SHORT REPORT: MOLECULAR EVALUATION OF THE EFFICACY OF CHLOROQUINE TREATMENT OF UNCOMPPLICATED PLASMODIUM FALCIPARUM MALARIA IN EAST TIMOR

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Abstract. The efficacy of chloroquine treatment of uncomplicated Plasmodium falciparum malaria in East Timor was investigated via molecular tools. Genotyping of the polymorphic markers msp1 and msp2 was performed to investigate the number and type of parasite alleles in pre- and posttreatment blood samples collected from 48 patients. Patients were infected with a minimum of 8 msp1 and 14 msp2 allelic types of parasite, and 43% of the patients had more than one allelic type before treatment. The genotyping also revealed that 66.7% of the patients were infected with at least one identical allelic type of parasite before and after treatment and therefore were likely to have experienced recrudescence. All parasites in pre- and posttreatment blood samples carried the K76T mutation in pfcrt, regardless of the clinical response to chloroquine. The sequence polymorphism patterns in pfcrt in the majority of parasites examined were identical to those observed in Bougainville, Papua New Guinea.

INTRODUCTION

Chloroquine has been used as first-line therapy for uncomplicated falciparum malaria in East Timor. However, until recently, reliable data on the efficacy of chloroquine in this region have been lacking. In mid-2000, MERLIN (Medical Emergency Relief International) conducted an in vivo chloroquine efficacy study in Lautem district, Los Palos, a hyperendemic area in the eastern sector of East Timor (Ezard N and others, unpublished data). Forty-eight East Timorese patients with uncomplicated Plasmodium falciparum malaria, who had been aged between 8 months and 29 years and who lived within a 1-hour car journey, were enrolled. Results of a questionnaire on chloroquine usage before the initiation of the trial revealed that 9 of the 48 patients had taken chloroquine within a 1-month period preceding the trial. Overall, 48 patients, two-thirds (32 of 48) experienced recurrent parasitemia after treatment with 1,500 mg chloroquine over 3 days, all but one patient failed to respond to late treatment (recurrent parasitemia occurred 7–28 days after treatment) (Ezard N and others, unpublished data).

After clinical investigation, molecular analysis was performed on pre- and posttreatment blood samples collected from these patients to investigate whether the recurrent parasitemia resulted from parasites recrudesced under chloroquine treatment or from new infections and whether sequence polymorphism in the pfcrt gene can be used as a molecular marker to predict clinical outcomes after chloroquine treatment in this region. Blood samples were collected and preserved either on filter paper or in 6 M guanidine hydrochloride on days 0, 14, and 28 after commencing chloroquine treatment, or on the day when symptoms recurred. We extracted DNA via the Wizard Plus Miniprep DNA Purification System (Promega, Madison, WI) according to the manufacturer’s instructions. Msp1 and msp2 were amplified by polymerase chain reaction (PCR) and analyzed by agarose gel electrophoresis.

Nested PCR was performed to amplify the pfcrt gene. Briefly, the first round of PCR was carried out in a 50-μL reaction mixture containing 1.5 μg/mL of each primer 5’-GTGGAGGTCTTGTCTTGTG-3’ and 5’-TCCAGTAGT-200 μM of dNTPs, buffer (50 mM KCl, 10 mM Tris-HCl, pH 8.3, 2.5 mM MgCl2), and 1.25 units of AmpliTaq Gold DNA polymerase (Perkin-Elmer, Norwalk, CT). The samples were denatured at 94°C for 10 minutes before 40 cycles of amplification (94°C for 50 seconds, 51°C for 50 seconds, and 70°C for 1 minute). The second round PCR were performed under the same conditions by using the following primers: 5’-TGTGCTCATGTGTTTAAACTT-3’ and 5’-AAAGCTCGGTGTCGTT-3. The nested PCR product was purified with a QIAquick PCR Purification Kit (Qiagen, Valencia, CA), then sequenced in an ABI PRISM 370 sequencer (Applied Biosystems, Inc., Foster City, CA).

Genotyping of 2 polymorphic markers, msp1 and msp2, revealed a minimum of 8 (410–580 bp) and 14 (380–800 bp) allelic types, respectively, indicating that many allelic types of P. falciparum were transmitted in the area. Multiple allelic types of P. falciparum were detected in 45.8% (22 of 48) of the patients before treatment, indicating a high level of malaria transmission in the area. The genotyping also revealed that 66.7% (32 of 48) of patients had at least one allelic type of parasite in posttreatment blood samples identical to those in pretreatment samples (Table 1, original types). Twenty-eight of these patients came from the in vivo resistant group and 4 from the in vivo susceptible group. Given the number of allelic types in the area, the chance of reinfecting with the same allelic type is low. Therefore, these patients are likely to have experienced recrudescence resulting from parasites that grew in the presence of chloroquine. Approximately 10% (5 of 48) of patients had different allelic types of parasites in their pre- and posttreatment blood samples, indicating new infections (Table 1, new types) during the 28 day follow-up period. Of the 5 patients with new infections, 4 were in the in vivo resistant group and 1 in the susceptible group. In the 16 patients classified as in vivo susceptible to chloroquine, genetic analysis revealed 4 patients to have recrudescent parasites and 1 patient to have a new infection. This finding suggests that these patients were infected with very low number of parasites that were below the limit of microscopic detection.

