CLINICAL ISSUES AND MOLECULAR CHARACTERISATION OF
SALMONELLA TYPHI ISOLATES FROM SOUTH EAST ASIA

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degree of Doctor of Philosophy
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Statement

I, Christiane Dolecek, declare that with the exception of the invaluable help and assistance outlined in the acknowledgements, the work described in this thesis is my own work and has not been submitted for a degree or other qualification to this or another university. Where information has been derived from other sources, I confirm that this has been indicated in the thesis.
Abstract

Due to the spread of antimicrobial drug resistance, typhoid fever has become increasingly difficult to treat. In Vietnam, more than 50% of S. Typhi isolates are multidrug resistant and 90% are quinolone resistant.

This thesis examines three aspects of typhoid fever; treatment, genotyping of bacteria and the clinical development of an oral vaccine.

We enrolled 358 children and adults with suspected typhoid fever into a randomised controlled trial to compare the efficacy and safety of gatifloxacin (10 mg/kg/day) versus azithromycin (20 mg/kg/day) for 7 days. In the blood culture confirmed group, 145 patients received gatifloxacin and 142 patients received azithromycin. Overall treatment failure occurred in 13/145 (9%) patients in the gatifloxacin group and 13/140 (9.3%) patients in the azithromycin group (HR = 0.93; 95% CI 0.43 – 2.0; p = 0.854).

We found a statistically significant relationship between drug exposure to gatifloxacin and clinical response. In patients with AUC$_{0-24}$: MIC ratios of greater than 92.7, 93.5% of patients had a favourable response; whilst in patients with AUC$_{0-24}$: MIC ratios equal or less than 92.7, only 75% had a favorable response (OR = 4.81; 95% CI 1.23-18.9; p = 0.02).

We investigated the genetic variability and relationship between the S. Typhi trial isolates by using a novel SNP genotyping array. The majority of isolates (98%)
belonged to the H58 haplotype, a quinolone resistant haplotype that has expanded globally. Within this group three main subgroups could be distinguished.

We conducted a randomised placebo controlled trial to determine the safety and immunogenicity of a novel oral typhoid vaccine (M01ZH09) with two independently-attenuating deletions (Ty2 aroC- ssaV-) in healthy 5 to 14 year old children in Vietnam. One hundred and fifty-one children were enrolled and followed up for 28 days. Twenty-six percent of M01ZH09 subjects and 22% of placebo subjects experienced an adverse event. There were no serious adverse events and no bacteraemia.

Ninety-seven percent of the subjects showed a positive immune response. M01ZH09 was immunogenic and had an appropriate safety and reactogenicity profile in children in an area with endemic typhoid fever.
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This PhD thesis describes two randomised controlled trials (Chapter 2 and Chapter 5), which inherently require to be conducted by big teams. I am deeply indebted to the doctors who supervised the day to day running of the clinical trial, Dr Tran Thi Phi La, head of the Infectious Ward at An Giang Provincial Hospital and Dr Doan Cong Du, Dr Duong Thanh Long and Dr Nguyen Ngoc Rang; to Dr Le Thi Phuong who recruited patients at Dong Thap Provincial Hospital and to Dr Ha Vinh, head of Ward E at the Hospital for Tropical Diseases. I am grateful to all these doctors for enrolling patients, taking samples and caring for the patients in this trial. The microbiology work included in this thesis was done by Nguyen Van Minh Hoang, Cao Thu Thuy, Pham Van Minh and Tran Thi Thu Nga at the Hospital for Tropical Diseases, Ho Chi Minh City. My special thanks goes to Jim Campbell for supervising the microbiology work, for his patience and for giving me a refresher course in basic microbiology. I am grateful to Dr Nguyen Van Vinh Chau and Dr To Song Diep, both at different times heads of the microbiology department at the
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This thesis is dedicated to four very special people, Sam, Georgina Anna, Charlie and Jeremy. I look forward to spending more time with you!
### Abbreviations

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Definition</th>
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<tbody>
<tr>
<td>FCT</td>
<td>Fever Clearance Time</td>
</tr>
<tr>
<td>OR</td>
<td>Odds Ratio</td>
</tr>
<tr>
<td>HR</td>
<td>Hazard Ratio</td>
</tr>
<tr>
<td>95% CI</td>
<td>95% confidence interval</td>
</tr>
<tr>
<td>MDR</td>
<td>multidrug resistant</td>
</tr>
<tr>
<td>ITT</td>
<td>intention to treat analysis</td>
</tr>
<tr>
<td>PP</td>
<td>per protocol analysis</td>
</tr>
<tr>
<td>CLSI</td>
<td>Clinical and Laboratory Standards Institute</td>
</tr>
<tr>
<td>CRF</td>
<td>Case Record Form</td>
</tr>
<tr>
<td>LPS</td>
<td>Lipopolysaccharide</td>
</tr>
<tr>
<td>IgA</td>
<td>Immunoglobulin A</td>
</tr>
<tr>
<td>IgG</td>
<td>Immunoglobulin G</td>
</tr>
<tr>
<td>ACS</td>
<td>antibody secreting cells</td>
</tr>
<tr>
<td>ELISA</td>
<td>Enzyme Linked Immunosorbent Assay</td>
</tr>
<tr>
<td>ELISPOT</td>
<td>Enzyme Linked Immunospot Assay</td>
</tr>
<tr>
<td>PBMC</td>
<td>peripheral blood mononuclear cells</td>
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Chapter 1

Introduction
1.1 Typhoid and paratyphoid fever

Typhoid and paratyphoid fever are septicaemias caused by the Gram negative bacteria *Salmonella enterica* serovar Typhi (S. Typhi) and *Salmonella enterica* serovar Paratyphi (S. Paratyphi) A, B and C. Typhoid and paratyphoid fever are summarized as enteric fevers. Whilst S. Typhi and S. Paratyphi A and B infections are restricted to humans, S. Paratyphi C can affect a variety of mammals.

1.2 Epidemiology

Typhoid fever is endemic in Africa, Asia, Central and South America and is also found in parts of the Middle East, southern and eastern Europe (Parry et al., 2002). Improvement of infrastructure and sanitation has virtually eliminated typhoid fever in developed countries and infections seen in Europe, Australia, and North America are usually acquired abroad (mostly from the Indian subcontinent, South East Asia and South America) (Steinberg et al., 2004). Current estimates from the World Health Organization (WHO) suggest that the global burden of typhoid fever is approximately 21 million cases annually with more than 210 000 deaths and that paratyphoid fever causes an additional 5 million cases (Crump et al., 2004). These numbers are based on extrapolating data from 22 studies that used blood culture, the gold standard for the diagnosis of typhoid fever (World Health Organization, 2003). Many institutions in endemic countries lack blood culture facilities, so the true extent of typhoid and paratyphoid fever is difficult to establish. It is likely that the proportion of disease caused by S. Paratyphi A particularly in Asia has been underestimated.
Recent data show that the proportion of diagnosed enteric fevers caused by *S. Paratyphi* A was 64% in China, 24% in India and 33% in Nepal (Maskey *et al.*, 2006; Ochiai *et al.*, 2005).

Transmission of typhoid fever occurs via the faeco-oral route by ingesting contaminated water or food or through direct contact (person to person transmission through poor hygiene). Risk factors for acquiring typhoid fever are eating food prepared outside the home, drinking contaminated water, eating shellfish from polluted water, vegetables that have been fertilised with human waste, the non-use of
soap and having a relative with a recent history of typhoid fever living in the same house (Luxemburger et al., 2001; Parry, 2004b). Chronic typhoid carriers involved in food handling are an important reservoir of infection.

The incidence of typhoid fever varies considerably. In population based surveillance studies from Asia conducted between 2002 and 2004, the annual typhoid incidence (per 100 000 persons per year) among the 5 to 15 year olds was low (24 and 29, respectively) at sites in Vietnam and China and high at sites in Indonesia, Pakistan and India (180, 413 and 493, respectively) (Ochiai et al., 2008). In endemic areas typhoid fever has been traditionally considered to be a disease of school children and young adults. However, recent data from community based studies emphasize that enteric fever is a common cause of morbidity in children between 1 and 5 years and that pre-school children experience similar or greater infection rates than school children (Lin et al., 2000; Ochiai et al., 2008; Sinha et al., 1999).

1.3 The bacterium and identification

The genus Salmonella belongs to the family of Enterobacteriaceae and is currently divided into two species, bongori and enterica (Brenner et al., 2000). The species Salmonella enterica is divided into six subspecies (I, enterica; II, salamae; III, arizonae; IV, diarizonae; V, houtenae and VI, indica) and contains more than 2400 serotypes based on the Kaufmann-White scheme (Grimont and Weill, 2007). Most of the Salmonella that cause disease in humans (including S. Typhi, S. Paratyphi and S. Typhimurium) are in the sub-species I (enterica). In contrast to other S. serovars, i.e. S. enteritidis and typhimurium, which show a wide host range, S. Typhi and S.
Paratyphi (with the exception of S. Paratyphi C) are highly adapted to humans and have no other known natural hosts.

S. Typhi and S. Paratyphi are flagellated, non-spore bearing, facultative anaerobic Gram negative bacilli. They are non-lactose fermenters and are identified by a characteristic biochemical pattern on triple sugar iron (TSI) agar slants (acid butt without gas, an alkaline slant and a moderate amount of \( \text{H}_2\text{S} \) production) (World Health Organization, Communicable Disease Surveillance & Response, 2003). The identification is confirmed by serological identification of their somatic lipopolysaccharide (O) and flagellar protein (H) antigens. S. Typhi and S. Paratyphi C sometimes possess a polysaccharide capsular Vi (virulence) antigen that coats the O antigen and potentially masks it from antibodies.

S. Typhi is O9, 12 (group D), Vi and Hd positive and S. Paratyphi A is identified as O1,2,12; Ha [1,5] positive. Unique flagella types, Hj and Hz66 are present in S. Typhi from Indonesia (Baker et al., 2007; Frankel et al., 1989).

1.4 The genome of S. Typhi CT18

The sequenced S. Typhi isolate CT18 (Parkhill et al., 2001a) is multidrug resistant (resistant to all first line antibiotics) and was isolated in 1993 from a child with typhoid fever in the Mekong Delta region of Vietnam. The genome of S. Typhi CT18 is 4.8 million base pairs in length and encodes approximately 4600 genes (Parkhill et al., 2001a). S. Typhi CT18 strain has several large insertions, believed to originate from bacteriophages or plasmids, termed the *Salmonella* pathogenicity islands that
encode genes that are important for survival in the host. *Salmonella enterica* has two type III secretion systems (TTSS), which are important virulence factors of Gram negative bacteria used to translocate proteins into the cytoplasm of eukaryotic host cells and are encoded by *Salmonella* pathogenicity islands SPI-1 and SPI-2. The invasion of epithelial cells is mediated by the SPI-1 TTSS, which is active on contact and injects virulence proteins into the host cell, leading to macropinocytosis of the bacteria and cytoskeletal rearrangement of the host cell to allow translocation. SPI-2 encoded TTSS is expressed after phagocytosis of bacteria by host cells and secretes effectors required for survival and replication in *Salmonella*-containing vesicles (SCV) inside phagocytes and epithelial cells (House *et al.*, 2001; Miao and Miller, 2000).

Another important feature of *S. Typhi* is the presence of more than 200 pseudogenes. The majority of these pseudogenes (124 out of 204) have arisen from introduction of a single frameshift or stop codon, some genes (45) have been inactivated by frameshifts that are due to changes in the length of homopolymeric tracts and some (27) genes are the remnants of insertion sequence (IS) transposases, integrases and genes of bacteriophage origin (Parkhill *et al.*, 2001a). The inactivation of these genes may explain the human host restriction of *S. Typhi*. CT18 harbours two plasmids, one large 220 kbp conjugative multiple drug resistance incH1 plasmid (pHCM1) which shows a high degree (more than 99%) of sequence identity with R27, an incH1 plasmid first isolated in the 1960s from *S. enterica* (Sherburne *et al.*, 2000) and a smaller 110 kbp
cryptic plasmid (pHCM2), which shows recent common ancestry with a virulence plasmid of *Yersinia pestis* (Kidgell *et al.*, 2002a; Prentice *et al.*, 2001).
1.5 Pathogenesis and pathology

The best studied model of typhoid fever is the “typhoid-like” illness of mice infected by *S. Typhimurium*, but not all findings from this infection model can be extrapolated to humans (House *et al.*, 2001).

Volunteer studies have shown that the infective dose of *S. Typhi* is between $10^3$ to $10^9$ bacteria (Hornick *et al.*, 1970). Gastric acidity destroys the organisms but gastric hypoacidity (following gastrectomy, intake of histamine-2 receptor antagonists or proton pump inhibitors) allows a greater number of organisms to enter the small intestine. In a study from India, *Helicobacter pylori* infection has been associated with an increased risk of typhoid fever (Bhan *et al.*, 2002).

After the ingestion in water or food, *S. Typhi* bacteria reach the small intestine where they adhere to the mucosal epithelial cells. They penetrate the mucosal epithelium either via the M (membranous) cells, specialised cells overlying the Peyer’s patches, enterocytes or via a paracellular route. *S. Typhi* bacteria arrive in the lamina propria where they elicit a local influx of macrophages. They are taken up by macrophages and multiply in the mononuclear phagocytic cells of the small intestine, are drained into mesenteric lymph nodes and it is believed that they reach the general circulation (causing an asymptomatic primary bacteraemia) by lymph drainage from the thoracic duct. The incubation period, which depends on the inoculum size and host defence factors, varies between 7 and 14 days. During this phase the bacteria reside and multiply within the organs of the reticuloendothelial system (spleen, liver, bone marrow and lymph nodes and especially the Peyer’s patches of the terminal ileum).
Bacteria are then shed again into the blood stream, marking the onset of fever and symptomatic disease. During the symptomatic stage *S. Typhi* can be cultured from blood, although this may be difficult in low level bacteraemia. In a study that performed quantitative blood cultures in a large number (*n* = 369) of patients with typhoid fever, the median *S. Typhi* count in blood was 1 colony forming unit per ml (range, <0.3 to 387 CFU/ml), of which a mean of 63% (95% CI, 58 to 67%) were intracellular (Wain *et al*., 1998). If left untreated, the *S. Typhi* bacteraemia persists for several weeks. In this phase the organism disseminates widely to the organs of the reticuloendothelial system (House *et al*., 2001; Parry *et al*., 2002; Wain *et al*., 2002).

*S. Typhi* infection produces hyperplasia of the Peyer’s patches in the first week, which can resolve or progress to necrosis. Ulcers can lead to perforation and haemorrhage, usually in the third week, although these may occur earlier or later during the disease (Owen, 1994; Parry *et al*., 2002). It has been hypothesized that the significant inflammation in the ileum causing necrosis and ulceration might be due to the re-exposure of Peyer’s patches to *S. Typhi* via the gallbladder, a mechanism similar to the Shwartzman and Koch reactions (Everest *et al*., 2001). The majority of patients mount local and systemic humoral and cellular immune responses but these do not give complete protection against relapse or re-infection. The mortality of typhoid fever in the pre-antibiotic era used to be about 10 to 20% (Herzog, 1976).
1.6 Clinical presentation

Typhoid fever typically presents with fever, headache, anorexia and abdominal discomfort with either diarrhoea or constipation. This can be accompanied by nausea, vomiting and a dry cough. Diarrhoea is more common in children, whereas constipation is more often found in adults. Profuse diarrhoea has been described in typhoid patients with HIV infection (Parry et al., 2002). On examination, abdominal tenderness, hepatomegaly (in 40 to 70% of patients) and splenomegaly are common. It is rare for patients with typhoid fever to not have any abdominal symptoms and normal bowel movement, however even then typhoid fever cannot be excluded. A small percentage of patients (less than 5%) show rose spots, small blanching erythematous maculopapular lesions of about 2 to 4 mm diameter on the trunk. Haemoglobin levels, white cell counts and platelet counts are normal or reduced. Liver enzymes (AST, ALT) are usually elevated two to three times the upper limit of normal and bilirubin is normal or slightly raised. Abdominal sonography may demonstrate enlargement of liver and spleen and prominent mesenteric lymph nodes.

It has been frequently cited that S. Paratyphi causes a milder disease, however recent prospective clinical trials have reported that enteric fever caused by S. Typhi and S. Paratyphi A are clinically indistinguishable (Maskey et al., 2006; Vollaard et al., 2005). S. Paratyphi A has also been described as the cause of severe enteric fever in Indonesia (Hoffman et al., 1984).
1.6.1 Complications and severe typhoid fever

Complications of typhoid fever are more likely to occur in patients who have been sick for longer periods without receiving treatment and in patients infected with non susceptible *S*. Typhi who do not receive appropriate treatment. Complications may develop in up to 10% of hospitalised patients (World Health Organization, 2003). The development of septic shock and acute respiratory distress syndrome are serious complications when treatment is delayed.

Gastrointestinal bleeding (occurs in approximately 10% of patients), intestinal perforation and typhoid encephalopathy are the most common complications. Gastrointestinal bleeding results from a necrotic Peyer’s patch eroding the wall of an enteric blood vessel. Often the bleeding is slight and resolves without intervention, however in approximately 2% of cases the bleeding is significant and requires blood transfusion. Gastrointestinal perforation (usually at the terminal ileum) is the most serious complication, and occurs in up to 3% of hospitalised cases (Parry *et al*., 2002). It manifests as acute abdomen or as worsening of abdominal pain accompanied by shock. Perforation is associated with a high mortality (van Basten and Stockenbrugger, 1994) and needs urgent surgical intervention.

A reduced level of consciousness or encephalopathy, often accompanied by shock, is a serious complication associated with a mortality of up to 50% (Hoffman *et al*., 1984). Typhoid encephalopathy is a complex neuropsychiatric syndrome with a wide range of symptoms and signs ranging from agitation to delirium and coma. These
symptoms might be worsened by associated liver failure, haematogenic dissemination to the brain or other as yet unknown mechanisms. The incidence of this presentation varies between different countries; ranging from 10 to 40% of hospitalised cases in Indonesia, and Papua New Guinea but less than 2% in Pakistan and Vietnam.

Figure 1.2 Gastrointestinal perforation, usually of the terminal ileum, is one of the most serious complications of typhoid fever.

The picture shows the intraoperative picture of a patient with perforated necrotic ulcer. Photo credit: Pukar Maskey, Patan Hospital, Kathmandu.
This variation is unexplained (Parry et al., 2002). Seizures have been described as frequent complication (up to 10%) in hospitalised children under the age of 10 in Bangladesh (Butler et al., 1991). In patients with encephalopathy, cerebrospinal fluid should be obtained to exclude tuberculous meningitis, other bacterial meningitis and encephalitis. The prognosis of typhoid fever during pregnancy has improved with the use of antibiotics (Seoud et al., 1988), although the optimal treatment for pregnant women remains unclear. Typhoid fever acquired through intrauterine infection can lead to neonatal typhoid fever, a severe sepsis with a mortality of up to 10% or to asymptomatic persistent secretion (Reed and Klugman, 1994).

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**Table 1-1. Important complications of typhoid fever.**

Modified from (Parry et al., 2002)
1.6.2 Relapse

The re-occurrence of symptoms within one month after the treatment has been completed and symptoms have been resolved is considered a relapse. Depending on the efficacy of the antibacterial treatment to clear the bacteria, relapse rates vary from 0% to 10% in patients (Parry et al., 2002; Parry et al., 2007).

1.6.3 Chronic Carriage

One to five percent of patients with a history of enteric fever become chronic carriers, which means they harbour S. Typhi or S. Paratyphi A or B in their gall bladder and are shedding bacteria intermittently in their stools for at least one year after the illness (World Health Organization, 2003; Ristori et al., 1982). These carriers are an important reservoir of infection and are usually asymptomatic. Up to 25% of chronic carriers do not have a history of typhoid fever. The rate of carriers is higher among females and patients with cholelithiasis. An association between urinary carriage of S. Typhi and S. Paratyphi A and schistosomiasis has been described, caused by obstructive lesions of the urinary tract (Hathout et al., 1966).

1.6.4 Case Fatality

A WHO report has estimated the case fatality rate in typhoid fever at 1% (Crump et al., 2004). There seems to be considerable geographic variation. In Vietnam and Pakistan the case fatality rate among hospitalised patients is less than 2%, but in patients with severe typhoid fever in Papua New Guinea and Indonesia it can vary
between 30 and 50% (Parry et al., 2002). The most important contributor to a poor outcome is probably a delay in appropriate antibiotic treatment.

1.6.5 Differential diagnosis

Typhoid fever presents with nonspecific symptoms and this makes the diagnosis difficult. Other endemic illnesses, most importantly malaria have to be ruled out. Typhoid can occasionally present as gastroenteritis with vomiting and diarrhoea. The differential diagnosis is broad and varies geographically but includes leptospirosis, rickettsial disease (scrub and murine typhus (rickettsial disease), tuberculosis, brucellosis, other bacterial sepsis, encephalitis, amoebic liver abscesses, visceral leishmaniasis, viral diseases (dengue fever, infectious mononucleosis, hepatitis, influenza), lymphoproliferative disease and autoimmune diseases including systemic lupus erythematosus (SLE).

1.7 Diagnosis

1.7.1 Blood culture and bone marrow culture

The definitive diagnosis of enteric fever requires the isolation of S. Typhi or S. Paratyphi from blood, bone marrow or an anatomic lesion. Blood culture is the gold standard in the diagnosis of enteric fever. However, the low level of bacteraemia (between 1 and 10 bacteria per ml of blood) is a characteristic feature of typhoid fever and the sensitivity of blood culture is estimated to be only 50 to 60%. Therefore obtaining a large volume of blood is one of the most important factors in the successful isolation of S. Typhi. Ideally 10 to 15 ml of blood should be taken from
school children and adults and 2 to 4 ml for toddlers and pre-school children (World Health Organization, 2003; Wain et al., 1998). Bone marrow culture is more sensitive (up to 80%), because of the higher concentration of bacteria found in the bone marrow (Wain et al., 2001).

Antimicrobial susceptibility testing should be performed against a fluoroquinolone, nalidixic acid (the prototype quinolone; strains that are nalidixic acid resistant show reduced susceptibility to fluoroquinolones, even when still within the current breakpoints for fluoroquinolone susceptibility), a third generation cephalosporin, other drugs currently used for treatment and the previous first line antibiotics to which the strains could be resistant (chloramphenicol, ampicillin, trimethoprim–sulfamethoxazole, streptomycin and tetracycline) (World Health Organization, 2003).

### 1.7.2 Serology

The Widal test was first described more than 100 years ago. It is a tube dilution test based on the presence of agglutinating antibodies to the O and H antigens of *Salmonella*. It is usually performed in settings where culture facilities are not available. In the original format, paired sera (acute and convalescent) were required and a four fold increase in the antibody titre (to O and H antigens) provided support for the diagnosis of typhoid fever. However, the test is usually performed on acute serum only as a screening assessment and there is no consensus regarding the
interpretation of the test, standardisation of the reagents and it lacks sensitivity and specificity.

One of the main problems with the interpretation of the Widal test is the wide variation in the antibody responses of individuals and populations. This is because not everybody mounts a detectable antibody response to *S. Typhi*, healthy populations in endemic areas and patients who received typhoid vaccine show high levels of antibodies and there is cross-reactivity to other *Salmonella* serotypes. For the accurate interpretation of results it is necessary to know the antibody levels of the "background" population in the area where the test is being applied.

Rapid tests have been developed for the serological diagnosis of typhoid fever. The typhidot test (Malaysian Biodiagnostics Research Ltd, Malaysia) is an immunodot ELISA based on the detection of IgG and IgM antibodies specific for the 50 kD outer membrane protein of *S. Typhi*. The Tubex test (IDL Biotech, Sweden) is a semiquantitative colorimetric test which detects anti-Salmonella O9 antibodies from a patient's serum by the ability of these antibodies to inhibit the binding between an indicator antibody-bound particle and a magnetic antigen-bound particle. A recent prospective community based study in Kolkata examined more than 6000 blood samples from patients with fever for more than 3 days and compared the performance of the Widal test, Typhidot and Tubex test to the gold standard blood culture (Dutta *et al.*, 2006). An anti-TO titer of 1/80 in the Widal test had a sensitivity, specificity, positive predictive value and negative predictive value of 58%, 85%, 69%, and 77%, respectively for the diagnosis of typhoid fever. The overall performance of sensitivity,
specificity, positive predictive value and negative predictive value of Typhidot and Tubex was found to be 47%, 83%, 85%, and 42% and 56%, 88%, 81%, and 69%, respectively.

1.7.3 Molecular diagnosis

PCR based assays have been developed to diagnose S. Typhi infection in blood samples. Most of these assays target the flagellin gene (\(fliC\)) of S. Typhi. Whilst PCR assays which use Salmonella isolates show robust results and high sensitivity and specificity (Levy et al., 2008), the results of PCR assays based on patient’s blood samples are more variable. In a study by Massi et al. real-time PCR based on the amplification of \(fliC\) was applied to detect S. Typhi in blood samples from patients with clinically diagnosed typhoid (Massi et al., 2005). The TaqMan assay detected more than \(10^3\) (range \(1.01 \times 10^3 - 4.35 \times 10^4\)) copies/ml blood of S. Typhi in the blood culture positive samples and less than \(10^3\) copies/ml blood in the blood culture negative samples. Given the low bacterial loads in blood that are characteristic of typhoid fever (Wain et al., 1998), these high copy numbers are surprising. A recent study found that a real-time PCR assay had less than 50% sensitivity when tested on DNA extracted from 2 ml of blood taken from patients with blood culture confirmed typhoid fever (Nga et al., 2010).
1.8 Antimicrobials for the treatment of typhoid and paratyphoid fever

1.8.1 First-line antimicrobial agents for the treatment of enteric fever

1.8.1.1 Chloramphenicol

Chloramphenicol is a broad spectrum antibiotic that was developed in 1947 from the soil bacterium *Streptomyces venezuelae* (Ehrlich *et al.*, 1947). Chloramphenicol is active against many Gram positive and Gram negative organisms (aerobes and anaerobes), rickettsiae, chlamydiae and mycoplasma. It demonstrates mostly bacteriostatic activity and binds to the bacterial 50S ribosomal subunit where it prevents the binding of aminoacyl-tRNA and terminates polypeptide chain synthesis. It was the first antibiotic to be manufactured synthetically on a large scale. It dramatically changed the management of typhoid fever (Woodward *et al.*, 1948).

Chloramphenicol treatment has reduced the typhoid fever mortality from 20% to less than 1%, and the duration of fever from 2 to 4 weeks to four to five days (White, 2002; Woodward *et al.*, 1948; Woodward *et al.*, 1954) and has been the first line drug for the treatment of typhoid fever. However, disadvantages of chloramphenicol are that it does not influence the relapse rate nor the typhoid carrier rate (Herzog, 1976) and the need for prolonged treatment durations of 14 to 21 days (Woodward and Smadel, 1964).

Chloramphenicol is available in three forms, as base, palmitate ester and sodium succinate ester (Neuhauser and Pendland, 2005). Chloramphenicol base is well absorbed and produces serum peak levels within 1 to 2 hours. The palmitate ester is
more soluble and palatable and used as the paediatric formulation, whereas the succinate ester is used for parenteral administration. The esters must be hydrolysed to yield the microbiologically active chloramphenicol base and therefore serum levels achieved with oral base are higher than with the palmitate ester and succinate ester. Chloramphenicol has good penetration into most tissues and body fluids with the exception of bile. It readily crosses the blood-brain barrier and is still used for the treatment of bacterial meningitis in many parts of the world.

The most important adverse effect of chloramphenicol is a dose related, reversible bone marrow depression that results from inhibition of mitochondrial protein synthesis (Yunis, 1989). This is relatively common and results in reversible (when the drug is stopped) reticulocytopenia, anaemia, leukopaenia, or thrombocytopaenia. In contrast, the chloramphenicol associated "idiosyncratic" aplastic anemia is very rare but is not dose related, non reversible and invariably fatal. Aplastic anemia is estimated to occur in 1 in 24500 to 40800 patients who receive the antibiotic, a risk that is about 13 times greater than in the general population (Wallerstein et al., 1969).

Resistance to chloramphenicol was first reported in the 1970s and has been widely spread (Herzog, 1976). The most common mechanism of resistance is the inactivation of the drug by the enzyme chloramphenicol acetyl transferase. The catI gene is usually carried on large incH11 plasmids (Parkhill et al., 2001a). Despite these limitations chloramphenicol remains an effective first line treatment for typhoid fever in many regions of the world where the bacteria remain sensitive (World Health Organization, 2003; Parry et al., 2002; Thaver et al., 2009)
1.8.1.2 Ampicillin and amoxicillin

The aminopenicillins ampicillin and amoxicillin have been evaluated for the treatment of typhoid fever in several clinical trials and have given similar or slightly inferior results to those obtained with chloramphenicol (Herzog, 1976; White, 2002). Fever clearance times are 1 to 3 days longer than with chloramphenicol and failure rates slightly higher (Herzog, 1976). Relapse and faecal carriage rates are similar to those achieved with chloramphenicol. Ampicillin and amoxicillin have been the treatment of choice in pregnancy and neonates. Resistance is widespread and generally due to the production of the bacterial enzyme β-lactamase that opens the β-lactam ring and causes inactivation of the antibiotic. The gene responsible for resistance in S. Typhi has been TEM-1 and is plasmid encoded (White, 2002).

1.8.1.3 Trimethoprim-Sulfamethoxazole (cotrimoxazole)

Trimethoprim-sulfamethoxazole has been widely used for the treatment of typhoid fever and has been show to be an effective alternative to chloramphenicol (Herzog, 1976). Resistance in S. Typhi is mediated by the acquisition of a plasmid encoded sulfonamide resistant dihydropteroate synthase and trimethoprim resistant dihydrofolate reductase (Goldstein and Stein, 2005).

1.8.2 Fluoroquinolones

Nalidixic acid, the prototype 4-quinolone antibiotic was discovered in 1962 (Lesher et al., 1962), it is active against Gram negative bacteria and only achieves modest serum and tissue concentrations.
Almost 20 years later, the addition of a fluorine molecule at position C6 created the fluoroquinolones. The 6-fluoro substituent confers a greater spectrum of activity against Gram negative and Gram positive pathogens, possibly by improving tissue penetration and binding to the DNA gyrase enzyme.

All quinolone derivatives have a dual ring structure with nitrogen at position 1, a carbonyl group at position 4 and a carboxyl group attached to the carbon at position 3 of the first ring (Hooper, 1995). Several structural modifications have led to compounds with enhanced antibacterial activity. Addition of a piperazinyl group (norfloxacin, enoxacin), methyl-piperazinyl group (pefloxacin, ofloxacin, amifloxacin, lomefloxacin, fleroxacin, temafloxacin), or dimethyl-piperazinyl group (sparfloxacin) at position 7 enhances activity against aerobic Gram negative bacteria.
Ciprofloxacin (a second generation fluoroquinolone) which was discovered in 1981 possesses a cyclopropyl group on position 1 of the quinolone ring which confers excellent activity against Gram negative organisms (Enterobacteriaceae, Haemophilus influenza, Neisseria meningitides and Moraxella catarrhalis) and Pseudomonas aeruginosa (Davis et al., 2005).

Ofloxacin (a second generation fluoroquinolone) received FDA approval in 1990 and possesses an additional ring structure bridging positions 1 and 8. Due to its availability and affordability, ofloxacin has been widely used for the treatment of typhoid fever in Vietnam.

Figure 1.4 Structure activity relationship of the fluoroquinolones.

From (Domagala, 1994)
Gatifloxacin is a broad spectrum 8-methoxy fluoroquinolone with enhanced activity against Gram positive organisms, which has received U.S. Food and Drug Administration (FDA) approval in 1999. It features a cyclopropyl group at position 1 similar to ciprofloxacin. The addition of a methoxy group at position 8 targets both topoisomerase II and IV and probably prevents (or delays) the development of quinolone resistance.
**1.8.2.1 Mode of action**

Fluoroquinolones are considered bactericidal agents and have excellent *in vitro* activity against a wide range of Gram negative and Gram positive organisms. The quinolones rapidly inhibit bacterial DNA synthesis, causing rapid cell death. The targets for the fluoroquinolones are the bacterial topoisomerase enzymes, DNA gyrase (topoisomerase II) and Topoisomerase IV. DNA gyrase supercohls strands of bacterial DNA into the bacterial cell and transiently nicks each chromosomal domain during supercoiling. When supercoiling is complete, DNA gyrase seals the nicked DNA. Topoisomerase IV separates the two linked daughter DNA molecules when replication is complete. These two enzymes are essential in DNA replication and cell partitioning of DNA molecules (Andriole, 2004). DNA gyrase is a tetramer composed of a Gyrase A dimer and Gyrase B dimer which are encoded by *gyrA* and *gyrB* genes, respectively. Topoisomerase IV is a tetramer composed of a ParC and ParE dimer, which are encoded by *parC* and *parE* genes, respectively. For many fluoroquinolones, DNA gyrase is the primary target in Gram negative bacteria and topoisomerase IV may be a secondary target (Piddock, 2002). In Gram positive bacteria, topoisomerase IV is the primary target. Recent microarray data identified an oxidative damage-mediated cell death pathway, which involves reactive oxygen species (ROS) generation and a breakdown in iron regulatory dynamics following norfloxacin-induced DNA damage (Kohanski *et al*., 2010).
1.8.2.2 Mechanism of resistance

The main mechanism of quinolone resistance in *S. Typhi* is the accumulation of amino acid substitutions in the bacterial target enzyme DNA gyrase. The most commonly identified alteration has been a serine to phenylalanine substitution at position 83 of GyrA (Chau *et al.*, 2007; Wain *et al.*, 1997). Amino acid changes at position 87 (aspartate to tyrosine, glycine or asparagine) of GyrA are less frequent. These mutations are focused around a region called the quinolone resistance determining region (QRDR). The QRDR of GyrA is close to tyrosine at position 122, the active site of the enzyme, which is covalently linked to DNA during strand breakage (Drlica, 1999). Single point mutations in *gyrA* of *S. Typhi* lead to nalidixic acid resistance (MIC ≥ 32 µg/ml) and reduced susceptibility to the fluoroquinolones (typically ciprofloxacin MICs ranging from 0.125 µg/ml to 1.0 µg/ml, compared to the wild type MIC of 0.03 µg/ml or below). Single isolates of fully fluoroquinolone resistant *S. Typhi* and *S. Paratyphi A* have been reported from India (Parry and Threlfall, 2008). The high-level fluoroquinolone resistance seen in these *S. Typhi* (ciprofloxacin MIC ≥ 4 mg/ml) isolates was conferred by dual mutations in *gyrA* and a single mutation in *parC* (Dutta *et al.*, 2008; Gaind *et al.*, 2006).

Alteration in drug transport has been described as an additional mechanism of fluoroquinolone resistance in *E. coli* (Mazzariol *et al.*, 2000) and recently in *Pseudomonas aeruginosa, Staphylococcus aureus, Streptococcus pneumonia, Klebsiella pneumonia* and *S. Typhimurium* (Baucheron *et al.*, 2002; Baucheron *et al.*, 2004; Mazzariol *et al.*, 2002). The expression of the AcrAB-TolC system, the major
multidrug efflux pump, is under the regulation of ramA, marA, soxS or rob. Constitutive over expression of AcrAB is present in most ciprofloxacin resistant E.coli and also occurs in ciprofloxacin resistant S. Typhimurium phage type DT204 (Baucheron et al., 2002). The MarA global activator, which can be derepressed by tetracycline or chloramphenicol, simultaneously up-regulates the AcrAB-TolC transport complex and down-regulates the synthesis of the larger porin OmpF, a mechanism that synergistically blocks the drug penetration and accumulation in the cell (Parry, 2003).

Plasmid mediated quinolone resistance was first described in 1998 in an isolate of Klebsiella pneumonia (Martinez-Martinez et al., 1998). Since then five major groups of quinolone resistance determinants, qnrA, qnrS, qnrB, qnrC and qnrD, have been identified (Strahilevitz et al., 2009). The qnr genes encode for a pentapeptide repeat protein that confers reduced susceptibility to the fluoroquinolones (typically with an 8 to 64 fold increased quinolone MIC). Qnr proteins are able to protect DNA gyrase from the quinolones. Aquatic bacteria are thought to be the origin of plasmid encoded quinolone resistance genes. qnr genes have been found on plasmids of varying size and incompatibility groups.

Recently additional plasmid mediated quinolone resistance genes have been described. aac(6')-lb-cr encodes a variant aminoglycoside acetyltransferase, which confers resistance to tobramycin, amikacin and kanamycin (Robicsek et al., 2006b). This enzyme reduces the activity of ciprofloxacin by N-acetylation at the amino nitrogen on its piperazinyl substituent. AAC(6')-lb-cr is selective only for
ciprofloxacin and norfloxacin, which both have an unsubstituted piperazinyl nitroge
AAC(6')-lb-cr confers only a modest increase in MIC (3 to 4 fold), but has shown to cause a dramatic increase in the mutant prevention concentration (Robicsek et al., 2006a). The aac(6')-lb-cr gene is located in an integron cassette with an associated attC site. It is often found on incF11 plasmids expressing CTX-M-15 that have spread rapidly and become the predominant ESBL in many countries worldwide (Strahilevitz et al., 2009).

So far, qnr genes and aac(6')-lb-cr have only been reported in non-Typhi Salmonella (Strahilevitz et al., 2009), with the exception of a multiple drug resistant S. Typhi strain isolated from an Iraqi traveler that was characterized by the bla_{CTX-M15}, qnrB2 and the GyrA Ser83Phe amino acid substitution (Pfeifer et al., 2009).

1.8.2.3 Adverse events
The frequency of adverse reactions to quinolones is between 6 and 11% with less than 1% of adverse events being recorded as serious (Andriole, 2004). The most frequent adverse effects reported are nausea, upper gastrointestinal discomfort and central nervous system effects such as headache, insomnia and dizziness. The adverse events are typically mild, self limited and mostly resolve when the drug is stopped.

Some adverse effects do not seem to be related to specific modifications, whereas phototoxicity and CNS effects are linked to a specific structure. Each fluoroquinolone tends to produce a characteristic profile of adverse effects.
In their preclinical evaluation, all quinolones studied caused arthropathy in immature animals, especially in young beagle dogs and usually in the major weight bearing joints (Gough et al., 1979; Stahlnmann et al., 1990). Histopathological examination showed localized blister formation and erosions in the joint cartilage (Schaad and Wedgwood, 1992). The concern that the fluoroquinolones might also cause cartilage damage in children, have led to cautious use in many countries. However, extensive experience with the fluoroquinolones in children suffering from cystic fibrosis, typhoid fever and bacillary dysentery has provided a body of evidence suggesting that the joint damage seen in young dogs does not occur in children and these antibiotics are safe in children (Bethell et al., 1996; Organization, 2003; Parry et al., 2002; Schaad et al., 1991; Schaad and Wedgwood, 1992).

Fluoroquinolones have been associated with tendinitis and tendon rupture in adults, primarily affecting the Achilles tendon, risk factors were renal dysfunction and concomitant corticosteroid use (Owens and Ambrose, 2005).

Severe neurotoxic reactions are rare. However, hallucinations, depression, and psychotic reaction have been reported. Some fluoroquinolones may inhibit transmission of gamma-aminobutyric acid (GABA) leading to CNS stimulation. These CNS effects may be potentiated by interactions with other medications such as theophyllin (Andriole, 2004; Davis et al., 2005). Thus the quinolones should be used with caution in patients with known CNS disorders (e.g., epilepsy) or conditions predisposing to seizures (Andriole, 2004; Davis et al., 2005).
The most common skin reactions are non specific skin rashes, pruritis and urticaria. Phototoxicity is a rare dermatologic complication of quinolone therapy which is inextricably related to the chemical structure (Owens and Ambrose, 2005).

The “double halogenated” quinolones which possess a halogen moiety (chlorine, fluorine) at position 8 together with the fluorination of position 6 have demonstrated significant phototoxic potential. Agents with these modifications are fleroxacin, lomefloxacin and sparfloxacin. Thrombocytopenia, leucopenia and anaemia are rare (Andriole, 2004). Recently the cardiovascular effects of the quinolones, especially of the newer agents have been closely evaluated. Dose related prolongation of the QTc interval and rare cases of significant arrhythmias including torsades de pointes were reported in patients treated with sparfloxacin and to a lesser extent with grepafloxacin, these two antibiotics were therefore withdrawn.

A study based on post marketing surveillance data reported that the crude incidence rate (95% confidence interval, 95% CI) of cases of Torsades de Pointes (TdP) per 10 million prescriptions in the United States was 0.3 (0.0-1.1) for ciprofloxacin, 2.1 (0.3-7.6) for ofloxacin, 5.4 (2.9-9.3) for levofloxacin and 27 (12-53) for gatifloxacin (Frothingham, 2001). However questions regarding the validity of both the numerators and denominators used in these incidence calculations remain (Owens and Ambrose, 2002). Preclinical and clinical data indicate that levofloxacin, moxifloxacin, and gatifloxacin prolong the QTc interval. The potential for TdP to develop as a result of this is rare and is influenced by many independent variables, especially by concurrent administration of class IA and III antiarrhythmic agents, genetic
susceptibility, underlying cardiac disease, electrolyte imbalance and organ impairment. Therefore gatifloxacin, levofloxacin, moxifloxacin or gemifloxacin should not be used in patients with risk factors predisposing them to TdP (Owens and Ambrose, 2002).

The quinolones as a class have demonstrated the ability to close $K^+$-ATP channels in the $\beta$ cells of the pancreas, resulting in the release of insulin and subsequent hypoglycaemia. However the mechanism for hyperglycaemia remains poorly understood and might be caused by overexposure (failure to adjust the dose in patients with renal failure) (Owens and Ambrose, 2002). Product labels for ciprofloxacin, gatifloxacin, levofloxacin, and moxifloxacin mention the possibility of hypoglycaemia and hyperglycaemia, whereas the product label for gemifloxacin mentions hyperglycaemia only. Although glucose disturbances appear to be a class effect, the odds of hypo- and hyperglycaemia appear to vary among the agents (Aspinall et al., 2009). A retrospective study in Texas reviewed records of dysglycaemia in hospitalised patients receiving gatifloxacin, levofloxacin, ciprofloxacin or ceftriaxone (Mohr et al., 2005). Dysglycaemic events were more likely to occur in patients receiving gatifloxacin (relative risk, 3.29; 95% CI, 2.33–4.65) or levofloxacin (relative risk, 1.55; 95% CI, 1.29–1.88) versus ceftriaxone.

In another study of elderly inpatients who received gatifloxacin or levofloxacin, gatifloxacin was independently associated with hypoglycaemia (OR, 2.4; 95% CI, 1.1–5.6) and hyperglycaemia (OR, 2.5; 95% CI, 1.6–3.9) versus levofloxacin (Lodise et al., 2007). In diabetic patients treated with gatifloxacin, the overall incidence of
hypoglycaemia was 0.4%, 0.7%, and 1.6% for patients below 65 years, 65 to 69 years and 80 years and above, respectively. The corresponding incidences of hyperglycaemia were 1.0%, 1.6%, and 3.3%, respectively (Owens and Ambrose, 2005).

When exposure to gatifloxacin was simulated in patients with severe hyperglycaemia, AUC values were 2 to 3 times those observed in patients with normal renal function (Ambrose et al., 2003). Therefore the authors suggested to empirically adjust the dose of gatifloxacin to 200 mg daily for patients aged above 65 years with community acquired respiratory tract infections. A detailed discussion of the risk benefit ratio of gatifloxacin for the treatment of enteric fever is presented in Chapter 2.

Only ciprofloxacin, clinafloxacin, enoxacin, grepafloxacin, pefloxacin, and tosufloxacin can inhibit the hepatic cytochrome P450 isoform CYP 1A4 isoenzymes. Few drugs are metabolized by these isoenzymes, but important drugs include the methylxanthines (theophylline and caffeine) and warfarin.

1.8.3 Extended spectrum cephalosporins

![Figure 1.7 Basic structure of cephalosporins](image-url)
The basic structure of the cephalosporins consists of a four membered β-lactam ring fused with a six-membered dihydrothiazine ring. Cephalosporins exert bactericidal activity by interfering with the later stages of the bacterial cell wall synthesis (Capitano and Kays, 2005). The target site of the β-lactam antibiotics including the cephalosporins are the penicillin-binding proteins (PBPs). During the process of peptidoglycan synthesis, the cephalosporin β-lactam ring becomes covalently bound to the PBPs, acting as a false substrate. This process inhibits the cross linking of the peptidoglycan structure and ultimately leads to bacterial cell lysis.

Production of β-lactamases is the most common mechanism of bacterial resistance. In the late 90s, non-Typhi Salmonella producing extended spectrum β-lactamases (ESBL) have been reported in numerous countries. Resistance generally results from the production of Ambler class A or C (also known as AmpC β-lactamases) ESBL.

Class A enzymes such as TEM, SHV, OXA, PER and CTX-M are plasmid mediated and confer resistance against oxyimino-β-lactams such as cefotaxime, ceftazidime and aztreonam, but are not active against cephamycins and can be inactivated by clavulanic acid. Ambler class C enzymes are able to hydrolise all β-lactams to some extent and are not inhibited by clavulanic acid. Over-expression confers resistance to all β-lactam including the cephamycins, but not to cefpirome, cefpime and the carbapenems (Parry, 2003).

Salmonella producing the β-lactamase CMY-2 have been isolated from food producing animals in Northern America and Europe (Aarestrup et al., 2004; Allen and
Poppe, 2002) and from hospitalised patients in the USA and Taiwan (Parry, 2003). Recent studies in the US, Mexico and South Africa have shown a wider range of ESBL enzymes in non-Typhi \textit{Salmonella} (Parry and Threlfall, 2008). However, prevalence of extended spectrum cephalosporin resistance (ESC) was low in human non-Typhi \textit{Salmonella} isolates collected across 10 European countries in 2000 (Threlfall \textit{et al.}, 2003). Only 0.6\% of 27000 \textit{Salmonella} isolates showed resistance to cefotaxime.

Resistance to extended spectrum cephalosporins has been reported in single isolates of \textit{S. Typhi} from Bangladesh and Italy and Paratyphi A from Pakistan and Nepal, however the mechanism was not described in these reports (Parry, 2003; Pokharel \textit{et al.}, 2006). In 2009, a \textit{S. Typhi} isolate with ESBL phenotype caused by \textit{bla}_{\text{CTX-15}} was described in a patient returning from Iraq (Pfeifer \textit{et al.}, 2009).

The cephalosporins exhibit time dependent bactericidal activity, therefore the target for antimicrobial therapy is to optimise the duration of exposure (Time above the MIC, T > MIC). Cephalosporins penetrate well into most tissues and body fluids (Capitano and Kays, 2005). High concentrations of ceftriaxone have been demonstrated in human monocytes. Overall, the cephalosporins are a safe class of antibiotics, hypersensitivity reactions are the most common adverse events. Gastrointestinal reactions, including nausea, vomiting and diarrhoea are also reported frequently.
The third generation cephalosporins ceftriaxone and cefixime have been widely used for the treatment of MDR typhoid fever. The average fever clearance times in randomised trials using ceftriaxone have been 7 days and 5 to 10% of patients failed clinically. Relapse rates varied between 4% and 6% (Parry et al., 2002). A study in Pakistan evaluated either 7 or 14 days of ceftriaxone treatment in children with typhoid fever and found a relapse rate of 14% (4 out of 28 patients) in the 7 day treatment group compared to no relapse in the 14 day group (Bhutta et al., 2000). The disadvantage of ceftriaxone is the need for parenteral administration and the high cost, especially for prolonged treatment courses.

Oral cefixime has been a popular choice for the treatment of typhoid fever in children. In randomised controlled trials in children the mean fever clearance times ranged from 5 to 8 days and clinical failure rates were reported to be below 3% (Bhutta et al., 1994; Girgis et al., 1995; Memon et al., 1997). However, a typhoid treatment trial in Vietnam reported much higher failure rates of 23% (10 out of 44 patients) when cefixime was used in children (Cao et al., 1999).

1.8.4 Azithromycin

Azithromycin belongs to the macrolide class of antibiotics and is a derivative of erythromycin. Erythromycin was isolated in 1952 from a strain of *Streptomyces erythreus* obtained from soil from the Philippines. The structure of erythromycin is a 14-membered lactone ring, substituted by two sugars, desosamine and cladinose.
Erythromycin is unstable in acidic medium which causes poor and inconsistent bioavailability.

Azithromycin has a 15-membered macrocycle and a methyl-substituted nitrogen, hence the name azalides has been given to this class. Azithromycin exhibits increased activity against Gram negative bacteria and a longer half life.

Macrolides are inhibitors of protein synthesis by impairing the elongation of the peptidyl chain. The main interaction site is the domain V of the 23S rRNA, which lies at the center of the peptidyl transferase site (Mulazimoglu et al., 2005). The macrolide binding site is located at the exit tunnel of the growing peptide chain. The critical interaction occurs between the 2'-OH group of the desosamine and the adenosine residue 2058. The binding site of the macrolides on the 50S subunit of the ribosome overlaps with that of chloramphenicol and the lincosamides, leading to antagonism and cross-resistance between these classes.

Acquired resistance in macrolides can involve three mechanisms; modification of the target, antibiotic inactivation or active efflux (Mulazimoglu et al., 2005). Methylation of the rRNA is currently the most prevalent mechanism of resistance in pathogenic bacteria. This is mediated by the acquisition of *erm* genes which encodes for methyltransferases. Methylation of the N(6) position of adenine 2058 in 23S rRNA results in inhibition of macrolide binding. Monomethylation confers high levels of resistance to lincosamides and streptogramins and low-level resistance to macrolides, whilst dimethylation causes high level resistance to all three drug classes, leading to
the MLSB phenotype. More than 30 *erm* genes have been described, which are located on conjugative and transferable transposons. The expression of the methylase is either constitutive or inducible. Inducers include the 14-, 15- and 16-membered macrolides, the lincosamides and the streptogramins, but not the ketolides.

Another mechanism of resistance is the substitution of the adenine at position 2058 with guanine, this has been described in *Helicobacter pylori*, *Mycoplasma* and *Mycobacterium spp.* (Mulazimoglu *et al.*, 2005).

Erythromycin-inactivating enzymes have been reported in *Enterobacteriaceae*. These are phosphorylases or esterases (encoded by *ereA* and *ereB*) that confer resistance to all 14-, 15- and 16-membered macrolides.

In Gram positive bacteria, exposure to the antibiotic can induce over-expression of efflux pumps conferring resistance. Examples of inducible efflux pumps are the Msr(A) pump in *Staphylococci* and the Mef efflux system in *Streptococci* (Mulazimoglu *et al.*, 2005).

A *S. Paratyphi* A isolate with an azithromycin MIC (Etest) of 64 mg/L. was recently reported to have caused treatment failure in an enteric fever patient returning from Pakistan, who was treated with oral azithromycin (Molloy *et al.*, 2010). Azithromycin has a bioavailability of 30% to 50%. The serum peak level is typically reached after 2 hours. Azithromycin has a large volume of distribution which is related to the ability to accumulate inside eukaryotic cells. The ratio of tissue to serum concentration for azithromycin is 50 to 1150 (Mulazimoglu *et al.*, 2005). The half life
is 35 to 40 hours, which allows a single daily dose and shortened treatment regimen (3 to 5 days).

Macrolides are primarily metabolised through cytochrome P450 and eliminated through the bile. Gastrointestinal adverse events are relatively frequent with macrolides. Macrolides have been associated with prolongation of the QT interval and should not be used in patients with concurrent administration of class IA and III anti-arrhythmic agents and underlying cardiac disease.

Azithromycin has become a popular treatment choice for the treatment of MDR typhoid fever. The MICs for S. Typhi to azithromycin range from 4 to 16 μg/ml (Metchock, 1990). The peak serum level after a single dose of 500 mg of azithromycin is 0.4 mg/L (Mulazimoglu et al., 2005). However, as azithromycin is concentrated more than 100-fold inside polymorphonuclear cells and macrophages (Panteix et al., 1993) and S. Typhi is primarily an intracellular pathogen (Wain et al., 1998), effective drug concentrations are considerably above the MIC.

In randomized clinical trials, azithromycin has been used for the treatment of MDR typhoid fever in children and adults in Egypt, India and Vietnam (Butler et al., 1999; Chinh et al., 2000; Frenck et al., 2000; Frenck et al., 2004; Girgis et al., 1999). Cure rates were excellent and outcomes in patients infected with nalidixic acid resistant S. Typhi were satisfactory (Chinh et al., 2000).
1.9 Antimicrobial drug resistance of S. Typhi and S. Paratyphi A

In 1948 the introduction of chloramphenicol revolutionised the management of typhoid fever (Woodward et al., 1948). Chloramphenicol was effective for more than 20 years, but in the 1970s outbreaks of chloramphenicol resistant typhoid fever took place in Mexico, India and Vietnam. In the late 1980s and early 1990s outbreaks of typhoid fever occurred that were resistant against all ‘first line’ antimicrobials (multidrug resistance (MDR) defined as resistance to chloramphenicol, ampicillin and trimethoprim-sulfamethoxazole) (Parry et al., 2002). These MDR S. Typhi isolates have been responsible for numerous outbreaks in countries in the Indian subcontinent, South East Asia and Africa (Bhan et al., 2005). All MDR strains so far examined, have been harbouring plasmids of the incHI1 incompatibility group.

Consequently, the fluoroquinolones have become the treatment of choice for typhoid fever. The fluoroquinolones show excellent tissue penetration, accumulation in monocytes and macrophages and high drug levels in the gall bladder. However, there have been reports from Vietnam, India and Tajikistan of the emergence of S. Typhi isolates that respond less well to the fluoroquinolones (Bhan et al., 2005; Parry et al., 2002). In 1997, a typhoid epidemics in Tajikistan caused by such isolates caused more than 10000 illnesses and 108 deaths (Mermin et al., 1999). Technically these isolates remain within the breakpoints set for fluoroquinolone susceptibility by the Clinical Laboratory Standard Institute (CLSI) (Clinical Laboratory Standard Institute, 2007), but they are resistant to nalidixic acid (the prototype quinolone) and show higher
MICs to the fluoroquinolones. Patients infected with these isolates show a poor clinical response when treated with ciprofloxacin or ofloxacin.

Nalidixic acid resistance is usually caused by single point mutations in the bacterial target enzyme GyrA, either at codon 83 or 87 (Chau et al., 2007). High-level ciprofloxacin resistant S. Typhi (Dutta et al., 2008; Gaind et al., 2006) and S. Paratyphi A (Gaind et al., 2006) with double mutations in gyrA and single mutation in parC have been described in the Indian subcontinent. Recently there have been reports of S. Typhi isolates with reduced susceptibility to the fluoroquinolones that test nalidixic acid sensitive (Cooke et al., 2007), suggesting another mechanism of resistance. There have been sporadic reports of ceftriaxone resistant S. Typhi, but these isolates still seem to be rare (Parry and Threlfall, 2008). A decreasing trend of chloramphenicol resistant S. Typhi has been reported in recent years from the Indian subcontinent (Dutta et al., 2005; Mohanty et al., 2006). MDR as well as nalidixic acid resistant S. Paratyphi A is an emerging problem in the Indian subcontinent (Chandel et al., 2000; Maskey et al., 2006).

1.10 Treatment of typhoid and paratyphoid fever

Enteric fevers are systemic infections and appropriate antimicrobial treatment should be initiated early. It is important to provide supportive measures, such as oral and intravenous fluids, appropriate nutrition and antipyretics. More than 90% of patients are managed as outpatients, with oral antibiotics, reliable care and close medical follow up for complications or failure to respond to therapy. Patients with persistent
vomiting, severe diarrhoea and abdominal distension need admission to hospital (World Health Organization, 2003).

The management of patients with enteric fever should include blood cultures and stool cultures after completion of treatment to check for failure to clear the bacteria in the blood and stools (convalescent stool carriage), as well as follow up for at least 6 months to identify chronic faecal carriage. However in most endemic areas such follow up is not possible and therefore the management of the acute illness with effective drugs, that also prevent chronic carriage and relapse, are essential.

1.10.1 Current recommendations of the World Health Organization for the treatment of typhoid fever

The choice of treatment depends on the antimicrobial susceptibility of the isolates, but also on the cost, which is an important factor especially in endemic regions. Table 1-2 shows the current recommendations of the World Health Organization (WHO) for the treatment of typhoid fever (World Health Organization, 2003).

The fluoroquinolones are the most effective treatment for typhoid fever. In patients infected with nalidixic acid susceptible isolates, fever usually resolves within 4 days, cure is achieved in 96% of patients and rates for faecal carriage and relapse are below 2% (Parry et al., 2002).

The fluoroquinolones are also recommended for the treatment of children with typhoid fever. Extensive experience with the fluoroquinolones in children suffering from cystic fibrosis, typhoid fever and bacillary dysentery has provided a body of
evidence suggesting that the cartilage damage seen in young animals does not occur in children (Bethell et al., 1996; World Health Organization, 2003; Parry et al., 2002). Alternatives to the fluoroquinolones are third generation cephalosporins (cefixime or ceftriaxone) and azithromycin. For infections with nalidixic acid (quinolone) resistant S. Typhi, azithromycin, prolonged courses of high dose fluoroquinolones (e.g. ofloxacin at 20 mg/kg/day) and third generation cephalosporins (ceftriaxone) are recommended. Ceftriaxone should be used for 10 to 14 days. Ceftriaxone therapy for 7 days was associated with a relapse rate of 14% (Bhutta et al., 2000; Frenck et al., 2000).
<table>
<thead>
<tr>
<th>Susceptibility</th>
<th>Antibiotic</th>
<th>Daily dose (mg/kg)</th>
<th>Days</th>
<th>Antibiotic</th>
<th>Daily dose (mg/kg)</th>
<th>Days</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fully sensitive</td>
<td>Fluoroquinolone</td>
<td>15</td>
<td>5-7¹</td>
<td>Chloramphenicol</td>
<td>50-75</td>
<td>14-21</td>
</tr>
<tr>
<td></td>
<td>e.g. ofloxacin or ciprofloxacin⁴</td>
<td></td>
<td></td>
<td>Amoxycillin</td>
<td>75-100</td>
<td>14</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Trimethoprim-sulfamethoxazole</td>
<td>8-40</td>
<td>14</td>
</tr>
<tr>
<td>Multidrug resistance</td>
<td>Fluoroquinolone</td>
<td>15</td>
<td>5-7</td>
<td>Azithromycin</td>
<td>8-10</td>
<td>7</td>
</tr>
<tr>
<td></td>
<td>or cefixime</td>
<td>15-20</td>
<td>7-14</td>
<td>Cefixime</td>
<td>15-20</td>
<td>7-14</td>
</tr>
<tr>
<td>Quinolone (nalidixic acid) resistance⁵</td>
<td>Azithromycin or ceftriaxone</td>
<td>8-10</td>
<td>7</td>
<td>Cefixime</td>
<td>20</td>
<td>7-14</td>
</tr>
<tr>
<td></td>
<td></td>
<td>75</td>
<td>10-14</td>
<td></td>
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</tr>
</tbody>
</table>

¹ Three day courses are also effective and are particularly so in epidemic containment.

⁴ The optimum treatment for quinolone resistant typhoid fever has not been determined. Azithromycin, the third generation cephalosporins, or a 10-14 day course of high-dose fluoroquinolones is effective. Combinations of these are now being evaluated.

Table 1-2. World Health Organization treatment recommendations for uncomplicated typhoid fever.

From (World Health Organization, 2003)
There are few data on the treatment of typhoid fever in pregnancy (Seoud et al., 1988). Ampicillin for fully susceptible isolates and ceftriaxone are considered safe for this indication (World Health Organization, 2003; Parry et al., 2002).

1.10.2 Management of severe typhoid fever

Both, in- and out-patients should be closely monitored for the development of complications. The parenteral fluoroquinolones are probably the first choice for the treatment of severe typhoid fever (Dutta et al., 1993; World Health Organization, 2003) but there have been no randomised trials to date. In severe typhoid fever, the fluoroquinolones should be given for a minimum of 10 days. For patients infected with nalidixic acid resistant isolates, ceftriaxone is effective (World Health Organization, 2003).

A trial conducted in the 1980s showed a dramatic beneficial effect of high dose steroid treatment (dexamethasone at 3 mg/kg for the first dose given over 30 minutes and 1 mg/kg every 6 hours for 48 hours) in severely sick typhoid fever patients with encephalopathy and shock, given in addition to chloramphenicol. Dexamethasone adjunctive treatment reduced the mortality from 56% to 10% when compared to placebo (Hoffman et al., 1984). Hydrocortisone at a lower dose was not effective (World Health Organization, 2003).

Intestinal perforation is a surgical emergency. Early intervention is crucial, and mortality rates increase when surgery cannot be performed immediately and vary between 10% and 32% (van Basten and Stockenbrugger, 1994). Metronidazole should
be added to the antibiotic regimen to treat leakage of intestinal bacteria into the abdominal cavity. Patients with intestinal haemorrhage need intensive care, monitoring and blood transfusion. Intervention is needed if there is significant blood loss, then crossmatched blood should be ready and the operating theatre should be prepared (Parry et al., 2002).

In patients presenting with a relapse, cultures should be obtained and patients should be treated according to the susceptibility pattern of the infecting isolate.

1.10.3 Typhoid carriers

Chronic carriers play an important role in the transmission of typhoid and paratyphoid fever. S. Typhi and S. Paratyphi are only shed intermittently in the faeces. Therefore, stool samples need be obtained repeatedly to detect typhoid carriers. Long antimicrobial treatment courses of up to six weeks should be given according to the susceptibility of the isolates to eradicate carriage (World Health Organization, 2003). In susceptible isolates, clearance was achieved in up to 80% with the administration of 750 mg ciprofloxacin or 400 mg norfloxacin twice daily for 28 days (Ferreccio et al., 1988; Gotuzzo et al., 1988). If cholelithiasis is present the patient may require antibiotic therapy as well as cholecystectomy. In patients with chronic urinary carriage resulting from infection with Schistosoma haematobium, antiparasitic medication in addition to antibiotics is needed to achieve bacteriological cure (World Health Organization, 2003).
1.11 Control and prevention of typhoid fever

Typhoid fever can be prevented by the provision of safe drinking water, good food hygiene and safe sewage disposal. Chronic carriers pose a special risk to the community, therefore programmes to detect and treat chronic carriers should be in place.

There are two licensed, safe typhoid vaccines available, the parenteral (intramuscular injectable) Vi polysaccharide and the oral live attenuated Ty21 vaccine, both vaccines are based on the pathogenic S. Typhi strain Ty2 (Felix and Pitt, 1951). The oral Ty21 vaccine (Vivotif, Bema) needs to be administered in three doses (day 1, 3, 5) and is licensed for adults and children above 6 years. Field studies with the oral Ty21 vaccine in the 1980s have shown a protective efficacy after 3 years of 96% in Egypt (Wahdan et al., 1982) and up to 77% in Chile when using the liquid formulation (Levine et al., 1990). The parenteral Vi vaccine is licensed for adults and children above 2 years. A single intramuscular injection confers a protective efficacy of 77% after 21 months in South Africa (Klugman et al., 1987). The WHO recommends that the immunization of school-age children should be undertaken wherever the control of the disease is a priority (World Health Organization, 2003). Unfortunately, these two vaccines are both underutilised in developing countries.
1.12 Vietnam

1.12.1 Introduction

The Socialist Republic of Vietnam is the second largest country in South East Asia. Vietnam borders to China, Laos and Cambodia and stretches 1650 km north to south. Vietnam's coastline along the South China Sea extends 3400 km. The country is divided in the Red River Delta in the north, the Central Highlands and the Mekong Delta in the south. Vietnam has an estimated population of 87 million with a median age of 27 years (Central Intelligence Agency, 2009). The capital is Hanoi. There are four other municipalities (Ho Chi Minh City, Danang, Can Tho and Hai Phong) and 58 provinces.

Economically, Vietnam is classified as a developing low income country by the World Bank. In 2008, the gross domestic product (GDP) was US$ 90 billion and the GNI (gross national income) per capita (Atlas method) was US$ 890 (World Bank, 2009). Twelve % of the population are estimated to be below the poverty line (i.e. living on less than US$ 1 per day) (Central Intelligence Agency, 2009). The total expenditure on health care is 7.1% of the GDP or US$ 58 per capita per annum. The government expenditure on healthcare is US$ 23 per capita or 39% of the total expenditure (World Health Organization, 2010). There are six doctors, eight nurses and three pharmaceutical personnel and 28 hospital beds per 10,000 population. The maternal mortality rate is 150 per 100 000 live births and the mortality rate in children under 5 years was 14 per 1000 live births in 2007. Life expectancy at birth is currently
74 years and the adult literacy rate is 90% (Central Intelligence Agency, 2009). Adult
HIV prevalence is estimated at 0.5%.

Figure 1.8. Map of Vietnam, showing the major cities.

From (Central Intelligence Agency, 2009)

1.12.2 The Hospital for Tropical Diseases, Ho Chi Minh City

The Hospital for Tropical Diseases was initially built in 1865 and is a 500 bed
infectious diseases hospital in Ho Chi Minh City, Vietnam and was formerly known
as the Centre for Tropical Diseases and before that as Cho Quan Hospital. It serves the local community in Ho Chi Minh City and is a tertiary referral centre for infectious diseases for the southern provinces of the country. Randomised controlled trials for the treatment of typhoid fever have been conducted on the adult and paediatric wards since 1992. The Wellcome Trust Major Overseas Programme Vietnam, Oxford University Clinical Research Unit, Ho Chi Minh City is based within the Hospital for Tropical Diseases, in a state of the art modern research facility, allowing close collaborations between clinicians and researchers. The research undertaken in this PhD was based at the Oxford University Clinical Research Unit, The Hospital for Tropical Diseases, Ho Chi Minh City.

1.12.3 Typhoid fever and antimicrobial drug resistance in Vietnam

Typhoid fever has been endemic in Vietnam, especially in the densely populated Mekong Delta area.

Chloramphenicol resistant typhoid fever was first described at the Hospital for Tropical Diseases in 1973 (Butler et al., 1973). In 1993, during the initial outbreak of MDR \textit{S. Typhi} in Kien Giang province in the south of Vietnam, the fluoroquinolone antibiotics were introduced as the first choice for the treatment of typhoid fever (Nguyen et al., 1993). Since 1993, the proportion of MDR \textit{S. Typhi} plateaued at high levels in southern Vietnam and there has been a dramatic increase in nalidixic acid resistance. In 2004, 50% (101/202) of the \textit{S. Typhi} isolates from southern Vietnam were MDR. In 1998, five years after ofloxacin and ciprofloxacin become widely used
to treat typhoid fever but also a broad range of other febrile illnesses, often purchased without prescription in an uncontrolled market, 87% of the S. Typhi isolates were resistant to nalidixic acid (Chau et al., 2007).

In 2004, 97% (196/201) of the S. Typhi isolates were resistant to nalidixic acid and showed reduced susceptibility to the older fluoroquinolones, such as ofloxacin. This combination of MDR and nalidixic acid resistance is a particular problem in Vietnam, leading to poor clinical response and high failure rates (up to 36% clinical failure rates) in typhoid fever patients treated with ofloxacin (Chinh et al., 2000; Parry et al., 2006), and severely restricts the therapeutic options in patients with typhoid fever. Data from a cross-sectional study from eight Asian countries (Bangladesh, China, India, Indonesia, Laos, Nepal, Pakistan and Vietnam) underline that antimicrobial drug resistance in S. Typhi is a problem in Asia (Chau et al., 2007). In 2003 and 2004, the prevalence of chloramphenicol resistant S. Typhi remained high with 18% (9/50) of isolates in Laos, 19% (28/149) in Nepal, 26% (6/23 and 9/34 isolates, respectively) in India and Pakistan and 40% (16/40) in Bangladesh. All countries in the region, with the exception of China and Laos, faced an additional problem of widespread nalidixic acid resistance. Again southern Vietnam was a particular hot spot with more than 90% of all S. Typhi resistant to nalidixic acid. Roumagnac et al recently suggested that fluoroquinolone use has stimulated the clonal expansion of a nalidixic acid resistant S. Typhi haplotype H58 in southeast Asia (Roumagnac et al., 2006).
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<tr>
<td>Ho Chi Minh City</td>
<td>106</td>
<td>0</td>
<td>75</td>
<td>0</td>
<td>42</td>
<td>0</td>
</tr>
<tr>
<td>An Giang</td>
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<td>0</td>
<td>724</td>
<td>0</td>
<td>545</td>
<td>0</td>
</tr>
<tr>
<td>Dong Thap</td>
<td>700</td>
<td>1</td>
<td>557</td>
<td>0</td>
<td>413</td>
<td>0</td>
</tr>
<tr>
<td>Southern Provinces</td>
<td>2707</td>
<td>1</td>
<td>3088</td>
<td>0</td>
<td>2173</td>
<td>0</td>
</tr>
<tr>
<td>Whole country</td>
<td>4323</td>
<td>1</td>
<td>5030</td>
<td>5</td>
<td>3018</td>
<td>0</td>
</tr>
</tbody>
</table>

Table 1-3. Reported cases of syndromic typhoid fever in Vietnam, 2004 to 2006.

Table 1-3 summarises the reported cases of syndromic typhoid fever in Vietnam (blood culture confirmed and unconfirmed) between 2004 and 2006 shown for three selected provinces (Ho Chi Minh City, An Giang and Dong Thap province), the southern provinces and the whole country. Source: Statistics on Infectious Diseases, National Institute of Health and Epidemiology (NIHE), Ministry of Health, Vietnam

Compared to the 1990s, the number of reported cases of typhoid fever has declined in Vietnam. In 1995, more than 700 *S. Typhi* strains were isolated from blood cultures from patients admitted at the Hospital for Tropical Diseases in Ho Chi Minh City (Parry, 2004a). In 2009, there were less than 50 blood culture confirmed cases of typhoid fever at this hospital. The reduction in the incidence of typhoid fever in Vietnam has been attributed to improvements in infrastructure that have accompanied the economic development and to better treatment. There have been limited targeted
vaccination campaigns, using the Vi vaccine (Lin et al., 2001), however the extent to which vaccination contributed to the reduction in incidence is not clear.

1.13 Nepal

Nepal is a landlocked country in Southern Asia that shares borders with the Republic of India in the south, west and east and with the Peoples Republic of China in the north. The total land area is about 140 000 km$^2$, of which only 16% are arable land. Nepal is a very mountainous country with eight of the world's ten highest peaks on its territory. Mount Everest, the world's tallest mountain with a height of 8844 m is located on the Nepalese-Tibetian border. Kanchenjunga, the world's third tallest mountain (8586 m) is located on the Nepalese-Indian border.

The Tarai plain, the northern rim of the Ganges plain, is situated at 300 m above sea level in the south of Nepal. Due to the diverse geography and enormous range of altitudes, the weather in Nepal varies from cool summers and extreme alpine winters in the north to sub tropic summers and mild winters in the south.

Nepal has an estimated population of 29 million and is among the poorest and least developed countries in the world. Approximately 31% of its population are living below the poverty line (less than 1 US$ per day). Agriculture provides an income for 75% of the population and accounts for approximately one third of the GDP.
After ten years of civil war (from 1996 to 2006) which was led by Maoist insurgents, nationwide elections took place in 2008 and the newly elected Constituent Assembly declared Nepal a Federal Democratic Republic and abolished the 240 year old monarchy.

The gross national income (GNI) per capita is 400 US$ (Central Intelligence Agency, 2009). The adult literacy rate (above 15 years) is 57% and the life expectancy is 67 years. The maternal mortality rate (adjusted) is one of the world's highest with 830 deaths per 100,000 live births and the infant mortality rate is 41 deaths per 1000 live births (World Health Organization, 2010). The mortality rate in children under 5 years is 51 per 1000 live births. Access to trained health care workers is a major problem in
this mountainous country, where travel is often by foot. There is a huge disparity in
the quality of health care offered in urban and rural areas. In Kathmandu 10 doctors
serve for every 10 000 people, whereas in rural Nepal 0.3 doctors serve 10 000
inhabitants. Only 19% of pregnant women have access to a skilled medical
professional (doctor, nurse or midwife) at delivery, in some rural areas this percentage
tends to be as low as 3% (Unicef, 2009).

1.13.1 Patan Hospital, Kathmandu

Kathmandu, Nepal’s capital, has approximately 1.5 million inhabitants and is situated
at an elevation of 1300 m. Kathmandu has four seasons, cold winters (December to
February), spring (March to May), hot monsoon summers (June to August) and
autumn (September to November). Patan Hospital is one of the three general hospitals
serving the Kathmandu metropolitan area. The hospital has 450 beds and provides
inpatient and outpatient medical, surgical, paediatric, gynaecology and obstetric
services for approximately 300 000 outpatients and 16 000 inpatients per year. It
serves as a primary and secondary health care facility.

Part of the research presented in Chapter 3 of this thesis was conducted at Patan
Hospital, Kathmandu.

1.13.2 Enteric fever in Nepal

Enteric fever is a major public health problem in Nepal. Data regarding the burden of
disease are difficult to obtain, this is partially due to self medication which is
purchased without prescription from local pharmacies and the absence of diagnostic
facilities in rural areas. A recent study reported that S. Typhi and S. Paratyphi A accounted for 75% (9124 out of 12252) of all positive blood cultures that were performed at Patan Hospital from 1993 till 2003, during an 11 year period (Maskey et al., 2008). The proportion of enteric fever caused by S. Paratyphi A increased from 18% in 1993 to 34% in 2003.

Multidrug resistant (MDR) S. Typhi was first reported in Nepal in 1991 and ciprofloxacin replaced chloramphenicol as first line treatment in 1994, but increasing rates of treatment failure were noted since 2000 (Maskey et al., 2008). Faecal contamination of water sources is significant. In 2002, an outbreak of enteric fever in 5936 people in Bharatpur was reported (Lewis et al., 2005). The source of the outbreak was the municipal water supply.

Kathmandu is served by an antiquated water supply. The water frequently contains coliform bacteria due to possible cross connections between water supply and sewage system. Chlorination is often inadequate. Often inhabitants do not have access to piped water in their homes and collect their water from local water spouts (Figure 1. 9) (Karkey et al., 2008).
Figure 1.10. Community water spout in Kathmandu, Nepal.

Villagers, mostly women and children are seen collecting their daily water provision from the community’s stone spouts. This water is usually not boiled.

1.14 Aims of the thesis

The work described in this thesis includes two clinical trials (Chapters 2 and 5) and two laboratory studies (Chapters 3 and 4) that examine different aspects of typhoid fever and aim to improve our understanding of this disease. The work for this thesis was undertaken at the Hospital for Tropical Diseases in Ho Chi Minh City, Vietnam and partly (Chapter 3) at Patan Hospital, Kathmandu, Nepal, in collaboration with the
Wellcome Trust Sanger Institute, UK and the Institute for Clinical Pharmacodynamics, US.

Chapter 2 describes a randomised controlled trial conducted in the Mekong Delta region of Vietnam with a high proportion of multidrug and nalidixic acid resistant S. Typhi strains. This chapter examines whether the newer fluoroquinolone gatifloxacin or azithromycin is the better treatment for uncomplicated typhoid fever in Vietnam. In the discussion the results of this trial are compared with two recent enteric fever trials using gatifloxacin, performed in Kathmandu, Nepal.

Chapter 3 uses existing data (patients’ weight, height, serum creatinine and drug doses) from the gatifloxacin treatment trial (Chapter 2) to model the patients’ drug exposure and put this into context with their clinical response to gatifloxacin treatment. It also identifies evidence based S. Typhi gatifloxacin MIC breakpoints to predict treatment success or failure.

The second section of Chapter 3 evaluates the pharmacokinetics of gatifloxacin in patients with typhoid fever. Blood samples were taken during a randomised trial of gatifloxacin versus chloramphenicol in Nepal and gatifloxacin plasma concentrations were measured. The pharmacokinetic profile of the Nepalese enteric fever patients is compared to North American adult subjects and paediatric patients with otitis media.

Chapter 4 explores the question of why the Mekong Delta has continued to be a hot spot for typhoid fever infections, particularly multidrug and nalidixic acid resistant typhoid fever, whilst the incidence of typhoid fever has declined in the rest of
Vietnam. This chapter looks at the population structure of the *S. Typhi* population isolated in the Mekong delta region during the clinical trial described in Chapter 2 and attempts to determine whether typhoid infections in this area are due to a certain genotype of *S. Typhi*.

Chapter 5 highlights possible mechanisms of prevention and describes a randomised controlled Phase II clinical trial of a novel oral typhoid fever vaccine in healthy Vietnamese children. The M01ZH09 (*S. Typhi* (Ty2 *aroC ssaV*) ZH9) vaccine has a well-defined dual mechanism of attenuation and is given in a single oral dose. This chapter describes the safety and immunogenicity of this vaccine in healthy children in an endemic area.

In the conclusion the key findings of this thesis are summarised and other research, current developments and possible future directions are discussed.
Chapter 2

A Multi-Center Randomised Controlled Trial of Gatifloxacin *versus* Azithromycin for the Treatment of Uncomplicated Typhoid Fever in Children and Adults in Vietnam
2.1 Introduction

The emergence of antimicrobial drug resistance in S. Typhi is a major problem particularly in South East Asia and the Indian sub-continent (Bhan et al., 2005; Bhutta, 2006; Parry et al., 2002). There is a need for an efficacious, safe and affordable oral treatment, particularly in regions with a high proportion of both multidrug and nalidixic acid resistant S. Typhi.

The World Health Organization (see Chapter 1) recommends the fluoroquinolones or cefixime for the treatment of MDR typhoid fever and azithromycin, the third-generation cephalosporins, or a 10-14 day course of high-dose older generation fluoroquinolones (e.g. ofloxacin or ciprofloxacin) for the treatment of nalidixic acid resistant typhoid fever (World Health Organization, 2003).

A trial from southern Vietnam used ofloxacin at the maximum recommended dose of 20 mg/kg/day for 7 days for the treatment of MDR and nalidixic acid resistant typhoid fever and showed high clinical failure rates (36%), high immediate post-treatment faecal carriage (19%), which may lead to transmission in the community after discharge from hospital, and prolonged mean fever clearance times of 8.2 days (95% CI, 7.2-9.2 days) (Parry et al., 2007). These results underline that the older generation fluoroquinolones are clearly failing in the treatment of nalidixic acid resistant typhoid fever.

Of the newer fluoroquinolones, gatifloxacin, a broad spectrum synthetic 8-methoxyfluoroquinolone is available and affordable in South and South East Asia.
including Vietnam. Of all the fluoroquinolones, gatifloxacin showed the lowest minimum inhibitory concentrations (MICs) for nalidixic acid resistant S. Typhi from Nepal (Maskey et al., 2006) and Vietnam and a rapid bactericidal effect in time-kill experiments involving S. Typhi isolates with single and double mutations in gyrA of S. Typhi (Chau et al., 2007). Gatifloxacin can be administered as a once daily oral dose.

Gatifloxacin was shown to be safe and efficacious in a pilot study in patients with a median fever clearance time (FCT) of 76 hours (unpublished data Dr. Nguyen Chinh).

Azithromycin, an azalid antibiotic, has achieved excellent clinical results in the treatment of MDR and nalidixic acid resistant typhoid fever (Chinh et al., 2000; Parry et al., 2007). However azithromycin is expensive and often not available in developing countries.

We conducted a randomised controlled trial comparing the efficacy of gatifloxacin to azithromycin in southern Vietnam, an area characterised by a very high proportion of MDR (88%) and nalidixic acid resistant (93%) S. Typhi isolates (Parry et al., 2007).

2.2 Methods

2.2.1 Study design and objectives

The study was designed as a multicenter, open-label randomised controlled trial to compare the efficacy and safety of gatifloxacin versus azithromycin for the treatment of uncomplicated typhoid fever in children and adult in-patients in southern Vietnam.
The overall objective of the trial was to identify an efficacious, safe, available and affordable oral treatment for MDR and nalidixic acid resistant typhoid fever.

2.2.2 Participants

Patients were eligible to be included in the study if they had clinically suspected or culture confirmed uncomplicated typhoid fever and if fully informed written consent had been obtained. For children, consent was obtained from the parent. Exclusion criteria were pregnancy, age under 6 months, history of hypersensitivity to either of the trial drugs, any signs of severe typhoid fever (shock, deep jaundice, encephalopathy, convulsions, bleeding, suspicion or evidence of gut perforation), or previous reported treatment with a fluoroquinolone antibiotics, a third generation cephalosporin or macrolide antibiotics within one week prior to hospital admission.

