Risk association, linkage disequilibrium, and haplotype analyses of ß-like globin gene polymorphisms with malaria risk in the Sabah population of Malaysian Borneo

ABSTRACT

Single nucleotide polymorphisms (SNPs) in the β-like globin gene of the human hosts to the risk of malaria are unclear. Therefore, this study investigates these associations in the Sabah population, with a high incidence of malaria cases. In brief, DNA was extracted from 188 post-diagnostic blood samples infected with *Plasmodium* parasites and 170 healthy controls without a history of malaria. Genotyping of the β-like globin C-158T, G79A, C16G, and C-551T SNPs was performed using a polymerase chain reaction-restriction fragment length polymorphism approach. Risk association, linkage disequilibrium (LD), and haplotype analyses of these SNPs were assessed. This study found that the variant allele in the C-158T and C16G SNPs were protective against malaria infections by 0.5-fold, while the variant allele in the G79A SNP had a 6-fold increased risk of malaria infection. No SNP combination was in perfect LD, but several haplotypes (CGCC, CGCT, and CGGC) were identified to link with different correlation levels of malaria risk in the population. In conclusion, the C-158T, G79A, and C16G SNPs in the β-like globin gene are associated with the risk of malaria. The haplotypes (CGCC, CGCT, and CGGC) identified in this study could serve as biomarkers to estimate malaria risk in the population. This study provides essential data for the design of malaria control and management strategies.