



RESEARCH REPORT ON

GEOSPATIAL AND ETHNIC MAPPING OF

PLASMODIUM KNOWLESI

GENETIC VARIANTS IN SABAH

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ABSTRACT

Plasmodium knowlesi, an originally zoonotic malaria parasite is now increasingly recognized as a potentially virulent type of human malaria, particularly in South East Asia. Naturally acquired human infections with *P. knowlesi* emerged either as single infection or associated with other human *Plasmodium*, across the Southeast Asia with the highest prevalence in the Malaysian Borneo. Sabah is the second largest state of Malaysia situated on the Borneo Island. And this simian parasite *Plasmodium knowlesi* is a common cause of severe and fatal human malaria in Sabah, Malaysia. This study focused on the *P. knowlesi* isolates of Sabah principally on the blood samples of *P. knowlesi* malaria sent to the public health laboratory of Kota Kinabalu confirmed by Nested PCR Assay. From the DNA samples of *P. knowlesi* isolates, DNA sequencing was done to detect the genetic variants of *P. knowlesi* in different regions of Sabah. The PCR – DNA sequencing of *SSUr* RNA gene of *P. knowlesi* isolates points out that SNPs at continuous three nucleotide positions 278, 279 and 280 can produce the genotypic characteristics important from the epidemiological point of view. Although these genotypes are not consistent for each district of Sabah, these can help in epidemiological surveillance as only four genotypes are circulating in this area. For district specific genetic identity, genetic variations of the *csp* gene of *P. knowlesi* isolates should be attempted in the future studies.