2.2.3 The study sites and ethical approval

The study was conducted at three hospitals in the south of Vietnam (Figure 2.1.). Adult and paediatric patients were recruited at the Hospital for Tropical Diseases in Ho Chi Minh City, at the Dong Thap Provincial Hospital in Cao Lanh, Dong Thap province and at the An Giang Provincial Hospital in Long Xuyen in An Giang province.
The trial was conducted as a multicenter trial in three hospitals in southern Vietnam.

The study was approved by the Ethical and Scientific Committee of the Hospital for Tropical Diseases in Ho Chi Minh City and the Oxford University Tropical Research Ethics Committee (OXTREC), UK for all three study sites. The clinical and microbiological data from the first 40 patients recruited to each arm of the study were sent to the independent Data Safety and Monitoring Committee for their advice regarding the continuation of the study. The study was not stopped. The trial was registered at Current Controlled Trials (ISRCTN67946944).

2.2.4 Intervention

According to their randomisation number patients were assigned to oral treatment with either 20 mg/kg azithromycin (Zithromax® suspension, Pfizer, USA; 200 mg/5 mL or Zithromax® tablets, Pfizer, USA; 500 mg/tablet) or 10 mg/kg gatifloxacin (Tequin®, Bristol-Myers Squibb, USA; 400 mg/tablet) once daily for 7 days. Tablets
were cut to obtain the appropriate study dosage and administered with water. Inevitably, the dose administered was an estimate of 10 mg/kg/day of gatifloxacin or 20 mg/kg/day of azithromycin (number of tablets or proportions of tablets were documented in the CRFs). Gatifloxacin was only available as tablets, which were cut to obtain the appropriate dosage and crushed if necessary for children.

The maximum dose of azithromycin was 1 g per day. All drugs were purchased commercially.

2.2.5 Procedures

2.2.5.1 In-patient procedures

On admission to the hospital the patient’s full history was taken, a standard clinical examination was performed and axillary temperature, weight and height were measured. Before treatment, full blood counts including white blood differential counts, serum aspartate transaminase (AST), serum alanine transaminase (ALT) and bilirubin were checked and blood cultures were obtained. For adult patients, creatinine, blood urea nitrogen (BUN) and glucose levels were additionally measured. In some patients bone marrow cultures were obtained. Urines were checked with dipstick and pre-treatment stool cultures were obtained. Chest X-ray and abdominal ultrasound were performed and repeated as clinically indicated. Randomisation and initiation of therapy took place either immediately on admission to hospital or patients were observed until results of blood tests including blood cultures were available and then randomised. Vital signs including measurement of axillary temperatures were measured and recorded every 6 hours (at 6, 12, 18 and 24 hours) until discharge.
Patients were examined daily until discharge from hospital, with particular reference to clinical symptoms, FCT, side effects of the drug and any complication of the disease. Additionally laboratory tests were scheduled if clinically indicated. All adverse events were recorded. On day 7 to 9 after the start of treatment full blood counts, liver function tests, blood and stool cultures were checked. In case of insufficient response to therapy, development of complications or drug-associated adverse events, the initial treatment was suspended and parenteral ceftriaxone (2 g per day) in two divided doses was used as rescue treatment for 10 days.

2.2.5.2 Follow-up procedures

Out-patient follow-up appointments were scheduled at 1 month, 3 months and 6 months after discharge from hospital to seek evidence for relapse (1 month visit) and check for chronic typhoid carriage (all visits). At these appointments a full history was taken, relevant examinations performed and stool cultures obtained. Blood or bone marrow cultures were only obtained if clinical symptoms were indicative of acute infection. If patients did not attend their follow up appointment, they were reminded by letter or a member of the study team visited their home. If stool samples were not available, a rectal swab was obtained.

Patients with convalescent stool carriage of *S. Typhi* or *S. Paratyphi A* were retreated according to the sensitivity of the isolate and were further followed up. Ultrasound was performed to exclude biliary or kidney stones if carriage was persistent.
2.2.6 Microbiology

Five to 8 mL of blood was collected from adults and inoculated into Bactec Plus Aerobic Blood bottles, and 3 to 5 mL of blood from children was inoculated into Bactec Peds Plus culture bottles (Becton Dickinson, New Jersey, USA). The bottles were incubated at 37°C in the BACTEC 9050 automated analyser for 7 days and sub-cultured according to standard methods when the machine indicated a positive signal, or incubated at 37°C in a standard laboratory incubator (An Giang hospital) and examined daily.

Stool samples or rectal swabs were inoculated onto MacConkey agar and Xylose Lysine Decarboxylase (XLD) agar plates, and in 10 mL of selenite F broth. Plates and broth were incubated at 37°C overnight and the broth was sub-cultured on MacConkey and XLD agar plates the next morning.

Isolates were screened using standard biochemical tests and S. Typhi and S. Paratyphi A were identified using API20E (BioMerieux, Paris, France) and slide agglutination with specific antiserum (Murex, Dartford, UK).

Antimicrobial susceptibility testing was performed by disc diffusion according to Clinical Laboratory Standards Institute (CLSI) guidelines (CLSI, 2006), using CLSI breakpoints (CLSI, 2007). Antimicrobial agents tested were: ampicillin, chloramphenicol, trimethoprim-sulfamethoxazol, nalidixic acid, ofloxacin, ciprofloxacin and ceftriaxone (Oxoid, Basingstoke, UK). MICs for amoxicillin, chloramphenicol, nalidixic acid, ofloxacin, ciprofloxacin, gatifloxacin, ceftriaxone
and azithromycin were determined by E-test (AB Biodisk, Solna, Sweden). Multidrug resistance (MDR) of isolates was defined as resistance to chloramphenicol (MIC ≥ 32 μg/mL), ampicillin (MIC ≥ 32 μg/mL) and trimethoprim-sulfamethoxazole (MIC ≥ 8/152 μg/mL). Nalidixic acid resistance was defined as an MIC ≥ 32 μg/mL. The CLSI breakpoints for ofloxacin and gatifloxacin were ≤ 2 μg/mL susceptible and ≥ 8 μg/mL resistant, for ciprofloxacin ≤ 1 μg/mL susceptible and ≥ 4 μg/mL resistant and for ceftriaxone ≤ 8 μg/mL susceptible and ≥ 64 μg/mL resistant. There were no CLSI MIC breakpoints for azithromycin (CLSI, 2007). The control strains used for all susceptibility tests were E. coli ATCC 25922, Pseudomonas aeruginosa ATCC 27853, Staphylococcus aureus ATCC 29213.

All cultures, identification of S. Typhi and S. Paratyphi A and disc diffusion were performed at the three study sites. All isolates were sent to the Hospital for Tropical Diseases, Ho Chi Minh City, for confirmation of identity, susceptibility testing and MIC testing.

### 2.2.7 Outcomes of the study

The primary endpoint of the study was the resolution of fever (fever clearance time, FCT), which was defined as the time from the start of the antibiotic treatment to when the axillary temperature first fell ≤ 37.5°C and remained there for at least 48 hours. Secondary endpoints were the overall failure to treatment, which was defined a priori as any of the following: clinical failure (persistence of fever and symptoms two days after the end of treatment, i.e. on day 10) or need for re-treatment due to insufficient
treatment response as judged by the treating physician; microbiological failure (positive blood culture on day 7 to 9 after the start of treatment); the development of typhoid fever-related complications during hospital-stay; the occurrence of relapse (symptoms and signs suggestive of typhoid fever) within 1 month after completion of treatment or the detection of faecal carriage of S. Typhi at the follow-up visits at 1, 3 and 6 months (to exclude faecal carriage a minimum of two consecutive follow-up visits had to be attended).

2.2.8 Sample Size

The primary outcome measure for the study was the fever clearance time (FCT).

Previous studies that used azithromycin to treat typhoid fever patients, reported a mean fever clearance time of 130 hours (Chinh et al., 2000) and 139 hours (Parry et al., 2007). For gatifloxacin, clinical observations from a small number of typhoid fever patients were available and indicated a mean FCT of 76 hours. We calculated that 139 patients with culture confirmed typhoid fever would be needed in each treatment arm to detect a Hazard Ratio of 1.40 with two-sided alpha of 0.05 and power of 0.80 (Machin et al., 1997). Therefore, assuming a median fever clearance time of 130 hours for azithromycin, the sample size of 140 patients with culture-confirmed typhoid fever in each arm would give power of at least 0.80 to detect a difference between treatments if the fever clearance time in the gatifloxacin group was 92 hours or less.
2.2.9 Randomisation

An administrator independent from the study generated the random number sequence in Excel using RAND function. These randomised codes were blocked in a size of 50. Treatment assignments were folded and kept in opaque, sealed, sequentially numbered envelopes at all three study sites. Due to logistic reasons randomisation was not stratified by centre.

After all inclusion and exclusion criteria were checked, and informed consent given, the study doctor opened the envelope to determine which treatment the subject would receive. The sealed envelopes were opened in strict numeric sequence. This study was conducted as an open study.

2.2.10 Statistical methods

Binary outcomes (clinical failure, microbiological failure, typhoid fever-related complications) were compared between the two treatment groups using Fisher’s exact test, assuming the worst case scenario (all lost to follow up treated as failures). The un-adjusted Odds Ratio (OR) and Cornfield’s 95% Confidence Interval (Breslow and Day, 1980) were calculated to show the relative risk of developing individual secondary outcomes (clinical, microbiological failure, typhoid fever-related complications) in the gatifloxacin group compared to the azithromycin group.

Fever clearance time, time to relapse and time to overall failure were analysed using survival methods. The time to overall failure equaled the earliest time individual failure was recorded. Kaplan-Meier estimates of probabilities of each event were
calculated at any time-point, and they were compared between the two treatment
groups using the log-rank test. Data of patients who were lost to follow-up were
censored at the time of the last recorded outcome. The Hazard Ratio was derived from
Cox proportional hazard model (Collett, 2003).

All patients with positive blood or bone marrow culture for *S. Typhi* and *S. Paratyphi
A* (per protocol analysis) and separately all randomised patients (intention to treat
analysis) were analysed.

All data were recorded prospectively into individual Case Record Forms (CRF) and
entered into an electronic database (Epi Info 2003, CDC, Atlanta, USA) and double-
checked.

Analysis was performed using STATA version 8.0 (Stata Corporation, Texas, USA)
statistical software program.

2.3 Results

2.3.1 Participant flow and recruitment

During the study period, 460 patients were assessed for eligibility (Figure 2.2). One
hundred and two patients were ineligible; the main reason was the reported previous
use of fluoroquinolone, macrolide or third generation cephalosporin antibiotics (41
patients) in the week before hospitalisation.

Between April 2004 and August 2005, 358 patients with suspected typhoid fever were
randomised to receive either gatifloxacin or azithromycin. Two hundred eighty-eight
of these patients had blood or bone marrow confirmed typhoid fever and 70 patients were culture negative for S. Typhi. One culture positive patient was excluded from the per protocol analysis (PP), because he had received ciprofloxacin before entry to the trial. The PP group consisted of 287 patients, 145 in the gatifloxacin group and 142 in the azithromycin group. All PP patients, except two in the azithromycin group, finished the full course of treatment.

The total number of patients visiting the follow-up at 1 month was 275 out of 287 (96%), at 3 months 268 out of 287 (93%), at 6 months 128 out of 287 (44%) patients.
Adults and children with clinically suspected typhoid fever assessed for eligibility during trial period, n=460

Not eligible, n=102
- Previous antibiotics, n=41
- Complicated typhoid fever, n=8
- Age under 6 months, n=6
- Refused consent, n=16
- Study doctor absent, n=30
- Allergic reaction to antibiotics, n=1

Intention to treat analysis

358 Patients randomised

186 Patients randomised to gatifloxacin, all received gatifloxacin

145 Patients with culture confirmed typhoid fever (S. typhi, n=144, S. paratyphi A, n=1)

41 Patients culture negative

145 analysed in the per protocol analysis

All patients completed treatment
- 13 Patients with overall treatment failure
- 132 Patients successfully treated

Follow-up:
- At 1 month, 138 of 145 patients
- At 3 months, 137 of 145 patients
- At 6 months, 65 of 145 patients

172 Patients randomised to azithromycin, all received azithromycin

142 Patients with culture confirmed typhoid fever (S. typhi, n=138, S. paratyphi A, n=4)

29 Patients culture negative

142 analysed in the per protocol analysis

2 did not complete treatment
- 13 Patients with overall treatment failure
- 1 moderate severe adverse event
- 126 Patients successfully treated

Follow-up:
- At 1 month, 137 of 142 patients
- At 3 months, 131 of 142 patients
- At 6 months, 63 of 142 patients

Figure 2.2. Profile of the trial
All 358 randomised patients were analysed in the intention to treat (ITT) analysis. Two hundred and eighty-seven patients with culture confirmed typhoid fever, 145 treated with gatifloxacin and 142 with azithromycin, were analysed in the pre-specified PP analysis.

### 2.3.2 Baseline Data

The median age of patients recruited in this trial was 11 years (range 1-41) in the PP group.

The baseline characteristics of the patients were similar in the two treatment groups and in the culture negative patients (Table 2-1)

Patients with suspected and blood culture confirmed typhoid fever were eligible for this trial. In the PP group, the median delay in time between hospital admission and randomisation was 3 days (interquartile range 1-4) in the gatifloxacin group and 3 days (interquartile range 2-4) in the azithromycin group. In the ITT group, the median delay in time between hospital admission and randomisation was 2 days (interquartile range 0-4) in the gatifloxacin group and 3 days (interquartile range 1-4) in the azithromycin group.
<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Culture confirmed patients treated with</th>
<th>Azithromycin, n=142</th>
<th>Blood culture negative patients, n=70</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Gatifloxacin, n=145</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Median age in years (range)</td>
<td>11 (2-30)</td>
<td>11 (1-41)</td>
<td>9 (2-42)</td>
</tr>
<tr>
<td>Number of children defined as age under 15 (%)</td>
<td>109 (75.2)</td>
<td>101 (71.1)</td>
<td>56 (80)</td>
</tr>
<tr>
<td>Number of males (%)</td>
<td>71 (49)</td>
<td>76 (53.5)</td>
<td>29 (41)</td>
</tr>
<tr>
<td>Median weight in kilograms (range)</td>
<td>25 (8.5-55)</td>
<td>24.5 (9.5-57)</td>
<td>19.5 (10.5-53)</td>
</tr>
<tr>
<td>Median duration of fever before admission in days (range)</td>
<td>7 (2-30)</td>
<td>7 (2-30)</td>
<td>7 (3-30)</td>
</tr>
<tr>
<td>Number of patients who received pretreatment (%)</td>
<td>21 (14.5)</td>
<td>18 (12.7)</td>
<td>16 (22.9)</td>
</tr>
<tr>
<td>Median temperature at admission in °C (range)</td>
<td>39 (37-40.5)</td>
<td>39 (37.3-41)</td>
<td>38.75 (37-40)</td>
</tr>
<tr>
<td>Hepatomegaly, number (%)</td>
<td>69 (47.6)</td>
<td>63 (44.4)</td>
<td>36 (51.4)</td>
</tr>
<tr>
<td>Splenomegaly, number (%)</td>
<td>17 (11.7)</td>
<td>14 (9.8)</td>
<td>2 (2.9)</td>
</tr>
<tr>
<td>Abdominal pain, number (%)</td>
<td>82 (56.5)</td>
<td>76 (53.5)</td>
<td>43 (61.4)</td>
</tr>
<tr>
<td>Weight loss, numbers (%)</td>
<td>69 (47.6)</td>
<td>71 (50)</td>
<td>21 (30)</td>
</tr>
<tr>
<td>Vomiting, number (%)</td>
<td>47 (32.4)</td>
<td>54 (38)</td>
<td>19 (27.1)</td>
</tr>
<tr>
<td>Diarrhoea, number (%)</td>
<td>95 (65.5)</td>
<td>82 (57.7)</td>
<td>49 (70)</td>
</tr>
<tr>
<td>Mild jaundice, number (%)</td>
<td>12 (8.3)</td>
<td>20 (14.1)</td>
<td>1 (1.4)</td>
</tr>
<tr>
<td>Median haematocrit in % (range)</td>
<td>34.3 (19.2-54.3)</td>
<td>34.6 (20.7-60.5)</td>
<td>34.2 (24.6-46.7)</td>
</tr>
<tr>
<td>Median white cell count, 10⁹/L (range)</td>
<td>6.9 (2-17.2)</td>
<td>7.05 (2.4-16.8)</td>
<td>7.25 (2.8-11.7)</td>
</tr>
<tr>
<td>Median platelet count, 10⁹/L (range)</td>
<td>172 (34-500)</td>
<td>172.5 (45-578)</td>
<td>208 (51-496)</td>
</tr>
<tr>
<td>Median AST, U/L(range)</td>
<td>85 (16.9-773)</td>
<td>72 (17.6-1190)</td>
<td>50.1 (11-533)</td>
</tr>
<tr>
<td>Median ALT, U/L (range)</td>
<td>67.4 (10.3-276)</td>
<td>59.4 (10.2-734)</td>
<td>44.1 (10-375)</td>
</tr>
<tr>
<td>Numbers of S.Typhi/S.Paratyphi A isolated from culture</td>
<td>144/1</td>
<td>138/4</td>
<td>0</td>
</tr>
<tr>
<td>Positive pretreatment faecal cultures, numbers (%)</td>
<td>11/124 (8.9)</td>
<td>6/118 (5.1)</td>
<td>0</td>
</tr>
</tbody>
</table>

AST, Serum Aspartate Aminotransferase AST (normal range, 12-30 U/L)
ALT, Serum Alanine Aminotransferase ALT (normal range, 13-40 U/L)

Table 2-1. Baseline characteristics of culture confirmed (PP analysis) and culture negative typhoid fever patients
2.3.3 Protocol deviations

At one study site, the An Giang Provincial Hospital, the follow-up visit at 6 months was not possible due to logistic reasons. It was therefore agreed to carry out two follow-up visits at 1 and 3 months and to schedule additional (cross-sectional) follow-up dates to invite as many patients as possible to a third follow-up visit. From the PP population, 22 out of 91 patients in the gatifloxacin arm and 17 out of 87 patients in the azithromycin arm attended the third visit.

2.3.4 Primary outcomes

There was no significant difference in the resolution of fever (FCT) between the two treatment groups (Table 2-2).
<table>
<thead>
<tr>
<th>Outcome Type</th>
<th>Outcomes</th>
<th>Sub-Categories</th>
<th>Treatment group (n=287)</th>
<th>p-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primary</td>
<td>Fever Clearance Time in hours (95% CI)</td>
<td>106 (94-118)</td>
<td>106 (88-112)</td>
<td>0.984^</td>
</tr>
<tr>
<td>Secondary</td>
<td>Overall Treatment Failure, numbers of patients (%)</td>
<td>13/145 (9)</td>
<td>13/140 (9.3)*</td>
<td>0.854^</td>
</tr>
<tr>
<td></td>
<td>Did not complete full treatment course, n (%)</td>
<td>0</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Clinical failure, n (%)</td>
<td>6/145 (4.3)</td>
<td>6/140 (4.2)</td>
<td>1.000#</td>
</tr>
<tr>
<td></td>
<td>Microbiological failure, n (%)</td>
<td>2/145 (1.4)</td>
<td>3/140 (2.2)</td>
<td>0.680#</td>
</tr>
<tr>
<td></td>
<td>Typhoid-fever related complications, n (%)</td>
<td>0/145 (0)</td>
<td>8/140 (5.7)</td>
<td>0.003#</td>
</tr>
<tr>
<td></td>
<td>Gastrointestinal bleeding</td>
<td>0</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pneumonia</td>
<td>0</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Liver dysfunction</td>
<td>0</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Relapse after discharge from hospital, n (%)</td>
<td>4/137 (2.9)</td>
<td>0/127 (0)</td>
<td>0.052^</td>
</tr>
<tr>
<td></td>
<td>Number of patients with faecal carriage&amp; (%)</td>
<td>1/137 (0.7)</td>
<td>0/131 (0)</td>
<td></td>
</tr>
</tbody>
</table>

Patients can fail in more than one subcategory. *In the worst case scenario: 15/142 (10.6%) showed overall treatment failure in the azithromycin group, p = 0.570. ^The p value is based on the logrank test. #The p value is based on Fisher's exact test. &Evaluated in patients who attended at least two follow up visits.

Table 2-2. Primary and secondary outcomes of culture confirmed patients (PP analysis)
By PP analysis, the median FCT was 106 hours in both treatment arms (95% Confidence Interval [CI]; 94 to 118 hours for gatifloxacin versus 88 to 112 hours for azithromycin), (logrank test $p = 0.984$, HR = 1.0; 95% CI 0.80 to 1.26). The Kaplan-Meier survival curve for the fever clearance time is shown in Figure 2.3. At day 7, fever clearance rate was 82.8% (95% CI; 76.2% to 88.4%) in the gatifloxacin group and 80.5% (95% CI; 73.6 % to 86.6%) in the azithromycin group.

![Graph showing Kaplan-Meier survival curve for fever clearance time.](image)

**Figure 2.3** Proportion of culture confirmed patients still febrile.

Kaplan-Meier survival curve showing the proportion of culture confirmed patients (PP analysis) still febrile through time by treatment group.
In the ITT population, the median FCT was 100 hours in both treatment arms (95% CI; 92 to 106 hours for gatifloxacin versus 88 to 112 hours for azithromycin), (logrank test p = 0.914, HR = 1.01; 95% CI 0.82 to 1.25). At day 7, fever clearance rate was 84.2% (95% CI; 78.5% to 89%) in the gatifloxacin group and 82.6% (95% CI; 76.5% to 87.9%) in the azithromycin group (Figure 2.4).

Figure 2.4. Proportion of all randomised patients still febrile.

Kaplan-Meier survival curve showing the proportion of all randomised patients (ITT analysis) still febrile through time by treatment group.
2.4 Secondary outcomes

There was no death in the study. There was no significant difference in overall failure to treatment between the two groups (Table 2-2).

By PP analysis, the number of patients that showed overall failure to treatment was 13/145 (9%) in the gatifloxacin group and 13/140 (9.3%) in the azithromycin group (logrank test $p = 0.854$, HR = 0.93; 95% CI 0.43 to 2.0), or when assuming the worst case scenario, that all dropped-out patients were failures, 15/142 (10.6%) failures in the azithromycin group (logrank test $p = 0.570$, HR = 0.81; 95% CI 0.38 to 1.7). Figure 2.5 shows the proportion of patients failing through time after the start of treatment.

In the azithromycin arm, more than one failure event occurred in individual patients (Table 2-2). Clinical failure occurred in 6/145 (4.3%) patients in the gatifloxacin group and in 6/140 (4.2%) in the azithromycin group ($p = 1.000$, OR = 0.96; 95% CI 0.25 to 3.7). Three patients in each study arm were re-treated with ceftriaxone, the other patients resolved their symptoms within 24 hours.

Microbiological failure (defined as positive blood culture on day 8) was seen in 2 out of 145 patients in the gatifloxacin arm (1.4%) and in 3 out of 140 (2.2%) in the azithromycin arm ($p = 0.680$, OR = 0.64; 95% CI 0.05 to 5.7). Two of the azithromycin recipients showed additionally signs of clinical failure.

There were no typhoid fever-related complications in the 145 gatifloxacin patients compared to 8 out of 140 (5.7%) patients in the azithromycin arm ($p = 0.003$, OR = 0; 95% CI 0 to 0.4). Two azithromycin recipients developed signs of liver dysfunction
(elevated AST and ALT, deepening of jaundice) in addition to signs of clinical failure. Study treatment was continued and symptoms resolved by the time of discharge. Four patients, three children and one adult, suffered from gastrointestinal bleeding on day 3, day 5 (2 cases) and day 7 of treatment respectively, three patients received blood transfusions. One of these patients developed shock but responded to intravenous fluids and supportive treatment. Treatment was discontinued immediately in all the patients and re-treatment with ceftriaxone was initiated. Two adult patients developed pneumonia during treatment.
Figure 2.5 Proportion of patients with overall failure in the culture confirmed population.

Kaplan-Meier survival curve showing the proportion of patients with overall failure in the culture confirmed population (PP analysis) by treatment group.

Relapse was evaluated only in patients that were initially categorised as successfully treated, patients with clinical failure, microbiological failure or complications were not evaluated. Four patients out of 137 (2.9%) relapsed in the gatifloxacin group compared to none out of 127 in the azithromycin group (logrank test $p = 0.052$, HR = not
estimable due to zero observations in one group), (Figure 2.6). These relapses with symptoms suggestive of typhoid fever occurred on day 7, 11, 13 and 15 respectively, after completion of treatment, three patients were confirmed culture positive for *S. Typhi*. One patient developed acute respiratory distress syndrome (ARDS) and needed ventilation. The patient was treated with ceftriaxone and pefloxacine and subsequently made a complete recovery.
Figure 2.6 Proportion of patients with relapse in the culture confirmed population.

Kaplan-Meier survival curve showing the proportion of patients with relapse in the culture confirmed population (PP analysis) by treatment group.

Chronic faecal carriage was evaluated in patients who attended at least two follow-up appointments, 137 in the gatifloxacin group and 131 in the azithromycin group. Only one patient with chronic faecal carriage was detected after 6 months (An Giang study site), the patient had received gatifloxacin.
In the ITT analysis (all 358 randomised patients), overall treatment failure was reported in 13 out of 185 (7%) in the gatifloxacin group compared to 14 out of 168 (8.4%) in the azithromycin group (logrank test $p = 0.615$, HR = 0.82; 95% CI 0.39 to 1.76). One culture negative patient in the azithromycin group had a positive blood culture on day 7 after start of treatment. There were no clinical failures or typhoid fever-related complications in the culture negative patients.

2.4.1 Adverse events

Both treatments were well tolerated. One adverse event related to azithromycin was reported, a maculopapular rash that occurred after the first dose of treatment. Azithromycin was discontinued immediately and the patient was treated with ceftriaxone.

Gastrointestinal side effects (change in consistency and frequency of stools) that were probably typhoid fever related were relatively frequent in both treatment arms at the start of treatment. In the gatifloxacin group, one patient experienced vomiting on day 2 and day 3 and one patient experienced diarrhoea (4 episodes/day) on day 4 and day 5 of treatment. These episodes were self-limiting and did not require the interruption of therapy.

The median levels of serum AST and ALT fell in both groups after 7 days of therapy. In the PP group, the median post-treatment AST was 46.4 U/L (range 12.8 – 217.5) in the gatifloxacin arm and 45 U/L (range 5 – 358) in the azithromycin arm. The median post-treatment ALT fell to 46.8 U/L (range 7.4 – 278) and 49.9 (1.1 – 494),
respectively. In the culture-negative patients, the median post-treatment AST was 44.8 U/L (range 12 – 654) and ALT was 40 U/L (range 10 – 424.4).

2.4.2 Antimicrobial susceptibilities of S. Typhi and S. Paratyphi A isolates

From the PP population, 282 (98%) S. Typhi and 5 (2%) S. Paratyphi A strains were isolated. Two hundred and sixty three S. Typhi and five S. Paratyphi A were received at the Hospital for Tropical Diseases for antimicrobial susceptibility testing.

Fifty-eight percent of the S. Typhi isolates were MDR and 96% were nalidixic acid resistant and showed reduced susceptibility to the older generation fluoroquinolones (Table 2-3). However technically, using current CLSI breakpoints, all isolates remained susceptible in vitro to ciprofloxacin and ofloxacin. The MIC90 of gatifloxacin was the lowest of all the fluoroquinolones tested at 0.19 µg/mL (range 0.004 - 0.5). All isolates were susceptible to ceftriaxone.

The 5 S. Paratyphi A strains were fully susceptible to all the antimicrobials tested.
<table>
<thead>
<tr>
<th>Treatment with</th>
<th>All isolates</th>
<th>Gatifloxacin</th>
<th>Azithromycin</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n = 263</td>
<td>n = 137</td>
<td>n = 126</td>
</tr>
<tr>
<td>Multidrug resistant, numbers (%)</td>
<td>153 (57)</td>
<td>87 (63)</td>
<td>66 (50.8)</td>
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<tr>
<td>Nalidixic acid resistant, numbers (%)</td>
<td>254 (94.8)</td>
<td>132 (95.6)</td>
<td>121 (93)</td>
</tr>
<tr>
<td><strong>Amoxicillin (µg/ml)</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MIC 50</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
</tr>
<tr>
<td>MIC 90</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
</tr>
<tr>
<td>range</td>
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<td>0.5 to &gt;256</td>
<td>0.125 to &gt;256</td>
</tr>
<tr>
<td><strong>Chloramphenicol (µg/ml)</strong></td>
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<td></td>
<td></td>
</tr>
<tr>
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<tr>
<td>MIC 90</td>
<td>&gt;256</td>
<td>&gt;256</td>
<td>&gt;256</td>
</tr>
<tr>
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<td>2 to &gt;256</td>
<td>0.38 to &gt;256</td>
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<td><strong>Nalidixic acid (µg/ml)</strong></td>
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<td>0.75</td>
<td>1</td>
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<tr>
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<td>1.5</td>
<td>1.5</td>
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<td>0.32-2</td>
<td>0.23-2</td>
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<tr>
<td><strong>Ofloxacin (µg/ml)</strong></td>
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<td></td>
<td></td>
</tr>
<tr>
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<td>0.38</td>
<td>0.38</td>
</tr>
<tr>
<td>MIC 90</td>
<td>0.5</td>
<td>0.5</td>
<td>0.5</td>
</tr>
<tr>
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<td>0.006-0.75</td>
<td>0.004-0.38</td>
</tr>
<tr>
<td><strong>Gatifloxacin (µg/ml)</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
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<td>0.125</td>
<td>0.125</td>
<td>0.125</td>
</tr>
<tr>
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<td>0.19</td>
<td>0.19</td>
</tr>
<tr>
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<td>0.004-0.5</td>
</tr>
<tr>
<td><strong>Ceftriaxone (µg/ml)</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MIC 50</td>
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<td>0.125</td>
<td>0.125</td>
</tr>
<tr>
<td>MIC 90</td>
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<td>0.125</td>
<td>0.19</td>
</tr>
<tr>
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<td>0.064-0.25</td>
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<tr>
<td><strong>Azithromycin (µg/ml)</strong></td>
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<td></td>
</tr>
<tr>
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<tr>
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<td>12</td>
</tr>
<tr>
<td>range</td>
<td>1.5-16</td>
<td>1.5-16</td>
<td>4-16</td>
</tr>
</tbody>
</table>

Table 2-3 Antimicrobial susceptibilities and MICs of 263 S. Typhi isolates.

MIC\textsubscript{50/90}, at which 50% and 90% of the organisms are inhibited respectively. MDR is defined as resistance to chloramphenicol, ampicillin and trimethoprim-sulfamethoxazole. CLSI MIC breakpoints are as follows: for chloramphenicol, ampicillin and nalidixic acid resistance ≥ 32 µg/mL; ofloxacin and gatifloxacin ≤ 2 µg/mL susceptible and ≥ 8 µg/mL resistant; ciprofloxacin ≤ 1 µg/mL susceptible and ≥
4 μg/mL resistant; ceftriaxone ≤ 8 μg/mL susceptible and ≥ 64 μg/mL resistant; there are none for azithromycin.

2.5 Discussion

The results of this trial show that both antibiotics worked well for the treatment of MDR and nalidixic acid resistant typhoid fever in Vietnam. A seven day oral course of gatifloxacin had similar efficacy and safety as a seven day course of azithromycin, which is recommended for the treatment of MDR and nalidixic acid resistant typhoid fever (Chinh et al., 2000; World Health Organization, 2003).

However, azithromycin is not available throughout much of the developing world and it is expensive. The costs of a 7-day treatment course of gatifloxacin (at 10 mg/kg per day) for an adult patient in Vietnam were approximately 25 US$, the costs of azithromycin (at 20 mg/kg per day) were more than 90 US$.

The results for gatifloxacin in this trial are comparable to the excellent clinical outcomes achieved with ofloxacin in Vietnam in the early 1990s, when S. Typhi isolates were still nalidixic acid susceptible (Cao et al., 1999; Tran et al., 1995; Vinh et al., 1996).

Gatifloxacin has a higher affinity to GyrA and is less inhibited by the common mutations in the gyrA gene (Lu et al., 1999). The gatifloxacin MIC50 of the study isolates was 0.125 μg/mL compared to the ofloxacin MIC50 of 0.75 μg/mL. We would not recommend the continued use of the older generation fluoroquinolones (ofloxacin and ciprofloxacin) in regions with high rates of nalidixic acid resistant typhoid fever for
fear of selecting further mutations in gyrA (Tam et al., 2007). This could put at risk the potential clinical benefit of the newer fluoroquinolones, including gatifloxacin.

There have been several case reports of gatifloxacin-associated dysglycaemia in patients with type II diabetes mellitus, overweight or with other comorbidity (Ambrose et al., 2003; Baker and Hangii, 2002; Frothingham, 2005). There have been concerns about the use of gatifloxacin, after a retrospective case-control study in 1.4 million individuals over the age of 66 years (mean age 77 years) in Canada was published ((Park-Wyllie et al., 2006). Subsequently, the US FDA required a ‘Black Box’ warning to be added to the package insert information. Later, “Tequin” (gatifloxacin) was voluntarily withdrawn in the US, Canada and Japan.

However, gatifloxacin remains approved in many countries where enteric fever is endemic and drug resistant strains are present, including India, Vietnam, Nepal, Bangladesh and China. It is also still available as an ophthalmic solution for eye infections in Canada and the US (Olliaro P., 2011).

As our trial was completed before publication of this report (Park-Wyllie et al., 2006), we did not systematically monitor for hypo- and hyperglycaemia. Blood glucose levels taken as part of the routine care were normal. All patients were managed as in-patients and potential symptoms of hypo- and hyperglycaemia would have been noted by the study physicians. No dysglycaemia events were reported during the in-patient period or during the follow up period of 3 to 6 months.
The patients in our trial were healthy, young and non-obese individuals. In our setting and in our patient population gatifloxacin was highly effective despite very high rates of drug resistance and was well tolerated.

A trial in 867 children with otitis media with glucose monitoring and a one year follow-up (Pichichero et al., 2005), as well as two recent enteric (typhoid and paratyphoid) fever trial in Nepal used gatifloxacin and did not report any clinically relevant dysglycaemias (Arjyal et al., 2011; Pandit et al., 2007). Other newer generation fluoroquinolones, i.e. gemifloxacin and moxifloxacin have shown low MICs for nalidixic acid resistant S. Typhi and S. Paratyphi A (Maskey et al., 2006), unfortunately these drugs are not available in Vietnam and they are considerably more expensive. The *in vitro* results seen with these other newer generation fluoroquinolones should be evaluated in clinical trials.

The emergence of nalidixic acid resistant S. Typhi and S. Paratyphi A with reduced susceptibility to the fluoroquinolones is a widespread problem throughout Asia and therefore our study is relevant to the whole region (Bhan et al., 2005; Chau et al., 2007). Many case reports and some randomised controlled trials have described the worsening clinical response to ciprofloxacin and ofloxacin (Aarestrup et al., 2003; Kadhiravan et al., 2005; Parry et al., 2007).

The search for effective antibiotics to treat typhoid fever is imperative.

Typically trials in typhoid fever are limited by small sample sizes. A recent Cochrane review stressed the need for large well-designed trials in enteric fever (Thaver et al.,
2005). The evidence from our trial is strengthened by a sample size of 287 patients with culture confirmed typhoid fever (358 patients randomised). Both antibiotics also worked well for the patients with negative blood cultures. This is an important finding because the sensitivity of blood culture for the diagnosis of typhoid fever is only approximately 50 to 80% (World Health Organization, 2003).

One possible limitation of our trial was the low rate of stool cultures positive for *S. Typhi*. Faecal carriage is usually characterised by intermittent shedding and the stool culture for *S. Typhi* is not very sensitive. When comparing our data with other studies that demonstrate that azithromycin is highly efficacious for the treatment of typhoid fever, we find similar low rates of faecal carriage at follow-up (Chinh *et al*., 2000; Frenck *et al*., 2004). It could be hypothesized that antibiotics that show high intracellular concentrations and good tissue penetration like azithromycin and the fluoroquinolones, achieve rapid bacterial killing and elimination throughout the body, which reduces faecal carriage.

The dose of gatifloxacin and azithromycin tablets was prepared by careful cutting of the tablets (proportions of the tablets administered were recorded in the CRFs). Inevitably, it was therefore an estimation of the exact dose. Hence we cannot guarantee that each patient received exactly 10 mg/kg/day of gatifloxacin or 20 mg/kg/day of azithromycin.

A MEDLINE search for "azithromycin, clinical trial, typhoid/enteric fever" and the recent enteric fever Cochrane review (Thaver *et al*., 2008) identified 6 clinical trials in the literature. In total, 251 typhoid fever patients were treated with azithromycin.
Four trials, three from Egypt and one from India, used azithromycin to treat MDR typhoid fever (Butler et al., 1999; Frenck et al., 2000; Frenck et al., 2004; Girgis et al., 1999). Azithromycin achieved cure rates between 88% and 100%, the mean FCT ranged from 3.8 to 4.5 days. Two trials performed in Vietnam used azithromycin at 20 mg/kg/day (Chinh et al., 2000) and at 10 mg/kg/day (Parry et al., 2007) for the treatment of MDR and nalidixic acid resistant typhoid fever. In total, 107 patients with culture confirmed typhoid fever were enrolled. The cure rate was 93% and 82% and the FCT was 5.6 and 5.8 days, respectively. Our results concur with these excellent data.

Two recently completed trials conducted in Kathmandu, Nepal also used gatifloxacin at the same dose and duration for the treatment of nalidixic acid resistant typhoid and paratyphoid fever (Arjyal et al., 2011; Pandit et al., 2007). Both trials reported excellent results for patients treated with gatifloxacin. The first trial compared the efficacy of gatifloxacin versus cefixime (20 mg/kg per day given in two divided doses for 7 days) (Pandit et al., 2007). Successful treatment in the gatifloxacin group was achieved in 96.5% (85 out of 88) patients and the median FCT (95% CI) was 92 hours (84-114 hours). This trial was stopped early by the independent Data and Safety Monitoring Committee as a result of the poor clinical response in the patients randomised to cefixime. In the cefixime group the overall failure rate was 37.6 % (26 out of 70 patients) and the median FCT was 138 hours.

The second trial compared the efficacy of gatifloxacin versus chloramphenicol (75 mg/kg per day in four divided doses for 14 days) (Arjyal et al., 2011). Treatment failure occurred in 12 out of 177 patients (6.8%) in the gatifloxacin arm compared to 14 out of
175 (8%) in the chloramphenicol arm \((HR \ 0.86, \ 95\%\ CI \ 0.40\ \text{to} \ 1.86; \ p = 0.70)\). The median FCT was 3.9 days in both treatment groups.

I believe on the basis of this and other recently published trials, that gatifloxacin or azithromycin are now the treatments of choice for enteric fever in areas of MDR and nalidixic acid resistance (Arjyal \textit{et al.}, 2011; Chinh \textit{et al.}, 2000; Pandit \textit{et al.}, 2007; Parry \textit{et al.}, 2007). However it is important to use these antimicrobial agents sparingly (i.e. at the recommended dose and duration) because indiscriminate use would inevitably encourage further drug resistance.
Chapter 3

Population Pharmacodynamics and Population Pharmacokinetics of Gatifloxacin in Patients with Typhoid Fever
3.1 Introduction

3.1.1 Pharmacokinetics

Pharmacokinetics (PK) describes the changes of drug concentrations over time in the body. The concentration versus time is a result of the processes of adsorption, distribution, metabolism and elimination.

The appropriate use of antimicrobial agents requires an understanding of the characteristics of the drug, host factors and the pathogen. Pharmacokinetic studies describe parameters such as the peak serum concentration $C_{\text{max}}$, the serum half life $t_{1/2}$ and the cumulative exposure to an agent by the area under the concentration time curve (AUC) for a 24 hour period (McKinnon and Davis, 2004). Severe disease and sepsis can significantly alter the pharmacokinetics of drugs, especially distribution and elimination.

3.1.2 Pharmacodynamics

Pharmacodynamics (PD) describes the relationship between the drug exposure in serum, tissues and body fluids and the pharmacological and toxicological effects of the drugs (Craig, 2007). For antimicrobials, the success of a given drug dose depends on a measure of drug exposure (such as the area under the concentration-time curve, the serum peak concentration and the duration of time the serum concentrations exceed a certain level) and a measure of the potency of the drug against the infecting organisms, e.g. the minimum inhibitory concentration (MIC) or the minimum bactericidal concentration (Craig, 2001). The relationship between drug exposure and MIC of the
pathogen has been shown to be predictive of microbiological eradication, this is often summarised as exposure-response relationship (Craig, 2007).

PK/PD indices that are used as surrogate markers for clinical and antimicrobial efficacy are the ratio of peak plasma concentration (C\text{max}) of the antimicrobial to MIC of the pathogen (C\text{max}/\text{MIC}), the ratio of the area under the concentration/time curve 0 to 24 hours to the MIC (AUC\text{0-24}/\text{MIC}) and the time above MIC (T>MIC).

![Concentration versus time with MIC superimposed and pharmacokinetic and pharmacodynamic markers.](image)

**Figure 3.1** Concentration versus time with MIC superimposed and pharmacokinetic and pharmacodynamic markers.

From (McKinnon and Davis, 2004).

There is renewed interest in pharmacodynamic concepts as clinicians and scientists realise that our antimicrobial armamentarium is limited (Becker et al., 2006) and only few new antibiotics are likely to be developed.
PD concepts can help to determine how to best use current available antibiotics and how to prevent antibiotic resistance. Mathematical modelling and pharmacodynamics have demonstrated that it is possible to delineate a drug exposure that would prevent the emergence of mutant subpopulations (Jumbe et al., 2003).

3.1.3 Population pharmacokinetics and pharmacodynamics

Population pharmacokinetics and pharmacodynamics has been developed in the late 1980s and aims to quantify determinants of drug concentration (PK) or response (PD) in a population of patients (Sheiner and Ludden, 1992). In general, population PK models provide precise estimates of the variance and covariance between PK parameters, this is useful for subsequent simulation experiments and the models are applicable to sparse sampling strategies (Rubino et al., 2007). Various software programmes are available, including NONMEM (non-linear mixed effects model) which was developed by Lewis Sheiner and Stuart Beal and S-ADAPT, which performs Monte Carlo Expectation Maximization (MCPEM) algorithm, as well as Bayesian estimation (Bauer et al., 2007).

3.1.4 Patterns of antimicrobial killing

Antimicrobials exhibit two primary patterns of microbial killing (Graig, 2007). The first pattern is characterised by concentration dependent killing which occurs over a wide range of concentrations and also shows moderate to prolonged persistent effects. Higher drug concentrations result in a greater rate and extent of microbial killing. This pattern
is observed with the fluoroquinolones, aminoglycosides, daptomycin, ketolides, metronidazole and amphotericin B.

The second pattern is the time dependent (or minimal concentration dependent) killing. The extent of the microbial killing is primarily dependent on the duration of the exposure. The killing rate is saturated at low multiples of the MIC, usually around four or five times the MIC. Higher drug concentrations do not kill microbes faster or more extensively. Time dependent killing with minimal to none persistent effects are observed with β-lactam antibiotics and flucytosine. Macrolides, clindamycin, glycopeptides, tetracyclines and linezolid exhibit a time dependent pattern with moderate to prolonged persistent effects that can prevent re-growth of bacteria during the dosing interval (Graig, 2007).

3.1.5 The pharmacokinetics and pharmacodynamics of gatifloxacin

Gatifloxacin (see Chapter 1) is a broad spectrum 8-methoxy fluoroquinolone with enhanced activity against Gram positive and Gram negative organisms, anaerobes and mycobacteria, which received U.S. Food and Drug Administration (FDA) approval in 1999. In clinical trials, gatifloxacin was shown to be effective in the treatment of acute respiratory infections, including community-acquired pneumonia, acute exacerbation of chronic bronchitis, sinusitis and urinary tract infections in adults and otitis media in children (Capparelli et al., 2005).

Gatifloxacin is readily absorbed from the gastrointestinal tract, with an absolute bioavailability of approximately 96% (LaCreta et al., 2000). Gatifloxacin has a large
volume of distribution (approximately 1.8 L/kg), low protein binding (approximately 20%), broad tissue distribution and is primarily (more than 80%) excreted unchanged in the urine (Grasela, 2000b; Nakashima et al., 1995). It has an elimination half life of 8 to 10 hours, independently of the dose (Grasela, 2000b; Nakashima et al., 1995).

In a single dose study, gatifloxacin concentrations in serum reached a peak between 1 and 2 hours and the peak concentrations were 0.87, 1.71, 3.35, and 5.41 μg/ml at the doses of 100, 200, 400, and 600 mg, respectively (Nakashima et al., 1995).

The PK/PD profile of the fluoroquinolones has been well characterized (Ambrose et al., 2007). For fluoroquinolones, the area under the concentration-time curve at 24 hours to MIC ratio (AUC₀₋₂₄: MIC) has correlated most strongly with efficacy in animal and in vitro models and in patients with a variety of diseases (Ambrose et al., 2007). Studies by Forrest A. et al. evaluated intravenous ciprofloxacin for the treatment of pneumonia caused predominantly by Gram negative organisms and Pseudomonas aeruginosa in seriously ill patients (Forrest et al., 1993). At an AUC₀₋₂₄: MIC above 125 the probability of therapeutic response, defined as clinical and microbiological cure was 80%.

In patients with hospital acquired pneumonia treated with levofloxacin, patients in whom AUC₀₋₂₄: MIC ratios ≥ 87 were attained had a 90% probability of a positive microbiological response, while those with lesser exposures had only a 43% favourable response to therapy ($p = 0.01$) (Drusano et al., 2004).
In vitro gatifloxacin PK/PD data against S. Typhi suggest that similar AUC: MIC ratios (approximately 105) correlate with bacterial eradication (Booker et al., 2005).

However, no clinical PK/PD data exist for infections involving S. Typhi. This chapter describes the pharmacokinetics and pharmacodynamics of gatifloxacin and is divided into two sections. The first section uses data from a randomised controlled trial of gatifloxacin versus azithromycin (described in Chapter 2) for the treatment of typhoid fever in Vietnam, to model the relationship between drug exposure (AUC_{0-24}: MIC) and therapeutic response in patients treated with gatifloxacin and to identify appropriate susceptibility breakpoints for gatifloxacin. The current CLSI breakpoints for Enterobacteriaceae (including Salmonella) for ofloxacin and gatifloxacin are ≤ 2 mg/L susceptible and ≥ 8 mg/L resistant, for ciprofloxacin ≤ 1mg/L susceptible and ≥ 4 mg/L resistant (CLSI, 2007). The breakpoints for nalidixic acid are ≥ 32 mg/L (resistant) and ≤ 16 mg/L (susceptible). There has been discussion whether the current fluoroquinolone breakpoints are not too generous and therefore misleading clinicians (Aarestrup et al., 2003; Crump et al., 2003). The CLSI guidelines (2007) on the “Performance Standards for Antimicrobial Susceptibility testing” have responded to this criticism and recommend that extraintestinal Salmonella isolates should be screened for nalidixic acid resistance, and that in case of nalidixic acid resistance the physician should be informed that the isolate may not be eradicated by fluoroquinolone treatment (Institute, 2007).

However some of the newer fluoroquinolones do remain effective against nalidixic acid resistant S. Typhi infection and therefore this recommendation is leading clinicians
towards less effective treatments. Therefore a review of the breakpoints for *Salmonella* is necessary but prospective clinical and pharmacological data are lacking. We also determined the positive and negative predictive value of the nalidixic acid screening test for the clinical efficacy of gatifloxacin treatment in the same patient population.

The second section describes the pharmacokinetics of gatifloxacin in adult and paediatric patients with enteric fever in Nepal. Blood samples to measure gatifloxacin concentrations in Nepalese adults and children with enteric fever were obtained during a randomised trial of gatifloxacin *versus* chloramphenicol, described in the discussion of Chapter 2. The pharmacokinetics (PK) of gatifloxacin has been reported in healthy volunteers and in selected North American patient populations, who included adult patients with community-acquired respiratory tract infections and paediatric patients with acute or recurrent otitis media (Grasela, 2000a; Grasela et al., 1998; Rubino et al., 2007). However, the PK of gatifloxacin in adult and paediatric patients with enteric fever is unknown. Such data will be useful to construct exposure-response relationships for the efficacy of gatifloxacin in this patient population.

3.2 Materials and Methods

3.2.1 Section 1. Pharmacodynamics of gatifloxacin in adult and paediatric typhoid fever patients in Vietnam

3.2.1.1 Patients and procedures

Typhoid fever patients who were treated with an oral dose of 10 mg/kg/day of gatifloxacin (Tequin®, Bristol-Myers Squibb, USA; 400 mg/tablet) once daily for 7
days in a randomised clinical trial conducted in Vietnam were analysed (Trial registration: http://controlled-trials.com/ISRCTN67946944).

Patients, inclusion and exclusion criteria, procedures and outcomes have been described in detail in Chapter 2 of this thesis. In brief, favourable clinical response was defined as the resolution of fever and symptoms within 48 hours of the end of therapy (i.e. on day 10). Fever was evaluated every 6 hours. Relapse was defined as the recurrence of fever and symptoms and/or the isolation of S. Typhi from blood within 1 month after the completion of therapy. Patients were followed up at 1, 3 and 6 months, at these visits the recent history was obtained, physical examination carried out and stool cultures were performed to check for chronic faecal carriage of S. Typhi.

3.2.1.2 Antimicrobial susceptibility testing of S. Typhi

The antimicrobial susceptibility testing of S. Typhi has been described in chapter 2. Multidrug resistance was defined as resistance to ampicillin, chloramphenicol, and trimethoprim-sulfamethoxazole.

3.2.1.3 Drug exposure determination

For children under 16 years we used a previously validated population pharmacokinetic model to determine the drug exposure as expressed by the area under the concentration time curve at 24 hours (AUC$_{0-24}$) (Rubino et al., 2007). The PK model used is a one-compartment model with first order absorption and elimination, and linear relationships between body surface area (BSA) and apparent oral clearance (CL/F; where F is the oral bioavailability), and weight and apparent volume of distribution (V/F), respectively. We used patients' specific demographic and baseline information (age,
sex, weight, height and serum creatinine) to estimate individual patient drug exposures.

Body surface area (BSA) was calculated according to the method of Gehan and George (Gehan and George, 1970).

EQUATION 1: BSA (m²) = 0.0235 × Height (cm)⁰.⁴²²⁴⁶ × Weight (kg)⁰.⁵¹⁴⁵⁶

For patients below 16 years, clearance was estimated according to Rubino et al. (Rubino et al., 2007).

EQUATION 2: Clearance (<16 years) = 8.46 × body surface area

For patients above 16 years of age, creatinine clearance (CL_cr) was estimated according to the Cockcroft-Gault formula (Cockcroft and Gault, 1976), which estimates the glomerular filtration rate:

EQUATION 3: estCL_cr = (140 – age) × weight (kg) / 72 × serum creatinine (mg/dL) *

* Multiply with factor 0.85 if female

Clearance was estimated for patients above the age of 16 years according to Ambrose et al. (Ambrose et al., 2001).

EQUATION 4: Clearance (>16 years) = 8.11 + 0.0629 (creatinine clearance – 75.0)

The clearance estimates were then used in conjunction with dose to estimate gatifloxacin exposure AUC₀-₂₄ for each patient:

EQUATION 5: AUC₀-₂₄ = dose/clearance
The ratio of drug exposure to MIC (AUC\textsubscript{0-24}: MIC ratio) was calculated by dividing the AUC\textsubscript{0-24} by the MIC of the patient’s infecting *S. Typhi* isolate:

**EQUATION 6:** \( \text{AUC}_0-24 : \text{MIC ratio} = \frac{\text{AUC}_0-24}{\text{MIC}} \)

The analysis included all patients with sufficient data to estimate the AUC\textsubscript{0-24}, who were blood culture positive and for whom the gatifloxacin MICs of the infecting *S. Typhi* isolate was available.

### 3.2.1.4 Pharmacodynamic analysis

All statistical analyses were implemented in the statistical program SYSTAT 11, Richmond, CA. Univariate and multivariate logistic regression were used to evaluate the probability of clinical response. Multivariate logistic regression modelling was carried out using likelihood ratio testing and backwards stepping. Categorical breakpoint values for continuous variables, such as AUC\textsubscript{0-24}: MIC ratio, were determined by classification and regression tree (CART) analysis. Variables evaluated included age, sex, weight, multidrug resistance, AUC\textsubscript{0-24}, MIC, and AUC\textsubscript{0-24}: MIC ratio.

Stratified Kaplan-Meier and Cox proportional hazards regression analyses were used to examine the relationship between independent variables of interest and the time to fever resolution. The time until fever resolution was defined as the first time the patient’s axillary temperature was less than 37.5 °C and remained so for a minimum of 48 hours.
3.2.2 Section 2. Pharmacokinetics of gatifloxacin in paediatric and adult enteric fever patients in Nepal

3.2.2.1 Patient population, ethical approval, inclusion and exclusion criteria

Blood samples were collected during a randomised controlled trial comparing the efficacy and safety of an oral dose of 10 mg/kg/day of gatifloxacin (Broadband, Acme Formulation Private Limited, Solan, India; marketed by Novartis AG, Basel, Switzerland; 400 mg/tablet) once daily for 7 days versus an oral dose of 75 mg/kg/day of chloramphenicol (Chloro, National Healthcare, Nepal) in four divided doses for 14 days for the treatment of enteric fever.

The trial was conducted at Patan Hospital, Kathmandu, Nepal. Patients aged 2 years to 60 years with suspected enteric fever (more than 3 days of fever and clinically diagnosed typhoid fever) were invited to participate. The trial was approved by the Oxford University Tropical Research Ethics Committee and the Nepal Health Research Council. The trial registration number was ISRCTN53258327 (http://www.controlled-trials.com/ISRCTN53258327).

Patients who lived in a pre-designated area of approximately 20 square kilometres in urban Lalitpur and who gave fully informed written consent were eligible for the study. Exclusion criteria were pregnancy or lactation, age under 2 years or weight less than 10 kg, shock, jaundice, gastrointestinal bleeding or any other signs of severe typhoid fever, previous history of hypersensitivity to either of the trial drugs, known previous treatment with chloramphenicol, quinolone antibiotic or third generation cephalosporin or macrolide within one week of hospital admission. Patients who had received
amoxicillin or cotrimoxazole were included as long as they did not show evidence of clinical response.

3.2.2.2 Procedures

Patients were enrolled into the study by dedicated physicians at Patan hospital, who took a full history and carried out the clinical examination. Once the study physicians had enrolled the patient, they were managed as outpatients. Trained community medical auxiliaries (CMAs) visited each patient’s house every 12 hours until the patient was cured, as described previously (Pandit et al., 2007). At each visit the CMAs recorded oral temperature, inquired about symptoms and directly observed each patient ingesting the single dose of gatifloxacin and the two doses of chloramphenicol coinciding with their daily visits.

Patients were re-examined by the study physicians at Patan Hospital on day 8 and blood and stool cultures were collected if the initial blood culture was positive. Patients also visited the study physicians on day 15, and at one, three and six months. At these visits stool of blood culture positive patients was checked for faecal carriage. Also febrile illnesses in household members were inquired. Random plasma glucose was measured on day 1, days 2 to 7 (using finger prick testing using OneTouch SureStep, Johnson & Johnson, USA during the CMAs’ evening visits), on day 8, day 15 and one month. Haemoglobin A1C was measured at three months. Full blood counts, liver enzymes and creatinine were studied on days 1, 8, and 15.
3.2.2.3 Outcomes

In brief, favourable clinical response was defined as the resolution of fever and symptoms within 48 hours of the end of therapy (i.e. on day 10). Fever was evaluated every 12 hours. Relapse was defined as the recurrence of fever and symptoms and/or the isolation of S. Typhi or S. Paratyphi A from blood within 1 month after the completion of therapy. At the 1, 3 and 6 months follow up visits, stool cultures were performed to check for chronic faecal carriage of S. Typhi or S. Paratyphi A.

3.2.2.4 Blood samples and sparse plasma sampling schedule

Blood sampling was performed in steady state concentrations. Steady state concentrations describe equilibrium between administration and elimination, which is usually reached after 5 drug half lives. For gatifloxacin with a half life of approximately 8 hours, steady state is reached after administration of the second dose.

Two ml of blood were collected into lithium heparin tubes using a sparse sampling scheme. The first of two samples was taken 3 to 6 hours after administration of the third or a later dose and the second sample was taken 12 to 24 hours after the third or a later dose. Blood tubes were inverted several times and immediately placed on ice. Samples were processed as soon as possible after collection. The samples were centrifuged for 10 minutes at 100 x g in a centrifuge which cups have been chilled. The plasma layer was transferred to polypropylene screw-capped tubes and labelled with the study number, study day, date and the actual sampling time. Plasma and cell pellets were immediately stored at -80°C. Information about each blood sample (date, time), the
exact time and doses (in mg; all tablets were weighed before administration) of all
previous gatifloxacin administrations were recorded in a spreadsheet.

For children, one sample was taken 6 to 24 hours after the third dose. Sampling times
were spread out to allow for the best possible validation using a single sample.

3.2.2.5 Gatifloxacin assay

Human plasma samples (50 μl) were deproteinated with 250 μl acetonitrile. The
samples were centrifuged and an aliquot of the supernatant (50 μl) was transferred into
an autosampler vial containing 1 ml of HPLC water.

Samples were analyzed by high pressure liquid chromatography tandem mass
spectrometry (LC/MS/MS). The LC/MS/MS system consists of a Shimadzu
Prominence HPLC system and an Applied Biosystems/MDS Sciex API5000
LC/MS/MS.

Chromatographic separation was performed using a Phenomenex Luna Phenyl-Hexyl
column, 5 μm, 150 x 3.0 mm column and a mobile phase consisting of 85% 0.1%
formic acid in water and 15% 0.1% formic acid in acetonitrile, at a flow rate of 0.75
ml/min. Gatifloxacin concentrations were obtained using LC/MS/MS monitoring the
MS/MS transition m/z 376 → m/z 332. Analysis run time was 4.0 minutes.

The assay was linear over a range of 0.050 to 10.0 μg/ml (r² > 0.996). The inter-day
precision (%CV) ranged from 2.61 to 9.69%, with an accuracy ranging from 106% to
111% on quality control samples at three levels (0.10 μg/ml, 1.00 μg/ml, and 8.00
μg/ml) in replicates of three at each level on each analysis day.
3.2.2.6 Development of a population pharmacokinetic model

Population PK datasets were constructed using the exact dose and sampling times. The data were vetted for the presence of errors in dose and/or sampling times. Potential outlier concentrations were explored using accepted methodology.

Separate population pharmacokinetic candidate models for adults (>16 years of age) and paediatric patients (≤16 years of age) were fit to the data using Monte-Carlo parametric expectation maximization (MCPEM) as implemented in the open-source software program S-ADAPT, which was written by Robert J. Bauer and is available at http://bmsr.usc.edu/Software/ADAPT/SADAPTSOFTWARE.html (Bauer and Guzy, 2004). The program performs parametric population analysis, including maximum likelihood estimation, via the Expectation Maximization (EM) algorithm with sampling as implemented in the Monte Carlo Expectation Maximization (MCPEM) algorithm, as well as Bayesian estimation (University of South Carolina, 2009).

Due to the sparse nature of the PK sampling scheme, the structure and covariate relationships from previous gatifloxacin adult and paediatric population PK models derived from North American patients were retained, but were revised to fit the data from this population (Grasela, 2000a; Grasela et al., 1998; Rubino et al., 2007).

These PK models had the structure of one compartment models with first-order absorption and elimination.

The equations and covariate relationships are provided below.
For the adult patients (>16 years) the following equations were used to estimate total clearance (CLt) and central volume of distribution (Vc). Creatinine clearance (CLcr) was calculated using the method of Cockcroft and Gault (Cockcroft and Gault, 1976).

\[ CLt (L/hr) = CLt-intercept + CLt-slope \times CLcr (ml/min/1.73m^2) \]

\[ Vc (L) = Vc-slope \times \text{Body Weight (kg)} \]

The following equations were used for the paediatric patients (≤ 16 years) to estimate total clearance (CLt) and central volume of distribution (Vc). Body surface area (BSA) was estimated according to the Gehan and George method (Gehan and George, 1970).

\[ CLt (L/hr) = CLt-slope \times BSA (m^2) \]

\[ Vc (L) = Vc-slope \times \text{Body Weight (kg)} \]

3.3 Results

3.3.1 Section 1. Pharmacodynamics of gatifloxacin in adult and paediatric typhoid fever patients in Vietnam

3.3.1.1 Patient population and clinical data

Of the 186 patients randomised to receive gatifloxacin therapy in this trial, 185 could be evaluated for this analysis. Of these, 144 patients were blood culture positive for S. Typhi and 124 patients had sufficient data to estimate gatifloxacin exposure.

These 124 patients represent the population used in all pharmacodynamic analyses. Sixty three patients were male and 61 were female; their mean (standard deviation, SD)
Age was 11.3 (5.48) years; their mean (SD) weight was 27.8 (12.4) kg; and their mean (SD) body surface area was 1.02 (0.299) m². Nine of the 124 (7%) patients had positive bone marrow cultures for S. Typhi in addition to their positive blood cultures. Five (6/124) percent of patients were infected with nalidixic acid susceptible (MIC ≤ 16 mg/L) and 95% (118/124) with nalidixic acid resistant (MIC ≥32 mg/L) S. Typhi strains. Sixty one (76/124) percent of patients were infected with multidrug resistant S. Typhi strains.

The median (range) gatifloxacin MIC of S. Typhi isolates was 0.018 (0.006-0.09) mg/L for nalidixic acid susceptible isolates and 0.12 (0.06-0.25) mg/L for nalidixic acid resistant isolates. The median (range) ciprofloxacin MIC value for nalidixic acid susceptible S. Typhi isolates was 0.014 (0.006-0.12) mg/L and for nalidixic acid resistant isolates was 0.38 (0.12-0.75) mg/L.

3.3.1.2 Pharmacodynamic analysis
Clearance estimates from previously validated adult and paediatric population pharmacokinetic models were used in conjunction with the dose to obtain an estimate for AUC (Ambrose et al., 2001; Rubino et al., 2007).

In these typhoid fever patients, there was a statistically significant relationship between the intensity of the drug exposure to gatifloxacin and clinical response.
<table>
<thead>
<tr>
<th>Risk Factor</th>
<th>$p$ value</th>
<th>Risk Factor</th>
<th>$p$ value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>0.206</td>
<td>MDR</td>
<td>0.867</td>
</tr>
<tr>
<td>Sex</td>
<td>0.795</td>
<td>AUC$^1$</td>
<td>0.519</td>
</tr>
<tr>
<td>Weight</td>
<td>0.136</td>
<td>AUC$^2$</td>
<td>0.0833</td>
</tr>
<tr>
<td>S. Typhi in bone marrow</td>
<td>0.165</td>
<td>MIC$^1$</td>
<td>0.0256</td>
</tr>
<tr>
<td></td>
<td></td>
<td>MIC$^2$</td>
<td>0.0716</td>
</tr>
<tr>
<td></td>
<td></td>
<td>AUC:MIC$^1$</td>
<td>0.0849</td>
</tr>
<tr>
<td></td>
<td></td>
<td>AUC:MIC$^2$</td>
<td>0.0243</td>
</tr>
</tbody>
</table>

$^1$Treated as a continuous variable  
$^2$Treated as a categorical variable

Table 3-1 Univariate logistic regression analysis results.

Risk factors were tested for association with clinical response in typhoid fever patients ($n = 124$) using univariate logistic regression analysis.

We could identify a significant dichotomous categorical breakpoint for $\text{AUC}_{0-24}: \text{MIC}$ ratio which was predictive of clinical success. Patients in whom an $\text{AUC}_{0-24}: \text{MIC}$ ratio of greater than 92.7 was obtained, had a favourable response to treatment in 93.5%, whilst in patients with $\text{AUC}_{0-24}: \text{MIC}$ ratios $\leq 92.7$ only 75% had a favourable response ($\text{Odds Ratio} = 4.81$, 95% CI 1.23-18.9; $p = 0.02$) (Figure 3.2).
Figure 3.2 Relationship between gatifloxacin exposure and clinical response in typhoid fever patients.

Univariate logistic regression analysis with AUC: MIC as a continuous variable, for AUC: MIC breakpoint (92.7); $p = 0.02$.

The mean time to fever resolution was 113 hours in patients in whom AUC$_{0-24}$: MIC ratios greater than 92.7 were attained, compared to 142 hours in those patients with lesser exposures ($p = 0.08$) (Figure 3.3). The proportion of patients who had a positive clinical response was 91% (113/124) for all patients. All six patients infected with nalidixic acid susceptible strains had successful clinical response to therapy; while 91% (107/118) of those patients infected with nalidixic acid resistant strains had a positive
therapeutic response (Fisher exact test $p = 1.0$). Similarly high cure rates of 91% (69/76) were obtained among the patients infected with multidrug resistant S. Typhi.

![Mean time to fever resolution: 113 vs. 142 hrs $P = 0.08$](image)

**Figure 3.3 Kaplan-Meier survival curve.**

The Kaplan-Meier survival curve shows the proportion of culture confirmed patients still febrile through time stratified by AUC$_{0-24}$: MIC ratio breakpoint. The mean time to fever resolution tended to be shorter in patients with AUC$_{0-24}$: MIC $> 92.7$ (blue line) than those patients with AUC0-24: MIC ratios $\leq 92.7$ (red line).

We could identify a borderline significant dichotomous categorical gatifloxacin MIC breakpoint for S. Typhi, which was predictive for clinical response. S. Typhi gatifloxacin MIC values $\geq 0.19$ mg/L were associated with 83.8% of patients having a
positive clinical response, while patients with gatifloxacin MIC values less than 0.19 mg/L had in 94.3% positive response \((p = 0.0716; \text{ odds ratio } 3.17, 95\% \text{ CI } 0.93-11.2)\). The positive (predicts success) and negative (predicts failure) predictive value of the nalidixic acid screening test for gatifloxacin treatment was 100% and 9.3%, respectively.

3.3.2 Section 2. Pharmacokinetics of gatifloxacin in paediatric and adult enteric fever patients in Nepal

3.3.2.1 Patient population and blood samples

Thirty six patients (aged 3 to 54 years) participated in the PK study and contributed 68 plasma samples for the population pharmacokinetic analysis. The majority of patients (31 [86\%] out of 36) contributed at least two samples. Seventeen adult patients contributed 31 PK samples and 19 paediatric patients contributed 37 PK samples. The median age of the 19 children was 10 years (range 5 to 16) and that of the 17 adult patients was 23 years (range 17 to 54 years), respectively. The following co-variables were analysed: age, sex, weight, height, body surface area (BSA), and serum creatinine concentrations. The demographic characteristics of the 36 patients are shown in Table 3-2.
<table>
<thead>
<tr>
<th>Variable</th>
<th>Population</th>
<th>N</th>
<th>Mean (SD)</th>
<th>Median</th>
<th>Range</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Age (years)</strong></td>
<td>Adults</td>
<td>17</td>
<td>27.4 (10.6)</td>
<td>23.0</td>
<td>17.0 - 54.0</td>
</tr>
<tr>
<td></td>
<td>Children</td>
<td>19</td>
<td>10.5 (3.01)</td>
<td>10.0</td>
<td>5.0 - 16.0</td>
</tr>
<tr>
<td><strong>Weight (kg)</strong></td>
<td>Adults</td>
<td>17</td>
<td>56.6 (9.28)</td>
<td>53.0</td>
<td>44.0 - 72.0</td>
</tr>
<tr>
<td></td>
<td>Children</td>
<td>19</td>
<td>26.9 (8.87)</td>
<td>25.0</td>
<td>15.0 - 50.0</td>
</tr>
<tr>
<td><strong>BSA (m²)</strong></td>
<td>Adults</td>
<td>17</td>
<td>1.61 (0.152)</td>
<td>1.58</td>
<td>1.36 - 1.87</td>
</tr>
<tr>
<td></td>
<td>Children</td>
<td>19</td>
<td>0.999 (0.212)</td>
<td>0.955</td>
<td>0.665 - 1.53</td>
</tr>
<tr>
<td><strong>CLcr (mL/min/1.73m²)</strong>*</td>
<td>Adults</td>
<td>17</td>
<td>67.1 (12.2)</td>
<td>69.4</td>
<td>46.2 - 93.0</td>
</tr>
<tr>
<td></td>
<td>Children</td>
<td>19</td>
<td>79.6 (11.8)</td>
<td>79.8</td>
<td>56.7 - 104</td>
</tr>
</tbody>
</table>

n number of patients

*a* calculated using the method of Cockcroft and Gault (Cockcroft and Gault, 1976)

*b* calculated using the Schwartz equation (Schwartz et al., 1976)

Table 3-2 Demographic characteristics of the adult and paediatric pharmacokinetic analysis population

### 3.3.2.2 Pharmacokinetic analysis and population pharmacokinetic model

Gatifloxacin pharmacokinetics was best fit by a linear one compartment model with first order absorption and elimination. Fits of data were excellent ($R^2 > 0.9$ for paediatric and adult data); the inter-individual variability in pharmacokinetics was modest. None of the gatifloxacin concentrations were deemed to be significant outliers.

Standard diagnostic goodness-of-fit and weighted residual plots were employed to establish whether the pharmacokinetic model was adequate for describing the data. Figure 3.4 shows the goodness-of-fit plots for the observed versus the individual fitted
gatifloxacin concentrations for the final adult (Panel A) and paediatric population (Panel B) PK model, respectively. Panels C and D are the plots of individual weighted residuals versus individual fitted gatifloxacin concentrations for the final adult and paediatric population PK models, respectively.

Figure 3.5 shows a scatter plot of gatifloxacin concentrations (μg/ml) measured in blood versus the time since the previous dose was administered for adult and paediatric patients, respectively. Gatifloxacin steady state concentrations measured at 3 hours after the previous dose ranged from 4.5 μg/ml to 8.9 μg/ml in children and from 5 μg/ml to 9.8 μg/ml in adults, respectively.

Table 3-3 presents the final population pharmacokinetic parameter estimates for the adult and paediatric data. Given the relatively small size of the datasets and the sparseness of the sampling scheme, the precision of parameter estimates was acceptable.

We compared the gatifloxacin PK parameter estimates between the previous PK models, developed from North American patients/subjects and those resulting from the application of this model to Nepalese patients with enteric fever (Table 3-4). Compared to the North American children with otitis media (Rubino et al., 2007), the Nepalese paediatric enteric fever patients had approximately 50% slower clearance (Table 3-4). The distributions of age and body surface area (BSA) were similar between the North American and Nepalese paediatric populations, but the Nepalese population had higher serum creatinine values, suggesting comparatively lower renal function (Figure 3.6).
Figure 3.4 Goodness-of-fit plots.

Goodness-of-fit plots for the observed versus the individual fitted gatifloxacin concentrations for the final adult (Panel A) and paediatric population (Panel B) PK model, respectively. Panels C and D are the plots of individual weighted residuals.
versus individual fitted gatifloxacin concentrations for the final adult and paediatric population PK models, respectively.

Figure 3.5 Scatter plot of gatifloxacin concentrations versus time since the last dose, stratified by population.

Adult patients (red squares) are defined as age above 16 years, paediatric patients (grey dots) as age ≤ 16 years.
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Adult Population PK Model&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Pediatric Population PK Model&lt;sup&gt;b&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Population Mean</td>
<td>Magnitude of Interindividual Variability (%CV)</td>
</tr>
<tr>
<td></td>
<td>Final Estimate</td>
<td>%SEM</td>
</tr>
<tr>
<td>Ka (1/hr)</td>
<td>3.34</td>
<td>116</td>
</tr>
<tr>
<td>Vc/F (L/kg)</td>
<td>1.28</td>
<td>17.7</td>
</tr>
<tr>
<td>CL/F, non-renal (L/hr)</td>
<td>2.91</td>
<td>21.9</td>
</tr>
<tr>
<td>CL/F, renal slope&lt;sup&gt;c&lt;/sup&gt; (L/hr/mL/min)</td>
<td>0.0629</td>
<td>-</td>
</tr>
<tr>
<td>CL/F(L/hr/m²)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>SD&lt;sub&gt;sl&lt;/sub&gt;</td>
<td>0.250</td>
<td>17.2</td>
</tr>
</tbody>
</table>

<sup>a</sup>Minimum value of the objective function = 6.34; <sup>b</sup>Minimum value of the objective function = -6.50; <sup>c</sup>This parameter was not fit due to the narrow range of renal function in this population; Ka absorption rate constant; Vc/F central volume of distribution; CL/F apparent oral clearance; SD<sub>sl</sub> standard deviation of the slope

Table 3-3 Final PK parameter estimates and associated standard errors for the adult and paediatric population PK models
### Table 3-4 Comparison of gatifloxacin PK parameters.

Comparison of gatifloxacin PK parameters between previous PK models (developed from North American patients/subjects) and the application of this model in the analysis of Nepalese patients with enteric fever (current data).

<table>
<thead>
<tr>
<th>Patient population</th>
<th>PK parameter</th>
<th>Mean (%SEM) parameter estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Paediatric</td>
<td>CL/F (L/h/m²)</td>
<td>Previous models</td>
</tr>
<tr>
<td></td>
<td>8.46 (3.50)</td>
<td>4.41 (5.65)</td>
</tr>
<tr>
<td></td>
<td>Vc (L/kg)</td>
<td>2.15 (3.30)</td>
</tr>
<tr>
<td></td>
<td>CL/F, nonrenal (L/h)</td>
<td>8.11 (35.3)</td>
</tr>
<tr>
<td>Adult</td>
<td>CL/F, renal-slope (L/h/mL/min)</td>
<td>0.0629 (37.8)</td>
</tr>
<tr>
<td></td>
<td>Vc (L/kg)</td>
<td>1.45 (7.9)</td>
</tr>
</tbody>
</table>

Vc central volume of distribution; CL/F apparent oral clearance
Figure 3.6 Box plots of age, serum creatinine (in mg/dl) and body surface area (BSA) in paediatric patients.

The data are stratified by population (Nepal = current analysis, US = model development population). The line inside the box represents the median, the upper and lower limits of the box are the 75th and 25th percentiles, respectively, and the upper and lower error bars indicate the values that are 1.5 times the inter-quartile range.
Individual points outside the error bars represent values that are >1.5 times the inter-quartile range (i.e., outliers).

### 3.4 Discussion

This chapter describes two studies that analyse the pharmacodynamic (section 1 of this chapter) and the pharmacokinetic profile (section 2) of gatifloxacin in patients infected with *S.* Typhi and *S.* Paratyphi A.

The first study had two objectives, to examine the relationship between gatifloxacin exposure and clinical efficacy and to determine the positive and negative predictive value of the nalidixic acid screening test for the clinical efficacy of gatifloxacin in the same patient population. A relationship between exposure to gatifloxacin and clinical response was identified. In patients in whom an AUC$_{0-24}$: MIC ratio of greater than 92.7 was attained, 93.5% were classified as clinically cured, while in patients in whom AUC$_{0-24}$: MIC ratios of less than or equal to 92.7 were achieved only 75% of patients had a favourable response (Odds Ratio = 4.81, 95% CI 1.23 - 18.9; *p* = 0.02). These findings are supported by clinical (Drusano *et al.*, 2004; Forrest *et al.*, 1993) and non-clinical studies (Booker *et al.*, 2005). A study in critically ill patients infected with Gram negative enteric pathogens and *Pseudomonas aeruginosa* (Forrest *et al.*, 1993) treated with intravenous ciprofloxacin, concluded that achieving an AUC$_{0-24}$: MIC ratio of greater than 125 was associated with improved clinical outcomes. Drusano *et al.* showed that an AUC$_{0-24}$: MIC ratio of greater than 100 also prevented the emergence of bacterial resistance, particularly in the critically ill (Drusano *et al.*, 2004).
In a one compartment in vitro pharmacodynamic model of gatifloxacin and S. Typhi, a \( fAUC_{0-24}:MIC \) ratio of 105 correlated with 90% bacterial eradication (Booker et al., 2005). Importantly, the relationship between exposure and response based on this model did not differ for a strain that was gatifloxacin susceptible (MIC 0.5 mg/L) and one that was resistant (MIC 4.0 mg/L), despite the latter having two GyrA (Ser83\( \rightarrow \)Tyr; Asp87\( \rightarrow \)Gly) and two ParC (Thr 57\( \rightarrow \)Ser; Ser80\( \rightarrow \)Ile) mutations. This observation is supported by a neutropenic murine thigh infection model involving Salmonella and levofloxacin, where the AUC\(_{0-24}:MIC\) ratios necessary for net bacterial stasis or a 90% reduction in bacterial burden did not differ by nalidixic acid susceptibility status (Craig et al., 2006).

Patients in whom AUC\(_{0-24}:MIC\) ratios greater than 92.7 were attained also tended towards a more rapid time (29 hours) to fever resolution \((p = 0.08)\). Administering drugs in a manner that leads to clinical improvements, such as fever and symptom resolution or the more rapid eradication of faecal pathogens, may have profound public health implications. As large epidemics are often related to faecal contamination of food and water supplies, decreasing the duration of S. Typhi shedding may limit secondary infections ((Luxemburger et al., 2001). Perhaps more importantly, it has been demonstrated that for fluoroquinolones and other Enterobacteriaceae and P. aeruginosa, it is possible to suppress the emergence of resistant subpopulations by administering high intensity (e.g. large AUC\(_{0-24}:MIC\) ratio) regimens for shorter durations (Jumbe et al., 2003).
The predictive value of the nalidixic acid screening test for gatifloxacin in patients with typhoid fever was poor \( (p = 1.0) \). While all patients infected with nalidixic acid susceptible strains were treated successfully, so were 90.7\% of patients infected with nalidixic acid resistant strains.

This is not true for the older generation fluoroquinolones such as ofloxacin and ciprofloxacin for which the nalidixic acid screening test was highly predictive of clinical success in the treatment of typhoid fever (Parry, 2004a). This observation has important clinical implications, as current CLSI guidelines state that “Fluoroquinolone-susceptible strains of Salmonella that test resistant to nalidixic acid may be associated with clinical failure or delayed response in fluoroquinolone-treated patients with extra-intestinal Salmonellosis. Extra-intestinal isolates of Salmonella should also be tested for resistance to nalidixic acid. For isolates that test susceptible to fluoroquinolones and resistant to nalidixic acid, the physician should be informed that the isolate may not be eradicated by fluoroquinolone treatment” (CLSI, 2007). As fluoroquinolones are associated with higher cure rates and more rapid fever resolution than other agents (Parry et al., 2002), these CLSI guidelines may direct clinicians to use other suboptimal antimicrobial therapies.

The explanation for the failure of the nalidixic acid screening test to predict gatifloxacin efficacy likely relates to the methoxy group at the 8-position of the quinolone bicyclic aromatic core of gatifloxacin. The C-8 methoxy group allows for dual enzymatic targeting of DNA gyrase and DNA topoisomerase IV in Escherichia coli, which results in a modest MIC increase in DNA gyrase mutants (Lu et al., 1999). This is exemplified
by the ratio of median MIC of nalidixic acid susceptible strains to the median MIC of resistant strains which was 7-fold for gatifloxacin compared to 27-fold for ciprofloxacin.

This data represent, to our knowledge, the first clinical validation of the importance of this structure-activity relationship for Enterobacteriaceae and highlights that not all fluoroquinolones are the same. The poorer clinical responses to the older fluoroquinolones now reported for enteric fever should not be extrapolated to the latest generation of drugs from this class.

