TLR4 genetic variation is associated with inflammatory responses in Gram-positive sepsis


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ABSTRACT

Objectives: To identify important pathogen recognition receptor (PRR) pathways regulating innate immune responses and outcome in Staphylococcus aureus sepsis.

Methods: We analysed whether candidate PRR pathway genetic variants were associated with killed S. aureus–induced cytokine responses ex vivo and performed follow-up in vitro studies. We tested the association of our top-ranked variant with cytokine responses and clinical outcomes in a prospective multicentre cohort of patients with staphylococcal sepsis.

Results: An intronic TLR4 polymorphism and expression quantitative trait locus, rs1927907, was highly associated with cytokine release induced by stimulation of blood from healthy Thai subjects with S. aureus ex vivo. S. aureus did not induce TLR4-dependent NF-κB activation in transfected HEK293 cells. In monocytes, tumor necrosis factor (TNF)–β release induced by S. aureus was not blunted by a TLR4/MD-2 neutralizing antibody, but in a monocyte cell line, TNF–β was reduced by knockdown of TLR4. In Thai patients with staphylococcal sepsis, rs1927907 was associated with higher interleukin (IL)-6 and IL-8 levels as well as with respiratory failure. S. aureus–induced responses in blood were most highly correlated with responses to Gram-negative stimulants whole blood.

Keywords:
Genetic
Humans
Immunity
Sepsis
Staphylococcus
Introduction

The incidence of Gram-positive sepsis has been continually increasing in recent years and is the predominant type of sepsis in the United States [1]. *Staphylococcus aureus* is the most common Gram-positive organism implicated in severe sepsis, with a mortality rate of 30% [2]. Infection with *S. aureus* can be acquired in both community and healthcare settings, and methicillin resistance in both arenas is a major ongoing concern. A better understanding of the host–pathogen interaction that may lead to novel approaches to treating Gram-positive sepsis is therefore of paramount importance.

Pattern recognition receptors (PRRs) on host immune cells mediate much of the inflammatory response to infection upon activation by conserved pathogen-associated molecular patterns (PAMPs) [3]. The PAMP-PRR interaction is a central driver of the host response in sepsis, and a better comprehension of the PAMP-PRR axis in human sepsis may unveil new targets for therapeutic exploitation. As a Gram-positive organism, *S. aureus* cell wall components activate membrane-bound PRRs such as Toll-like receptor (TLR) 2 (as a heterodimer with TLR1 or TLR6) and cytoplasmic NOD-like receptors [4]. Many of these PRRs are also activated by PAMPs of Gram-negative organisms [3]. Lipopolysaccharide (LPS) has long been considered to be an essential precipitant of the host inflammatory response to Gram-negative infection, however [5]. In contrast to Gram-negative organisms, *S. aureus* does not express LPS. Although various PRRs may be activated by different bacteria, downstream signaling pathways may converge or be interrelated [3]. It remains unclear whether and how the fundamental inflammatory pathways activated in Gram-positive and Gram-negative sepsis differ from one another and drive outcome [6].

Innate immune genetic variation modulates the host response to infection [7]. We hypothesized that key PRR genes regulating inflammatory responses to *S. aureus* sepsis could be identified by identifying human genetic variation associated with cytokine production and clinical outcome. To test this hypothesis, we assessed the relationship between *ex vivo* blood cytokine responses to *S. aureus* and PRR pathway genetic variation in a large cohort of healthy individuals, then validated our findings in a prospective multicentre cohort of patients with staphylococcal sepsis.

Methods

**Ex vivo blood stimulation assays**

Three hundred healthy Thai subjects donating blood at the blood donation centre at Sunpasitthiprasong Hospital, Ubon Ratchathani, Thailand, were recruited for a blood sample as previously reported [8]. Those who met enrollment criteria gave written informed consent to participate and provided a postdonation blood sample in citrate tubes. A batch of 96-well immunoassay plates was generated by adding 20 µL of stimuli in appropriate concentrations to each well. Plates were frozen at −80 °C until the day of use, when they were thawed to 37 °C. Fresh whole blood (380 µL) anti-coagulated with citrate and mixed 1:1 with RPMI media was added to each well [8]. Final concentrations of stimuli were as follows: whole heat-killed *S. aureus* strain Newman 2.5 × 10^7 CFU/mL and 5.0 × 10^7 CFU/mL, whole heat-killed *Burkholderia pseudomallei* K96243 2.5 × 10^7 CFU/mL, *Salmonella typhimurium* flagellin 500 ng/µL, *Pam3CSK4* 100 ng/µL (InvivoGen, San Diego, CA, USA), *Pam2CSK4* 100 ng/µL (InvivoGen), MDP (10-meramyl dipeptide) 10 µg/µL (InvivoGen), TriDAP 10 µg/µL (InvivoGen), *Escherichia coli* O111:B4 LPS 10 ng/µL (List Biological Laboratories, Campbell, CA, USA) and *Salmonella minnesota* Res595 LPS 10 ng/µL (List Biological Laboratories). Plates were placed on a shaker at 37 °C under 5% CO2 for 6 hours before being spun down; the plasma supernatant was removed and frozen at −80 °C. Monocyte counts were performed in the hospital clinical laboratory.

