Short Report: Therapeutic Efficacy of Chloroquine in *Plasmodium vivax* and the *pvmdr1* Polymorphisms in the Republic of Korea Under Mass Chemoprophylaxis

Young Keun Kim, Changsoo Kim, Inho Park, Hyo Youl Kim, Jun Yong Choi, and June Myung Kim*

Department of Internal Medicine, Yonsei University, Wonju College of Medicine, Wonju, Korea; Konyang University, Myunggok Medical Research Institute, Daejeon, Korea; Department of Preventive Medicine, Yonsei University College of Medicine, Seoul, Korea; Department of Preventive Medicine, The Armed Forces Medical Command, Sungnam, Korea; Department of Internal Medicine, Yonsei University College of Medicine, Seoul, Korea

**Abstract.** Chemoprophylaxis with hydroxychloroquine (HCQ) and primaquine has been used in the Republic of Korea (ROK) Army since 1997. It may facilitate the development of chloroquine (CQ)-resistant strains of *Plasmodium vivax*. We investigated the therapeutic efficacy of HCQ and the *pvmdr1* gene polymorphisms in *P. vivax*. From June to September 2006, 102 soldiers with vivax malaria near the demilitarized zone in Gyeonggi-do, ROK, were enrolled in the study. We determined the status of compliance of chemoprophylaxis. In 85 patients, therapeutic efficacy was monitored 28 days after standard HCQ treatment; 66 (64.7%) of 102 malaria patients had taken all chemoprophylaxis with HCQ. In all patients enrolled in the therapeutic efficacy monitoring, parasitemia had not been observed since 3 days after standard HCQ treatment. However, the ubiquitous presence of the F1076L mutation of the *pvmdr1* was observed. There was no evidence that the F1076L mutation of *pvmdr1* could contribute to failure of HCQ treatment.

**INTRODUCTION**

By the end of 1970s, the World Health Organization (WHO) declared that *Plasmodium vivax* had been eradicated in the Republic of Korea (ROK).1 In 1993, one case of malaria reemerged near the demilitarized zone (DMZ) that separates ROK (south) from the Democratic People’s Republic of Korea (north).2 Since 1993, the number of malaria cases has increased exponentially, not only among soldiers but also among civilians living near the DMZ.3–5 Although malaria did initially increase exponentially, the increase has since been tempered by control measures. Since 1997, the number of soldiers who received chemoprophylaxis with hydroxychloroquine (HCQ) and primaquine has continuously increased to over 200,000 in 2005. Nonetheless, the number of cases of malaria has increased again since 2005 in the ROK Army. Military antimalarial chemoprophylaxis has contributed, in part, to the decrease in the number of malaria cases among military personnel. However, long-term chemoprophylaxis may facilitate the development of chloroquine (CQ)-resistant strains of *P. vivax*.

Although the mechanism of *P. vivax* CQ resistance is unknown, it has been suggested that the mutation of *pvmdr1* that is the orthologue of the *pfmdr1* of *P. falciparum* is related to the CQ resistance.3,6 We investigated the breakthrough malaria infection and the therapeutic efficacy of CQ in *P. vivax* in ROK. Additionally, the *pvmdr1* gene polymorphisms and their relevance to CQ resistance in *P. vivax* were evaluated.

**MATERIALS AND METHODS**

**Study subjects.** From June 1 to September 30, 2006, we investigated the malaria patients who were admitted to the three referral Armed Forces Hospitals, Byeoje, Yangju, and Ildong Hospitals, located in the Northern Kyunggi province near the DMZ. The patients were diagnosed when they had any febrile illness and *P. vivax* in peripheral blood films. Blood samples were obtained from all patients who had given the informed consent. The protocol was approved by the Institutional Ethic Committee at the Armed Forces Medical Command (April 13, 2006).

**Compliance of chemoprophylaxis.** The chemoprophylaxis with HCQ sulfate (400 mg, one time per week) was started on May 8, 2006, and it continued throughout the transmission season (May to September). Therefore, the chemoprophylaxis was provided throughout the study period. Fourteen-day prophylaxis with primaquine (15 mg base, one time per day) was started on the first day of the last week of CQ administration.

The status of chemoprophylaxis was determined by the military record, which was a malaria case report form submitted by the military doctor after the interview with the patient. According to the status of chemoprophylaxis, the patients were classified as complete compliance when they took all doses before malaria infection, poor compliance when they did not take the dose more than one time before malaria infection, and no prophylaxis when they did not take the dose at all.