Finally, these clinical data suggest gatifloxacin, and perhaps other 8-methoxy fluoroquinolone, specific susceptibility breakpoints. Gatifloxacin MIC values ≥ 0.19 mg/L were associated with 83.8% of patients having a positive clinical response, while patients with MIC values less than 0.19 mg/L had a 94.3% positive response \( (p = 0.0716) \). This MIC breakpoint is similar to that derived from the aforementioned in vitro PK/PD S. Typhi infection model and Monte Carlo simulation (Booker et al., 2005). Simulation results suggested susceptible breakpoint of 0.12 mg/L for gatifloxacin. Moreover, these data indicate that the nalidixic acid screening test does not predict gatifloxacin efficacy. Gatifloxacin attained high favourable clinical response rates regardless of nalidixic acid susceptibility or multidrug resistance status. Continued use of this screening test to predict gatifloxacin efficacy, and perhaps that of other 8-methoxy fluoroquinolones, may drive clinical use away from effective treatment regimens to less effective regimens. One possible remedy is the use of S. Typhi specific susceptibility breakpoints, which to date have not been determined by the CLSI.
As drug clearance was markedly lower in Nepalese enteric fever patients compared to North American infected patients, these data demonstrate the importance of evaluating pharmacokinetics in different patient populations. The PK models described in this chapter will be used in future pharmacokinetics-pharmacodynamics analyses of efficacy in Asian populations with enteric fever.
Chapter 4

High throughput genotyping of *S. Typhi* strains isolated in the Mekong Delta region of Vietnam
4.1 Introduction

*S.* Typhi is a recently evolved and genetically monomorphic organism. *S.* Typhi is exceptional amongst the 2400 serovars of *S.* enterica, as it doesn’t have a promiscuous life style infecting a wide range of animals and has an ecologically adapted niche as a human invasive pathogen. This host restriction has been attributed to the acquisition of several *Salmonella* pathogenicity islands (SPIs) and the accumulation of pseudogenes (Achtman, 2008; Parkhill et al., 2001a).

The *S.* Typhi genome contains several large insertions, which encode virulence-associated genes, the *Salmonella* pathogenicity islands (SPI) (Parkhill et al., 2001a). Bacterial pathogenicity islands often exhibit features of mobile genetic elements (Hou, 1999) and are believed to be acquired through recent horizontal acquisition from other bacteria. Features of SPIs include a GC content that differs from that of the rest of the bacterial genomes, the presence of flanking direct repeats and insertion elements that are reminiscent of those of phages and plasmids and the ability to encode ‘mobility genes’, such as integrases, transposases and origins of plasmid replication (Hou, 1999). Often these elements overlap with tRNA genes suggesting that the 3’ sites of transfer RNAs may serve as recombination site for pathogenicity islands (Hou, 1999).

Two hundred and four pseudogenes have been described in the genome of *S.* Typhi strain CT 18 (Parkhill et al., 2001a). Most of these pseudogenes have been introduced by a single frameshift or stop codon and many of these pseudogenes are found in housekeeping genes and genes that are potentially involved in virulence (Parkhill et al., 2001a).
As a young and monophyletic organism, *S. Typhi* shows little DNA sequence variation. The analysis of a global collection of 334 *S. Typhi* isolates by multilocus enzyme electrophoresis (MLEE), which tested 24 conserved neutral cytoplasmic enzymes for variation in charge identified only two multilocus enzyme genotypes (Selander *et al.*, 1990). Multi Locus Sequence Typing (MLST) of seven *S. Typhi* housekeeping genes also demonstrated that genetic polymorphisms were rare in *S. Typhi* (Kidgell *et al.*, 2002b). Only three polymorphic sites were found when seven genes from a diverse collection of 26 *S. Typhi* isolates were sequenced. It was estimated that the last common ancestor of *S. Typhi* is approximately 50,000 years (Kidgell *et al.*, 2002b).

For epidemiological purposes to identify genetic relationship of isolates, especially in outbreak situations and to trace sources of infection, different typing schemes for *S. Typhi* have been deployed. These include Pulsed Field Gel Electrophoresis (PFGE) (Thong *et al.*, 1994; Thong *et al.*, 1995), Variable Number of Tandem Repeat (VNTR) analysis (Liu *et al.*, 2003), IS200 typing (Threlfall *et al.*, 1994) and ribotyping ((Navarro *et al.*, 1996)). These typing schemes can identify multiple variants and can capture strain variation and properties, especially in outbreak situations. It has been shown that differences in PFGE and ribotype patterns of *S. Typhi* reflect the genomic rearrangement of the chromosome through recombination between rRNA loci (Ng *et al.*, 1999). Also the modular nature and distribution of prophages can contribute significantly to strain variation (Hou, 1999). However, whilst these techniques capture variation, there are some disadvantages, as they are difficult to standardise within and in
between laboratories and they do not readily provide phylogenetic relationships (Achtman, 2008).

Recently, Roumagnac et al. (Roumagnac et al., 2006) have developed a typing scheme based on Single Nucleotide Polymorphisms (SNP) for S. Typhi. Denatured High Performance Liquid Chromatography (dHPLC) was performed to analyse the diversity of 199 gene fragments of a global collection of 105 S. Typhi isolates. Fifty-five polymorphic gene fragments were analysed in an additional 350 isolates, which were isolated mostly in Southern Asia. Mutation discovery detected 97 bi-allelic Polymorphisms (BiPs). S. Typhi was resolved into a fully parsimonious phylogenetic tree defining 85 distinct haplotypes (H1-H85), which developed from a common root node, S. Typhi H45 (Figure 4.1) (Achtman, 2008; Roumagnac et al., 2006).

This study revealed that S. Typhi has a neutral population structure, which is defined by the absence of strong selection in housekeeping genes and pathogenicity genes. However, on the backbone of this neutral population structure the clonal expansion of nalidixic acid (quinolone) resistant S. Typhi haplotype H58 emerged recently in South East Asia, presumably due to high antibiotic selective pressure. This clone has become the predominant S. Typhi haplotype in Vietnam. S. Typhi haplotype H58 is more closely related to Ty2 than to CT 18 (Figure 4.1) (Roumagnac et al., 2006).
Figure 4.1 Minimal spanning tree of 105 global S. Typhi isolates.

Minimal spanning tree of 105 global S. Typhi isolates based on sequence polymorphisms in 199 gene fragments (88,739 base pairs). From (Roumagnac et al., 2006). The tree shows 59 haplotypes (nodes) based on 88 BiPs, the colour coding of the pie charts indicates the continental source of the S. Typhi strains. The numbers along some edges indicate the number of BiPs that separate the nodes that they connect; unlabeled edges reflect single BiPs. The genomes of the CT18 and Ty2 strains have been fully sequenced. z66 refers to a flagellar variant that is common in Indonesia.
Very recently, new technologies that allow high throughput parallel sequencing (454 pyrosequencing technology, Roche Diagnostics and Solexa sequencing, Illumina) and high throughput genotyping (GoldenGate genotyping assay, Illumina) have been developed and have vastly increased the pace at which large datasets of genomic information can be obtained and analysed (Fan et al., 2006).

Nineteen S. Typhi isolates from central and radial haplotype groups of this phylogenetic tree (Figure 4.1) were chosen for whole genome sequencing using a combination of 454 pyrosequencing (Roche Diagnostics) and Solexa sequencing (Illumina) (Holt et al., 2008). Repetitive sequences (including Variable Number of Tandem Repeats, VNTRs) were excluded from the analysis. In total 1964 SNPs were identified in the S. Typhi genome. The SNPs traced the same phylogenetic tree as defined by Roumagnac (Roumagnac et al., 2006), but provided better resolution, especially of the H58 and H59 haplotypes (Holt et al., 2008) (Figure 4.2). The study revealed that pseudogene formation has occurred independently in different lineages of S. Typhi and is ongoing. This supports the hypothesis that evolution in this human restricted pathogen is dominated by loss of gene function (Holt et al., 2008). Reduction in genome size and accumulation of large numbers of pseudogenes have been described as mechanisms of host restriction in other pathogens, including Yersinia pestis (Parkhill et al., 2001b) and Mycobacterium leprae (Vissa and Brennan, 2001).
Figure 4.2 Phylogenetic tree of *S. Typhi* based on SNP data from whole-genome sequencing of 19 *S. Typhi* isolates.

From (Holt *et al.*, 2008). Branch colours indicate different lineages of *S. Typhi*; branch lengths are measured in number of SNPs (scale as indicated). Central, small black circle indicates the ancestral root, dashed line represent the *Salmonella* lineage; phage (ST) and SPI15 insertion events are shown along branches; plasmids detected in each isolate are indicated by filled circles (IncHI1 multidrug resistance plasmids), open circles (cryptic plasmid) and filled lines (linear plasmids carrying z66 flagella variant).

In this chapter we used a GoldenGate (Illumina) assay to type 1500 single nucleotide polymorphisms (SNPs) and analyse the genetic variation of *S. Typhi* isolated from 264 typhoid fever patients during a randomised multicenter treatment trial (reported in Chapter 2) conducted in the Mekong delta region of Vietnam between 2004 and 2005.
Nearly all S. Typhi isolates from these patients were resistant to nalidixic acid (96%) and 58% were multidrug resistant (Chapter 2).

The incidence of typhoid fever has declined in Vietnam. Whilst between 1991 and 2001 approximately 17,000 cases of typhoid fever (blood culture confirmed and syndromic cases) were reported annually through the Vietnamese national surveillance system (Kelly-Hope et al., 2007; Kelly-Hope et al., 2008), only 4,323 and 5,030 annual typhoid fever cases were reported in 2004 and 2005, respectively (Source: National Institute of Health and Epidemiology, Ministry of Health, Vietnam). However, 75% of these cases occurred in the Mekong delta (Kelly-Hope et al., 2007; Kelly-Hope et al., 2008).

4.2 Methods

4.2.1 S. Typhi isolates

S. Typhi isolates were collected during a multicenter clinical trial (described in Chapter 2), conducted at the (a) the Hospital for Tropical Diseases in Ho Chi Minh City (n=10), (b) Dong Thap Provincial Hospital, Cao Lanh, Dong Thap province (n=25) and (c) An Giang Provincial Hospital, Long Xuyen, An Giang province (n=232). Children (above 6 months) and adults were eligible to be included in the study if they had clinically suspected or culture confirmed uncomplicated typhoid fever and if fully informed written consent had been obtained.
4.2.2 Bacterial isolation and DNA preparation

After initial isolation, *S*. Typhi isolates were stored at -70°C in a 20% glycerol solution until required for further analysis and DNA extraction. To revive frozen organisms, MacConkey and Xylose Lysine Decarboxylase (XLD) agar plates were inoculated from the glycerol solution and incubated at 37°C overnight. To ensure correct identification, colonies were checked using slide agglutination with serotype specific antiserum (Vi, O9) and an irrelevant antiserum as a negative control (O4) (Murex, Dartford, United Kingdom). Two mL of nutrient broth were inoculated with single *S*. Typhi colonies and incubated overnight. Overnight cultures were centrifuged and *S*. Typhi DNA was extracted using Wizard Genomic DNA Purification kit (Promega, USA) as recommended by the manufacturer's guidelines. DNA was stored at -20°C and was quantified using the Quant-IT PicoGreen dsDNA Reagent and Kit (Invitrogen, UK). *S*. Typhi DNA concentrations were adjusted to 50 ng/mL and 250 ng of DNA were pipetted into 96-well plates. Each 96-well plate contained two isolates in duplicate and the sequenced *S*. Typhi isolate CT18 as control for assay reproducibility.

4.2.3 Selection of *S*. Typhi SNPs

*S*. Typhi SNPs identified by dHPLC (Roumagnac *et al*., 2006) and by whole genome sequencing of 19 *S*. Typhi isolates (Holt *et al*., 2008), were used to design a custom GoldenGate assay (Figure 4.3). In total, 1485 chromosomal SNPs, (listed in (Holt *et al*.; Kariuki *et al*.) and 172 IncH11 plasmid haplotype SNPs (Kariuki *et al*.; Phan *et al*.,
2009) including antibiotic resistance gene sequences were probed in sample S. Typhi using the GoldenGate assay.

### 4.2.4 High throughput SNP genotyping

The GoldenGate assay (Illumina) provides high throughput SNP genotyping platform. The assay was originally developed for high throughput SNP calling in complex human genetic linkage studies and is modified in this study for SNP identification in bacteria. The assay generates SNP specific PCR products that are subsequently hybridised to beads either on a solid matrix or in solution (Figure 4.3). Three oligonucleotides are synthesized for each SNP, two allele specific oligonucleotides that distinguish the SNP, and a locus specific sequence just downstream of the SNP. The allele specific and locus specific oligonucleotide sequences also contain target sequences for a set of universal primers (universal PCR sequences 1-3). Each locus specific oligonucleotide also contains a unique sequence (address or “illumicode”) which is complementary to sequences attached to the 3 μM beads. The pooled oligonucleotides are hybridized simultaneously to genomic DNA in a single DNA sample per well reaction. Highly multiplexed allele specific oligonucleotide hybridization, ligation and extension assays are followed by universal PCR amplification, which reduces amplification bias to a minimum. The address sequences of the PCR amplification products hybridize with its cognate sequences on the 3 μM beads in the 96-sample Sentrix Array Matrices (SAMs). The fluorescence on each bead is quantified. Each address sequence translates to a particular SNP locus and the presence of Cy3 and Cy5 indicates the allele. For the
GoldenGate array designed in this study facilitated the interrogation of 1536 custom designed SNPs per sample.
Figure 4.3 Schematic representation of GoldenGate assay workflow

(GoldenGate, Illumina).

4.2.5 Genotype calling

The raw data provided by the Illumina GoldenGate assay is, for each SNP in each sample, a fluorescence signal corresponding to each allele-specific fluorescent-labelled probe. Raw data was normalised using the proprietary Illumina BeadStudio software, but the mean normalised signal intensities and signal to noise ratios vary among SNPs. Thus turning allele-specific signals into genotype calls requires each SNP to be analysed individually, across a range of samples. This process is known as genotype clustering, and is essentially a two-dimensional clustering problem, where each allele-specific probe contributes one dimension. Since each SNP needs to be clustered individually, manual genotype clustering is extremely time consuming and is considered to introduce bias into genotyping results. An automated clustering algorithm is implemented in the Illumina software (BeadStudio), but has been optimised for clustering genotypes in diploid samples, i.e. where three clusters are expected for each locus, corresponding to two homozygous and one heterozygous genotype (AA, BB or AB). However for the present study involving haploid bacterial genotyping, we expect no heterozygous genotype clusters but some 'no signal' genotype clusters. Illumina BeadStudio is proprietary software and unable to be modified, but third-party opensource genotype clustering algorithms are available. Among the best performing for the Illumina genotyping platform is Illuminus (Teo et al., 2007), whose author Y. Teo modified to search for a third 'no signal' cluster centred at the origin rather than a heterozygous cluster. This version, referred to hereafter as Illuminus-P, was applied to genotype clustering of all GoldenGate data presented in this thesis.
4.2.6 Phylogenetic analysis

Alleles determined by genotype clustering with Illuminus-P as described above were analysed as follows. A Perl script was written to extract allele data from subsets of high-quality SNPs. The script outputs alignments of concatenated strings of SNP alleles in phylip format, suitable for analysis using phylogenetic methods. Chromosomal alleles from a global collection of 180 S. Typhi isolates plus 19 sequenced isolates were analysed in ModelTest (Posada and Crandall, 1998), a tool to select the best-fit model of nucleotide substitution (implemented in FindModel at http://www.hiv.lanl.gov/content/sequence/findmodel/findmodel.html). The analysis suggested a general time reversible (GTR) model provided the most appropriate phylogenetic model for these data. Phylogenetic analysis was performed using maximum likelihood approaches to fit a GTR model, implemented in the software program RAxML (Stamatakis et al., 2005). SNP genotyping with the Illumina GoldenGate only provides genetic information at the specific assayed loci; in the case of chromosomal SNPs, these are mostly loci determined by whole genome comparison of 19 S. Typhi strains (Holt et al., 2008). Thus the genotyping analysis essentially places each S. Typhi isolate at the appropriate position along branches defining the phylogenetic tree of these 19 strains, and branch lengths reflect genetic divergence only at the assayed loci. Short branches separating very closely related clusters (e.g. within the H58 group) were verified by manually inspecting cluster plots for SNPs that differentiated within those clusters.
4.2.7 Statistical analysis

Clinical data were deposited into an electronic database (Epi Info 2003, CDC, Atlanta, USA). For comparison of patient characteristics according to infecting *S. Typhi* haplotypes, Kruskal-Wallis tests were used for analysis of continuous variables (age, length of stay in hospital, fever clearance time) and $\chi^2$ tests were used for categorical variables (presence of symptoms). Two-tailed p-values are reported; statistical analysis was performed using the R package (http://www.r-project.org/).

4.2.8 PCR amplification and sequencing of *gyrA* gene in *S. Typhi*

Oligonucleotide primers for the amplification of the quinolone resistance determining regions in *gyrA* gene in *S. Typhi* were as follows (Chau *et al.*, 2007): GYR/A P1 5' TGTCCGAG ATGGCCTGAAGC and GYR/A P2 5' TACCCTGACAATATTCCACG. Predicted PCR amplicon size was 347 bp. PCR was performed under the following conditions; 30 cycles of: 92°C for 45 seconds, 45 - 62°C for 45 seconds and extension at 74°C for 1 minute, followed by a final extension step at 74°C for 2 minutes. PCR products were purified and directly sequenced using the CEQ DTCS - Quick Start Kit (Beckman Coulter, USA) and the CEQ 8000 capillary sequencer. The resulting DNA sequence was analyzed using CEQuence Investigator CEQ2000XL (Beckman Coulter, USA). All sequences were verified, aligned and manipulated using Bioedit software (http://www.mbio.ncsu.edu/BioEdit/bioedit.html) and compared to other *gyrA* sequences by BLASTn at NCBI.
4.2.9 Spatial data collection and analysis

Patient addresses were recorded at the time of hospital admission. The latitude and longitude of the residences of typhoid fever patients (to the hamlet/village level) was assigned from the collected address data using 1/50,000 scale maps (Source: Cartographic Publishing House and VinaREN, Ministry of Natural Resources and Environment, Vietnam) and cross-checked using the websites http://www.basao.com.vn and http://ciren.gov.vn.

Location data was analysed using Quantum GIS version 1.4.0 (http://www.qgis.org/). Locations were colour coded according to S. Typhi haplotype and clustering of specific haplotypes was calculated using the nearest neighbour analysis function. Nearest neighbour analysis examines the distances between each point and the closest point to it, and then compares these to expected values for a random sample of points from a CSR (complete spatial randomness) pattern. Significant clustering was inferred by Z-score value (standard normal variate) of less than 0; a positive score was interpreted as dispersion of locations.

4.3 Results

4.3.1 S. Typhi population structure

A recently developed typing system, which is based on the simultaneous interrogation of 1,485 single nucleotide polymorphisms (SNPs) distributed in the S. Typhi chromosome using a custom Illumina GoldenGate array, was used to analyse each of the S. Typhi isolates. This approach facilitates the unequivocal assignment of isolates to
haplotypes, allowing closely related strains to be distinguished phylogenetically based on single nucleotide changes (Holt et al., 2010; Kariuki et al., 2010). From the 287 patients with culture confirmed typhoid fever recruited between January 2004 and December 2005, 267 S. Typhi were available for SNP typing. This included 264 S. Typhi isolated from blood culture at admission (see clinical trial described in Chapter 2), one relapse S. Typhi isolate and two S. Typhi faecal carriage isolates. A total of 261 isolates (98%) were of the common H58 haplogroup. The remaining isolates were of haplotypes H1 (n=3), H45, H50 and H52 (see Figure 4.4 and Table 4-1).

The H58 S. Typhi isolates displayed variation at 10 SNP loci (detailed in (Holt et al., 2010)), which differentiated seven distinct sub-H58 haplotypes, shown in Figure 4.4. However, 242 (93%) of these isolates belonged to just three closely related H58 haplotypes, designated C, E1 and E2 in Figure 4.4. The genome of S. Typhi strain AG3, isolated during the study (March 2004) from a typhoid fever patient living in An Giang province, was sequenced previously (Holt et al., 2008). AG3 belongs to the H58-E2 haplotype, and the SNPs separating E2 from haplotypes E1 and C were originally identified by analysis of the AG3 genome. Therefore, the ability to differentiate within the cluster of 242 S. Typhi isolates was dependant on the inclusion of strain AG3 in the initial SNP detection study (Holt et al., 2008).
Figure 4.4 Phylogenetic distribution of *S. Typhi* isolates from the Mekong delta region of Vietnam.

From (Holt et al., 2011).

Grey nodes represent control isolates (labelled by isolate code and haplotype group), unfilled grey circle indicates tree root (H45 (Roumagnac et al., 2006)), white nodes correspond to non-H58 *S. Typhi* isolated in this study (labelled with isolate code), black nodes show H58 isolates. Inset: Enlargement of the H58 haplogroup; grey nodes represent control isolates (labelled by isolate code or haplotype code), unfilled grey circle indicates tree root; coloured circles indicate nodes corresponding to H58 *S. Typhi* isolated in this study, node labels are as in the text, node colours indicates the haplotype of the *S. Typhi* isolate, node sizes indicate the number of isolates on the scale as
indicated by numbered circles. The tree was rooted using alleles from other *Salmonella* serovars as outgroups.

All 231 (out of 232) *S*. Typhi strains isolated from the blood culture of patients admitted to An Giang Provincial Hospital as well as the two faecal *S*. Typhi strains isolated from chronic carriers belonged to the *S*. Typhi H58 haplogroup. The remaining *S*. Typhi isolate was of the H45 haplotype and was isolated from a patient who was resident in neighbouring Can Tho province. One patient at An Giang Provincial Hospital relapsed with symptoms of typhoid fever and had *S*. Typhi isolated from blood culture 11 days after the initial treatment had been completed. The mother of the patient was found to be a chronic *S*. Typhi carrier. All three *S*. Typhi strains, the patient's admission and relapse blood culture isolates and the mother's faecal isolate belonged to the *S*. H58-E2 subtype. The patients' isolates were both MDR and carried the IncHI1 ST6 plasmid (see below), whereas the mother's *S*. Typhi isolate was susceptible to all first line antimicrobials at the time of isolation. Patients were followed up at 1, 3 and 6 months to obtain stool samples. Chronic faecal carriage of *S*. Typhi was detected in only one trial patient. This was a MDR H58-C strain isolated from stool after 6 months of follow-up, which was indistinguishable in all SNP loci from the patient's original blood culture isolate.

At Dong Thap Provincial Hospital, only 3 of the 25 *S*. Typhi isolates did not belong to the H58 haplogroup. Two H1 isolates (BJ63 and BJ64) were identical at all assayed SNP loci (Figure 4.4) and were isolated on consecutive days from two patients in Dong Thap. A third H1 strain (BJ105; Figure 4.4) differed from BJ63 and BJ64 at 16 SNP
loci and was isolated in Dong Thap 14 months after these isolates. Two siblings (BJ75 and BJ76) from Dong Thap province were admitted on two consecutive days in 2004 and were both infected with MDR S. Typhi of the haplotype H58-C.

Figure 4.5 Location of the hospitals in the Mekong delta of Vietnam.

The map shows the 8 Vietnamese regions. Highlighted in grey is Mekong delta region in the south, which covers 40,000 km$^2$. The dotted box corresponds to the area magnified in Figure 1b. Highlighted in Figure 1 B are An Giang province (green) and Dong Thap province (grey) and the provincial hospitals of An Giang province (x) and Dong Thap (y). The direct distance between the two hospitals is 22.5 km.
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<th>Total study n=267</th>
<th>Characteristics n (% of all isolates)</th>
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<td>1</td>
<td>15</td>
<td></td>
</tr>
<tr>
<td>MDR</td>
<td>12</td>
<td>2</td>
<td>1</td>
<td>15</td>
<td></td>
</tr>
<tr>
<td>NaR</td>
<td>12</td>
<td>2</td>
<td>1</td>
<td>15</td>
<td></td>
</tr>
<tr>
<td>MDR and NaR</td>
<td>12</td>
<td>2</td>
<td>1</td>
<td>15</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>107</td>
<td>1</td>
<td>1</td>
<td>109</td>
<td>(41%)</td>
</tr>
<tr>
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<td>1</td>
<td>92</td>
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<td>ST6</td>
<td>16</td>
<td>1</td>
<td>0</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>MDR</td>
<td>20</td>
<td>1</td>
<td>0</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td>NaR</td>
<td>107</td>
<td>1</td>
<td>1</td>
<td>109</td>
<td></td>
</tr>
<tr>
<td>MDR and NaR</td>
<td>20</td>
<td>1</td>
<td>0</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>17</td>
<td>2</td>
<td>0</td>
<td>19</td>
<td>(7%)</td>
</tr>
<tr>
<td>no plasmid</td>
<td>3</td>
<td>0</td>
<td>0</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td>ST6</td>
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<td>2</td>
<td>0</td>
<td>16</td>
<td></td>
</tr>
<tr>
<td>MDR</td>
<td>14</td>
<td>2</td>
<td>0</td>
<td>16</td>
<td></td>
</tr>
<tr>
<td>NaR</td>
<td>14</td>
<td>2</td>
<td>0</td>
<td>16</td>
<td></td>
</tr>
<tr>
<td>MDR and NaR</td>
<td>14</td>
<td>2</td>
<td>0</td>
<td>16</td>
<td></td>
</tr>
<tr>
<td><strong>Other HS8 subtypes</strong></td>
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<tr>
<td>Total</td>
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<td>3*</td>
<td>2*</td>
<td>6</td>
<td>(2%)</td>
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<td>6</td>
<td></td>
</tr>
<tr>
<td>ST6</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>MDR</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>NaR</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>MDR and NaR</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>

Table 4-1 S. Typhi haplotypes according to region.
S. Typhi haplotypes are listed according to the hospital (An Giang Provincial Hospital, An Giang; Dong Thap Provincial Hospital, Dong Thap and the Hospital for Tropical Diseases, Ho Chi Minh City) where they were isolated.

*One S. Typhi H45 haplotype was isolated. &Three S. Typhi H1 haplotypes were collected. ^One S. Typhi isolate of the H50 and one of the H52 haplotype were isolated. NaR nalidixic acid resistance.

Of the ten S. Typhi strains isolated at the Hospital for Tropical Diseases in Ho Chi Minh City, eight were members of the H58 haplogroup, with patients reporting to be residents in Ho Chi Minh City (n=5), Long An (n=1), Kien Giang (n=2) and An Giang (n=1) provinces, reflecting the larger catchment area of the hospital. The remaining two S. Typhi were of haplotypes H52 (BJ3) and H50 (BJ9) and were isolated from patients living in Binh Hoa province (north of Ho Chi Minh City) and Ho Chi Minh City, respectively. There was no obvious association between S. Typhi haplotype and patient age, length of stay in hospital, fever clearance time or relapse (Table 4-2). However, upon admission, patients infected with S. Typhi haplotype H58-E2 tended to report lower frequencies of diarrhoea and headache and higher frequencies of constipation compared to patients infected with other haplotypes, including H58-C (see Table 4-2).
<table>
<thead>
<tr>
<th></th>
<th>S. Typhi H58-E2 n=107</th>
<th>Non-H58-E2 S. Typhi n=157</th>
<th>S. Typhi H58-C n=117</th>
<th>H58-E2 vs all other S. Typhi [95% CI]</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (yrs)</td>
<td>11.9</td>
<td>12.2</td>
<td>12.7</td>
<td>Diff. -0.8 (-2.0, 1.0)</td>
<td>0.83</td>
</tr>
<tr>
<td>Time in hospital (days)</td>
<td>13.9</td>
<td>13.7</td>
<td>13.8</td>
<td>Diff. 0.2 (-1.0, 1.0)</td>
<td>0.74</td>
</tr>
<tr>
<td>Fever clearance (hrs)</td>
<td>116</td>
<td>115</td>
<td>121</td>
<td>Diff. 1 (-12, 18)</td>
<td>0.70</td>
</tr>
<tr>
<td>Constipation</td>
<td>13.6%</td>
<td>5.8%</td>
<td>6.0%</td>
<td>OR 2.6 (1.1, 6.1)</td>
<td>0.03</td>
</tr>
<tr>
<td>Headache</td>
<td>55.7%</td>
<td>70.1%</td>
<td>70.1%</td>
<td>OR 0.54 (0.32, 0.90)</td>
<td>0.02</td>
</tr>
<tr>
<td>Diarrhoea</td>
<td>55.1%</td>
<td>72.6%</td>
<td>73.5%</td>
<td>OR 0.46 (0.28, 0.78)</td>
<td>0.004</td>
</tr>
</tbody>
</table>

**Table 4-2 Selected characteristics of 264 typhoid fever patients, based on baseline presentation, history and outcomes.**

For continuous variables age, time in hospital and fever clearance, values shown are means and test statistic given is the difference in means (Diff.); other variables indicate frequency of constipation, headache or diarrhoea self-reported at time of admission, test statistic is odds ratio (OR); 95% confidence intervals are given in brackets. All comparisons shown are for patients infected with H58-E2 S. Typhi versus those infected with other S. Typhi haplotypes (including H58-C and others).
4.3.2 Plasmids and antimicrobial resistance

The GoldenGate SNP assay incorporated probes targeting IncH1I plasmid sequences, allowing for detection of the presence of IncH1I plasmid within the S. Typhi genomic DNA. The SNP assay indicated that a total of 139 of the S. Typhi isolates harboured an IncH1I plasmid. All plasmids were of the IncH1I ST6 sequence type (Phan et al., 2009) and all plasmid-bearing isolates belonged to the S. Typhi H58 haplogroup (see Table 4-1). The MDR IncH1I plasmid was more common among H58-C isolates than H58-E2 isolates (86% vs 19%, see Table 4-1). Of the 139 S. Typhi isolates giving positive signals for IncH1I SNP loci, 137 (99%) were classified as MDR by antimicrobial susceptibility testing conducted at the time of isolation (see Chapter 2). One other IncH1I-positive isolate tested positive by GoldenGate SNP typing for the genes sul1, sul2, dfrA7, tetACDR, strAB, bla and cat, like the MDR isolates, yet had low MICs for chloramphenicol, ampicillin and co-trimoxazole. An additional S. Typhi isolate, BJ5, was resistant to ampicillin and co-trimoxazole but sensitive to chloramphenicol. This was consistent with GoldenGate results, which gave positive signals for the repC replication initiation gene of IncH1I, resistance genes strAB, bla, sul1, sul2, dfrA7, but no signal for sequences from the cat gene which encodes chloramphenicol resistance. A further 17 S. Typhi isolates were recorded as MDR according to their antimicrobial susceptibility pattern at the time of isolation, but did not test positive for IncH1I plasmid SNPs. This likely reflects loss of the IncH1I plasmid during culture or in storage between the time of isolation and DNA extraction.
A total of 257 S. Typhi isolates were resistant to nalidixic acid. All of these isolates belonged to the H58 haplogroup and all were susceptible to gatifloxacin, ciprofloxacin and ofloxacin according to current CLSI guidelines (Clinical and Laboratory Standards Institute, 2007). S. Typhi haplotypes H58-C, H58-E1 and H58-E2 were uniformly resistant to nalidixic acid with the exception of a single H58-C isolate which had an intermediate MIC of 28 µg/mL (resistance defined as MIC ≥ 32 µg/mL). The sequenced H58-E2 isolate AG3 harbours a mutation changing serine (TCC) to phenylalanine (TTC) at codon 83 in the gyrA gene (Holt et al., 2008), which is known to confer resistance to nalidixic acid (Hopkins et al., 2005). In the present study we sequenced the gyrA gene in 223 of the nalidixic acid resistant isolates (88%) and found the GyrA Ser83Phe amino acid substitution in all isolates tested.

4.3.3 Spatial and temporal distribution

Figure 4.6 shows the spatial distribution of the residences of 160 of the 267 typhoid patients (this information was not available for the remaining patients). At the time of the study prospective GPS mapping of patients’ residences was not possible, however we used patients address data to allocate longitude and latitude. Of the patients admitted at An Giang Provincial Hospital and Dong Thap Provincial hospital, sufficient address detail to allow for assignment of latitude and longitude was provided in 61% and 73% of cases, respectively. In An Giang, the patients’ homes clustered around the An Giang Provincial Hospital, but also around the Sông Hậu branch of the Mekong river (arrow in Figure 4.6). Mainly S. Typhi of the H58-E2 haplotype were isolated from patients living near this point in An Giang province and this group demonstrated significant
clustering using nearest neighbour analysis (orange in Figure 4.6; n = 57, Z-score = -14.145). In contrast, *S.* Typhi of the H58-C haplotype were isolated relatively frequently in neighbouring provinces and had a more sporadic, yet significant, clustering pattern (red in Figure 4.6; n = 31, Z-score = -5.747).

Figure 4.6 The spatial distribution of *S.* Typhi haplotypes surrounding An Giang provincial hospital in 2004 (a) and 2005 (b).
Each point corresponds to the residential location of a typhoid fever patient and the colour represents the haplotype of the S. Typhi isolate (with or without plasmid): dark orange, H58-E2 with MDR plasmid; light orange, H58-E2 without MDR plasmid; dark red, H58-C with MDR plasmid; pink, H58-C with MDR plasmid; grey, other S. Typhi haplotypes. Locations of the hospitals are shown by a white cross on a red background. The pink circle corresponds to a range of 15 km from An Giang Provincial Hospital. The arrow distinguishes the Sông Hậu branch of the Mekong river.

In 2004, S. Typhi H58-E2 (103 isolates) and H58-C (62 isolates) were both prevalent. In 2005, 55 S. Typhi H58-C isolates were observed, but only 4 H58-E2 Typhi. The decline of H58-E2 may be associated with selection for the IncH11 MDR plasmid, which was much more common in H58-C. As Figure 4.7 highlights, the majority of isolates collected during the second season were MDR and carried the IncH11 plasmid ST6.

The temporal distribution of S. Typhi haplotypes over 2004 and 2005 is shown in Figure 4.7. Typhoid incidence peaked just prior to the onset of the wet season in each year (see monthly rainfall, solid line in Figure 4.7).
Figure 4.7 Monthly incidence of typhoid fever cases by haplotype in An Giang province

Bar heights indicate the total number of *S. Typhi* isolated each month during the study, according to the scale given on the left-hand y-axis; colours indicate *S. Typhi* haplotype and presence of IncHI1 plasmid as given in the legend. Solid black line = total rainfall each month recorded in An Giang, dashed line = maximum rainfall occurring in a 24 h period during each month in An Giang; scale given on right-hand y-axis.
4.4 Discussion

We used high throughput SNP typing as tool to discriminate the population structure and genetic relationship of 267 $S$. Typhi strains which were isolated during a clinical treatment trial between 2004 and 2005 in the Mekong river delta region of Vietnam.

The $S$. Typhi population in this study was very homogenous, with the vast majority of $S$. Typhi isolates ($n = 261, 98\%$) belonging to the H58 haplogroup. Furthermore, 242 (91\%) belonged to a single sublineage of $S$. Typhi H58 (nodes C, E1, E2), demonstrating remarkable clonality in the $S$. Typhi population in this location over the study period. The observed level of clonal dominance is greater than that observed in previous haplotyping studies of local $S$. Typhi populations.

Among 54 $S$. Typhi isolates from Jakarta, Indonesia, a total of nine haplotypes were detected, with the dominant H59 haplotype accounting for 53\% of isolates; the next most frequent haplotype was genetically distant from H59 and comprised 24\% of isolates (Baker et al., 2008). In Kathmandu, Nepal, a collection of $S$. Typhi isolated from children hospitalised with typhoid fever was dominated by the H58-G haplotype (66\%) but the distant H42 haplotype was also present at a significant frequency (19\%) (Holt et al.). Among $S$. Typhi isolated between 2001 and 2008 in Nairobi, Kenya, 87\% were H58, although two distinct lineages of this haplogroup (nodes B and J) were co-circulating at high frequencies (>40\% each) over the period between 2004 to 2008 (Kariuki et al.). $S$. Typhi H58 nodes B and J (concomitant in Nairobi) represent distinct lineages, each acquiring unique SNPs since the last common ancestor of H58 (Figure 4.2). H58 nodes C, E1 and E2, which account for 91\% of isolates in this study in
Vietnam, are closely related and formed a tight clonal complex differentiated by just two SNPs (Figure 4.4). The overall level of clonality of the S. Typhi population analysed in this study was unexpectedly high. The clonal complex comprising H58-C, H58-E1 and -E2 was not detected in study populations in Nepal and Kenya where the same SNP typing method was used (Holt et al., 2010; Kariuki et al., 2010), suggesting it may have arisen locally in Vietnam.

Despite the genetic homogeneity we observed, the availability of whole-genome sequence data for S. Typhi isolate AG3 (Holt et al., 2008), collected during the study, allowed us to differentiate closely related organisms within the H58 group. Just two SNPs identified in strain AG3 (haplotype H58-E2) subdivided the homogeneous group into three nodes (Figure 4.2), of which two, subgroup C and E2 were dominant (> 40% of isolates each). Isolates belonging to the H58-C node were present at a constant rate during the two years of the study (62 isolates in 2004 and 55 in 2005). However, isolates belonging to the H58-E2 node were common during 2004 (103 isolates), yet were virtually undetected in 2005 (3 isolates). This change in both haplotype distribution and total number of typhoid cases from 2004 to 2005 is striking, and suggests an outbreak caused by S. Typhi H58-E2 during 2004. This decline is also reflected in hospital data from the An Giang Provincial Hospital, where in 2004 193 patients were admitted with blood culture confirmed typhoid fever, whereas in 2005 only 91 patients had S. Typhi isolated from blood culture.

It was additionally found that H58-C strains had a much stronger association with the ST6 IncHI1 MDR plasmid than H58-E2 (Table 4-2). It is possible to speculate that the
persistence of H58-C strains and the corresponding disappearance of H58-E2 may be associated with a competitive phenotypic advantage conferred by the IncHII MDR plasmid. However, it is important to remember that node C is a precursor of node E2 and we can only differentiate E2 from C because we had whole genome sequence data for an H58-E2 strain from which to identify SNPs (Holt et al., 2008). Thus the population of S. Typhi isolates assigned to node C by our SNP typing assay may be more diverse than that assigned to H58-E2.

We identified two cases of chronic faecal carriage of S. Typhi during the course of the study, one in a patient’s relative and one in a patient after 6 months of follow-up. This underlines the importance of screening procedures to identify carriers and effective treatment to eliminate carriage and reduce transmission. The faecal S. Typhi isolates were of the dominant H58-E2 and H58-C haplotypes, respectively. In a previous case-control study performed in the Mekong delta, close contact with a patient with typhoid fever was significantly associated with developing the disease compared to hospital controls (adjusted odds ratio (OR) = 5.2; 95% CI 1.7-15.9) or community controls (adjusted OR = 11.9; 95% CI 2.3-60.7) (Luxemburger et al., 2001). This suggests that close contacts and faecal carriers play an important role in the transmission and persistence of these haplotypes in the community.

We were able to collect residential location data from 160 typhoid patients (61%); these provided roughly equal representation of patients infected with S. Typhi H58-C (65%) and H58-E2 (62%). Spatial clustering of S. Typhi H58-E2 was evident particularly around the Sông Hậu branch of the Mekong river, while other S. Typhi haplotypes were
more broadly distributed. The spatial clustering of H58-E2 S. Typhi further supports an outbreak in 2004 caused by these isolates. In contrast, the broader spatial and temporal distribution of S. Typhi H58-C during the study suggests it may be well established in the community and can persist over longer distances and time periods.

We also observed that some symptoms of patients infected with H58-E2 S. Typhi differed from those infected with other S. Typhi haplotypes (Table 4.2). Infections associated with H58-E2 S. Typhi were less likely to be associated with diarrhoea and headache compared with other S. Typhi haplotypes (Odds Ratio 0.46; 95% CI 0.28-0.78 and OR 0.54; 95% CI 0.32-0.9, respectively), but were more commonly associated with constipation (OR 2.6; 95% CI 1.1 – 6.1). This suggests there may be some differences between H58-E2 and other S. Typhi with respect to the disease phenotype, however these were post-hoc analyses, no adjustments were made for multiple comparisons and hence these associations should be interpreted with caution. However, if confirmed in subsequent prospective studies, it would be of interest to know whether these phenotypic characteristic were associated with specific mutations in the H58-E2 clone.

The two SNPs differentiating the E2 node from E1 and C are both synonymous mutations (C->T in melA (nt 315); G->A in rbsA (nt 576)) and the phage insertions and large deletions detected in our earlier analysis of the AG3 strain sequence data were also detected in other sequenced H58 isolates (Holt et al., 2008). However, we were unable to verify if other single-base insertions or deletions were present, which may result in gene inactivation with corresponding phenotypic effects.
Patterns of antimicrobial resistance of S. Typhi tend to vary markedly between different typhoid endemic regions. In this present work, as in the recent study of Kenyan isolates (Kariuki et al., 2010), there were high rates of MDR associated with IncHI1 ST6 plasmids among strains of the S. Typhi H58 haplogroup. This suggests that the presence of the plasmid may contribute to the success of the dominant S. Typhi haplotypes, and the results of our study corroborate this hypothesis. The S. Typhi H58-E2 subtype (which was generally not associated with a plasmid) was only transient, while the H58-C subtype (which was more commonly associated with the IncHI1 MDR plasmid) was present in 2004 and 2005 in southern Vietnam. In a Kenyan study, almost all isolates of the dominant haplotypes carried the MDR plasmid, while the plasmid-free H58-G subtype was only detected twice (Kariuki et al., 2010). All the H58 isolates analysed in the present study were resistant to nalidixic acid, conferred by an identical mutation in gyrA. This is consistent with previous studies reporting strong associations between the nalidixic acid resistance phenotype and the H58 haplogroup of S. Typhi (Holt et al., 2010; Kariuki et al., 2010; Roumagnac et al., 2006). The presence of the same mutation conferring nalidixic acid resistance in all isolates of H58-C, -E1 and -E2 suggests that this mutation may have arisen in the common ancestor of this clonal complex, perhaps in situ in the Mekong delta region, and its continued presence is likely maintained by selective pressure exerted by the administration of fluoroquinolones.
Chapter 5

Safety and Immunogenicity of the Novel Single Oral Dose Live Typhoid Vaccine M01ZH09 in Healthy Vietnamese Children
5.1 Introduction

The previous chapters of this thesis have highlighted the problem of antimicrobial drug resistance of *S. Typhi*. In industrialised countries typhoid fever has been essentially eliminated. The most potent measures to eliminate typhoid fever are improvements in infrastructure and sanitation.

Typhoid vaccines are another effective strategy to prevent typhoid fever. Whole-cell typhoid fever vaccines have been introduced by Almroth E. Wright in England and by Richard Pfeiffer in Germany at the end of the 19th century. These vaccines were given to soldiers in developing and developed countries and were applied in mass vaccination campaigns in several countries in the 1960s (DeRoeck *et al.*, 2008; Engels *et al.*, 1998; Tarr *et al.*, 1999). The three year cumulative efficacy of the whole-cell typhoid vaccine was 73% for two doses (based on seven trials), however fever after vaccination occurred in 15.7% of recipients (Engels *et al.*, 1998). The high rates of adverse events necessitated the introduction of new generation vaccines.

There are currently two licensed, safe typhoid vaccines available, the live oral Ty21a vaccine and the parenteral (intramuscular injectable) Vi polysaccharide. The World Health Organization recommends that countries should consider the programmatic use of these typhoid vaccines for controlling endemic diseases and that the immunization of school age and/or pre-school age children should be undertaken particularly in areas where antibiotic resistant *Salmonella enterica* serovar Typhi (*S. Typhi*) is prevalent (World Health Organization, 2008).
Ty21a typhoid vaccine was developed in the 1970s by random chemical mutagenesis of the pathogenic S. Typhi strain Ty2. The mutations responsible for its attenuation include an inactivation of galE (which encodes UDP-galactose-4-epimerase, involved in synthesis of lipopolysaccharide), an inability to express Vi polysaccharide presumably through mutation and other mutations that are collectively responsible for the stable, highly attenuated phenotype (Germanier and Fuer, 1975; Kopecko et al., 2009).

Ty21a vaccine is available in enteric-coated capsules or liquid formulation. It is administered in three doses (four doses in the US and Canada) two days apart and is licensed for adults and children above 6 years. Field studies with the oral Ty21a vaccine in the 1980s have shown a protective efficacy between of 96% after 3 years in Egypt (Wahdan et al., 1982), 77% in Chile after 3 years when using the liquid formulation (Levine et al., 1999) and up to 53% in Indonesia after 2.5 years (Simanjuntak, 1991 #920. Ty21a cannot be used in immunocomprised patients and pregnant women, and antibiotics should be avoided seven days before and after immunisation. Revaccination is recommended every 5 years.

The parenteral capsular polysaccharide Vi vaccine is given in a single dose (25 μg) and is licensed for individuals above 2 years. A single intramuscular injection conferred a protective efficacy of 77% after 21 months in South Africa (Klugman, 1987 #616), 72% after 17 months in Nepal (Acharya et al., 1987) and 61% after 2 years in India (Sur et al., 2009). Revaccination is recommended every three years.
Similar to other T-cell-independent polysaccharide vaccines, Vi vaccine is not immunogenic in children under 2 years of age and does not induce immunological memory. To overcome this limitation, a conjugate Vi vaccine bound to recombinant protein *Pseudomonas aeruginosa* exotoxin A (rEPA) was developed (Szu et al., 1994). Two doses of the conjugate Vi-rEPA vaccine administered 6 weeks apart had a protective efficacy of 91.5% in children aged two to five years in Vietnam after 27 months (Lin et al., 2001), but this vaccine is not yet commercially available.

The major limitation of the Ty21a vaccine is the need to administer at least 3 doses. From a public health perspective, a single dose oral typhoid vaccine would have major advantages (Fraser et al., 2007; Levine, 2003). Modern genetic techniques allow the construction of oral one dose typhoid vaccines with defined attenuating mutations. These next generation typhoid vaccines include *S. Typhi* strain Ty800 (attenuated by a double deletion in the genes *phoP* and *phoQ*) (Hohmann et al., 1996), CVD908-*htrA* (attenuated by deletion mutations in *aroC, aroD* and *htrA* genes) (Tacket et al., 2000) and M01ZH09.

M01ZH09 (*S. Typhi* (Ty2 *aroC ssaV*) ZH9) is a promising defined attenuated typhoid vaccine candidate, it has a well-defined dual mechanism of attenuation (Hindle et al., 2002) and has been safe and immunogenic in a single dose in Western (Hindle et al., 2002; Kirkpatrick et al., 2005b; Kirkpatrick et al., 2006) and Vietnamese adult volunteers (Hien TT, unpublished).
Historically, oral live vaccines often showed reduced immunogenicity in developing country populations compared to Western populations (Levine, 2006), therefore M01ZH09 was evaluated at an early stage of its development in children in an endemic country.

This chapter describes the results of a randomised placebo controlled trial that evaluated the safety and immunogenicity of M01ZH09 in 151 healthy Vietnamese children aged between 5 and 14 years.

5.2 Methods

5.2.1 Study design and objectives

The study was designed as a randomised placebo controlled single blind trial to evaluate the safety and immunogenicity of the novel oral single dose live typhoid vaccine M01ZH09 in Vietnamese children aged 5 to 14 years (inclusive).

5.2.2 The study site and ethical approval

The trial was conducted at the Hospital for Tropical Diseases in Ho Chi Minh City, Vietnam. Ethical approval for the trial and all trial related documents was obtained from the Oxford Tropical Research Ethics Committee (OXTREC) and the Institutional Review Board of the Ministry of Health, Hanoi, Vietnam. The trial was conducted in accordance with the Declaration of Helsinki and its amendments and according to Good Clinical Practice guidelines and was monitored by Matrix Contract Research Ltd., UK
The trial was also conducted under an US Investigational New Drug (IND) license. Trial registration: www.controlled-trials.com/ISRCTN91111837.

5.2.3 Investigator and sponsor roles

The trial was sponsored by Emergent Product Development UK Ltd., UK and funded by a Strategic Translational Award from the Wellcome Trust, UK (grant code: B9RKYTO).

The data were subject to a confidentiality agreement between the sponsor and investigator, which established full access to the study data. Prior to publication the manuscript was reviewed by the sponsor but there was no obligation on behalf of the academic authors to modify the publication. The data entry and analysis of data were managed by Statwood (now Quanticate), UK, an independent Clinical Research Organisation.

5.2.4 Participants

Healthy Vietnamese children aged 5 to 14 years (inclusive) were invited to participate in the trial. Recruitment was carried out by word of mouth and flyers. Families who were interested in the trial were invited to attend one of several information evenings at the Hospital for Tropical Diseases. At these meetings the study was presented by the principal investigator (TTH) and all questions could be discussed and answered. Families who remained interested in the trial were invited to attend the screening visit. Children were eligible if they were available during the trial period and at least one of their parents gave written informed consent for their child to participate after the trial
procedures and potential risks were carefully explained by the study investigators. All children were invited to give their assent to the study and written informed assent was obtained from subjects starting at the age of 6 years. After informed consent was obtained, screening tests were performed. Children were screened by history, physical examination (including height, weight and vital signs), blood tests (biochemistry, haematology and HIV test), urine dipsticks and pregnancy tests (for female subjects of 11 years and above). Stool cultures were performed to check for the presence of *Salmonella species*.

Subjects with a history of typhoid fever, Ty21a vaccination in the last 10 years or any other typhoid vaccine in the last 5 years, any clinically significant illness, abnormal blood test results, immune suppression, positive HIV or pregnancy test were excluded. Also excluded were subjects whose body weight was under 17 kg in the 5 to 10 year old group or under 27 kg in the 11 to 14 year old group and subjects who suffered from an acute febrile illness at the time of dosing. Only one child per family was allowed to participate in the trial.

The results of the screening tests were reviewed and subjects who continued to meet the inclusion criteria were invited to continue in the trial.

### 5.2.5 The M01ZH09 vaccine and dose

*S. Typhi* (Ty2 *aroC ssaV*) ZH9 was constructed using a rational genetic attenuation strategy. Two defined independently attenuating deletion mutations were introduced into *S. Typhi* Ty2. Deletion of *aroC*, encoding chorismate synthase, prevents the
biosynthesis of aromatic amino acids and deprives the live vaccine bacterium of essential nutrients. Deletion of ssAV, encoding a structural component of the Salmonella pathogenicity island-2 (SPI-2) type III secretion system, which prevents systemic spread of S. Typhi (Hindle et al., 2002). The vaccine was manufactured according to Good Manufacturing Practice protocols by Eurogentec S.A. and SynCo Bio Partners B.V; batch number M-STZH9-F16 was shipped to Vietnam. The vaccine kits were stored at 2-8°C.

Previous studies in adult volunteers demonstrated that a nominal dose of 5 x 10⁹ CFU of the vaccine strain was immunogenic and safe (Hindle et al., 2002; Kirkpatrick et al., 2005b; Kirkpatrick et al., 2006). The Ty21a oral typhoid vaccine capsules are licensed for adults and children above 6 years using the same dose and immunization schedule and large Ty21a field trials in children used the same dose and regimen as in adults (Levine et al., 1987). It was therefore determined that the appropriate dose for the children’s study was a nominal dose of 5 x 10⁹ CFU of S. Typhi (Ty2 aroC ssAV) ZH9.

The vaccine (containing 5 x 10⁹ CFU of vaccine strain plus excipients) and the placebo (vaccine excipients only) were supplied as freeze-dried formulations in single dose vials, which were labeled identically, containing “M01ZH09 oral typhoid vaccine or placebo” but with a unique subject number corresponding to the randomisation list. The bicarbonate solution was prepared by dissolving one effervescent bicarbonate tablet (provided in the vaccine kit and containing 2.6 g sodium bicarbonate, 1.65 g ascorbic acid and 30 mg aspartame) in 150 ml of bottled drinking water (final concentration: 1.75% wt/vol sodium bicarbonate, 1.1% wt/vol ascorbic acid, and 0.02% wt/vol
aspartame). The lyophilised vaccine or placebo was reconstituted in either 150 ml (for children above 10 years) or in 75 ml of the bicarbonate solution (the other 75 ml were discarded) for children below 10 years and was administered immediately.

The study used two age group specific randomisation lists, one for the 11 to 14 year old and one for the 5 to 10 year old children to ensure at least 70% children were between 5 to 10 years old.

5.2.6 Intervention

On the day of vaccination (day 0) which took place within 28 days of the screening, inclusion and exclusion (including history of antibiotic medication in the last 2 weeks) criteria were reviewed. Pregnancy tests (female subjects of 11 years and above only), urine dipstick test and stool cultures were performed. Blood samples for haematology, biochemistry, ELISA and ELISPOT assays (only in children 11 years and above) were obtained. After the subjects had fasted for at least 2 hours (with the exception of drinking water), the candidate typhoid vaccine or placebo was administered.

Subjects were allocated the next age-group specific subject number and the medication pack bearing the same number was prepared and issued by the pharmacist, who was otherwise not involved in the trial. The subjects were randomly assigned to receive either M01ZH09, consisting of \(5 \times 10^9\) CFU of \(S.\ Typhi (Ty2 aroC^{ss}saV') \) ZH9 or the placebo reconstituted in bicarbonate solution as described above.

Volunteers were observed for at least 90 minutes at the hospital. During this time pulse and blood pressure were recorded periodically and only drinking water was provided.
Diary cards were issued for all the volunteers and all subjects received a basic hygiene kit containing soap, gloves and spatulas for the collection of stool samples. The subjects and their parents were instructed to measure and record the oral temperature of the children twice daily (morning and evening) and to record any adverse events (including headache, fever, nausea, vomiting, abdominal pain, frequency and consistency of stools and any other symptoms) for 14 days.

5.2.7 Follow up procedures and monitoring of adverse events

Children were followed up daily from days 1 to 14 and again on day 28 after dosing. At these appointments diary cards were checked and adverse events and concomitant medication reviewed. A history of the last 24 hours with special emphasis on temperatures of 38.5°C and above and adverse events (diarrhoea, loss of appetite, vomiting, headache and chills) was obtained. Oral temperatures and vital signs were recorded and children were examined for signs of splenomegaly. Stool cultures were performed daily from day 1 to day 14. Blood samples for biochemistry and haematology were obtained on days 7, 14 and 28; for the LPS specific serum IgA ELISA on days 7 and 14; for the IgG ELISA on days 14 and 28 and for the LPS specific IgA antibody secreting cell (ASC) ELISPOT assay (only in subjects aged 11 years and above) on day 7. The total amount of blood taken during this study was approximately 28 ml from the 5 to 10 years old and 44 ml from the 11 to 14 years old children.
5.2.8 Unscheduled visits

Subjects and parents were instructed to make additional visits to the clinic, if the child felt unwell and/or had a fever of $\geq 38.5^\circ C$. At these visits the subject was assessed and samples taken for culture as clinically indicated. Blood cultures to investigate for the presence of *S. Typhi* in blood would be obtained if a fever of $\geq 39.0^\circ C$ was recorded twice over a 48 hours period, or a severe fever of $\geq 39.5^\circ C$ was recorded once.

5.2.9 Definition and reporting of serious adverse events

There was no Data Safety and Monitoring Committee for this trial. Data from all children were reviewed daily and there were *a priori* defined stopping rules which would trigger a suspension of the trial and a safety review. Serious adverse events were reported to AKOS Ltd (Hitchin, UK), a pharmacovigilance company within 24 hours.

5.2.10 Detection of *Salmonella* in stool samples at the screening visit and day 0

The detection of *Salmonella* species at the screening visit and on day 0 was performed according to microbiological standard procedures. In brief, stool samples were inoculated onto MacConkey agar and xylose lysine deoxycholate (XLD) agar plates, and in 10 ml of selenite F broth. Plates and broth were incubated at 37°C overnight and the broth was sub-cultured on MacConkey and XLD agar plates the next morning. Isolates were screened using standard biochemical tests and *Salmonella* were identified by slide agglutination with specific antisera (Oxoid Ltd., UK) and API20E profiling (bioMérieux, UK).
5.2.11 Detection of S. Typhi in stool samples

Stool samples were collected daily between days 1 and 14. Stool samples were cultured directly on deoxycholate citrate agar (DCA) Hynes plates (direct method) and in selenite F broth (enriched method). Both media were supplemented with aromatic compounds (DCA-aro and selenite F-aro, respectively) to detect S. Typhi, including the auxotrophic vaccine strain, in stools. Following overnight incubation at 37°C, an aliquot of the inoculated selenite F-aro broth was sub-cultured on DCA-aro Hynes plates. Suspected S. Typhi colonies were inoculated on brain heart infusion agar plates supplemented with aromatic compounds (BHI-aro). Oxidase negative colonies were evaluated by agglutination with Hd, Vi and O9 anti-sera (Oxoid Ltd., UK) and API20E profiling (bioMérieux, UK). Stool samples containing isolates that were positive in at least 2 out of 3 agglutinations and identified as S. Typhi by API20E profiling were considered to be positive for S. Typhi. All isolates were stored in 10% (v/v) glycerol at -80°C.

5.2.12 Detection of S. Typhi in blood samples

Blood samples were collected into either Bactec Peds Plus/F culture bottles (1-3 ml blood; BD, USA) or Bactec Plus Aerobic/F culture bottles (4-10 ml blood; BD, USA) and supplemented with aromatic compounds. Blood cultures were incubated at 35°C in the Bactec detection system and monitored for up to 5 days. Gram stain was performed on all bottles triggering a positive reaction. Positive cultures and all cultures that were negative after 5 days of incubation were sub-cultured on XLD agar plates. Suspected S.
Typhi colonies were sub-cultured onto BH1-aro agar plates. Oxidase negative isolates were evaluated by agglutination and API20E profiling (bioMérieux, UK) as above.

5.2.13 PCR identification of S. Typhi isolates

Genomic DNA was isolated from glycerol stocks of S. Typhi isolates using a DNeasy blood and tissue kit (Qiagen, UK). Multiplex PCRs were performed using a Taq PCR core kit (Qiagen, UK). Each reaction mixture contained 200 μM dNTPs, 0.4 μM ssaV4 (5' ATCCCCACGACTTCAGCAAG 3') and ssaV7 (5' CTTTCTGGCTCATCATGAGG 3'), and 0.1 μM aroC.Z1 (5' GACAACCTCTTTTCGTAACC 3') and aroC.Z3 (5' TTACATCCGCATTCTGTGCC 3'), 10 ng genomic DNA and 1.25 u Taq DNA polymerase in a total volume of 50 μl reaction buffer. PCRs were performed for 25 cycles as follows: 94°C for 30 sec, 57°C for 30 sec and 72°C for 2.5 min. The PCR products were visualised by ethidium bromide staining and UV transillumination after electrophoresis on a 0.8% (w/v) TAE agarose gel. The expected sizes of the PCR products were 1.04 kb (aroC) and 2.59 kb (ssaV) for S. Typhi wild-type strains and 0.45 kb (aroC) and 0.70 kb (ssaV) for S. Typhi (Ty2 aroC ssaV) ZH9.

5.2.14 Detection of antibody secreting cells producing S. Typhi LPS specific IgA antibodies by ELISPOT assay

ELISPOT assays to detect antibody secreting cells (ACS) producing S. Typhi LPS specific IgA antibodies were performed on days 0 and 7 as described previously (Kirkpatrick et al., 2005a; Kirkpatrick et al., 2006). In brief, whole blood was collected in
heparinised cell preparation tubes (Vacutainer CPT; BD, UK) and centrifuged. Peripheral blood mononuclear cells (PBMCs) were washed, resuspended in culture medium and adjusted to three cell concentrations (1 x 10⁷/ml, 5 x 10⁶/ml and 2.5 x 10⁶/ml). One hundred microlitres of each concentration were added to LPS coated and uncoated wells (for subtraction of non-specific results) of nitrocellulose microtiter plates (Millipore, USA) and incubated overnight at 37°C in a 5% CO₂ incubator. PBMC collected from a healthy volunteer who had received three doses of Ty21a (Vivotif, Berna, Switzerland) were included as positive control and PBMC from a non-vaccinated person as negative control. Plates were washed and an alkaline phosphatase-conjugated anti-human IgA antibody (Immune Systems Ltd., UK) was added and incubated for one hour. Plates were washed and spots were visualised by the addition of 5-bromo-4-chloro-3-indolyl-phosphate/nitro blue tetrazolium (BCIP/NBT) substrate. Antibody secreting cell (ASC) spots were counted manually using an inverted microscope. If more than 100 spots per well were present, the result was described as “too many spots to be counted”. A positive response in the ELISPOT assay on day 7 was defined as ≥ 4 IgA ASC specific for LPS per 10⁶ PBMCs and a negative response as < 4 IgA ASC specific for LPS per 10⁶ PBMCs. Subjects with a day 0 result of ≥ 4 ASC per 10⁶ PBMC were excluded from the ELISPOT analysis. ELISPOT assays were performed at the Hospital for Tropical Diseases.
5.2.15 Analysis of S. Typhi LPS specific serum IgG and IgA by ELISA and definition of a positive immune response

Quantitative ELISA methods for measuring S. Typhi LPS specific serum IgG and IgA were developed and qualified by Emergent Product Development UK Ltd using serum samples from recipients of M01ZH09 who participated in prior clinical trials and who had given informed consent for retention and usage of their samples. For the IgG ELISA, serum which demonstrated more than 4-fold increase from pre-dose in a previously described end point titre assay (Kirkpatrick et al., 2005b) were pooled and used as reference standard. The LPS specific IgG concentration in the standard serum was set arbitrarily at 30,000 units/ml. For the IgA ELISA, serum from past recipients of M01ZH09 who demonstrated positive response in IgA ELISPOT were pooled and used as reference standard. The LPS specific IgA concentration in the standard serum was set arbitrarily at 100 units/ml.

The standard error of measured sample means and the least significant difference (LSD) between two samples at the 1% significance level were calculated using PRISM (PRISM Training & Consultancy Ltd, UK). This was used as the cut-off value for a positive result in the respective assay. A positive serum IgG response was defined as a 70% increase (fold change of 1.7) as compared to the corresponding baseline sample, whereas a positive serum IgA response was defined as a 50% increase (fold change of 1.5) as compared to baseline.
Serum samples for measurement were frozen at -20°C and shipped to Emergent Product Development UK Ltd for the ELISA analyses. For the IgG ELISA, microtiter plates were coated with *S.* Typhi LPS, washed and then blocked. Washing occurred between each step. Calibration standards and diluted test samples were added, and the plates were incubated. Bound IgG was detected using an anti-human IgG antibody conjugated to horseradish peroxidise (HRP) (Dako, Denmark) followed by the addition of 3,3',5,5'-Tetramethylbenzidine (TMB) substrate. The plates were read at 450 nm within 30 minutes of stopping the reactions with 0.3 mol/L sulphuric acid. The standard curve was constructed by plotting the optical densities (ODs) of standards against concentrations and fitted by a 4-parameter logistic equation (SoftMax Pro 4.6, Molecular Devices, USA). The concentration of LPS specific IgG in each sample was determined from the standard curve. The IgA quantitative ELISA was performed in a similar manner, except using a double detection system of biotinylated anti-human IgA antibody (Southern Biotech, USA) followed by streptavidin-HRP conjugate (Dako, Denmark).

5.2.16 Outcomes of the study

5.2.16.1 Safety Outcomes

The primary safety endpoint was the proportion of subjects with any adverse events attributed to M01ZH09. The secondary safety endpoint was the proportion of subjects with any serious related adverse events; any related or unrelated adverse events; persisting faecal shedding of *S.* Typhi (Ty2 aroC\(^{-}\) ssaV\(^{-}\)) ZH9 after day 7; and/or had a fever of 38.5°C or greater in the 14 days post vaccination, withdrew from the trial due
to adverse events, including bacteremia, and/or had clinically significant changes in laboratory parameters related to the candidate vaccine.

All subjects who received a dose of the vaccine or placebo were analysed in the safety population. Post-vaccination adverse events were categorised according to body system and preferred term using the Medical Dictionary for Regulatory Activities (MedDRA, Version 9.1), allocated before unblinding. Adverse events were graded by severity (mild, moderate, severe) and judged for the relatedness to the study vaccine (unlikely, possibly, probably) by the investigator. Only possibly and probably related adverse events were attributed to the vaccine. Moderate fever was defined as an oral temperature of ≥ 38.5°C and severe fever as an oral temperature of ≥ 39.5°C. Moderate diarrhoea was defined as more than 4 unformed stools and severe diarrhoea as more than 6 unformed stools in a 24 hour period or evidence of significant dehydration. All adverse events were recorded in the CRFs and monitored until return to normal.

The numbers and proportion of subjects reporting adverse events were listed by body system. A per subject analysis of adverse events was performed e.g., if a subject reported the same adverse event on three occasions that adverse event was only counted once. Subjects reporting more than one adverse event per body system were counted only once in that body system total.

5.2.16.2 Immunogenicity Outcomes

The primary immunogenicity endpoint was the proportion of subjects who developed a positive immune response to S. Typhi LPS defined by an increase of 70% (1.7 fold
change) in LPS specific serum IgG on day 14 or 28 and/or an increase of 50% (1.5 fold change) in LPS specific serum IgA on day 7 or 14 compared to baseline.

The secondary immunogenicity endpoints were defined as the proportion of subjects who developed a positive immune response in each of the following assessments: *S.* Typhi LPS specific IgA ELISA assay on days 7 or 14, *S.* Typhi LPS specific IgG ELISA assay on days 14 or 28 and *S.* Typhi LPS specific IgA ELISPOT on day 7. A positive ELISPOT was defined as ≥ 4 IgA antibody secreting cells specific for *S.* Typhi LPS per 10⁶ PBMCs.

### 5.2.17 Sample Size

The planned sample size was 150 subjects, of whom at least 70% should be aged 10 years or younger, as this was the target age of the vaccine, randomised to M01ZH09 or placebo in a 2:1 ratio.

No formal sample size calculation was considered appropriate; it was aimed to include a sufficient sample size to assess safety and immunogenicity based on previous observations in adult studies and immunogenicity rates of licensed typhoid vaccines in children.

### 5.2.18 Randomisation procedures

Randomisation codes were computer generated in blocks of 9 by Statwood Ltd, UK. The vaccine and the placebo were labeled identically but with a unique subject number corresponding to the randomisation list. The study used two age group specific
randomisation lists, one for the 11 to 14 year old and one for the 5 to 10 year old children to ensure at least 70% children were between 5 to 10 years old.

Subjects were allocated the next age-group specific subject number in strict numerical sequence from this list and the medication pack bearing the same number was prepared by the pharmacist.

5.2.19 Blinding

This study was formally a single blind study due to slight differences in taste and aroma between the treatment preparations but it was conducted under the principles of a double blind study. M01ZH09 and placebo were packaged and labeled identically but with a unique sequential number. Possible sources of unblinding could have been the preparation of the vaccine. Therefore the study pharmacist was otherwise not involved in the trial. The subjects were asked to not report the taste of the vaccine. Microbiology results were not reviewed by the investigators for at least 14 days after vaccination to avoid potential unblinding through shedding in stools. Immunology results were not reviewed by the investigators. The study site received code break envelopes in case an emergency made unblinding for a single subject necessary. No codes were broken during this study. The unblinding of treatment allocations took place after the trial had been completed and the whole database had been entered and locked.

5.2.20 Data collection, data entry and statistical methods

All data were recorded in Case Record Forms (CRFs). CRFs were reviewed and collected by the study monitor. Data entry, data management and statistical analysis
were conducted by Statwood, UK using SAS software (version 9.1). Data were double entered and analysed according to an *a priori* defined statistical analysis plan which included the definition of all subject populations and the trial endpoints. The safety population included all subjects who received the study medication. The intention to treat (ITT) population comprised all dosed subjects who had any post-dose immunogenicity data available. The per protocol (PP) population excluded major protocol violators (failure to meet the inclusion/exclusion criteria, to comply with the study medication or use of other vaccinations or antibiotics two weeks before until 2 weeks after vaccination, or use of antacids or proton-pump inhibitors prior to vaccination and/or did not provide samples for the ELISAs). The protocol stated that a confirmatory analysis of the primary immunogenicity endpoint in the PP population was planned if more than 5% of subjects were excluded.

The proportion of subjects who experienced post-dose adverse events was presented together with their two-sided 95% confidence intervals (95% CI). Post dose adverse events, adverse events considered to be related to the vaccine and adverse events that occurred in more than 10% of the trial population were tested using a two-sided Fisher’s exact test to compare between the two groups.

The proportion of subjects who developed a positive immune response was presented together with their two-sided 95% CI calculated by using an exact binomial distribution. The treatment difference and associated 95% CI were presented as above. All available data from withdrawn subjects was included in the analysis.
5.3 Results

5.3.1 Participant flow and recruitment

The trial was conducted between April and July 2007. In total, 205 healthy Vietnamese children between 5 and 14 years (inclusive) were screened for eligibility. Fifty-four children were not eligible (Figure 5.1), the most common reasons were unavailability for the whole study period (n = 10) and a positive stool culture for Salmonella species at screening (non-typhoid Salmonella, n = 22). No S. Typhi or S. Paratyphi A were detected in stools at the screening visits.

One hundred and fifty-one children were randomised, 101 children received the candidate typhoid vaccine M01ZH09 and 50 children received placebo. All subjects fulfilled the inclusion and exclusion criteria at screening and dosing, however two subjects (both in the M01ZH09 group) had clinically significant elevated white blood counts (16.3 and 18.2 x 10⁹/L respectively) on day 0; these results were only available after dosing.

One subject in the M01ZH09 group vomited after taking approximately 50% of the required vaccine dose. The subject agreed to take another dose, but failed to retain it. Three subjects withdrew from the study, one placebo recipient withdrew due to non-compliance (refused to provide stool samples) after day 2 and two vaccine recipients left the study after day 6 (one wished to withdraw, the second subject went on holiday).

All three subjects attended the day 28 visit. The remaining subjects attended all study visits. Two subjects had unscheduled visits. One subject in the vaccine group attended
the clinic on day 16 because of fever of 38.1°C and one subject in the placebo group returned on day 26 with a temperature of 38.0°C. Blood cultures were obtained from both subjects and both cultures were negative. One M01ZH09 recipient had unscheduled tests performed. The subject presented on day 10 with a temperature of 38.6°C and reported diarrhoea, vomiting and fever on the previous day. The white blood count was elevated with 14.2 x 10^9/L and the blood culture result was negative.

5.3.2 Numbers analysed

All 151 children who were randomised and received either M01ZH09 (n=101) or placebo (n=50) constituted the intention to treat (ITT) population. Seven subjects, 4 in the vaccine group and 3 in the placebo group were protocol violators (see Figure 5.1) and were excluded from the per protocol (PP) population. The analysis of the primary endpoints in the PP population was planned if more than 5% of subjects were excluded from the ITT. The PP population comprised 95% (144/151) of subjects and therefore no per protocol analysis was conducted.

All outcomes were evaluated for the ITT population.

5.3.3 Baseline data

The two groups did not differ significantly at enrolment in terms of sex, age and laboratory parameters (Table 5-1). One hundred and seven (71%) children were aged 10 years or younger.
Two subjects in the M01ZH09 group had clinically significant elevated white blood counts on day 0 (see above). Twelve subjects in total, five in the placebo group and seven in the M01ZH09 group (this included the subject who vomited on the day of dosing) had a positive stool culture for non-typhoid *Salmonella* on day 0, these results were only available after dosing.
Healthy Vietnamese children aged 5 to 14 years (inclusive) were screened for eligibility, n = 205

Not eligible, n = 54
- Age under 5 years, n = 1
- Fever on day 0, n = 1
- Body weight below 27 kg (11-14 year old), n = 2
- Withdrawal from the study, n = 4
- Abnormal laboratory result, n = 6
- No stool sample provided, n = 8
- Not available for the duration of the study, n = 10
- Stool sample positive for any S. species at screening, n = 22

151 children randomised

101 children assigned to M01ZH09
- 1 subject did not take the required dose of M01ZH09
- 2 subjects withdrew after day 6
- 1 subject took antibiotics between day -14 and day 14
- 1 subject had one unscheduled visit on day 16 because of fever
- 1 subject had unscheduled blood tests on day 10 because of fever

101 children received M01ZH09
- All 101 subjects attended the day 28 visit
- All 101 subjects analysed in the ITT analysis

50 children assigned to placebo
- 1 subject withdrew after day 2
- 2 subjects took antibiotics between day -14 and day 14
- 1 subject took antibiotics between day 1, 2, and 6
- 1 subject had one unscheduled visit on day 26 because of fever

50 children received placebo
- All 50 subjects attended the day 28 visit
- All 50 subjects analysed in the ITT analysis

Figure 5.1 Flow of patients
<table>
<thead>
<tr>
<th>Characteristics</th>
<th>M01ZH09 group (n = 101)</th>
<th>Placebo group (n = 50)</th>
<th>Overall (n = 151)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age in years</td>
<td>9 (5-14)</td>
<td>9 (5-14)</td>
<td>9 (5-14)</td>
</tr>
<tr>
<td>Number of children under 10 years (%)</td>
<td>109 (75.2)</td>
<td>101 (71.1)</td>
<td>56 (80)</td>
</tr>
<tr>
<td>Number of males (%)</td>
<td>54 (53)</td>
<td>27 (54)</td>
<td>81 (54)</td>
</tr>
<tr>
<td>Weight in kilograms</td>
<td>28 (17-53)</td>
<td>26.5 (17-66)</td>
<td>27 (17-66)</td>
</tr>
<tr>
<td>Height in cm</td>
<td>132 (97-165)</td>
<td>130.50 (100-165)</td>
<td>132 (97-165)</td>
</tr>
<tr>
<td>Oral temperature in °C</td>
<td>36.80 (36.1-37.5)</td>
<td>36.75 (35.1-37.4)</td>
<td>36.80 (35.1-37.5)</td>
</tr>
<tr>
<td>Haemoglobin, g/dl*</td>
<td>13.3 (10.5-15.3)</td>
<td>13.4 (10.9-15.5)</td>
<td>13.3 (10.5-15.5)</td>
</tr>
<tr>
<td>White cell count, 10^9/L ^</td>
<td>7.2 (5-18.2)</td>
<td>8.0 (4.9-10.7)</td>
<td>7.4 (4.9-18.2)</td>
</tr>
<tr>
<td>Lymphocytes, %^</td>
<td>39.6 (14.9-55.5)</td>
<td>39.9 (21.4-67.4)</td>
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</tr>
<tr>
<td>Neutrophils, %^</td>
<td>48.6 (29.2-70)</td>
<td>50.5 (19.5-73.8)</td>
<td>49.9 (19.5-73.8)</td>
</tr>
<tr>
<td>Monocytes, %^</td>
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<td>5.0 (1.4-13.2)</td>
<td>5.2 (1.4-13.2)</td>
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<tr>
<td>Basophiles, %^</td>
<td>0.3 (0-0.7)</td>
<td>0.3 (0-0.7)</td>
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</tr>
<tr>
<td>Eosinophiles, %^</td>
<td>4.0 (0.1-18.4)</td>
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<td>3.8 (0.1-18.4)</td>
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<td>Platelet count, 10^9/L &amp;</td>
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<td>311 (190-467)</td>
<td>300 (190-503)</td>
</tr>
<tr>
<td>AST, U/L</td>
<td>27 (14-52)</td>
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<td>27 (14-52)</td>
</tr>
<tr>
<td>ALT, U/L</td>
<td>16 (6-58)</td>
<td>17 (5-43)</td>
<td>16 (5-58)</td>
</tr>
<tr>
<td>Creatinine, mM/L</td>
<td>0.47 (0.33-0.70)</td>
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</tr>
<tr>
<td>Stool culture positive for <em>Salmonella sp.</em></td>
<td>7</td>
<td>5</td>
<td>12</td>
</tr>
</tbody>
</table>

Table 5-1 Baseline characteristics of the subjects on day 0 (Intention to Treat population).

All data are presented as median (range) unless otherwise specified. Data from one*, two^ and seven& subjects not available.
5.3.4 Protocol deviations

The protocol stated that the primary safety endpoint would be the proportion of subjects reporting serious adverse events attributed to M01ZH09. Due to concerns that these numbers might be small and would not be sufficient to detect a difference in safety between the two groups, the primary endpoint was changed to the proportion of subjects with any related adverse event. This change was made after the completion of the clinical phase but prior to database lock and unblinding.

5.3.5 Outcomes and estimation

5.3.5.1 Safety Outcomes

There were no serious adverse events, no bacteraemia and none of the subjects withdrew due to adverse events in this trial.

Similar proportion of subjects reported adverse events in both treatment groups during the 28 days of follow up, but the total number of events was higher in the M01ZH09 group. In the vaccine group, 26 (26%; 95% CI 18-35%) of 101 subjects reported 64 adverse events compared to 11 (22%; 95% CI 12-36%) of 50 subjects in the placebo group who reported 17 adverse events (odds ratio (OR) = 1.23, 95% CI 0.550-2.747; \( p = 0.691 \)) (Table 5-2). Repeated occurrences of a particular adverse event in the same subject were included in the total number of 64 and 17 adverse events, respectively. Of the 64 adverse events reported by M01ZH09 recipients, 55 were mild (8 of these were considered to be related to the candidate vaccine), 8 moderate (one related) and one was
severe and related to M01ZH09 (Table 5-2). Of the 17 adverse events in the placebo group, 12 were mild, 5 moderate and none was related.

Four (4%) M01ZH09 recipients experienced 10 adverse events that were related to the candidate vaccine compared to none in the placebo group \((p = 0.302)\). Of these, 8 were mild, one moderate (diarrhoea) and one event of pyrexia was severe. The moderate and the severe related adverse events occurred in the same subject. This subject had a normal temperature on day 0, but the pre-dose blood test showed an elevated white blood cell count \((16.3 \times 10^9/L)\). The subject experienced five post vaccination adverse events occurring on day 0, including fever of 38.5 and 39.0°C, diarrhoea, headache, abdominal pain and anorexia. The subject received paracetamol and recovered.

Similar proportions of subjects experienced fever post vaccination (Table 5-2), only one subject reported fever related to M01ZH09 (see above).

Adverse events classified as gastrointestinal disorders, nervous system disorders and investigations were experienced by a higher proportion of M01ZH09 recipients (Table 5-2). Twelve (12%) vaccine recipients experienced gastrointestinal disorders compared to 1 (2%) placebo recipient \((p = 0.061)\). Nervous system disorders (headache) occurred in 9 (9%) vaccine recipients compared to 1 (2%) placebo recipient \((p = 0.166)\) and investigations were reported by 4 (4%) vaccine recipients compared to none of the placebo recipients \((p = 0.302)\). Cough was the most frequently reported adverse event, occurring in 6 (6%) M01ZH09 recipients versus 7 (14%) placebo recipients \((p = 0.124)\).
On day 1 after vaccination, faecal shedding of *S.* Typhi occurred in 47 (49%) of 95 vaccine recipients; shedding was detected by the direct method in 11 (12%) subjects and by the enriched method of culturing stools in 36 (38%) subjects. On day 2 after vaccination, faecal shedding was detected in 12 (12%) of 97 subjects (in 1 (1%) subject by direct and in 11 (11%) subjects by enriched method). Only one (1%) of 98 subjects experienced shedding on Day 3 (detected by enrichment method). In total, 51 (51%; 95% CI 41-61%) of 100 M01ZH09 subjects experienced shedding on either days 1, 2 or 3 and no subjects experienced shedding on day 4 after vaccination or later.

The presence of *S.* Typhi was detected in the stools of 1 (2%; 95% CI 0-11%) of 50 subjects in the placebo group. This occurred on day 2 and was detected using the enriched method. No fever or adverse events were recorded for this subject. The finding of a positive stool culture for *S.* Typhi in a placebo subject was only available after unblinding of the trial. All previous and all sequential stool cultures up to day 14 of this subject were negative. This isolate was identified as the vaccine strain *S.* Typhi (Ty2 *aroC* *ssaV*) ZH9 by subsequent PCR analysis.