**Staphylococcal sepsis study**

A prospective observational study of community onset *S. aureus* sepsis was conducted at four hospitals in northeast Thailand between March 2010 and December 2013 [9]. Study sites were Sunpasitthiprasong Hospital, Ubon Ratchathani; Udon Thani Hospital, Udon Thani; Sirinagarind Hospital, Khon Kaen; and Khon Kaen Hospital, Khon Kaen. Potential study patients were identified by daily screening at each hospital diagnostic microbiology laboratory for clinical samples taken from sterile sites that grew a pure growth of *S. aureus*. Subsequent genetic analysis of isolates revealed that a minority subset (19%) were *S. argenteus* [9], a recently described closely related *Staphylococcus* species that is indistinguishable from *S. aureus* in the diagnostic laboratory. Written informed consent was obtained from all patients or their designee. Inclusion criteria were as follows: age at least 14 years (who are admitted to the adult wards), positive culture taken within 2 days of hospital admission or after 2 days when sampling from a patient admitted with suspected infection was delayed and at least two of four systemic inflammatory response criteria met within 48 hours of culture. These criteria were as follows: temperature <36 °C or >38 °C, heart rate >90 beats per minute, respiratory rate >20 breaths per minute or PaCO2 <32 mm Hg or requiring mechanical ventilation, white blood cell count <4000 or >12 000 cells/µL or >10% band forms. Baseline clinical information was obtained from the medical records. Blood was drawn at the time of enrollment, and plasma was separated and frozen at −80 °C. Patients were followed until hospital discharge, and mortality was ascertained on the 28th day. Respiratory failure was defined as requirement for mechanical ventilation; shock was defined as requirement for vasopressors or inotropes.

LPS and TLR4-stimulation assays

The presence of LPS in the heat-killed *S. aureus* strain Newman preparation was determined by *Limulus* Ameocyte Lysate gel-clot

Conclusions: A genetic variant in TLR4 is associated with cytokine responses to *S. aureus* ex vivo and plasma cytokine levels and respiratory failure in staphylococcal sepsis. While *S. aureus* does not express lipopolysaccharide or activate TLR4 directly, the innate immune response to *S. aureus* does appear to be modulated by TLR4 and shares significant commonality with that induced by Gram-negative pathogens and lipopolysaccharide.
assay (Associates of Cape Cod, East Falmouth, MA, USA) according to the manufacturer's instructions (sensitivity 0.03 EU/mL). TLR4-dependent NF-κB activation by S. aureus was assessed by stimulation of hTLR4/hMD-2/hCD14-transfected HEK293 cells, using a modified version of a previous approach [10]. Cells were cultured in a 96-well flat-bottomed tissue culture plate at 35 000 cells per well in Dulbecco modified Eagle medium (DMEM) plus 10% fetal bovine serum and 1% L-glutamine. The following day, cells were transiently transfected with 100 μL of transfection mixture comprising plasmid, transfection reagent (Polyfect; Qiagen, Valencia, CA, USA) and DMEM. DNA was added in the following amounts per well: ELAM mids, transfection reagent (Polyfect; Qiagen, Valencia, CA, USA) and lysis buffer (Promega, Madison, WI, USA), and NF-κB was activated in 10 μL of lysis by the ratio of firefly to Renilla luciferase light emission by the use of the Dual-Luciferase reporter system (Promega).

**Primary monocyte/monocyte cell line stimulations and TLR4 knockdown**

Peripheral blood mononuclear cells were isolated from blood obtained from fasting subjects who avoided recent strenuous exercise drawn into 8 mL Vacutainer CPT tubes (Becton Dickinson (BD), San Diego, CA, USA). Subjects were between 18 and 65 years of age, weighed between 100 and 350 pounds, were of Southeast Asian ancestry, had no chronic medical conditions, were not pregnant and had not delivered a child in the last 9 months, were nonsmokers, took no medications other than oral contraceptives and had no recent illness or vaccinations. Peripheral blood mononuclear cells were further processed to monocytes using the Monocyte Isolation Kit II (Miltenyi Biotec, San Diego, CA, USA). Monocytes were plated in a 96-well plate at 50 000 cells per well and rested overnight in complete RPMI media (10% fetal bovine serum, 1% L-glutamine). The next day, cells were treated with a monoclonal TLR4/MD-2 neutralizing antibody (mab-htr4md2, InvivoGen) or control isotype antibody (mabg1-ctrlm, InvivoGen) at 20 μg/mL, 1 hour before addition of stimulus. Cells were stimulated for 6 hours with LPS from B. pseudomallei (InvivoGen), derived from the human THP-1 monocyte cell line, at a concentration of 1 ng/mL or heat-killed S. aureus or E. coli O111:B4 LPS (List Biological Laboratories, Campbell, CA, USA) as a positive control. After 48 hours of incubation, transfected cells were stimulated with heat-killed S. aureus or E. coli O111:B4 LPS (List Biological Laboratories, Campbell, CA, USA) as a positive control. After 4 hours, cells were washed with phosphate-buffered saline and lysed with passive lysis buffer (Promega, Madison, WI, USA), and NF-κB activation was determined in 10 μL of lysate by the ratio of firefly to Renilla luciferase light emission by the use of the Dual-Luciferase reporter system (Promega).