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Allelic types and sequence polymorphisms detected in pre- and posttreatment blood samples and their correlations with in vivo response to chloroquine treatment.

<table>
<thead>
<tr>
<th>In vivo chloroquine susceptibility</th>
<th>No. of patients (n = 48)</th>
<th>MSP1/MSP2 in posttreatment samples</th>
<th>Polymorphism in PfCRT protein</th>
<th>Pretreatment</th>
<th>Posttreatment</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>MSP/M SP2 types</td>
<td>No. of patients</td>
<td>K76 SVMNT*</td>
<td>SVMNT*</td>
</tr>
<tr>
<td>Susceptible</td>
<td>16</td>
<td>Original type</td>
<td>4</td>
<td>0</td>
<td>16</td>
</tr>
<tr>
<td></td>
<td></td>
<td>New type</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Undetected</td>
<td>11</td>
<td>0</td>
<td>32</td>
</tr>
<tr>
<td>Resistant</td>
<td>32</td>
<td>Original type</td>
<td>28</td>
<td>0</td>
<td>28</td>
</tr>
<tr>
<td></td>
<td></td>
<td>New type</td>
<td>4</td>
<td>0</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Undetected</td>
<td>0</td>
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</tr>
</tbody>
</table>

* SVMNT and CVIET represent amino acids at positions 72 to 76 in PfCRT.

The pre- and posttreatment blood samples were also examined for sequence polymorphisms in the pfcr gene at positions corresponding to amino acids 72, 74, 75, and 76. Mutation K76T in pfcr has been demonstrated to correlate with decreased susceptibility to chloroquine in vitro, and sequence polymorphisms at amino acids 72, 74, and 75 are associated with geographical origins of parasite samples.1,2,5 K76T was detected in all parasites in both pre- and posttreatment blood samples, regardless of the clinical response to chloroquine (Table 1). The patients with new infections were all reinfected with parasites carrying the K76T mutation (Table 1). The results are in accord with a recent study conducted in Laos, which showed that although K76T was perfectly associated with in vivo chloroquine resistance, the mutation was present in all amplifiable in vivo susceptible isolates.6 In the 16 patients cured of malaria, the elimination of mutation carrying parasites may be due to a stronger antiparasitic immune response in these individuals. A correlation in patient age and predictive value of K76T mutation reported recently supports this explanation.7 However, in this group of patients, there was no correlation (chi-square test, $P > 0.5$) between the age group and patient’s age when patients were grouped as age <5 (n = 11), 5–10 (n = 16) and >10 (n = 21), or <5 (n = 11) and >5 (n = 37), or <1 (n = 2), 2–3 (n = 2), 4–5 (n = 7) and >5 (n = 37) years. This could have resulted from relatively small number of volunteers in each age group. There is also a possibility that the parasites in these individuals have lower levels of chloroquine resistance compared with those in patients not responding to the treatment. Therefore, the presence of mutation K76T in pfcr is necessary, but not sufficient, to predict clinical outcome of chloroquine treatment. In accord with the in vivo findings, our molecular analysis also indicated that chloroquine-resistant P. falciparum is widespread in this region of East Timor (Ezard N and others, unpublished data).

As to the sequence polymorphisms at other positions in pfcr, S72, M74, and N75 were detected in all but one sample (C72, I74, and E75) (Table 1). In previous studies, it was found that polymorphisms at codon positions 74, 75, 271, 326, 356, and 371 in pfcr were linked into blocks in parasites with the K76T mutation.1,2,5 So far, M74/N75/Q271/D326/L356/R371 has been identified in pfcr of all analyzed chloroquine resistant samples from the mainland Papua New Guinea (PNG), the island of Bougainville, PNG, and Brazil, whereas I74/E75/E271/S326/T(I)356/I371 has been found mainly in isolates from Southeast Asia and Africa.1,2,5 At amino acid 72, however, a S or C has been observed in the South American/PNG isolates.1,2,5 A synonymous DNA sequence polymorphism of $S_{AGT}$ or $S_{CTT}$ was also observed in the isolates from mainland PNG.5 However, in our set of samples from East Timor and Bougainville, PNG, AGT was the only codon type identified in chloroquine-resistant parasites for S72. These findings suggest that majority of the chloroquine-resistant parasites from East Timor and Bougainville, PNG, may be derived from a common origin as a result of the geographical proximity of the 2 islands.

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