Seven (7%) of 101 M01ZH09 recipients and 3 (6%) of 50 placebo recipients were detected to have a positive stool culture for non-typhoid *Salmonella* between day 1 and 14 after vaccination.
<table>
<thead>
<tr>
<th>Event</th>
<th>M01ZH09 (n=101)</th>
<th>Placebo (n=50)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Any adverse event</td>
<td>26 (18-35)</td>
<td>11 (12-36)</td>
</tr>
<tr>
<td>Gastrointestinal disorders (%)</td>
<td>12 (6-20)</td>
<td>1 (0-11)</td>
</tr>
<tr>
<td>Abdominal pain (%)</td>
<td>8 (6-20)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Constipation (%)</td>
<td>2 (2-4)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Diarrhoea</td>
<td>5 (2-10)</td>
<td>1 (0-7)</td>
</tr>
<tr>
<td>Nausea</td>
<td>3 (0-5)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Vomiting</td>
<td>3 (0-5)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>General disorders and administration site conditions</td>
<td>9 (4-16)</td>
<td>5 (3-22)</td>
</tr>
<tr>
<td>Chills</td>
<td>1 (0-5)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Fatigue</td>
<td>0 (0-7)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Pyrexia</td>
<td>8 (3-6)</td>
<td>3 (0-7)</td>
</tr>
<tr>
<td>Infections and infestations</td>
<td>1 (0-5)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Viral infection</td>
<td>1 (0-7)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Investigations</td>
<td>4 (1-10)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Urine colour abnormal</td>
<td>2 (0-7)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>White blood cell count increased</td>
<td>2 (0-7)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Metabolism and nutrition disorders</td>
<td>3 (1-8)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Anorexia</td>
<td>1 (0-7)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Decreased appetite</td>
<td>2 (0-7)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Nervous system disorders</td>
<td>9 (4-16)</td>
<td>1 (0-11)</td>
</tr>
<tr>
<td>Headache</td>
<td>9 (2-12)</td>
<td>14 (6-27)</td>
</tr>
<tr>
<td>Respiratory, thoracic and mediastinal disorders</td>
<td>6 (2-12)</td>
<td>7 (14)</td>
</tr>
<tr>
<td>Cough</td>
<td>6 (7)</td>
<td>14</td>
</tr>
<tr>
<td>Rhinorrhoa</td>
<td>1 (0-7)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Skin and subcutaneous tissue disorders</td>
<td>1 (0-5)</td>
<td>2 (0-11)</td>
</tr>
<tr>
<td>Rash</td>
<td>1 (0-5)</td>
<td>0 (0-7)</td>
</tr>
<tr>
<td>Hypertension</td>
<td>1 (0-5)</td>
<td>0 (0-7)</td>
</tr>
</tbody>
</table>

Table 5-2 Incidence of adverse events after vaccination during 28 days of follow up
(Intention to Treat population)
Per-subject analysis of adverse events (unlikely, possibly and probably related to the vaccine) reported during 28 days of follow up. Subjects could experience more than one adverse event. Each adverse event was only counted once for each subject and system class. There were 56 adverse events in the M01ZH09 group and 16 in the placebo group, when repeated occurrences of a particular event in the same patient were only counted once. Adverse events that were possibly or probably related to the vaccine are presented in italic. * One severe adverse event was reported.

5.3.5.2 Immunogenicity Outcomes

Ninety-eight (97%; 95% CI, 92-99%) of 101 subjects in the M01ZH09 group and 8 (16.0%; 95% CI, 7-29%) of 50 subjects in the placebo group developed a positive immune response in either the S. Typhi LPS specific serum IgG or IgA ELISA, defined as the primary endpoint (Table 3). The difference in proportions of responders between the vaccine group and the placebo group was 81.0% (95% CI; 68-89%), the lower limit of the 95% CI of this difference was greater than 50% and fulfilled the a priori defined criterion for an acceptable immune response.

Median baseline LPS specific antibody levels were comparable in both groups (Figure 5.2). In the M01ZH09 group, median IgA antibody levels increased from 3 (IQR; 3-7.2) units/ml at baseline to 94 (IQR; 19.8-231.5) units/ml and 103 (IQR; 23.9-253.5) units/ml on days 7 and 14 respectively. On day 7, the 88 immune responders in the vaccine group (Table 5-3) displayed a median 16.4 (IQR 3.75-60.25) fold rise in serum IgA antibodies relative to baseline (Table 5-4).
In the vaccine group, median LPS specific IgG antibody levels were 66650 (IQR; 31075-123900) units/ml and 55700 (IQR; 25450-106800) units/ml on day 14 and 28, respectively, compared to median baseline levels of 6300 (IQR 3620-16560) units/ml. On day 14, the 91 immune responders in the M01ZH09 group (Table 5-3) showed a median 8.18 (IQR; 3.57-20.68) fold increase in serum IgG antibodies relative to baseline.

Forty-two out of 44 eligible subjects provided samples for the ELISAPOT assay on day 7. All baseline ELISAPOT samples were negative (defined as < 4 ASC per 10^6 PBMC). On day 7, 28 (100%) of 28 M01ZH09 subjects who provided samples showed a positive ELISAPOT response compared to none (0%) of the 14 evaluable subjects in the placebo group. Sixteen (57%) of 28 M01ZH09 recipients displayed results of >100 spots per 10^6 PBMC and among the remaining 12 vaccine subjects numbers of spots ranged from 8 to 128 per 10^6 PBMC. The median number of spots in the M01ZH09 recipients was > 100 (IQR 46.5->100) spots per 10^6 PBMC, as counting stopped above 100 spots, this was recorded as "too many spots to be counted". All 14 placebo recipients showed < 4 spots per 10^6 PBMC, this was recorded as "too few spots to be counted."

There was strong correlation between the results of the IgA ELISA and the IgA ELISAPOT assays on day 7. Twenty-eight (100%) of 28 M01ZH09 recipients showed a positive immune response and 14 (100%) of 14 placebo recipients showed a negative response in both assays.
<table>
<thead>
<tr>
<th>M01ZH09 group n=101</th>
<th>Placebo group n=50</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Positive Immune response</td>
</tr>
<tr>
<td></td>
<td>No.</td>
</tr>
<tr>
<td>Detected in IgA ELISA assay</td>
<td></td>
</tr>
<tr>
<td>Day 7</td>
<td>99</td>
</tr>
<tr>
<td>Day 14</td>
<td>99</td>
</tr>
<tr>
<td>Day 7 or day 14</td>
<td>99</td>
</tr>
<tr>
<td>Detected in IgG ELISA assay</td>
<td></td>
</tr>
<tr>
<td>Day 14</td>
<td>99</td>
</tr>
<tr>
<td>Day 28</td>
<td>101</td>
</tr>
<tr>
<td>Day 14 or 28</td>
<td>101</td>
</tr>
<tr>
<td>Detected in either IgA or IgG ELISA assay</td>
<td></td>
</tr>
<tr>
<td>Day 7, 14 or 28</td>
<td>101</td>
</tr>
<tr>
<td>Detected in IgA ELISPOT</td>
<td></td>
</tr>
<tr>
<td>Day 7</td>
<td>28</td>
</tr>
</tbody>
</table>

Table 5-3 Proportions of responders to the candidate typhoid vaccine M01ZH09 (Intention to Treat population).
No., number of subjects who provided samples.

A positive immune response in the ELISA assay was defined by an increase of 50% (1.5 fold change) in LPS specific serum IgA and/or an increase of 70% (1.7 fold change) in LPS specific serum IgG compared to baseline.

*44 subjects aged 11 years and above (29 subjects in the M01ZH09 group and 15 subjects in the placebo group) were eligible for the ELISPOT.

A positive ELISPOT result was defined as ≥ 4 IgA antibody secreting cells specific for S. Typhi LPS per 10^6 PBMCs. None of the subjects had a positive day 0 ELISPOT result.
<table>
<thead>
<tr>
<th>Day</th>
<th>M01ZH09 group</th>
<th>Placebo group</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n=101</td>
<td>n=50</td>
</tr>
<tr>
<td>Median</td>
<td>IQR</td>
<td>Median</td>
</tr>
<tr>
<td>units/ml</td>
<td>units/ml</td>
<td></td>
</tr>
<tr>
<td>Serum IgA antibody levels specific for LPS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Day 0</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td>3-7.2</td>
<td>3-7.9</td>
</tr>
<tr>
<td>Day 7</td>
<td>94^</td>
<td>3.1*</td>
</tr>
<tr>
<td></td>
<td>19.8-231.5</td>
<td>3-7.4</td>
</tr>
<tr>
<td>Day 14</td>
<td>103^</td>
<td>3.4*</td>
</tr>
<tr>
<td></td>
<td>23.9-253.5</td>
<td>3-7.4</td>
</tr>
<tr>
<td>Serum IgG antibody levels specific for LPS</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Day 0</td>
<td>6300</td>
<td>6925</td>
</tr>
<tr>
<td></td>
<td>3620-16560</td>
<td>3950-10762.5</td>
</tr>
<tr>
<td>Day 14</td>
<td>66650^</td>
<td>7680*</td>
</tr>
<tr>
<td></td>
<td>31075-123900</td>
<td>4170-11500</td>
</tr>
<tr>
<td>Day 28</td>
<td>55700</td>
<td>8175</td>
</tr>
<tr>
<td></td>
<td>25450-106800</td>
<td>4402.5-12437.5</td>
</tr>
</tbody>
</table>

Data from one* and two^ subjects missing.

IQR interquartile range

Table 5-4 Serum IgA and IgG antibody levels specific for S. Typhi LPS (Intention to Treat population)
Figure 5.2 Time course of LPS specific serum IgA and IgG antibody levels.
Time course of LPS specific serum IgA (A) and IgG (B) antibody levels, according to vaccination groups (Intention to Treat population).

Box and whisker plots showing the distribution of antibodies according to time point and vaccination groups. The horizontal line within each box represents the median, the top and bottom of each box represents the 75th and 25th percentiles, respectively, and the I bar represents the highest and lowest values within 1.5 times the interquartile range. Circles show outliers.
5.4 Discussion

This is the first evaluation of a novel oral typhoid vaccine in school children in an endemic country. *S. Typhi* (Ty2 *aroC* *ssaV*) ZH9 (contained in M01ZH09) is characterised by two well defined deletion mutations, one in an aromatic amino acid biosynthesis pathway gene and the other in a functional gene of the SPI-2 type III secretion system (Hindle *et al.*, 2002). A single dose of $5 \times 10^9$ CFU of the vaccine strain was well tolerated and had an acceptable safety profile. There were no serious adverse events, no withdrawals due to adverse events and none of the subjects experienced bacteraemia.

In general, adverse events were mild. Similar proportions of subjects, 26% (26 of 101) in the candidate vaccine group and 22% (11 of 50) in the placebo group reported adverse events during the 28 day follow up period ($p = 0.691$). The overall number of adverse events tended to be higher in the M01ZH09 group, especially those classified as gastrointestinal disorders, nervous system disorders and investigations.

There was one severe related adverse event in this trial, a high fever of 39.0°C which occurred on day 0 after vaccination in a subject who had a pre-dose elevated white blood count ($18.2 \times 10^9$/L) and might have suffered from an underlying infection. One other subject vomited after drinking approximately half of the vaccine dose, this subject was found to have a positive stool culture for non-typhoid *Salmonella* on day 0.

*S. Typhi* was isolated from the stools of one placebo recipient on day 2 after vaccination which was later identified as *S. Typhi* (Ty2 *aroC* *ssaV*) ZH9 by PCR
analysis. The previous stool cultures and all following stool cultures of this subject up to day 14 were negative. After a thorough check, which included the randomisation codes and vaccination paperwork, the possibility that the subject received M01ZH09 by error was excluded. The subject also did not display any positive results in the immunogenicity assays. It was concluded that the most likely cause for isolating S. Typhi (Ty2 aroC ssaV) ZH9 in the stools of a placebo recipient was the mislabelling or mismatch of stool samples.

The candidate vaccine elicited a positive immune response in 97% (98/101) of the M01ZH09 recipients by ELISA and in 100% (28/28) of M01ZH09 recipients who were evaluable by ELISPOT assay. In conclusion M01ZH09 was safe and immunogenic in Vietnamese children.

The observed safety and immunogenicity profile of the candidate typhoid vaccine in children compares favourably to that seen in Western adult volunteers. M01ZH09 has been tested so far up to a nominal dose level of $5 \times 10^9$ CFU in nine UK volunteers (Hindle et al., 2002) and 80 US volunteers (Kirkpatrick et al., 2005b; Kirkpatrick et al., 2006). Immunogenicity results from previously published M01ZH09 trials used a 4 fold or higher increase in LPS specific IgG antibody levels as definition of a positive immune response in the endpoint titre ELISA and seroconversion rates were 50% (8/16 subjects) (Kirkpatrick et al., 2006) and 77.4% (24/31 subjects) (Kirkpatrick et al., 2005b). In this study, allowing for these different cut-offs, the magnitude of the immune response seen in the children was approximately 30 fold and 10 fold increase of median levels of LPS specific IgA and IgG antibodies, respectively. Furthermore, the
median number of ASCs producing LPS specific IgA antibodies, a measure for priming of the mucosal immune system, was greater than 100 per $10^6$ PBMC in this trial, this compares favourably to an arithmetic mean of 118 ASC/$10^6$ PBMC seen in a previous M01ZH09 trial in adults (Kirkpatrick et al., 2006) and a geometric mean of 119 ASC/$10^6$ PBMC (producing IgA and IgG) seen in American volunteers who received 4 doses of the licensed Ty21a typhoid vaccine at a dose of $2-6 \times 10^9$ CFU (Kantele et al., 1998).

This is encouraging as one major concern for the development of many oral vaccines has been their reduced immunogenicity when tested in developing country populations compared to Western volunteers (Dougan et al., 2002; Levine, 2006). For oral vaccines a brisk colonisation of the intestine is necessary to become immunogenic, it might be possible that drug resistant commensals, bacterial overgrowth, enteric viruses or helminths interfere with the colonisation of the new vaccine (Levine and Campbell, 2004). In this study, 51% (51/100) of vaccine recipients shed S. Typhi (Ty2 aroC ssaV ) ZH9 in stools after vaccination, one subject excreted the vaccine strain on day 3, but no shedding was observed on day 4 and beyond. In Western adult volunteers shedding of S. Typhi in stools was reported for slightly longer durations and ranged from 1 to 6 days and 1 to 7 days in a small number of volunteers, respectively (Hindle et al., 2002; Kirkpatrick et al., 2005b).

Typhoid fever is still a major health problem in developing countries, with high incidence (Crump et al., 2004; Ochiai et al., 2008) and high rates of antimicrobial drug resistance, especially in Asia (Chau et al., 2007; Ochiai et al., 2008). The WHO
recommends the immunisations of school and preschool children in endemic areas, especially where drug resistant typhoid fever is prevalent as well as in epidemic situations (World Health Organization, 2006, 2008). M01ZH09 is a promising novel oral one dose typhoid vaccine and large trials are necessary to evaluate vaccine efficacy. If protection from typhoid fever is demonstrated, M01ZH09 may facilitate large vaccination campaigns due to its simpler logistic and broader acceptance from children.
Chapter 6

Conclusions
This thesis aims to evaluate different aspects of typhoid fever and to provide better understanding of this disease. This chapter will summarise key findings from the thesis and point at future avenues of research.

Chapter 2 described a randomised clinical trial conducted in the Mekong Delta in Vietnam that compared gatifloxacin to azithromycin for the treatment of multidrug and nalidixic acid resistant typhoid fever. Two hundred and eighty-seven patients, both adults and children, with blood culture confirmed typhoid fever were enrolled, 145 were treated with gatifloxacin and 142 patients with azithromycin. Both antibiotics showed an excellent efficacy and safety profile. The median FCT was 106 hours in both arms and overall treatment failure (defined as any of the following: persistence of fever till day 10, need for re-treatment, blood culture positive on day 7, development of complications, relapse or faecal carriage) occurred in approximately 9% of patients in both arms (13/145 patients in the gatifloxacin group and 13/140 patients in the azithromycin group, respectively). Ninety-six percent (254/263) of the S. Typhi isolates were resistant to nalidixic acid and 58% (153/263) were multidrug resistant.

This trial was part of a series of clinical trials to evaluate the antibiotic regimen recommended for the treatment of typhoid fever by the WHO (World Health Organization, 2003). Particular attention was paid to the design of these trials, to respond to criticism made by the authors of a recent Cochrane review (Thaver et al., 2008). Typically clinical trials in typhoid fever have been small, outcomes have been defined at the discretion of the investigators, length of follow up varied, and they have often not included children, although this is the age group predominantly affected by
the disease (Thaver et al., 2008). The trial presented in this thesis and subsequent work (not included here) aimed to address these reasonable criticisms by designing large clinical trials using a standardised trial design with adequate sample sizes that include all age groups to facilitate subsequent meta-analyses.

Blood culture, the gold standard for the diagnosis of typhoid fever is estimated to have only 40% to 60% sensitivity (World Health Organization, 2003; Parry et al., 2002). Therefore, a large proportion of patients in typhoid trials is blood culture negative for S. Typhi and only diagnosed clinically (World Health Organization, 2003), until now these patients have been excluded from the analysis. The trial described in Chapter 2 reported an a priori defined “intention to treat” analysis including blood culture negative patients, as well as the “per protocol” analysis of those patients with blood culture confirmed typhoid fever. In my view this has addressed some of the criticisms from the Cochrane review (Thaver et al., 2008) and has helped establishing standard methods for the design of clinical trials in typhoid fever.

These excellent results for gatifloxacin seen in this trial are supported by two subsequent trials conducted in Kathmandu, Nepal (Arjyal et al., 2011; Pandit et al., 2007). In total, these two trials enrolled 265 patients with culture confirmed typhoid fever who were treated with gatifloxacin (Arjyal et al., 2011; Pandit et al., 2007), both trials also monitored daily blood glucose levels. There were no clinically relevant dysglycaemias in these young patients.
Gatifloxacin has also been used for the treatment of pulmonary tuberculosis. A randomised controlled trial evaluating gatifloxacin-containing short-course (4 months) regimen against standard regimen for the treatment of pulmonary tuberculosis has been conducted in 5 African countries (Benin, Guinea, Kenya, Senegal and South Africa) between 2005 and 2011 (Olliaro P., 2011). A total of 1836 patients have been recruited in this trial, 917 were randomised to the gatifloxacin arm. The incidence rates of dysglycaemic events were similar in the gatifloxacin and control arms (Olliaro P., 2011).

As outlined in the discussion of Chapter 2, gatifloxacin was withdrawn from the US and Canadian market following a report of increased risk of dysglycaemia in elderly Canadians (Park-Wyllie et al., 2006). A group of investigators including myself has recently submitted an application to WHO to include gatifloxacin in the Essential Medicines List (EML) for the indications typhoid fever and tuberculosis (Olliaro P., 2011). Unfortunately, this has been rejected by the WHO committee in April 2011 on the basis, that there were alternative therapeutic options available. We are in the process of challenging the decision from the WHO committee and discussing options to try and ensure gatifloxacin remains available for specific populations and indications.

There is clearly a different risk/benefit ratio of gatifloxacin in different populations. Whilst there have been side effects of hypo- and hyperglycaemia in multimorbid elderly patients, possibly because of age-related decreases in renal function (Ambrose et al., 2003), these side effects have not been seen in young and otherwise healthy patients. We have few drugs available for the treatment of multidrug and nalidixic acid resistant
typhoid fever. The third generation cephalosporins are no real alternatives, as intravenous ceftriaxone shows slow fever clearance and clinical response (average FCT of one week) (Parry et al., 2002), and a clinical trial using oral cefixime had to be stopped early by the Data and Safety Monitoring Board due to poor performance (Pandit et al., 2007).

From the evidence of these studies in predominantly young and otherwise healthy patients gatifloxacin is effective, safe and affordable. It would be a shame if gatifloxacin were not available for the treatment of typhoid fever and tuberculosis in young people due to adverse events in a different patient population, i.e. elderly multimorbid Canadians. We are running out of antibiotics, we should be careful before we discard effective and safe drugs.

A lot of thought and effort has been put into the development of protocols and the design of case record forms (CRFs) during these studies. These resources will be made available for other researchers on www.enterics.org, which will be linked with the e-research hub, accessible via http://ght.globalhealthhub.org/.

The WHO guidelines (World Health Organization, 2003) which still recommend cefixime for the treatment of multidrug and nalidixic acid resistant S. Typhi, urgently need to be updated on the basis of clinical evidence. The Oxford University Clinical Research Unit Vietnam is involved in producing up-to-date guidelines in collaboration with the Coalition Against Typhoid.
Chapter 3 described the pharmacodynamic analysis of the gatifloxacin arm of the trial presented in Chapter 2. A dichotomous categorical breakpoint for $\text{AUC}_{0-24}: \text{MIC}$ ratio was identified. Patients in whom an $\text{AUC}_{0-24}: \text{MIC}$ ratio of greater than 92.7 was obtained, had a favourable response to treatment in 93.5%, whilst in patients with $\text{AUC}_{0-24}: \text{MIC}$ ratios $\leq 92.7$ only 75% had a favourable response. A borderline significant dichotomous categorical gatifloxacin MIC breakpoint for *S. Typhi*, predictive for clinical response, could be identified. *S. Typhi* gatifloxacin MIC values $\geq 0.19$ mg/L were associated with 83.8% of patients having a positive clinical response, while patients with gatifloxacin MIC values less than 0.19 mg/L had in 94.3% positive response. In gatifloxacin treated patients infected with nalidixic acid susceptible (n=6) and nalidixic acid resistant (n=118) organisms, clinical success rates were 100% and 91%, respectively. Thus, based on the nalidixic acid screening test, nalidixic acid susceptibility predicts success 100% of the time (n=6/6), whereas nalidixic acid resistance predicts failure only 9.3% of the time (n=11/118). Therefore the nalidixic acid screening test is not suited to predict gatifloxacin failure.

There has been criticism that the CLSI fluoroquinolone breakpoints for *Salmonella* were too generous. The MIC breakpoints for ciprofloxacin against extraintestinal *Salmonella* have been recently revised by CLSI and these new breakpoints will be published in 2012. In June 2011 the gatifloxacin breakpoints will be reviewed. The data presented in Chapter 3 has been made available to CLSI.

Chapter 4 described the population structure of the *S. Typhi* strains isolated during the clinical trial. The *S. Typhi* isolates were very homogenous, the vast majority of *S. Typhi*
(n = 261, 98%) in the Mekong delta region belonged to the H58 haplogroup, which expanded and persisted under antibiotic pressure.

Chapter 5 looked at novel and improved typhoid vaccines and described the safety and immunogenicity trial of a novel oral one dose typhoid vaccine in healthy Vietnamese children.

The adverse events were generally mild and the vaccine showed acceptable immunogenicity in these children. The next step would require an efficacy trial in an endemic region, however these trials are prohibitively expensive, at an estimated cost of 1 Million US per 1000 subjects. Therefore the next phase for the M01ZH09 vaccine is a typhoid challenge study that is currently being performed at Oxford University, UK (Principal Investigator Professor Andrew Pollard).

This thesis has addressed clinical issues, in particular aiming to establish a standard design for randomised clinical trials in typhoid fever and the use of pharmacokinetic and pharmacodynamic parameters, a better understanding of the population structure of S. Typhi in a region of high transmission and the assessment of a one dose oral typhoid vaccine.

In 2011, it is the tenth anniversary of the publication of the genome sequence of S. Typhi CT18, isolated in Vietnam (Parkhill et al., 2001a). A lot has been accomplished in the last decade since this seminal publication, but much still remains to be done.

We need to define the best treatment strategies and ensure we design trials in a way that permits more informative meta-analyses. There has been renewed interest in the
development of new vaccines for typhoid and paratyphoid fever and also for non-Typhi
*Salmonella*. Although there are great challenges to the development of these vaccines,
it should be possible. Perhaps a greater question is whether these vaccines can be fully
developed and made available to low income countries.

It is possible to consider the elimination or even eradication of typhoid fever. To do this
a multidisciplinary approach would be required, including appropriate treatment of
patients with effective antibiotics that cure the patient and also prevent secondary
transmission and chronic carriage, the use of appropriate vaccines and the improvement
of the infrastructure in low-income countries.
Publications arising from this thesis


Relationship thesis-publications

Chapter 1 of this thesis is in part based on the Review “Typhoid fever and other enteric fevers” written for “Infectious diseases. J. Cohen, W.G. Powderley (Eds.)”. Parts of Chapter 1 have been used for the gatifloxacin EML application to WHO (http://www.who.int/selection_medicines/committees/expert/18/applications/Cochrane_Gatifloxacin.pdf). The results of the clinical trial reported in Chapter 2 have been published in PLoS One (Dolecek et al., 2008). The discussion has been updated to include more recent trials. Part of the results described in Chapter 3 of this thesis, have been reported at the Interscience Conference on Antimicrobial Agents and Chemotherapy (ICAAC) 2008, Washington D. C. Chapter 4 is based on a publication in PLoS Negl Trop Dis. 2011 (Holt et al.). The results described in Chapter 5 have been published in PLoS ONE 2010 (Tran et al.).
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Bacterial agents of enteric diseases of public health concern. Manual for the laboratory 
identification and antimicrobial susceptibility testing of bacterial pathogens of public 
health concern in the developing world. 

use in tsunami-affected areas. 

Epidemiol Rec* 49-60.

Appendix
Gatifloxacin versus chloramphenicol for uncomplicated enteric fever: an open-label, randomised, controlled trial

Amid Agar, Paubha Basnyat, Samir Koirala, Abhijit Karki, Sahil Dangol, Krishna Kumar Agrawal, Niki Shrestha, Kehin Shrestha, Manish Sharma, Saraju Lemos, Kantai Shrestha, Noly Shrestha Bhuital, Umesh Shrestha, James Campbell, Stephen Baker, Jeremy Fazal, Mark Welber, Christiane Dobroch

Summary

Background We aimed to investigate whether gatifloxacin, a new generation and affordable fluoroquinolone, is better than chloramphenicol for the treatment of uncomplicated enteric fever in children and adults.

Methods We did an open-label randomised superiority trial at Patan Hospital, Kathmandu, Nepal, to investigate whether gatifloxacin is more effective than chloramphenicol for treating uncomplicated enteric fever. Children and adults clinically diagnosed with enteric fever received either gatifloxacin (10 mg/kg) once a day for 7 days, or chloramphenicol (75 mg/kg per day) in four divided doses for 14 days. Patients were randomly allocated treatment (1:1) in blocks of 50, without stratification. Allocations were placed in sealed envelopes opened by the study physician once a patient was enrolled into the trial. Masking was not possible because of the different formulations and ways of giving the two drugs. The primary outcome measure was treatment failure, which consisted of at least one of the following: persistent fever at day 10, need for rescue treatment, microbiological failure, relapse until day 31, and enteric-fever-related complications. The primary outcome was assessed in all patients randomly allocated to disease treatment and reported separately for culture-positive patients and for all patients. Secondary outcome measures were fever clearance time, late relapse, and face carriage. The trial is registered on controlled-trials.com, number ISRCTN 53258327.

Findings 844 patients with a median age of 16 (IQR 9–22) years were enrolled in the trial and randomly allocated a treatment. 852 patients had blood-culture-confirmed enteric fever: 175 were treated with chloramphenicol and 177 with gatifloxacin. 14 patients had treatment failure in the chloramphenicol group, compared with 12 in the gatifloxacin group (hazard ratio [HR] of time to failure 0.86, 95% CI 0.49–1.52, p=0.60). The median time to fever clearance was 3–95 days (95% CI 2.68–4.68) in the chloramphenicol group and 3–90 days (1.55–4.27) in the gatifloxacin group (HR 1.06, 0.86–1.32, p=0.59). At month only, 3 of 148 patients were stool-culture positive in the chloramphenicol group and none in the gatifloxacin group. At the end of 3 months only one person had a positive stool culture in the chloramphenicol group. There were no other positive stool cultures even at the end of 6 months. Late relapses were noted in 3 of 175 patients in the culture-confirmed chloramphenicol group and two of 177 in the gatifloxacin group. There were no culture-relapse failures after day 62. 99 patients (24%) experienced 168 adverse events in the chloramphenicol group and 59 (14%) experienced 73 events in the gatifloxacin group.

Interpretation Although no more efficacious than chloramphenicol, gatifloxacin should be the preferred treatment for enteric fever in developing countries because of its shorter treatment duration and fewer adverse events.

Funding Wellcome Trust.

Introduction

Enteric fever is a disease that predominantly affects children and is caused by the faecal–oral transmission of *Salmoneilla enterica* serotypes Typhus (S. typhi) and *Salmonella enterica* Paratyphii A (S. paratyphi A). There are an estimated 26 million infections and over 200,000 deaths caused by the disease worldwide each year. In parts of south Asia, the incidence of enteric fever in children can be as high as 573 cases per 100,000 person years.

Chloramphenicol was the standard treatment for enteric fever from the 1950s until the development and spread of multidrug-resistant (MDR; defined as resistance to all first-line antibiotics: chloramphenicol, amoxicillin, and co-trimoxazole) S. typhi and S. paratyphi A in the early 1990s. Subsequently, fluoroquinolones became first choice for the treatment of enteric fever. However, increased resistance to the older generation fluoroquinolones (ciprofloxacin and ofloxacin) has emerged. This reduces the options for treatment, and raises the specter of fully resistant enteric fever. Conflicting reports have emerged from randomised controlled trials with relatively small sample sizes that assessed older fluoroquinolones (ciprofloxacin and ofloxacin) versus chloramphenicol for the treatment of enteric fever. Additionally, no trials have been done to investigate the efficacy of chloramphenicol versus a newer fluoroquinolone, such as gatifloxacin, in the
treatment of enteric fever in children. Recent reports suggest a general decline in the prevalence of MDR typhoid fever in Asia, and two recent studies of patients with enteric fever in Kathmandu, Nepal, reported a low prevalence of chloramphenicol resistance in S. typhi and S. paratyphi A isolates: nine (1.7%) of 522 strains of S. typhi and three (1.2%) of 247 strains of S. paratyphi A. Gatifloxacin was effective in the treatment of nalidixic-acid-resistant enteric fever in two previous randomized trials done in Nepal and Vietnam. The drug targets both DNA gyrase and topoisomerase IV and hence is less inhibited by the common mutations of the gyrA gene of S. typhi than are ciprofloxacin or ofloxacin. We designed a randomized controlled trial to assess whether gatifloxacin had superior efficacy compared with chloramphenicol in adults and children with uncomplicated enteric fever in Nepal.

**Methods**

**Patients**
The study physicians enrolled patients who presented to the outpatient or emergency department of Patan Hospital, Lalitpur, Nepal from May 2, 2006, to August 30, 2008. Patients with fever for more than 3 days who were clinically diagnosed to have enteric fever (undiagnosed fever with no clear focus of infection on physical exam and laboratory tests) whose residence was in a predesignated area of about 20 km² in urban Lalitpur and who gave fully informed written consent were eligible for the study. Exclusion criteria were pregnancy or lactation, age under 2 years or weight

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**Figure 2: Trial profile**

*Two culture-positive patients in both the chloramphenicol and gatifloxacin groups were lost to follow-up before day 8.*
less than 30 kg, shock, jaundice, gastrointestinal bleeding, or any other signs of severe typhoid fever, previous history of hypersensitivity to either of the trial drugs, or known previous treatment with chloramphenicol, quinuprine, gatifloxacin, third generation cephalosporin, or macrolide within 1 week of hospital admission. Patients who had received amoxicillin or cotrimoxazole were included as long as they did not show evidence of clinical response. Ethical approval was granted by both Nepal Health Research Council and Oxford Tropical Research Ethics Committee.

Randomisation and masking
Randomisation was done in blocks of 50 without stratification by an administrator otherwise not involved in the trial. The random allocations were placed in sealed opaque envelopes, which were kept in a locked drawer and opened by the study physician once each patient was enrolled into the trial after meeting the inclusion and exclusion criteria. Patients were enrolled in the order they presented and the sealed envelopes were opened in strict numerical sequence. Masking was not possible because of the different formulations and ways of giving the two drugs.

Procedures
Each enrolled patient was randomly assigned to treatment with either gatifloxacin tablets (400 mg) 10 mg per kg per day in a single oral dose for 7 days or chloramphenicol capsules (250 mg or 500 mg) 75 mg per kg per day in four divided oral doses for 14 days. Gatifloxacin tablets were cut and weighed and the patients’ daily doses were prepared in sealed plastic bags. The pre-protocol planned duration of chloramphenicol treatment of 14 days was modified for blood-culture-negative patients, who received at least 8 days of chloramphenicol and stopped either on day 8 or 5 days after being afebrile, whichever came later. Gatifloxacin was given for 7 days in all patients.

After enrolment, patients were managed as outpatients and seen by trained community medical auxiliaries (CMAs), as described previously. The CMAs made a visit to each patient’s house every 12 h for either 10 days (gatifloxacin group) or 14 days (chloramphenicol group) or until the patient was cured. The CMA directly observed each patient ingesting the single dose of gatifloxacin and two doses of chloramphenicol. The physicians re-examined the patients on days 8 and 15, and at 1, 3, and 6 months. All examinations were standardised and entered into case record forms.

Complete blood counts were done on days 1, 8, and 15. On day 1, serum creatinine, bilirubin, aspartate aminotransferase (AST), and alanine aminotransferase (ALT) were also checked. Random plasma glucose was measured on day 1, day 8, day 15, and 1 month. On days 2–7, during the evening visit, the blood glucose was measured by finger-prick testing (OneTouch SureStep, Johnson and Johnson, USA) by the CMAs. Haemoglobin Acr was measured at 3 months.

Blood culture was done as described previously in all patients at admission, in the culture-positive patients on day 8, and if symptoms and signs suggested further infection.

Blood cultures were done on admission in all patients, and in culture-positive patients after completion of treatment and at the 1 month, 3 month, and 6 month visits in 10 ml of Selenite F broth and incubated at 37°C. After the overnight incubation, the broth was subcultured onto MacConkey agar and xylene lysine deoxycholate agar media.

Isolates were screened using standard biochemical tests, and 5 multiplex of 5 pat ways A were identified using API 20E (BioMerieux, Paris, France) and slide agglutination with specific antisera (Murex Biotech, Dartford, UK).

Minimum inhibitory concentrations (MICs) were calculated for amoxicillin, azithromycin, chloramphenicol, cotrimoxazole, nalidixic acid, ofloxacin, ciprofloxacin, tetracycline, gatifloxacin, and cefixime by Etest (AB Biodeck, Solna, Sweden).

The primary endpoint of this study was the composite endpoint of treatment failure, which consisted of any one of the following: persistence of fever of more than 37.5°C at day 10 of treatment; the need for rescue treatment with

<table>
<thead>
<tr>
<th>Procedure</th>
<th>Chloramphenicol</th>
<th>Gatifloxacin</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blood test</td>
<td>1-5(8-22)</td>
<td>1-5(8-22)</td>
</tr>
<tr>
<td>Mac testing</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
<tr>
<td>Blood culture</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
<tr>
<td>Abdominal pain</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
<tr>
<td>Gastroenteritis</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
<tr>
<td>Nausea</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
<tr>
<td>Vomiting</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
<tr>
<td>Diarrhoea</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
<tr>
<td>Constipation</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
<tr>
<td>Hepatitis</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
<tr>
<td>Gastroonenteritis</td>
<td>100(5-95)</td>
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<tr>
<td>Gastroonenteritis</td>
<td>100(5-95)</td>
<td>100(5-95)</td>
</tr>
</tbody>
</table>

Table 1: Baseline characteristics of patients according to treatment group.
Articles

<table>
<thead>
<tr>
<th>Chloramphenicol (n=75)</th>
<th>Gatifloxacin (n=77)</th>
<th>Comparison</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total number of treatment failures*</td>
<td>14</td>
<td>12</td>
</tr>
<tr>
<td>Proven fever at day 10</td>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td>Need for rescue treatment</td>
<td>5</td>
<td>3</td>
</tr>
<tr>
<td>Microbiological failure</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>Relapse until day 72</td>
<td>7</td>
<td>4</td>
</tr>
<tr>
<td>Enteric fever-related complications</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Probability of treatment failure</td>
<td>0.068 (CI 0.00 to 0.11)</td>
<td>0.047 (CI 0.00 to 0.09)</td>
</tr>
<tr>
<td>Median time to fever clearance (day)**</td>
<td>3.9 (95% CI 3.4 to 4.4)</td>
<td>1.9 (95% CI 1.8 to 2.7)</td>
</tr>
<tr>
<td>Microbiological failure</td>
<td>0/7 (0%)</td>
<td>2/10 (20%)</td>
</tr>
<tr>
<td>Relapse until day 31</td>
<td>5</td>
<td>4</td>
</tr>
<tr>
<td>Number of culture confirmed relapses</td>
<td>5</td>
<td>3</td>
</tr>
<tr>
<td>Number of syndromic relapses</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>Probability of relapse until day 31</td>
<td>0.44 (95% CI 0.00 to 0.05)</td>
<td>0.09 (95% CI 0.00 to 0.09)</td>
</tr>
<tr>
<td>Relapse until day 62</td>
<td>10</td>
<td>9</td>
</tr>
<tr>
<td>Number of culture confirmed relapses</td>
<td>8</td>
<td>6</td>
</tr>
<tr>
<td>Number of syndromic relapses</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>Probability of relapse until day 62</td>
<td>0.44 (95% CI 0.00 to 0.09)</td>
<td>0.06 (95% CI 0.00 to 0.09)</td>
</tr>
<tr>
<td>Relapse after day 62 (all of which were syndromic)</td>
<td>4</td>
<td>10</td>
</tr>
</tbody>
</table>

*Includes only patients with diabetes. **Includes the difference [based on Kaplan-Meier estimates]. Patients can have more than one type of treatment failure.

Table 2: Summary of primary and secondary outcomes for culture-positive patients (per-protocol analysis)

cotrimoxazole or ceftriaxone as judged by the treating physician; microbiological failure, defined as a positive blood culture for S. typhi or S. paratyphi A on day 8 relapse; that is reappearance of culture-confirmed (including mismatch of serotypes e.g. day 1 blood culture positive for S. typhi and relapse blood culture positive for S. paratyphi A or vice versa) or syndromic enteric fever on or after day 11 to day 31 in patients who were initially categorised as successfully treated; and occurrence of enteric-fever-related complications. Time to treatment failure was defined as the time from the first dose of treatment until the date of the earliest failure event of that patient, and patients without an event were censored at the date of their last follow-up visit.

Secondary endpoints were fever clearance time (FCT); time from the first dose of treatment given until the temperature was <37.5°C and the patient remained afebrile for at least 48 h; time to relapse until day 31, day 62, or month 6 of follow-up; and fecal carriage at the follow-up visits at 1, 3, and 6 months. The patients' FCTs were calculated electronically on the basis of twice-daily recorded temperatures. Patients without recorded fever clearance or relapse were censored at the date of their last follow-up visit. To reduce possible bias, an investigator not involved in the recruitment of patients decided patients' final outcomes by use of a masked database.

Statistical analysis

The trial was designed as a superiority trial with the hypothesis that gatifloxacin was superior to chloramphenicol in patients with enteric fever. The sample size was calculated to detect a difference of 10% between the two groups in the proportion of patients reaching treatment failure at the two-sided 5% significance level with 80% power. We assumed treatment failure rates of 15% in the chloramphenicol and 3% in the gatifloxacin group, leading to a total required sample size of 160 patients with culture-confirmed enteric fever per group—320 patients in total. On the basis of results from a previous study, we assumed that about 40% of patients who were randomly assigned treatment had culture-confirmed enteric fever. To allow for a loss to follow-up rate of about 5%, a total of 853 patients with suspected enteric fever were recruited to the trial.

Times to treatment failure, fever clearance, and relapse were analysed by use of survival methods. The cumulative incidence of events was calculated with the Kaplan-Meier method, and comparisons were based on Cox regression models with the treatment group as the only covariate. For the primary endpoint (treatment failure), we also compared the absolute risk of treatment failure until day 31 on the basis of Kaplan-Meier estimates and standard errors according to Greenwood's formula.

Additionally, the time to treatment failure was analysed in the subgroups defined by culture result, pathogen (S. typhi or S. paratyphi A), and age (<46 years or ≥46 years), and heterogeneity of the treatment effect was tested with a Cox regression model that included an interaction between treatment and subgroup.

The per-protocol analysis population consisted of all patients with blood-culture-confirmed enteric fever.
We also analysed all patients who were assigned treatment, with the exception of those patients who were mistakenly randomised or withdrew before the first dose of study treatment, for treatment failure and safety.

All reported tests were done at the two-sided 5% significance level, and 95% CIs are reported. All analyses were done with the statistical software R version 2.9.1.10

The trial is registered on controlled-trials.com, number ISRCTN 53313327.

Role of the funding source
The sponsor of the study had no role in study design, data collection, data analysis, data interpretation, or writing of the report. The corresponding author had full access to all the data in the study and had final responsibility for the decision to submit for publication.

Results
Of 1151 patients assessed, 853 were assigned treatment; 844 were analysed. 418 assigned chloramphenicol and
46 gatifloxacin (figure 1). The baseline characteristics of the patients were similar in the two treatment groups (table 1). The proportion of patients with treatment failure was similar in the two treatment groups in patients with culture-positive disease (table 2). Of the five patients with persistent fever on day 10 in the gatifloxacin group, two became afebrile on day 11 and did not require rescue treatment. The other three patients were effectively treated with intravenous ceftriaxone 50 mg/kg per day in a single dose for 7 days. The five patients in the chloramphenicol group who needed rescue treatment were successfully treated with ceftriaxone 20 mg/kg per day in two divided doses per day for 7 days. In all cases, rescue treatment was initiated on either day 10 or day 11.

Two patients with microbiological failure in the gatifloxacin group also had persistent fever, and responded well to ceftriaxone 50 mg/kg per day in a single daily dose for 7 days. All relapse patients, consisting of seven (five of whom were culture confirmed) in the gatifloxacin group, were also treated with ofloxacin 20 mg/kg per day, and recovered.

The secondary outcome measures, which included fewer clearance time (median 3.95 days in the chloramphenicol group and 3.90 in the gatifloxacin group) and time to relapse until day 31 or day 62 also showed no significant difference between the groups (table 2). Only systemic relapses were documented between day 62 and 6 months. Figure 2 shows the Kaplan-Meier estimates for the time to treatment failure, fever clearance, and relapse.

Stool samples at baseline were positive for S. typhi or S. paratyphi A in 16 (30%) of 52 patients in the chloramphenicol group and 14 (7%) of 162 patients in the gatifloxacin group. The proportion of positive stool samples at 1-6 months of follow-up was low in both groups: at 1 month, only three (2%) of 148 and none of 154 patients were stool-culture-positive in the chloramphenicol and gatifloxacin groups (p=0.12), respectively.

At the end of 3 months, only one patient (in the chloramphenicol group) had a positive stool culture, and at 6 months no patients had a positive stool culture.

Table 1 shows the primary and secondary endpoints in all randomized patients, with the exception of patients who were mistakenly randomly allocated to treatment or withdrew before the first dose of study treatment. There was a slightly greater risk of treatment failure in patients receiving chloramphenicol (p=0.09). Results in selected subgroups (table 6) suggest that this is primarily due to a higher failure rate of chloramphenicol in the culture-negative population, especially a higher rate of relapses until day 31 [nine (three confirmed, six suspected) vs two (both confirmed): HR of time to relapse=0.22, 95% CI 0.05-0.91, p=0.05]. The median duration of chloramphenicol treatment was 9 days (IQR 8-11) in the culture-negative population, but there was not a significant association between the duration of treatment and the time to relapse (HR=0.93, 95% CI 0.66-1.30, p=0.66).

Table 4: Comparison of treatment failure in the culture-positive and culture-negative population and selected subgroups

<table>
<thead>
<tr>
<th>Chloramphenicol</th>
<th>Gatifloxacin</th>
<th>p for heterogeneity*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Population</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Culture-positive</td>
<td>14 (75%)</td>
<td>12 (72%)</td>
</tr>
<tr>
<td>Culture-negative</td>
<td>5 (25%)</td>
<td>5 (28%)</td>
</tr>
<tr>
<td>Rathmann</td>
<td>6/12 (50%)</td>
<td>3/10 (30%)</td>
</tr>
<tr>
<td>Sites of infection</td>
<td>11 (72%)</td>
<td>8 (56%)</td>
</tr>
<tr>
<td>Salmonella typhi</td>
<td>3/16 (19%)</td>
<td>2/20 (10%)</td>
</tr>
<tr>
<td>Afebrile</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age &lt; 10 years</td>
<td>18/32 (56%)</td>
<td>17/30 (56%)</td>
</tr>
<tr>
<td>Mortality</td>
<td>1 (1.6%)</td>
<td>3 (4.6%)</td>
</tr>
</tbody>
</table>

*Heterogeneity was tested with a Cochran-Mantel-Haenszel test that included an interaction between treatment and subgroup.

Table 5: Adverse events comparison of overall frequency and frequency of selected adverse events between the two treatment groups

<table>
<thead>
<tr>
<th>Adverse event</th>
<th>Chloramphenicol (n=88)</th>
<th>Gatifloxacin (n=44)</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Any adverse event</td>
<td>96 (104)</td>
<td>48 (109)</td>
<td>0.0306</td>
</tr>
<tr>
<td>Adverse event</td>
<td>Number of patients with event (%)</td>
<td>Number of events</td>
<td>Number of patients with event (%)</td>
</tr>
<tr>
<td>Acute</td>
<td>32/88 (36%)</td>
<td>17/44 (39%)</td>
<td>0.063</td>
</tr>
<tr>
<td>Diarrhea</td>
<td>24/88 (27%)</td>
<td>12/44 (27%)</td>
<td>0.907</td>
</tr>
<tr>
<td>Nausea</td>
<td>36/88 (40%)</td>
<td>29/44 (66%)</td>
<td>0.010</td>
</tr>
<tr>
<td>Gastrointestinal</td>
<td>8/44 (18%)</td>
<td>8/44 (18%)</td>
<td>0.713</td>
</tr>
<tr>
<td>Gastrointestinal</td>
<td>4/44 (9%)</td>
<td>4/44 (9%)</td>
<td>0.713</td>
</tr>
</tbody>
</table>

All adverse events in column 1 were less than 5% in grade 1, grade 2, or grade 3, except for one grade 1 demerit in the chloramphenicol group and one grade 1 severe event in the gatifloxacin group. *Based on Fisher's exact test.
There was no indication of treatment effect heterogeneity in the subgroups defined by pathogen or age (table 6).

Most adverse events were mild (grade 1 and 2; table 3). Adverse events were slightly more common in the culture-positive patients than the culture-negative patients. In the chloramphenicol group, 44 (25%) of 175 culture-positive patients experienced at least one adverse event (81 events in total). In the gatifloxacin group, 30 (16.7%) of 177 culture-positive patients experienced at least one adverse event (58 events in total). Three patients in the chloramphenicol group had a white-blood-cell count between 1500 and 3000 cells per 1 on day 3-8, and had their chloramphenicol stopped. No grade 3 or 4 leucopenia was recorded (table 6). No grade 4 hypoglycemia was recorded (table 7), and there were no life-threatening complications of enteric fever in this cohort.

Of all the strains of S paratyphi A and S typhi isolated, 251 (73%) of 345 were nalidixic acid resistant, and two (0.6%) were multidrug resistant (table 8). Both MDR strains were S typhi isolated from patients in the gatifloxacin group. Two S paratyphi A isolates were resistant to chloramphenicol, one of which was isolated from a patient in the gatifloxacin group and one of which was isolated from a patient in the chloramphenicol group.

In culture-positive patients, nalidixic acid resistance was significantly associated with a slower rate of fever clearance (HR 0.57, 95% CI 0.40-0.81, p=0.02) for patients on gatifloxacin, but there was no significant difference in speed of fever clearance between patients with nalidixic acid-resistant strains and those without in the chloramphenicol group (0.80, 0.56-1.14, p=0.22).

Discussion
Both chloramphenicol, which is a readily available drug in many resource-poor settings, and gatifloxacin, which is a newer generation fluoroquinolone, had excellent efficacy
in the treatment of culture-positive enteric fever, and both drugs had a favourable side-effect profile. Gatifloxacin did as well, but was not superior to, chloramphenicol in an area with a high proportion (72%) of nalidixic-acid-resistant Salmonella strains, but almost no chloramphenicol resistance. With 844 patients analysed (figure 1), this is to our knowledge the largest randomised controlled trial in enteric fever, and the biggest trial comparing chloramphenicol with a fluoroquinolone. This is also the first trial to compare chloramphenicol to a fluoroquinolone in a predominantly paediatric population (table 1). We also assessed the—to our knowledge—largest population of blood-culture-negative patients with enteric fever. In patients who had blood-culture-negative syndromic enteric fever, both drugs were effective, but gatifloxacin was more effective in reducing syndromic clinical relapse.

There are underlying technical issues for typhoid and enteric fever treatment trials. One of the central limitations is the low sensitivity of the blood culture technique, which is estimated to be between 40% and 50%.1 That most patients with enteric fever are categorised as syndromic, and treated empirically without a definitive diagnosis for enteric fever, is therefore not surprising. For the same reason, syndromic relapse was included as an outcome event in the a-priori defined analysis plan in this study.

The antibiotics used in this trial show different pharmacological properties. Gatifloxacin has important features likely to help with treatment adherence compared with chloramphenicol: gatifloxacin only needs to be taken once a day for 7 days, whereas chloramphenicol requires four doses per day for 14 days. There was no difference between the two drugs in terms of treatment failure and fever clearance time in the culture-positive group however, the adverse effects profile showed that anorexia, nausea, diarrhoea, and dizziness, were significantly worse in the chloramphenicol group (table 5).

We monitored blood glucose levels closely in both treatment groups chiefly because of a recent Canadian retrospective case-controlled study of 1,404 elderly individuals (mean age 77) that showed that gatifloxacin was associated with dysglycaemia.21 After this report, gatifloxacin was withdrawn from the US and Canadian markets. In our trial, between day 2 and day 7, the proportion of patients with a high (grade 2: 161-250 mg/dL) non-fasting blood glucose on finger-stick testing was higher in the gatifloxacin group versus the chloramphenicol group. However, there was no difference on days 15 and days 30. Similarly, at the end of 3 months, HbA1c concentrations were not different in the two groups (table 7). Additionally, previous studies using gatifloxacin in a younger population have not reported clinically relevant dysglycaemia.22 Finally, in another study comparing gatifloxacin with ofloxacin for the treatment of enteric fever we are doing (ISRCTN63006567), we have not recorded any dysglycaemia. The gatifloxacin-associated dysglycaemia in the Canadian study might be attributed to an age-related decrease in renal function. In elderly patients receiving gatifloxacin, there might well be a pharmacokinetic or pharmacodynamic rationale for a potential age-related dose reduction.23 Treatment options for enteric fever are clearly limited. Gatifloxacin is an efficacious drug for the treatment of enteric fever in young and otherwise healthy patients, and should be available for indication in this neglected disease. It would be prudent not to use gatifloxacin in patients over 50 years of age, or in patients with comorbidities such as diabetes or renal failure. Most enteric fever trials are done in an inpatient setting, which does not reflect reality in developing countries, where most uncomplicated enteric fever treatment is done in an outpatient setting.24 Our trial was completed
in an outpatient setting with the help of CMAs, as described in our earlier trial. This model is more applicable to developing countries.

A very attractive feature, especially for resource-poor settings, is the insensitivity of the antibiotics studied here. The average price for a 14-day treatment course with chloramphenicol was USS7. The average price for a 7-day treatment with gatifloxacin was USS1.8.

A recent Cochrane review (panel) of fluoroquinolones for the treatment of enteric fever pointed out the weaknesses of typhoid fever treatment trials that have small sample sizes, inadequate randomisation and concealment of allocation, and a lack of paediatric patients and standardised endpoints. We tried to address these criticisms by recruiting a large sample of patients, by precisely defining our endpoints, and by attempting to reduce bias within the limits of an open trial.

Two other trials used gatifloxacin for the treatment of enteric fever (panel). The first trial compared gatifloxacin to cefixime, and enrolled children and adult outpatients in Nepal. This trial was to be prematurely stopped on the advice of the independent data safety monitoring committee because of the poor performance of cefixime. There was a high rate of overall treatment failure (persistent fever at day 7, relapse and death) with 29 (18%) of 70 patients failing in the cefixime group compared with three (5%) of 88 patients in the gatifloxacin group (HR 0.08, 0.03-0.28, p=0.003). There was one death in the cefixime group.

The second trial compared gatifloxacin with azithromycin, and was done in paediatric and adult inpatients in Vietnam. There was no statistical difference between the two antibiotics, and both showed excellent efficacy. The median fever clearance times were 106 h in both groups. 13 (9%) of 145 patients in the gatifloxacin group had overall treatment failure as did 13 (9%) of 140 in the azithromycin group (HR 0.93, 0.43-2.0, p=0.85). Both trials were done in regions with high rates of multidrug-resistant strains: 83% in Nepal and 96% in Vietnam. In previous trials in Vietnam, patients treated with the older generation fluoroquinolone ofloxacin given at 20 mg/kg per day showed high clinical failure rates of 36% (23 of 63 patients) and prolonged mean fever clearance times of 8-12 days (95% CI 7.2-9.2 days).

Gatifloxacin is not superior to chloramphenicol in terms of efficacy. However, on the basis of its shorter treatment duration, fewer adverse events, and lower cost, gatifloxacin should be the preferred treatment of enteric fever in developing countries.

Conflicts of interest
Bh, IF, and CD are applying an application to the WHO Essential Medicines list (EML) in support of Gatifloxacin for treating enteric fever, Submission in the 10th Expert Committee on the Selection and Use of Essential Medicines. All other authors declared no conflicts of interest.

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1 Summary statement of the proposal for inclusion

Enteric fever (Salmonella typhi and S. paratyphi) affects 26 million mostly young people in resource limited setting annually (conservative estimates). Resistance has developed and spread widely against all the traditional treatments and there are few therapeutic options that treat the patient effectively and prevent long term carriage. No antibiotics have ever been developed specifically for the treatment of enteric fever. Very few countries use typhoid vaccines and there is no vaccine for paratyphoid.

Multidrug resistance (MDR = resistance to chloramphenicol, ampicillin and trimethoprim/sulfamethoxazole) and nalidixic acid resistance (reducing the sensitivity to the classical fluoroquinolones ofloxacin and ciprofloxacin) is widespread. Resistance causes higher failure rates and prolonged carriage, increasing the risk of complications in an individual and increasing the potential for continued transmission to the community.

There is good evidence from a series of randomised controlled trials that gatifloxacin can be applied universally in all endemic areas, irrespective of Salmonella susceptibility profiles. There is also pre-clinical and clinical pharmacokinetic/pharmacodynamic (PK/PD) information to support the proposed gatifloxacin treatment.

A once-a-day gatifloxacin 7-day regimen is effective and safe against both sensitive, MDR and nalidixic acid resistant strains of Salmonella typhi and S. paratyphi. No susceptibility screening is required. It is the least expensive treatment currently available.

1.1 Rationale for this submission

The claim is supported by
- In-vitro, clinical (randomised controlled trials, RDTs and meta-analysis) and pharmacological (PK/PD) evidence that gatifloxacin is effective for the treatment of enteric fever, including multi-drug resistant and nalidixic acid resistant strains.
- Safety information based on RDTs of enteric fever and longer exposure for the treatment of tuberculosis.
- Cost and cost-effectiveness data - gatifloxacin is the least expensive option for treating enteric fever.

The product is widely available across disease-endemic countries as a generic product; while approved as a general antibiotic it is not specifically indicated at present for the treatment of enteric fever. However, gatifloxacin has been approved for treating urinary tract infections involving non-Salmonella Enterobacteriaceae, such as Escherichia coli, which is genetically closely related to Salmonella.

2 Focal point in WHO submitting the application

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4 International Nonproprietary Name (INN, generic name) of the medicine

**INN: Gatifloxacin**

Chemical name: (1R,1S)-1-Cyclopropyl-6-fluoro-1,4-dihydro-8-methoxy-7-(3-methyl-1-piperazinyl)-4-oxo-3-quinoxalinecarboxylic acid sesquihydrate

Molecular formula: C<sub>21</sub>H<sub>22</sub>F<sub>2</sub>N<sub>3</sub>O<sub>9</sub>•1/2H<sub>2</sub>O = 402.4

CAS: 160738-57-8 (anhydrous gatifloxacin); 180200-66-2 (gatifloxacin sesquihydrate)

ATC code: J01MA16; S01AX21

Chemical structure:

![Chemical structure of Gatifloxacin](image)

5 Formulation proposed for inclusion

Solid oral forms (200mg and 400mg tablets and capsules) are available. No specific paediatric formulation currently exists.
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5.1 Prospective formulation improvements
Ways of stimulating manufacturers to optimize gatifloxacin formulation will be sought. The enteric fever patient population is generally young and small and dosing is based on body weight. While tablet crushing is customary, and a practical dosing schedule is proposed here, smaller (lower strength) tablets, scored tablets or a suspension will improve dosing accuracy.

An oral suspension was developed and used in Phase 3 clinical trials as part of the Bristol-Myers Squibb Company gatifloxacin paediatric New Drug Application. Additionally, a 50 mg paediatric tablet was also studied. Formulation details will be sought from the Bristol-Myers Squibb Company (Princeton, New Jersey, USA) for possible technology transfer. Scored 200mg and 400mg tablets could be developed easily.

6 International availability
Several generic products are on the market.

6.1 Patent status
The patent situation for gatifloxacin is publicly available in "Drugs in Focus January '10" (1), (details in Appendix 1). In addition WHO/TDR commissioned a search to Withers & Rogers in 2009.

Of the four patent families reported by the Key Patent Indicator (KPI), only the first family (claims to its chemical formula) is relevant to the use of gatifloxacin products for enteric fever. All expired in 2010 or earlier, except: (i) 2012 in Germany and Austria (through extension of patent) and (ii) 2011 in Germany, France and UK (data exclusivity expiry) but (a) extension in Australia and Germany were granted for brand name Tequin® which is discontinued and (b) no marketing authorization exists for gatifloxacin in Australia, France or UK. The latest patent to expire is in Canada although the product was voluntarily discontinued. There is no patent in the disease-endemic countries.

6.2 Production
Gatifloxacin is currently manufactured and sold by generic companies in India and China and freely available for export. In India, the principal manufacturer of Approved Pharmaceutical Ingredient (API) is CIPLA Pharmaceuticals of Mumbal, who manufacture gatifloxacin sesquihydrate as bulk material for export (2) and use by other companies in India (3).

CIPLA also manufacture gatifloxacin as tablets under the trade name Gatiquin as 200 and 400 mg Tablets (4). There are at least 80 generic manufacturers currently supplying gatifloxacin formulated material in India. The individual presentations of generic gatifloxacin in India are in Appendix 2.

In China, there are a number of producers of API recorded, several of which produce to GMP standards, although the status of formulated gatifloxacin in the China market is more difficult to determine. Gatifloxacin is also available in Nepal, Vietnam, Pakistan and other countries in the region. Availability in other countries with endemic enteric fever is difficult to determine.

7 Listing is requested as an individual medicine
Individual medicine - gatifloxacin
Reasons are: resistance to first-generation fluoroquinolones; specific efficacy, safety data and supportive pharmacokinetic/pharmacodynamic and in vitro data; specific cost of product.
8 Information supporting the public health relevance

Enteric fever is widespread; conservative estimates have 26 million cases per year between *S. typhi* and *S. paratyphi*.

Multidrug resistance (MDR = resistance to chloramphenicol, ampicillin and trimethoprim/sulfamethoxazole) and nalidixic acid resistance (NAR = reducing the sensitivity to the classical fluoroquinolones ofloxacin and ciprofloxacin) is widespread.

Where MDR and NAR are common azithromycin and gatifloxacin are now the best options for treatment and can additionally treat other pathogens which may cause a clinical syndrome similar to enteric fever.

8.1 Epidemiology

Typhoid fever and paratyphoid fever are septicaemias caused by the Gram negative bacteria *Salmonella enterica* serovar Typhi (*S. typhi*) and *Salmonella enterica* serovar Paratyphi (*S. paratyphi*) A, B and C. Typhoid and paratyphoid fever are summarized as enteric fevers. Whilst *S. typhi* and *S. paratyphi* A and B infections are restricted to humans, *S. paratyphi* C can affect a variety of animals.

Enteric fever is endemic in Africa, Asia, Central and South America and found in parts of the Middle East, southern and eastern Europe (5). Improvement of infrastructure and sanitation has virtually eliminated typhoid fever in developed countries and infections seen in Europe, Australia, and North America are usually acquired abroad (mostly from the Indian Subcontinent, South East Asia and South America) (6). Current estimates from the World Health Organization (WHO) suggest that the global burden of typhoid fever is approximately 21 million cases annually with more than 210,000 deaths and that paratyphoid fever causes an additional 5 million cases (7). These numbers are based on extrapolating data from 22 studies that used blood culture, the gold standard for the diagnosis of typhoid fever. Many institutions in endemic countries lack blood culture facilities and the sensitivity of blood culture is less than 50% and so the true magnitude of the problem is undoubtedly greater. Transmission of typhoid fever occurs via the faeco-oral route by ingesting contaminated water or food or through direct contact. Chronic typhoid carriers involved in food handling are an important reservoir of infection. In endemic areas enteric fever is a disease of young school children through to young adults.

A WHO report has estimated the case fatality rate in enteric fever at 1% (7). The most important contributor to a poor outcome is a delay in appropriate antibiotic treatment made more likely by the presence of drug resistant strains in the community.

The geographical distribution of *S. typhi* and areas of multi-drug and nalidix acid resistance are in Figure 1.
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Figure 1 Areas of typhoid fever endemicity and distribution of antimicrobial drug resistance to Salmonella enterica serotype Typhi, 1990 to 2005. Modified from (8). MRD = Multidrug Resistance; NAR = Nalidixic Acid Resistance.

8.2 Current treatment options and antibiotic resistance

8.2.1 Chloramphenicol
Chloramphenicol is a broad spectrum antibiotic with bacteriostatic activity. It was developed in 1947. Chloramphenicol was the first antibiotic to be used in the treatment of typhoid fever (9).

Chloramphenicol treatment reduced typhoid fever mortality from 20% to approximately 1%, and the duration of fever from 2-4 weeks to 4-5 days (9-11). The most important adverse effect of chloramphenicol is a dose related, reversible bone marrow depression that results from inhibition of mitochondrial protein synthesis. This is relatively common and is reversible when the drug is stopped. In contrast, the chloramphenicol associated "idiosyncratic" aplastic anemia is very rare but is not dose related, non reversible and invariably fatal. Aplastic anemia is estimated to occur in 1 in 24,500 to 40,800 exposed (12). Resistance to chloramphenicol was first reported in the 1970s and has spread widely (13). Chloramphenicol remains of use for enteric fever in regions of the world where the bacteria are fully sensitive (5, 14, 15). However, disadvantages of chloramphenicol include the need for knowledge of the local sensitivity pattern, higher relapse and typhoid carrier rates (13) plus the need for treatment four times a day for 14-21 days (16) which reduces adherence.

8.2.2 Ampicillin and amoxicillin
The aminopenicillins ampicillin and amoxicillin have been evaluated for the treatment of typhoid fever in several clinical trials proved inferior to chloramphenicol (10, 13). Resistance is widespread and generally due to the production of the bacterial enzyme β-lactamase.
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8.2.3 Trimethoprim-Sulfamethoxazole (cotrimoxazole)
Trimethoprim-sulfamethoxazole was widely used for the treatment of typhoid fever but with widespread resistance and an inferior efficacy it is rarely used today (13).

8.2.4 Extended spectrum cephalosporins
Cephalosporines exert bactericidal activity by interfering with the later stages of the bacterial cell wall synthesis (17). The target site of the β-lactam antibiotics including the cephalosporines are the penicillin-binding proteins (PBP5). Production of β-lactamases is the most common mechanism of bacterial resistance. In the late 90s, non-Typh Salmonella producing extended spectrum β-lactamases (ESBL) have been reported in numerous countries. Resistance to extended spectrum cephalosporins has been reported in isolates of S. typhi from Bangladesh and Italy and S. paratyphi A from Pakistan and Nepal (18, 19). In 2009, a S. typhi isolate with ESBL phenotype caused by blaoCTE, B5 has been described in a patient returning from Iraq (20). The cephalosporines exhibit time dependent bactericidal activity.

Overall, the cephalosporines are a safe class of antibiotics, hypersensitivity reactions are the most common adverse events. Gastrointestinal reactions, including nausea, vomiting and diarrhoea are also reported frequently. The third generation cephalosporines ceftiraxone and cefixime have been used for the treatment of MDR typhoid fever. The fever clearance times in randomised trials using intravenous ceftiraxone have been 7-10 days and 10% of patients failed clinically. Relapse rates varied between 4% and 6% (5). A study in Pakistan evaluated either 7 or 14 days of ceftiraxone treatment in children with enteric fever and found a relapse rate of 14% (4 out of 28 patients) in the 7 day treatment group compared to no relapse in the 14 day group (21). The major disadvantage of ceftiraxone is the need for parenteral administration, the high cost, especially for what is often a prolonged treatment course.

Oral cefixime was a popular choice for the treatment of typhoid fever in children. In randomised controlled trials in children the mean Fever Clearance Times ranged from 5 to 8 days and clinical failure rates were reported to be below 3% (22-24). However, a typhoid treatment trial in Vietnam reported much higher failure rates of 23% (10 out of 44 patients) when cefixime was used in children (25) and a recent trial in Nepal using Cefixime was stopped by the Independent Data and Safety Monitoring Committee because of an unacceptably high failure and relapse rate in those receiving cefixime. The overall treatment failure in this trial (acute treatment failure, relapsed patients plus one death) was determined to be (95% confidence interval) 37.5% (27.14%-50.2%) in the cefixime group (26). Both S. typhi and S. paratyphi are predominantly intracellular organisms and the cephalosporines do not penetrate well intracellularly. This may explain the prolonged fever clearance times, higher relapse and carriage rates seen when these drugs are used.

8.2.5 Azithromycin
Azithromycin belongs to the macrolide class of antibiotics. Macrolides are inhibitors of protein synthesis by impairing the elongation of the peptidyl chain. Azithromycin resistance has not yet been reported in S. Typhi. Azithromycin has a bioavailability of 30% to 50%, The serum peak level is typically reached after 2 hours. Azithromycin has a large volume of distribution which is related to the ability to accumulate inside eukaryotic cells. The ratio of tissue to serum concentration for azithromycin is 50 to 1150 (27). The half life is 35 to 40 hours, which allows a single daily dose and shortened treatment regimen (3 to 5 days). Macrolides are primarily metabolised through cytochrome P450 and eliminated through the bile.
The high level of amino acid activity against effectiveness of both activity and ofloxacin (second generation fluoroquinolones) have excellent activity against Gram negative bacteria and only achieves modest serum and tissue concentrations. Almost 20 years later, the addition of a fluoro molecule at position C6 created the fluoroquinolones. The 6-fluoro substituent confers a greater spectrum of activity against Gram negative and Gram positive pathogens, possibly by improving tissue penetration and binding to the DNA gyrase enzyme.

Ciprofloxacin and Ofloxacin have excellent activity against Gram negative organisms (37). Due to its availability and affordability, ofloxacin has been widely used for the treatment of typhoid fever. However over the last few years strains resistant to nalidixic acid have appeared and spread widely. These strains are much less susceptible to both ciprofloxacin and ofloxacin with patients suffering from prolonged fever clearance times, clinical failures and prolonged carriage. Therefore the effectiveness of both of these drugs has declined leaving few options for treatment in regions with both multi-drug and nalidixic acid resistance.

Gatifloxacin is a broad spectrum 8-methoxy fluoroquinolone with enhanced activity against Gram positive organisms, which has received U.S. Food and Drug Administration (FDA) approval in 1999. It features a cyclopropyl group at position 1 similar to ciprofloxacin. The addition of a methoxy group at position 8 targets both topoisomerase II and IV and probably prevents (or delays) the development of quinolone resistance.

Fluoroquinolones are considered bactericidal agents and have excellent in vitro activity against a wide range of Gram negative and Gram positive organisms. The quinolones rapidly inhibit bacterial DNA synthesis, causing rapid cell death. The targets for the fluoroquinolones are the bacterial topoisomerase enzymes, DNA gyrase (topoisomerase II) and topoisomerase IV.

The main mechanism of quinolone resistance in S. Typhi is the accumulation of amino acid substitutions in the bacterial target enzyme DNA gyrase. The most commonly identified alteration has been a serine to phenylalanine substitution at position 83 of gyrA (38, 39). These mutations are focused around a region called the quinolone resistance determining region (QRDR). The QRDR of gyrA is close to tyrosine at position 122, the active site of the enzyme, which is covalently linked to DNA during strand breakage (40). Single point mutations in gyrA of S. Typhi leads to nalidixic acid resistance (MIC ≥ 32 µg/ml) and reduced susceptibility to the older generation fluoroquinolones. Single isolates of fully fluoroquinolone resistant S. Typhi and S. Paratyphi A have been reported from India (41). The high-level fluoroquinolone resistance seen in these S. Typhi (ciprofloxacin MIC ≥ 4 mg/ml) isolates was conferred by dual mutations in gyrA and a single mutation in parC (42, 43). Gatifloxacin binds with greater affinity to the QRDR and is less susceptible to the mutations remaining effective against these strains.
Gatifloxacin for enteric fever

The frequency of adverse reactions to quinolones is between 6 and 11% of the subjects exposed with less than 1% of adverse events being recorded as serious (44). The most frequent adverse effects reported are nausea, upper gastrointestinal discomfort and central nervous system effects such as headache, insomnia and dizziness. The adverse events are typically mild, self limited and mostly resolve when the drug is stopped. Some adverse effects do not seem to be related to specific modifications, whereas phototoxicity and CNS effects are linked to a specific structure. Each fluoroquinolone tends to produce a characteristic profile of adverse effects.

In their preclinical evaluation, all quinolones studied caused arthropathy in immature animals, especially in young beagle dogs and usually in the major weight bearing joints (45, 46). The concern that the fluoroquinolones might also cause cartilage damage in children has led to cautious use in many countries. However, extensive experience with the fluoroquinolones, especially ciprofloxacin and levofloxacin, in children suffering from cystic fibrosis, enteric fever and bacillary dysentery has provided a body of evidence suggesting that the joint damage seen in young dogs does not occur in children and these antibiotics are safe in children (5, 14, 47-49).

Gatifloxacin, levofloxacin, moxifloxacin or gemifloxacin should not be used in patients with risk factors predisposing them to TdP (52).

The quinolones as a class have demonstrated the ability to close K⁺-ATP channels in the β cells of the pancreas, resulting in the release of insulin and subsequent hypoglycaemia. However the mechanism for hyperglycaemia remains poorly understood and might be caused by overexposure (failure to adjust the dose in patients with renal failure) (52). Product labels for ciprofloxacin, gatifloxacin, levofloxacin, and moxifloxacin mention the possibility of hypoglycaemia and hyperglycaemia. Although glucose disturbances appear to be a class effect, the odds of hypo- and hyperglycaemia appear to vary among the agents (53). A retrospective study in Texas reviewed records of dysglycaemia in hospitalised patients receiving gatifloxacin, levofloxacin, ciprofloxacin or ceftriaxone (54). Dysglycemic events were more likely to occur in patients receiving gatifloxacin (relative risk, 3.29; 95% CI, 2.33–4.65) or levofloxacin (relative risk, 1.55; 95% CI, 1.29–1.88) versus ceftriaxone.

In another study of elderly in-patients who received gatifloxacin or levofloxacin, gatifloxin was independently associated with hypoglycaemia (OR, 2.4; 95% CI, 1.1–5.6) and hyperglycaemia (OR, 2.5; 95% CI, 1.6–3.9) versus levofloxacin (55). In diabetic patients treated with gatifloxacin, the overall incidence of hypoglycaemia was 0.4%, 0.7%, and 1.6%.
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for patients below 65 years, 65 to 69 years and 80 years and above, respectively. The corresponding incidences of hyperglycaemia were 1.0%, 1.6%, and 3.3%, respectively (50).

When exposure to gatifloxacin was simulated in patients with severe hyperglycemia, who were often also older Type-2 diabetics with renal dysfunction, AUC values were 2 to 3 times those observed in patients with normal renal function (56). Therefore the authors suggested to empirically adjust the dose of gatifloxacin to 200 mg daily for patients aged above 65 years with community acquired respiratory tract infections. Only ciprofloxacin, clinafloxacin, enoxacin, grepafloxacin, pefloxacin, and tosufloxacin can inhibit the hepatic cytochrome P450 isoform CYP 1A4 isoenzymes. Few drugs are metabolized by these isoenzymes, but important drugs include the methylxanthines (theophylline and caffeine) and warfarin.

8.2.7 Summary of treatment options
In regions of the world where MDR and Nalidixic Acid strains of S. typhi and S. paratyphi are common azithromycin and gatifloxacin are now arguably the best options for treatment. Intravenous antibiotics are not appropriate in most settings where patients are treated as out-patients. In most parts of the world where enteric fever is common the sensitivity of the strains is not known as microbiological confirmation of the infection is lacking and formal testing of sensitivities is not undertaken. Hence most patients are treated empirically. In such circumstances a 7-day regimen of azithromycin or gatifloxacin are excellent choices for all strains of S. typhi and S. paratyphi. The added value of these antibiotics is that they are effective against other pathogens which may cause a clinical syndrome similar to enteric fever. (see Section 9.2)

9 Treatment details

9.1 Dosage regimen and duration

| The data presented in this application support the use of gatifloxacin at 10 mg/kg/day for 7 days (not to exceed 600 mg/day). |

This Section presents the pharmacological basis for this regimen. Efficacy results from randomised controlled studies are in Section 10).

We also present in this Section practical dosing schedules with existing formulations and prospective dosing with improved formulations.

9.2 Current clinical guidelines
There have been no formal WHO Guidelines published on the specific treatment for Enteric Fever. In 2003 the WHO Department of Vaccines and Biologicals produced an expert committee report "Background document: The diagnosis, treatment and prevention of typhoid fever" (14) in which the following recommendations were made:
Table 1. WHO recommendations from 2003 on optimal and alternative treatments for typhoid fever (NOTE: this table pre-dates the updated Cochrane Reviews and recent trials)

<table>
<thead>
<tr>
<th>Susceptibility</th>
<th>OPTIMAL THERAPY</th>
<th>ALTERNATIVE EFFECTIVE DRUGS</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Antibiotic</td>
<td>Daily dose (mg/kg)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fully sensitive</td>
<td>Fluoroquinolone</td>
<td>15</td>
</tr>
<tr>
<td>e.g. ciprofloxacin</td>
<td></td>
<td></td>
</tr>
<tr>
<td>or ciprofloxacin*</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Multidrug resistance</td>
<td>Fluoroquinolone</td>
<td>15</td>
</tr>
<tr>
<td>or cefixime</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Quinolone</td>
<td>Azithromycin</td>
<td>8-10</td>
</tr>
<tr>
<td>(nalidixic acid)</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Cefixime</td>
<td>75</td>
</tr>
</tbody>
</table>

* Three day courses are also effective and are particularly so in epidemic containment.
* The optimum treatment for quinolone resistant typhoid fever has not been determined. Azithromycin, the third generation cephalosporines, or a 10-14 day course of high-dose fluoroquinolones is effective. Combinations of these are now being evaluated.

There have been a series of reviews since that date (5, 8, 57). The treatment options depend on local knowledge of the sensitivity patterns of the circulating strains of S. typhi and S. paratyphi [see Table 1]. When culture facilities are not available and knowledge of the sensitivity patterns are unknown treatment decisions must be made empirically and consideration also given to the potential other causes and the differential diagnosis.

9.3 Summary target product profile

The ideal therapy would be an oral regimen; the drug would cure the patient quickly preferably as an outpatient, prevent the development of complications, and reduce the incidence of both short and long term carriage. The regimen would be easy to administer to enhance adherence, be effective against all strains of S. typhi and S. paratyphi, with no need for an anti-yeast and it would have minimal adverse events and be affordable. As much enteric fever is managed empirically it would be ideal if the therapy is also potentially effective against the common bacterial illnesses that can present like enteric fever.

Of all the treatments currently available the two drugs that fit this profile are gatifloxacin and azithromycin.

9.4 Pharmacological basis of gatifloxacin treatment regimen for enteric fever

Work presented in the Section provides evidence that:
- the main determinant of gatifloxacin is the AUIC<sub>90</sub> to MIC. A ratio >92.7 predicts a favourable response in enteric fever.
- This ratio is achieved with a daily dose of 10mg/kg which produces consistent levels of exposure (little inter-individual variability) both in children and adults.
- Nalidixic acid resistant organisms remain susceptible to gatifloxacin.
- Susceptibility screening and in vitro Salmonella-specific breakpoints are not required for gatifloxacin.
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9.4.1 Summary of antimicrobial drug resistance
In the late 1980s and early 1990s outbreaks of typhoid fever occurred that were resistant against all "first line" antimicrobials (multidrug resistance (MDR) defined as resistance to chloramphenicol, ampicillin and trimethoprim-sulfamethoxazole) [5]. These MDR S. Typhi isolates have been responsible for numerous outbreaks in countries in the Indian subcontinent, southeast Asia and Africa [8]. All MDR strains so far examined have plasmids of the incHI incompatibility group. Consequently, the fluoroquinolones have become the treatment of choice for typhoid fever especially in areas of the world with MDR strains. The fluoroquinolones show excellent tissue penetration, accumulation in monocytes and macrophages and high drug levels in the gall bladder. However, there have been reports from Vietnam, India and Tajikistan of the emergence of S. Typhi isolates that respond less well to the fluoroquinolones [5, 8]. In 1997, a typhoid epidemics in Tajikistan caused by such isolates caused more than 10000 illnesses and 108 deaths [58]. Technically these isolates remain within the breakpoints set for fluoroquinolone susceptibility by the Clinical Laboratory Standard Institute (CLSI) [59], but they are resistant to nalidixic acid (the prototype quinolone) and show higher MICs to the fluoroquinolones. Patients infected with these isolates show a poor clinical response when treated with ciprofloxacin or ofloxacin. Of all the fluoroquinolones assessed, gatifloxacin showed the lowest minimum inhibitory concentrations (MICs) for nalidixic acid resistant S. typhi from Nepal [60] and Vietnam [38]. In vitro time-kill experiments showed a reduction in the efficacy of ofloxacin against strains harbouring a single amino acid substitution at codon 83 or 87 of GyrA, this effect was more marked against a strain with a double substitution. The 8-methoxy fluoroquinolone gatifloxacin showed rapid killing of S. typhi harbouring both the single and double amino acid substitutions [38].

9.4.2 Pharmacodynamics and Pharmacokinetics of gatifloxacin in patients with enteric fever
Pre-clinical PK/PD models have long served as a basis for dose regimen selection in early drug development and, subsequently, PK/PD analyses of clinical data have served to confirm or refine pre-clinical PK/PD model predictions [61]. The pre-clinical and clinical PK/PD of fluoroquinolone are better understood than perhaps any other class of antibacterial agents. The PK-PD relationship between exposure and response are understood in a wide range of indications, including community-acquired pneumonia, acute exacerbations of chronic bronchitis, acute maxillary sinusitis, urinary tract infections, hospital-acquired pneumonia and typhoid fever [61].

Figure 2 presents the PK/PD indices that are used as surrogate markers for clinical and antimicrobial efficacy are the ratio of peak plasma concentration (C_max) of the antimicrobial to the minimum inhibitory concentration (MIC) of the pathogen (C_max/MIC), the ratio of the area under the concentration time curve 0 to 24 hours to the MIC (AUC/MIC) and the time above MIC (T>MIC). For the fluoroquinolones family in general antibacterial activity depends on the C_max/MIC and the AUC-MIC.
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Figure 2. Concentration versus time curve with minimum inhibitory concentration superimposed and pharmacokinetic and pharmacodynamic markers.

Pharmacodynamics of gatifloxacin in patients with typhoid fever (see Appendix 3)
Clinical data from patients (randomised controlled trial of gatifloxacin versus azithromycin; see Section 10.4.) with typhoid fever were used to investigate the exposure-response relationship of gatifloxacin and the positive- and negative-predictive value of the nalidixic acid screening test. There are few non-clinical PK-PD data available and essentially no clinical PK-PD data for fluoroquinolones and S. typhi among patients with typhoid fever. If available, such data could be used to evaluate the adequacy of dosing regimens and in vitro susceptibility breakpoints. In an effort to clarify these issues, gatifloxacin exposure-response relationships were modelled for patients with enteric fever.

Abstract
Background. The pharmacodynamics of gatifloxacin in patients with typhoid fever and the positive- (predicts clinical cure) and negative- (predicts clinical failure) predictive value of the nalidixic acid screening test were evaluated in a randomized clinical trial.
Methods. Gatifloxacin-treated [10 mg/kg/day given orally for 7 days] patients with typhoid fever were analyzed. Previously validated population pharmacokinetic models were used in conjunction with patient-specific demographics to estimate individual patient drug exposures, as measured by the area under the concentration-time curve at 24 hours (AUC$_{24}$). Analyses included all patients with sufficient data to estimate AUC$_{24}$ and who had a defined minimum inhibitory concentration (MIC) value (N = 124). Fever was evaluated every 6 hours. Favourable clinical response was defined as the resolution of fever and symptoms within 48 hours of the end of therapy. Relapse was defined as the recurrence of fever and symptoms and/or the isolation of S. typhi from blood after completion of therapy and discharge from hospital. A medical history, physical examination and stool cultures to determine chronic faecal carriage were performed at 1, 3 and 6 months after the end of therapy.
Findings. Statistically significant relationships between drug exposure intensity and clinical response were detected. In patients with a AUC$_{24}$/MIC ratios of greater than
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92.7, 93.5% had a favourable response; while for those with AU/MIC ratios ≤ 92.7, only 75% had a favourable response (odds ratio = 4.81, 95% CI 1.83, 18.9; P = 0.02). The positive- (predicts cure) and negative- (predicts failure) predictive value of the nalidixic acid screening test was 100.0% and 9.3%, respectively.

