RESEARCH NOTE

GENETIC DIVERSITY OF *PLASMODIUM VIVAX*MEROZOITE SURFACE PROTEIN-3α (*Pvmsp-3α*) GENE IN JHAPA DISTRICT OF NEPAL

Madhav Adhikari¹, Samir Ranjitkar², Mette Leth Schousboe², Michael Alifrangis², Mallika Imwong³, Dwij Raj Bhatta¹ and Megha Raj Banjara¹

¹Central Department of Microbiology, Tribhuvan University, Kirtipur, Kathmandu, Nepal; ²Center for Medical Parasitology, Department of International Health, Immunology and Microbiology, Copenhagen University Hospital, Copenhagen, Denmark; ³Department of Clinical Tropical Medicine, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

Abstract. In Nepal, *Plasmodium vivax* accounts for approximately 80-90% of the malaria cases, but limited studies have been conducted on the genetic diversity of this parasite population. This study was carried out to determine the genetic diversity of *P. vivax* population sampled from subjects living in an endemic area of Jhapa District by analyzing the polymorphic merozoite surface protein-3 α (*Pvmsp-3* α) gene by using PCR-restriction fragment length polymorphism. Three distinct genotypes were obtained from 96 samples; type A: 40 (71%), type B: 7 (13%), and type C: 9 (16%) which could be categorized into 13 allelic patterns: A1-A9, B1, B2, C1 and C2. These results indicated a high genetic diversity within the studied *P. vivax* population. As the transmission rate of malaria is low in Nepal, the diversity is most likely due to migration of people between the malaria endemic regions, either within the country or between Nepal and India. Similar prevalence of the three genotypes of *Pvmsp-3* α between the two countries likely supports the latter explanation.

Keywords: *Plasmodium vivax*, genetic diversity, merozoite surface protein-3α, Nepal

Correspondence: Madhav Adhikari, Central Department of Microbiology, Tribhuvan University, Kirtipur, Kathmandu, Nepal.

Tel: +977 98 41492485, +977 (0) 11681919

E-mail: madi_may@hotmail.com