PP 10 Geographic structure of *Plasmodium vivax* in Sri Lanka

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Introduction and rationale

Sri Lanka plans to eliminate malaria within the next 5 years. The reported cases of *P. vivax* malaria in Sri Lanka have reduced drastically from 240,324 in 1999 to 445 in 2009 (World Malaria Report, 2009). In this backdrop, knowledge regarding genetic diversity and population structure of *P. vivax* in Sri Lanka would help to differentiate indigenous from imported parasite isolates within the country, enabling meaningful surveillance and control strategies to be implemented for the success of the elimination program. The aim of this study was to determine the genetic diversity and population structure of *P. vivax* patient isolates collected from Sri Lanka.

Methodology

Microsatellite typing was done on 190 *P. vivax* field isolates collected from Sri Lanka between1999 and 2008 using 14 highly polymorphic microsatellite markers. DNA templates for PCR amplification were extracted either from venous blood or filter paper blood spots. PCR was done using 1.5µl of genomic DNA in a final reaction volume of 20µl. All samples were PCR-amplified using fluorescent labelled primers and the PCR products were size fractionated by capillary gel electrophoresis. The single/predominant allele at each locus was used in computing allele frequencies. The presence of more than one allele at a particular locus was interpreted as a multiple-clone infection. Genetic diversity was determined by calculating heterozygosity (H_E) and standardized index of association (I^S_A) used to test for multilocus linkage disequilibrium. STRUCTURE software was used to test for clustering of haplotypes according to geographic and temporal origins.

Results

The parasite population was highly polymorphic with 189 unique haplotypes. The number of alleles per locus varied between 13 and 47. Almost 66% (n=125) had multiple-clone infections. Mean genetic diversity (H_E) was 0.8747. Significant multilocus linkage disequilibrium was present (I^S_A=0.0265, P<0.001). The population structure revealed temporal variations and partial clustering of *P. vivax* isolates according to geographic locations.

Conclusion

Microsatellite typing would serve as a useful tool for surveillance of *P. vivax* malaria within Sri Lanka enabling effective strategies for control depending on the origin of the parasite.

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