Interpretation. The exposure-response relationships identified provide a paradigm for dose regimen evaluation of existing and new fluoroquinolones for the treatment of typhoid fever. The results of this study also indicate that the nalidixic acid screening test was not predictive of clinical failure for gatifloxacin and Salmonella-specific susceptibility breakpoints may be warranted.

Population pharmacokinetics of gatifloxacin in south east Asian adult and paediatric patients with typhoid fever (see Appendix 4)

Background: An understanding of patient pharmacokinetics (PK) is critical for the rational use of antibiotics. This is especially true for pathogens such as Salmonella typhi in South East Asian countries where the development of multi-drug resistance is an increasing concern. Gatifloxacin is a commonly used treatment in South East Asia for typhoid fever. We investigated gatifloxacin PK in paediatric patients and adult patients from Nepal with uncomplicated typhoid fever.

Methods: PK data were collected during routine clinical care. Each patient had ≤ 3 plasma samples for PK drawn after 3 - 6 days of oral gatifloxacin therapy. Separate candidate models for adults and children were fit to the data using Monte Carlo parametric expectation maximization with S-ADAPT. Due to the sparse nature of the PK sampling, the structure and covariate relationships from previous gatifloxacin adult and paediatric population PK models derived from infected North American patients were retained but were revised to fit the data from this population.

Results: 68 PK samples from 36 patients (aged 3 - 54 years) were analyzed. Gatifloxacin PK were best fit by a linear 1-compartment model. Fits of data were excellent (r² > 0.9 for children and adult data); Interindividual variability in PK was modest. Compared to North American paediatric patients, the Nepalese paediatric patient population had ~50% slower clearance (Table 2).

Conclusions: As drug clearance was markedly lower in South East Asian typhoid fever vs infected North American patients, these data demonstrate the importance of evaluating PK in varying patient populations. The PK models described herein will be used in future pharmacokinetics-pharmacodynamics (PK-PD) analyses of efficacy in South East Asian populations with typhoid fever.

Table 2. Main parameters of gatifloxacin derived from population kinetics of Asian enteric fever patients

<table>
<thead>
<tr>
<th>Patient population</th>
<th>PK parameter</th>
<th>Mean (%SEM) parameter estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Previous models</td>
<td>Current data</td>
</tr>
<tr>
<td>Pediatric</td>
<td>CL/F (L/h/m²)</td>
<td>8.46 (5.50)</td>
</tr>
<tr>
<td></td>
<td>Vc (L/kg)</td>
<td>2.15 (5.30)</td>
</tr>
<tr>
<td>Adult</td>
<td>CL/F, nomenal (L/h)</td>
<td>8.11 (35.3)</td>
</tr>
<tr>
<td></td>
<td>CL/F, renal-corrected (L/h/mL/min)</td>
<td>0.0629 (37.8)</td>
</tr>
<tr>
<td></td>
<td>Vc (L/kg)</td>
<td>1.45 (7.9)</td>
</tr>
</tbody>
</table>

This parameter was not fit due to the narrow range of renal function.
Gatifloxacin for enteric fever

**9.5 Proposed dosing regimens**

Gatifloxacin is currently formulated as 200mg and 400mg strength non scored tablets. Tablet fractionation is custom both in clinical practice and clinical trials.

We present here proposed practical dosing regimens using the current formulations and prospected improved formulations. The target dose was set at 10mg/kg and the therapeutic window at 7-13.5mg/kg/d not to exceed 600mg/d. This range is consistent with how gatifloxacin was originally developed by Bristol-Myers Squibb and with the pharmacokinetic/pharmacodynamic data and safety margins in children and adults.

The objective was to administer whole tablets and minimize tablet crushing. We also wanted to predict what proportion of the typical enteric fever patient population will be receiving which dose. The proportions of the overall population in the tables below refer to the weight frequencies found in the Nepal plus Vietnam database of 1208 enteric fever patients (weight distribution in Figure 3 below.)

*Figure 3. Weight distribution of Asian enteric fever patients*

Option 1 uses the current non scored 200mg and 400mg tablets. It was not possible to give whole tablets for patients under 15kg body weight (*) for whom tablet crushing remains the only option. Patients weighing 29kg taking one 200mg tablet will be receiving 6.9mg/kg instead of the 7mg/kg. Because of the 600mg maximum dose patients weighing >=87kg will received <7mg/kg.
Gatifloxacin for enteric fever

Table 3. Practical dosing of gatifloxacin with current non scored 200mg and 400mg tablets

<table>
<thead>
<tr>
<th>Option 1</th>
<th>200mg and 400mg strength not scored</th>
<th>mg/kg/d</th>
<th>mean</th>
<th>min</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>weight band</td>
<td>% population</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;15kg</td>
<td>9.8%</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>15 to 29</td>
<td>34.2%</td>
<td>200</td>
<td>9.5</td>
<td>6.9</td>
<td>13.3</td>
</tr>
<tr>
<td>30 to 49</td>
<td>29.6%</td>
<td>400</td>
<td>10.4</td>
<td>8.2</td>
<td>13.3</td>
</tr>
<tr>
<td>&gt;= 50</td>
<td>28.5%</td>
<td>600</td>
<td>8.8</td>
<td>6.7</td>
<td>12.0</td>
</tr>
</tbody>
</table>

Option 2 refers to the possibility that manufacturers will accept to develop 200mg and 400mg tablets scored in half (or 400mg tablets scored to give four 100mg units). (*: patients weighing less than 15kg the dosing range displayed is for the weight range 8.5kg to <15kg, below which tablet crushing is required to avoid overdosing. Because of the 600mg maximum dose, patients weighing =>87kg will received <7mg/kg.

Table 4. Practical dosing of gatifloxacin with scored 200mg and 400mg tablets

<table>
<thead>
<tr>
<th>Option 2</th>
<th>200mg strength scored &amp; 400mg strength scored</th>
<th>mg/kg/d</th>
<th>mean</th>
<th>min</th>
<th>max</th>
</tr>
</thead>
<tbody>
<tr>
<td>weight band</td>
<td>% population</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;15kg</td>
<td>9.8%</td>
<td>100</td>
<td>9.4</td>
<td>7.1</td>
<td>12.5</td>
</tr>
<tr>
<td>15 to 24</td>
<td>27.1%</td>
<td>200</td>
<td>10.5</td>
<td>8.3</td>
<td>13.3</td>
</tr>
<tr>
<td>25 to 34</td>
<td>12.0%</td>
<td>300</td>
<td>10.3</td>
<td>8.8</td>
<td>12.0</td>
</tr>
<tr>
<td>35 to 49</td>
<td>24.6%</td>
<td>400</td>
<td>9.6</td>
<td>8.2</td>
<td>11.4</td>
</tr>
<tr>
<td>&gt;= 50</td>
<td>26.5%</td>
<td>600</td>
<td>8.8</td>
<td>6.7</td>
<td>12.0</td>
</tr>
</tbody>
</table>

10 Summary of comparative effectiveness

10.1 Identification of clinical evidence

The current Cochrane review (57) is being updated. We completed a comprehensive search in October 2010 and have screened this and retrieved full text articles. The inclusion criteria remain the same as the current published Cochrane review.

In the updating of this review, we will use the Cochrane new risk of bias assessment. We will use GRADE to summarize the results. This will be using relative risk with confidence intervals across meta-analysis of comparisons for standard outcomes where this is appropriate. (the updated review will be submitted at a later stage as Appendix 5.)

10.2 Recent randomised comparative clinical trials

Recent clinical trials compared gatifloxacin to:

Azithromycin:
Dolecek C, Tran TP, Nguyen MH, Le TP, Ha V, Phung QT, Doan CD, Nguyen TB, Duong TL, Luong BM, Nguyen TB, Nguyen TA, Pham ND, Mai NL, Phan VB, Vo AH, Nguyen VM, Tran TT, Tran TC, Schultsz C, Dunstan SJ, Stepniewska K, Campbell JI, To SQ, Basnyat B,
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Background: Drug resistant typhoid fever is a major clinical problem globally. Many of the first line antibiotics, including the older generation fluoroquinolones, ciprofloxacin and ofloxacin, are failing.

Objectives: We performed a randomised controlled trial to compare the efficacy and safety of gatifloxacin (10 mg/kg/day) versus azithromycin (20 mg/kg/day) as a once daily oral dose for 7 days for the treatment of uncomplicated typhoid fever in children (above 6 months) and adults in Vietnam.

Methods: An open-label multi-centre randomised trial with pre-specified per protocol analysis and intention to treat analysis was conducted. The primary outcome was fever clearance time, the secondary outcome was overall treatment failure (clinical or microbiological failure, development of typhoid fever-related complications, relapse or faecal carriage of S. typhi). Patients were followed up at 1, 3 and 6 months.

Principal findings: We enrolled 358 children and adults with suspected typhoid fever, 186 patients were treated with gatifloxacin and 172 with azithromycin. There was no death in the study. 287 patients had blood culture confirmed typhoid fever, 145 patients received gatifloxacin and 142 patients received azithromycin. The median FCT was 106 hours in both treatment arms (95% Confidence Interval [CI]; 94-112 hours for gatifloxacin versus 88-112 hours for azithromycin). (logrank test p = 0.984, HR [95% CI] = 1.0 [0.60-1.76]).

Overall treatment failure occurred in 13/145 (9%) patients in the gatifloxacin group and 13/140 (9.3%) patients in the azithromycin group, (logrank test p = 0.854, HR [95% CI] = 0.93 [0.43-2.0]). 96% (254/263) of the Salmonella enterica serovar Typhi isolates were resistant to nalidixic acid and 58% (153/263) were multidrug resistant.

Conclusions: Both antibiotics showed an excellent efficacy and safety profile. Both gatifloxacin and azithromycin can be recommended for the treatment of typhoid fever particularly in regions with high rates of multidrug and nalidixic acid resistance. The cost of a 7-day treatment course of gatifloxacin is approximately one third of the cost of azithromycin in Vietnam.

Trial registration: Current Controlled Trials ISRCTN 67946944

Cefixime:


Objective. To assess the efficacy of gatifloxacin versus cefixime in the treatment of uncomplicated culture positive enteric fever.

Design. A randomized, open-label, active control trial with two parallel arms. Setting. Emergency Room and Outpatient Clinics in Patan Hospital, Lalitpur, Nepal.

Participants. Patients (aged two to sixty-five years) with clinically diagnosed uncomplicated enteric fever meeting the inclusion criteria. Interventions. Patients were allocated to receive one of two drugs, Gatifloxacin or Cefixime. The dosages used were Gatifloxacin: 10 mg/kg, given once daily for 7 days, or Cefixime 20 mg/kg/day given in two divided doses for 7 days.

Outcome Measures. The primary outcome measure was fever clearance time. The secondary outcome measure was overall treatment failure (acute treatment failure and relapse). Patients were followed up for 6 months.

Results. Randomization was carried out in 390 patients before enrollment was suspended on the advice of the independent data safety monitoring board due to
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significant differences in both primary and secondary outcome measures in the two arms and the attainment of a priori defined endpoints. Among all randomized patients, 187 patients were assigned to receive cefixime and 203 to gatifloxacin. 77 patients assigned to receive cefixime were blood culture positive for enteric fever whilst 92 of those assigned to receive gatifloxacin were culture positive.

Median (95% confidence interval) fever clearance times were 92 hours (84–114 hours) for gatifloxacin recipients and 138 hours (105–164 hours) for cefixime-treated patients (Hazard Ratio [95% CI] = 2.171 [1.545–3.051], p=0.0001). 19 out of 70 (27%) patients who completed the 7 day trial had acute clinical failure in the cefixime group as compared to 1 out of 88 patients (1%) in gatifloxacin group (Odds Ratio [95% CI] = 0.031 [0.004–0.237], p=0.001). Overall treatment failure patients (relapsed patients plus acute treatment failure patients plus death) numbered 29. They were determined to be (95% confidence interval) 37.6% (27.14%–50.2%) in the cefixime group and 3.5% (2.2%–11.5%) in the gatifloxacin group (HR [95% CI] = 0.084 [0.025–0.280], p=0.0001). There was one death in the cefixime group. This trial was stopped early by the independent Data Safety and Monitoring Board due to the inferior performance of cefixime.

Conclusions. Based on this study, gatifloxacin is a better treatment for uncomplicated enteric fever than cefixime.

Trial Registration. Current Controlled Trials ISRCTN75784880

Chloramphenicol (Appendix 4):
A randomised controlled trial of gatifloxacin versus chloramphenicol for the treatment of uncomplicated enteric fever in Nepalese children and adults:
Background: It is unclear whether chloramphenicol is a reliable therapy for enteric fever or whether gatifloxacin, a newer generation and affordable fluoroquinolone, would be the better choice.
Objectives: To determine the efficacy of chloramphenicol versus gatifloxacin in the treatment of uncomplicated enteric fever.
Participants: Patients (aged two to sixty-five years) from Patan Hospital, Kathmandu, Nepal with clinically diagnosed with enteric fever who met the inclusion criteria.
Intervention: Patients received either gatifloxacin (10 mg/kg) once a day for 7 days or chloramphenicol (75 mg/kg/day) in four divided doses for 14 days.
Outcome measures: The primary outcome measure was treatment failure which comprised of persistent fever at day 10, need for rescue treatment, microbiological failure, relapse until day 31, and enteric fever related complications. The secondary outcome measure was fever clearance time, late relapse, and faecal carriage. Patients were followed up for 6 months.
Results: One thousand one hundred and fifty one patients were assessed for eligibility of which 853 were randomized and 844 were analyzed. Of these 418 were in the chloramphenicol arm and 426 were in the gatifloxacin arm. Out of the 844 patients, 352 patients had blood culture confirmed enteric fever, 175 in the chloramphenicol arm and 177 in the gatifloxacin arm. There were 14 treatment failure patients in the chloramphenicol arm and 12 in the gatifloxacin arm (Hazard Ratio [95% CI] = 0.86 [0.40 to 1.86], p=0.70). Major side effects for chloramphenicol (bone marrow suppression) or gatifloxacin (dysglycemia) were not encountered although, nausea, dizziness, and diarrhea were worse in the chloramphenicol group. Only 0.5% (2/352) of the isolates were multidrug resistant (MDR), but 71% (251/352) were nalidixic acid resistant.
Conclusion: This large clinical trial of culture confirmed enteric fever showed that both chloramphenicol and gatifloxacin had an excellent efficacy in this young population, in
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A region with full sensitivity to chloramphenicol and over 70% resistance to nalidixic acid. Treatment duration, ease of administration, decreased side effects and expense favours the usage of gatifloxacin. Trial Registration. Current Controlled Trials ISRCTN 53258337. Funding: Wellcome Trust.

Ofl oxacin:
An open randomised comparison of gatifloxacin versus ofloxacin for the treatment of uncomplicated enteric fever; ISRCTN63009657. This is an ongoing trial. As of November 2010 approximately 500 patients have been enrolled.

10.3 Meta-analysis of the above RCTs of gatifloxacin for enteric fever

Two of the above RCTs (gatifloxacin vs. azithromycin and vs. ceftazime) were already included in the previous Cochrane systematic review. A third study (vs. chloramphenicol) is being submitted for publication and will be included in the updated systematic review. These studies total 414 gatifloxacin and 394 active control patients.

This preliminary meta-analysis is based on overall failures (primary failure and relapse). No difference is found between gatifloxacin and azithromycin and between gatifloxacin and chloramphenicol; gatifloxacin is significantly more effective than ceftazime. The latter comparison explains the heterogeneity found on aggregate (I-square = 87%).

<table>
<thead>
<tr>
<th>Study or Subgroup</th>
<th>Events</th>
<th>Control</th>
<th>Odds Ratio</th>
<th>Odds Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>ML: 95% Cl</td>
<td>ML: 95% Cl</td>
</tr>
<tr>
<td><strong>Gatifloxacin vs. azithromycin</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dibakar_Neuro700</td>
<td>19</td>
<td>142</td>
<td>20.0%</td>
<td>0.64 [0.44, 1.19]</td>
</tr>
<tr>
<td>Subtotal [95% Cl]</td>
<td>146</td>
<td>142</td>
<td>20.0%</td>
<td>0.64 [0.44, 1.19]</td>
</tr>
<tr>
<td>Total events</td>
<td>13</td>
<td>13</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Inhomogeneity: Not applicable</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Test for overall effect: Z = 0.36 (P = 0.71)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Gatifloxacin vs. Ceftazime</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hostel_Neuro7</td>
<td>7</td>
<td>52</td>
<td>67.3%</td>
<td>0.11 [0.04, 0.31]</td>
</tr>
<tr>
<td>Subtotal [95% Cl]</td>
<td>82</td>
<td>77</td>
<td>67.3%</td>
<td>0.11 [0.04, 0.31]</td>
</tr>
<tr>
<td>Total events</td>
<td>7</td>
<td>76</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Inhomogeneity: Not applicable</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Test for overall effect: Z = 0.15 (P = 0.88)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Gatifloxacin vs. Chloramphenicol</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dibakar_Neuro700</td>
<td>13</td>
<td>117</td>
<td>23.0%</td>
<td>0.64 [0.36, 1.14]</td>
</tr>
<tr>
<td>Subtotal [95% Cl]</td>
<td>170</td>
<td>170</td>
<td>23.0%</td>
<td>0.64 [0.36, 1.14]</td>
</tr>
<tr>
<td>Total events</td>
<td>12</td>
<td>14</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Inhomogeneity: Not applicable</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Test for overall effect: Z = 1.04 (P = 0.30)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total [95% CI]</td>
<td>0.64</td>
<td>0.36</td>
<td>1.00%</td>
<td>0.46 [0.36, 1.17]</td>
</tr>
<tr>
<td>Total events</td>
<td>32</td>
<td>66</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Inhomogeneity: Chi² = 14.64, df = 2 [P = 0.0004]; I² = 87%</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Test for overall effect: Z = 3.40 (P = 0.0006)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Test for sub-group differences: Not applicable</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Gatifloxacin for enteric fever

11 Summary of comparative evidence on safety

- The class and product-specific safety liabilities are known
- The safety profile presented here is derived from RCTs of enteric fever and pulmonary tuberculosis
- There is no evidence from studies at the target dose in the target population that patients on gatifloxacin will be at a particular risk of dysglycaemia. This is further confirmed by data from tuberculosis patients exposed to 25 times the total dose used for enteric fever.
- The drug is well-tolerated in patients with enteric fever; the gatifloxacin safety profile is similar to that of the comparator drugs.

11.1 Class and product-specific safety liabilities

Gatifloxacin is a fourth-generation fluoroquinolone antibiotic that, like other members of that family, inhibits the bacterial enzymes DNA gyrase and topoisomerase IV. Gatifloxacin is generally well tolerated. In common with all broad-spectrum antibiotics, gastrointestinal disturbances may be encountered. The fluoroquinolones are also known to have a number of adverse effects that are considered to be common to the class, although the severity of these varies considerably between compounds. These include effects on cardiac conduction, collagen formation (e.g. tendon rupture), photosensitivity, and dysglycaemia. While another 4th generation fluoroquinolone, moxifloxacin, has significant effects on cardiac repolarisation (prolongation of QT interval), this appears to be absent with gatifloxacin. In contrast, dysglycaemic effects (hypoglycaemia at the beginning of treatment, followed later by hyperglycaemia) are most commonly reported with gatifloxacin. (see also Section 8.2.6)

Hints of gatifloxacin-associated effects on glucose homeostasis were first noted during preclinical development. Preclinical studies which administered up to 19 times the 400 mg dose for up to 6 months demonstrated a dose related decrease in insulin release in pancreatic β-cells in all species studied (62). Shortly after gatifloxacin was introduced, case reports of effects on glucose homeostasis began to emerge. Patients identified as “at risk” included those with non-insulin-dependent diabetes on therapy and elderly patients with age-related decreases in renal function (55).

In summary, these data demonstrate
- a mechanism of gatifloxacin-associated dysglycaemia that is
- dose-(exposure) dependent,
- patients especially at risk include non-insulin-dependent diabetics treated with oral hypoglycaemic medications, and
- elderly patients with age-related changes in renal function.

Gatifloxacin-associated dysglycaemia was not noted during the course of the paediatric development programme and a large trial in children with otitis media followed for one year demonstrated no dysglycaemia adverse effects (53). The concerns of dysglycaemia in elderly Canadian patients were further heightened with the retrospective report in 2006 in the NEJM, concerning older, severely ill in-patients with a history of diabetes (64). That study received worldwide publicity leading to the drug being withdrawn in many countries.

Subsequent work (far less publicized) questioned whether these effects were any more severe or common compared to other fluoroquinolones and comparable antibiotics in an outpatient setting (65). In addition, patients with enteric fever are typically children and young adults and thus are very rarely non-insulin-dependent diabetics and have good kidney function. Clearly in these two very different populations gatifloxacin’s dysglycaemia adverse effect profile is very different.
Gatifloxacin for enteric fever

Between Nepal and Vietnam in recent years in registered clinical trials almost 1500 young patients suffering from enteric fever, shigellosis and TB meningitis were treated with gatifloxacin with no problems noted in glucose control. Of these, over 600 patients were followed up for six months and no episodes of dysglycaemia have been seen (26, 66) and ISRCTN53253837 (An open randomised study to assess the efficacy of gatifloxacin versus chloramphenicol for the treatment of uncomplicated typhoid fever in Kathmandu, Nepal; manuscript submitted as appendix) and ISRCTN63006567 (An open randomised comparison of gatifloxacin versus ofloxacin for the treatment of uncomplicated enteric fever; ongoing).

In addition, dysglycaemia has not emerged as a side effect attributable to gatifloxacin in 917 patients receiving gatifloxacin daily for four months as part of a drug combination regimen for the treatment of pulmonary tuberculosis in a multicentre RCT in Africa (Senegal, Benin, Guinea, Kenya and South Africa). Blood glucose analysis from the above studies is presented below.

As compared to the elderly Canadian patients, the profile of the enteric fever patients as derived from 1211 patients with age recorded enrolled in two RCTs in Nepal and Vietnam is that of a younger population (overall: median age 13 year, interquartile range 8-21 years; median weight 36kg, interquartile range 19.5-50kg).

Table 5. Age(n=853) and weight(n=850) profile of enteric fever patients from two RCTs in Nepal and Vietnam.

<table>
<thead>
<tr>
<th></th>
<th>Nepal</th>
<th>Vietnam</th>
<th>Combined</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Age</td>
<td>Weight</td>
<td>Age</td>
</tr>
<tr>
<td>count</td>
<td>853</td>
<td>850</td>
<td>358</td>
</tr>
<tr>
<td>median</td>
<td>16</td>
<td>42</td>
<td>11</td>
</tr>
<tr>
<td>Q25</td>
<td>9</td>
<td>21</td>
<td>7</td>
</tr>
<tr>
<td>Q75</td>
<td>22</td>
<td>52</td>
<td>15</td>
</tr>
</tbody>
</table>

11.2 Analysis of blood glucose in RCTs of enteric fever and pulmonary tuberculosis

We present here an analysis of blood glucose as dysglycaemia has been identified as a particular safety liability for this compound (see above.) We have detailed data from randomised controlled trials (RCTs) on enteric fever (20mg/kg/d x 7d; n=422 gatifloxacin-treated patients) and tuberculosis (400mg/d 6 days a week in combination with rifampicin,
Gatifloxicin for enteric fever

isoniazid and pyrazinamide for initial 2 months and in combination with rifampicin and isoniazid for the following 2 months, n=917 gatifloxicin-treated patients).

11.2.1 Blood glucose levels in enteric fever

Blood glucose levels were monitored during the trial of gatifloxicin versus chloramphenicol in Nepalese children (above 2 years) and adults (ISRCTN63258327). Random blood glucose (RBG) was measured daily on days 1 to 8, on day 15 and at one month. On days 2 to 7, during the evening visit, the blood glucose was measured by finger-prick testing (OneTouch SureStep™, Johnson & Johnson, USA) by the Community Medical Assistants. HbA1c was measured at 3 months.

For the analysis and grading of adverse events including blood glucose, the NIH Division of AIDS Table for Grading the Severity of Adult and Pediatric Adverse Events ("DAIDS AE grading table") was used.

Table 6. Parameters used in the analysis of severity of diabetes

<table>
<thead>
<tr>
<th>PARAMETER</th>
<th>GRADE 1</th>
<th>GRADE 2</th>
<th>GRADE 3</th>
<th>GRADE 4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nonfasting Glucose, serum. high hyperglycaemia</td>
<td>Mild (50-100 mg/dl)</td>
<td>Moderate (100-200 mg/dl)</td>
<td>Severe (200-400 mg/dl)</td>
<td>Potentially life-threatening (&gt;400 mg/dl)</td>
</tr>
<tr>
<td>Nonfasting Glucose, serum. low hypoglycaemia</td>
<td>50-60 mg/dl</td>
<td>40-50 mg/dl</td>
<td>30-39 mg/dl</td>
<td>&lt;30 mg/dl</td>
</tr>
</tbody>
</table>

The following information regarding RBG and HbA1c was summarised:
- Median (IQR) levels for each visit (e.g. daily until day 8, day 15, and month 1 for random glucose and at day 90 for HbA1c)
- Worst hyperglycaemia grade overall, during days 1-8, at day 15, or at month 1 (contingency tables of frequencies by treatment arm)
- Worst hypoglycaemia grade overall, during days 1-8, at day 15, or at month 1 (contingency tables of frequencies by treatment arm)
- Median (IQR) levels of HbA1c at month 3.
- Proportion of patients with HbA1c >6% at month 3.

Table 7 shows the numbers of hyper- and hypoglycaemias in both treatment arms and Table 8 shows the median random glucose levels. There were more non-fasting grade 2 hyperglycaemias (150-250 mg/dl) in patients in the gatifloxicin group with 42/414 (10.14%) compared to 25/407 (6.14%) in the chloramphenicol group (p=0.04) during treatment (day 2 to day 7). There were no non-fasting hyperglycaemia events noted on day 15. The proportion of patients with an elevated glycosylated Haemoglobin (HbA1C) level between 6 and 7.5% at 3 months was similar in the two groups.

Table 8 (median glucose levels) showed that levels to be higher on days 2 to 7 during treatment in both arms. Median glucose levels on days 4 to 8 were slightly, but significantly, higher in the gatifloxicin arm compared to the chloramphenicol arm.
Gatifloxacin for enteric fever

Table 7 Di glycaemia. Patients with abnormal non-fasting blood glucose. Numbers with (% of those tested)  

<table>
<thead>
<tr>
<th></th>
<th>Chloramphenicol</th>
<th>Gatifloxacin</th>
<th>Comparison (p-value)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Hyperglycaemia, Grade 2</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>At Baseline</td>
<td>1/414 (0.24)</td>
<td>2/422 (0.47)</td>
<td>-</td>
</tr>
<tr>
<td>On Day2 to Day7†</td>
<td>25/407 (6.14)</td>
<td>42/414 (10.14)</td>
<td>0.04</td>
</tr>
<tr>
<td>On Day8</td>
<td>0/402 (0)</td>
<td>1/403 (0.25)</td>
<td>0.5</td>
</tr>
<tr>
<td>On Day15</td>
<td>1/368 (0.27)</td>
<td>0/383 (0)</td>
<td>1</td>
</tr>
<tr>
<td>On Month1</td>
<td>1/375 (0.27)</td>
<td>0/383 (0)</td>
<td>0.50</td>
</tr>
<tr>
<td><strong>Hypoglycaemia, Grade 2 or worse</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>At Baseline</td>
<td>4/414 (0.97)</td>
<td>4/426 (0.95)</td>
<td>-</td>
</tr>
<tr>
<td>On Day2 to Day7†</td>
<td>1/407 (0.26)</td>
<td>1/414 (0.24)</td>
<td>-</td>
</tr>
<tr>
<td>On Day8</td>
<td>2/402 (0.50)</td>
<td>2/403 (0.50)</td>
<td>1.00</td>
</tr>
<tr>
<td>On Day15</td>
<td>3/368 (0.82)</td>
<td>3/351 (0.85)</td>
<td>1.00</td>
</tr>
<tr>
<td>On Month1</td>
<td>3/375 (0.80)</td>
<td>4/383 (1.04)</td>
<td>1</td>
</tr>
<tr>
<td><strong>HbA1c &gt;6</strong></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>On Month3</td>
<td>22.8 (0.27)</td>
<td>20.5 (5.57)</td>
<td>0.75</td>
</tr>
</tbody>
</table>

* On Day 2 to 7 all patients were monitored with fingerstick glucose testing.
† Hyperglycaemia grade 2 defined as non-fasting plasma glucose level between 161 and 250 mg/dl. No grade 3 hyperglycaemias were observed.
‡ Hypoglycaemia grade 2 defined as non-fasting plasma glucose between 40 and 54 mg/dl.

Table 8 Median daily random blood glucose level in enteric fever patients treated with chloramphenicol or gatifloxacin. Median glucose levels in mg/dl. n = Number of patients. Comparisons based on Wilcoxon test.

<table>
<thead>
<tr>
<th></th>
<th>All patients Glucose</th>
<th>Chloramphenicol Glucose</th>
<th>Gatifloxacin Glucose</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n mg/dl</td>
<td>n mg/dl</td>
<td>n mg/dl</td>
<td></td>
</tr>
<tr>
<td><strong>Day 1</strong></td>
<td>836 67.77-98</td>
<td>414 68.77-98</td>
<td>422 67.76-98</td>
<td>0.581</td>
</tr>
<tr>
<td><strong>Day 2</strong></td>
<td>805 105.92-119</td>
<td>396 106.93-121</td>
<td>409 103.92-118</td>
<td>0.092</td>
</tr>
<tr>
<td><strong>Day 3</strong></td>
<td>784 106.94-119</td>
<td>389 104.94-118</td>
<td>395 107.95-120</td>
<td>0.16</td>
</tr>
<tr>
<td><strong>Day 4</strong></td>
<td>776 108.97-121.25</td>
<td>383 125.95-118</td>
<td>393 110.100-123</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td><strong>Day 5</strong></td>
<td>767 107.96-121</td>
<td>393 104.95-114</td>
<td>394 111.99-125</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td><strong>Day 6</strong></td>
<td>769 105.96-119</td>
<td>380 102.95-114</td>
<td>389 109.96-122</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td><strong>Day 7</strong></td>
<td>754 106.96-117</td>
<td>379 102.93-114</td>
<td>375 110.96-121</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td><strong>Day 8</strong></td>
<td>802 64.74-95</td>
<td>402 83.73-25</td>
<td>400 88.75-98</td>
<td>0.007</td>
</tr>
<tr>
<td><strong>Day 15</strong></td>
<td>717 61.73-91</td>
<td>366 81.73-92</td>
<td>351 81.72-90</td>
<td>0.412</td>
</tr>
<tr>
<td><strong>Day 30</strong></td>
<td>758 83.74-93</td>
<td>375 83.74-50.92</td>
<td>383 84.74-94.50</td>
<td>0.51</td>
</tr>
</tbody>
</table>

11.2.2 Blood glucose levels in pulmonary tuberculosis (Appendix 7)

Context

The data analysed are from a randomised open-label controlled trial of a 4 month gatifloxacin-containing regimen versus standard 6 month regimen for the treatment of adult patients with pulmonary tuberculosis. This trial has been conducted in 5 countries in Africa (Benin, Guinea, Kenya, Senegal and South Africa). The recruitment started in January 2005 and the study will end in April 2011.
Method
Male or female patients, aged 18 to 65 years, currently suffering from recently diagnosed microscopically proven pulmonary tuberculosis and providing informed consent were eligible for inclusion in the study. In the Gatifloxacin arm, patients took Gatifloxacin at the dose of 400mg daily (5 days per week), irrespective of weight, for 4 months; in association with Rifampicin, Isoniazid and Pyrazinamide during the first 2 months of TB treatment and Rifampicin, Isoniazid for the last 2 months.

Initially blood glucose measurements were taken at baseline (pre-randomisation; visit 1), week 4 (visit 3), 8 (visit 4) and end of treatment visits (either visit 6 or 8 depending on treatment arm), by finger-prick or full blood tests. During the study recruitment period additional sampling times were incorporated based on the recommendation from the Data Monitoring Committee. These were: 4 hours following first treatment dose, day 7, 14 and week 12 (visit 5) from randomisation. The measurement taken 4 hours after first dose was not taken when fasting as patients were allowed to eat 30 minutes after first drug intake.

This report provides a summary, by treatment arm, of the (i) frequency of hypoglycaemic (less than or equal to 3.5 mmol/L), normal (3.51-6.39 mmol/L) and hyperglycaemic (greater than or equal to 6.4 mmol/L) events, (ii) severity of these events, and (iii) incidence rates of dysglycaemic events.

Results and conclusion
A total of 1,836 patients have been recruited in this trial of whom 917 were randomised to the Gatifloxacin arm. In the Gatifloxacin arm the approximate mean age and weight were 30 years and 55 kg, respectively. Based on the data analysed, the incidence rates of dysglycaemic events were similar in the Gatifloxacin and control arms.

11.3 Summary of comparative safety against comparators in RCTs of enteric fever
In randomized controlled trials comparing gatifloxacin to azithromycin (66), cefixime (26) and chloramphenicol, gatifloxacin was extremely well tolerated.

Gatifloxacin versus azithromycin
Both treatments were well tolerated. One adverse event related to azithromycin was reported, a maculopapular rash that occurred after the first dose of treatment. Azithromycin was discontinued immediately and the patient was treated with ceftriaxone.

Gastrointestinal side-effects (change in consistency and frequency of stools) that were probably typhoid fever related were relatively frequent in both treatment arms at the start of treatment. In the gatifloxacin group, one patient experienced vomiting on day 2 and day 3 and one patient had diarrhoea (4 episodes/day) on day 4 and day 5 of treatment. These episodes were self-limiting and did not require the interruption of therapy.

The median levels of serum AST and ALT fell in both groups after 7 days of therapy. In the culture positive group, the median post-treatment AST was 46.35 U/L (range 12.8 – 217.5) in the gatifloxacin arm and 45 U/L (range 5 – 358) in the azithromycin arm.

Gatifloxacin versus cefixime
There was one death in the cefixime group. This might have been due to the development of disease-related complications during treatment. The 16 year old patient was enrolled on the fourteenth day of his illness. On day 6 of treatment the patient complained of reddish stool and petechiae and was immediately admitted to hospital where he developed severe thrombocytopenia and gastrointestinal bleeding. He developed acute respiratory distress syndrome and was mechanically ventilated. He developed disseminated intravascular coagulation and succumbed to his illness on day 21 of entry into the trial. His pretreatment
Gatifloxacin for enteric fever

Blood culture grew S. Paratyphi A which was sensitive to cefixime with an MIC of 0.38 mg/mL. One patient developed erythematous skin rash which needed two doses of oral antihistamine.

Among all patients who received gatifloxacin there were 2 patients with excessive vomiting, which required intravenous anti-emetics and fluids and observation in the hospital emergency room for up to 6 hours. There was an additional 23 patients who complained of excessive nausea and occasional vomiting after ingestion of the drug. Of these, two needed oral antiemetics; in the remaining 21 patients no intervention was required.

Gatifloxacin versus chloramphenicol

A comparison of adverse events in the two randomized arms is shown in Table 9. Adverse events were mild (grades 1 and 2). Anorexia, diarrhoea, nausea and dizziness were significantly more common in the chloramphenicol arm of the study. Three patients in the chloramphenicol arm who had a white cell count between 1500-1999/mm³ on day 5 to 8 and had their chloramphenicol stopped. The fever had already defervesced when the drug was stopped and they did not relapse for 6 months. There were no life-threatening complications of enteric fever in this study.

Table 9. Adverse events in enteric fever patients treated with chloramphenicol or gatifloxacin.

<table>
<thead>
<tr>
<th>Adverse Event</th>
<th>Chloramphenicol (n=418)</th>
<th>Gatifloxacin (n=426)</th>
<th>Comparison (p value)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Any selected AE</td>
<td>99 (23.6%)</td>
<td>73 (17.1%)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Abdominal pain</td>
<td>11 (2.6%)</td>
<td>8 (1.9%)</td>
<td>0.5</td>
</tr>
<tr>
<td>Acne</td>
<td>2 (0.4%)</td>
<td>0 (0%)</td>
<td>0.25</td>
</tr>
<tr>
<td>Anorexia</td>
<td>9 (2.1%)</td>
<td>1 (0.2%)</td>
<td>0.01</td>
</tr>
<tr>
<td>Diarrhoea</td>
<td>24 (5.7%)</td>
<td>26 (6.1%)</td>
<td>0.001</td>
</tr>
<tr>
<td>Dizziness</td>
<td>11 (2.6%)</td>
<td>11 (2.6%)</td>
<td>0.47</td>
</tr>
<tr>
<td>Nausea</td>
<td>26 (6.2%)</td>
<td>29 (6.7%)</td>
<td>0.905</td>
</tr>
<tr>
<td>Oral candidiasis</td>
<td>4 (0.9%)</td>
<td>4 (0.9%)</td>
<td>0.6</td>
</tr>
<tr>
<td>Vomiting</td>
<td>36 (8.6%)</td>
<td>35 (8.2%)</td>
<td>0.9</td>
</tr>
<tr>
<td>Weakness</td>
<td>4 (0.9%)</td>
<td>4 (0.9%)</td>
<td>0.6</td>
</tr>
</tbody>
</table>

Note: All adverse events in this list were non-severe, ie Grade I or Grade II

12 Summary of available data on comparative cost and cost-effectiveness within the pharmacological class or therapeutic group

A variety of generic products is on the market, all generally cheap. We retrieved information and compared costs with alternative treatment options. We also used enteric fever patient data to produce specific estimates of cost of drug when enteric fever is treated with gatifloxacin. Other direct costs and indirect costs could not be quantified for the moment. The cost of illness of enteric fever is poorly characterised.
This section shows that:
- Gatifloxacin is the cheapest of all treatments of enteric fever. Azithromycin (the only alternative that could be used in areas of MRD and NAR) is 2-5 times as expensive.
- Treating 1000 patients with the current products (200 and 400mg tablets) will cost 4150s.

12.1 Economic burden of enteric fever

There have been very few studies of the economic burden of illness in regions where enteric fever is endemic. In 2004 from India the estimated direct and indirect costs to the family of an episode of enteric fever ranged between 150US$ - 550US$ depending on whether the patient was treated as an out-patient or required admission to hospital (67). Neither of these estimates included the costs incurred during relapses or the costs associated with patients who develop long term carriage and pass on the infection to others in their community.

12.2 Direct costs: comparison of drug costs for treatment of enteric fever with gatifloxacin vs. other options

Cost of treatment of enteric fever with gatifloxacin and several other antibiotics was estimated using data obtained from an on-line pharmacy database in India <http://chemistparadise.com>. Generally accepted dosage regimens for adults of 50 kg and 75 kg body weight, and children of 15 kg and 25 kg body weight were used to estimate the overall cost of treatment for these different classes. For gatifloxacin, the maximum daily dose was set at 600mg.

Table 10. Dose and duration of therapy of enteric fever with gatifloxacin and other regimens. Examples of total dose for a 15kg and 25kg child and a 50kg and 75kg adult are provided.

<table>
<thead>
<tr>
<th>Drug</th>
<th>Dose (mg/kg/d)</th>
<th>Days</th>
<th>75 Kg (adult)</th>
<th>50 Kg (adult)</th>
<th>25 Kg (child)</th>
<th>15 Kg (child)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gatifloxacin</td>
<td>10</td>
<td>7</td>
<td>600</td>
<td>500</td>
<td>250</td>
<td>150</td>
</tr>
<tr>
<td>Chloramphenicol</td>
<td>75</td>
<td>14</td>
<td>5625</td>
<td>3750</td>
<td>1875</td>
<td>1125</td>
</tr>
<tr>
<td>Cefixime</td>
<td>20</td>
<td>14</td>
<td>1500</td>
<td>1000</td>
<td>500</td>
<td>300</td>
</tr>
<tr>
<td>Ceftriaxone</td>
<td>14</td>
<td>4000</td>
<td>2000</td>
<td>2000</td>
<td>1000</td>
<td>1000</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>20</td>
<td>7</td>
<td>1500</td>
<td>1000</td>
<td>500</td>
<td>300</td>
</tr>
<tr>
<td>Ofloxacin</td>
<td>20</td>
<td>7</td>
<td>1500</td>
<td>1000</td>
<td>500</td>
<td>300</td>
</tr>
<tr>
<td>Azithromycin</td>
<td>7</td>
<td>1000</td>
<td>1000</td>
<td>500</td>
<td>500</td>
<td>500</td>
</tr>
</tbody>
</table>

All gatifloxacin products available in India on 1st November 2010 were identified, and per tablet costs obtained in US$. Similarly, the costs of chloramphenicol, ceftriaxone, ciprofloxacin, ofloxacin, and azithromycin were obtained. These were wholesale costs to pharmacy of single packs of, in general, 10 tablets. Since there were a large number of products available, with a wide price range, the mean cost was obtained for each compound and strength. Only solid dosage forms (capsule/tablet) were considered, although examination of the costs of specific paediatric formulations and parenteral formulations, where available, showed similar price structures. The mean single tablet costs were estimated, and applied to the different dosage regimens to give per treatment costs, using the most appropriate dose sizes for the different weight classes. The derived data (in US$) are tabulated below.
Gatifloxacin for enteric fever

**Table 11. Cost of treating children and adults with enteric fever with gatifloxacin and other regimens**

<table>
<thead>
<tr>
<th>Drug</th>
<th>Cost per tablet</th>
<th>Cost for 75 Kg Adult*</th>
<th>Cost for 50 Kg Adult*</th>
<th>Cost for 25 Kg Child*</th>
<th>Cost for 15 Kg Child*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gatifloxacin 400</td>
<td>0.01-1.00 $</td>
<td>$0.55 $</td>
<td>$6.30 $</td>
<td>$5.25 $</td>
<td>$3.83 $</td>
</tr>
<tr>
<td>Ciprofloxacin 500</td>
<td>0.09-0.81 $</td>
<td>$0.46 $</td>
<td>$12.66 $</td>
<td>$6.84 $</td>
<td>$4.32 $</td>
</tr>
<tr>
<td>Azithromycin 250</td>
<td>0.08-3.26 $</td>
<td>$0.69 $</td>
<td>$18.47 $</td>
<td>$12.40 $</td>
<td>$12.40 $</td>
</tr>
<tr>
<td>Ofloxacin 400</td>
<td>0.09-0.59 $</td>
<td>$0.62 $</td>
<td>$20.60 $</td>
<td>$14.00 $</td>
<td>$7.20 $</td>
</tr>
<tr>
<td>Chloramphenicol</td>
<td>0.17-0.23</td>
<td>$0.38 $</td>
<td>$59.22 $</td>
<td>$38.48 $</td>
<td>$19.74 $</td>
</tr>
<tr>
<td>Ceftriaxone 200</td>
<td>0.65</td>
<td>$0.65 $</td>
<td>$137.34 $</td>
<td>$91.58 $</td>
<td>$91.58 $</td>
</tr>
<tr>
<td>Cefixime 200</td>
<td>0.08-0.88 $</td>
<td>$1.56 $</td>
<td>$103.50 $</td>
<td>$109.00 $</td>
<td>$54.50 $</td>
</tr>
</tbody>
</table>

*usually half-strength tablets/capsules used for these estimates

Gatifloxacin appears to be the cheapest option. The next least expensive drug is ciprofloxacin, which is 13%-69% more expensive. Ofloxacin is 1.83-2.05 and azithromycin is 3-5 times more expensive. Chloramphenicol is 5-9 times as expensive. The most costly options are ceftriaxone (17-24) and cefixime (16-26) times as expensive.

**Figure 4. Comparative costs of treatment with gatifloxacin vs. other regimens for enteric fever (in the Table: relative costs, Gatifloxacin = 1)**

A very large number of products (often in excess of 100 alternatives for each dose formulation) are available, with widely differing costs, except for ceftriaxone where only a single product was listed. Costs for the better-known manufacturers were in general higher, but not always so. Although product costs have been estimated for treatments, this is a
Gatifloxacin for enteric fever

basic analysis, and no attempt has been made to assess quality of product, which would be a significant factor in determining true cost and efficacy of treatment. While single tablet costs of other products are often lower than gatifloxacin, cost of treatment is determined by the regimen used, and when this is considered, the cost of gatifloxacin treatment, using Indian derived material, is lower than with other accepted treatments. Some limited data are available for other countries and roughly follows that of the Indian data (much of the material used is of Indian origin, especially in the sub-continent), but detailed information on costs of all products within a country are not available to allow a similar analysis.

12.3 Direct costs of treatment of enteric fever with gatifloxacin practical dosing

Using the anthropometric database of Nepalese and Vietnamese patients, and applying the practical dosing schedule with the current 200mg and 400mg tablets, we calculated the costs of treating 1,000 cases of enteric fever. These amount to $4,150.

Using the Vietnamese patients’ profile, the projected cost of drug for treating all estimated ~4,500 cases occurring in one year in Vietnam will cost ~$15,800.

Table 12. Cost of drug for treating 1,000 enteric fever patients with gatifloxacin using the practical dosing schedule with the current non-scored 200mg and 400mg tablets

<table>
<thead>
<tr>
<th>Body weight class (kg)</th>
<th>No. per 1000 pts</th>
<th>Total No. tablets required</th>
<th>cost/Rx</th>
<th>cost/1000 Rx</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;15</td>
<td>97</td>
<td>7 x 200mg</td>
<td>$2.66</td>
<td>$258.02</td>
</tr>
<tr>
<td>15 to 29</td>
<td>342</td>
<td>7 x 200mg</td>
<td>$2.66</td>
<td>$909.72</td>
</tr>
<tr>
<td>30 to 49</td>
<td>296</td>
<td>7 x 400mg</td>
<td>$4.06</td>
<td>$1,201.76</td>
</tr>
<tr>
<td>50+</td>
<td>265</td>
<td>7 x 600mg</td>
<td>$6.72</td>
<td>$1,780.80</td>
</tr>
<tr>
<td>TOTAL</td>
<td>1000</td>
<td></td>
<td></td>
<td>$4,150.30</td>
</tr>
</tbody>
</table>

When applying these calculations to Vietnam, the total costs of treating all the ~4,500 cases per annum of the entire country will be ~$15,800 for drug costs.

Table 13. Cost of drug to treat all cases occurring in one year in Vietnam

<table>
<thead>
<tr>
<th>Body weight class (kg)</th>
<th>% population</th>
<th>Total No. tablets required</th>
<th>cost/1000 Rx</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;15</td>
<td>14%</td>
<td>7 x 200mg</td>
<td>$1,671.76</td>
</tr>
<tr>
<td>15 to 29</td>
<td>49%</td>
<td>7 x 200mg</td>
<td>$5,817.82</td>
</tr>
<tr>
<td>30 to 49</td>
<td>26%</td>
<td>7 x 400mg</td>
<td>$4,593.02</td>
</tr>
<tr>
<td>50+</td>
<td>12%</td>
<td>7 x 600mg</td>
<td>$3,716.65</td>
</tr>
<tr>
<td>TOTAL</td>
<td></td>
<td></td>
<td>$15,799.27</td>
</tr>
</tbody>
</table>
12.4 Total direct and indirect costs
We are not in a position at present to submit a complete cost-effectiveness analysis. Cost of illness has not been entirely quantified for enteric fever. To account for all direct costs, we are collecting information on cost of care in Nepal and Vietnam. We are also attempting to collect more anthropometric data on enteric fever patients from different settings to generate more complete projections of the applicability of the practical dosing and costs of drug.
Using gatifloxacin will also mean that an antibiogram is not needed - this cost should also be factored in.

13 Summary of regulatory status of the medicine
Gatifloxacin was originally granted licences in the USA (Bristol-Myers Squibb) and Japan (Kyorin) in 1999. The indications included general infections sensitive to fluoroquinolones and community acquired pneumonia. In 2002, there were indications that some patients might suffer dysglycaemia, and warnings were added to the SPC. Following publication of a review of dysglycaemia related deaths [64] and an editorial [68] in March 2006 in NEJM, the US FDA required a 'Black Box' warning to be added to the SPC. Subsequently, in May 2006, Bristol-Myers Squibb stopped manufacture of Tequin®. Similar action was taken in 2008 in Japan. In addition, The US FDA in September 2008 decided that, since "Tequin (gatifloxacin) Tablets, Injections and Oral Suspensions were withdrawn from sales for reasons of safety or effectiveness" gatifloxacin had become ineligible to the abbreviated new drug application (ANDA) should a new submission be filed for any of the previously approved dosage forms and indications of Tequin®[69].
Although the licence for oral products has not been renewed or has been voluntarily withdrawn in countries such as the USA and Japan, the product remains approved in many countries where enteric fever is endemic and drug resistant strains are present - including India, Vietnam, Nepal, Bangladesh and China. It also remains widely available as an ophthalmic solution for eye infections.

14 Availability of pharmacopoeial standards (British Pharmacopoeia, International Pharmacopoeia, United States Pharmacopoeia)
A 'Pending USP Standard' was approved May 23 2008 [70]. API and analytical standards exist in the Indian and Chinese Pharmacopoeias.

15 Proposed (new) text for the WHO Model Formulary
Gatifloxacin
Tablet, 200mg, 400 mg (as sesqulhydrate)

General information
Gatifloxacin is a synthetic fluoroquinolone that acts as a specific inhibitor of bacterial DNA gyrase and topoisomerase IV. It has a broad spectrum of efficacy against both Gram-

1 The US Food and Drug Administration requires that - when serious adverse events are identified by the agency as being of particular concern - the drug's printed materials carry a warning about those adverse effects surrounded by a printed black box - thus the name. As an example, since July 2008 fluoroquinolones as a family are required to have a black box warning for tendon rupture.
Gatifloxacin for enteric fever

Gatifloxacin is rapidly absorbed from the gastrointestinal tract. Peak plasma levels occur 1-2 hours after dosing. It is widely distributed in body tissues and concentrated in the bile. It has a plasma half-life of approximately 8 hours and is excreted in the urine mainly as unchanged drug. Elimination half-life 7-14 hours, with more than 70% of a given dose being excreted in 48 hours. Bioavailability 96%; protein binding 20%.

Clinical Information

Uses
Treatment of typhoid and paratyphoid fever and infectious enteritis due to Salmonella enteritidis.

Dosage and administration
Children and adults: 10mg/kg orally (maximum 600mg/d) every 24 hours for 7 days. A practical dosing with 200mg and 400mg strength tablets will be as follows:

<table>
<thead>
<tr>
<th>weight band</th>
<th>daily dose</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;15kg</td>
<td>10mg/kg</td>
</tr>
<tr>
<td>15kg to 29kg</td>
<td>200mg</td>
</tr>
<tr>
<td>30kg to 49kg</td>
<td>400mg</td>
</tr>
<tr>
<td>&gt;=50kg</td>
<td>600mg</td>
</tr>
</tbody>
</table>

Contraindications
- Hypersensitivity to any quinolone antibiotic.
- Diabetes mellitus.
- Pregnancy and lactation.

Precautions
DISTURBANCES OF BLOOD GLUCOSE, INCLUDING SYMPTOMATIC HYPOGLYCEMIA AND HYPERGLYCEMIA, HAVE BEEN REPORTED WITH GATIFLOXACIN, USUALLY IN DIABETIC PATIENTS. HOWEVER, HYPOGLYCEMIA AND PARTICULARLY HYPERGLYCEMIA HAVE OCCURRED IN PATIENTS WITHOUT A HISTORY OF DIABETES. IN ADDITION TO DIABETES, OTHER RISK FACTORS ASSOCIATED WITH DYSGLYCEMIA WHILE TAKING GATIFLOXACIN INCLUDE OLDER AGE, RENAL INSUFFICIENCY AND CONCOMITANT GLUCOSE-ALTERING MEDICATIONS (PARTICULARLY HYPOGLYCEMIC MEDICATIONS). PATIENTS WITH THESE RISK FACTORS SHOULD BE CLOSELY MONITORED FOR GLUCOSE DISTURBANCES. IF SIGNS AND SYMPTOMS OF EITHER HYPOGLYCEMIA OR HYPERGLYCEMIA OCCUR IN ANY PATIENT BEING TREATED WITH TEOQUIN, APPROPRIATE THERAPY MUST BE INITIATED IMMEDIATELY AND GATIFLOXACIN SHOULD BE DISCONTINUED.

Reduced dosage should be considered in patients with hepatic or renal impairment.

Gatifloxacin has the potential to prolong the QTc interval of the electrocardiogram in some individuals, with an increased risk of ventricular arrhythmias. Care should be taken in individuals taking Class 1A or Class 3 anti-arrhythmic agents.

Gatifloxacin has been rarely associated with tendon rupture, usually in elderly patients and those receiving corticosteroids.
Galiloxacin for enteric fever

Galiloxacin should be administered cautiously to patients with epilepsy or raised intracranial pressure since seizures have been reported with other drugs of this class.

Use in pregnancy and early childhood
Galiloxacin should not be used during pregnancy or during lactation. Use in children is controversial, since quinolones have been shown to induce arthropathy in the weight-bearing joints of young animals. Although damage to growing cartilage has not been demonstrated in humans, use of quinolones is not generally recommended in children and adolescents. However, in severe infections such as enteric fever the benefits are considered to outweigh the risk.

Adverse effects
Galiloxacin is generally well tolerated. The most frequently reported adverse effects are nausea, diarrhoea, vomiting, dyspepsia, abdominal pain, headache, restlessness, tremor, confusion, rash, dizziness and pruritus. Myalgia, tendinitis, and hepatic and renal disturbances have also been reported. Rapid heartbeat, mental confusion, hallucinations, agitation, nightmares, depression; photophobia; tendon rupture; insomnia, chills, fever; back pain; constipation, inflammation of the tongue, mouth sores; abnormal vision, ringing in the ears occur occasionally. Hyperosmolar nonketotic hyperglycaemic coma, diabetic ketoacidosis, and hypoglycaemic coma have been reported and are potentially fatal if untreated.

Drug interactions
Systemic exposure to galiloxacin is increased with concomitant administration of probenicid and reduced with concomitant administration of oral iron compounds and antacids containing aluminium or magnesium salts. Significant interactions are not seen as a result of affects on major cytochrome P450 enzymes (3A, 1A2, 2C9, 2C19, and 2D6).

Overdosage
Gastric lavage is of value if performed promptly. Electrolyte balance must be maintained and cardiac function monitored. Serum concentrations of galiloxacin may be lowered by dialysis.

Storage
Tablets should be stored in well-closed containers.
APPENDICES

Appendix 1. Patent status
Appendix 2. Individual presentations of generic gatifloxacin in India
Appendix 3. ACCESS RESTRICTED TO REVIEWERS UNTIL PUBLISHED - Pharmacodynamics of gatifloxacin in patients with typhoid fever
Appendix 4. ACCESS RESTRICTED TO REVIEWERS UNTIL PUBLISHED - Population pharmacokinetics of gatifloxacin in south east Asian adult and pediatric patients with typhoid fever
Appendix 5. Updated Cochrane systematic review and meta-analysis of fluoroquinolones for enteric fever - will be submitted later
Appendix 6. ACCESS RESTRICTED TO REVIEWERS UNTIL PUBLISHED - A randomised controlled trial of gatifloxacin versus chloramphenicol for the treatment of uncomplicated enteric fever in Nepalese children and adults
Appendix 7. ACCESS RESTRICTED TO REVIEWERS UNTIL PUBLISHED - Blood glucose levels in pulmonary tuberculosis patients treated with gatifloxacin
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REFERENCES


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Temporal Fluctuation of Multidrug Resistant Salmonella Typhi Haplotypes in the Mekong River Delta Region of Vietnam

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Abstract

Background: Typhoid fever remains a public health problem in Vietnam, with a significant burden in the Mekong River delta region. Typhoid fever is caused by the bacterial pathogen Salmonella enterica serovar Typhi (S. Typhi), which is frequently multidrug resistant with reduced susceptibility to fluoroquinolone-based drugs, the first choice for the treatment of typhoid fever. We used a GoldenGate (Illumina) assay to type 1,500 single nucleotide polymorphisms (SNPs) and analyze the genetic variation of S. Typhi isolated from 267 typhoid fever patients in the Mekong delta region participating in a randomized trial conducted between 2004 and 2005.

Principal Findings: The population of S. Typhi circulating during the study was highly clonal, with 91% of isolates belonging to a single clonal complex of the S. Typhi HS8 haplogroup. The patterns of disease were consistent with the presence of an endemic haplotype HS8-C and a localized outbreak of S. Typhi haplotype HS8-E2 in 2004. HS8-E2-associated typhoid fever cases exhibited evidence of significant geo-spatial clustering along the Sang Hau branch of the Mekong River. Multidrug resistance was common in the established clone HS8-C but not in the outbreak clone HS8-E2, however all HS8 S. Typhi were nalidixic acid resistant and carried a Ser72Met aminoglycoside acetyl transferase in the gyrA gene.

Significance: The HS8 haplogroup dominates S. Typhi populations in other endemic areas, but the population described here was more homogeneous than previously examined populations, and the dominant clonal complex (HS8-C, -E1, -E2) observed in this study has not been detected outside Vietnam. In CH1 plasmid-bearing S. Typhi HS8-C was endemic during the study period whilst HS8-E2, which rarely carried the plasmid, was only transient, suggesting a selective advantage for the plasmid. These data add insight into the outbreak dynamics and local molecular epidemiology of S. Typhi in southern Vietnam.


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Competing Interests: The authors have declared that no competing interests exist.

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These authors contributed equally to this work.

Introduction

The Mekong river delta is located in the south of Vietnam (Figure 1) in an area of 40,000 square kilometres (12% of Vietnam's land mass) and is home to over 30% of Vietnam's population. It is the area where the Mekong river divides into multiple channels and drainage into the South China sea. The low-lying nature of the land and the seasonal fluctuation in water level make the region particularly vulnerable to flooding. The human-resistant disease typhoid fever is endemic to the Mekong delta region [1,7], with a mean incidence of ~80 cases per 100,000 people per year [1,2,3,7]. Salmonella Typhi (S. Typhi), the bacterium causing typhoid fever, is transmitted human-to-human in areas with poor sanitation.

The first multidrug resistant (MDR) defined as resistance to chloramphenicol, ampicillin and co-trimoxazole typhoid outbreak in Vietnam occurred in Kien Giang in the Mekong river delta in 1991 [5], and since then the fluoroquinolones have become the first choice for the treatment of typhoid fever. MDR & Typhi is usually associated with self-transferable IncH1 plasmids carrying...
Author Summary

Typhoid fever remains a serious public health issue in some parts of Vietnam, including the Mekong delta region. Typhoid is caused by the bacterium Salmonella Typhi, which is frequently multidrug resistant and shows reduced susceptibility to fluoroquinolone-based drugs. We assayed single nucleotide variation in the genomes of S. Typhi organisms isolated from 267 patients with typhoid fever in the Mekong delta between 2004 and 2005, and identified genetically distinct S. Typhi strains. We also detected the presence of genes or mutations that confer drug resistance in these strains. We found that the vast majority of typhoid cases were caused by one of two subgroups of H58 S. Typhi, referred to as H58-C and H58-E2. The H58-E2 group appeared to cause an outbreak in 2004, affecting patients living in a small zone near the Mekong River. The other group, H58-C, was present throughout the study period and affected patients living in a broader area of the Mekong River delta. Most of the H58-C strains were resistant to multiple drugs and carried a plasmid encoding multiple resistance genes. However, very few H58-E2 strains were multidrug resistant, which may explain why the strain did not persist after the initial outbreak.

multiple resistance genes encoded within mobile genetic elements [6,7,8,9,10]. Between 1994 to 1998, over 80% of S. Typhi strains isolated in the Mekong delta region were reported to be MDR [11], and declined to approximately 50% between 2002 and 2004 [3,11,12]. This decline may have been catalyzed by the change in treatment policy and the widespread use of fluoroquinolones (such as ciprofloxacin and ofloxacin), which are effective against MDR strains [13,14].

While high-level resistance to fluoroquinolones remains uncommon in Vietnam and other endemic typhoid regions, there has been a sharp increase in the proportion of S. Typhi isolates that are resistant to nalidixic acid [11]. Nalidixic acid (NA) is a quinolone antimicrobial (the precursor of fluoroquinolones) and the main mechanism for NA resistance in S. Typhi is mutation of the DNA gyrase gene, gyr [12,15]. S. Typhi strains with NA resistance-conferring mutations in the gyr gene usually have elevated minimum inhibitory concentrations (MIC) to fluoroquinolone antibiotics such as ciprofloxacin (MIC ≥0.125 µg/mL) [16]. However, these organisms are not resistant according to CLSI guidelines, which are currently defined by MIC ≥4 µg/mL to ciprofloxacin [17]. Even though these strains are not classified as resistant, they are of clinical importance since typhoid patients infected with such strains respond less well to fluoroquinolone therapy [14,15,16,18]. Such patients frequently have a prolonged fever and an increased rate of relapse, compared to those infected with strains that do not have an elevated MIC to fluoroquinolones (MIC <0.125 µg/mL to ciprofloxacin and <0.25 µg/mL to ofloxacin) [15,18,19]. Resistance to NA is therefore often used as a marker to predict how well a patient will respond to therapy with fluoroquinolones.

The incidence of typhoid fever has declined in Vietnam. Between 1991 and 2001 approximately 17,000 cases of typhoid fever (blood culture confirmed and typhoid cases) were reported

Figure 1. Location of hospitals in the Mekong river delta of Vietnam. (A) Map showing the 8 Vietnamese regions stretching from the People's Republic of China in the north to the Mekong river delta in the south. Highlighted in grey is Mekong river delta (Dong Thap, Soc Trang, and Long) region, which is the southernmost of the eight regions and covers 40,000 km². The dotted box corresponds to the area magnified in B. (B) Map showing a ~22,000 km² of the Mekong river delta. Highlighted are An Giang province (green) and Dong Thap province (grey). Also highlighted are the provincial hospitals of An Giang province (a) and Dong Thap (g). The direct distance between the two hospitals is 22.5 km.

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annually through the Vietnamese national surveillance system [1,2], while only 4,352 and 5,030 annual typhoid fever cases were reported in 2004 and 2005, respectively (Source: National Institute of Health and Epidemiology, Ministry of Health, Vietnam). However, 75% of these cases occurred in the Mekong delta [1,2], likely associated with high population density and the propensity of the land to become saturated with floodwaters. In this region, the occurrence of S. Typhi isolates that are MDR and Nal resistant severely limits treatment options. More than 95% of S. Typhi isolated in the Mekong delta are now resistant to Nal, placing a considerable pressure on the effective use of fluoroquinolones [1,12]. To compare alternative therapies for typhoid fever patients infected with strains that are MDR and Nal resistant, a randomized controlled trial comparing ciprofloxacin (a newer fluoroquinolone) and azithromycin (a macrolide) was conducted during 2004-2005 in the Mekong delta region [30]. Typhoid patients aged 18 years and older were recruited into the study at three hospitals in the south of Vietnam (details in Materials and Methods; locations are highlighted in Figure 1B). Here, we used a high-throughput single nucleotide polymorphism (SNP) typing assay to investigate the population structure of S. Typhi collected during the study [29], and to determine the genetic mechanism of drug resistance in this S. Typhi population.

Materials and Methods

Eths statement

The study was conducted according to the principles expressed in the Declaration of Helsinki and approved by the Institutional Review Board of the Hospital for Tropical Diseases and the Oxford Tropical Research Ethics Committee (OXTREC). All patients provided written informed consent for the collection of samples and subsequent analysis (written informed consent was provided by the parents or guardians of children under 18 years of age).

Patient recruitment

S. Typhi isolates were collected during a multicenter clinical trial [29] conducted between January 2004 and December 2005 at (a) the Hospital for Tropical Diseases in Ho Chi Minh City (n = 180), (b) Dong Thap Provincial Hospital, Cao Lãnh, Dong Thap province (n = 28) and (c) An Giang Provincial Hospital, Long Xuyen, An Giang province (n = 232). Locations of (b) and (c) are shown in Figure 1B. Adults and children over 6 months of age were eligible to be included in the study if they had clinically suspected or culture-confirmed uncomplicated typhoid fever and if fully informed written consent had been obtained. Patients were tested for typhoid carriage (via stool culture) during follow-up appointments at 1, 3 and 6 months after discharge from hospital. The 367 isolates presented in this study constitute nearly the full complement of 387 S. Typhi isolated from culture-confirmed typhoid patients enrolled in the trial; the recruitment flow for which is described in detail in [30].

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was performed at the time of initial isolation by the diffusion according to Clinical Laboratory Standards Institute (CLSI) guidelines [17]. Antimicrobial agents tested were: ampicillin, chloramphenicol, trimethoprim-sulfamethoxazole (co-trimoxazole), nalidixic acid, ciprofloxacin and cotrimoxazole (Bacto, Basingstoke, UK). Minimum Inhibitory Concentrations (MICs) for amoxicillin, chloramphenicol, nalidixic acid, ciprofloxacin, gentamycin, cotrimoxazole and azithromycin were determined by Etest (AB Biodisk, Selma, Sweden). Multidrug resistance (MDR) of isolates was defined as resistance to chloramphenicol (MIC ≤32 μg/mL), ampicillin (MIC ≤35 μg/mL) and trimethoprim-sulfamethoxazole (MIC ≤1/125 μg/mL). Nalidixic acid resistance was defined by an MIC ≤32 μg/mL.

Bacterial isolation and DNA preparation

After initial isolation, S. Typhi was stored at −70°C in a 20% glycerol solution until required for further analysis and DNA extraction. To revive from colonies, MacCordox and Xylex Elyte DecadeBact (SLD) agar plates were inoculated from the glycerol solution and incubated at 37°C overnight. To ensure correct identification, colonies were checked using slide agglutination with serotype specific antisera (V1, V6) and an irreverent antisera at a negative control (O4) (Murex, Dartford, United Kingdom). Two mL of nutrient broth were inoculated with single S. Typhi colonies and incubated overnight. Overnight cultures were centrifuged and S. Typhi DNA was extracted using Wizard Genomic DNA Purification Kit (Promega, USA) as recommended by the manufacturer's guidelines. DNA was stored at −20°C. DNA was quantified using the Quant-it PicoGreen ARDNA Resgent Kit (Invitrogen, UK). S. Typhi DNA concentrations were adjusted to 50 ng/mL and 250 μg of DNA were pipetted into 96-well plates. Each 96-well plate contained two isolates in duplicate and the sequenced S. Typhi isolate CT/0 as control for assay reproducibility.

Determination of chromosomal and plasmid haplotypes

The chromosomal haplotype of S. Typhi isolates was determined based on alleles present at 1,485 chromosomal SNP loci identified previously from genome-wide survey [12,21] and listed in [22,23]. In [11], plasmid haplotypes were determined based on eight SNPs identified previously [22,24] and resistance gene sequences were interrogated using additional oligonucleotide probes (listed in Table S1). All loci were interrogated using a GoldenGate custom oligonucleotide array according to the manufacturer's standard protocols (Illumina), as described previously [22,23]. A maximum-likelihood phylogenetic tree based on chromosomal SNPs was constructed using the RAxML software [25].

Statistical analysis

Clinical data were entered into an electronic database (Epi Info 2003, CDC, Atlanta, USA). For comparison of patient characteristics according to infection S. Typhi haplotypes, Kruskal-Wallis tests were used for analysis of continuous variables (age, length of stay in hospital, fever clearance time) and logistic regression was used for categorical variables (presence of symptoms). Odds ratios were adjusted for duration of fever prior to admission and use of antibiotics prior to admission by including these variables in the logistic regression model. Where data was missing for a particular patient and variable, that patient was excluded from analysis of that variable (N=33 patients). Two-tailed p-values are reported; statistical analysis was performed using the R package (https://www.r-project.org/).

PCR amplification and sequencing of gyrA gene in S. Typhi

Oligonucleotide primers for the amplification of the quinolone resistance determining regions in the S. Typhi gyrA gene were as follows [11]: GYRA/PI 5′-TGTCGCGAGTGGCGTGAAGGC-3′ and GYRA/P2 5′-TACGGCATAATTTCACTGCG-3′. Predicted PCR amplicon size was 347 bp. PCR was performed...
under the following conditions: 30 cycles of: 92°C for 45 seconds, 45°C for 45 seconds and extension at 74°C for 1 minute, followed by a final extension step at 74°C for 3 minutes. PCR products were purified and directly sequenced using the CEQ DTCS - Quick Start Kit (Beckman Coulter, USA) and the CEQ D300 capillary sequence. The resulting DNA sequence was analyzed using CLARion sequence CEQ2000XL (Beckman Coulter, USA). All sequences were verified, aligned and manipulated using Bioedit software (http://www.mbio.ncsu.edu/BioEdit/bioedit.html) and compared to other gene sequences by BLAST at NCBI.

Spatial data collection and analysis

Patient addresses were recorded at the time of hospital admission. The latitude and longitude of the residences of typhoid fever patients (to the hamlet/village level) was assigned from the collected address data using 1/50,000 scale maps. Source: Cartographic Publishing House and VinaREN, Ministry of Natural Resources and Environment, Vietnam and cross-checked using the websites https://www.bvaco.com.vn and http://viren.vn. Location data was analyzed using Quantum GIS version 1.4.0 (http://www.qgis.org/). Locations were colour-coded according to S. Typhi haplotype and clustering of specific haplotypes was calculated using the nearest-neighbour analysis function. Nearest-neighbour analysis examines the distances between each point and the closest point to it, and then compares these to expected values for a random sample of points from a CSR (complete spatial randomness) pattern. Significant clustering was inferred by Z-score values (standard normal variable) of less than 0; a positive score was interpreted as dispersion of locations.

Results
S. Typhi population structure

A recently developed typing system, based on the simultaneous interrogation of 1,485 S. Typhi chromosomal single nucleotide polymorphisms (SNPs) using a custom Illumina GoldenGate array [22,23], was used to analyze each of the S. Typhi isolates. This approach facilitates the unequivocal assignment of isolates to haplotypes, allowing closely related strains to be distinguished phylogenetically based on single nucleotide changes. From 287 patients with culture confirmed typhoid fever recruited between January 2004 and December 2005 [26], 267 S. Typhi were available for SNP typing. Those included 294 S. Typhi isolated from blood culture at admission [30] one relapse isolate and two fecal carriage isolates. A total of 24 S. Typhi (22) isolated from An Giang and one from Dong Thap, randomly distributed throughout the study period, were not available for SNP typing. A total of 261 S. Typhi isolates (91%) were of the common H58 haplogroup. The remaining isolates were of haplotypes H1 (isolates B1, B63, B102), H5, H65, H116 (isolates B1, B75, H50, H53) and H58 (isolates B1, and H53 and 38 SNPs were displayed at 10 SNP loci (detailed in [26]), which differentiated seven distinct sub-H58 haplotypes, shown in Figure 2. However, 247 (93%) of these isolates belonged to just three closely related H58 haplotypes, designated C, E1 and E2 in

Figure 2. Phylogenetic distribution of S. Typhi isolates. Grey nodes represent control isolates (labelled by isolate code and haplotype group), unfilled grey circle indicates tree root, white nodes correspond to non-H58 S. Typhi isolated in this study (labelled with isolate code), black nodes show H58 isolates. Inset: zoom-in on the H58 haplogroup; grey nodes represent control isolates (labelled by isolate code or haplotype code), unfilled grey circles indicate tree root; coloured circles indicate nodes corresponding to H58 S. Typhi isolated in this study; node labels are as in the text; node colours are as in Figures 3-4; node sizes indicate the number of isolates on the scale as indicated by numbered circles. doi:10.1371/journal.pntd.0000290.g002

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Table 1. Antimicrobial resistance pattern of S. Typhi haplotypes.

<table>
<thead>
<tr>
<th>S. Typhi Haplotype</th>
<th>Total (% of all isolates)</th>
<th>Naïd resistant (% of haplotype)</th>
<th>MDR (% of haplotype)</th>
<th>incH1 plasmid (% of haplotype)</th>
<th>MDRNaïd (% of haplotype)</th>
</tr>
</thead>
<tbody>
<tr>
<td>H58-C</td>
<td>118 (44%)</td>
<td>117 (99%)</td>
<td>152 (80%)</td>
<td>92 (79%)</td>
<td>102 (84%)</td>
</tr>
<tr>
<td>H58-E1</td>
<td>15 (06%)</td>
<td>15 (100%)</td>
<td>15 (100%)</td>
<td>14 (100%)</td>
<td>15 (100%)</td>
</tr>
<tr>
<td>H58-E2</td>
<td>169 (61%)</td>
<td>169 (100%)</td>
<td>21 (13%)</td>
<td>17 (13%)</td>
<td>21 (13%)</td>
</tr>
<tr>
<td>Other H58</td>
<td>19 (7%)</td>
<td>19 (100%)</td>
<td>16 (84%)</td>
<td>16 (84%)</td>
<td>13 (68%)</td>
</tr>
<tr>
<td>New H58</td>
<td>6 (0%)</td>
<td>0 (0%)</td>
<td>0 (0%)</td>
<td>0 (0%)</td>
<td>0 (0%)</td>
</tr>
<tr>
<td>Total</td>
<td>267 (100%)</td>
<td>257 (96%)</td>
<td>267 (100%)</td>
<td>267 (100%)</td>
<td>267 (100%)</td>
</tr>
</tbody>
</table>

All S. Typhi were isolated from blood culture, except two that were isolated from the stools of two chronic carriers.

*Includes one fecal carriage S. Typhi isolate. Naïd = Naïdistic acid. MDR = multi-drug resistant. Presence of incH1 plasmid was inferred from GoldenGate assay results of all isolates.

Antimicrobials resistance testing conducted at the time of isolation. One other IncH1-positive isolate tested positive by GoldenGate assay for the genes astA, astB, aac(3)-Ie, aadA, and cat (resistance genes: functions outlined in Table S1) like the MDR isolates, yet had low MICs for chloramphenicol, ampicillin and trimethoprim-sulfamethoxazole. An additional S. Typhi isolate, B73, was resistant to ampicillin and trimethoprim-sulfamethoxazole but sensitive to chloramphenicol. This was consistent with GoldenGate assay results, which gave positive signals for the astA replication infection gene of IncH1, resistance genes astA, astB, aadA, aac(3)-Ie, and cat (resistance genes: functions outlined in Table S1). For the IncH1 plasmid, this likely reflects loss of the IncH1 plasmid in culture or storage between the time of isolation and DNA extraction. The MDR status of the infecting S. Typhi isolate was not associated with fever clearance time (p = 0.3, two-sided t-test) or treatment failure (p = 0.18, Chi² test).

Plasmids and antimicrobial resistance

The GoldenGate assay incorporated probes targeting IncH1 plasmid sequences, allowing for detection of the presence of IncH1 plasmid within the genomic DNA extracted from each S. Typhi isolate. The assay indicated that a total of 139 S. Typhi isolates harboured an IncH1 plasmid. All plasmids were of the IncH1 ST5 sequence type [22] and all plasmid-bearng isolates belonged to the S. Typhi H58 haplogroup (see Table 1). The MDR IncH1 plasmid was more common among H58-C isolates than H58-E2 isolates (86% vs 19%; see Table 1). Of the 139 S. Typhi isolates giving positive signals for IncH1 SNP loci, 137 (99%) were classified as MDR by antimicrobial susceptibility testing conducted at the time of isolation. One other IncH1-positive isolate tested positive by GoldenGate assay for the genes astA, astB, aac(3)-Ie, aadA, and cat (resistance genes: functions outlined in Table S1) like the MDR isolates, yet had low MICs for chloramphenicol, ampicillin and trimethoprim-sulfamethoxazole. An additional S. Typhi isolate, B73, was resistant to ampicillin and trimethoprim-sulfamethoxazole but sensitive to chloramphenicol. This was consistent with GoldenGate assay results, which gave positive signals for the astA replication infection gene of IncH1, resistance genes astA, astB, aadA, aac(3)-Ie, and cat (resistance genes: functions outlined in Table S1). For the IncH1 plasmid, this likely reflects loss of the IncH1 plasmid in culture or storage between the time of isolation and DNA extraction. The MDR status of the infecting S. Typhi isolate was not associated with fever clearance time (p = 0.3, two-sided t-test) or treatment failure (p = 0.18, Chi² test).
A total of 257 S. Typhi isolates were resistant to nalidixic acid (Nal). All of these isolates belonged to the H58 haplogroup (Table 1) and were susceptible to chloramphenicol, ciprofloxacin and ofloxacin according to current CLSI guidelines [17]. S. Typhi haplotypes H58-C, H58-E1 and H58-E2 were uniformly resistant to Nal, with the exception of a single H58-C isolate which had an intermediate MIC of 20 μg/mL (resistance defined as MIC ≥32 μg/mL). The sequenced H58-E2 isolate AG3 harbours a mutation changing alanine to threonine (TCC to phenylalanine (TTG) at codon 63 in the groE gene (Gyra-ScrE1B) [21], which is known to confer resistance to Nal [26]. In the present study we sequenced the groE gene in 223 of the Nal resistant isolates (87%) and found the same Gyra-ScrE1B allele amino acid substitution in all isolates tested.

Spatial and temporal distribution

Figure 3 shows the spatial distribution of the residences of 160 typhoid patients (this information was not available for the remaining patients). Of the patients admitted at An Giang Provincial Hospital and Dong Thap Provincial Hospital, sufficient address detail to allow for assignment of latitude and longitude was provided in 41% and 73% of cases, respectively. This represents 50% and 30% of all blood culture confirmed typhoid fever patients at An Giang Provincial Hospital and Dong Thap Provincial Hospital, respectively, during 2004-2005. In An Giang, patients' homes clustered around the An Giang Provincial Hospital, but also around the Song Hia branch of the Mekong River (see Figure 3). Most S. Typhi isolates from patients living near this point in An Giang province were of the H58-E2 haplotype (orange in Figure 3), and this group demonstrated significant clustering using nearest-neighbour analysis (n = 57, Z-score = 14.145). In contrast, S. Typhi of the H58-C haplotype were isolated relatively frequently in neighbouring provinces and had a more sporadic clustering pattern (red in Figure 3). While isolates from An Giang Provincial Hospital are overrepresented in this spatial analysis, the apparent increase in typhoid density in An Giang is consistent with total Typhi isolation rates at the two hospitals during the study period [24] at An Giang Provincial Hospital and 90 at Dong Thap Provincial Hospital.

The temporal distribution of S. Typhi haplotypes over 2004 and 2005 is shown in Figure 4. Typhoid fever cases peaked just prior to the onset of the wet season in each year, as has been observed previously in this region [13] (see monthly rainfall, solid line in Figure 4). In 2004, H58-E2 and H58-C were both prevalent (82% and 18% in Figure 4; 103 E2, orange in Figure 4), whereas few isolates of H58-E2 Typhi were observed during 2005 (55 C, 4 E2; see Figure 4). The decline of H58-C Typhi may be associated with selective advantage of the incH1 MDRI plasmid, which was much more common in H58-C (Table 1). As Figure 4 highlights, the majority of isolates collected during the second season were MDRI and carried the incH1 plasmid ST8.

Discussion

Our data show the usual majority of S. Typhi isolates (n = 251, 98%) isolated from the Mekong delta during the two-year study period belonged to the H58 haplogroup. Furthermore, 92% of isolates (n = 245) belonged to a single clonal complex of S. Typhi H58 (nodes C, E1, E2 shown in Figure 2), demonstrating remarkable homogeneity in the S. Typhi population in this location during the study period. The observed level of clonal dominance is greater than that observed in previous haplotyping studies of local S. Typhi populations. Among 54 S. Typhi isolates from Jakarta, Indonesia between 1975 and 2005, a total of nine

Table 2. Selected characteristics of typhoid fever patients, based on baseline presentation history and outcomes.