**Monitoring of therapeutic efficacy.** All patients diagnosed with vivax malaria received standard treatment: 2 g HCQ sulfate (day 1 dose, 1,200 mg; day 2 dose, 400 mg; day 3 dose, 400 mg) and 15 mg primaquine one time daily for 14 days. The patients were followed-up 28 days after the start of antimalarial treatment; the protocol used was a slightly modified version of that antimalarial drug resistance monitoring that was originally suggested by WHO (Table 1).7

**Identification of *pvmdr1* polymorphism.** Parasite genomic DNA from all blood samples collected into ethylene-diaminetetraacetic acid (EDTA) tubes was extracted with a QIAamp DNA blood kit (QIAGEN Inc., Valencia, CA) following the manufacturer’s instructions with minor modifications: the incubation time with proteinase K was increased to 1 hour at 56°C to improve the yield of the extraction, and DNA was eluted from the column by use of 100 μL polymerase chain reaction (PCR)-grade H2O. Genomic DNA from *P. vivax* was amplified in a total volume of 20 μL containing 0.20 mmol/L 2'-deoxynucleoside 5'-triphosphate (dNTP), 1 μmol/L each primer, 1 μU Platinum Taq DNA Polymerase (Invitrogen), 1.5 mmol/L MgCl2, and 5 μL 10× PCR buffer.
The sequences of PCR primers were as follows: *pvmdr1*-F (5′-CACCTTGGCCTTCTTGCG-3′), *pvmdr1*-R (5′-TTCCTTTGTTGCATAAAC-3′), *pvmdr1*-S (5′-ATAGTCA TGCCCTCAGGATTG-3′), and *pvmdr1*-AS (5′-ACGTTCGG TCTGGACAAGTATC-3′). PCR was performed under the following conditions: 37 cycles of denaturation at 94°C (5 min in the first cycle and 30 s in subsequent cycles), annealing for 30 s at 55°C, extension for 30 s at 72°C, and a final extension for 7 min. PCR products were sequenced using the ABI Prism 3100 Genetic Analyzer (Applied Biosystems, Foster City, CA). The sequences were compared with the GenBank accession number AY618622 of Sal-1, a CQ-susceptible strain from Salvador, using a basic local alignment search tool (BLAST) search of the National Center for Biotechnology Information databases (http://blast.ncbi.nlm.nih.gov/Blast.cgi).

RESULTS

During the study period, a total of 149 patients were diagnosed as *P. vivax* malaria in the study hospitals. The status of chemoprophylaxis was determined for 102 patients whose military records were available, and the therapeutic efficacy was monitored for 28 days after standard HCO treatment in the 85 patients who had given the informed consent (Figure 1); 66 (64.7%) patients were classified as complete compliance, 11 (10.8%) patients had poor compliance, and 25 (24.5%) patients had no prophylaxis (Table 2). All peripheral blood smears needed for monitoring had been done in all 85 patients, and all enrolled patients cleared their parasites within 3 days.

The PCR was performed from the blood samples that were obtained from the 85 patients who enrolled in therapeutic efficacy monitoring. After PCR, the 78 isolates were obtained from the 85 patients who had given the informed consent (Table 2). All peripheral blood smears needed for monitoring had been done in all 85 patients, and all enrolled patients cleared their parasites within 3 days.

The PCR was performed from the blood samples that were obtained from the 85 patients who enrolled in therapeutic efficacy monitoring. After PCR, the 78 isolates were obtained from the 85 patients who had given the informed consent (Table 2). All peripheral blood smears needed for monitoring had been done in all 85 patients, and all enrolled patients cleared their parasites within 3 days.

The mass chemoprophylaxis for the soldiers based in the risk area reduced the number of malaria cases, but long-term chemoprophylaxis could facilitate the development of drug resistance/tolerance or prophylaxis failure. In this study, 66 patients were defined as complete compliance by the military record. The drug level in whole blood of the patients with chemoprophylaxis was not measured at the malaria infection; it is highly likely that the drug concentration in patients with complete compliance could be higher than 100 ng/mL, because it is usually known that the drug concentration is maintained higher than 100 ng/mL by the long-term CQ prophylaxis given one time per week. *P. vivax* may be classified as biologically resistant if malaria infection that persists in the CQ level in whole blood is greater than 100 ng/mL, and it should completely cure blood-stage CQ-sensitive *P. vivax*. However, Lee and others showed that the HCO and its metabolite could not be found in the blood of 46 of 74 soldiers who had taken HCO chemoprophylaxis weekly, although the blood concentration of the HCO and its metabolites was above 100 ng/mL in eight patients. Therefore, it is not truly breakthrough malaria in the 66 patients regarded as complete compliance group.

