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Letter to the Editor

Genetic diversity of *Plasmodium falciparum* erythrocyte membrane protein 1 in field isolates: Correspondence

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To the Editor

Dear Editor, we would like to share ideas on the publication "Genetic diversity of *Plasmodium falciparum* erythrocyte membrane protein 1 in field isolates from central Myanmar [1]." By examining field isolates from central Myanmar for the *P. falciparum* Duffy-binding-like domain (PfDBL), Dinzouna-Boutamba et al. sought to describe the diversity of var repertoires. Their genetic research indicated that the D-H segments of the var in Myanmar populations contain a wide variety of polymorphic repertoires, with many distinct sequence types in each individual [1]. The anthors found that independent of regional origins, var genes from the worldwide population, including Myanmar, shared close genetic lineages, suggesting that they had not experienced fast evolutionary changes [1].

The discussion of hereditary attributes in this article may or may not be applicable. We both agree that the genetic factor under investigation may be relevant to the outcome. The important concern is on the source of isolation. It was mentioned that the origin is from central Myanmar but it is necessary to recognize the local ethnic diversity and the transnational migration of the local people between Myanmar and nearby country such as Thailand. In that area heterogenic pattern of the genetic variants is reported [2]. The importation of the infection is possible, and this might be an important factor that must be carefully interpreted. Second, it might be interpreted that there is a high similarity between the observed pattern in the current report and previous data from other settings, but it might be difficult to conclude about the evolutionary changes. The evolutionary change should be based on a long-term follow-up and data should be collected from the same area.

Reply from Dr. Youn-Kyoung Goo (corresponding author: kuku1819@knu.ac.kr)

We appreciate Drs. Kleebayoon and Wiwanitkit for their interests and comments on our recent publication [1].

1. **The important concern is on the source of isolation. It was mentioned that the origin is from central Myanmar but it is necessary to recognize the local ethnic diversity and the transnational migration of the local people between Myanmar and nearby country such as Thailand. In that area, heterogenic pattern of the genetic variants is reported [3]. The importation of the infection is possible, and this might be an important factor that must be carefully interpreted.**

Response: We agree with your opinion that the site of initial malaria infection is impor-

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tant. The travel history has been checked with questionnaires prior to sample collection. To determine the difference of genetic variant patterns between Myanmar and nearby country populations such as Thailand, the var sequences of Thailand populations obtained from GenBank have been added for phylogenetic analysis, in which no specific relationship has found between 2 populations [1]. However, we have not considered the local ethnic diversity of patients for evaluation of the genetic polymorphism of var genes, because var gene is the gene of *Plasmodium falciparum* parasite, but not of humans. The ethnic group diversity would be carefully interpreted in a study to investigate whether human genetics could influence malaria mortality or treatment efficacy [3,4].

2. Second, it might be interpreted that there is a high similarity between the observed pattern in the current report and previous data from other settings, but it might be difficult to conclude about the evolutionary changes. The evolutionary change should be based on a long-term follow-up and data should be collected from the same area.

Response: Long-term follow-up data are recommended to discuss evolutionary changes. The rapid evolutionary change can be caused by strong selective pressure such as species interactions and community structure [5]. To overcome the limitations of samples, we selected samples exposed to various species interactions and community structures. Then, a phylogenetic tree was created using var gene sequences reported around the world as well as obtained from culture-adapted malaria strain (3D7 and Dd2 strains) to examine the evolutionary degree and relationships among the populations. In the phylogenetic tree, it was analyzed that no rapid evolutionary changes would occur depending on sample distribution in clusters and the branch length [6].

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