**Cytokine and chemokine measurements**

Cytokine/chemokine assays were performed using Luminex multiplex bead system with RD Systems reagents or enzyme-linked immunosorbent assay (BD; and RD Systems, Minneapolis, MN, USA).

**Statistical analyses**

Continuous data following a normal distribution are reported as mean ± standard deviation; continuous data following a nonnormal distribution are reported as median ± interquartile ranges. Plasma cytokine data were log10 transformed before analysis, given their generally nonnormal distribution. For the immunoassay data set, cytokine correlations were assessed using a Pearson correlation coefficient, and correlation matrices were used to created heat maps [12] and relatedness dendrograms. To maximize power for identifying genetic associations, a composite cytokine response was created. The monocyte-normalized responses for five cytokines (interleukin (IL)-6, IL-8, tumor necrosis factor (TNF)-α, granulocyte-colony stimulating factor (G-CSF) and IL-1β) were summed after subtracting the mean and dividing by the standard deviation of the 300 observations within each cytokine. These cytokines were chosen on the basis of the relatedness score in a cluster dendrogram. Linear regression of each SNP on composite cytokine response was performed assuming an additive genetic model, adjusting for log monocyte count. Eight of the 51 SNPs had observed minor allele frequencies of <0.05 and were removed from the primary analysis because of low power in the face of multiple test adjustment, leaving 43 SNPs for testing with the composite DNA.
cytokine outcome. Adjustment for multiple testing was done via permutation testing [13]. The distribution of the ordered p values under the null hypothesis was produced by permuting the outcomes 2000 times and recomputing the 43 p values for each permutation. The distribution of the minimum of the 43 p values for each of the permutations was compared with the observed minimum p value to obtain the probability of observing this minimum under the null hypothesis (i.e. a multiple-test corrected p value). Corrected p values for the second and third most significant SNPs (and so on) were obtained analogously. Associations were considered significant if the corrected p value was ≤0.05. Further tests of association of candidate SNPs with individual cytokines were performed on log10-transformed cytokine data using linear regression, adjusting for log monocyte count, again assuming an additive genetic model. For monocyte/monocyte cell line experiments, data were analysed with the t test. For the clinical study, association of genotype with cytokine response or clinical outcome was performed with Fisher’s exact test (for clinical outcomes) or with regression, adjusting for age, sex, comorbidity index and site. The comorbidity index is a 10-point score, with 1 each given for lung disease, heart disease, kidney disease, liver disease, neurologic disease, haematologic disease, autoimmune disease, cancer, diabetes and alcoholism. Secondary analyses were performed adjusting for bacterial species. Analyses were performed by Stata 11.2 software (StataCorp, College Station, TX, USA), or R (R Foundation for Statistical Computing, Vienna, Austria; http://www.r-project.org/).

Ethics

Ethical approval was obtained from the ethics committees of the following institutions: Faculty of Tropical Medicine, Mahidol University, Bangkok; Sunpasitthiprasong Hospital, Ubon Ratchathani; Udon Thani Hospital, Udon Thani; Khon Kaen Hospital, Khon Kaen; and Faculty of Medicine (Srinagarind Hospital), Khon Kaen University, Khon Kaen, Thailand; and the University of Washington, Seattle.

Results

S. aureus induces robust inflammatory responses in blood

To evaluate the inflammatory response to S. aureus in human blood, we assayed pro- and anti-inflammatory cytokines and chemokines in plasma after stimulation of fresh whole blood from 200 healthy individuals with two different concentrations of heat-killed S. aureus (Fig. 1A). As expected, S. aureus induced significant increases above baseline values for all mediators (IL-1ra, IL-1β, IL-6, IL-8, IL-10, TNF-α, G-CSF and monocyte chemotactic protein (MCP)-1), with considerable interindividual variation in responses.

A human TLR4 variant is associated with cytokine responses to S. aureus

We next analysed the association of candidate PRR pathway genetic variants with cytokine responses induced by S. aureus. We generated a composite cytokine response by performing pairwise comparisons between different cytokines produced from whole blood of each donor after activation with S. aureus and creating a cluster dendrogram based on intermediator relatedness scores (Fig. 1B). The most closely related mediators were IL-1β, IL-8, G-CSF, IL-6 and TNF-α (r = 0.6–0.9). We selected these mediators to use as the composite measure. We genotyped 96 SNPs in candidate PRR pathway genes, selected as described in the Methods, in all 300 subjects. Five assays failed and 39 assays had no variation. One assay was excluded because of a call rate of <97%. The remaining 51 variants are listed in Supplementary Table S1. Eight variants had observed minor allele frequencies (MAF) of <0.05 and were excluded because of low power. Forty-three variants were tested for an