The *pfmdr1* gene of *P. falciparum* is classified as the adenine 5′-triphosphate (ATP) binding cassette (ABC) transporter, and it has been known to relate with the resistance against CQ, artemisinin, quinine, mefloquine, and halofantrine. The *pfmdr1* gene of *P. vivax* is the orthologue of the *pfmdr1* of *P. falciparum*, and there is controversy regarding whether the *pfmdr1* gene relates with the CQ resistance. A recent study showed that the amplification of *pfmdr1* and single-nucleotide polymorphisms was correlated with susceptibility of *P. vivax* to multiple antimalarial drugs and that the *pfmdr1 Y976F* allele had reduced susceptibility to CQ. In this study, the F → L change at codon 1076 of the *pfmdr1*, which was caused by a single mutation (TTT → TCT), was observed in all 78 isolates. Therefore, this ubiquitous presence of the F1076L mutation of *pvmdr1* might be correlated with geographical characteristics in Korean vivax malaria rather than drug resistance.

In this study, no treatment failure was observed after the standard treatment of CQ/primaquine in 85 patients for the 28 days of monitoring. Considering the blood schizontidal effect of primaquine, it could not be determined that there was absolutely no CQ treatment failure, but it could be determined that there was no standard treatment failure.

### Table 2

<table>
<thead>
<tr>
<th>Characteristics (N = 102)</th>
<th>Measurement</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Mean age (in years)</strong></td>
<td>22.5 ± 3.3 (17–36)</td>
</tr>
<tr>
<td><strong>Residency</strong></td>
<td></td>
</tr>
<tr>
<td>Northwestern, Kyonggi (Byeokje)</td>
<td>44 (43.1%)</td>
</tr>
<tr>
<td>Mid-north, Kyonggi (Yangju)</td>
<td>36 (35.3%)</td>
</tr>
<tr>
<td>Northeastern, Kyonggi (Ildong)</td>
<td>23 (22.6%)</td>
</tr>
<tr>
<td><strong>Compliance</strong></td>
<td></td>
</tr>
<tr>
<td>Complete</td>
<td>66 (64.7%)</td>
</tr>
<tr>
<td>Poor</td>
<td>11 (10.8%)</td>
</tr>
<tr>
<td>No</td>
<td>25 (24.5%)</td>
</tr>
<tr>
<td><strong>Median parasitemia count per microliter (IQR)</strong></td>
<td>2,250 (490–8050)</td>
</tr>
</tbody>
</table>

*All patients were male.*
†IQR = interquartile range.
‡Complete compliance group (2.0571 μL) vs. poor and no prophylaxis groups (4.5581 μL).

![Figure 1](image-url)
In this study, there were limitations. For example, the blood levels of CQ and its metabolites, desethylchloroquine and desethylhydroxychloroquine, were not measured after the vivax malaria was developed. In conclusion, there was no treatment failure of HCQ and primaquine in Korea, and there was no evidence that that the F1076L mutation of pvmdr1 could contribute to HCQ resistance in *P. vivax*.

Received September 1, 2010. Accepted for publication January 15, 2011.

Acknowledgments: The authors thank Kyeongman Jeon and Taekyoung Park in the Armed Forces Capital Hospital for assistance in collecting the data, and we also thank many medical officers in Byeokje, Yangju, and Ildong Hospitals for collecting the blood samples.

Financial support: This work was supported in part by Konyang Myung Gok Research Fund of 2007.

Authors’ addresses: Young Keun Kim, Department of Internal Medicine, Yonsei University, Wonju College of Medicine, Kangwon-do, Republic of Korea, E-mail: amo@yonsei.ac.kr. Changsoo Kim, Department of Preventive Medicine, Yonsei University College of Medicine, Seoul, Republic of Korea, E-mail: preman@yuhs.ac.kr. Inho Park, Chief of Professional Service, Armed Forces Seoul Hospital, Seoul, Republic of Korea, E-mail: park_in_ho@yahoo.co.kr. Hyoung Youl Kim, Yonsei University, Wonju College of Medicine, Kangwon-do, Republic of Korea, E-mail: bykys@yonsei.ac.kr. Jun Yong Choi and June Myung Kim, Department of Internal Medicine, Yonsei University College of Medicine, Seoul, Republic of Korea, E-mails: seran@yuhs.ac and jmkim@yuhs.ac.

REFERENCES