<table>
<thead>
<tr>
<th>Variable</th>
<th>S. Typhi H58-E2</th>
<th>Non-H58-E2</th>
<th>S. Typhi H58-C</th>
<th>H58-E2 vs all other S. Typhi (95% CI)</th>
<th>p-value</th>
<th>Missing data</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>n</strong></td>
<td>107</td>
<td>117</td>
<td>117</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age (yr)</td>
<td>11.9 (1.2)</td>
<td>12.3 (1.2)</td>
<td>12.7 (1.7)</td>
<td>DIF = 0.8 (0.1, 1.6)</td>
<td>0.83</td>
<td>0</td>
</tr>
<tr>
<td>Time in hospital (days)</td>
<td>13.9 (1.3)</td>
<td>13.7 (1.3)</td>
<td>13.8 (1.3)</td>
<td>DIF = 0.2 (0.1, 0.4)</td>
<td>0.07</td>
<td>0</td>
</tr>
<tr>
<td>Fever clearance (hrs)</td>
<td>116 (1)</td>
<td>115 (1)</td>
<td>121 (1)</td>
<td>DIF = 1.0 (0.8, 1.2)</td>
<td>0.70</td>
<td>2</td>
</tr>
<tr>
<td>Conjugation</td>
<td>1.8 (1)</td>
<td>1.9 (1)</td>
<td>2.0 (1)</td>
<td>DIF = 2.0 (1.5, 2.6)</td>
<td>0.03</td>
<td>1</td>
</tr>
<tr>
<td>Headache</td>
<td>5.7 (1.2)</td>
<td>1.6 (1.2)</td>
<td>6.5 (1.2)</td>
<td>DIF = 4.5 (3.6, 5.5)</td>
<td>0.01</td>
<td>35</td>
</tr>
<tr>
<td>Diarrhoea</td>
<td>1.1 (0.1)</td>
<td>1.0 (0.1)</td>
<td>1.1 (0.1)</td>
<td>DIF = 0.5 (0.3, 0.8)</td>
<td>0.02</td>
<td>1</td>
</tr>
<tr>
<td>Abdominal pain</td>
<td>1.4 (0.1)</td>
<td>1.3 (0.1)</td>
<td>1.3 (0.1)</td>
<td>DIF = 0.5 (0.4, 0.6)</td>
<td>0.02</td>
<td>34</td>
</tr>
<tr>
<td>Urine output</td>
<td>2.6 (1.3)</td>
<td>2.1 (1.3)</td>
<td>2.7 (1.3)</td>
<td>DIF = 4.1 (2.8, 4.9)</td>
<td>0.01</td>
<td>34</td>
</tr>
<tr>
<td>Hemoglobin</td>
<td>50.3 (13.3)</td>
<td>49.3 (13.3)</td>
<td>51.3 (13.3)</td>
<td>DIF = 2.0 (1.0, 3.0)</td>
<td>0.37</td>
<td>6</td>
</tr>
</tbody>
</table>

Comparisons of selected characteristics among 264 typhoid fever patients (i.e., excluding carriage and enzootic isolates), for continuous variables age, time in hospital, and fever clearance, values shown are means and test statistic given in the difference in means (DIF = mean value for S. Typhi - mean value for non-H58-E2 S. Typhi). Other variables indicate frequency of symptoms self-reported at time of admission and of clinician diagnosed hemagglutination tests statistic is odds ratio (OR) for H58-E2 S. Typhi vs non-H58-E2 S. Typhi. Both crude OR and adjusted OR are reported (adjusted for duration of fever prior to admission and use of antibiotics prior to admission, using logistic regression). All comparisons shown are for patients infected with H58-E2 S. Typhi vs those infected with other S. Typhi haplotypes including H58-C and other; 95% confidence intervals (CI) are given in brackets.

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Figure 3. Spatial distribution of S. Typhi isolates by haplotype and year. The spatial distribution of S. Typhi haplotypes surrounding An Giang provincial hospital in (A) 2004 and (B) 2005. Each point corresponds to the residential location of a typhoid fever patient; colour indicates the haplotype of the S. Typhi isolate (with or without plasmid); dark orange = H58-E2 with MDR plasmid; light orange = H58-E2 without MDR plasmid; dark red = H58-C with MDR plasmid; pink, H58-C with MDR plasmid; grey = other S. Typhi haplotypes. Locations of the hospitals are indicated by a white cross on a red background; pink circle indicates a radius of 15 km from An Giang Provincial Hospital; arrow indicates the Sông Hậu branch of the Mekong river.
doi:10.1371/journal.pmed.0000092.s003

Haplotypes were detected, with the dominant H29 haplotype accounting for 54% of isolates; the next most frequent haplotype was genetically distant from H58 and comprised 24% of isolates.

[37] In Kathmandu, Nepal, a collection of S. Typhi isolated from children hospitalised with typhoid fever in 2003–2006 was dominated by the H58-G haplotype (66%) but the distant H42 haplotype.
haplotype was also present at high frequency (19%) [25]. Among S. Typhi isolated between 2001 and 2005 in Ninh Binh, Vietnam, 87% were H58, although two distinct subtypes (nodes B and J, see Figure 2) were co-circulating at equally high frequencies (>40% each) between 2004 and 2005 [22]. S. Typhi H58 nodes B and J (co-circulating in Ninh Binh) represent distinct lineages, each acquiring unique SNPs since the last common ancestor of H58 (Figure 2). However H58 nodes C, E1, and E2, which account for 91% of isolates in this study in Vietnam, are closely related and formed a tight clonal complex differentiated by just two SNPs (Figure 2). Thus, the overall level of clonality of the S. Typhi population analysed in this study was unexpectedly high. The clonal complex comprising H58-C, E1 and E2 was not detected in study populations in Nepal and Kenya where the same SNP typing method was used [22,25], suggesting it may have arisen locally in Vietnam.

Despite the genetic homogeneity we observed, the availability of whole-genome sequence data for S. Typhi H58-E2 isolate AG3 [21], collected during the study, allowed us to differentiate closely-related organisms within the H58 group. Just two SNPs identified in strain AG3 subdivided the homogeneous group into three nodes: C, E1 and E2 (Figure 2), of which two (C and E2) were dominant (>40%) each. Isolates belonging to the H58-C node were present at a consistent rate during the two years of the study (62 isolates in 2004 and 55 in 2005). However, isolates belonging to the H58-E2 node were common during 2004 (203 isolates), yet were virtually undetected in 2005 (3 isolates). This change in both haplotype distribution and total number of typhoid cases from 2004 to 2005 is striking, and suggests an outbreak caused by S. Typhi H58-E2 during 2004. We additionally found that H58-C strain had a much stronger association with the ST6 IncH1 MDR plasmid than H58-E2 (Table 1). This indicates that the persistence of H58-C strain and the corresponding disappearance of H58-E2 may be associated with a competitive phenotypic advantage conferred by the IncH1 MDR plasmid. However, it is important to remember that node C is a precursor of node E2 and we can only differentiate E2 from C because we had whole genome sequence data for an H58-E2 strain from which to identify SNPs [21]. Thus the population of S. Typhi isolates assigned to node C by our SNP typing may be more diverse than that assigned to H58-E2. It is also important to note that since our data covers just two years, it is possible that any competitive advantage of H58-C strain may be short-lived and there is no evidence for long-term replacement of H58-E2.

We identified two cases of chronic faecal carriage of S. Typhi during the course of the study, one in a patient's relative and one in a patient after 6 months of follow-up. This underlines the importance of screening procedures to identify carriers and effective treatment to eliminate carriage and reduce transmission. The fecal S. Typhi isolates were of the dominant H58-E2 and H58-C haplotypes, respectively. In a previous case-control study performed in the Mekong delta, close contact with a patient who

Figure 4. Monthly incidence of typhoid cases by haplotype. Bar heights indicate the total number of S. Typhi isolated each month during the study, according to the scale given on the left-hand y-axis. colours indicate the combination of S. Typhi haplotype and presence of IncH1 ST6 plasmid as given in the legend. Solid black line = total rainfall each month recorded in An Giang, dashed line = maximum rainfall occurring in a 24 h period during each month in An Giang, and rainfall scale is shown on the right-hand y-axis.

doi:10.1371/journal.pmed.0000929.g004
typhoid fever was significantly associated with developing the disease compared to hospital controls (adjusted odds ratio [OR] = 3.2, 95% confidence interval [95% CI] = [1.7, 5.9]) or community controls (adjusted OR = 11.9, 95% CI = [2.3, 60.7]) [26].

We were able to collect residential location data from 60 typhoid patients (61%). While typhoid patients reporting to An Giang Provincial Hospital are overrepresented in this data set (50% of all confirmed cases vs. 26% of all confirmed cases at Dong Thap Hospital), the apparent clustering in An Giang (Figure 3) is consistent with the overall isolation rates at the two hospitals, which during the study period were more than three times higher at An Giang Provincial Hospital than Dong Thap Hospital. The data set provides roughly equal representation of patients infected with S. Typhi H58-C (65%) and H58-E2 (82%), thus any differences in spatial distribution between patients presenting at the different hospitals should not affect the differences between spatial distribution of these haplotypes. Spatial clustering of S. Typhi H58-E2 was evident particularly around the Song Hia branch of the Mekong river, while other S. Typhi haplotypes were more broadly distributed (Figure 4). The spatial clustering of H58-E2 S. Typhi further supports a localized outbreak in 2004 caused by these isolates. In contrast, the broader spatial and temporal distribution of S. Typhi H58-C during the study suggests it may be well established in the community and can persist over longer distances and time periods.

We also observed that some symptoms reported by patients infected with H58-E2 S. Typhi differed from those infected with other S. Typhi haplotypes (Table 2). After adjusting for antibiotic use and duration of fever prior to admission, patients infected with H58-E2 S. Typhi were more likely to report diarrhea and headache compared with other S. Typhi haplotypes (OR = 0.56, 95% CI = [0.34, 0.93]) and OR = 0.96, 95% CI = [0.40, 1.93], respectively), but were more commonly associated with constipation (OR = 2.6, 95% CI = [1.1, 6.1]). This suggests there may be some pathogenic differences between H58-E2 and other S. Typhi with respect to disease, however these were post-hoc analyses and no adjustments were made for multiple comparisons, hence these associations should be interpreted with caution. However if confirmed in subsequent prospective studies, it would be of interest to know whether these phenotypic characteristics were associated with specific mutations in H58-E2 S. Typhi. The two SNPs differentiating the E2 node from E1 and C are both synonymous mutations (C>T in snm [nt 315]; G>T in ymd [nt 570]) and our earlier analysis of the AGI sequence data detected no single-base insertions or deletions that were not also detected in other sequenced H58 isolates [21]. However, we were unable to verify if other single-base insertions or deletions were present, which may result in gene inactivation and corresponding phenotypic effects.

Patterns of antimicrobial resistance of S. Typhi tend to vary markedly between different typhoid-endemic regions. In this project work, as in the recent study of Kenyan isolates [22], there were high rates of MDR associated with IncHI1-RT6 plasmids among strains of the S. Typhi H58 haplgroup. This suggests that the presence of the plasmid may contribute to the success of the dominant S. Typhi haplotypes, and the results of our study corroborate this hypothesis. The S. Typhi H58-E2 subtype (which was generally not associated with a plasmid) was only transient, while the H58-C subtype (which was more commonly associated with the IncHI1 MDR plasmid) was present in 2004 and 2005 in withdrew Vietnam. In Kenya, almost all isolates of the dominant H58 haplotypes carried the MDR plasmid, while the plasmid-free H58-G subtype was only detected twice [22]. All the H58 isolates analysed in the present study were resistant to nal, conferring an identical mutation in 


References


Supporting Information

Checklist S1. Strebe Checklist

Found at: doi:10.1371/journal.pmed.0009299.e001 (0.99 MB DOC)

Table S1. IncH1 plasmid and resistance-associated gene targets.

Found at: doi:10.1371/journal.pmed.0009299.e002 (0.03 MB XLS)

Translation S1. Translation of the abstract into Vietnamese by Ng. Tran Vu Thien.

Found at: doi:10.1371/journal.pmed.0009299.e003 (0.09 MB RTF)

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Author Contributions

Conceived and designed the experiments: KEH CD NVVC TTH JF GD SB. Performed the experiments: TTC PTD TTH NVME TVTN JBC BHM NVVC. Analyzed the data: KEH CD BM SB. Contributed reagents/materials/analysis tools: TTH GD. Wrote the paper: KEH CD NVVC TTH JF GD SB.

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S. Typhi in the Mekong Delta
Suitable Disk Antimicrobial Susceptibility Breakpoints Defining *Salmonella enterica* Serovar Typhi Isolates with Reduced Susceptibility to Fluoroquinolones

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Infections with *Salmonella enterica* serovar Typhi isolates that have reduced susceptibility to ciprofloxacin (MIC ≥ 0.25 µg/ml) or ciprofloxacin (MIC ≥ 0.125 µg/ml) have been associated with a delayed response or clinical failure following treatment with these antimicrobials. These isolates are not detected as resistant using current disk susceptibility breakpoints. We examined 816 isolates of S. Typhi from seven Asian countries. Screening for nalidixic acid resistance (MIC ≥ 16 µg/ml) identified isolates with an ciprofloxacin MIC of ≥ 0.25 µg/ml with sensitivity of 97.3% (253/260) and specificity of 99.3% (552/556). For isolates with a ciprofloxacin MIC of ≥ 0.125 µg/ml, the sensitivity was 92.9% (248/267) and specificity was 98.4% (540/549). A zone of inhibition of ≤25 mm around a 5-µg ciprofloxacin disc detected strains with an ciprofloxacin MIC of ≥ 0.25 µg/ml with a sensitivity of 94.4% (246/260) and specificity of 94.2% (524/556). A zone of inhibition of ≤30 mm detected isolates with a ciprofloxacin MIC of ≥ 0.125 µg/ml with sensitivity of 94.6% (231/247) and specificity of 94.8% (317/334). An MIC of ≤0.25 µg/ml and a ciprofloxacin MIC of ≤0.125 µg/ml detected 74.5% (406/546) of isolates with an identified quinolone resistance-inducing mutation and 81.5% (311/386) of the most common mutant (carrying a serine-to-phenylalanine mutation at codon 83 in the gyrB gene). Screening for nalidixic acid resistance or ciprofloxacin and ciprofloxacin disk inhibition zone are suitable for detecting S. Typhi isolates with reduced fluoroquinolone susceptibility.

Enteric fever is an infection caused by *Salmonella enterica* serovar Typhi and Paratyphi A. These human restricted pathogens are transmitted by the fecal-oral route, and enteric fever is common in regions with poor standards of hygiene and sanitation. There are 27 million new enteric fever infections each year, of which approximately 200,000 are fatal (16). Antimicrobials are essential for appropriate clinical management of enteric fever, but antimicrobial resistance in S. Typhi and S. Paratyphi A have become a problem in regions where they are endemic (6, 8). Multiple-drug-resistant (MDR) S. Typhi and S. Paratyphi A (resistant to chloramphenicol, trimethoprim-sulfamethoxazole, and ampicillin) are particularly common in some locations in Asia and have led to large epidemiologic data. An MDR S. Typhi strain was responsible for an outbreak in Tajikistan in the late 1990s, causing over 24,000 infections (39). The occurrence of MDR strains limits the options for antimicrobial therapy of enteric fever. The current WHO guidelines suggest that the fluoroquinolones are the optimal group of antimicrobials for the treatment of uncomplicated typhoid fever in adults (44). The fluoroquinolones, such as ciprofloxacin and ofloxacin, are comparatively inexpensive and well tolerated and in early randomized clinical trials were very effective. However, S. Typhi and S. Paratyphi A isolates with reduced susceptibility to fluoroquinolones have become common in Asia and are increasingly common in Africa (6, 8, 13, 26, 32, 37). Infections with S. Typhi strains with elevated MICs to ciprofloxacin and ofloxacin have been

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associated with the failure of treatment with these antimicrobials and increased disease severity (15, 30, 33, 36, 43). Investigations of S. Typhi with reduced susceptibility to fluoroquinolones has shown the appearance of elevated MIC with several single-base-pair mutations in the DNA gyrase gene, gyrB, and the topoisomerase gene, parC (4, 6, 33, 42). Furthermore, extensive genome sequencing and single nucleotide polymorphism (SNP) investigation of S. Typhi strains have further shown the dramatic impact of strains with gyrB mutations on the population structure of this monophyletic organism (35). Genotyping studies identified at least 15 independent gyr mutations that have occurred within a decade and stimulated clonal expansion in Asia and Africa (6, 35). These data suggest that such strains have evolved rapidly and are maintained by a strong selective pressure.

The laboratory detection and identification of strains with reduced susceptibility to fluoroquinolones are important for the treating clinician, but such strains are categorized as susceptible by the current interpretive guidelines for fluoroquinolone disk susceptibility testing (3, 11, 19). These isolates are invariably resistant to nalidixic acid, and susceptibility testing with a nalidixic acid disk has been suggested as a suitable screening method for reduced fluoroquinolone susceptibility (11, 19). The British Society for Antimicrobial Chemotherapy (BSAC) has recommended that for invasive isolates of Salmonella, an MIC for reduced susceptibility to fluoroquinolones should be determined (5).

Here we have examined the relationship between gyr and parC mutations, nalidixic acid resistance, ofloxacin and ciprofloxacin disk inhibition zone sizes, and MIC for a large number of S. Typhi clinical isolates from multiple locations in Asia over a 16-year period. We suggest disk susceptibility breakpoints for strains with reduced susceptibility to ciprofloxacin and ofloxacin, which may permit the diagnostic laboratory to detect such isolates and aid the clinical management of enteric fever.

MATERIALS AND METHODS

S. Typhi strain collection. The S. Typhi strains used in this study were comprised of isolates collected as part of independent investigations. The majority of the strains (216 strains) were collected from continuous control trials conducted between 1992 and 2002 in southern Vietnam. These trials were conducted using a standard protocol, except for the treatment regimens used, as described in detail elsewhere (5, S, 26, H, 36, 40, 41). One hundred and forty-five S. Typhi strains were isolated in a pantropical controlled trial (gatifloxacin versus chloramphenicol [DSSCT/MS052/02ATTT]) at Ponta Hospital, Kundasang, Malaysia, and 60 isolates were from a randomized controlled trial (gatifloxacin versus chloramphenicol [DSSCT/MS052/02ATTT]) at Ponta Hospital, Kundasang, Malaysia, for the treatment of uncomplicated acute fever between 2004 and 2008. The remaining 53 S. Typhi strains (a total of 196) were collected between 2002 and 2008 as part of population-based prospective surveillance studies conducted by multiple teams in Jakarta, Indonesia (n = 27), Dhaka, Bangladesh (n = 40), Hanoi City, Guang Xi, China (n = 51), Kolkata, India (n = 25), and Karachi, Pakistan (n = 53) (6). A subset of the strains described above (n = 100) from Vietnam, Indonesia, China, India, and Pakistan) and a collection of contemporary S. Typhi strains from Vietnam and India (n = 275) were additionally selected for screening for gyr, parC, and par mutations. These strains are presented in the supplemental material.

Microbiological methods. The isolates were identified by standard bacteriological means and agglutination with Salmonella-specific antisera (Murex Diagnostics, Dartford, United Kingdom). Antimicrobial susceptibilities were tested at the time of isolation by the modified Bauer-Kirby disk diffusion method, with zone size interpretation based on CLSI guidelines (8, 11). Antimicrobial disks tested were chloramphenicol (CLM) (30 μg), ampicillin (AMP) (10 μg), trimethoprim-sulfamethoxazole (SXT) (1.25/23.75 μg), ceftriaxone (CRO) (30 μg), ofloxacin (CFOX) (5 μg), and nalidixic acid (NAL) (30 μg). Müller-Hinton agar and antimicrobial discs were purchased from Unipath, Basingstoke, United Kingdom.

Antimicrobial disks were applied to Mueller-Hinton agar by CLSI methods for NAL (30 μg), ciprofloxacin (CIP) (5 μg), and ofloxacin (CFOX) (5 μg). The zone of inhibited growth for each antimicrobial was assessed for three separate measurements (30 μg) to the result of the measurement of the others. The average zone size recorded for the three readers was calculated. The MICs for the isolates were determined by the standard agar plate dilution method according to CLSI guidelines or by Etest according to the manufacturer's recommendations (AB Biodisk, Sweden) (19).

The antimicrobial disks were run (0.008 μg/ml to 4 μg/ml) disk with 6.25 μg/ml to 12 μg/ml). Antimicrobial pressure for the agar plate dilution MICs were purchased from Sigma, United Kingdom. The MIC end points were read by two independent investigators, each blind to the result determined by the other. Discrepancies were resolved by discussion. Iso- enches coli ATCC 25922 and Neisseria gonorrhoeae ATCC 25922 were used as control strains for these assays. The results were interpreted according to CLSI guidelines, susceptible being values of ≤8 μg/ml for nalidixic acid, ≤1 μg/ml for ofloxacin, and ≤1 μg/ml for ciprofloxacin. An isolate was defined as MDR if it was resistant to chloramphenicol, trimethoprim-sulfamethoxazole, and ampicillin by disk susceptibility testing.

PCR amplification and sequencing of gyrB, gyr parC, and par genes in S. Typhi. DNA from the strains that were selected for PCR amplification of the gyrB, gyr parC, and par genes was extracted using the Wizard genomic DNA purification kit (Promega) according to the manufacturer's recommendations. Briefly, a single colony was inoculated in 1.5 ml of Luria-Bertani broth and incubated overnight at 37°C with shaking at 200 rpm to reach 10 cutoff turbidity. One ml of the bacterial culture was transferred to a microcentrifuge tube and centrifuged in a microcentrifuge at 13,000 rpm for 2 min. The supernatant was removed, and the bacterial pellet was used for DNA extraction. The extracted DNA was stored at −20°C until required.

Oligonucleotide primers for the amplification of the quinolone resistance-determining region of gyrB, parC, and par genes was designed. The primers were as follows (36): gyrB, GYR1A (5′-TCTTCGAGATGCGTGAAGG) and GYR2F (5′-TACGCGATCAGACCTCAAGG) (ammonium temperature, 60°C; PCR, 25°C; GC value, 0.6°C) and parC1F (5′-TCCGCGATCAGACCTCAAGG) and parC2R (5′- TAA CAGAACGTGGTCAATT) (ammonium temperature, 60°C; PCR, 25°C; GC value, 0.6°C). PCR amplification and sequencing of gyrB, gyr parC, and par genes were performed using the CEQ 2000 falsification kit (Biorad) and was sequenced using a CEQ 2000 capillary sequencer, and the resulting DNA sequence was analyzed using CEQ Sequence Interpreter CEQ2000XL (Biorad). All sequencing were verified, aligned, and manipulated using EBI software (http://www.ncbi.nlm.nih.gov/BLAST/blasttutorial.html). All gyrB, gyr parC, and par sequences were compared to other gyrB, gyr parC, and par sequences by BLASTN and TBLASTX at NCBI. The DNA sequence of the various S. Typhi sequences of gyrB, gyr parC, and parB were deduced and aligned with the predicted sequences.

Data analysis. Zone size interpretable of clindamycin and interpretive disc susceptibility tests were calculated by the rule of thumb-based method of Motluk and DellaFaus (27). The MIC breakpoints for reduced susceptibility were ≤25 μg/ml for clindamycin and ≤39 μg/ml for ciprofloxacin. The zone size breakpoints were adjusted until the number of false-negative disk diffusion test results (very major discrepancies) and false-positive disk zones (major discrepancies) were held to a minimum. Guidelines for acceptable discrepancy rates were according to the CLSI recommendation (12). Normally distributed data were compared using the Student's t test, nonnormally distributed data using the Mann-Whitney U test, and proportions by the chi-squared test. Statistical analysis was performed using Epilize, version 6 (CDC, Atlanta, GA), and SPSS for Windows version 11.0 (SPSS, Inc., Chicago, IL).

RESULTS

Antimicrobial susceptibility testing of S. Typhi isolates. We investigated 816 S. Typhi isolates collected between 1992 and 2008 from seven Asian countries: Vietnam, Nepal, Indonesia, India, Bangladesh, Pakistan, and China. Only one isolate (the
Strain isolated on admission to the health care facility) from each patient was included for microbiological examination and analysis.

Of the 816 S. Typhi isolates tested, 466 (57.1%) were MDR (resistant to chloramphenicol, ampicillin, and trimethoprim-sulfamethoxazole), while 30/816 (37%) were fully susceptible to chloramphenicol, ampicillin, and trimethoprim-sulfamethoxazole. Two hundred fifty-three of the 816 isolates (31%) were resistant to nalidixic acid (MIC, \( \geq 32 \) \( \mu \)g/ml) and 4 isolates had an MIC of 16 \( \mu \)g/ml (intermediate) to nalidixic acid but were classified as resistant according to the zone sizes from disk susceptibility testing (\( \geq 13 \) mm). Of the 466 MDR isolates, 145 (31.1%) were additionally resistant to nalidixic acid compared to 80/303 (26.4%) isolates that were fully susceptible to chloramphenicol, ampicillin, and trimethoprim-sulfamethoxazole (\( P = 0.16 \)).

All 816 S. Typhi isolates were classified as susceptible to ciprofloxacin according to MIC testing (MIC \( \leq 1 \) \( \mu \)g/ml), yet 12 gave a discrepant result with disk testing. These strains exhibited an inhibition zone size of \( \leq 20 \) mm and were, therefore, classified as intermediate by disk testing. Two of the 816 S. Typhi strains were graded with intermediate resistance to ofloxacin with an MIC of 4 \( \mu \)g/ml but had inhibition zone sizes of \( \geq 16 \) mm and were, therefore, classified as susceptible.

The distribution of the MIC levels to ciprofloxacin and ofloxacin for all 816 S. Typhi isolates is presented in Fig. 1. The histograms of the levels of MIC to ciprofloxacin and ofloxacin both demonstrate a bimodal distribution. The two distinct groups are partially divided by nalidixic acid susceptibility (Fig. 1, black shading denotes resistance to nalidixic acid). The 563 isolates that were susceptible to nalidixic acid had an MIC\(_{50}\) (range) to ciprofloxacin of 0.03 \( \mu \)g/ml (0.008 to 0.5 \( \mu \)g/ml) and of 0.06 \( \mu \)g/ml (0.016 to 0.5 \( \mu \)g/ml) to ofloxacin. The 253 isolates that were resistant to nalidixic acid had an MIC\(_{50}\) (range) to ciprofloxacin of 0.5 \( \mu \)g/ml (0.064 to 1 \( \mu \)g/ml) and to ofloxacin of 1.0 \( \mu \)g/ml (0.125 to 4 \( \mu \)g/ml).

Antimicrobial susceptibility test interpretive categories of S. Typhi to ciprofloxacin and ofloxacin. The current CLSI intermediate breakpoints are 2 \( \mu \)g/ml and 4 \( \mu \)g/ml, respectively, for ciprofloxacin and ofloxacin. Only 2 of the 816 strains tested had MIC levels greater than or equal to those of the current MIC breakpoints (Fig. 1). The MICs for nalidixic acid were compared with those of ciprofloxacin and ofloxacin in scatter plots (Fig. 2). The current interpretive breakpoints are shown in Fig. 2 as dark shading in red for ofloxacin and ciprofloxacin and in gray for nalidixic acid. The suggested interpretive breakpoints for reduced susceptibility are depicted by a broken line with an arrow (Fig. 2). As predicted, there was a linear relationship between the nalidixic acid MIC and the ofloxacin (Fig. 2a) and ciprofloxacin MICs (Fig. 2b).

Screening strains using nalidixic acid resistance (MIC \( \geq 16 \) \( \mu \)g/ml) for the detection of isolates with an MIC of \( \geq 0.25 \) \( \mu \)g/ml for ofloxacin had a sensitivity of 97.3% (253/260) and a specificity of 99.3% (552/556) (Fig. 2a). The number of very major discrepancies was 7/260 (2.7%), with none more than two dilutions above the breakpoint, and the number of major discrepancies was 8/260 (3.1%), with none more than two dilutions below the breakpoint. Screening for the detection of isolates with a ciprofloxacin MIC of \( \geq 0.125 \) \( \mu \)g/ml, using nalidixic acid resistance (MIC of \( \geq 16 \) \( \mu \)g/ml), was not as reliable as that for ofloxacin, as it had a sensitivity of 92.9% (248/267) and a specificity of 98.4% (540/549). The number of very major discrepancies was 19/267 (7.1%), with 1/267 (0.4%) more than two dilutions above the breakpoint, and the number of major discrepancies was 9/249 (3.6%), with none more than two dilutions below the breakpoint.

We explored the relationship between the diameter of the zone of inhibition and the MICs for ciprofloxacin and ofloxacin, using 5-\( \mu \)g disks (Fig. 3). A zone of inhibition of \( \geq 28 \) mm around a 5-\( \mu \)g ofloxacin disk correlated with an MIC of \( \geq 0.25 \) \( \mu \)g/ml, with the least number of discrepancies (Fig. 3a). The number of very major discrepancies was 14/260 (5.4%), with none more than two dilutions above the breakpoint, and the number of major discrepancies was 32/556 (5.7%), with 14/556 (2.5%) more than two dilutions below the breakpoint. A zone of inhibition of \( \geq 28 \) mm around a 5-\( \mu \)g ciprofloxacin disk detected strains with an ofloxacin MIC of \( \geq 0.25 \) \( \mu \)g/ml, with a sensitivity of 94.6% (246/260) and a specificity of 94.2% (524/556). A zone of inhibition of \( \geq 30 \) mm around a 3-\( \mu \)g ciprofloxacin disk correlated with an MIC of \( \geq 0.125 \) \( \mu \)g/ml, with the least num-
FIG. 2. Scatter plots relating oxytetracycline and ciprofloxacin MICs to nalidixic acid MIC for 316 Asian S. Typhi isolates. Scatter plots comprised of MIC data from 316 S. Typhi isolates from Nepal (n = 104), India (n = 25), Indonesia (n = 27), Bangladesh (n = 40), Pakistan (n = 53), China (n = 51), and Vietnam (n = 51). Plois show the relationship between the MIC to nalidixic acid (y axis) and the MIC to oxytetracycline (a) and ciprofloxacin (b) (x axis). The vertical and horizontal shading in each scatter plot indicates the current CLSI recommendations for breakpoints between susceptibility (white), intermediate (light gray), resistant (light red), oxytetracycline, and resistance (dark gray, nalidixic acid; dark red, oxytetracycline and ciprofloxacin) (nalidixic acid MIC, ≤8 μg/ml and ≥32 μg/ml; oxytetracycline MIC, ≥2 μg/ml and ≥8 μg/ml; and ciprofloxacin MIC, ≥0.1 μg/ml and ≥4 μg/ml). The red broken line corresponds to the proposed MIC breakpoint identifying strains with reduced susceptibility to fluoroquinolones (oxytetracycline MIC of ≥0.25 μg/ml and ciprofloxacin MIC of ≥0.125 μg/ml).

ber of discrepancies (Fig. 3b). The number of very major discrepancies was 16/267 (6.0%), with 4/267 (1.5%) more than two dilutions above the breakpoint, and the number of major discrepancies was 32/249 (13.0%), with 22/249 (4.0%) more than two dilutions below the breakpoint. A zone of growth inhibition of <50 mm detected isolates with a ciprofloxacin MIC of >0.125 μg/ml, with a sensitivity of 94.0% (231/257) and a specificity of 94.2% (517/548).

Reduced susceptibility to fluoroquinolones and gyrA, gyrB, parC, and parE mutations. To further define the S. Typhi population with reduced susceptibility to fluoroquinolones, we produced PCR amplicons and then sequenced the quinolone resistance-determining region of the gyrA, gyrB, parC, and parE genes from a collection of 475 S. Typhi strains from Vietnam, China, India, Indonesia, and Pakistan. One hundred of these strains were described in the previous section, and 375 were more recent strains from Vietnam and India. The MIC range of these strains was 1 to 512 μg/ml to nalidixic acid, 0.008 to 6 μg/ml to ciprofloxacin, and 0.03 to 12 μg/ml to oxytetracycline. These strains and the corresponding data from these strains are described in the supplemental material.

Fifteen of the 475 S. Typhi strains examined by PCR and sequencing of gyrA, gyrB, parC, and parE had no mutations in the quinolone resistance-determining regions of any gene. No strains had a mutation in the quinolone resistance-determining region of gyrB or parE. Four hundred sixty strains had either a single mutation or a combination of double or triple mutations in the gyrA and parC genes. DNA sequencing identified seven different amino acid substitutions: D97A, aspartic acid to asparagine at codon 87 in the gyrA gene; S83F/D87N, serine to phenylalanine at codon 83 and aspartic acid to asparagine at codon 87 in the gyrA gene; S83F/D87G, serine to phenylalanine and aspartic acid to glycine at codon 87 in the gyrA gene; S83F/D87G/S80I, serine to phenylalanine at codon 83 and aspartic acid to glycine at codon 87 in the gyrA gene and serine to isoleucine at codon 80 in the parC gene. The most commonly identified amino acid replacement was S83F, constituting (88%) 406/460 strains with a mutation, with S83Y the second most common mutant (10%) 46/460.

We compared the MICs to oxytetracycline and ciprofloxacin of the 460 strains with the seven different mutation patterns and the 15 strains with no mutation detected (Fig. 4). When grouped into strains with and without a single mutation in the gyrA gene, the single mutation group had significantly higher MICs to oxytetracycline (Fig. 4a) and ciprofloxacin (Fig. 4b) than those without a mutation. The most common amino acid substitution, S83F, had mean MICs of 0.75 μg/ml and 0.33 μg/ml to oxytetracycline and ciprofloxacin, respectively. Figure 4 also shows the current CLSI breakpoints and the suggested oxytetracycline breakpoint of 0.25 μg/ml and ciprofloxacin breakpoint of 0.125 μg/ml. An MIC of 0.25 μg/ml to oxytetracycline and an MIC of 0.125 μg/ml to ciprofloxacin detected 74.5% (341/460) of the S. Typhi strains with an identified fluoroquinolone resistance mutation and 81.5% (331/406) of the most common S. Typhi mutant (S83F) with reduced susceptibility to fluoroquinolones.

DISCUSSION

The increasing recognition that S. Typhi isolates with reduced susceptibility to oxytetracycline and ciprofloxacin may lead to treatment failure has led to calls for a revision of their break-
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**FIG. 3.** Scatter plots relating offoxacin and ciprofloxacin MIC to inhibition zone diameter for 816 Asian 5. Typhi isolates. Scatter plots for 816 5. Typhi isolates comparing the inhibition zone diameters using a 5-μg ciprofloxacin disc (a) and a 5-μg offoxacin disc (b) (y axis) and the corresponding MIC of ciprofloxacin (a) and offoxacin (b) (x axis). The numbers in brackets relate to the 253 nalidixic acid-resistant isolates. The vertical red shading in each scatter plot is the current CLSI disc zone breakpoint for resistance (offoxacin inhibition zone diameter, ≤16 mm; ciprofloxacin inhibition zone diameter, ≤21 mm). The horizontal red shading distinguishes strains with an MIC of >2 μg/mL for offoxacin or an MIC of >1 μg/mL for ciprofloxacin. The gray shading is the proposed breakpoint for 5. Typhi isolates with reduced susceptibility (offoxacin MIC, ≥0.25 μg/mL; ciprofloxacin MIC, ≥0.125 μg/mL). The red broken line corresponds with the proposed breakpoints for strains with reduced susceptibility (offoxacin inhibition zone diameter, ≤25 mm; ciprofloxacin inhibition zone diameter, ≤30 mm).

**TABLE 3.** Breakpoints. Breakpoints of >0.25 μg/mL for offoxacin and levofloxacin and ≥0.125 μg/mL for ciprofloxacin and gatifloxacin have been suggested (1, 2, 14, 32). Nalidixic acid resistance and disk susceptibility testing have both been proposed as laboratory screening methods to detect such isolates. We have explored the performance of these methods with a large number of strains that are representative of 5. Typhi isolates circulating in countries in Asia where it is endemic.

Nalidixic acid resistance had a sensitivity of 96.2% and 91.8% and a specificity of 99.5% and 98.5% for the detection
of isolates with reduced susceptibility to ofloxacin and ciprofloxacin, respectively. Alternatively, using disk sensitivity testing, isolates with reduced susceptibility were detected by an ofloxacin (5-µg) disk inhibition zone diameter of ≤28 mm with a sensitivity of 94.6% and specificity of 94.2% and by a ciprofloxacin (5-µg) disk inhibition zone diameter of ≤30 mm with a sensitivity of 94.0% and specificity of 94.2%. Therefore, both methods had sufficiently high sensitivity for them to be used for screening and acceptably low levels of discrepancies (12). Disk inhibition zone size did, however, demonstrate a slightly lower specificity than nalidixic acid disk testing with this panel of isolates. Similar data for the relationship between nalidixic acid resistance and a decreased ciprofloxacin MIC have been presented for S. Typhi isolates in the United States (14) and India (23) and in non-S. Typhi Salmonella isolates in the United States (14) and Finland (21). For nalidixic acid-susceptible and -resistant S. Typhi isolates in India (23), the average disk inhibition zone sizes for ciprofloxacin were greater than those that we observed here. The non-S. Typhi study in Finland proposed a ciprofloxacin (5-µg) disk inhibition zone diameter of ≤37 mm as the breakpoint (21). The sensitivity of this approach was 100%, yet the specificity was only 51.9%.

In some isolates in this study, the nalidixic acid, ofloxacin, and ciprofloxacin MIC results were discrepant, in that isolates were nalidixic acid susceptible but with a reduced ofloxacin (n = 10) or ciprofloxacin susceptibility (n = 22). Similar results have been seen in other studies (13, 15, 22, 26). The clinical significance of these isolates is unclear, as there have been limited documented cases of infection with such strains treated with fluoroquinolones. It is likely that isolates that are nalidixic acid susceptible but with reduced ofloxacin and ciprofloxacin susceptibility contain resistance mechanisms other than mutations in the quinolone resistance-determining region of the gyrA gene. Possibilities include decreased permeability, an increase in active efflux, and the presence of plasmid-mediated genes, such as the qnr genes that encode a protein that protects the DNA gyrase from ciprofloxacin or aac(6')-Ib-cr, an aminoglycoside-modifying enzyme with activity against ciprofloxacin (32).

The mutations that we detected in DNA gyrase genes and topoisomerase genes were consistent with previous reports (4, 6, 34, 42). The most common amino acid substitution detected was S83F, which has been found to be particularly associated with the H85 haplotype (35). This haplotype has become dominant in many areas of Asia in recent years and has also been found to have spread into Kenya in East Africa (24). Approx-
imately 20 to 25% of the isolates with a gyrA mutation had an MIC below the suggested breakpoints of 0.25 μg/mL for ofloxacin and 0.125 μg/mL for ciprofloxacin. The effect on the response to fluoroquinolone treatment of infection with isolates with a single gyrA mutation but with an MIC below the suggested breakpoints is not known. It is also possible that the isolate with a single gyrA mutation but an MIC above the suggested breakpoint have additional resistance mechanisms present (32).

The lack of universally observed guidelines for the detection of S. Typhi isolates with reduced susceptibility has meant that such isolates are frequently unrecognized by microbiology laboratories.

Qplofloxacín and ofloxacin for these infections may be driving the emergence of fully fluoroquinolone-resistant isolates of S. Typhi and S. Paratyphi A (20, 25, 34). Gatifloxacín, azithromycin, and ceftriaxone are better options for treating such infections, if the isolates also demonstrate resistance to first-line antimicrobials (7, 15, 18, 21, 31).

The use of nalidixic acid as a surrogate screening test is often confusing because it is not used to detect the treatment of enteric fever. Furthermore, the emergence of nalidixic acid-resistant isolates with reduced ofloxacin and ciprofloxacin susceptibility may mean that some isolates are missed. Therefore, a straightforward solution would be to modify the S. Typhi breakpoints to ≥30 mm and ≤28 mm for ciprofloxacin and ofloxacin, respectively. Interpretative breakpoints for the disk susceptibility tests with the antimicrobials actually used for treatment will need to be determined in this therapy for enteric fever and will allow the collection of accurate surveillance data. Our data suggest disk breakpoints of ≥30 mm and ≤28 mm for ciprofloxacin and ofloxacin, respectively. These breakpoints have high specificity and sensitivity, permitting the detection of S. Typhi strains that have reduced susceptibility to ciprofloxacin and ofloxacin.

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We dedicate that we have no competing interests.

REFERENCES


13. Cure, P., F. J. White, J. White, and E. J. Threlfall. 2003. Antimicrobial treatment of enteric fever and will allow the collection of accurate surveillance data. Our data suggest disk breakpoints of ≥30 mm and ≤28 mm for ciprofloxacin and ofloxacin, respectively. These breakpoints have high specificity and sensitivity, permitting the detection of S. Typhi strains that have reduced susceptibility to ciprofloxacin and ofloxacin.
A Randomised Trial Evaluating the Safety and Immunogenicity of the Novel Single Oral Dose Typhoid Vaccine M01ZH09 in Healthy Vietnamese Children

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Abstract

**Background:** The emergence of drug resistant typhoid fever is a major public health problem, especially in Asia. An oral single dose typhoid vaccine would have major advantages. M01ZH09 is a live oral single dose typhoid vaccine candidate vaccine containing Salmonella enterica serovar Typhi (Ty2 arcC strain) Z19 with two independently attenuating deletions. Studies in healthy adults demonstrated immunogenicity and an acceptable safety profile.

**Objectives:** We conducted a randomised placebo controlled, single-blind trial to evaluate the safety and immunogenicity of M01ZH09 in healthy Vietnamese children aged 5 to 14 years.

**Methods:** Subjects were randomly assigned to receive either a nominal dose of 5×10^9 CFU of M01ZH09 or placebo and were followed up for 28 days. The primary safety outcome was the proportion of subjects with any adverse event attributed to M01ZH09. The primary immunogenicity endpoint was the proportion of subjects who showed a positive immune response to M01ZH09 in the Salmonella Typhi lipopolysaccharide (LPS) specific serum IgA and IgG ELISA.

**Principal Findings:** One hundred and fifty-one children were enrolled, 101 subjects received M01ZH09 and 50 subjects received placebo. An intention to treat analysis was conducted. There were no serious adverse events and no bacteraemias. In the M01ZH09 group, 26 (26%) 95% CI, 18-35% of 101 subjects experienced adverse events compared to 11 (22%) 95% CI, 12-36% of 50 subjects in the placebo group (odds ratio [OR] [95% CI] = 1.23 [0.50-2.747], p = 0.691). Faecal shedding of S. Typhi (Ty2 arcC strain) Z19 was detected in 11 (21%) 95% CI, 41-61% of 101 M01ZH09 subjects. No shedding was detected beyond day 4. A positive immune response, defined as 70% increase (1.7 fold change) in LPS specific serum IgG (day 14 or 28) and/or 50% increase (1.5 fold change) in LPS specific serum IgA (day 7 or 14) from baseline was detected in 90% 95% CI, 92-99% of 101 M01ZH09 recipients and 8 (16%) 95% CI, 7-29% of 50 placebo recipients. Twenty-eight (100%) 95% CI, 88-100% of 28 vaccine recipients who were evaluated in the LPS specific IgA ELISPOT assay showed a positive response compared to none of the 14 placebo recipients tested.

**Conclusions:** This was the first phase II trial of a novel oral candidate typhoid vaccine children in an endemic country. M01ZH09 had an appropriate safety profile and was immunogenic in children.

**Trial Registration:** Controlled-trials.com ISRCTN91111837


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Introduction

Typhoid fever remains a major public health burden in developing countries with approximately 21 million cases and more than 210,000 deaths worldwide per year [1].

Drug-resistant typhoid fever has emerged and spread globally narrowing the treatment options [2, 4]. The World Health Organization therefore recommends that countries should consider the programmed use of typhoid vaccines for controlling endemic disease and that the immunization of school age and/or preschool age children should be undertaken particularly in areas where antibiotic-resistant Salmonella enterica serovar Typhi (S. Typhi) is prevalent [5].

Two licensed and safe typhoid vaccines are available. The oral live attenuated Ty21a vaccine is moderately immunogenic and needs to be administered in three to four doses. Ty21a enterically-coated capsules and Ty21a liquid formulation (which is currently not manufactured) are licensed for children above 6 years and 2 years, respectively. The single dose injectable Vi polysaccharide vaccine is licensed for children above 2 years. The liquid formulation of Ty21a and Vi vaccine provide about 55 to 70% protection from culture confirmed typhoid fever and protection lasts for 3 to 5 years [6].

From a public health perspective, a single dose oral typhoid vaccine would have major advantages [7, 8]. M01ZH09 (S Typhi (Ty2 acm− rtionF) ZH9) is a promising candidate of such a novel typhoid vaccine, it has a well-defined dual mechanism of attenuation [9] and has been safe and immunogenic in a single dose in Western [9, 11] and Vietnamese adult volunteers [10, TT, unpublished].

Historically, oral live vaccines often showed reduced immunogenicity in developing country populations compared to Western populations [12], therefore M01ZH09 was evaluated at an early stage of its development in children in an endemic country.

We describe here the results of a randomized placebo-controlled trial that evaluated the safety and immunogenicity of M01ZH09 in 151 healthy Vietnamese children aged 5 to 14 years.

Methods

The protocol for this trial and supporting CONSORT checklist are available as supporting information; see Protocol S1 and Checklist S1.

Study design and objectives

The study was designed as a randomized placebo controlled single blind trial to evaluate the safety and immunogenicity of the novel oral single dose live typhoid vaccine M01ZH09 in Vietnamese children aged 5 to 14 years (inclusive).

The study site and ethical approval

The trial was conducted at the Hospital for Tropical Diseases in Ho Chi Minh City, Vietnam. Ethics approval for the trial and all trial related documents was obtained by the Oxford Tropical Research Ethics Committee (OXTREC) and by the Institutional Review Board of the Ministry of Health, Hanoi, Vietnam. The trial was conducted in accordance with the Declaration of Helsinki and its amendments and according to Good Clinical Practice guidelines and was monitored by Marius Contract Research Ltd., UK (now Novella Clinical). The trial was also conducted under an US Investigational New Drug (IND) license.

Participants

Healthy Vietnamese children aged 5 to 14 years (inclusive) were invited to participate in the trial. Recruitment was carried out by word of mouth. Families who were interested in the trial were invited to attend one of several information evenings at the Hospital for Tropical Diseases. At these meetings the study was presented by the principal investigator (TTH) and all questions could be discussed and answered. Families who remained interested in the trial were invited to attend the screening visit. Children were eligible if they were available during the trial period and at least one of their parents gave written informed consent for their child to participate after the trial procedures and potential risks were carefully explained by the study investigators. All children were invited to give their assent to the study and written informed consent was obtained from subjects starting at the age of 6 years. After informed consent was obtained, screening tests were performed. Children were screened by history, physical examination (including height, weight and vital signs), blood tests (biochemistry, haematology and HIV test), urine dipsticks and pregnancy tests (for female subjects of 11 years and above). stool cultures were performed to check for the presence of Salmonella species.

Subjects with a history of typhoid fever, Ty21a vaccination in the last 10 years or any other typhoid vaccine in the last 5 years, any clinically significant illness, abnormal blood test results, immune suppression, positive HIV or pregnancy test were excluded. Also excluded were subjects whose body weight was under 17 kg in the 5 to 10 year old group or under 27 kg in the 11 to 14 year old group and subjects who suffered from an acute febrile illness at the time of dosing (the complete list of exclusion criteria is available in the trial protocol). Only one child per family was allowed to participate in the trial.

The results of the screening tests were reviewed and subjects who continued to meet the inclusion criteria were invited to continue in the trial.

The M01ZH09 vaccine and dose

S Typhi(Ty2 acm− rtionF) ZH9 was constructed with a rational attenuation strategy. Two defined independently attenuating deletion mutations were introduced into S Typhi Ty2. Deletion of acm encoding chorismate synthase, prevents the biosynthesis of aromatic amino acids and depletes the live vaccine bacterium of essential nutrients. Deletion of rtf encoding a structural component of the Salmonella pathogenicity island-2 (SPI-2) type III secretion system, prevents systemic spread of S Typhi [9]. The vaccine was manufactured according to Good Manufacturing Practice protocols by Emergent S.A. and Syntec Bio Partners-B.V.; batch number M01ZTH9-F was shipped to Vietnam. The vaccine kits were stored at 2 °C.

Previous studies in adult volunteers demonstrated that a nominal dose of 5x10^9 CFU of the vaccine strain was immunogenic and safe [9, 11]. The Ty21a oral typhoid vaccine capsules are licensed for adults and children above 6 years using the same dose and immunization schedule and large Ty21a field trials in children used the same dose and regimen as in adults [12]. It was
therefore determined that the appropriate dose for the children's study was a nominal dose of 5 x 10^7 CFU of S. Typhi (TY2 acc^−

ZHB).

The vaccine (containing 5 x 10^7 CFU of vaccine strain plus

exipients) and the placebo (vaccine exipients only) were supplied as freeze-dried formulations in single dose vials, which were

labeled identically, containing "M612/98 tubercoid vaccine or

placebo" but with a unique subject number corresponding to the

randomization list. The bicomponent solution was prepared by
dissolving one different bicomponent tablet (provided in the

vaccine kit and containing 2.6 g sodium bicarbonate, 1.65 g

sucrose, and 30 mg aspartame) in 150 ml of chilled drinking

water (final concentration 1.72%, 0.1% wet/wet sucrose, and

0.02% wet/wet aspartame). The

hypothalamic vaccine or placebo was reconstituted in either 150 ml

for children above 15 years or in 75 ml of the bicomponent solution

for children below 10 years and was administered immediately.

The study used two age group specific randomization lists, one

for the 11 to 14 year old and one for the 5 to 10 year old children
to ensure at least 70% children were between 5 to 10 years old.

Intervention

On the day of vaccination (day 0) which took place within 28
days of the screening, inclusion and exclusion (including history of

antibiotic medication in the last 2 weeks) criteria were reviewed.

Pregnancy (female subjects of 11 years and above only), urine

dipstick test and stool cultures were searched for. Bacterial,

haematology, biochemistry, ELISA and EISPOT assays (only in

children 11 years and above) were obtained. After the subjects had

fasted for at least 2 hours (with the exception of drinking water),

the candidate typhoid placebo or placebo was administered.

Subjects were allocated the next age group specific subject

number and the medication pack bearing the same number was

prepared and issued by the pharmacist, who was otherwise not

involved in the trial. The subjects were randomly assigned to

receiving one (containing of 5 x 10^7 CFU of S. Typhi (TY2 acc^−

ZHB) or the placebo reconstituted in bicomponent solution as
described above.

Subjects were observed for at least 90 minutes at the hospital.

Duration this time pulse and blood pressure were recorded

periodically and only drinking water was provided.

Diary cards were filled for all the volunteers and all subjects

received a basic hygiene kit containing soap, gloves and

guttas for the collection of stool samples. The subjects and their

parents were instructed to measure and record the oral temperature of the

toddlers twice daily in the morning and evening) and record any

adverse events (including headache, fever, nausea, vomiting, abdominal

pain, frequency and consistency of stools and any other

symptoms) for 14 days.

Follow up procedures and monitoring of adverse events

Children were followed up daily from days 1 to 14 and again on
day 28 after dosing. At these appointments diary cards were

checked and adverse events and concomitant medication reviewed.
A history of the last 24 hours with special emphasis on

temperatures of 38.5°C and above and adverse events (diarrhoea,

loss of appetite, vomiting, headache and shill) was obtained. Oral

temperatures and vital signs were recorded and children were

examined for signs of splenomegaly. Stool cultures were performed
daily from day 1 to day 14. Blood samples for biochemistry and

haematology were obtained on days 7, 14 and 28 for the LPS

specific serum IgA ELISA on days 7 and 14; for the IgA ELISA on
days 14 and 28 and for the LPS specific IgA antibody secreting cell

(ASC) EISPOT assay (only in subjects aged 11 years and above)
on day 7. The total amount of blood taken during this study was

approximately 20 ml from the 11 to 14 years old and 9 ml from

the 5 to 10 years old children.

Unscheduled visits

Subjects and patients were instructed to make additional visits to

the clinic, if the child felt unwell and/or had a fever of ≥38.5°C.

At these visits the subject was assessed and samples taken for

culture as clinically indicated. Blood cultures to investigate the

presence of S. Typhi in blood would be obtained if a fever of

≥39.0°C was recorded twice over a 48 hours period, or a severe

fever of ≥39.5°C was recorded once.

Definition and reporting of serious adverse events and
definition of stopping rules

There was no Data Safety and Monitoring Committee for this

trial. Data from all children were reviewed daily and there were a

few defined stopping rules which would trigger a suspension of the

trial and a safety review (Protocol S1). Serious adverse events

were reported to AKOS Ltd (Hitchin, UK), a pharmacovigilance

company within 24 hours.

Detection of Salmonella in stool samples at the screening

visit and day 0

The detection of Salmonella species at the screening visit and on
day 0 was performed according to microbiological standard

procedures. In brief, stool samples were inoculated onto

MacConkey agar and xylose lysine deoxycholate (XLD) agar

plates, and incubated at 37°C for 24 hours. Blood and broth were

incubated at 37°C overnight and the broth was sub-cultured on

MacConkey and XLD agar plates the next morning. Isolates were

identified using standard biochemical tests and salmonella were

identified by slide agglutination with specific antiserum (Oxoid Ltd.,

UK) and API20E profiling (bioMérieux, UK).

Detection of S. Typhi in stool samples

Stool samples were collected daily between days 1 and 14. Stool

samples were cultured directly on deoxycholate citrate agar (DCA)

Hynes plates (direct method) and in saline F broth (enriched

method) both of which were supplemented with aromatic

compounds (DCA-aro and saline F-aro, respectively) to detect

S. Typhi, including the nonmotile vaccine strain, in stools. Following

overnight incubation at 37°C, an aliquot of the inoculated saline F-broth was sub-cultured on DCA-aro

Hynes plates. Suspected S. Typhi colonies were inoculated on

brain heart infusion agar plates supplemented with aromatic

compounds (BHI-aro). Oxide negative colonies were evaluated

by agglutination with H5, V1 and O9 anti-serum (Oxoid Ltd.,

UK) and API20E profiling (bioMérieux, UK). Stool samples containing

isolates that were positive in at least 2 out of 3 agglutinations and

identified as S. Typhi by API20E profiling were considered to be

positive for S. Typhi. All isolates were stored in 10% (v/v) glycerol

at −70°C.

Detection of S. Typhi in blood samples

Blood samples were collected into either Bactec Pedi Plus/F

culture bottles (1 3 ml blood; BD, USA) or Bectec Pedi Anaerobic/F

culture bottles (4 10 ml blood; BD, USA) and supplemented with

antimicrobial compounds. Blood cultures were incubated at 35°C in

the Bactec detection system and monitored for up to 5 days. Gram

stains was performed on all bottles triggering a positive reaction.

Positive cultures and all cultures that were negative after 5 days of

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incubation were sub-cultured on XLD agar plates. Suspected S. Typhi colonies were sub-cultured onto BH-trypt agar plates. Opaque negative isolates were evaluated by agglutination and APSE tissue culture isolation (BoMérimex, UK) as above.

PCR identification of S. Typhi isolates

Genomic DNA was isolated from glycerol stocks of S. Typhi isolates using a DNeasy blood and tissue kit (Qiagen, UK). Multiplex PCRs were performed using a Takara PCR core kit (Qiagen, UK). Each reaction mixture contained 200 μl of (10 nM each) SATCAGAGCCTTACCAAGG (5') and msaVT (5' CTITTTCTGCATCATGAGG 3'), and 0.1 μM each Hvr1-Z3 (5' GAGAAGCCTTGCTGTAACC 3') and msaG-Z3 (5' TTAACTCTACATAGGTCGTGC 3'). 10 ng genomic DNA and 1.25 μl Taq DNA polymerase in a total volume of 50 μl reaction buffer. PCRs were performed for 25 cycles as follows: 94°C for 30 sec, 57°C for 30 sec and 72°C for 2.5 min. The PCR products were visualized by ethidium bromide staining and UV transillumination after electrophoresis on a 0.8% (w/v) TAE agarose gel. The expected size of the PCR products were 1.8 kb (mSA) and 0.59 kb (maS) for S. Typhi wcb-type strains and 0.55 kb (mS) and 0.70 kb (maS) for S. Typhi (Ty2) (mS mS maS maS) Z1H9.

Detection of antibody secreting cells producing S. Typhi LPS specific IgA antibodies by ELISPOT assay

ELISPOT assays to detect antibody secreting cells (ACS) producing S. Typhi LPS specific IgA antibodies were performed on days 0 and 7 as described previously [10,14]. In brief, whole blood was collected in heparinized cell preparation tubes (Vacutainer CPT, BD, UK) and centrifuged. Peripheral blood mononuclear cells (PBMCs) were washed, resuspended in culture medium and assayed to three cell concentrations (×10^4/mL, 5×10^4/mL and 2.5×10^4/mL). One hundred microliters of each concentration were added to LPS coated and uncoated wells. The plates were read at 450 nm within 30 minutes of stopping the reactions with 0.3% and 0.15% dextran sulphonate. The standard curve was constructed by plotting the optical densities (ODs) of standards against concentrations and fitted by a 4-parameter logistic equation (SollMax® Pro 4.6, Molecular Devices, USA). The concentration of LPS specific IgA in each sample was determined from the standard curve. The IgA quantitative ELISA was performed in a similar manner, except using a double detection system of biotinylated anti-human IgA antibody (Southern Biotech, USA) followed by streptavidin-HRP conjugate (Dako, Denmark).

Outcomes of the study

Safety Outcomes. The primary safety endpoint was the proportion of subjects with any adverse events at both dose levels of M0129H9. The secondary safety endpoint was the proportion of subjects with any serious related adverse event; any related or unrelated adverse event; any severe related adverse event; any severe adverse event; any severe, unexpected, and/or serious adverse event. Adverse events were assessed and graded by severity (mild, moderate, severe) and judged for the relatedness to the study vaccine (likely, probably) by the investigator. Only possibly and probably related adverse events were attributed to the vaccine. Moderate fever was defined as an oral temperature of 38.5°C or greater in the 4 days post vaccination, with a further rise in the urine due to serious adverse events, including haemorrhages, and/or had clinically significant changes in laboratory parameters related to the candidate vaccine.

All subjects who received a dose of the vaccine or placebo were analysed in the safety population. Post-vaccination adverse events were categorised according to the MedDRA (Medical Dictionary for Regulatory Activities; MedDRA, Version 9.1), allocated before unblinding. Adverse events were graded by severity (mild, moderate, severe) and judged for the relatedness to the study vaccine (unlikely, probably) by the investigator. Only possibly and probably related adverse events were attributed to the vaccine. Moderate fever was defined as an oral temperature of 38.5°C or greater in the 4 days post vaccination, with a further rise in the urine due to serious adverse events, including haemorrhages, and/or had clinically significant changes in laboratory parameters related to the candidate vaccine.
The numbers and proportion of subjects reporting adverse events were fitted by body system. A per subject analysis of adverse events was performed e.g. if a subject reported the same adverse event on three occasions that adverse event was only counted once. Subjects reporting more than one adverse event per body system were counted only once in that body system total.

Immunogenicity Outcomes. The primary immunogenicity endpoint was the proportion of subjects who developed a positive immune response to S. Typhi LPS defined by an increase of 70% (1.5 fold change) in LPS specific IgG on day 14 or 28 and/ or an increase of 50% (1.5 fold change) in LPS specific IgA on day 7 and 14 compared to baseline.

The secondary immunogenicity endpoints were defined as the proportion of subjects who developed a positive immune response in each of the following assessments: S. Typhi LPS specific IgA ELISA assay on days 7 or 14, S. Typhi LPS specific IgG ELISA assay on days 14 or 20 and S. Typhi LPS specific IgA ELISPOT assay on day 7. A positive ELISPOT was defined as ≥40 IgA antibody secreting cells specific for S. Typhi LPS per 30^6 PBMCs.

Sample Size. The planned sample size was 150 subjects, of whom at least 70% should be aged 10 years or younger, as this was the target age of the vaccine, randomized to M01/ZH09 or placebo in a 2:1 ratio.

No formal sample size calculation was considered appropriate; it was aimed to include a sufficient sample size to assess safety and immunogenicity based on previous observations in adult studies and immunogenicity rates of licensed typhoid vaccines in children.

Randomization procedures and assignment of intervention (sequence generation, allocation concealment, implementation). Randomization codes were computer generated in blocks of 9 by Statwise Ltd, UK. The vaccine and the placebo were labeled identically but with a unique subject number corresponding to the randomization list. The study used two age group specific randomization lists, one for the 1.1 to 14 years old and one for the 5 to 10 year old children to ensure at least 70% children were between 5 to 10 years old.

Subjects were allocated the next age-group specific subject number in strict numerical sequence from this list and the medication pack bearing the same number was prepared by the pharmacist.

Blinding. This study was formally a single blind study due to slight differences in taste and aroma between the treatment preparations but it was conducted under the principles of a double blind study. M01/ZH09 and placebo were packaged and labeled identically but with a unique sequential number. Possible sources of unblinding could have been the preparation of the vaccine, therefore the study pharmacist was otherwise not involved in the trial. The subjects were asked to not report the taste of the vaccine. Microbiology results were not reviewed by the investigators for at least 14 days after vaccination to avoid potential unblinding through shedding in stools. Immunology results were not reviewed by the investigators. The study site received code break envelopes in case an emergency mode unblinding for a single subject necessary. No codes were broken during this study. The unblinding of treatment allocations took place after the trial had been completed and the whole database had been entered and locked.

Data collection, data entry and statistical methods. All data were recorded in Case Report Forms (CRF). CRFs were reviewed and collected by the study monitor. Data entry, data management and statistical analysis were conducted by Statwood, UK using SAS® software (version 9.1). Data were double entered and analyzed according to an a priori defined statistical analysis plan which included the definition of all subject populations and the trial endpoints. The safety population included all subjects who received the study medication. The intention to treat (ITT) population comprised all consented subjects who had any post-dose immunogenicity data available. The per protocol (PP) population excluded major protocol violations (failure to meet the inclusion/exclusion criteria, to comply with the study medication or use of other vaccinations or antibiotics two weeks before until 2 weeks after vaccination, or use of aspirin or protoserpil inhibitors prior to vaccination and/or did not provide samples for the ELISA). The protocol stated that a confirmatory analysis of the primary immunogenicity endpoint in the PP population was planned if more than 5% of subjects were excluded.

The proportion of subjects who experienced post-dose adverse event was presented together with their two-sided 95% confidence intervals (95%CI). Post-dose adverse events, adverse events considered to be related to the vaccine and adverse events that occurred in more than 10% of the trial population were tested using a two-sided Fisher's exact test to compare between the two groups.

The proportion of subjects who developed a positive immune response was presented together with their two-sided 95% confidence intervals calculated by using an exact Binomial distribution. The treatment difference and associated 95% confidence interval were presented as above. All available data from withdrawn subjects was included in the analysis.

Results. Participant flow and recruitment. The trial was conducted between April and July 2007. In total, 205 healthy Vietnamese children between 5 and 14 years inclusive were screened for eligibility. Fifty-four children were not eligible (Figure 1), the most common reasons were unavailability for the whole study period (n=10) and a positive stool culture for Salmonella species at screening (non-typhoidal Salmonella, n=25). No S. Typhi or S. Paratyphi A were detected in stools at the screening visits. One hundred and fifty-one children were randomized, 101 children received the candidate typhoid vaccine M01/ZH09 and 50 children received placebo. All subjects fulfilled the inclusion and exclusion criteria at screening and dosing, however two subjects (both in the M01/ZH09 group) had clinically significant elevated white blood counts (16.3 and 18.2 x/10^9/L respectively) on day 0, these results were only available after dosing.

One subject in the M01/ZH09 group withdrew after taking approximately 50% of the required vaccine dose. The subject agreed to take another dose, but failed to return it. Three subjects withdrew from the study, one placebo recipient withdrew due to non-compliance (refused to provide stool sample) after day 2 and two vaccine recipients left the study after day 6 (one wished to withdraw, the second subject went on holiday). All three subjects attended the day 28 visit. The remaining subjects attended all study visits. Two subjects had unscheduled visits. One subject in the vaccine group attended the clinic on day 16 because of fever of 38.1°C and one subject in the placebo group returned on day 26 with a temperature of 38.3°C. Blood cultures were obtained from...
Healthy Vietnamese children aged 5 to 14 years (inclusive) were screened for eligibility, n = 205

- Not eligible, n = 54
- Age under 5 years, n = 1
- Fever on day 0, n = 1
- Body weight below 27 kg (11-14 year old), n = 2
- Withdrawal from the study, n = 4
- Abnormal laboratory result, n = 6
- No stool sample provided, n = 8
- Not available for the duration of the study, n = 10
- Stool sample positive for any S. species at screening, n = 22

151 children randomised

101 children assigned to MO1ZH09
101 children received MO1ZH09
50 children assigned to placebo
50 children received placebo

1 Subject did not take the required dose of MO1ZH09
2 Subjects withdrew after day 6
1 Subjects took antibiotics between day -14 and day 14
1 Subjects had one unscheduled visit on day 16 because of fever
1 Subject had unscheduled blood tests on day 10 because of fever

All 101 subjects attended the day 28 visit
All 101 subjects analysed in the ITT analysis

1 Subject withdrew after day 2
1 Subject had one unscheduled visit on day 26 because of fever
2 Subjects took antibiotics between day -14 and day 14

All 50 subjects attended the day 28 visit
All 50 subjects analysed in the ITT analysis

Figure 1. Flow of subjects.

Both subjects and both cultures were negative. One MO1ZH09 recipient had unscheduled tests performed. The subject presented on day 16 with a temperature of 38.6°C and reported diarrhoea, vomiting and fever on the previous day. The white blood count was elevated with 14.2x10³/L and the blood culture result was negative.

Numbers analysed

All 151 children who were randomised and received either MO1ZH09 (n = 101) or placebo (n = 50) constituted the intention to treat (ITT) population. Seventy subjects, 4 in the vaccine group and 3 in the placebo group were protocol violators (see Fig. 1) and were excluded from the per-protocol (PP) population. The analysis of the primary endpoints in the PP population was planned if more than 5% of subjects were excluded from the ITT. The PP population comprised 95% (144/151) of subjects and therefore no per protocol analysis was conducted.

All outcomes were evaluated for the ITT population.

Baseline data

The two groups did not differ significantly at enrolment in terms of sex, age and laboratory parameters (Table 1). One hundred and seven (71%) children were aged 16 years or younger. Two subjects in the MO1ZH09 group had clinically significant elevated white blood counts on day 0 (see above). Twelve subjects...
Table 1. Baseline characteristics of the subjects on day 0 (intention to Treat population).

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>M01ZH09 group (n = 101)</th>
<th>Placebo group (n = 50)</th>
<th>Overall (n = 151)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (yr)</td>
<td>9 (5–14)</td>
<td>9 (5–14)</td>
<td>9 (5–14)</td>
</tr>
<tr>
<td>Number of males (%)</td>
<td>54 (53)</td>
<td>27 (54)</td>
<td>51 (41)</td>
</tr>
<tr>
<td>Height in cm</td>
<td>132 (97–165)</td>
<td>130 (96–160)</td>
<td>131 (97–160)</td>
</tr>
<tr>
<td>Oral temperature °C</td>
<td>36.40 (36.1–37.5)</td>
<td>36.75 (37.1–37.4)</td>
<td>36.63 (35.1–37.5)</td>
</tr>
<tr>
<td>Haemoglobin, g/dL</td>
<td>13.3 (10.5–15.5)</td>
<td>13.4 (10.9–16.1)</td>
<td>13.3 (10.5–15.5)</td>
</tr>
<tr>
<td>White cell count, 10^9/L</td>
<td>7.15 (5.8–10.2)</td>
<td>7.05 (5.2–8.5)</td>
<td>7.15 (5.2–8.5)</td>
</tr>
<tr>
<td>Leucocytes, %</td>
<td>38.4 (14.3–55.5)</td>
<td>39.8 (24.7–47.4)</td>
<td>38.8 (24.7–47.4)</td>
</tr>
<tr>
<td>Neutrophils, %</td>
<td>46.4 (29.2–70)</td>
<td>52.5 (43.5–73.0)</td>
<td>50.9 (43.5–73.0)</td>
</tr>
<tr>
<td>Monocytes, %</td>
<td>5.1 (2.1–12.3)</td>
<td>5.6 (4.4–13.3)</td>
<td>5.3 (4.4–13.3)</td>
</tr>
<tr>
<td>Basophils, %</td>
<td>0.3 (0–0.7)</td>
<td>0.3 (0–0.7)</td>
<td>0.3 (0–0.7)</td>
</tr>
<tr>
<td>Eosinophils, %</td>
<td>4.0 (0–12.6)</td>
<td>3.6 (0–12.3)</td>
<td>3.8 (0–13.6)</td>
</tr>
<tr>
<td>Platelet count, 10^9/L</td>
<td>285 (196–503)</td>
<td>211 (179–403)</td>
<td>231 (179–403)</td>
</tr>
<tr>
<td>Serum Aspartate Aminotransferase, AST, U/L</td>
<td>27 (14–32)</td>
<td>26 (14–31)</td>
<td>27 (14–32)</td>
</tr>
<tr>
<td>Serum Alanine Aminotransferase, ALT, U/L</td>
<td>16 (6–10)</td>
<td>17 (5–8)</td>
<td>16 (5–10)</td>
</tr>
<tr>
<td>Creatinine, mG/d</td>
<td>0.47 (0.33–0.70)</td>
<td>0.47 (0.27–0.73)</td>
<td>0.47 (0.27–0.73)</td>
</tr>
<tr>
<td>Good culture positive for Salmonella species</td>
<td>5</td>
<td>13</td>
<td>18</td>
</tr>
</tbody>
</table>

All data are presented as median (range) unless otherwise specified.

Data from enrolment and randomisation phases not available.

Four (4%) M01ZH09 recipients experienced 10 adverse events that were related to the candidate vaccine compared to none in the placebo group (p = 0.302). Of these, 8 were mild, one moderate (diarrhoea) and one event of pneumonia was severe. The moderate and the severe related adverse events occurred in the same subject.

This subject had a normal temperature on day 0, but the pre-dose blood test showed an elevated white blood cell count (18.3 x 10^9/L). The subject experienced five post vaccination adverse events occurring on day 0, including fever of 39.5 and 39.0°C, diarrhoea, headache, abdominal pain and anorexia. The subject received paracetamol and recovered.

Similar proportions of subjects experienced fever post vaccination (Table 2), only one subject reported fever related to M01ZH09 (see above).

Adverse events classified as gastrointestinal disorders, nervous system disorders and investigations were experienced by a higher proportion of M01ZH09 recipients (Table 2). Twelve (22%) vaccine recipients experienced gastrointestinal disorders compared to 1 (2%) placebo recipient (p = 0.061). Nervous system disorders (headache) occurred in 9 (18%) vaccine recipients compared to 1 (2%) placebo recipient (p = 0.160) and investigations were reported by 4 (8%) vaccine recipients compared to none of the placebo recipients (p = 0.302).

Cough was the most frequently reported adverse event, occurring in 6 (8%) M01ZH09 recipients versus 7 (14%) placebo recipients (p = 0.124).

On day 3 after vaccination, faecal shedding of S Typhi occurred in 47 (89%) of 53 vaccine recipients; shedding was detected by the direct method in 31 (72%) subjects and by the enrichment method of culturing stools in 36 (86%) subjects. On day 2 after vaccination, faecal shedding was detected in 12 (12%) of 97 subjects (in 1% subject by direct and in 11 (11%) subjects by enrichment method. Only one (1%) of 58 subjects experienced shedding on Day 3 (detected by enrichment method). In total, 51 (51%), 95% CI, 41–61% of 100 M01ZH09 subjects experienced...
Table 2. Incidence of adverse events after vaccination during 28 days of follow up (intention to Treat population).

<table>
<thead>
<tr>
<th>Event</th>
<th>MD01ZH09 (n = 101)</th>
<th>Placebo (n = 50)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Any adverse event</td>
<td>26</td>
<td>23</td>
</tr>
<tr>
<td>Gastrointestinal disorders (%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>related to vaccine</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>Abdominal pain (%)</td>
<td>8</td>
<td>6</td>
</tr>
<tr>
<td>related to vaccine</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Constipation (%)</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Diarrhea (%)</td>
<td>5</td>
<td>1</td>
</tr>
<tr>
<td>related to vaccine</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Nausea (%)</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>related to vaccine</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Vomiting (%)</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>General disorders and administration site conditions (%)</td>
<td>9</td>
<td>10</td>
</tr>
<tr>
<td>Chills (%)</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Fatigue (%)</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Pyrexia (%)</td>
<td>8</td>
<td>6</td>
</tr>
<tr>
<td>related to vaccine and fever*</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Infections and infestations</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Oral infestations</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Infections</td>
<td>4</td>
<td>0</td>
</tr>
<tr>
<td>Urine colour abnormal</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>White blood cell count increased</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Metabolism and nutrition disorders (%)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Appetite (%)</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>related to vaccine</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Decreased appetite</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Nervous system disorders</td>
<td>9</td>
<td>2</td>
</tr>
<tr>
<td>headache (%)</td>
<td>9</td>
<td>2</td>
</tr>
<tr>
<td>related to vaccine</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Respiratory, thoracic and mediastinal disorders (%)</td>
<td>6</td>
<td>14</td>
</tr>
<tr>
<td>Cough (%)</td>
<td>6</td>
<td>14</td>
</tr>
<tr>
<td>Sinusitis (%)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Skin and subcutaneous tissue disorders (%)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Rash (%)</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Vascular disorders</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Hypersensitivity</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

Per subject analysis of adverse events (likely, possibly and probably related to the vaccine) reported during 28 days of follow up. Subjects could experience more than one adverse event. Each adverse event was only counted once for each subject and system class. There were 56 adverse events in the MD01ZH09 group and 10 in the placebo group, when repeated occurrences of a particular event in the same patient were only counted once. Adverse events that were possibly or probably related to the vaccine are presented in bold.

*One serious adverse event was reported.

doi:10.1371/journal.pone.0017770.003

The presence of S. Typhi was detected in the stools of 1 (2%) 55%CI 0.11% and 2 of 50 subjects in the placebo group. This occurred on day 2 and was detected using the enriched method. No fever or adverse events were recorded for this subject. The finding of a positive stool culture for S. Typhi in a placebo subject was only available after unblinding of the trial, all previous and all sequential stool cultures up to day 14 of this subject were negative.

This isolate was identified as the vaccine strain S. Typhi (Ty2 and C' and ZH2) by subsequent PCK analysis. Seven (7%) of 101 MD01ZH09 recipients and 3 (6%) of 50 placebo recipients were detected to have a positive stool culture for non-typhoidal Shigella between day 1 and 14 after vaccination.

Immunogenicity Outcomes. Ninety-eight (97%; 95%CI, 92.99%) of 101 subjects in the MD01ZH09 group and 8 (16.0%; 95%CI, 7.29%) of 50 subjects in the placebo group developed a positive immune response in either the S. Typhi LPS specific.
serum IgG or IgA ELISA, defined as the primary endpoint (Table 3). The difference in proportions of responders between the vaccine group and the placebo group was 81.6% (85% CI: 69.95%, the lower limit of the 95% CI of the difference was greater than 50% and fulfilled the a priori defined criterion for an acceptable immune response.

Median baseline LPS specific antibody levels were comparable in both groups (Figure 2). In the MOI Z H09 group, median IgA antibody levels increased from 3 (IQR: 9.20 212) units/ml at baseline to 29 (IQR: 19.2 231.3) units/ml and 103 (IQR: 28 253.5) units/ml on days 7 and 14 respectively. On day 7, 28 immune responders in the vaccine group (Table 3) displayed a median 16.4 (IQR: 3.75 60.25) fold rise in serum IgA antibodies relative to baseline (Table 4, Supplementation).

In the vaccine group, median LPS specific IgG antibody levels were 66650 (IQR: 5125 139500) units/ml and 55700 (IQR: 25450 160000) units/ml on day 14 and 28, respectively, compared to median baseline levels of 6300 (IQR: 2030 16560) units/ml. On day 14, the 91 immune responders in the MOI Z H09 group (Table 3) showed a median 5.18 (IQR: 3.57 20.68) fold increase in serum IgG antibodies relative to baseline.

Forty-two out of 44 eligible subjects provided samples for the ELISPOT assay on day 7. All baseline ELISPOT samples were negative (defined as <5 ASC per 10⁶ PBMC). On day 7, 26 (100% of 26) MOI Z H09 subjects who provided samples showed a positive ELISPOT response compared to none (0%) of the 14 evaluable subjects in the placebo group. Sixteen (57%) of 28 MOI Z H09 recipients displayed results of >100 spots per 10⁶ PBMC and among the remaining 12 vaccine subjects numbers of spots ranged from 6 to 126 per 10⁶ PBMC. The median number of spots in the MOI Z H09 group was >100 (IQR 46 5 100) greater spots per 10⁶ PBMC, as counting stopped above 100 spots, this was recorded as "too many spots to be counted". All 14 placebo recipients showed <4 spots per 10⁶ PBMC, this was recorded as "too few spots to be counted."

There was strong correlation between the results of the IgA ELISA and the IgA ELISPOT assays on day 7. Twenty-eight (100%) of 28 MOI Z H09 recipients showed a positive immune response and 14 (100%) of 14 placebo recipients showed a negative response in both assays.

### Discussion

**Interpretation**

This is the first evaluation of a novel oral typhoid vaccine in school children in an endemic country. S Typhii (Ty2 serotype) ZH9 (contained in MOI Z H09) is characterised by two well-defined deletion mutations, one in an aromatic amino acid biosynthesis pathway gene and one in a functional gene of the type III secretion system encoded by SPI-2 [9]. A single dose of 5 x 10⁸ CFU of the vaccine strain was well tolerated and had an acceptable safety profile. There were no serious adverse events, no withdrawals due to adverse events and none of the subjects experienced bacteremia.

In general, adverse events were mild. Similar proportions of subjects, 26% (26 of 101) in the candidate vaccine group and 22% (11 of 50) in the placebo group reported adverse events during the 28 day follow up period (p = 0.699). The overall number of adverse events tended to be higher in the MOI Z H09 group, especially those classified as gastrointestinal disorders, nervous system disorders and investigations.

There was one severe related adverse event in this trial, a high fever of 39.9°C which occurred on day 0 after vaccination in a subject who had a pre-dose elevated white blood count (18.2 x 10⁹/L) and might have suffered from an underlying infection. One other subject, vaccinated after drinking approximately half of the vaccine dose, this subject was found to have a positive stool culture for non-typhoid Salmonella on day 0.

S Typhii was isolated from the stools of one placebo recipient on day 2 after vaccination which was later identified as S Typhii (Ty2)

Table 3. Proportions of responders to the candidate typhoid vaccine MOI Z H09 (Intention to Treat population).

<table>
<thead>
<tr>
<th>MOI Z H09 group n = 101</th>
<th>Placebo group n = 50</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Detected in IgA ELISA assay</strong></td>
<td><strong>Detected in IgG ELISA assay</strong></td>
</tr>
<tr>
<td>Day 7</td>
<td>Day 14</td>
</tr>
<tr>
<td>99 (88.9)</td>
<td>99 (91.9)</td>
</tr>
<tr>
<td>81-94</td>
<td>81-97</td>
</tr>
<tr>
<td>5 (7)</td>
<td>4 (12)</td>
</tr>
<tr>
<td><strong>Positive Immune response, n (%)</strong></td>
<td><strong>Positive Immune response, n (%)</strong></td>
</tr>
<tr>
<td>95% CI</td>
<td>95% CI</td>
</tr>
<tr>
<td><strong>Detected in IgA ELISA assay</strong></td>
<td><strong>Detected in IgG ELISA assay</strong></td>
</tr>
<tr>
<td>Day 7 or day 14</td>
<td>Day 14</td>
</tr>
<tr>
<td>99 (94.5)</td>
<td>99 (91.9)</td>
</tr>
<tr>
<td>81-99</td>
<td>81-97</td>
</tr>
<tr>
<td>0 (0)</td>
<td>4 (12)</td>
</tr>
<tr>
<td><strong>Positive Immune response, n (%)</strong></td>
<td><strong>Positive Immune response, n (%)</strong></td>
</tr>
<tr>
<td>95% CI</td>
<td>95% CI</td>
</tr>
<tr>
<td>Day 14</td>
<td>Day 28</td>
</tr>
<tr>
<td>90 (90.0)</td>
<td>101 (99.2)</td>
</tr>
<tr>
<td>81-94</td>
<td>92-99</td>
</tr>
<tr>
<td>4 (13)</td>
<td>0 (0)</td>
</tr>
<tr>
<td><strong>Positive Immune response, n (%)</strong></td>
<td><strong>Positive Immune response, n (%)</strong></td>
</tr>
<tr>
<td>95% CI</td>
<td>95% CI</td>
</tr>
<tr>
<td>Day 7, 14 or 28</td>
<td>Day 7</td>
</tr>
<tr>
<td>98 (97.0)</td>
<td>78 (78.0)</td>
</tr>
<tr>
<td><strong>Positive Immune response, n (%)</strong></td>
<td><strong>Positive Immune response, n (%)</strong></td>
</tr>
<tr>
<td>92-99</td>
<td>81-100</td>
</tr>
<tr>
<td>0 (0)</td>
<td>14 (28)</td>
</tr>
<tr>
<td><strong>Positive Immune response, n (%)</strong></td>
<td><strong>Positive Immune response, n (%)</strong></td>
</tr>
<tr>
<td>95% CI</td>
<td>95% CI</td>
</tr>
</tbody>
</table>

*44 subjects aged 11 years and above (29 subjects in the MOI Z H09 group and 15 subjects in the placebo group) were eligible for the ELISPOT.