![Fig. 1. SNP in TLR4 is associated with Staphylococcus aureus–induced cytokine release. (a) IL-1ra, IL-1β, IL-6, IL-8, IL-10, TNF-α, G-CSF and MCP-1 were measured in plasma supernatants by multiplex bead assay after stimulation of fresh whole blood from 300 healthy individuals with heat-killed S. aureus 2.5 × 10⁷ CFU/mL (S. aureus low) or 5 × 10⁷ CFU/mL (S. aureus high) for 6 hours at 37°C. Data are displayed on log scale. Boxes show median and interquartile range; whiskers show upper and lower adjacent values; outside values are not shown for clarity. All mediators induced by S. aureus are significantly greater than in unstimulated blood (p <0.001 for all). (b) Cluster dendrogram created from relatedness scores calculated from pairwise comparisons between cytokines induced by stimulation of whole blood with S. aureus 2.5 × 10⁷ CFU/mL used to derive composite outcome measure of TNF-α, IL-6, IL-8, G-CSF and IL-1β responses. (c) QQ plot (expected vs. observed log10 (1/p values)) for association of 43 SNPs with composite outcome of S. aureus–induced cytokine levels demonstrating several lower-than-expected p values (higher-than-expected log10 (1/p values)). Lowest p value is rs1927907, intronic SNP in TLR4. G-CSF, granulocyte-colony stimulating factor; IL, interleukin; MCP, monocyte chemotactic protein; SNP, single nucleotide polymorphism; TNF, tumor necrosis factor.](image-url)
association with cytokine response. We tested the association of each variant with the composite *S. aureus*-induced cytokine cluster (Fig. 1C). The top-ranked variant associated with cytokine response to *S. aureus* with p < 0.05 (adjusted for multiple comparisons via the permutation test) and a false discovery rate < 0.05 was rs1927907, an intronic TLR4 polymorphism that exchanges a C for a T. The MAF of rs1927907 in our cohort was 0.10. To determine if a particular cytokine drove the observed composite effect, the association between rs1927907 and individual cytokine concentrations was tested. We found that four of the five cytokines induced by *S. aureus*—TNF-α, IL-1β, IL-6 and G-CSF—were significantly higher for carriers of the rs1927907 minor allele (Table 1). By comparison, rs1927907 was also associated with cytokine responses to *E. coli* LPS (TNF-α, IL-1β, IL-6 and G-CSF) and Pam3CSK4 (TNF-α and IL-6), but not with cytokines induced by Pam2CSK4 or flagellin (data not shown).

rs1927907 is a TLR4 expression quantitative trait locus (eQTL) in whole blood; the minor allele is associated with increased whole blood TLR4 expression [14]. Moreover, the minor allele of rs1927907 is associated with increased TLR4 protein expression on CD4+ CD25^b^ regulatory T cells of asthmatic subjects as determined by flow cytometry [15]. These data, which are concordant with our observations of increased blood cytokine responses in carriers of the rs1927907 minor allele, implicate TLR4 itself in the response to *S. aureus*. However, TLR4 is the canonical LPS receptor and therefore is not anticipated to be involved in sensing of a Gram-positive pathogen. This prompted us to consider contamination of our *S. aureus* preparations with LPS as a potential explanation for these findings. We assayed our *S. aureus* preparations using a sensitive Limulus Amebo-cyte Lysate assay, but did not detect any LPS (data not shown).

**S. aureus does not activate TLR4 in vitro**

Because we did not find any LPS contamination in our preparations, we postulated that *S. aureus* might express other factors that would serve as ligands for TLR4. To address this question, we stimulated hTLR4/MD-2/CD14-transfected HEK293 cells with our *S. aureus* preparations to assess for a TLR4-dependent signal. We measured NF-κB activation by luciferase reporter assay but found no *S. aureus*-induced TLR4-dependent light emission (Fig. 2A). This observation suggested that *S. aureus* does not express a TLR4 ligand that signals through NF-κB. We next evaluated how blockade of TLR4 receptor function would affect cytokine responses to *S. aureus*. We stimulated primary blood monocytes from healthy subjects with *S. aureus* in the presence of a TLR4/MD-2 neutralizing antibody and assayed TNF-α concentrations in cell supernatants (Fig. 2B). We observed no change in TNF-α release when TLR4 receptor function was impaired. Together, these experiments indicated that *S. aureus* does not activate TLR4 to induce inflammatory cytokine responses.