A positive ELISPOT result was defined as <50 typhoid antibody secreting cells specific for S Typhii LPS per 10⁶ PBMC. None of the subjects had a positive day 0 ELISPOT result.

[1] 10.1371/journal.pone.0017793.003

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Figure 2. Time course of LPS specific serum IgA (A) and IgG (B) antibody levels according to vaccination groups (Intention to Treat population). Box and whisker plots showing the distribution of antibodies according to time point and vaccination groups. The horizontal line within each box represents the median, the top and bottom of each box represents the 75th and 25th percentiles, respectively, and the I-bar represents the highest and lowest values within 1.5 times the interquartile range. Circles show outliers.

doi:10.1371/journal.pone.0011778.g002
This is encouraging as one major concern for the development of many oral vaccines has been their reduced immunogenicity when tested in developing country populations compared to Western volunteers [1,16]. For oral vaccines a high Baldwination of the intestine is necessary to become immunogenic, it might be possible that drug resistant commensals, bacterial overgrowth, enteric viruses or helminths interfere with the colonization of the new vaccine [17]. In this study, 51% (51/100) of vaccine recipients shed S. Typhi (Ty2 and/or murk') ZH9 in stools after vaccination, one subject excreted the vaccine strain on day 3, but no shedding was observed on day 4 and beyond. In Western adult volunteers shedding of S. Typhi in stools was reported for slightly longer durations and ranged from 1-6 days and 1-7 days in a small number of volunteers, respectively [9,11].

Generalisation

Typhoid fever is still a major health problem in developing countries, with high incidence [1,18] and high rates of antimicrobial drug resistance, especially in Asia [4,18]. The World Health Organisation recommends the immunisation of school and preschool children in endemic areas, especially where drug resistant typhoid fever is prevalent as well as in epidemic situations [5,19]. M012190 is a promising novel oral dose typhoid vaccine and large trials are necessary to evaluate vaccine efficacy. If protection from typhoid fever is demonstrated, M012190 may facilitate large vaccination campaigns due to its simpler logistic and broader acceptance from children.

Supporting Information

Protocol 81. Trial protocol. The trial protocol is as a true and correct copy of the original document (PDF version) minus redacted lines (personal information, names and telephone numbers of employees have been removed to maintain their confidentiality). No part in the content of the trial protocol with the exception of the vaccine recipients has been reduced.

Found at: doi:10.1371/journal.pone.0017782.s011 (2.9 MB PDF)

Checklist S1. CONSORT Checklist. Found at: doi:10.1371/journal.pone.0017782.s002 (0.05 MB DOC)

Acknowledgments

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Author Contributions

Conceived and designed the experiments: TTH ES CS CPS WL FM JM AU RR GD JF NVNC GD. Performed the experiments: TTH NDTT NTT V NVNC GD. Analyzed the data: TTH ES CS CPS WL FM JM AU RR GD JF NVNC GD. Wrote the paper: TTH ES CS CPS WL FM JM AU RR GD JF NVNC GD.


Table 4. Serum IgA and IgG antibody levels specific for S. Typhi LPS (intention to Treat population).

<table>
<thead>
<tr>
<th>Serum IgA antibody levels specific for LPS</th>
<th>M012190 group n=101</th>
<th>Placebo group n=50</th>
</tr>
</thead>
<tbody>
<tr>
<td>Day</td>
<td>Median units/ml</td>
<td>IQR</td>
</tr>
<tr>
<td>Day 0</td>
<td>3.7</td>
<td>5.7</td>
</tr>
<tr>
<td>Day 7</td>
<td>9.6*</td>
<td>3.2*</td>
</tr>
<tr>
<td>Day 14</td>
<td>70*</td>
<td>3.4*</td>
</tr>
</tbody>
</table>

Data from one* and two* subjects missing

doi:10.1371/journal.pone.0017782.t004

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typhoid vaccine use in target-afflicted areas.
High-throughput sequencing provides insights into genome variation and evolution in *Salmonella* Typhi

Kathryn E Holt1, Julian Parkhill1, Camila J Mazzoni2,3, Philippe Roumagnac3,4, François-Xavier Weill1, Ian Goodhead1,2, Richard Rance1, Stephen Baker1,2, Duncan J Maskell1, John Wain1, Christiane Dolecek5, Mark Achtman1,2 & Gordon Dougan1

Isolates of *Salmonella enterica* serovar Typhi (Typhi), a human-restricted bacterial pathogen that causes typhoid, show limited genetic variation. We generated whole-genome sequences for 19 Typhi isolates using 454 (Roche) and Solexa (Illumina) technologies. Isolates, including the previously sequenced CT18 and FY2 isolates, were selected to represent major nodes in the phylogenetic tree. Comparative analysis showed little evidence of purifying selection, antigenic variation or recombination between isolates. Rather, evolution in the Typhi population seems to be characterized by ongoing loss of gene function, consistent with a small effective population size. The lack of evidence for antigenic variation driven by immune selection is in contrast to strong adaptive selection for mutations conferring antibiotic resistance in Typhi. The observed patterns of genetic isolation and drift are consistent with the proposed key role of asymptomatic carriers of Typhi as the main reservoir of this pathogen, highlighting the need for identification and treatment of carriers.

Typhoid fever, along with plague, diphtheria and smallpox, is one of the classical infectious diseases of humankind. The disease, which is spread via oral ingestion of contaminated food or water, is caused by *Salmonella enterica* serovar Typhi (Typhi), a Gram-negative bacterium classified as a serovar of the species *S. enterica*. *S. enterica* is a broad and promiscuous species with isolates able to cause gastroenteritis in a range of animals, including humans1. In contrast to most other *S. enterica* serovars, Typhi has forsaken the promiscuous lifestyle to become a human-restricted pathogen causing both acute systemic infections (typhoid fever) and chronic infections (asymptomatic carriers). A number of evolutionary processes have been implicated in the adaptation of Typhi to this specialized niche, including the horizontal acquisition of several *Salmonella* pathogenicity islands (SPIs)2,3 and extensive loss of gene function4.

Typhi, together with other human pathogens such as *Vibrio parahaemolyticus, Bordetella pertussis* and *Bacillus anthracis*, is regarded as a monomorphic organism, as the genomes of individual Typhi isolates are highly conserved and clonally related. A recent study involving the DNA sequencing of 199 gene fragments from a global collection of 105 Typhi isolates detected only 82 SNPs5. Analysis of the SNP database revealed Typhi to be a rooted, fully parsimonious phylogenetic tree defining 85 genetically distinct haplotypes (H1–H85, Supplementary Fig. 1 online). The availability of a robust phylogenetic tree proved to be a useful framework against which to investigate the recent evolution of phenotypic traits such as the acquisition of resistance to fluoroquinolones, a class of antibiotics used to treat typhoid fever2–5.

Because Typhi shows such low levels of genetic variation, further studies require a whole-genome approach. Complete genome sequences are available for two Typhi isolates, CT18 and FY2 (refs. 6, 8). However, several new sequencing technologies have been developed that make draft genome sequencing simpler and more cost effective6. In order to capture variation in Typhi at the whole-genome level and minimize sampling bias7, we sequenced an additional 17 Typhi isolates dispersed in the phylogenetic tree, using a combination of 454 (Roche) and Solexa (Illumina) sequencing technologies.

**RESULTS**

Choice of Typhi isolates for whole-genome sequencing

In order to capture as much information as possible about the distribution of genomic variation in the Typhi population, we prepared DNA from CT18, FY2 and 17 other isolates for a combination of 454 and Solexa sequencing (see Methods and Table 1). To limit selection bias as much as possible, we chose Typhi isolates from central haplotype clusters together with selected isolates from radial haplotype
ARTICLES

Table 1. Typhii isolates sequenced in this study

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Country</th>
<th>Year</th>
<th>Haplotypes</th>
<th>454 coverage</th>
<th>Solexa coverage</th>
<th>Paired</th>
</tr>
</thead>
<tbody>
<tr>
<td>E00-7866</td>
<td>Morocco</td>
<td>2000</td>
<td>14466</td>
<td>10.5×</td>
<td>–</td>
<td>n.d.</td>
</tr>
<tr>
<td>E01-45750</td>
<td>Senegal</td>
<td>2001</td>
<td>1452</td>
<td>8.16×</td>
<td>–</td>
<td>n.d.</td>
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<tr>
<td>ER0-6618</td>
<td>Uganda</td>
<td>1998</td>
<td>1450</td>
<td>10.6×</td>
<td>–</td>
<td>n.d.</td>
</tr>
<tr>
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<td>1985</td>
<td>1853</td>
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<tr>
<td>M223</td>
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<td>#3</td>
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<td>n.d.</td>
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<tr>
<td>E02-6483</td>
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<td>7.4×</td>
<td>–</td>
<td>n.d.</td>
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<tr>
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<td>2003</td>
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<td>18.9×</td>
<td>–</td>
<td>pHKU1</td>
</tr>
<tr>
<td>IS9-0347867</td>
<td>Mexico</td>
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<td>–</td>
<td>7.87×</td>
<td>pHKU1</td>
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<tr>
<td>IS9-0440573</td>
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<td>22.9×</td>
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<tr>
<td>72</td>
<td>Russia</td>
<td>1994</td>
<td>1413</td>
<td>–</td>
<td>8.6×</td>
<td>n.d.</td>
</tr>
</tbody>
</table>

Country and year of isolation are shown. Haplotypes correspond to those previously defined. Coverage refers to overampling in sequence data. n.d., not detected.

SNPs and phylogenetic analysis

We detected high quality SNPs by mapping 454 covers or Solexa reads to the finished CT18 sequence (see Methods). Our analysis focused on the nonrepetitive component of the genome, and we did not attempt to identify single-base insertions or deletions. Repetitive sequences, including VNTRs, exact repeats of >20 bp, >90% identical repeats of >50 bp and phase and insertion sequences (IS), account for 7.4% of the CT18 genome (Supplementary Table 1a online). Here, we excluded these classes of repetitive sequences from SNP analysis as (i) non-identical repeats can appear indistinguishable from SNPs, particularly with short sequencing reads (100-250 bp for 454, 25 bp for Solexa), (ii) assembly and mapping of short reads are unreliable in repetitive regions and (iii) repeated regions may be subject to different selective pressures compared to the rest of the genome, for example, recombination between repeat copies. After excluding these sequences, we identified a total of 1,864 SNPs in the nonrepetitive genome, approximately 1 every 2,500 bp. Details of these SNPs are given in Supplementary Table 2 online.

We determined complete allele data for 1,787 SNPs (missing data was due to low coverage or deletion of SNP loci in one or more isolates). These SNPs traced the same phylogenetic tree as previously defined (Supplementary Fig. 1) but provided better estimates of branch lengths and greatly increased resolution, particularly within the H58 and H159 groups (Fig. 1). By comparing sequence data from 454, Solexa and published sequences, we determined cut-offs for quality filtering (Supplementary Fig. 2 online) and estimated a false positive rate of 2.7% and SNP detection sensitivity of 82-99.7% for both sequencing platforms (see Methods and Supplementary Table 1b).

This apparently high false positive rate is due to the extreme paucity of true SNPs; the actual error rate of the sequencing technologies is very low (around 7 to 10 errors in 4.45×10⁸ base pairs for Solexa sequencing on CT18 and Ty2; see Supplementary Methods online). Only ten SNPs (0.56%) did not fit the previously determined phylogenetic tree, two of which are confirmed examples of convergent evolution at sites under adaptive selection in g6k (see below). Thus, we have little reason to suspect high error rates among allele assignments, or to doubt the phylogenetic tree structure shown in Figure 1.

Using the resulting rooted phylogenetic tree, we were able to group mutations into relative age groups: (i) recent mutations, farthest from the root and lying on intra-haplotype branches, (ii) intermediate mutations, lying on haplotype-specific branches, and (iii) older mutations, lying on branches closest to the root and shared by

Figure 1 Phylotree based on SNP data. Branch colors indicate different lineages of Ty2, branch lengths are measured in number of SNPs, scale as indicated. Central, small black circle indicates the ancestral root, dashed line represents Salmonella lineage, purple (S1) and SP;15 insertion events are shown along branches, plasmids detected in each isolate are indicated by filled circles (nIC): multi-strain resistance plasmid, open circles (cryptic plasmids) and filled lines (linear plasmid carrying 265 flagella operon).
multiple haplotypes. The distribution of SNPs and other variants in each group is shown in Table 2.

dN/dS as a measure of stabilizing selection

The ratio of non-synonymous to synonymous SNP rates, dN/dS, is a common measure of stabilizing selection. A dN/dS ratio close to 1 indicates no selection against non-synonymous SNPs, whereas dN/dS close to 0 indicates strong stabilizing selection. The mean dN/dS of each isolate compared to the last common ancestor was 0.66 ± 0.033 (s.d.), indicating either a weak trend in the direction of stabilizing selection or the last common ancestor of Typhi, or a combination of stabilizing selection in some genes and diversifying selection in others. As there is little evidence of diversifying selection in any Typhi genes (see below and Supplementary Table 3a online), weak stabilizing selection observed here may be due to too little time for selection to act, and/or genetic drift due to low effective population size. It has been previously shown that in closely related bacteria, the reciprocal of dN/dS, or 1/dN/dS, is related to time12; simulations indicated that when population size was large, this relationship was linear, but when effective population size was small, genetic drift became more important and 1/dN/dS reached a plateau. The relationship of 1/dN/dS to time (measured by the number of intergenic SNPs) for the sequenced Typhi isolates was nonlinear (Fig. 2a). Intergenic SNPs serve as an approximation of time, as they are less likely to be under purifying selection than SNPs in coding regions. However, intergenic SNPs may have regulatory or other functions that may be under selection, so as an alternative measure, we also calculated dN/dS among SNPs of different relative ages, which confirmed the same trajectory (Fig. 2b). In the light of the previously described model12, these patterns are suggestive of genetic drift in Typhi due to a small effective population size, which seems likely, as Typhi has no known reservoir outside of humans. A small effective population size (∼ = 2.3 × 10^6 – 1.0 × 10^8) has been calculated previously using Bayesian skyline plots based on 82 SNPs in 105 Typhi isolates5.

Table 2 Genetic variation detected in 19 Typhi genomes

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Intergenic</th>
<th>Intragenic</th>
<th>Prophage</th>
<th>Miscellaneous</th>
</tr>
</thead>
<tbody>
<tr>
<td>Conserved Total</td>
<td>Conserved Total</td>
<td>Conserved Total</td>
<td>Conserved Total</td>
<td>Conserved Total</td>
</tr>
<tr>
<td>Deviations</td>
<td>5</td>
<td>8</td>
<td>7</td>
<td>20</td>
</tr>
<tr>
<td>Prophage insertions</td>
<td>n.a.</td>
<td>5</td>
<td>4</td>
<td>9</td>
</tr>
<tr>
<td>Plasmids</td>
<td>3</td>
<td>2</td>
<td>0</td>
<td>5</td>
</tr>
</tbody>
</table>

SNPs (complete allele data)

- Intergenic: 93 (1.75%) 338 (1.78%)
- Intragenic: 61 (6.52%) 663 (48.9%) 176 (53.1%) 900
- Phage: 5 (0.45%) 39 (2.9%) 12 (3.6%) 56
- dN/dS: 0.38 0.46 0.52 0.43

SNPs (noncomplete allele data)

- Intergenic: 19 122 25 175
- Intragenic: 4 (21.1%) 24 (19.7%) 6 (17.3%) 34
- Phage: 3 (15.8%) 41 (33.3%) 12 (33.3%) 56
- Intragenic: 12 (36.2%) 57 (46.7%) 17 (48.6%) 66
- Non-coding: 0.00% 0.00% 0.00% 0
- dN/dS: 1.24 0.41 0.44 0.48

Potential signals of selection

We found very little evidence of adaptive selection in Typhi genes, which would be represented by an overabundance of non-synonymous SNPs or independent changes in the same or nearby amino acid residues. We found that 72% of genes contained no SNPs and that the distribution of SNPs per gene followed a Poisson distribution in the range of 0–6 SNPs per gene (Fig. 3). However, there were a few exceptions (Supplementary Table 3a). Three genes (yhuU, tviC and STY2875) contained more than six SNPs, which deviates from the Poisson model. STY2875 is an exceptionally large gene (3,625 bp compared to the genome mean of 910 bp), which may account for the high number of SNPS. However, yhuU and tviC are small (562–579 bp) and thus the high number of SNPs may be evidence of diversifying selection in these genes; the second of which is encoded within SPI2 and is involved with Vl synthesis9. Ten SNPs did not fit the phylogenetic tree, which may indicate either recombination or convergent evolution, whereby the same mutation arose independently in different lineages. If the latter explanation is true, it would suggest the possibility of adaptive selection at these sites, which include non-synonymous SNPs in three genes encoding membrane proteins (STY1204, yhuU and tviC) and two non-synonymous SNPs in gly that are known to increase resistance to fluoroquinolones, a class of antibiotics used to treat typhoid fever26,27. Fifteen genes contained clusters of non-synonymous SNPs, whereby two residues within five amino acids were mutated, which may indicate adaptive selection in localized regions of the encoded protein (Supplementary Table 3a).

Of the 26 genes in which we detected potential signals of adaptive selection, half encode proteins that are surface-exposed, exported or secreted, or affect synthesis of such proteins (Supplementary Table 3a). These weak signals may reflect selective pressures arising from interactions with the human host4, including selection for more virulent mutants or those with antigenic variants that better evade the human immune system. The genes identified here as potentially under selection warrant further investigation, illustrating the value of this approach, which could potentially be adapted to genetic association studies in pathogenic bacteria similar to those carried out routinely in eukaryotes25. However, most genes whose products are secreted or are surface-exposed showed no evidence of adaptive evolution. For example, with the exception of afa, which encodes a SPI1 effector protein (Supplementary Table 3a), no other genes encoding known secreted effector proteins showed evidence of immune selection.
Recombination

Other than the ten SNPs that do not fit the phylogenetic tree, which are potentially a result of convergent evolution, we found no evidence of recombination between Typhi isolates and very little evidence of recombination with other bacteria (see Methods, Supplementary Note and Supplementary Table 1c online). Imports from S. enterica serovar Typhimurium (Typhimurium) have been reported in two Typhi isolates including 40947, but realignment of the history of the isolates harbored revealed that these were introduced in the laboratory during the production of avr-knockout mutants and do not represent wild-type variation. Large-scale recombination has been proposed between Typhi and the human-restricted S. enterica serovar Paratyphi A19. However, this most likely occurred before the evolution of the common ancestor of extant Typhi, which seems to be genetically isolated.

15 elements, phage, pathogenicity islands and plasmids

As 454 reads were long enough to be assembled, DNA insertion events could be identified among 454 sequenced Typhi isolates and confirmed by PCR and capillary sequencing (see Methods). Known IS elements in the CT18 genome were not present at the same sites in any other isolates, although we detected an IS1 element at a different genomic site within H38 isolates (see Supplementary Note). CT18 harbors seven well-defined prophage-like elements11,12, and while all sequenced isolates showed conservation in most of these, some isolates harbored new phages. Figure 1 shows the occurrence of phage insertion events in the phylogenetic tree, and the number of insertion events occurring in each relative age group is shown in Table 1. The new phages are discussed further in the Supplementary Note.

We also observed variation in the 6-kbp genomic island SPI13 (ref. 18). This region includes an integrase gene adjacent to four hypothetical genes and was inserted within tRNA-Glu, generating direct flanking repeats. The region seemed to exist in three forms among the sequenced Typhi: (i) CT18; (ii) I8589G, 4094-903-4983; and (iii) all other isolates. In each case, the insertion site and direct repeats were identical, but three distinct but related alleles were present for the integrase gene (95% amino acid identity between forms i and ii, 70% between all three forms). Each of the three forms contained a unique set of core genes. The function of these genes is unknown, with no matches to known protein domains in the Pfam database (accessed July 3, 2008). These genes merit further investigation because of their potential contribution to virulence. Plasmids detected in seven of the sequenced Typhi isolates (see Methods) fall into three classes (Table 1a and Fig. 1), which are discussed in more detail in the Supplementary Note.

Genomic deletions

Genomic insertions were rare in the sequenced isolates, but deletions were twice as common and more conserved (Table 2). Note that in many comparative studies, insertions and deletions are indistinguishable, but we were able to separate these events by using the rooted phylogenetic tree. The deletions range in size from 60 bp to 6.5 kbp, and some correspond to variant regions previously identified using DNA microarrays (Supplementary Table 3b). Most of the deleted regions include protein-coding sequences, resulting in partial or total deletion of 42 Typhi genes.

In addition, SPI17, which harbors genes required for synthesis of the polysaccharide VI capsule, was missing from 4094 and 150085. The isolate I808-3196 seemed to be a mixed population in regards to SPI17, as its coverage in both 454 and Solexa reads was 25% that of genomic coverage (Supplementary Fig. 3 online). Note that the low mapping coverage in this region is most likely due to deletion of SPI17 rather than replacement with a similar island, as deletion is known to occur during culture52,53. No alternative island could be assembled from 454 reads. No other SPIs were deleted from the sequenced Typhi, indicating that they are relatively stable in the genome (although we observed three variants of the 6-kbp SPI13, as described above).

Ongoing functional gene loss

In addition to identifying 42 genes affected by deletion events, we detected 35 nonsense SNPs that had occurred since the last common ancestor of Typhi. These introduce stop codons into protein-coding genes, thereby cutting short translation. Read-through of stop codons has been reported22; however, the described mechanism applies to only two of the nonsense SNPs we detected. There was evidence of selection against nonsense SNPs, with a lower rate of occurrence than nonnonsynonymous SNPs. Nevertheless, many nonsense SNPs were fixed, making up 2.9% of SNPs in the intermediate and oldest age groups (Table 2).

CT18 and 32 each contain ~200 pseudogenes18, defined as genes that are putatively inactive by mutations including nonsense SNPs, frameshifts and truncation by deletion or rearrangement. This constitutes 4.5% of Typhi genes, much higher than the frequency in Typhimurium (0.9%) or Escherichia coli K12 (0.7%). High pseudogene frequencies are associated with host restriction in a variety of bacteria23-24, presumably as certain genes required for infection in a broad range of hosts are not required in the preferred host. This is potentially also attributable to high rates of mutation fixation resulting from accelerated genetic drift caused by evolutionary bottlenecks associated with host adaptation.

By mapping the deletions and nonsense SNPs to the phylogenetic tree, we found that 92 new pseudogenes have accumulated among the sequenced Typhi isolates since their last common ancestor (Supplementary Table 3c), which itself harbored ~180 pseudogenes25. Many of these genes fall into gene categories (metabolism, cohabitation utilization, peptide or sugar transport, virulence) previously associated with the natural environment, and some appear to be associated with genes for both the host and the natural environment.
with pseudogenes in host-restricted pathogens\(^a\) (Supplementary Table 3c). Figure 4 shows the rate of accumulation of inactivating mutations in each branch of the phylogenetic tree. Nearly all of these genes showed evidence of expression in Typhi according to microarray data accessible at the NCBI GEO database (Supplementary Methods and Supplementary Table 3c), thus most of the nonsense and deletion mutations we observed probably result in true inactivation of previously functional genes. Because the losses have occurred independently in different lineages, Typhi isolates at different points in the phylogenetic tree have varying complements of functional genes and may have different pathogenic potential. This may contribute to the differences observed in clinical manifestations of typhoid fever in different regions\(^5\). Of note, different lineages show variation in the relative rates of accumulation of SNPs and inactivating mutations (line slopes in Figure 4). This may be attributable to variation in mutation rates or different selective pressures for or against pseudogene formation in particular lineages.

As only 3% of possible SNPs in the Typhi genome are nonsense SNPs, we expect only 1-2 false nonsense SNP calls overall (3% of the estimated total of 53 false SNP calls). This constitutes ~2% of genes inactivated by nonsense or deletion mutation and thus would make little difference to conclusions regarding the continuous accumulation of pseudogenes. In addition, we did not attempt to analyze frame-shift mutations, as single-base insertions or deletions are currently difficult to detect reliably from 454 and Solexa sequence data. However, most of the genes identified as differentially inactivated between CT18 and 7Y2 were due to frame-shift mutations (20 frame-shifts versus 4 nonsense SNPs and 2 deletions\(^a\), thus we hypothesize that many more pseudogenes may have accumulated in the Typhi population than those caused by nonsense SNPs or deletions. Therefore, although our analysis demonstrates that gene loss is ongoing in Typhi, we most likely underestimate the extent of this phenomenon.

**DISCUSSION**

Few whole-genome intraspecies comparisons of this scale exist for pathogenic bacteria\(^7\) and none at this level of subspecies resolution. In addition, the choice of isolates for sequencing is usually driven by clinical phenotype or simply availability, rather than unbiased sampling from relevant phylogenetic trees. However, isolate selection is critically important for comparative analysis, which can only uncover mutations that differ between the sampled isolates. Sampling from one part of the phylogenetic tree will overlook much of the variation present in the population and collapse all isolates into a single type\(^a\). For example, when SNPs detected between CT18 and 7Y2 were typed in a larger Typhi collection\(^7\), most isolates were assigned to the same genotype even though they were probably more variable than the 2 isolates we sequenced. By sequencing isolates from major nodes in the previously defined phylogenetic tree (Supplementary Fig. 1), we expect to have captured much of the variation present in the Typhi population. We also anticipate that the SNPs we have detected among the sequenced isolates will serve as genotypic markers providing phylogenetic information at high resolution in future genotyping studies.

Our whole-genome analysis supports the proposals of small population size and genetic drift in Typhi. Although we detected signals of selection in gyrA, we did not detect signals of the same magnitude in other Typhi genes, suggesting that this level of selection is exceptional in Typhi. Furthermore, our whole-genome comparison provides the opportunity to gain broad insight into the spectrum of genetic variation in Typhi, including SNPs, insertions, deletions and recombinations as well as plasmid and phase content (although we did not analyze insertion or deletion of single nucleotides). The patterns of genome-wide variation we detected demonstrate that pseudogene formation is ongoing in Typhi (Fig. 4) and support the hypothesis that evolution in this host-restricted pathogen is dominated by genetic drift and loss of gene function rather than by diversifying selection or gain of function through point mutation, recombination or acquisition of new sequences. Although this amount of gene function seems to be rare, it may be occurring in a few genes through point mutations.

The lack of evidence for adaptive selection in general is in contrast with the known adaptive selection for mutations in gyrA associated with fluoroquinolone resistance. We detected the signal of selection in gyrA as clustered, homoplasmic non-synonymous SNPs in neighboring codons 83 and 87. Three other genes contained homoplasmic non-synonymous SNPs, one of which (yajE) encodes the membrane component of an ABC transporter in E. coli\(^13\). Thus, these genes therefore be associated with antibiotic resistance in Typhi (efflux proteins can act as pumps to remove antibiotics from the bacterial cell\(^13\)). However, no genes besides gyrA contained multiple homoplasmic SNPs, and few contained multiple non-synonymous SNPs, consistent with the hypothesis of genetic drift in the Typhi genome. The adaptive mutations evident in the gyrA gene highlight the strong selective pressure on the Typhi genome associated with antibiotic use in the human population. This is not particularly surprising, as the Fitness advantage associated with increased antibiotic resistance is likely to be very strong. However, the lack of similar evidence for other adaptive mutations suggests that Typhi is under relatively little selective pressure from its host or the environment in general.

The limited evidence of selection in Typhi gene sequences is particularly notable when compared to patterns observed among other human bacterial pathogens, which show a variety of mechanisms for antigenic variation. For example, antigenic variation is achieved by extensive recombination in the Helicobacter pylori and Chlamydia trachomatis populations\(^24\), whereas in Mycobacterium tuberculosis, antigenic variation is associated with duplication and diversification of antigen-associated gene families\(^25\). In contrast, only 3 Typhi genes contained more than 6 SNPs, and 16 genes contained independent non-synonymous SNPs in the same or neighboring amino acids (see Supplementary Table 3a). Although these may represent cases of antigenic variation, the level of variation is low, with most of the SNPs unique to a single haplotype and therefore most haplotypes
sharing identical sequences. Similarly, although there was some evidence of import of small fragments of non-Typhl sequences (see Supplementary Table 1c), the only indication of possible recombination between Typhl isolates were ten SNPs that do not fit the phylogenetic tree (Supplementary Table 3a), which could equally be due to convergent evolution. The sparsity of direct sequence evidence for antigenic diversity in the pathogen under strong selective pressures from the human immune system and may interact with its host in a different way, possibly favoring immune evasion and localization to immune privileged sites. However, it cannot be ruled out that Typhl may possess as yet unidentified mechanisms of generating antigenic diversity or that phage genes, which were excluded from SNP analysis in this study, may have a role.

It has long been suspected that human carriers provide the main reservoir driving the transmission of Typhl. The bacterium is relatively difficult to isolate from water and the environment even in endemic regions25,26, and it is generally believed that Typhl has a limited survival time outside the human host25. If human carriers provide the main persistent reservoir for Typhl, this could account for the patterns of genetic drift and lack of recombination or gene acquisition we observed, as the human reservoir is likely to be small and physiologically isolated25,26. Furthermore, adaptive mutations arising during symptomatic typhoid infections may have no fitness advantage in the carrier state and may therefore not persist in the long-term Typhl population. All nodes of the Typhl phylogenetic tree shown in Supplementary Figure 1 were detected among a set of approximately 450 extant Typhl isolates27, suggesting that the Typhl population is shaped by clonal replacement. These patterns are well described by the source-sink model of evolutionary dynamics, which distinguishes permanent 'source' and transient 'sink' populations and predicts that adaptive mutations arising in the sink (individuals with typhoid) may be short lived in the population if they provide no fitness benefit in the long-term source (carriers of Typhl)28. Similar dynamics may be occurring in other human-restricted bacterial populations.

An understanding of the evolutionary dynamics of the Typhl population has important implications for the control of typhoid. The SNP typing of individual Typhl isolates into distinct genotypes may lead to improved methods for tracking the spread of Typhl between human hosts29. Vaccination may be a crucial long-term strategy for disease control, as it could not only reduce the level of typhoid infections but also the level of asymptomatic Typhl carriage in the population, a key reservoir of typhoid infections.

METHODS

Bacterial strains. Details of Typhl isolates used in this study are provided in Table 1. Isolates were provided by the Oxford University Clinical Research Unit (CTA, JH585, AG3). B Holmes at the National Collection of Type Cultures (M223); the Wellcome Trust Sanger Institute (1049), (722) and F-XW (all isolates).

DNA sequencing. We reflected bacterial cells by centrifugation and prepared DNA using the Wizard Genomic DNA Kit (Promega) according to the manufacturer's instructions. We sequenced eight Typhl isolates using a 454 Life Sciences GS-20 sequencer (Roche), and an additional two isolates (M233, H20-1488) using the 454 Life Sciences GS-GFLX sequencer (Roche). Twelve isolates were sequenced using the Illuina/Solexa Genome Analyzer System according to the manufacturer's specifications. In all cases, we generated single-end reads. Two isolates, H20-2759 and SPS-04-0693, were each sequenced over seven Solexa lanes during protocol optimization and thus have much higher coverage than other isolates, which were sequenced in one Solexa lane each.

We used Sanger sequencing of PCR products to confirm insertion and deletion sites. Primers used for PCR and sequencing are provided in Supplementary Table 3d. PCR was done in a 25 µl volume using PCR Supermix Taq Polynucleos (Invitrogen) and cycled on an MJ Research thermal cycler. Products were checked on a 1% agarose gel and purified using QiAquick PCR Purification Kit (QIAGEN).

Plasmid identification. In order to verify the presence and size of plasmids within Typhl isolates, we prepared plasmid DNA from Typhl isolates, as described in Supplementary Methods. All plasmids detected in this way were represented in the sequence data for their host isolates and were identified by mapping to known plasmid sequences (using blum for 454 contigs and Mag t 0.6 for Solexa reads).

SNP detection from sequence data. We assembled 454 reads de novo into contigs (that is, without reference to any other sequence) using mirest (v1.1. Roche). We used MUMFinder (v3.6.1, newer algorithm30) to align contigs to the finished CTB13 sequence and to generate primary SNP calls. Solexa reads were too short to be assembled effectively using current software and thus were mapped directly to the CTB13 reference sequence using Mag t 0.61, which we used to also generate primary SNP calls. We filtered SNP calls according to quality criteria determined by comparison of data from: multiple sequencing platforms, as described in Supplementary Methods. We combined Ethor SNP calls into a single list of SNP loci and determined the allele at each locus in each of the 15 Typhl sequences and additional 3 etype strain (using tata) search for 454 contigs or finished sequences and Mag consensus base calls for Solexa data). This allowed recovery of some SNPs that were initially rejected in one isolate because of low confidence but detected with high confidence in a second isolate. Noname SNPs were verified by manually inspecting multiple alignments of all 454 and Solexa reads mapping to each nonsense SNP locus.

Estimation of sensitivity and specificity of SNP calls. We estimated SNP detection accuracy and sensitivity for 454 and Solexa by comparing results from three isolates sequenced using both platforms, as described in Supplementary Methods. Additional estimates for Solexa data were determined by comparing Solexa data from CTB17 and 7Y2 to the published sequences (see Supplementary Methods).

Phylogenetic analysis. SNPs lying within recombined regions (see below) or within repeat regions were excluded from analysis, leaving 1,784 SNP calls. We called alleles against an independent whole-genome multiple alignment of all 454 and published Typhl sequences generated using Kedon (Applied Maths). Alleles could be confirmed in all nineteen Typhl isolates for 1,787 (99%) SNPs. These support a single monophyletic tree, as determined by the parsimony algorithm in the PHYLIP package (Fig. 1), consistent with the reference phylogenetic tree (Supplementary Fig. 1).

SNP calculations. We calculated nSNVs according to the formula (Nc/nSwv), where Nc is sum of nonmousonuous; snv is nonmousonuous sites in nonrefereneprotein-coding sequences; s = sum of homozygous SNPs; s = sum of homozygous SNPs in nonrefereneprotein-coding sequences. The mean nSNVs since the last common ancestor was calculated by weighting nSNVs by 1/2 for I5H isolates, 1/2 for I5H isolates and 1/2 for all other isolates, so that each haplotype is represented equally. The error reported (0.03) is 1 s.d. of this weighted mean.

Detection of recombination events. We checked SNP calls from each Typhl isolate for SNP clusters (defined as >3 SNPs within 1,000 bp) and searched those regions against the EMU database using blast in order to identify potential recombination events (Supplementary Note).
Note: Supplementary information is available on the Nature Genetics website.

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AUTHOR CONTRIBUTIONS

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A Multi-Center Randomised Controlled Trial of Gatifloxacin versus Azithromycin for the Treatment of Uncomplicated Typhoid Fever in Children and Adults in Vietnam

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Abstract

Background: Drug resistant typhoid fever is a major clinical problem globally. Many of the first line antibiotics, including the older generation fluoroquinolones, cephalosporins and aminoglycosides, are failing.

Objectives: We performed a randomised controlled trial to compare the efficacy and safety of gatifloxacin (10 mg/kg/day) versus azithromycin (20 mg/kg/day) as a once daily oral dose for 7 days for the treatment of uncomplicated typhoid fever in children and adults in Vietnam.

Methods: An open-label multi-centre randomised trial with pre-specified per protocol analysis and intention to treat analysis was conducted. The primary outcome was fever clearance time; the secondary outcome was overall treatment failure (clinical or microbiological failure, development of typhoid fever-related complications, relapse or faecal carriage of S. typhi).

Principal Findings: We enrolled 358 children and adults with suspected typhoid fever. There was no death in the study. 287 patients had blood culture confirmed typhoid fever, 145 patients received gatifloxacin and 142 patients received azithromycin. The median ICT was 106 hours in both treatment arms (95% Confidence Interval [CI]: 94–118 hours for gatifloxacin versus 88–112 hours for azithromycin). (logrank test p = 0.984, HR 95% CI = 1.0 (0.80–1.26)). Overall treatment failure occurred in 13/145 (9%) patients in the gatifloxacin group and 13/142 (9.2%) patients in the azithromycin group. (logrank test p = 0.854, HR 95% CI = 0.99 (0.43–2.20)). 96% (254/263) of the Salmonella enterica serovar Typhi isolates were resistant to nalidixic acid and 58% (153/263) were multidrug resistant.

Conclusions: Both antibiotics showed an excellent efficacy and safety profile. Both gatifloxacin and azithromycin can be recommended for the treatment of typhoid fever particularly in regions with high rates of multidrug and nalidixic acid resistance. The cost of a 3-day treatment course of gatifloxacin is approximately one third of the cost of azithromycin in Vietnam.

Trial Registration: Controlled-Trials.com ISRCTN67946944

Introduction

There are approximately 21 million cases of typhoid fever annually, with more than 210,000 deaths [1]. The emergence of antimicrobial drug resistance in Salmonella enterica serovar Typhi [2–4] is a major problem particularly in South East Asia and the Indian sub-continent and challenges our current treatment options [2–4]. There is a need for an efficacious, safe and affordable oral
Treatment of Typhoid Fever

Participants

Patients were eligible to be included in the study if they had clinically suspected or culture confirmed uncomplicated typhoid fever and if fully informed written consent had been obtained. For children, consent was obtained from the parent. Exclusion criteria were pregnancy, age under 6 months, history of hypersensitivity to either of the trial drugs, any signs of severe typhoid fever (shock, deep jaundice, encephalopathy, coma, bleeding, ascension or evidence of gut perforation), or previous reported treatment with a fluorquinolone antibiotic, a third generation cephalosporin or macrolide antibotics within one week prior to hospital admission.

The study sites and ethical approval

The study was conducted at three hospitals in the south of Vietnam.

Adult and paediatric patients were recruited at the Hospital for Tropical Diseases in Ho Chi Minh City, at the Dong Da Provincial hospital in Cao Lãnh, Dong Thap province and at the An Giang Provincial hospital in Long Xuyen, An Giang province.

The study was approved by the Ethical and Scientific Committee of the Hospital for Tropical Diseases in Ho Chi Minh City and the Oxford University Tropical Research Ethics Committee (OXTREC), UK for all three study sites. The clinical and microbiological data from the first 40 patients recruited to each arm of the study were sent to the independent Data Safety and Monitoring Committee for their advice regarding the continuation of the study. The study was not stopped.

Intervention

According to their randomisation number patients were assigned to oral treatment with either 50 mg/kg azithromycin (Zithromax® suspension, Pfizer, USA; 300 mg/5 mL or Zithromax® tablets, Pfizer, USA; 500 mg/tablet) or 10 mg/kg nalidixic acid (Tepin®, Bristol-Myers Squibb, USA; 400 mg/tablet) once daily for 7 days. Tablets were cut to obtain the appropriate study dosage and administered with water. Informed consent was obtained from the dose administered was an estimate of 10 mg/kg/day of nalidixic acid or 50 mg/kg/day of azithromycin (number of tablets or proportion of tablets were documented in the CRFs). Gatifloxacin was only available as tablets, which were cut to obtain the appropriate dosage and crushed if necessary for children.

The maximum dose of azithromycin was 1 g per day. All drugs were purchased commercially.

Procedures

In-patient procedures. On admission to the hospital the patient's full history was taken, a standard clinical examination was performed and axillary temperature, weight and height were measured. Before treatment, full blood counts including white blood differential count, serum aspartate transaminase (AST), serum alanine transaminase (ALT) and bilirubin were checked and blood cultures were obtained. For adult patients, creatinine, blood urea nitrogen (BUN) and glucose levels were additionally measured. In some patients bone marrow cultures were obtained. Urines were checked with dipstick and pre-treatment used cultures were obtained. Chest X-ray and abdominal ultrasound were performed and repeated as clinically indicated. Randomisation and initiation of therapy took place either immediately on admission to hospital or patients were observed until results of blood tests including blood cultures were available and then randomised. Vital signs including measurement of axillary temperature were measured and recorded every 6 hour (at 6, 12, 18 and 24 hour) until discharge. Patients were examined

Methods

The protocol for this trial and supporting CONSORT checklist are available as supporting information; see Checklist S1 and Protocol S1.

Study design and objectives

The study was designed as a multicenter, open-label randomised controlled trial to compare the efficacy and safety of gatifloxacin versus azithromycin for the treatment of uncomplicated typhoid fever in children and adult in-patients in southern Vietnam.

The overall objective of the study was to identify an efficacious, safe, available and affordable oral treatment for MDR and nalidixic acid resistant typhoid fever.
study until discharge from hospital, with particular reference to clinical symptoms, FCT, side effects of the drug and any complication of the disease. Additionally laboratory tests were scheduled if clinically indicated. All adverse events were recorded. On day 3 to 7 and 9 after the start of treatment full blood counts, fever function tests, blood and stool cultures were checked. In case of insufficient response to therapy, development of complications or drug related complications, the current antibiotic therapy was suspended and parenteral cefixime (2 g per day) in two divided doses was used as rescue treatment for 10 days.

Follow-up procedures. Outpatient follow-up appointments were scheduled at 1 month, 3 months and 6 months after discharge from hospital to seek evidence for relapse (1 month visit) and check for chronic typhoid carriage (all visits). At these appointments full blood counts, relevant laboratory examinations performed and stool cultures obtained. Blood or bone marrow cultures were only obtained if clinical symptoms were indicative of acute infection. If patients did not attend their follow up appointment, they were reminded by letter or a member of the study team visited their home. If stool samples were not available, a rectal swab was obtained.

Patients with concurrent stool carriage of S. typhi or S. paratyphi A were retreated according to the sensitivity of the isolate and were further followed up. Ultrasound was performed to exclude bilary or kidney stones if carriage was persistent.

Microbiology

Five to 8 mL of blood was collected from adults and inoculated into Bectec Plus Aerobic Blood bottles, and 3 to 5 mL of blood from children was inoculated into Bectec Plus culture bottles (Bectec Dickinson, New Jersey, USA). The bottles were incubated at 37'C in the BACTEC 9120(Bectec) automated analyser for 7 days and sub-cultured according to standard methods when the machine indicated a positive signal, or incubated at 37'C in a standard laboratory incubator (Biolog, USA) and examined daily.

Stool samples or rectal swabs were incubated onto MacConkey agar and Xylose Lysine Deoxycholate (XLD) agar plates, and in 10 mL of sterile F broth. Plates and broth were incubated at 37°C overnight and the broth was sub-cultured on MacConkey and XLD agar plates the next morning.

Isolates were screened using standard biochemical tests and S. typhi and S. paratyphi A were identified using API 20E (BioMerieux, Paris, France) and slide agglutination with specific antisera (Merex, Dartford, UK).

Antimicrobial susceptibility testing was performed by disc diffusion according to Clinical Laboratory Standards Institute (CLSI) guidelines [12], using CLSI breakpoints [13]. Antimicrobial agents tested were ampicillin, chloramphenicol, trimethoprim-sulfamethoxazole, sulfisoxazole, ofloxacin, ciprofloxacin and ceftiraxone (Oxoid, Basingstoke, UK). Minimum Inhibitory Concentration (MIC) for amoxicillin, chloramphenicol, sulfisoxazole, ofloxacin, ciprofloxacin, ceftiraxone and azithromycin were determined by E-test (AB Biodisk, Solna, Sweden).

Medicine resistance (MDR) of isolates was defined as resistance to chloramphenicol (MIC > 32 mg/mL), sulfisoxazole (MIC > 32 mg/mL) and trimethoprim-sulfamethoxazole (MIC > 8/152 mg/mL).

Nalidixic acid resistance was defined as an MIC > 32 mg/mL. The CLSI breakpoints for ofloxacin and ciprofloxacin were < 1.0 mg/mL susceptible and 1.0 mg/mL resistant, for ciprofloxacin < 1.0 mg/mL susceptible and 2 mg/mL resistant and for ceftriaxone < 8 mg/ mL susceptible and 16 mg/mL resistant. There were no CLSI MIC breakpoints for azithromycin [13]. The control strains used for all susceptibility tests were E. coli ATCC 25922, Proteus mirabilis ATCC 27853, Staphylococcus aureus ATCC 29213.

All cultures, identification of S. typhi and S. paratyphi A and disc diffusion were performed at the study sites. All isolates were sent to the Hospital for Tropical Diseases, Ho Chi Minh City, for confirmation of identity, susceptibility testing and MIC testing.

Outcomes of the study

The primary endpoint of the study was the resolution of fever (fever clearance of 0.5°C and FCT), which will be defined as the end of the antibiotic treatment when the axillary temperature first fell ≤37.5°C and remained there for at least 48 hours. Secondary endpoints were the overall failure of treatment, which was defined as any of the following: clinical failure (resistance of fever and symptoms two days after the end of treatment, i.e. on day 10) or need for re-treatment due to insufficient treatment response as judged by the treating physician; microbiological failure (positive blood culture on day 7 to 9 after the start of treatment); the development of typhoid fever-related complications during hospital stay; the occurrence of relapse (symptoms and signs suggestive of typhoid fever within 3 months after completion of treatment or the detection of fecal carriage of S. typhi at the follow-up visits at 1, 3 and 6 months, to exclude fecal carriage a minimum of two consecutive follow-up visits had to be attended).

Sample Size

The primary outcome measure for the study was the fever clearance time (FCT).

Previous studies that used azithromycin to treat typhoid fever patients, reported a mean fever clearance time of 130 hours [7] and 139 hours [8]. For ciprofloxacin, clinical observations from a small number of typhoid fever patients were available and indicated a mean FCT of 76 hours. We calculated that 139 patients with culture-confirmed typhoid fever would be needed in each treatment arm to detect a Hazard Ratio of 0.40 with two-sided alpha of 0.05 and power of 0.80 [14]. Therefore, the estimated median fever clearance time of 130 hours for azithromycin, the sample size of 149 patients with culture-confirmed typhoid fever in each study arm, would be sufficient to detect a difference in treatment efficacy if the fever clearance time in the azithromycin group was 92 hours or less.

Randomization procedures and assignment of intervention (sequence generation, allocation concealment, implementation)

An administrator independent from the study generated the random number sequence in Excel using RAND function. These randomised codes were blocked in a size of 50. Treatment assignments were folded and kept in opaque, sealed, sequentially numbered envelopes at all three study sites. Due to logistic reasons randomisation was not stratified by centre.

After all inclusion and exclusion criteria were checked, and informed consent given, the study doctor opened the envelope to determine which treatment the subject would receive. The sealed envelopes were opened in strict numeric sequence.

Blinding

This study was conducted as an open study.

Statistical methods

Binary outcomes (clinical failure, microbiological failure, typhoid fever-related complications) were compared between the two treatment groups using Fisher's exact test, assuming the worst case scenario (all lost to follow up treated as failures). The un-
adjusted Odd Ratio (OR) and Cochrane's 95% confidence interval [15] were calculated to show the relative risk of developing individual secondary outcomes (clinical, microbiological failure, typhoid fever-related complications) in the gatifloxacin group compared to the azithromycin group.

Fever clearance time, time to relapse and time to overall failure were analysed using survival methods. The time to overall failure equaled the earlier time individual failure was recorded. Kaplan-Meier estimates of probabilities of each event were calculated at any time-point, and they were compared between the two treatment groups using the log-rank test. Data of patients who were lost to follow-up were censored at the time of the last recorded outcome. The Hazard Ratio was derived from Cox proportional hazard model [16].

All patients with positive blood or bone marrow culture for S. typhi and S. paratyphi A (per protocol analysis) and separately all randomized patients (intention to treat analysis) were analysed.

All data were recorded prospectively into individual Case Report Forms (CRF) and entered into an electronic database (EpInfo 2003, CDC, Atlanta, USA) and double-checked.

Analysis was performed using STATA version 8.0 (Stata Corporation, Texas, USA) statistical software program.

Results

Participant flow and recruitment
During the study period, 600 patients were assessed for eligibility (Figure 1). One hundred and two patients were non-eligible, the main reason was the reported previous use of fluoroquinolones, macrolid or third generation cephalosporin antibiotics (41 patients) in the week before hospitalisation.

Between April 2004 and August 2005, 358 patients with suspected typhoid fever were randomised to receive either gatifloxacin or azithromycin. Two hundred eighty-three of these patients had blood or bone marrow confirmed typhoid fever and 70 patients were culture negative for S. typhi. One culture positive patients was excluded from the per protocol analysis [PP], because he was received empirical treatment before to the trial. The PP group consisted of 287 patients, 145 in the gatifloxacin group and 142 in the azithromycin group. All PP patients, except two in the azithromycin group, finished the full course of treatment.

The total number patients visiting the follow-up at 1 month was 275 out of 287 (96%), at 3 months 268 out of 287 (93%), at 6 months 128 out of 287 (44%) patients.

Numbers analysed
All 358 randomised patients were analysed in the intention to treat (ITT) analysis. Two hundred eighty-seven patients with culture confirmed typhoid fever, 145 treated with gatifloxacin and 142 with azithromycin, were analysed in the pre-specified PP analysis.

Baseline Data
The median age of patients recruited in this trial was 11 years (range 1-41) in the PP group.

The baseline characteristics of the patients were similar in the two treatment groups and in the culture negative patients (Table 1).

Patients with suspected and blood culture confirmed typhoid fever were eligible for the trial. In the PP group, the median delay in time between hospital admission and randomisation was 3 days (interquartile range 1-4) in the gatifloxacin group and 3 days (interquartile range 2-4) in the azithromycin group. In the ITT group, the median delay in time between hospital admission and randomisation was 2 days (interquartile range 0-4) in the gatifloxacin group and 3 days (interquartile range 1-4) in the azithromycin group.

Protocol deviations and modifications
At one study site, the Ai Giang Provincial Hospital, the follow-up visit at 6 months was not possible for logistic reasons. It was therefore agreed to carry out two follow-up visits at 1 and 3 months and to whether additional (reintervention) follow-up data to invite as many patients as possible to a third follow-up visit.

From the PP population, 22 out of 91 patients in the gatifloxacin arm and 17 out of 87 patients in the azithromycin arm attended the third visit.

Outcomes and estimation

Primary outcomes. There was no significant difference in the resolution of fever (FCI) between the two treatment groups (Table 2).

By PP analysis, the median FCI was 106 hours in both treatment arms (95% Confidence Interval [CI]: 94-110 hours for gatifloxacin versus 98-112 hours for azithromycin, [log rank test p = 0.504, HR [95% CI] = 1.0 [0.89-1.20]]. The Kaplan-Meier survival curve for the fever clearance time is shown in Figure 2. At day 7, fever clearance rate was 82.8% (95% CI: 76.2-89.4%) in the gatifloxacin group and 83.5% (95% CI: 73.6% 93.6%) in the azithromycin group.

In the ITT population, the median FCI was 103 hours in both treatment arms (95% CI: 92-106 hours for gatifloxacin versus 81-122 hours for azithromycin, [log rank test p = 0.514, HR [95% CI] = 1.00 [0.82-1.25]]. At day 7, fever clearance rate was 84.2% (95% CI: 78.5-89.9%) in the gatifloxacin group and 83.6% (95% CI: 76.5-87.9%) in the azithromycin group (Figure 3).

Secondary outcomes. There was no death in the study.

There was no significant difference in overall failure to treatment between the two groups (Table 2).

By PP analysis, the number of patients that showed overall failure to treatment was 13/145 (9%) in the gatifloxacin group and 13/140 (9.3%) in the azithromycin group (log rank test p = 0.534, HR [95% CI] = 0.95 [0.43-2.01]), or when assuming the worst case scenario, that all dropped-out patients were failures, 15/142 (10.6%) failures in the azithromycin group (logrank test p = 0.570, HR [95% CI] = 0.81 [0.38-1.72]). Figure 4 shows the proportion of patients failing through time after the start of treatment.

In the azithromycin arm, more than one failure event occurred in individual patients (Table 2). Clinical failure occurred in 6/145 (4.2%) patients in the gatifloxacin group and in 6/140 (4.2%) in the azithromycin group (p = 1.000, OR [95% CI] = 0.96 [0.25-3.7]). Three patients in each study arm were re-treated with ceftriaxone, the other patients resolved their symptoms within 24 hours.

Microbiological failure was seen in 2 out of 143 patients in the gatifloxacin group (1.4%) and in 3 out of 140 (2.1%) in the azithromycin group (p = 0.600, OR [95% CI] = 0.44 [0.05-5.7]). Two of the azithromycin recipients showed additionally signs of clinical failure.

There were no typhoid fever-related complications in the 145 gatifloxacin patients compared to 8 out of 140 (5.7%) patients in the azithromycin arm (p = 0.003, OR [95% CI] = 0 [0.4]). Two azithromycin recipients developed signs of liver dysfunction (elevated AST and ALT, deepening of jaundice) in addition to signs of clinical failure. Study treatment was continued and symptoms resolved by the time of discharge. Four patients, three children and one adult, suffered from gastrointestinal bleeding on day 3, day 5 (2 cases) and day 7 of treatment respectively, three patients received blood transfusions. One of these patients
Developed shock but responded to intravenous fluids and supportive treatment. Treatment was discontinued immediately in all the patients and re-treatment with ceftriaxone was initiated. Two adult patients developed pneumonia during treatment.

Relapses were evaluated only in patients that were initially categorized as successfully treated, patients with clinical failure, microbiological failure or complications were not evaluated. Four patients out of 137 (2.9%) relapsed in the gatifloxacin group compared to 2/127 (1.6%) relapsed in the azithromycin group ($p = 0.052$, EBR [95% CI] = not estimable due to zero observations in one group). (Figure 5). These relapses with symptoms suggestive of typhoid fever occurred on day 7, 11, 13 and 15 respectively, after completion of treatment, three patients were confirmed culture positive for $S. \text{typhi}$. One patient developed acute respiratory distress syndrome (ARDS) and needed ventilation. The patient was treated with ceftriaxone and perfuson and subsequently made a complete recovery.

Chronic fecal carriage was evaluated in patients who attended at least two follow-up appointments, 137 in the gatifloxacin group and 131 in the azithromycin group. Only one patient with chronic...
Table 1. Baseline characteristics of culture confirmed patients (PP analysis) and culture negative patients.

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Culture confirmed patients treated with Gallofloxacin n = 143</th>
<th>Azithromycin n = 142</th>
<th>Blood culture negative patients, n = 70</th>
</tr>
</thead>
<tbody>
<tr>
<td>Median age in years (range)</td>
<td>11 (0-30)</td>
<td>11 (0-41)</td>
<td>9 (2-42)</td>
</tr>
<tr>
<td>Number of children defined as age under 15 (%)</td>
<td>101 (75.2)</td>
<td>101 (71.1)</td>
<td>56 (80)</td>
</tr>
<tr>
<td>Number of males (%)</td>
<td>71 (49)</td>
<td>76 (53.5)</td>
<td>29 (41)</td>
</tr>
<tr>
<td>Median weight in kilograms (range)</td>
<td>75 (65.5-111)</td>
<td>74 (65.5-117)</td>
<td>74 (65.5-117)</td>
</tr>
<tr>
<td>Median duration of fever before admission in days (range)</td>
<td>7 (0-32)</td>
<td>7 (0-32)</td>
<td>7 (0-32)</td>
</tr>
<tr>
<td>Number of patients who received treatment (%)</td>
<td>21 (14.5)</td>
<td>18 (12.7)</td>
<td>16 (23.9)</td>
</tr>
<tr>
<td>Median temperature at admission in °C (range)</td>
<td>39 (37-40.5)</td>
<td>39 (37.3-41)</td>
<td>38.75 (37-40)</td>
</tr>
<tr>
<td>Hypoalbuminemia, number of patients (%)</td>
<td>69 (47.6)</td>
<td>63 (44.4)</td>
<td>39 (51.4)</td>
</tr>
<tr>
<td>Splenomegaly, number of patients (%)</td>
<td>17 (11.9)</td>
<td>14 (9.8)</td>
<td>2 (2.9)</td>
</tr>
<tr>
<td>Abdominal pain, number of patients (%)</td>
<td>82 (56.5)</td>
<td>76 (53.5)</td>
<td>43 (61.4)</td>
</tr>
<tr>
<td>Weight loss, number of patients (%)</td>
<td>69 (47.0)</td>
<td>71 (50)</td>
<td>31 (45)</td>
</tr>
<tr>
<td>Vomiting, number of patients (%)</td>
<td>47 (32.4)</td>
<td>54 (38)</td>
<td>19 (27.1)</td>
</tr>
<tr>
<td>Diarrhea, number of patients (%)</td>
<td>95 (65.5)</td>
<td>82 (57.7)</td>
<td>49 (70)</td>
</tr>
<tr>
<td>SBI jaundice, number of patients (%)</td>
<td>12 (8.3)</td>
<td>20 (14.1)</td>
<td>1 (7.4)</td>
</tr>
<tr>
<td>Median hematocrit in % (range)</td>
<td>54.3 (19.3-54.3)</td>
<td>54.3 (18.7-60.3)</td>
<td>54.7 (24.8-46.5)</td>
</tr>
<tr>
<td>Median white cell counts, 10³ /L (range)</td>
<td>6.6 (1.9-100)</td>
<td>7.05 (2.6-16.8)</td>
<td>7.25 (2.8-11.3)</td>
</tr>
<tr>
<td>Median platelet count, 10⁵ /L (range)</td>
<td>173 (54-500)</td>
<td>173.3 (45-578)</td>
<td>290 (51-486)</td>
</tr>
<tr>
<td>Median AST, U/L (range)</td>
<td>85 (1.6-773)</td>
<td>72 (1.6-1190)</td>
<td>53.1 (11-533)</td>
</tr>
<tr>
<td>Median ALT, U/L (range)</td>
<td>87.4 (0.3-279)</td>
<td>39.4 (0.2-754)</td>
<td>44.1 (10-373)</td>
</tr>
<tr>
<td>Numbers of Serratia/Sporothrix A isolated from blood cultures</td>
<td>144/1</td>
<td>136/4</td>
<td>0</td>
</tr>
<tr>
<td>Positive pre-treatment fecal cultures, numbers (%)</td>
<td>11/24 (8.5)</td>
<td>6/118 (5.5)</td>
<td>0</td>
</tr>
</tbody>
</table>

AST, Serum Aspartate Aminotransferase; AST internal range, 7-30 U/L.
ALT, Serum Alanine Aminotransferase; ALT internal range, 1-40 U/L.
*Treatment with amoxicillin or cefalexin prior to hospital admission.
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Table 2.

<table>
<thead>
<tr>
<th>Outcome Type</th>
<th>Outcome Sub-Categories</th>
<th>Treatment group (n = 287)</th>
<th>p-Value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Gallofloxacin n = 143</td>
<td>Azithromycin n = 142</td>
<td></td>
</tr>
<tr>
<td>Primary</td>
<td>Fever Clearance Time in hours (95% CI)</td>
<td>106 (94-118)</td>
<td>106 (98-112)</td>
</tr>
<tr>
<td>Secondary</td>
<td>Overall treatment failure, number of patients (%)</td>
<td>13/145 (9)</td>
<td>13/140 (9.3)</td>
</tr>
<tr>
<td></td>
<td>Did not complete full treatment course, n (%)</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td>&quot;Clinical failure, n (%)</td>
<td>6/145 (4.2)</td>
<td>6/140 (4.2)</td>
</tr>
<tr>
<td></td>
<td>Microbiological failure, n (%)</td>
<td>2/145 (1.4)</td>
<td>3/140 (2.2)</td>
</tr>
<tr>
<td></td>
<td>&quot;Hyphoidal fever related complications, n (%)</td>
<td>5/145 (3.5)</td>
<td>6/140 (4.2)</td>
</tr>
<tr>
<td></td>
<td>Gastrointestinal bleeding</td>
<td>0</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td>Pneumonia</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td>Liver dysfunction</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td></td>
<td>Relapse after discharge from hospital, n (%)</td>
<td>4/137 (2.9)</td>
<td>0/137 (0)</td>
</tr>
<tr>
<td></td>
<td>*Number of patients with fecal carriage at follow-up, n (%)</td>
<td>1/137 (0.7)</td>
<td>0/137 (0)</td>
</tr>
</tbody>
</table>

*Patients can fall in more than one subcategory.
*The p value is based on the log rank test.
*The p value is based on Fisher's exact test.
*Evaluated in patients who attended at least two follow-up visits.
doi:10.1371/journal.pone.0002788.g007
Treatment of Typhoid Fever

![Graph](image)

**Figure 2.** Proportion of culture confirmed patients still febrile. Kaplan-Meier survival curve showing the proportion of culture confirmed patients still febrile through time by treatment group.

doi:10.1371/journal.pone.0021882.g002

A fecal carriage was detected after 6 months (Az. Giang study site), the patient had received gatifloxacin.

In the ITT analysis (all 358 randomized patients), overall treatment failure was reported in 13 out of 185 (7%) in the gatifloxacin group compared to 16 out of 168 (9.4%) in the azithromycin group. Logrank test $p = 0.613$, HR [95% CI] = 0.82 (0.39-1.76). One culture negative patient in the azithromycin group had a positive blood culture on day 7 after start of treatment. There were no clinical failures or typhoid fever-related complications in the culture negative patients.

![Graph](image)

**Figure 3.** Proportion of all randomized patients still febrile. Kaplan-Meier survival curve showing the proportion of all randomized patients still febrile through time by treatment group.

doi:10.1371/journal.pone.0021882.g003

May 2008 | Volume 3 | Issue 5 | e2188
Adverse events

Both treatments were well tolerated. One adverse event related to azithromycin was reported, a maculopapular rash that occurred after the first dose of treatment. Azithromycin was discontinued immediately and the patient was treated with ceftriaxone.

Gastrointestinal side-effects (change in consistency and frequency of stools) that were probably typhoid fever related occurred relatively frequent in both treatment arms at the start of treatment. In the gatifloxacin group, one patient experienced vomiting on day 2 and day 3 and one patient diarrhea (5 episodes/day) on day 4 and day 5 of treatment. These episodes were self-limiting and did not require the interruption of therapy.

The median levels of serum AST and ALT fell in both groups after 7 days of therapy. In the PP group, the median post-treatment AST was 46.35 U/L (range 12.8-217.5) in the gatifloxacin arm and 45 U/L (range 5-150) in the azithromycin arm. The median post-treatment ALT fell to 66.6 U/L (range 7.4-278) and 40.9 (1.1-464), respectively. In the culture-negative patients, the median post-treatment AST was 44.8 U/L (range 12.8-648) and ALT was 40 U/L (range 10-474).

Antimicrobial susceptibilities of S. typhi and S. paratyphi A isolates

From the PP population, 282 (98%) S. typhi and 5 (2%) S. paratyphi A strains were isolated. Two hundred and sixty-three S. typhi and 5 S. paratyphi A were received at the Hospital for Tropical Diseases for antimicrobial susceptibility testing.

Fifty-eight percent of the S. typhi isolates were MDR and 96% were nalidixic acid resistant and showed reduced susceptibility to the older generation fluoroquinolones (Table 3). However, technically, using current CLSI breakpoints, all isolates remained susceptible in vitro to ciprofloxacin and ofloxacin. The MIC90 of gatifloxacin was the lowest of all the fluoroquinolones tested at 0.08 μg/mL (range 0.004-0.5). All isolates were susceptible to ceftriaxone.

The S. paradoxus A strains were fully susceptible to all the antimicrobials tested.

Discussion

Interpretation

The results of this trial show that both antibiotics worked well for the treatment of MDR and nalidixic acid resistant typhoid fever in Vietnam. A seven day oral course of gatifloxacin had similar efficacy and safety as a seven day course of azithromycin, which is recommended for the treatment of MDR and nalidixic acid resistant typhoid fever [7,9].

However, azithromycin is not available throughout most of the developing world and it is expensive. The costs of a 7-day treatment course of gatifloxacin (at 10 mg/kg/day) for an adult patient in Vietnam are approximately 25 USD, the costs of azithromycin (at 20 mg/kg/day) are more than 90 USD.

The results for gatifloxacin in this trial are comparable to the excellent clinical outcomes achieved with ofloxacin in Vietnam in the early 1990s, when S. typhi isolates were still susceptible to nalidixic acid [7-10].

Gatifloxacin has a higher affinity to GyrA and is less inhibited by the common mutations in the GyrA gene [20]. The gatifloxacin MIC90 of the study isolates was 0.19 μg/mL compared to the ciprofloxacin MIC90 of 0.75 μg/mL. We would not recommend the continued use of the older generation fluoroquinolones (ofloxacin and ciprofloxacin) in regions with high rates of nalidixic acid resistant typhoid fever for fear of selecting further mutations in gyrA [21]. This could put at risk the potential clinical benefit of the newer fluoroquinolones, including gatifloxacin.

There have been several case reports of gatifloxacin-associated dysglycemia in patients with type II diabetes mellitus, overweight

![Figure 4. Proportion of patients with overall failure in the culture confirmed population. Kaplan-Meier survival curve showing the proportion of patients with overall failure in the culture confirmed population (PP analysis) by treatment group.](image-url)
The randomised controlled trial described the relevant A. salmonicidae and chloroquine monitoring and one patient period. Genera Z. luminescent described the study physicians. No dysglycemia events were reported during the inpatient period or during the follow-up period of 3 to 6 months. The patients in our trial were healthy, young and non-aboriginal individuals. A trial in 86 children with otitis media with glucose monitoring and a one-year follow-up [16], as well as a recent enteric typhoid and paratyphoid fever trial in Nepal used gatifloxacin and did not report any dysglycemia [10]. In our setting and in our patient population, gatifloxacin was highly effective despite very high rates of drug resistance and was well tolerated.

Other newer generation fluoroquinolones, i.e. gemifloxacin and moxifloxacin have shown low MICs for nalidixic acid resistant S. paratyphi and S. paratyphi A [16]. Unfortunately these drugs are not available in Vietnam, and they are considerably more expensive. The in vitro results seen with these other newer generation fluoroquinolones should be evaluated in clinical trials.

Generalizability

The emergence of nalidixic acid resistant S. paratyphi A with reduced susceptibility to the fluoroquinolones is a widespread problem throughout Asia and therefore our study is relevant to the whole region [2,5]. Many case reports and some randomised controlled trials have described the worsening clinical response to ciprofloxacin and ofloxacin [8,27,28].

The search for effective antibiotics to treat typhoid fever is imperative.

Typically trials in typhoid fever are limited by small sample sizes, a recent Cochrane Report has stressed the need for large well-designed trials in enteric fever [29]. The evidence from our trial is strengthened by a sample size of 287 patients with culture confirmed typhoid fever (256 patients randomised), which we believe is so far the largest RCT performed in typhoid fever.

Both antibiotics also worked well for the patients with negative blood cultures. This is an important finding, because the sensitivity of blood cultures for the diagnosis of typhoid fever is only approximately 50 to 80% [9].

Limitations of the study

The randomisation sequence was generated with a large block size of 50, which resulted in uneven numbers in the two treatment groups (86 versus 172 patients in the ITT populations).

One possible limitation was the low rate of stool cultures positive for S. paratyphi A. Faecal carriage is usually characterised by intermittent shedding and the stool culture for S. paratyphi A is not very sensitive.

When comparing our data with other studies that demonstrate that antibiotics are highly efficacious for the treatment of typhoid fever, we find similar low rates of faecal carriage at follow-up [7-30]. It could be hypothesised that antibiotics that show high intracellular concentrations and good time-penetration like amoxicillin and the fluoroquinolones, achieve rapid bacterial killing and elimination throughout the body, which reduces faecal carriage.

The dose of gatifloxacin and amoxicillin tablets was prepared by careful counting of the tablets (proportions of the tablets administered were recorded in the CRFs). Inevitably, it was therefore an estimate of the exact dose, hence we cannot guarantee that each patient received exactly 10 mg/kg/day of gatifloxacin or 25 mg/kg/day of amoxicillin.
Table 3. Antimicrobial susceptibilities and minimum inhibitory concentrations (MIC) of 263 S. typhi isolate.

<table>
<thead>
<tr>
<th></th>
<th>All isolates</th>
<th>Treatment with</th>
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<tbody>
<tr>
<td></td>
<td>n=245</td>
<td>Gatifloxacin</td>
</tr>
<tr>
<td>Antibiotic</td>
<td></td>
<td>n=137</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nitrofurantoin</td>
<td>151 (62%)</td>
<td>87 (33%)</td>
</tr>
<tr>
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<td></td>
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</tr>
<tr>
<td>Nitric acid</td>
<td>254 (94.5%)</td>
<td>132 (96.3%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aminoglycoside</td>
<td></td>
<td></td>
</tr>
<tr>
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<td>&gt;256</td>
</tr>
<tr>
<td>Micromethod</td>
<td></td>
<td></td>
</tr>
<tr>
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<td>0.725 to &gt;256</td>
<td>0.5 to &gt;256</td>
</tr>
<tr>
<td></td>
<td>&gt;256</td>
<td>&gt;256</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Chloramphenicol</td>
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<td></td>
</tr>
<tr>
<td>MIC 50 (µg/ml)</td>
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<td>&gt;256</td>
</tr>
<tr>
<td>Micromethod</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>0.38 to &gt;256</td>
<td>2 to &gt;256</td>
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<tr>
<td>Nitric acid</td>
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<td>MIC 50 (µg/ml)</td>
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<td>&gt;256</td>
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<tr>
<td>Micromethod</td>
<td></td>
<td></td>
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<tr>
<td></td>
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<td>1.5 to &gt;256</td>
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<td></td>
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<td></td>
</tr>
<tr>
<td>Nitrofurantoin</td>
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<td>0.75</td>
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<tr>
<td>MIC 50 (µg/ml)</td>
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<tr>
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<td>0.023-2</td>
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<td>0.5</td>
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<tr>
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</table>

Overall evidence. We performed a MEDLINE search for “azithromycin, clinical trial, typhoid-enteric fever” and used the recent enteric fever Cochrane report [29] to identify 6 clinical trials in the literature. In total, 251 typhoid fever patients were treated with azithromycin.

Four trials, three from Egypt and one from India, used azithromycin to treat MDR typhoid fever [30-33]. Azithromycin achieved cure rates between 83% and 100%, the mean FCT ranged from 3.8 to 4.3 days. Two trials performed in Vietnam used azithromycin at 50 mg/kg/day [7] and at 10 mg/kg/day [8] for the treatment of MDR and nitric acid resistant typhoid fever. In total, 107 patients with culture confirmed typhoid fever were enrolled. The cure rate was 93% and 82% and the FCT was 5.6 and 5.8 days, respectively. Our results concur with these excellent data.

A recent trial conducted in Kathmandu, Nepal used gatifloxacin at the same dose and duration for the treatment of nitric acid resistant typhoid fever [16]. Successful treatment was achieved in 96.5% (85 out of 88) patients and the median FCT (55% CE) was 92 hours (94: 114 hours). The trial in Nepal was stopped early by the independent Data and Safety Monitoring Committee as a result of the poor clinical response in the patients randomized to cefixime.

We believe on the basis of this and other recently published trials, that gatifloxacin or azithromycin are now the treatments of choice for enteric fever in areas of MDR and nitric acid resistance [7,9,10]. However it is important to use these antimicrobial agents cautiously because indications use would inevitably induce further resistance.

Supporting Information
Protocol 81 Trial Protocol
Found at: doi:10.1371/journal.pone.0002188.s001 (0.07 MB DOC)

Checklist 81 CONSORT Checklist
Found at: doi:10.1371/journal.pone.0002188.s002 (0.06 MB DOC)
Acknowledgments

We are grateful to all the doctors and nurses who cared for the patients in this study and to all the patients and their relatives. We wish to thank the members of the Data and Safety Monitoring Board, Dr. Christopher M. Parry, Liverpool University, UK and Professor Nichas J. White, Mahidol University, Bangkok, Thailand.

References


Author Contributions

Conceived and designed the experiments: TH JF SD PT NS NC KS CD BJ JC TS NV TP NR, LP HV DD NB ML FB VH CS. Performed the experiments: TH JF SD NS NC CD BJ JC TS NV TP NR, LP HV DD NB ML FB VH CS. Analyzed the data: TH JF PT NS NC KS CD NV TP NR, LP HV. Wrote the paper: TH JF PT NS NC KS CD NV TP NR, LP HV.
**BJ STUDY NOTES**

CASE RECORD FORM USED FOR THE GATIFLOXACIN VERSUS AZITHROMYCIN TYPHOID FEVER TRIAL DESCRIBED IN CHAPTER 2

1. PATIENT DETAILS

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<thead>
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</tr>
<tr>
<td>MOTHER NAME: (if patient child)</td>
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</tr>
<tr>
<td>BJ STUDY NO:</td>
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</tr>
<tr>
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<tr>
<td>HOSPITAL NUMBER:</td>
<td></td>
</tr>
<tr>
<td>SEX:</td>
<td>MALE / FEMALE</td>
</tr>
<tr>
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<td>_____ YEARS.</td>
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**ADDRESS DETAILS:**

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<th>Telephone number:</th>
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<td>Road:</td>
<td>Mobile number:</td>
</tr>
<tr>
<td>Town/City:</td>
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</tr>
<tr>
<td>District/Province:</td>
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**ADDRESS DETAILS**

<table>
<thead>
<tr>
<th>House number:</th>
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<tbody>
<tr>
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<td>Town/City:</td>
<td></td>
</tr>
<tr>
<td>District/Province:</td>
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</tbody>
</table>
INFORMATION SHEET
OXTREC No: BJ

An open randomized comparison of Azithromycin versus Gatifloxacin for the treatment of uncomplicated enteric fever

Introduction to the study
You (or your child) are being asked to be in a research study on typhoid fever. Typhoid fever is a serious infection and in Viet Nam is now becoming very difficult to treat. This study is designed to see if we can improve the treatment of typhoid fever.

Blood Tests:
Whether or not you take part in the study you will be given the same standard of care for your illness. If you wish to take part in the study we will randomize the treatment you receive to one of two alternatives. We do not know which one you will receive or which is the best treatment. We believe both treatments to be effective. We will ask to take blood and stool samples during your stay in hospital and for the next 6 months after you are discharged from hospital to ensure that you have cleared the infection. This is very important to ensure that your family and friends are not at risk of infection. We will study the cells in the blood that protect you against infection and also your genes to try and understand why you got sick. The blood will be stored in a freezer at the Hospital for Tropical Diseases in Ho Chi Minh City. Further tests on these stored samples may be undertaken in the future to further the understanding of this disease.

Confidentiality:
We will keep the information we get from you as private. Your name will not be on your test results—we will use a number instead of your name. The results of your blood tests will be told only to your doctor. These results will be under the authority and supervision of the doctor responsible for your inpatient care. Your doctor will discuss these results with you. All this information will be kept confidential in your medical records. Your name will not be mentioned in any papers or speeches about the study.

Risks:
There are very few risks to you from being in our study. All the drugs being used in this study are routinely used in Viet Nam. Taking blood by needle will hurt for a moment, and may leave a bruise.

Costs:
There will be no cost to you.

Refusal to participate
You may refuse to be in any parts of the study. If you do not want to be in the study that decision will not in any way interfere with your ability to receive proper medical care or attention.

Questions:
If you have any other questions about the study please ask the doctor on the ward or the doctors named at the top of this sheet.
(This is the doctor you see every day. Please ask any nurse or doctor who will help you)
CONSENT FORM:

OXTREC No: BJ:

An open randomized comparison of Azithromycin versus Gatifloxacin for the treatment of uncomplicated enteric fever

Consent from patient:
I have been fully informed of the possible risks and benefits of taking part in this study and agree to take part. I agree that the samples may be stored and that further tests may be undertaken on these samples in the future to further the understanding of this disease.

Name of patient: ____________________________ Date: ____________________________
Signature: ____________________________

Name of physician: ____________________________ Date: ____________________________
Signature: ____________________________

If the patient gives verbal consent to take part in the trial but is unable to sign, the physician can record the consent here:

Name of physician: ____________________________ Signature: ____________________________
Date: ____________________________

Reason for giving verbal consent: ____________________________

Consent from relative: (Only to be used when the patient is unable to give consent because the patient is a child)

I have been fully informed of the possible risks and benefits of this study. I agree that my relative ____________________________ may take part in the study.

Name of relative: ____________________________
Relationship with patient: ____________________________
Signature: ____________________________ Date: ____________________________

Name of physician: ____________________________ Date: ____________________________
Signature: ____________________________
Please note, the patient can only enter the study if the consent form has been signed.

### 2. History

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#### Duration of symptoms (record days, 0 = not reported)

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</tr>
<tr>
<td>Cough</td>
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<tr>
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<tr>
<td>Weight loss</td>
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<td>Abdominal pain</td>
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<tr>
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#### Past History

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<th>Diabetes:</th>
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<td>Y / N</td>
</tr>
<tr>
<td>Date if Yes:</td>
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<table>
<thead>
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</thead>
<tbody>
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<td>Y / N</td>
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<table>
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<th>Drug:</th>
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<td>If yes: Drug:</td>
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#### Treatment in the last 2 weeks

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<td>Other treatment (drug and dose):</td>
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#### Where:

### 3. Examination

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<tr>
<td>Temperature: 37°C</td>
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<tr>
<td>Blood pressure: 120 mmHg</td>
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<td>Pulse: 120 / min</td>
<td>Stiff neck: Y / N</td>
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BJ Study Notes
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<th>Respiratory rate: _____ /min</th>
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<tr>
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### 4. CULTURE

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### 5. ANTIBIOGRAM

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BJ STUDY Notes
### 6. BLOOD TESTS

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<td>Glucose</td>
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7. CHEST X-RAY (please summarize most important finding)

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<th>Date: (___)</th>
<th>Date: (___)</th>
<th>Date: (___)</th>
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8. OTHER TESTS

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9. MANAGEMENT

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<tr>
<th>Diagnosis:</th>
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<tbody>
<tr>
<td>General assessment:</td>
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<tr>
<td>Severe / Average / Mild.</td>
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<tr>
<td>Treatment prescribed:</td>
</tr>
<tr>
<td>Start of treatment: date __________</td>
</tr>
<tr>
<td>dose __________</td>
</tr>
<tr>
<td>Complications: Yes / No</td>
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</table>

<table>
<thead>
<tr>
<th>COMPLICATIONS</th>
<th>Date</th>
<th>Duration, level of illness, management</th>
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<tr>
<td>GI bleeding</td>
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<tr>
<td>Intestinal perforation</td>
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<tr>
<td>Hepatitis/Cholecystitis</td>
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<tr>
<td>Shock</td>
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<td>Others</td>
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10. HAND WRITTEN SUMMARY
## STUDY NOTES

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<th>Day 2 Date</th>
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<tr>
<td>Dose (po/im/iv)</td>
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</tr>
<tr>
<td>Hours since start treatment</td>
<td></td>
<td></td>
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<td></td>
</tr>
<tr>
<td>Time</td>
<td>6</td>
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<tr>
<td>Blood pressure</td>
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<tr>
<td>Respiratory rate</td>
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</tr>
<tr>
<td>GCS</td>
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<tr>
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<tr>
<td>Splenomegaly</td>
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<td>Day 5 Date:</td>
<td>Day 6 Date:</td>
<td>Day 7 Date:</td>
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<tr>
<td><strong>Dose (po/im/iv)</strong></td>
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<tr>
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<tr>
<td><strong>Pulse rate</strong></td>
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<td><strong>Blood pressure</strong></td>
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Date of admission:

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**Antibiotic**

**Dose (po/im/iv)**

**Hours since start treatment**

<table>
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<th>6</th>
<th>12</th>
<th>18</th>
<th>24</th>
<th>6</th>
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<th>24</th>
<th>6</th>
<th>12</th>
<th>18</th>
<th>24</th>
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</table>

**Fever °C**

- 40.0
- 39.0
- 38.0
- 37.0
- 36.0

**Pulse rate**

**Blood pressure**

**Respiratory rate**

**GCS**

**Hepatomegaly**

**Splenomegaly**

**Diarrhoea**

**Melaena**

**Roseolae**

---
**ADMISSION OUTCOME**

<table>
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<th>Fever clearance time: <em>(Time from the start of treatment until the temp. falls below 37.5°C and remains at or below 37.5°C for at least 48 hours)</em></th>
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<td>If No, describe:</td>
<td>= ___________ hours</td>
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<td>Duration of antibiotic treatment: (days)</td>
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<td>Treatment failure:</td>
<td>Clinical (fever after 7 days of treatment) Yes/No</td>
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<tr>
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<td>Microbiological (positive stool culture on day 9) Yes/No</td>
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<td>Date of death:</td>
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<td>Date of discharge:</td>
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**SIDE-EFFECTS OF STUDY DRUGS**

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<td>Allergic reaction</td>
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<td>Nausea</td>
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<td>Vomiting</td>
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<td>Headache</td>
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<td>Others</td>
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</tbody>
</table>
FOLLOW-UP

Follow-up 1 after 1 MONTH

Date: __________

Time since finished treatment: __________ (days)

Complaint: ____________________________

Clinical examination: __________________

Temperature: _____ °C

Other symptoms: ______________________

Relapse: Yes/No

Comments: ____________________________

Stool culture (1 sample): __________

Faecal carriage: Yes/No

Name of doctor ___________________________ Date: __________

Follow-up 2 after 3 MONTH

Date: __________

Time since finished treatment: __________ (days)

Complaint: ____________________________

Clinical examination: __________________

Temperature: _____ °C

Other symptoms: ______________________

Relapse: Yes/No

Comments: ____________________________

Stool culture (1 sample): __________

Faecal carriage: Yes/No

Name of doctor ___________________________ Date: __________
Follow-up 3

Date: 
Time since finished treatment: __________ (days)

Complaint: 

Clinical examination: 

Temperature: __________ °C

Other symptoms: 

Relapse: Yes/No

Comments: 

Stool culture: (1 sample): 

Fecal carriage: Yes/No

Name of doctor: ______________________ Date: ____________
Antimicrobial Drug Resistance of Salmonella enterica Serovar Typhi in Asia and Molecular Mechanism of Reduced Susceptibility to the Fluoroquinolones

Tran Thuy Chau,1,2 James Ian Campbell,1,2 Claudia M. Galindo,3 Nguyen Van Minh Hoang,1,2 To Song Diep,2 Tran Thu Thi Nga,1,2 Nguyen Van Vinh Chau,2 Phung Quoc Tuan,1,2

Anne Laure Page,4 R. Leon Ochiai,5 Constance Schultze,1 John Wain,5 Zulfikar A. Bhutta,5 Christopher M. Parry,1,5 Sujit K. Bhattacharyya,5 Shanta Dutta,2 Magdalina Agtini,8 Baiqing Dong,2 Yang Honghui,2 Deng Duc Anh,9 Do Gia Canh,10 Aliya Naheed,11 M. John Albert,12 Rattanaphone Photonsawat,16 Paul N. Newton,13,16 Bach M. Bang,14

Amit Arjyal,4 Tran Thii Phi La,17 Nguyen Ngoc Rang,17 Le Thi Phuong,18

Phan Van Be Bay,10 Lorenz von Seidlein,1 Gordon Dougan,12 John D. Clemens,5 Ha Vinh,1 Tran Tinh Hien,2 Nguyen Tran Chinh,1 Camilo J. Acosta,3 Jeremy Farrar,5,14 and Christiane Dolecek1,2,14

Oxford University Clinical Research Unit, Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam;1 The Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam;2 Centre for Tropical Medicine, Nuffield Department of Clinical Medicine, John Radcliffe Hospital, Oxford, United Kingdom;2 Patan Hospital, Kathmandu, Nepal;6 International Vaccine Institute, Seoul, South Korea;3 Department of Paediatrics, Aga Khan University, Karachi, Pakistan;4 National Institute of Cholera and Enteric Diseases, Kolkata, India;5 National Institute of Health Research and Development, Jakarta, Indonesia;6 Guangxi Center for Disease Control and Prevention, Nanning, Guangxi, China;7 National Institute of Hygiene and Epidemiology, Hanoi, Vietnam;8 International Centre for Diarrhoeal Disease Research (ICDDR), Dhaka, Bangladesh;11 The Wellcome Trust Sanger Institute, Cambridge, United Kingdom12; Department of Medical Microbiology and Genito-urinary Medicine, Duncan Building, University of Liverpool, United Kingdom13; London School of Hygiene and Tropical Medicine, London, United Kingdom14; Department of Microbiology, Faculty of Medicine, Kuwait University, Kuwait;15; Wellcome Trust-Mahathir Hospital-Oxford Tropical Medicine Research Collaboration, Microbiology Laboratory, Mahathir Hospital, Vientiane, Lao People’s Democratic Republic;16; An Giang Provincial Hospital, Long Xuyen, An Giang, Vietnam17; and Dong Thap Provincial Hospital, Cao Lãnh, Dong Thap, Vietnam18.

Received 1 March 2007/Returned for modification 28 May 2007/accepted 24 September 2007

This study describes the pattern and extent of drug resistance in 1,714 strains of Salmonella enterica serovar Typhi isolated across Asia between 1993 and 2001 and characterizes the molecular mechanisms underlying the reduced susceptibilities to fluoroquinolones of these strains. For 1,353 serovar Typhi strains collected in southern Vietnam, the proportion of multidrug resistance has remained high since 1993 (50% in 2004) and there was a dramatic increase in nalidixic acid resistance between 1993 (4%) and 2005 (97%). In a cross-sectional sample of 281 serovar Typhi strains from 8 Asian countries, Bangladesh, China, India, Indonesia, Laos, Nepal, Pakistan, and central Vietnam, collected in 2002 to 2004, various rates of multidrug resistance (15 to 37%) and nalidixic acid resistance (5 to 18%) were found. The eight Asian countries involved in this study are home to approximately 80% of the world’s typhoid fever cases. These results document the scale of drug resistance across Asia. The SerR3—the substitution in gyrA was the predominant alteration in serovar Typhi strains from Vietnam (117/127 isolates; 92.1%). No mutations in parC1,2 or parE2 were detected in 55 of these strains. In vitro time kill experiments showed a reduction in the efficacy of ciprofloxacin against strains harboring a single amino acid substitution at codon 83 or 87 of gyrA; this effect was more marked against a strain with a double substitution. The 8-methoxy fluoroquinolone gatifloxacin showed rapid killing of serovar Typhi harboring both the single- and double-amino-acid substitutions.

There are approximately 21 million cases of typhoid fever worldwide, with a particularly high incidence in Asia. An estimated 220,000 deaths per year occur as a consequence of the disease (11). This article describes the extent and pattern of drug resistance of Salmonella enterica serovar Typhi across Asia. This information is vital for guiding treatment and is also important for helping policy makers to plan vaccination campaigns. The emergence and spread of drug resistance have limited treatment options for typhoid fever in many countries. Since the isolation of multidrug-resistant (MDR) serovar Typhi strains which show resistance to all third-generation cephalosporins (chloramphenicol, ampicillin, and trimethoprim-sulfamethoxazole) in the 1980s, the fluoroquinolone class of antibiotics has become the treatment of choice for enteric fever (4, 38). Unfortunately, outbreaks of serovar Typhi strains that were resis-
tant to nalidixic acid (the prototype quinolone, which is used for in vitro screening tests) and showed reduced susceptibility to the fluoroquinolones have been reported subsequently in a number of countries (25). Vietnam and particularly the Mekong Delta region of Vietnam faced a series of typhoid fever epidemics over the last decade, imposed on a background of endemic disease, that reflected changes in resistance patterns and pointed to a serious problem of drug resistance (24). MDR is associated with a transferable plasmid (36), while reduced susceptibility to the fluoroquinolones in serovar Typhi is usually associated with point mutations in the bacterial target genes encoding DNA gyrase and/or DNA topoisomerase IV.

This work was presented in part at the American Meeting of Hygiene and Tropical Medicine, Atlanta, GA, December 2005.)

**MATERIALS AND METHODS**

Bacterial isolates. (i) Serovar Typhi strains isolated in southern Vietnam from 1993 to 2005. One thousand three hundred thirty-three serovar Typhi isolates were collected consecutively from patients with uncomplicated typhoid fever during prospective hospital-based clinical studies between 1993 and 2005 conducted at Dong Thap Provincial Hospital, Dong Nai Provincial Hospital, An Giang Provincial Hospital, and the Hospital for Tropical Diseases, Ho Chi Minh City, all located in southern Vietnam. These studies have been described previously (7, 8, 22, 26, 32-35).

(ii) Serovar Typhi isolates from eight Asian countries in 2002 to 2004. One hundred forty-nine serovar Typhi isolates were collected in March and April 2003 during a hospital-based descriptive study at Patna Hospital, Kathmandu, Nepal. Fifty isolates were collected consecutively during a clinical trial in 2003 and at the Watkhun Tham-Mahaphol Hospital-Orphan Tropical Medicine Research Collaboration, Lao People's Democratic Republic, Laos (27). One hundred eighty-two serovar Typhi isolates were collected, as part of population-based prospective surveillance studies conducted by multiple teams in collaboration with the International Vaccine Institute (IVI), Seoul, South Korea (11). These surveillance sites included whole townships (China and Vietnam), specific slum areas (Bangladesh, Pakistan, and India), and an impoverished urban slum (Indonesia). Forty isolates were collected from February 28 to March 6, 2005, in a urban slum in Dhaka, Bangladesh; the setting has been described (15, 21) isolates were collected, from 2002 to 2004 in Hucuq city, Guang Xi, China; 23 strains were collected from May to July 2003 in urban areas in Kolkata, West Bengal, India; 17 isolates were collected from July to September 2002 in North Jakarta, Indonesia; 34 strains were isolated between January 2002 and March 2003 in one slum area in Karachi, Pakistan; and 47 isolates were collected between July 2002 and September 2004 in Hoa city, central Vietnam.

All serovar Typhi isolates were collected consecutively from inpatient patients during the indicated periods and came from geographically contiguous areas. The isolates were uncultured, and were representative of the population they came from.

**Identification and antimicrobial susceptibility.** Isolates were identified using the API20E biochemical identification system (BioMerieux, Paris, France). Susceptibility was carried out using selective anaerobic (polystyren, O, 09, 06, and 09) (Merex, Darlington, United Kingdom).

Antimicrobial susceptibility testing with ampicillin, chloramphenicol, trimethoprim-sulfamethoxazole, nalidixic acid, ofloxacin, ciprofloxacin, gentamicin, and ceftriaxone was performed using diffusion according to Clinical and Laboratory Standards Institute (CLSI) methods and interpreted following CLSI guidelines (9). The control strains used for all susceptibility tests were Escherichia coli ATCC 25922, Pseudomonas aeruginosa ATCC 27853, and Staphylococcus aureus ATCC 29213. MICs were determined by using the E-test (AB Biologics, Solna, Sweden). MDR of isolates was defined as resistance to chloramphenicol (MIC ≤ 32 μg/ml), ampicillin (MIC ≤ 32 μg/ml), and trimethoprim-sulfamethoxazole (MIC ≤ 32 μg/ml). Nalidixic acid resistance was defined as a MIC of ≥32 μg/ml. The breakpoints for ceftriaxone and gentamicin were ≤2 μg/ml (susceptible) and ≥8 μg/ml (resistant), whereas, for ciprofloxacin, ≤1 μg/ml (susceptible) and ≥8 μg/ml (resistant). All tests were performed at the Hospital for Tropical Diseases (HTD), Ho Chi Minh City, Vietnam, except for the isolates from Nepal, which were tested at Patna Hospital, Kathmandu, Nepal, using identical methodologies.

DNA isolation. A single colony was inoculated in 6 ml of LB broth (Sigma) and incubated overnight at 37°C. DNA was extracted using the GenElute Genomic-DNA Mini and Cellyzer DNA buffer set (Sigma, Ltd., Hillsden, Germany) or the acid-phenol/chloroform method of DNA extraction (2). DNA stock was stored at −20°C and −80°C. Four hundred nanograms of DNA was used for each PCR.

PCR and sequencing. Galleria mellonella primers were as shown in Table 1. PCR amplification of gyrA (371 bp), parC (341 bp), parE (270 bp), and gyrB (240 bp) were performed with 30 cycles of denaturation at 95°C for 1 min, annealing at 62°C for 1 min, and extension at 74°C for 2 min, followed by a final extension step at 74°C for 1 min.

PCR products were purified using the QIAquick PCR purification kit (QIAGEN, Hilden, Germany) and used directly as templates for sequencing, which was performed with the CEG EQPCR-Quick start kit and analyzed using an automated sequencer, the CEBIO9000 genetic analysis system (Beckman Coulter, Inc., Fullerton, CA). Selected strains were removed for the presence of the gyrA and parC genes by PCR. The PCR conditions for the amplification of parC were as follows: 94°C for 2 min, 34 cycles of 94°C for 45 s, 45°C for 45 s, and 72°C for 1.5 min; and 72°C for 3 min. PCR conditions for parE were as follows: 94°C for 1 min, 15 cycles of 94°C for 45 s, 50°C for 45 s, and 72°C for 1 min; and 72°C for 3 min. PCR conditions for gyrA were as follows: 94°C for 1 min, 15 cycles of 94°C for 45 s, 50°C for 45 s, and 72°C for 1 min; and 72°C for 7 min.

Selected strains were removed for the presence of the gyrB and parE genes by PCR. The PCR conditions for the amplification of gyrB were as follows: 94°C for 2 min, 34 cycles of 94°C for 45 s, 45°C for 45 s, and 72°C for 1.5 min; and 72°C for 3 min. PCR conditions for parE were as follows: 94°C for 1 min, 15 cycles of 94°C for 45 s, 50°C for 45 s, and 72°C for 1 min; and 72°C for 3 min. PCR conditions for gyrA were as follows: 94°C for 1 min, 15 cycles of 94°C for 45 s, 50°C for 45 s, and 72°C for 1 min; and 72°C for 7 min.

**TABLE 1. Oligonucleotide primer sequences used for PCR amplification**

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primer</th>
<th>Primer sequence (5′→3′)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>GyrA</td>
<td>GYRA/B1</td>
<td>TCTTCCGAGATGCTGGCCTGACG</td>
<td>16</td>
</tr>
<tr>
<td>GyrA</td>
<td>GYRA/B2</td>
<td>GATTCCATGATGGCCTGACG</td>
<td>20</td>
</tr>
<tr>
<td>GyrB</td>
<td>StripyB1</td>
<td>TCTTCCGATGATGGCCTGACG</td>
<td>20</td>
</tr>
<tr>
<td>parC</td>
<td>StripyC</td>
<td>GATTCCATGATGGCCTGACG</td>
<td>20</td>
</tr>
<tr>
<td>parE</td>
<td>StripyE1</td>
<td>GATTCCATGATGGCCTGACG</td>
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</tr>
<tr>
<td>parE</td>
<td>StripyE2</td>
<td>GATTCCATGATGGCCTGACG</td>
<td>20</td>
</tr>
<tr>
<td>parE</td>
<td>StripyE3</td>
<td>GATTCCATGATGGCCTGACG</td>
<td>20</td>
</tr>
<tr>
<td>parE</td>
<td>StripyE4</td>
<td>GATTCCATGATGGCCTGACG</td>
<td>20</td>
</tr>
</tbody>
</table>

* Sequences for the parC primers were designed based on the sequence of Staphylococcus aureus (17).
in order to obtain 6%, 4%, 2%, and 1% MIC. The growth control contained no antibiotic.

The cultures were inoculated at 35 to 37°C for 24 h. Visible zones were measured immediately prior to the addition of the antibiotic and at 30 min and 1, 2, 4, 6, and 24 h after the addition of the antibiotic. Visible zones were performed by using the Mikes and Mazza technique on nutrient agar plates following serial dilutions in maximum-recovery volumes (Oxoid, United Kingdom). The lower limit of detection was 10 CFU/ml.

Nucleotide sequence accession numbers. The partial DNA sequences of the

_âluminate_ sequences of the

...sequence database under the accession numbers EF506960 and EF506961, respectively.

RESULTS

Antimicrobial susceptibility testing. (i) _Serovar Typhi_ isolated in southern Vietnam from 1993 to 2005. Between 1993 and 2005, 1,393 isolates of _serovar Typhi_ were collected (Fig. 1). The proportion of MDR _serovar Typhi_ was 63.2% (36/57 strains) in 1993 and increased to more than 80% in the late 1990s and early 2000. During the same period, there was a dramatic increase in nalidixic acid resistance. In 1993, 2 out of 57 (3.5%) _serovar Typhi_ isolated from patients in southern Vietnam were nalidixic acid resistant (respective MICs of ciprofloxacin, 0.250 and 0.125 μg/ml) (37). Nalidixic acid resistance surged to 88.6% (109/123) in 1998. It has remained at high levels since then, with 99% (190/202) of isolates in 2004. Since 1998, a high proportion of _serovar Typhi_ isolates show the combination of

M RDR and nalidixic acid resistance (Fig. 1).

The antimicrobial susceptibility data of 202 _serovar Typhi_ isolated in 2004 in southern Vietnam are shown in more detail in Table 2.

(ii) _Serovar Typhi_ strains isolated in eight Asian countries in 2002 to 2004. The antimicrobial resistances of 381 _serovar Typhi_ isolates collected in 2002 to 2004 from eight Asian countries were analyzed (Table 2). There were various rates of MDR across the sites, ranging from 16% (8/50) of isolates from Laos to 37.5% (15/40) from Bangladesh. China and Indonesia were exceptions, with no MDR _serovar Typhi_ identified.

The percentages of nalidixic acid-resistant _serovar Typhi_ isolates ranged from 0% in Indonesia and Laos and 4.8% (1/21) in China to 51% (76/140) in Nepal (Table 2). The com-

TABLE 2. Antimicrobial drug resistance of _serovar Typhi_ isolates in 2002 to 2004 across eight Asian countries

<table>
<thead>
<tr>
<th>Country</th>
<th>% Nalidixic acid-resistant isolates*</th>
<th>MIC of ciprofloxacin (μg/ml) Range</th>
<th>% Ciprofloxacin-resistant isolates*</th>
<th>MIC of gentamicin (μg/ml) Range</th>
<th>% Chloramphenicol-resistant isolates*</th>
<th>% MDR isolates*</th>
</tr>
</thead>
<tbody>
<tr>
<td>China</td>
<td>4.8 (1/21)</td>
<td>0.006-0.25 0.015 0.03</td>
<td>0</td>
<td>0.012-0.190 0.023 0.029</td>
<td>0 (0/21)</td>
<td>0 (0/21)</td>
</tr>
<tr>
<td>Indonesia</td>
<td>0 (0/17)</td>
<td>0.006-0.25 0.015 0.015</td>
<td>0</td>
<td>0.012-0.20 0.016 0.025</td>
<td>0 (0/17)</td>
<td>0 (0/17)</td>
</tr>
<tr>
<td>Laos</td>
<td>0 (0/50)</td>
<td>0.006-0.25 0.012 0.016</td>
<td>0</td>
<td>0.012-0.047 0.016 0.023</td>
<td>18 (9/50)</td>
<td>18 (9/50)</td>
</tr>
<tr>
<td>Bangladesh</td>
<td>49 (16/49)</td>
<td>0.006-0.38 0.25 0.38</td>
<td>0</td>
<td>0.012-0.19 0.016 0.019</td>
<td>18 (9/50)</td>
<td>373 (37/40)</td>
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<tr>
<td>India</td>
<td>47.8 (11/23)</td>
<td>0.006-0.25 0.004 0.25</td>
<td>4 (6/149)</td>
<td>0.012-1.590 0.044 0.25</td>
<td>19 (26/149)</td>
<td>26 (6/235)</td>
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<td>Nepal</td>
<td>51 (76/149)</td>
<td>0.004-0.25 0.012 0.25</td>
<td>0</td>
<td>0.012-0.20 0.023 0.19</td>
<td>28.5 (9/34)</td>
<td>263 (9/34)</td>
</tr>
<tr>
<td>Pakistan</td>
<td>38.3 (13/34)</td>
<td>0.006-0.5 0.023 0.38</td>
<td>0</td>
<td>0.006-0.025 0.016 0.19</td>
<td>213 (10/47)</td>
<td>213 (10/47)</td>
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<tr>
<td>Central Vietnam  (IV)</td>
<td>59 (23/47)</td>
<td>0.006-0.5 0.023 0.38</td>
<td>0</td>
<td>0.006-0.250 0.125 0.19</td>
<td>50 (10/150)</td>
<td>50 (10/150)</td>
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<tr>
<td>Southern Vietnam (IIID)</td>
<td>97 (106/202)</td>
<td>0.006-0.75 0.38 0.5</td>
<td>0</td>
<td>0.006-0.25 0.125 0.19</td>
<td>50 (101/202)</td>
<td>50 (101/202)</td>
</tr>
</tbody>
</table>

*Paper thickness numbers indicate no. of resistant isolates, no. tested.

NA, not available.

FIG. 1. Antimicrobial drug resistance of _serovar Typhi_ strains isolated during clinical studies in southern Vietnam from 1993 to 2005. Percentages of MDR and nalidixic acid-resistant _serovar Typhi_ isolates. The number of isolates from each year is shown on top of the bars.
<table>
<thead>
<tr>
<th>Isolate</th>
<th>Year of isolation</th>
<th>Country or province</th>
<th>Acine and substitution(s) in gD</th>
<th>Nucleotide change(s) in gD</th>
<th>gD 63% prob</th>
<th>Presence of MDR</th>
<th>MIC of drug (mg/mL)</th>
<th>Ciprofloxacin</th>
<th>Gentamicin</th>
<th>Ofloxacin</th>
<th>Quinoloxacin</th>
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<td>D 43*</td>
<td>2004 Indonesia</td>
<td>S31Y</td>
<td>TCC→TAC</td>
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<td>wt</td>
<td>wt</td>
<td>No</td>
<td>&gt;256</td>
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<td>0.5</td>
<td>0.25</td>
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<td>TCC→TAC</td>
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<td>Yes</td>
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<td>0.19</td>
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<td>TCC→TAC</td>
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<td>Yes</td>
<td>Yes</td>
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<td>wt</td>
<td>Yes</td>
<td>No</td>
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<td>Yes</td>
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<td>wt</td>
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<td>Yes</td>
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<td>wt</td>
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<td>Yes</td>
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<td>nar 104*</td>
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<td>wt</td>
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<td>Yes</td>
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<td>S33F</td>
<td>TCC→TTC</td>
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<td>Yes</td>
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<td>Yes</td>
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<td>Yes</td>
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<td>Yes</td>
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<td>TCC→TTC</td>
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<td>Yes</td>
<td>&gt;256</td>
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<td>Yes</td>
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<td>Yes</td>
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<td>Yes</td>
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<td>Yes</td>
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<td>Yes</td>
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<td>TCC→TTC</td>
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<td>wt</td>
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<td>Yes</td>
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<td>0.5</td>
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<td>Yes</td>
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<td>Yes</td>
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<td>Yes</td>
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<td>0.5</td>
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<td>DT 54</td>
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<td>wt</td>
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<td>Yes</td>
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<td>S33F</td>
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<td>Yes</td>
<td>&gt;256</td>
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<td>1</td>
<td>0.125</td>
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* Isolate names consist of an abbreviation for the study followed by the isolate number. *, strain screened for presence of gD1 and gD2 strains by PCR. 
† Indicates sensitivity of gD2 strains to gD2-specific PCR.
bination of MDR and nalidixic acid resistance was found in 4.3% (2/47) of serovar Typhi isolates from central Vietnam, 8.7% (2/23) of isolates from India, 23.5% (8/140) of isolates from Pakistan, and 30% (12/40) of isolates from Bangladesh. In Nepal, 18.1% (27/149) of serovar Typhi isolates were resistant to both amoxicillin and nalidixic acid.

However, using current CLSI breakpoints, all isolates remained susceptible in vitro to ciprofloxacin and ofloxacin, with the exception of one isolate from southern Vietnam, AG 152, with intermediate susceptibility (MIC, 3.0 μg/ml) to ofloxacin (Table 3) and six isolates (4%) from Nepal that were ciprofloxacin resistant. The highest MICs of gatifloxacin at which 50% and 90% of serovar Typhi isolates were inhibited were 0.125 μg/ml and 0.25 μg/ml, respectively (Table 2). All isolates were susceptible to ceftazidime.

DNA analysis of QRDR of DNA gyrase and DNA topoisomerase IV and effect of mutations on fluorquinolone susceptibility. One hundred twenty-seven nalidixic acid-resistant serovar Typhi isolates (118 from southern Vietnam, 5 from India, and 4 from Pakistan) with reduced susceptibilities to the fluorquinolones (MIC of ofloxacin ranging from 0.5 μg/ml to 3 μg/ml) were selected for molecular analysis of the quinolone resistance determining region (QRDR) of gyrE. Six different types of mutations were detected. The most prevalent amino acid substitution was Ser83→Phe (TCC→TTC) in 117/127 (92.1%) strains. Four isolates (3.1%) had an alteration at codon 83 changing Ser to Tyr (TCC→TAC). Two isolates showed the Asp87→Gly (GAC→Gly) substitution and two isolates the Asp87→Asn (GAC→GCC) substitution. Two serovar Typhi isolates had double-amino-acid substitutions in GyrA: isolates DT 18 (Ser83→Phe and Asp87→Gly) and AG 152 (Ser83→Phe and Asp87→Asn), as shown in Table 3.

Fifty-five of these strains were analyzed for mutations in the QRDR of gyrB, parC, and parE (13, 20); no mutations were detected (Table 3). Twenty-five isolates (indicated by an asterisk in Table 3) were screened for the presence of the plasmid-mediated quinolone resistance genes qnrS1 and qnrS5 (15); none were detected in these isolates.

In vitro time kill analysis. One isolate representing each mutant group was selected for in vitro time-kill experiments: CT 76, wild-type strain (MIC, 0.064 μg/ml for ofloxacin and 0.008 μg/ml for gatifloxacin); HTD 798 (Ser83→Phe; MICs, 1.0 μg/ml for ofloxacin and 0.13 μg/ml for gatifloxacin); CT 144 (Asp87→Gly; MICs, 1 μg/ml for ofloxacin and 0.064 μg/ml for gatifloxacin); and DT 18 (Ser83→Phe and Asp87→Gly; MICs, 2.0 μg/ml for ofloxacin and 0.25 μg/ml for gatifloxacin). The mean changes in log10 CFU/ml are presented in Fig. 2. Gatifloxacin showed rapid killing of wild-type strain CT 76 (Fig. 2a); viable counts of serovar Typhi HTD 798 and CT 144 decreased after 4 h at 4°C, but complete killing could not be achieved (Fig. 2b and c). No bactericidal activity was achieved against serovar Typhi DT 18 (Fig. 2d). Gatifloxacin at 4°C MIC decreased the bacterial population of CT 76, HTD 798 and CT 144 (Fig. 2e, f, and g) in the first 30 min and showed complete killing after 6 h. Viable counts of serovar Typhi DT 18 decreased after 4 h, followed by regrowth; higher concentrations (8× or 16× MIC) showed a more pronounced bactericidal effect against this double mutant (Fig. 2f).

DISCUSSION


In 1993, during the initial outbreak of MDR serovar Typhi in Ken Giang province in the south of Vietnam, the fluoroquinolone antibiotics were introduced for the treatment of typhoid fever (22). Since 1995, the proportion of MDR serovar Typhi has remained at high levels and there has been a dramatic increase in nalidixic acid resistance. In 1998, 5 years after ofloxacin and ciprofloxacin become widely available in an uncontrolled market, 87% of the isolates were resistant to nalidixic acid; this increased to 97% by 2004. The combination of MDR and nalidixic acid resistance is a particular problem in Vietnam, because it severely restricts the therapeutic options for patients with typhoid fever.

Patients infected with nalidixic acid-resistant serovar Typhi show poor clinical response, high failure rates (up to 36%), and prolonged focal carriage when treated with an older-generation fluoroquinolone, such as ofloxacin (8, 20). The antimicrobial resistance data from southern Vietnam are complemented by the results of a cross-sectional study from eight Asian countries: Bangladesh, China, India, Indonesia, Laos, Nepal, Pakistan, and Vietnam. These countries are home to approximately 80% of the world's typhoid fever cases (11).

While in southern Vietnam the MDR phenotype of serovar Typhi has remained at high levels over the last 13 years, there have been reports of a return to chloramphenicol sensitivity in some regions (14, 21). However, in our study the prevalence of chloramphenicol resistance remained high in many Asian countries (18% in Laos, 19% in Nepal, 26% in India and Pakistan, and 40% in Bangladesh), with the exception of China and Indonesia.

In 2002 to 2004, all countries in the region, with the exception of China and Laos, faced a problem of nalidixic acid resistance, with southern Vietnam as a particular hot spot. Roumagnac et al. recently suggested that fluoroquinolones use has driven the clonal expansion of a nalidixic acid-resistant serovar Typhi haplotype, H185, in Southeast Asia (28). The emergence of resistance of serovar Typhi to ciprofloxacin (6/149 isolates; 4%) in Nepal, together with reports of high-level ciprofloxacin resistance in India and Bangladesh (14, 28, 30), might be the prelude to a worsening drug resistance problem in Asia.

In this study carried out across Asia, mutations associated with nalidixic acid resistance and reduced susceptibility to fluoroquinolones for serovar Typhi were defined only in gyrA, as single-amino-acid substitutions at either codon 83 or 91 (6, 18, 31, 37), with the exception of two isolates from Vietnam, which had double-amino-acid substitutions. There have been two recent reports of serovar Typhi with the Ser83Phe and Asp87Gly double alteration in high-level-ciprofloxacin-resistant serovar Typhi (28, 30). In our study, the isolates with double mutations in gyrA were less susceptible to the fluoroquinolones, and this phenotype may become more widespread in the future if continued drug pressure is applied. This is a particular problem in many parts of Asia, where antibiotics are readily available in an unregulated marketplace and inadequate doses and durations of antibiotics are often used.
FIG. 2. In vitro time-killed experiments of wild type serovar Typhi and serovar Typhi harboring single and double amino acid substitutions in GyrA. Figure a to d shows exposure to ofloxacin, and Fig. e to h shows exposure to gatifloxacin at concentrations of 1× to 16× MIC over 24 h. Results represent means of duplicate values; the standard deviation is indicated by error bars.
DRUG RESISTANCE OF SALMONELLA SEROVAR TYPHI IN ASIA

e) Serovar Typhi CT 76 (wild type) v. Gatifloxacin

f) Serovar Typhi HTD798 (Ser83Phe) v. Gatifloxacin

g) Serovar Typhi CT 144 (Asp87Gly) v. Gatifloxacin

h) Serovar Typhi DT 18 (Ser83Phe and Asp87Gly) v. Gatifloxacin

FIG. 3—Continued
Our time-kill experiments suggest that the choice of the fluoroquinolone and the dose used for the treatment of septic Typhus may be critical and underline that clearly not all the fluoroquinolones are as susceptible to these common mutations. Continued use of the older-generation fluoroquinolones (ciprofloxacin and ofloxacin) may encourage the persistence of resistant isolates and lead to the development of new mutations which might compromise the efficacy of the newer generation. With lower MICs and better responses in the time-kill experiments, it is possible that gatifloxacin (and potentially other newer-generation fluoroquinolones) would prove a better choice for use in typhoid fever. This provides a clear rationale for the clinical assessment of these drugs in randomized controlled trials in typhoid fever. If these in vitro data are supported by clinical results, then this newer generation of fluoroquinolones should be recommended for the treatment of typhoid fever instead of ciprofloxacin and ofloxacin.

In conclusion, the emergence and persistence of MDR and multiresistant-antibiotic-resistant Typhus strains constitute a major problem across Asia. No drug has ever been developed specifically for typhoid fever, and there are very few potential targets in Salmonella against which new drugs could be designed (3). We need to use our current drugs better and use the best and most affordable drugs available in order to prevent further resistance. Knowledge of the extent of drug resistance should be an important factor when discussing the implementation of a comprehensive typhoid vaccination strategy.

ACKNOWLEDGMENTS
We are grateful to the directors of Dong Tang Provincial Hospital, An Giang Provincial Hospital, and the Hospital for Tropical Diseases, Ho Chi Minh City, Vietnam, for their support.

REFERENCES


An Open Randomized Comparison of Gatifloxacin versus Cefixime for the Treatment of Uncomplicated Enteric Fever

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Objective: To assess the efficacy of gatifloxacin versus cefixime in the treatment of uncomplicated culture positive enteric fever. Design: A randomized, open-label, active control trial with two parallel arms. Setting: Emergency Room and Outpatient Clinic in Patan Hospital, Lagankhel, Lalitpur, Nepal. Participants: Patients with clinically diagnosed uncomplicated enteric fever meeting the inclusion criteria. Interventions: Patients were allocated to receive one of two drugs, Gatifloxacin or Cefixime. The dosages used were Gatifloxacin 10 mg/kg, given once daily for 7 days, or Cefixime 20 mg/kg/day given in two divided doses for 7 days. Outcome Measures: The primary outcome measure was fever clearance time. The secondary outcome measure was overall treatment failure (acute treatment failure and relapse). Randomization was carried out in 390 patients before enrollment was suspended on the advice of the independent data safety monitoring board due to significant differences in both primary and secondary outcome measures in the two arms and the attainment of a priori defined endpoints. Median (95% confidence interval) fever clearance times were 92 hours (84-114 hours) for gatifloxacin recipients and 138 hours (103-164 hours) for cefixime-treated patients (Hazard Ratio [95% CI] = 2.171 [1.545-3.051], p < 0.0001). 19 out of 70 (27%) patients who completed the 7 day trial had acute clinical failure in the cefixime group as compared to 1 out of 88 patients (1%) in gatifloxacin group (Odds Ratio [95% CI] = 0.031 [0.004 - 0.237], p < 0.001). Overall treatment failure patients (relapsed patients plus acute treatment failure patients plus death) numbered 29. They were determined to be (95% confidence interval) 37.6% (27.4%-50.2%) in the cefixime group and 3.5% (2.2%-11.5%) in the gatifloxacin group (HR [95% CI] = 0.084 [0.025-0.280], p < 0.0001). There was one death in the cefixime group. Conclusions: Based on this study, gatifloxacin is a better treatment for uncomplicated enteric fever as compared to cefixime. Trial Registration: Current Controlled Trials ISRCTN75784880

INTRODUCTION

Enteric fever (Typhoid and Paratyphoid fever) is a systemic infection caused by the bacterium Salmonella enterica serovar Typhi (S. typhi) or Salmonella enterica serovar Paratyphi (S. paratyphi) which in humans is transmitted through the fecal-oral route [1,2]. Today the vast burden of disease is encountered in the developing world where sanitary conditions remain poor. The best global estimates are of at least 22 million cases of typhoid fever each year with 200,000 deaths [3]. Currently these are almost exclusively confined to resource poor countries. A recent Cochrane review [4] on typhoid treatments underscored the need for large sample size drug interventional trials, especially in children in whose disease predominate.

In 1948 the introduction of chloramphenicol revolutionized the treatment of typhoid fever [5]. Unfortunately the emergence of resistance to the "first line" antimicrobials for example, ciprofloxacin has been a major setback and has given rise to the possibility of untreatable enteric fever [7]. Gatifloxacin, a relatively inexpensive fluoroquinolone antibiotic in South Asia with recent oral administration, is a new broad spectrum synthetic 8-epi-7-deazafloquinolone which has the lowest minimum inhibitory concentration (MIC) against S. typhi from Nepal [9]. Clinically these are almost exclusively confined to resource poor countries. Cefixime, an orally administered third generation cephalosporin, is a commonly used drug in South Asia for the treatment of enteric fever. Although cefixime is recommended as a drug of choice by the World Health Organization (WHO) for the treatment of resistant typhoid fever [10] it is relatively expensive in South Asia and has to be administered for a longer duration than the currently used chloramphenicol. Clearly there is an urgent need for a treatment [11] that combines ease of oral administration, with speed of clinical response, reduction in secondary transmission and inconvenience. In this open randomized trial, we aimed to compare clinical outcomes for the treatment of uncomplicated enteric fever with gatifloxacin or cefixime in an outpatient setting.

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Competing Interests: The authors have declared that no competing interests exist.

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† These authors contributed equally to this work.
METHODS

Participants

The study was approved by Nepal Health Research Council and Oxford Tropical Ethics Committee. The protocol for this trial and supporting CONSORT checklist are available as supporting information; see Checklist S1 and Protocol S1. We enrolled patients who presented to the outpatient or emergency department of Patan Hospital, Lalitpur, Nepal from June 5, 2005 to September 16, 2005. Patan Hospital is a 318-bed hospital located in the Lalitpur district in Kathmandu Valley. Patients were eligible to enter the study if they had clinically diagnosed enteric fever and their residence was within approximately 2.5 km radius from the hospital. Other inclusion criteria were that patients must be aged between 2 and 65 years, able to take oral medications, non-pregnant and non-lactating, without a history of seizures, able to stay in the city for the duration of the treatment, not known to have concomitant infections or other causative agents and willing to give informed written consent to take part in the study. For children enrolled into the study, written informed consent was taken from a parent. Patients were excluded from the study if they had any signs of complicated typhoid defined as the presence of jaundice, gastrointestinal bleeding, peritonitis, shock, encephalopathy, convulsions, myocarditis or arrhythmia at the time of enrollment. Patients who had received a third-generation cephalosporin or fluoroquinolones in the week prior to presentation to our clinic were also excluded.

Interventions

On presentation to Patan Hospital all patients with fever without an obvious focus were referred to the enteric fever study clinic, where they were seen by the study physician. Patients who fulfilled the inclusion criteria were randomly assigned to receive Cefixime (Breedhaum® Novo) AG Basel, Switzerland); 10 mg/g kg/day [17], in a single dose orally for 7 days or Cefixime (Ciflex™, Aegia, Nærum, Copen) 20 mg/kg/day [17] in two divided doses orally for 7 days. Both drugs were administered in tablet form, cut and weighed in a sensitive scale to ensure that underdosing did not occur. To children who were apprehensive of swallowing the tablet, the drug was embedded in a banana and given. All patients were asked to follow the study drug under direct observation during each visit.

Each patient had hematoxina, total leucocyte count with differential, serum creatinine, total bilirubin, alanine aminotransferase (ALT), and aspartate aminotransferase (AST) measured, and blood and stool cultures were also performed before the start of the study intervention.

The exact location of the patient's home was recorded and the first dose of drug administered at the clinic. We employed five Community Medical Auxiliaries (CMAs) who had all received at least 13 months of prior formal primary health care worker training and been registered in a government recognized institution. The CMAs visited patients twice daily at their homes to perform a clinical examination, measure the oral temperature and give directly observed therapy with the study drugs. The CMA visited the patient's home every 12 hours, morning and evening, until day 10 following enrollment or complete resolution of illness, whichever came later. The oral temperature of the patient was recorded twice every day by the CMA and a note was made of the timing and dosages of antibiotic intake. The quality of patient care was ensured by regular unsupervised supervisory checks in which the study doctor accompanied the CMA during the visits to patients' homes.

CMAs were asked to send patients immediately to the hospital on encountering any severe symptoms, and the patient also were asked to attend clinic if they had any severe symptoms at any other time. A symptom questionnaire was used daily during each visit to monitor any adverse events. Any patient with any severe symptom was seen by the study physician. The CMAs and study physicians held daily case conferences at which all the study patients were discussed.

All patients regardless of the culture results were seen at hospital on Day 10 following enrollment. Blood and stool cultures were repeated on Day 10 in all culture positive patients and thereafter if the patient again became ill with probable enteric fever. All culture positive patients were followed up until six months after enrollment, and stool cultures were performed at the end of the first, third and sixth month.

Microbiological Procedures

Blood culture was performed on media containing tryptone soy broth and sodium polyanethol sulphonate, incubated at 37 C and examined daily for growth over 7 days [11]. Salmonella enterica serotype Typhi or Paratyphi A, B or C isolated in culture were identified using standard biochemical tests and specific antisera (Murex Biotech, Dartford, England). Antibiotic susceptibilities were determined during isolation using the Kirby-Bauer disc diffusion method involving antibiotic discs containing Nalidixic acid, Oxytetracycline, Chloramphenicol, Ampicillin, Cotrimoxazole, Ceftriaxone and Cefixime (Himedia Laboratories, Mumbai, India). Minimum Inhibitory Concentrations (MICs) were determined later for organisms stored in glycerol (bacterial preservative) at −70°C. The MICs were determined by Chlrophyllum, Nalidixic acid, Cefixime, Ceftriaxone and Cefotaxime E-test™ (AB Biodisk, Solna, Sweden), according to the manufacturer's instructions. The sensitivity results were interpreted using Clinical and Laboratory Standards Institute criteria for Enterobacteriaceae.

Objectives

The objective of the study was to compare the efficacy of Cefixime and Ceftriaxone in the treatment of uncomplicated culture positive enteric fever.

Outcomes

The primary outcome was the fever clearance time (FCT). FCT was defined as time to first drop in oral temperature ≤ 37.5°C, remaining ≤ 37.5°C for 48 hours. The secondary outcomes included acute treatment failure. Acute treatment failure was defined as including any severe complication; the persistence of fever (≥ 38°C); the persistence of symptoms for more than 7 days after the start of treatment, requiring additional or rescue treatment. If a patient had a temperature above 37.5° and below 30 for more than 7 days, but did not need additional or rescue therapy, and subsequently their fever cleared by day 10, that patient would not qualify as an acute treatment failure. Patients who failed the study treatment were given rescue treatment.

The rescue drug was Oxytetracycline 20 mg/kg/day orally in two divided doses for 14 days for the Cefixime group, and Ceftriaxone 40 mg/kg/day IV in a single daily dose for 14 days for the Cefixime group. For the Ceftriaxone group alone, if on day 9 of treatment the patient still had a fever of ≥ 38°C, the study drug was continued for 10 days and the patient categorized as acute treatment failure. If the temperature on Day 10 was ≤ 37.5°, rescue treatment was given.

A relapse was defined as fever with a positive blood culture within a month of completing treatment. All the relapses were....
patients that were initially categorized as successfully treated. Any patient given rescue treatment or prolonged treatment was precluded from the "relapse" group.

Patients categorized as "overall treatment failures" included patients experiencing acute treatment failure, plus those falling into the relapsed category, plus all deaths within the trial follow up period.

Sample size
The sample size was calculated to detect a FCT difference of approximately 40 hours between ceftriaxone (assumed median FCT 126 hrs) and ceftiraxone (assumed median FCT 204 hrs) [14] with \( p = 0.05 \) and power = 80%. The accrual time for recruitment was assumed to last 70 days, and that the last patient would be followed up until 8 days after recruitment. Therefore, we estimated the minimum sample size at 235 participants. Assuming a loss to follow-up of 5%, the sample size was calculated as 125 blood culture positive patients in each arm.

Before the recommended sample size had been reached, more 169 blood culture positive patients had been enrolled, the independent data safety monitoring committee (DSMC) advised the Principal Investigators to stop recruitment to the trial based on a prespecified difference (\( p=0.01 \)) between the two treatment arms in the primary endpoint of the study.

Randomization—Sequence generation
Patients were randomized in blocks of 100 from a computer-generated randomization list, by an investigator not involved in patient recruitment or assessment.

Randomization—Allocation concealment
The randomization sequence and block size was concealed from the physicians allocating treatment and managing the patients, prior to patient enrollment. Treatment allocations were kept in sealed opaque envelopes, which were opened only on enrollment of the patients to the study after all inclusion and exclusion criteria had been checked.

Randomization—Implementation
Participants were enrolled by the study physician in the same order in which they presented to the study clinic. The sealed envelopes were opened in strict numeric sequence.

Blinding
Blinding was not feasible in this trial due to logistical reasons.

Statistical methods
All data were entered into an electronic database (Microsoft Office Access, version 2003, WAUSA), and analysis was performed using Stata 9 (Stata Corp LP, Texas, USA). Continuous covariates were compared between groups of patients using the Mann-Whitney test, and categorical covariates were compared using the chi-square test or Fisher's exact test when appropriate. Fever clearance times and time to relapse were analyzed using Kaplan Meier survival curves and compared between the two groups using the logrank test. Binary outcomes (clinical failures) were compared between the two treatment groups using Fisher's exact test. Analyses were done in all randomized patients (intention to treat, IIT) and separately in patients with positive pretreatment culture (per protocol, PP) and negative pretreatment culture.

RESULTS

Participant flow
Of the 482 patients from the study area who were clinically diagnosed with enteric fever, 350 patients were enrolled into the study and randomized. 92 patients were ineligible, the main reason (49 patients) being a history of already having taken antibiotics (fluoroquinolone, macrolide, or third generation cephalosporin) within one week prior to study entry (Figure 1). Among all randomized patients, 187 patients were assigned to receive ceftriaxone and 203 to cefotaxime. 77 patients assigned to receive ceftriaxone were blood culture positive for enteric fever whilst 92 of those assigned to receive ceftriaxone were culture positive. There were unequal numbers of positive patients in each of the study arms. One possible reason for the difference in number of culture positive patients between study arms is that cultures were drawn and culture results obtained after randomization had been done.

Recruitment
We enrolled patients who presented to the outpatient or emergency department of Patan Hospital, Lalitpur, Nepal from June 5, 2000 to September 8, 2003. All enrolled patients were followed up for at least 10 days after recruitment. Patients with a positive pretreatment blood culture were followed up for six months after enrollment.

At the point that the DSMC asked to examine the trial data for the primary outcome measure in positive pretreatment patients, the median fever clearance time was 92 hours (25% CI, 84–114 hours) for the ceftriaxone treated patients and 138 (95% CI, 105–164 hours) for cefotaxime treated patients. The difference between the two treatment arms was 46 hours (\( p=0.0001 \)).

Baseline data
Admission characteristics are shown for all ITT patients (Table 1) and for all PP patients (Table 2). The median age of patients enrolled into the trial was 17 with a range of 2–64 years. There were no baseline differences in the culture positive and culture negative groups, other than temperature at presentation, AST and ALT which were higher and platelet and total WBC which were lower in the culture positive patients as compared to the culture-negative patients. Among all PP patients, there were no differences in the baseline characteristics between the two treatment groups.

There were 49 patients, 15 in the ceftriaxone arm and 25 in the cefotaxime arm, who had taken amoxicillin up to the week before study entry. Of these 4 and 7 were culture-positive respectively.

Numbers analyzed
Analysis was done in all 300 randomized patients (ITT) and separately in 169 patients with positive pre-treatment culture (PP). All endpoints were analyzed in the ITT and PP populations, apart from relapse which was only analyzed in the PP population.

Outcomes and estimation

Primary outcome
In all ITT patients, median (95% confidence interval) fever clearance time was 102 (90–117) hours for the ceftriaxone group and 72 (62–80) hours for the cefotaxime group. Log rank test statistic was 8.84 (\( p=0.003 \)). Hazard Ratio (95% Confidence Interval) was 1.271 (1.466 2.983). The proportion of all patients failing through time to clear fever is shown in Figure 2. At day 7 fever clearance rate was 73.9% (67.0%–80.3%) in ceftriaxone group and 94.3% (90.2%–96.8%) in cefotaxime group.

In the PP group, median (95% CI) fever clearance time was 92 hours (84–114 hours) for ceftriaxone recipients and 138 hours...
Figure 1. Profile of the Trial. The consort flow diagram showing the flow of participants through the trial.

(105–164 hours) for cefixime-treated patients [HR(95% CI) = 2.171 (1.545–3.051), p<0.0001]. The proportion failing to clear fever for each study drug through time after treatment is shown (Figure 5). At day 7 the fever clearance rate was 62.7% [95% CI = 51.5%–73.8%] in the cefixime group and 91.8% [95% CI = 86.8%–96.4%] in the gatifloxacin group.

In the group with negative blood culture but clinically diagnosed enteric fever (Fig 1), the PFT was 92 hours [95% CI = 44–94 hours] for the cefixime group and 39 hours [95% CI = 28–54 hours] for the gatifloxacin group [HR(95% CI) = 1.760 (1.099–2.112), p<0.0001]. Logrank test.

Secondary Outcomes. In the ITT group, overall, 30 out of 167 (18%) in the cefixime group and 2 out of 190 (1%) in the gatifloxacin group were acute clinical failures, OR(95% CI) = 0.049 [0.011–0.207], p<0.001, Fisher’s exact test.

In the PP group, 19 out of 97 (17%) patients who completed the 7-day trial had acute clinical failure in the cefixime recipients as compared to 1 out of 58 (1%) in the gatifloxacin recipients [Odds Ratio [95% CI] = 0.031; [0.004–0.237], p<0.001]. Considering all patients to be failures who dropped out of the study before completion of the seven day treatment course, 26 out of 77 (34%) failed in the cefixime group as compared to 5 out of 92 (5%) in the gatifloxacin group [OR(95% CI) = 0.112 (0.046–0.312), p<0.001].

138 patients were evaluable for relapse; 30 had acute treatment failure and 11 withdrew from the study before day 7. In total, eight relapses (Figure 1) were observed. Relapse rates were 12.4% (6/49) in the cefixime group and 3.6% (2/57) in gatifloxacin group [HR(95% CI) = 0.185 (0.037–0.915), p = 0.0159]. The Kaplan–Meier plots for the time of relapse are shown in Figure 4.

Overall failure (acute treatment failure plus relapse plus death) were 29 in number (Figure 1). Overall failure rate at 1 month was estimated as 37.4% [95% CI = 27.14%–47.52%] in the cefixime group and 9.5% [95% CI = 2.2%–11.9%] in the gatifloxacin group [HR(95% CI) = 0.081 (0.025–0.280), p<0.0001] (Figure 5).

From patients with negative cultures, 11 had acute clinical failures, 10 (out of 91, 10%) in Cefixime group and 1 (out of 103, 1%) in the Gatifloxacin group, OR(95% CI) = 0.006 (0.011–0.600), p = 0.004, Fisher’s exact test.

Similarly, treating drop-out as treatment failures, we had 50 out of 105 (27%) in the Cefixime group and 15 out of 203 (7%) in the Gatifloxacin group acute treatment failures, OR(95% CI) = 0.219 (0.118–0.405), p <0.001, Fisher’s exact test.
Ancillary analyses
Among all culture positive patients in the ceftriaxone group, one patient (1/70, 1.4%) had S. Paratyphi A cultured from her blood on day 10, but there were none (0/65, 0%) positive blood culture growth in the gentamicin group on day 10.
No patient was found to be a persistent carrier of S. Typhi or Paratyphi A in their stool. A positive stool culture for S. Typhi was seen for one patient on day 10 and for another on day 30. Subsequent cultures were negative for both patients. We were able to obtain stool cultures from 147 (28%), 141 (83%), and 130 (77%) pretreatment blood culture positive patients at one, three, and six months respectively.

Microbiology
Antibiotic sensitivity testing revealed that all strains were sensitive to gentamicin, ceftriaxone, cefotaxime or gentamicin. One strain was resistant to chloramphenicol, and 136 (83%) of the pretreatment isolates were sulfonamide acid resistant strains (NARST). Minimum inhibition concentration (MIC) was determined for 16I of the pretreatment blood culture isolates. The median (range) MICs for each antibiotic were as follows: gentamicin 0.123 (0.006 - 0.5) μg/mL, ceftriaxone 0.123 (0.016 - 2.0) μg/mL, sulfonamide acid > 256 (5.0 - > 256) μg/mL, chloramphenicol 0.0 (0.05 - > 1024) μg/mL, cefotaxime 0.123 (0.016 - 16) μg/mL, and amoxicillin 0.123 (0.004 - 0.5) μg/mL.

Adverse events
Among all patients who received ceftriaxone, there was one death, which might have been due to the development of disease-related complications during treatment. This patient was enrolled on the fourteenth day of his illness. On day 6 of treatment the patient complained of reddish stools and petechiae and was immediately admitted to hospital where he developed severe thrombocytopenia and gastrointestinal bleeding. He developed acute respiratory distress syndrome and was mechanically ventilated. He developed disseminated intravascular coagulation and succumbed to his illness on day 21 of entry into the trial. His pretreatment blood culture grew S. Paratyphi A which was sensitive to ceftriaxone with an MIC of 0.32 μg/mL. One patient developed erythema multiforme which needed two doses of oral antihistamines.

Among all patients who received gentamicin there were two patients with excessive vomiting, which required intravenous antibiotics and fluids and observation in the hospital emergency room for more than 6 hours. There were an additional 23 patients who complained of excessive nausea and occasional vomiting after ingestion of the drug. Of these, two needed oral antihistamines, in the remaining 21 patients no intervention was required.

DISCUSSION
Interpretation
In this study examining fever clearance time, acute treatment failure and relapse as indicators of treatment efficacy, that the results raise doubt on the usefulness of ceftriaxone and suggest that ceftriaxone is a potent choice for the treatment of uncomplicated enteric fever.
Fibric acid is one of the most common reasons for presentation to hospitals in many developing countries. In patients with fever, a very common clinical diagnosis is enteric fever, and S.
Table 2. Baseline characteristics at presentation of culture positive patients.

<table>
<thead>
<tr>
<th>PATIENT CHARACTERISTICS</th>
<th>GADIFLAXIN (n=92)</th>
<th>CEFOTAXIM (n=37)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (yr)</td>
<td>18 (11-40)</td>
<td>16 (3-60)</td>
</tr>
<tr>
<td>Number aged &lt; 14 years (%)</td>
<td>27 (29%)</td>
<td>33 (43%)</td>
</tr>
<tr>
<td>Weight (kg)</td>
<td>49 (10-85)</td>
<td>42 (11-70)</td>
</tr>
<tr>
<td>Duration of fever before treatment (days)</td>
<td>5.2</td>
<td>5.4</td>
</tr>
<tr>
<td>Median and range of temperature at presentation(%)</td>
<td>39 (O.0-5)</td>
<td>39 (O.0-40)</td>
</tr>
<tr>
<td>Median and range of WBC at presentation(%)</td>
<td>80 (10-100)</td>
<td>75 (10-100)</td>
</tr>
<tr>
<td>Median and range of Arterial PNI at presentation(%)</td>
<td>75 (75.3%)</td>
<td>56 (75.3%)</td>
</tr>
<tr>
<td>Median and range of Hemoglobin at presentation(%)</td>
<td>43 (5.6%)</td>
<td>42 (5.6%)</td>
</tr>
<tr>
<td>Median and range of Cough at presentation(%)</td>
<td>37 (45.3%)</td>
<td>22 (29%)</td>
</tr>
<tr>
<td>Median and range of Fungal infection at presentation(%)</td>
<td>21 (22%)</td>
<td>20 (22%)</td>
</tr>
<tr>
<td>Median and range of S. pneumonia at presentation(%)</td>
<td>17 (18%)</td>
<td>10 (13%)</td>
</tr>
<tr>
<td>Median and range of Sp. pneumonia at presentation(%)</td>
<td>14 (12%)</td>
<td>8 (10%)</td>
</tr>
<tr>
<td>Median and range of Hematocrit at presentation(%)</td>
<td>10 (10%)</td>
<td>8 (10%)</td>
</tr>
<tr>
<td>Median and range of White Cell Count at presentation(%)</td>
<td>5 (5.4%)</td>
<td>5 (5%)</td>
</tr>
<tr>
<td>Median and range of Monocyte Count at presentation(%)</td>
<td>1.05 (1.0-1.0)</td>
<td>1.0 (1-1)</td>
</tr>
<tr>
<td>Median and range of ALT at presentation(%)</td>
<td>35 (12-155)</td>
<td>35 (12-150)</td>
</tr>
<tr>
<td>Median and range of AST at presentation(%)</td>
<td>33 (14-155)</td>
<td>49 (21-168)</td>
</tr>
<tr>
<td>Median and range of Total bilirubin at presentation(%)</td>
<td>0.65 (0.1-2.5)</td>
<td>0.9 (0.1-2.5)</td>
</tr>
<tr>
<td>Median and range of Positive smear at presentation(%)</td>
<td>9 (9.0%)</td>
<td>5 (9.0%)</td>
</tr>
</tbody>
</table>

Baseline epidemiological, clinical and laboratory features at presentation of all blood culture positive patients showing a comparison between the parrotaxic and patients arms.

**ALT** (U/L) = alanine aminotransferase normal range 5-34 U/L
**AST** (U/L) = aspartate aminotransferase normal range 5-34 U/L

antigens type Typhi and Paratyphi A are the two most commonly isolated pathogens from the blood in febrile patients in our hospital [15]. Before the advent of multi-drug-resistant (MDR) S. Typhi, chloroquine, ampicillin or cotrimoxazole were successfully used as the first line drug in the treatment of enteric fever. After the emergence of MDR strain, fluoroquinolones and third-generation cephalosporins have been suggested and used as alternative antimicrobials [16,13]. However the emergence and spread of point mutations in the gyrA gene of the bacterial genome [17] has conferred resistance to nalidixic acid and reduced susceptibility to the commonly used fluoroquinolones such as ofloxacin, leading to a poorer clinical response [18,19]. A recent study in Viet Nam (CM Pury, unpublished) showed ofloxacin at the dose of 25 mg/kg/day was able to achieve a cure rate in only...
Generalizability

Despite the increased resistance to Nalidixic acid in Kathmandu, and rising MICs to the other fluoroquinolones, gatifloxacin and ofloxacin, gatifloxacin has proven to be a potent drug for the treatment of enteric fever. Our study has relevance to South Asia, as resistance to nalidixic acid is widely prevalent there. Initially there will be emergence of resistance to gatifloxacin in areas with both MDR and NARST, and in this situation alternative antibiotics may need to be used. Of interest, in keeping with anecdotal reports from elsewhere in South Asia, only one strain was resistant to chloramphenicol in the present study. In areas of the world where chloramphenicol susceptibility has reemerged there may be an argument for reusing chloramphenicol.

In the present study Gatifloxacin was associated with nausea in 12% of patients and it may be important to forewarn patients of this possible side effect. There have been sporadic reports of dysglycemia caused by gatifloxacin [24-26], and a recent population-based, case controlled study examining gatifloxacin usage amongst elderly individuals in Canada (mean age 77 years) who developed dysglycemia [27] also raised possible concern. We did not do any blood sugar testing to look for dysglycemia. However in a study involving a younger age group where blood sugar testing was done the results revealed no dysglycemia: 687 children were treated with gatifloxacin (10 mg/kg) for otitis media and were followed for a year with no signs of alteration of glucose homoeostasis either acutely or otherwise [28]. Clearly, it would be prudent to treat diabetics and elderly people suffering from enteric fever with an alternative antibiotic such as amoxicillin and avoid the potential problems in this specific population with gatifloxacin.

Limitations of the study

The DBSMC advised the Principal Investigators in this study to stop enrollment to the trial based on a priori defined difference (p<0.01) between the two treatment arms in the primary endpoints of the study. It is possible that if the trial had been continued with a larger sample size, other important information could have been garnered. In addition if patients and/or investigators had been blinded to treatment assignments, the
study would have been further strengthened; however, as in most typhoid trials, it was not possible to do this due to the difference in dosing schedule for the two drug being compared. Another limitation of this study was that temperature was only measured every 24 hours. In this instance, and to avoid missing increases in temperature, we checked temperatures for 10 days after enrolment, or for 48 hours after resolution of fever, whichever came later, in all patients. Finally, a telephone or interest based system of randomization would be ideal, but such a system does not exist here.

Overall evidence
We have compared the outcomes from our trial with those of other comparable studies, identified from a recent Cochrane review [4], WHO typhoid guidelines [16], and a search of Medline using these terms: "typhoid" and "typhus" and "typhoid fever in children." Overall evidence of treated typhoid fever in children[14]. However other studies have suggested caffeine can be successful in the treatment of enteric fever [29 33]. Overall these studies, both descriptive and randomized, have examining the use of caffeine in confirmed enteric fever (total of 292 patients) and with treatment durations of mostly 14 days, have found failure rates ranging from 4% to 23%. Besides the general underactivity of a longer course with caffeine with increased morbidity and possibly complications, this drug is also more expensive (a 7-day course costs US $7 (Blue Cross Lallah, India)). The present study is the largest randomized controlled trial ever conducted with caffeine in enteric fever and clearly shows, even in a setting with fully sensitive strains, that caffeine helps. These findings are contrary to the recommendation by many sources[3,11] including the World Health Organization[10] that caffeine can be used as first or second line therapy in the treatment of enteric fever. Based on the present study, we believe guidedlines to be an optimal choice in the treatment of uncomplicated enteric fever.

SUPPORTING INFORMATION

Checklist S1 CONSORT Checklist
Found at: doi:10.1371/journal.pone.000542.0001 (0.05 MB DOC)
Protocol S1 Trial Protocol
Found at: doi:10.1371/journal.pone.000542.0002 (0.05 MB DOC)

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Author Contributions

Conceived and designed the experiments: JF BB AP AA JD MZ BY CD BP. Performed the experiments: JF BB AP AA JD MZ BY CD BP. Analyzed the data: KS. Contributed reagents/materials/analysis tools: JF BB AP AA JD MZ BY CD BP. Wrote the paper: JF BB AP AA JD MZ BY CD BP. Other: Helped write the paper: JC KS SD.

REFERENCES


Evolutionary History of Salmonella Typhi

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Abstract

For microbial pathogens, phylogeographic differentiation seems to be relatively common. However, the neutral population structure of Salmonella enterica serovar Typhi reflects the continued existence of ubiquitous haplotypes over millennia. In contrast, clinical use of fluoroquinolones has yielded at least 15 independent gyrA mutations within a decade and stimulated clonal expansion of haplotype H58 in Asia and Africa. Yet, antibiotic-sensitive strains and haplotypes other than H58 still persist despite selection for antibiotic resistance. Neutral evolution in Typhi appears to reflect the asymptomatic carrier state, and adaptive evolution depends on the rapid transmission of phenotypic changes through acute infections.

Many bacterial taxa can be subdivided into multiple, discrete clonal groupings (clonal complexes, or ecotypes) that have diverged and differentiated as a result of clonal replacement, selective sweeps, periodic selection, and/or population bottlenecks (1). Geographic isolation and clonal replacement can also result in phylogeographic differences between bacterial pathogens from different parts of the world (2), even within young, genetically monomorphic pathogens (3) (supporting online material text) such as Mycobacterium tuberculosis (4) and Pseudomonas aeruginosa (5). Typhi is a genetically monomorphic (6), human-restricted bacterial pathogen that causes 21 million cases of typhoid fever and 200,000 deaths per year, predominantly in southern Asia, Africa, and South America (7). Typhi also enters a carrier state in rare individuals (such as Mortimer’s example of “Mr. W. the milkman” (8)), who can shed high levels of these bacteria for decades in the absence of clinical symptoms. Genome sequences are available from strains CT18 (9) and Ty2 (10), but the global diversity, population

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genetic structure, and evolutionary history of Typhi were poorly understood. It has been speculated that Typhi evolved in Indonesia, which is the exclusive source of isolates with the z66 flagellar antigen (11).

We investigated the evolutionary history and population genetic structure of Typhi by mutation discovery (12) within 200 gene fragments (~500 base pairs each) from a globally representative strain collection of 105 strains. The 200 genes included 121 housekeeping genes, 50 genes encoding cell surface structures, regulation, and pathogenicity; and 29 pseudogenes. Site variation of a poly-T67 homopolymeric stretch within one gene fragment was inconsistent with other phylogenetic patterns (homoplasies) and this fragment was excluded from further analysis. The other 199 gene fragments cover 88,789 base pairs, or 1.82% of the genome. Sixty-six were polymorphic as a result of 88 alternative allelic states [biallelic polymorphisms (BiPs)], for a frequency of approximately one BiP per kilobase. Five of the 88 BiPs probably represent three independent recombination events. Four seem to reflect two similar imports spanning 24 to 25 kb from S. enterica serovar Typhimurium (fig. S1), and a gene fragment with six single-nucleotide polymorphisms (SNPs) is identical to the corresponding gene fragment in S. enterica serovar Paratyphi A. The other 83 BiPs consisted of 37 nonsynonymous SNPs, 3 of which resulted in premature stop codons; 33 synonymous SNPs; 12 SNPs in pseudogenes; and one deletion of 4 base pairs.

We anticipated that housekeeping genes would exhibit diminished levels of nucleotide diversity, π, as a result of purifying selection, and that pathogenicity genes would exhibit elevated levels as a result of diversifying selection. However, π did not differ significantly with gene category (P > 0.05, analysis of variance) (table S1). Purifying selection should result in Ks/Ks (the ratio of nonsynonymous substitutions per nonsynonymous site to synonymous substitutions per synonymous site) values that are less than 1.0 and diversifying selection should result in ratios higher than 1.0. A trend in this direction was observed (table S1), but it was not particularly strong. We therefore concluded that these 88 BiPs largely reflect the lack of strong selection and are markers of neutral population structure in Typhi. It was somewhat surprising that a supposedly obligate pathogen such as Typhi should possess a neutral population structure, but the population structure of several other bacterial species that occasionally cause disease can also be explained by neutral genetic drift (13).

The distribution pattern of the 88 BiPs within Typhi is highly unusual because it is fully parsimonious according to maximum parsimony analysis (homoplasy index = 0). The 88 BiPs defined 59 haplotypes that form a unique path within a single minimal spanning tree of length 88, except for three hypothetical nodes (Fig. 1). These observations suggest that each BiP was caused by a unique genetic event, either a single mutation (83 BiPs) or the three imports described above (5 BiPs). The tree contains 19 informative BiPs that mark the evolutionary history of Typhi plus 69 noninformative BiPs that are specific to single haplotypes. A second, highly unusual feature of this data set is that the ancestral node, haplotype H45, is represented by extant bacteria. H45 must be the ancestral "root" node, because it possesses the identical nucleotides for all 82 SNPs, as did eight genomes of S. enterica of other serovars, whereas all other haplotypes result from one or more mutations. The general appearance of the tree (Fig. 1) suggests descent from H45 in multiple lineages, followed by diversification during multiple, independent population expansions that resulted in radial clusters of haplotypes containing the noninformative BiPs. For example, one cluster contains all seven Indonesian isolates with the z66 flagellar variant. The z66 cluster radiates from a single haplotype, indicating that it has arisen only once. Hence, z66 isolates cannot represent the evolutionary source of Typhi (11), because the z66 cluster is distant from H45.

The haplotype tree has a third, highly unusual feature: Most links between sequential haplotypes consist of single SNPs, and many longer edges, including one hypothetical node,
were resolved into steps of single SNPs when additional strains were surveyed (fig. S2). Even within this initial sample of 105 isolates, almost half of the mutational steps during the evolutionary history of Typhi are represented by extant haplotypes, indicating long persistence of individual haplotypes. If ecotypes associated with periodic selection were to exist within Typhi, the genetic continuum between haplotypes implies that ecotypes are subdivisions of haplotypes. Furthermore, haplotypes and haplotype clusters were found in multiple continents. For example, it is unclear where H45 evolved, because it has been isolated from five locations in Asia, Africa, and North America (3). Because each BIP is associated with a single, genetic event, each haplotype or haplotype cluster that is present in multiple continents marks at least one independent wave of global transmission. Global transmission has not been previously described for Typhi but is a well-known phenomenon with other human pathogens.

To place the time scale associated with neutral evolution in context, we calculated the time since the most recent common ancestor (tmrca) and the effective population size (N_e) from the selectively neutral data in Fig. 1. These calculations were performed with the use of two estimates of the molecular clock rate, a high rate corresponding to the long-term rate of accumulation of synonymous mutations between *Escherichia coli* and *S. enterica* (5) and a clock rate one-fifth as high, corresponding to the rate of accumulation of all mutations in conserved housekeeping genes between these species (14). For Typhi, tmrca is 10 to 43 thousand years (95% confidence limits of 5.7 to 15.8 thousand years for the high clock rate and 25.5 to 71 thousand years for the low rate) according to both Bayesian skyline plots (15) and maximum likelihood trees (fig. S3). Based on the same clock rates, N_e is currently 2.3 × 10^6 to 1.0 × 10^7 (confidence limits of 1.2 × 10^6 to 9.3 × 10^6 for the high clock rate and 5.3 × 10^6 to 4.1 × 10^6 for the low clock rate) (fig. S3A). Similar values were obtained from the nucleotide variation, θ_Mt, by an independent method (16) (table S1). The maximum likelihood tree also suggests that H45, the ancestral haplotype, and multiple descendent haplotypes arose after human migrations out of Africa but before the Neolithic period (fig. S3B).

The existence of an asymptomatic human carrier state for typhoid is formally similar to tuberculosis, for which the reactivation of granulomas after decades results in delays of centuries between initial new infections and subsequent epidemic peaks (17). Likewise, we propose that the human carrier state allowed persistence of infection with Typhi during periods of isolation and was essential for transmission between hunter-gatherer groups. Hence, the population structure and geographical distribution of Typhi may largely reflect the frequency of carriers.

The 55 polymorphic coding gene fragments (excluding pseudogenes) were screened by mutation discovery with 59 additional strains that were isolated between 1958 and 1967 from Africa and Vietnam. All but three strains were assigned to known haplotypes from the global sample (fig. S4). Twelve haplotypes were isolated on multiple occasions over a range of 22 to 44 years from eight countries (Table 1), demonstrating that Typhi haplotypes persist in single countries for decades, or longer. For example, CT18 (9) is a multidrug-resistant (MDR) strain of haplotype H1 that was isolated in Vietnam in 1993, soon after multidrug resistance emerged. However, a Vietnamese isolate from 1967 was also of haplotype H1, showing that H1 was present in Vietnam long before multidrug resistance emerged. The long-term persistence of Typhi may also reflect the carrier state and can help explain why Typhi remains endemic in regions of the world with poor drinking-water quality and limited sewage treatment (18).

Antibiotic-resistant typhoid fever has recently become an enormous public health problem in southern Asia because of the emergence of MDR Typhi followed by nalidixic acid resistance (NAL) with concomitant reduced susceptibility to fluoroquinolones (19). Fluoroquinolones were first used for antibiotic therapy in southeast Asia in 1989 (20) and NAL-resistant Typhi were reported in 1991 (21). Such strong selection should have led to a population expansion of
Naïve Typhi, and possibly to clonal replacement of existing haplotypes within southern Asia. We therefore performed mutation discovery with the 55 polymorphic coding fragments on 295 additional strains of Typhi that were isolated from southern Asia between 1990 and 2004. Again, most strains were assigned to known haplotypes and only a few defined new, peripheral haplotypes (Fig. 2E). However, the relative frequencies of isolates differed from those in the global set of 105 strains (Fig. 1), because most recent isolates from southern Asia, particularly Naïve isolates, belonged to haplotype HS8 (Fig. 2E). Thus, a recent population expansion of HS8 seems to have resulted from the general use of fluoroquinolones.

We also investigated the genetic diversity of a 489-base pair fragment of the gyrA gene encoding a DNA gyrase subunit, within which nonsynonymous mutations at codons 83 and 87 result in resistance to nalidixic acid (22). All 125 strains that were sensitive to nalidixic acid (Naïve) and all other strains with unknown resistance to nalidixic acid possessed the ancestral gyrA1 sequence. In contrast, all 119 Naïve strains, most of which were isolated in central south or southeast Asia (table S2), possessed one of six nonsynonymous mutations at codons 83 and 87 of gyrA (Fig. 2A), and no other mutations were detected in gyrA (or parC). We identified 13 independent mutational events (A through O in Fig. 2B) in distinct haplotypes that also possessed gyrA1 alleles. Assuming that they all arose between 1991 and 2004 (13 years), the identification of ≥15 mutations in two codons (6 base pairs) yields a minimum frequency of 0.19 per base pair per year, ≥2.5 × 10^8 greater than the long-term mutation clock rate within E. coli (14).

For most haplotypes with gyrA mutations, Naïve strains were detected only once or twice; however, Naïve variants of haplotype HS8 and its derivative haplotypes (H34, H57, and H60 to H65) were isolated in Vietnam, India, and Pakistan, and other countries in southern Asia (Table 2). These Naïve variants represent at least five distinct gyrA mutations (K, L, M, N, and O), which were rare or before the mid-1990s (Fig. 2C). The frequency of mutation L has remained fairly constant since the mid-1990s, but HS8 isolates with mutation K seem to have become more common in recent years, particularly in Vietnam (Table 2).

These results show that selection for antibiotic resistance has probably led to clonal expansion of HS8 and its Naïve derivatives in southern Asia. These strains have now also reached Africa, given that one MDR HS8 strain (isolated in Morocco in 2003) was included among nine rare, recent MDR isolates from Africa and that the sole MDR Naïve isolate from Africa that was tested (mutation K, isolated in central Africa in 2004) also belonged to HS8 (Table 2). Thus, HS8 is probably not ethnically restricted to southern Asia, and nalidixic acid-resistant typhoid fever may soon present an additional public health problem in Africa.

Despite the selection for resistance to nalidixic acid in southern Asia, the data do not show complete clonal replacement, which would be expected from periodic selection; about 20% of Typhi isolated in recent years in northern Vietnam and 5% of Typhi from southern Vietnam remain susceptible to nalidixic acid, as are many other recent HS8 isolates (Fig. 2C). Furthermore, recent isolates from southern Asia also belong to other haplotypes, where mutations in gyrA are rare (Fig. 2B). Thus, the population structure indicative of neutral evolution has not been disrupted by strong selection for resistance to nalidixic acid during the past 15 years, except for the clonal expansion of HS8. Possibly gyrA mutations in many haplotypes reduce fitness (23) or some cases of typhoid fever have not been treated with fluoroquinolones. But still another alternative is that the population structure of Typhi reflects two distinct epidemiological dynamics associated with different time scales: first, the human carrier state permitting slow neutral evolution (millennia), and second, infectious transmission facilitating a rapid response to selection in real time. Outbreaks of infections, similar to the recent expansion of HS8 in southeast Asia, may be responsible for independent chains of intercontinental transmission. These, in turn, create a global distribution of carriers for multiple...
haplotypes. According to this interpretation, it is exactly because the environment selects that everything is everywhere in Typhi, thus inverting a hotly disputed (24) tenet of microbial ecology that was proposed by L. G. M. Basa Becking in 1934 (25).

The results presented here open multiple avenues for future research. Long-term epidemiology with larger strain collections is now possible on the basis of neutral SNPs (fig. S2), whereas classical microbiological methods do not seem to provide reliable markers for such purposes (table S3). Surveillance of haplotypes is particularly appropriate to provide early warning of the continued spread of Na? H58. Our overview of the current global population diversity in Typhi will allow comparisons of genomic sequences from representative strains without the risk of phylogenetic discovery bias (26). Finally, we suggest that the human carrier state may be of much greater importance for neutral evolution and genetic buffering than had been previously appreciated, an interpretation that would demand major changes in public health campaigns to reduce the incidence of typhoid.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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References and Notes

3. Materials and methods are available as supporting material on Science Online.
Fig. 1.
Minimal spanning tree of 105 global isolates based on sequence polymorphisms in 199 gene fragments (88,739 base pairs). The tree shows 59 haplotypes (nodes) based on 88 B1Ps, the continental sources of which are indicated by colors within pie charts. The numbers along some edges indicate the number of B1Ps that separate the nodes that they connect; unlabeled edges reflect single B1Ps. The genomes of the CT18 and Ty2 strains have been sequenced (GenBank accession codes AL513382 and AE014613, respectively). z66 refers to a flagellar variant that is common in Indonesia (11).
Fig. 2. Selection for mutations in gyrA versus a neutral population framework in 483 strains. The strains consisted of 105 global isolates (Fig. 1), 59 older isolates from Africa and Vietnam (1958 to 1967) (Fig. 54 and Table 1), and 317 isolates from southeast Asia (1984 to 2004) and other sources. (A) Sequence of codons 81 to 89 of gyrA, showing all mutated nucleotides (bold) that were detected within a 489-base pair stretch. Each mutation is designated by the name of the resulting amino acid and codon position (left). NAS, nalidixic acid sensitive. (B) Minimal spanning tree of 85 haplotypes based on 97 bps within 55 polymorphic genes. Sizes of circles and arcs reflect numbers of isolates. Strains without mutations in gyrA are shown in white, whereas strains with mutations are indicated by colored arcs that correspond to the colors in (A). The 15 letters indicate independent mutations associated with resistance to nalidixic acid. (C) Time course of isolation of 118 isolates of haplotype H58 or its derivative haplotypes H34, H37, and H60 to H65. These isolates were selected for haplotyping and gyrA genotyping without prior knowledge of their susceptibility to nalidixic acid. Fifty-two other H58 isolates from Vietnam are not included because they were a nonrandom sample of NalR bacteria. The apparent increase of Pho83 in 2004 is based on a sample from the Mekong Delta province of Vietnam and may represent an outlier.

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<table>
<thead>
<tr>
<th>Haplotype</th>
<th>Persistence (years)</th>
<th>Years persisted</th>
<th>No. of isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vietnam</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>H1</td>
<td>37</td>
<td>1967-2004</td>
<td>25</td>
</tr>
<tr>
<td>H50</td>
<td>37</td>
<td>1950-1996</td>
<td>3</td>
</tr>
<tr>
<td>Madagascar</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>H15</td>
<td>31</td>
<td>1965-1996</td>
<td>4</td>
</tr>
<tr>
<td>H20</td>
<td>33</td>
<td>1967-2000</td>
<td>2</td>
</tr>
<tr>
<td>Algeria</td>
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</tr>
<tr>
<td>H36</td>
<td>34</td>
<td>1966-2000</td>
<td>3</td>
</tr>
<tr>
<td>Ivory Coast</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>H39</td>
<td>34</td>
<td>1967-2001</td>
<td>4</td>
</tr>
<tr>
<td>HR1</td>
<td>35</td>
<td>1987-2002</td>
<td>2</td>
</tr>
<tr>
<td>Senegal</td>
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<td></td>
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</tr>
<tr>
<td>H39</td>
<td>22</td>
<td>1966-1988</td>
<td>4</td>
</tr>
<tr>
<td>H32</td>
<td>39</td>
<td>1982-2001</td>
<td>4</td>
</tr>
<tr>
<td>Congo</td>
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<td></td>
</tr>
<tr>
<td>H46</td>
<td>34</td>
<td>1960-2000</td>
<td>3</td>
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<tr>
<td>Morocco</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>H52</td>
<td>34</td>
<td>1986-2000</td>
<td>2</td>
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<tr>
<td>Cameroon</td>
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<tr>
<td>H77</td>
<td>44</td>
<td>1958-2002</td>
<td>2</td>
</tr>
</tbody>
</table>
Table 2

Geographic sources of haplotypes with gyr mutations by haplotype. Where more than one isolate was found in a country, the number of isolates is indicated in parentheses.

<table>
<thead>
<tr>
<th>Haplotype</th>
<th>gyr‡ mutation (isolates)</th>
<th>gyr‡* (isolates)</th>
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</thead>
<tbody>
<tr>
<td>H15</td>
<td>A: India</td>
<td>Global (1)</td>
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<tr>
<td>H50</td>
<td>B: India</td>
<td>Global (55)</td>
</tr>
<tr>
<td>H12</td>
<td>E: India, F: Pakistan</td>
<td>Global (26)</td>
</tr>
<tr>
<td>H1</td>
<td>G: Vietnam</td>
<td>Vietnam (23), Laos (7), Bangladesh</td>
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<td></td>
<td>H: Vietnam</td>
<td>Indonesia</td>
</tr>
<tr>
<td>H55</td>
<td>I: India</td>
<td>Morocco, Pakistan, Indonesia</td>
</tr>
<tr>
<td>H52</td>
<td>J: India (2)</td>
<td>Global (5)</td>
</tr>
<tr>
<td>H58</td>
<td>K: Vietnam (46), Pakistan (5), India (6), Cambodia, Nepal, central Africa,</td>
<td>Vietnam (31), India (12), Laos (5), Pakistan (5), Hong Kong (2), Bangladesh, Sri Lanka, Morocco</td>
</tr>
<tr>
<td></td>
<td>L: India (6), Bangladesh (6), Vietnam (5), Indonesia</td>
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</tr>
<tr>
<td></td>
<td>M: Pakistan (2)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>N: Vietnam</td>
<td></td>
</tr>
<tr>
<td></td>
<td>O: Pakistan</td>
<td></td>
</tr>
<tr>
<td>1D4, 1D5, and 1D6-65</td>
<td>K: Vietnam (6), Bangladesh (2)</td>
<td>Nepal, Laos</td>
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<td></td>
<td>L: India (2)</td>
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