**Knockdown of TLR4 inhibits the TNF-α response to *S. aureus***

To explain our observations of differential cytokine response associated with rs1927907, we next evaluated whether differential expression of TLR4 in the cell may modify the host response to *S. aureus*. We surmised that even if *S. aureus* did not directly activate TLR4, there may be downstream modulatory effects of TLR4 on other signaling pathways. We and others have observed such an effect of TLRS on TLR4-dependent signaling (Dickey AK, West TE, paper presented at the 2013 American Thoracic Society International Conference, abstract A4556; Collin CJ, Sciuira J, Rice A, Aloor J, Cyphert J, Bulek K, et al., paper presented at the 2016 American Thoracic Society International Conference, abstract A2643). We developed an assay using human monocyte THP-1-Dual cells in which we transfected siRNA targeting TLR4 or control siRNA (Fig. 2C). We achieved approximately 50% decrease in TLR4 gene expression in this assay. We next stimulated cells with *S. aureus* after transfection of siRNA against TLR4 (Fig. 2D). We measured TNF-α concentration in cell supernatants and found that levels of this cytokine induced by *S. aureus* were significantly reduced after TLR4 knockdown. Collectively, these results supported the concept that *S. aureus* does not directly activate TLR4 but that TLR4 modulates the inflammatory response to *S. aureus*.

**TLR4 variant rs1927907 is associated with increased cytokine responses during staphylococcal sepsis***

Regulators of the inflammatory response to heat-killed *S. aureus* in experimental settings may be very different than host response determinants in clinical staphylococcal infection. To determine whether rs1927907 might predict cytokine/chemokine responses in a clinical setting, we genotyped the variant in a cohort of 327 individuals with community-onset staphylococcal sepsis recruited at four hospitals in northeast Thailand. The clinical characteristics of these patients are described in Table 2. After finding no evidence for deviation from Hardy-Weinberg equilibrium in this cohort (p = 0.61), we tested the association of rs1927907 with plasma cytokine concentration at enrolment. Minor allele homozygotes generated significantly higher levels of IL-6 and IL-8 in crude analyses and after adjusting for age, sex, comorbidity index and site (adjusted p = 0.01 and 0.045, respectively) (Fig. 3).

**TLR4 variant rs1927907 is associated with increased respiratory failure during staphylococcal sepsis***

We then tested whether rs1927907 genotype predicted clinical outcome from staphylococcal sepsis. In both crude and adjusted analyses, minor allele homozygotes developed significantly more respiratory failure (adjusted odds ratio 9.65, 95% confidence interval 1.60–58.08, p = 0.01) (Table 3). These individuals did not have significantly greater rates of shock or death, outcomes that were less frequent overall. Together, these cytokine and clinical data in an independent cohort of patients offer confirmatory evidence in support of the role of TLR4 as a modulator of the host response in staphylococcal sepsis.

### Table 1

<table>
<thead>
<tr>
<th>rs1927907 genotype</th>
<th>Median (IQR) (pg/mL) for:</th>
<th>IL-6</th>
<th>IL-8</th>
<th>TNF-α</th>
<th>IL-1β</th>
<th>G-CSF</th>
</tr>
</thead>
<tbody>
<tr>
<td>CC</td>
<td>1480 (861–2656)</td>
<td>4532 (3090–7610)</td>
<td>927 (574–1433)</td>
<td>763 (463–1328)</td>
<td>55 (34–99)</td>
<td></td>
</tr>
<tr>
<td>CT</td>
<td>1852 (1304–4117)</td>
<td>5687 (3990–10956)</td>
<td>1128 (726–2684)</td>
<td>1100 (699–1727)</td>
<td>82 (49–148)</td>
<td></td>
</tr>
<tr>
<td>TT</td>
<td>3096 (701–5492)</td>
<td>7658 (2772–12544)</td>
<td>1831 (219–3447)</td>
<td>2243 (399–3886)</td>
<td>99 (27–170)</td>
<td></td>
</tr>
<tr>
<td>p^a</td>
<td></td>
<td>0.012</td>
<td>0.065</td>
<td>0.017</td>
<td>0.002</td>
<td>0.001</td>
</tr>
</tbody>
</table>

G-CSF, granulocyte-colony stimulating factor; IL, interleukin; IQR, interquartile range; TNF, tumor necrosis factor.

^a^ Linear regression model on log-transformed cytokine concentrations assuming an additive genetic model and adjusting for monocyte count.
Inflammatory responses to S. aureus correlate with responses to LPS and B. pseudomallei

In light of our data implicating TLR4 in the immune response to S. aureus, we then sought to determine whether inflammatory responses induced by S. aureus in healthy individuals might be correlated with responses induced by LPS or by Gram-negative bacteria in our human blood immunoassay. We selected E. coli LPS, S. minnesota LPS and heat-killed B. pseudomallei for this comparison. As control stimulants, we chose TLR2/6 agonist Pam2CSK4, TLR2/1 agonist Pam3CSK4, TLR5 agonist S. typhimurium flagellin, NOD1 agonist Tri-DAP and NOD2 agonist MDP. We measured the correlations between each stimulus and created heat maps with derived relatedness dendrograms. Across all cytokines, the dendrograms indicated highest relatedness between responses to S. aureus and LPS or between S. aureus and B. pseudomallei. For example, the correlation between TNF-α induced by S. aureus and by S. minnesota LPS was 0.61 (p < 0.0001), and the correlation between IL-8 induced by S. aureus and by B. pseudomallei was 0.67 (p < 0.0001) (Fig. 4).

Discussion

The main findings of this study are as follows: blood inflammatory responses to S. aureus are associated with the TLR4 genetic polymorphism rs1927907, an eQTL, both ex vivo and in patients...
with staphylococcal sepsis; TLR4 is not activated by *S. aureus* but TLR4 knockdown impairs TNF-α release induced by *S. aureus*; rs1927907 predicts respiratory failure in patients with staphylococcal sepsis; and blood inflammatory responses to *S. aureus* are tightly correlated with responses to LPS and a Gram-negative organism. These findings raise intriguing new questions about the role of TLR4 in human staphylococcal sepsis.

TLR4 is not usually considered a fundamental participant in the host response to Gram-positive infections. The *S. aureus* cell wall is composed of peptidoglycan in combination with other substances such as lipoteichoic acid (LTA) and lipoprotein. These components and secreted proteins can induce inflammation and may contribute to sepsis [4]. PRRs on host immune cells involved in recognition of *S. aureus* include TLR2 in combination with TLR1 or TLR6 and/or CD36 and CD14 [4]. While the cell wall of Gram-negative bacteria shares many of the same PAMPs as Gram-positive bacteria [3], a cell wall component unique to Gram-negative organisms is LPS [5]. LPS is known as a TLR4 agonist and induces a robust proinflammatory response and septic shock [16], but it is not expressed by *S. aureus*. Therefore, when we found associations between inflammatory responses and genetic variation in TLR4 and observed tight correlation between responses to

### Table 2
Clinical characteristics and outcomes of 327 patients with staphylococcal sepsis

<table>
<thead>
<tr>
<th>Variable</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, years, median (IQR)</td>
<td>54 (42–65)</td>
</tr>
<tr>
<td>Female sex, n (%)</td>
<td>114 (34.9)</td>
</tr>
<tr>
<td>Preexisting conditions, n (%)</td>
<td></td>
</tr>
<tr>
<td>Diabetes mellitus</td>
<td>116 (35.5)</td>
</tr>
<tr>
<td>Heart disease</td>
<td>17 (5.2)</td>
</tr>
<tr>
<td>Kidney disease</td>
<td>53 (16.2)</td>
</tr>
<tr>
<td>Liver disease</td>
<td>13 (4.0)</td>
</tr>
<tr>
<td>Lung disease</td>
<td>18 (5.5)</td>
</tr>
<tr>
<td>Cancer</td>
<td>7 (2.1)</td>
</tr>
<tr>
<td>Alcoholism</td>
<td>5 (1.5)</td>
</tr>
<tr>
<td>Autoimmune disease</td>
<td>5 (1.5)</td>
</tr>
<tr>
<td>Neurologic disease</td>
<td>8 (2.5)</td>
</tr>
<tr>
<td>Haematologic disease</td>
<td>9 (2.8)</td>
</tr>
<tr>
<td>Comorbidity index, median (IQR)*</td>
<td>1 (0–1)</td>
</tr>
<tr>
<td>Outcome, n (%)</td>
<td></td>
</tr>
<tr>
<td>Respiratory failure</td>
<td>58 (17.7)</td>
</tr>
<tr>
<td>Shock</td>
<td>38 (11.6)</td>
</tr>
<tr>
<td>Death at 28 days</td>
<td>30 (9.2)</td>
</tr>
</tbody>
</table>

*Comorbidity index is a 10-point score with 1 point each given for lung disease, heart disease, kidney disease, liver disease, neurologic disease, haematologic disease, autoimmune disease, cancer, diabetes and alcoholism.

### Table 3
Association of TLR4 variant rs1927907 with clinical outcomes of patients with staphylococcal sepsis

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Respiratory failure</th>
<th>Shock</th>
<th>Death</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Yes</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>CC</td>
<td>42 (72%)</td>
<td>210 (78%)</td>
<td>29 (76%)</td>
</tr>
<tr>
<td>CT</td>
<td>12 (21%)</td>
<td>57 (21%)</td>
<td>7 (18%)</td>
</tr>
<tr>
<td>TT</td>
<td>4 (7%)</td>
<td>2 (1%)</td>
<td>2 (5%)</td>
</tr>
</tbody>
</table>

Unadjusted p* 0.018 0.22 0.51
Adjusted OR (95% CI) 9.65 (1.60–58.08) 4.31 (0.66–27.96) 1.75 (0.18–17.11)
Adjusted p 0.01 0.13 0.63

CI, confidence interval; OR, odds ratio.

*Unadjusted analyses performed by exact test.

* Adjusted analyses performed by logistic regression assuming recessive genetic model adjusting for age, sex, comorbidity index and site.

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Fig. 3. TLR4 variant rs1927907 is associated with plasma IL-6 and IL-8 in patients with staphylococcal sepsis. IL-6 (a) and IL-8 (b) were assayed by ELISA in plasma samples from patients with staphylococcal sepsis and are displayed by TLR4 variant rs1927907 genotype. Boxes show median and interquartile range; whiskers show upper and lower adjacent values; outside values are not shown for clarity. Values were log10 transformed, and linear regression was performed using recessive model (comparing CC and CT subjects to TT subjects), adjusting for age, sex, comorbidity index and site. n = 249 (CC), 69 (CT), 6 (TT). **p < 0.01; *p < 0.05. ELISA, enzyme-linked immunosorbent assay; IL, interleukin.

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S. aureus and to LPS, we first excluded detectable LPS contamination in our experiments. We also considered that activation of TLR4 may occur by bacterial ligands other than LPS [17]. For example, the S. aureus exotoxin leukocidin has been reported to induce TLR4-dependent immune responses [18]. Yet we did not find that TLR4 was activated by our preparations of S. aureus, at least via the transcription factor NF-κB.

Two other explanations may account for our findings. First, TLR4 may respond to endogenous ligands produced by the host [19]; during infection, this effect may be sufficiently strong to result in altered TLR4-dependent inflammatory responses and clinical outcomes. This is supported by a report that haemoglobin, a host blood product, can significantly enhance macrophage secretion and expression of several cytokines and receptors in a TLR4-dependent pathway when activated with low levels of TLR2 ligands such as LTA and Pam3CSK4. Haemoglobin can also lead to secretion of high mobility group box 1 protein (HMGB1), which synergizes with LTA to increase secretion of IL-6 [20].

Second, TLR4 may contribute to the inflammatory response without direct ligation of the receptor. This seems like the most likely explanation for our observations, as cytokine release in monocytes was not impaired by antibody-mediated blockade of TLR4, yet cytokine release in a monocyte cell line was blunted after transfection of siRNA reducing TLR4 gene expression. Cooperative behavior by TLRs may alter inflammatory responses even when the ligand is specific for only one of the interacting TLRs. For example, we and others have found that TLR5 may alter TLR4-dependent signaling (Dickey AK, West TE, paper presented at American Thoracic Society International Conference, 2013, abstract A4556; Collin CJ, Sciurba J, Rice A, Aloor J, Cyphert J, Bulek K, et al., paper presented at American Thoracic Society International Conference, 2016, abstract A2643). Furthermore, recent work suggests that TLR4

Fig. 4. High correlation between blood inflammatory responses induced by Staphylococcus aureus and LPS or Burkholderia pseudomallei. Heat maps of correlation between TNF-α (a) or IL-8 (b) responses induced by stimulation of whole blood from 300 healthy subjects with panel of purified innate immune ligands and heat-killed bacteria for 6 hours at 37°C. Stimulants were heat-killed S. aureus 2.5 × 10^7 CFU/ml (SAlow) and 5.0 × 10^7 CFU/ml (SAhigh), heat-killed B. pseudomallei 2.5 × 10^7 CFU/ml (BP), Salmonella typhimurium flagellin 500 ng/ml (Flg), Pam3CSK4 100 ng/ml (Pam3), Pam2CSK4 100 ng/ml (Pam2), Escherichia coli O111:B4 LPS 10 ng/ml (EClips) and Salmonella minnesota Re595 LPS 10 ng/ml (SMips). Dendrogram of hierarchical clustering results for correlation matrix for each mediator is shown. Lowest correlation is red (Pearson correlation coefficient r < 0.1) and highest correlation is white (r = 1). Scatter plots of individual TNF-α (c) or IL-8 (d) responses (log10 transformed) after stimulation of fresh whole blood from 300 healthy subjects with heat-killed S. aureus 5 × 10^7 CFU/ml, S. minnesota Re595 LPS (C) or heat-killed B. pseudomallei 2.5 × 10^7 CFU/ml (d) for 6 hours at 37°C. For each plot, relationship between variables as determined by linear regression (dotted line) and Pearson correlation (correlation coefficient, r) are shown. IL, interleukin; LPS, lipopolysaccharide; TNF, tumor necrosis factor.
contributes to murine macrophage responses to \textit{S. aureus} and that TLR2 and TLR4 may interact in this process [21]. Thus, although we present data that implicate TLR4 as a modulator of the host response to \textit{S. aureus}, the mechanism by which this may occur requires further elucidation.

Genetic variation in innate immunity is well established as a modulator of inflammatory responses and outcome in sepsis [22–24]. Our focus on Thai subjects offers important new data as population differences in genetic association studies of sepsis are critical to consider. For example, functional TLR1 variants are associated with outcomes from sepsis in white North American subjects [22], but we have shown that TLR1 genetic architecture is profoundly different and variants are nonfunctional in Southeast Asians [25]. rs1927907 is an intronic variant in TLR4 that is common throughout the world (MAF 0.11–0.25 [26]). Notably, the clinical associations reported to date are restricted to Chinese populations; the variant is associated with late-onset Alzheimer disease [27], asthma severity [15,28] and tacrolimus pharmacokinetics after liver transplantation [29], neonatal early Crohn disease [30] and chronic periodontitis in a TLR4 haplotype [31]. In the Southern Han Chinese population, the variant is in high linkage disequilibrium ($r^2 = 0.87$) with a TLR4 promoter region variant, rs10983755 [26]. Ragnarsdottir et al. have reported that rs10983755 disrupts a potential binding site for the transcription factor N-Myc and increases promoter activity in HEK293 cells on infection with \textit{E. coli} [32]. Moreover, rs1927907 is in high linkage disequilibrium with rs960312, a TLR4 polymorphism that we have found to be associated with susceptibility to melioidosis, a common Gram-negative infection in northeast Thailand [33]. Thus, the haplotype tagged by rs1927907 is of considerable interest.

Several lines of evidence link rs1927907 to altered TLR4 expression at both the gene and protein level. In a study of over 5300 whole blood specimens, rs1927907 was identified as a TLR4 eQTL, with increasing TLR4 gene expression observed in carriers of the minor allele [14]. Moreover, the minor allele of rs1927907 is associated with increased TLR4 protein expression on CD4$^+$CD25$^{\text{high}}$ regulatory T cells of asthmatic subjects as determined by flow cytometry [15]. While not excluding \textit{trans} (more distant) effects of rs1927907 on expression of other genes, these findings complement our findings of increased cytokine responses in carriers of the rs1927907 minor allele and more concretely implicate TLR4 in this process. Further work is required to more completely understand the variation driving the observed associations and to replicate the clinical associations in other populations.

In light of the overlapping but not identical pathways activated by Gram-positive and Gram-negative bacteria, whether and how Gram-positive sepsis differs from Gram-negative sepsis is debated [34,35]. In comparison to other PAMPs, we found that responses to LPS and to \textit{B. pseudomallei} were most highly correlated with \textit{S. aureus}—induced responses. This suggests a shared common pathway of inflammation precipitated by Gram-positive and Gram-negative bacteria. A study by Tang et al. showed that the human sepsis transcriptome in Gram-positive sepsis is similar to the transcriptome in Gram-negative sepsis [36]. While this report also supports a common host response in the pathophysiology of sepsis regardless of infecting organism, a potentially confounding factor in clinical or \textit{in vivo} studies is that LPS derived from gut bacteria may be released systemically during bowel hypoperfusion from sepsis of any etiology [37]. Our \textit{ex vivo} data, obtained under controlled experimental conditions, avoid confounding by gut bacteria LPS release and provide corroborating protein-level evidence of shared pathway activation.

Several important limitations to our study deserve mention. First, the use of killed bacteria may not mimic the innate immune responses induced by live pathogens. Second, our analysis is restricted to the optimal concentrations of specific PAMPs chosen that induced detectable cytokine responses; conceivably there may be additional dose-dependent effects that have not been identified. Third, our genetic analyses may be confounded by population stratification and may potentially differ in non-Thai subjects. Fourth, although we reported significant associations of rs1927907 with respiratory failure or plasma cytokines, the number of subjects with the recessive genotype in our clinical study was low, and our results may be biased by unmeasured confounding. While the association of rs1927907 with cytokine responses in whole blood stimulation \textit{ex vivo} was determined using an additive genetic model, the associations in the clinical study were apparent using a recessive genetic model. This may be due to inadequate power to distinguish between the relative contributions of these models in human infection, or it may reflect different biological effects \textit{ex vivo} versus in infected humans. Independent replication of these results in larger clinical cohorts is therefore important. Fifth, our study was likely underpowered to detect associations with shock or death, but we note that IL-6 and IL-8 levels strongly predict these outcomes in our cohort. Finally, the proinflammatory cytokines investigated in our study are mainly driven by shared NF-kB/MAP kinase—signaling pathways downstream of the PRRs. We did not investigate interferon production, such as that mediated by interferon regulatory factors (IRFs). It has been recently reported that \textit{S. aureus} RNA activates IRF5 via TLR8 and that this is antagonized by TLR2 activation [38]. How this sensing pathway relates to our findings necessitates further investigation.

Strengths of our immunoassay study include the prospective nature of healthy subject recruitment from a blood donor pool, the large number of subjects assayed and highly standardized blood processing techniques, as well as batched generation of assays, measurement of cytokines and genotyping. Furthermore, we replicated and extended our initial genetic associations in patients from the same region recruited in a prospective multisite study of staphylococcal sepsis. To our knowledge, our study is one of the first to identify innate immune genetic variants that predict outcomes from Gram-positive sepsis in Asians.

In conclusion, in Thais, a genetic variant in TLR4 that is an eQTL is associated with whole blood cytokine responses to \textit{S. aureus} \textit{ex vivo} and with plasma cytokine levels and respiratory failure in staphylococcal sepsis. While \textit{S. aureus} does not express LPS—the canonical TLR4 ligand—or activate TLR4 directly, the innate immune response to \textit{S. aureus} does appear to be modulated by TLR4 and shares significant commonality with that induced by Gram-negative pathogens and LPS. These data suggest a regulatory role for TLR4 beyond canonical LPS-receptor ligation in Gram-positive sepsis.

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Transparency Declaration

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Appendix A. Supplementary data

Supplementary data related to this article can be found at http://dx.doi.org/10.1016/j.cmi.2016.08.028.

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