Conclusion

Cutaneous leishmaniasis is prevalent in Polonnaruwa and affects both sexes and a wide age range. Clinical appearance of lesions is non-specific, hence confirmation of diagnoses using laboratory methods is recommended. Seasonal variation in case numbers observed in the study might be due to the changing vector prevalence associated with environmental factors, which need further investigations.

PP2 Determining the geographical origin of *Plasmodium vivax* using five microsatellite markers, instead of twelve markers: a more cost effective tool

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Introduction

Malaria transmission in Sri Lanka remains low and unstable with a plan in place for its elimination within the next 5 years. Recent epidemiology of malaria in Sri Lanka consists of infections imported from other endemic countries and locally acquired sporadic cases with focal spread among non-immune residents. Identifying the source of infection is vital for the implementation of vigorous and targeted control strategies enabling successful elimination. Twelve previously validated microsatellite markers have proved to be useful in revealing the geographic origin and population structure of *P. vivax* parasites, which is a costly method to adopt. Aim of this study was to determine the minimum number of markers required to achieve the same outcome.

Methods

Data from 425 field isolates genotyped using a previously validated panel of 12 microsatellite markers (MS1, MS2, MS3, MS4, MS5, MS7, MS8, MS10, MS12, MS15, MS16 and MS20) was used. These field isolates comprised samples collected from Sri Lanka (140), Myanmar (167) and Ethiopia (118). Different combinations of microsatellite haplotypes (varying from 3 to 5) were tested using 2/3rds of isolates as a model for predicting the ancestry by using the Bayesian algorithm software STRUCTURE. Isolates

with predominant ancestry (>70%) were considered as members of that particular population. Genetic diversity was determined by calculating virtual heterozygosity (H_E) and standardized index of association (I^S_A) was used to test for multilocus linkage disequilibrium computed using LIAN 3.5 software.

Results

A combination of 5 microsatellite loci (MS1, MS2, MS5, MS15 and MS16) was identified which gave comparable results to those with 12 microsatellite markers used previously. Of the 142 isolates that were tested on this model, 47 were from Sri Lanka, 56 from Myanmar and 39 from Ethiopia. Percentages of test isolates that were correctly identified to have a predominant ancestry from either Asian or African origin were: 72.3% (n=34) for Sri Lanka (Asian), 62.5% (n=35) for Myanmar (Asian) and 76.9% (n=30) for Ethiopia (African), giving an overall predictive power of 69.7% (n=99). Mean genetic diversity (H_E) was: 0.6363 (Ethiopia), 0.7627 (Myanmar) and 0.8195 (Sri Lanka). Significant linkage disequilibrium was maintained for the Asian region (I^S_A=0.0126; P=0.001).

Conclusion

Microsatellite analysis with 5 markers appears to give comparable results to the 12 markers previously tested in determining the geographical origin of *P. vivax* parasite isolates, at least to continent level (Asian or African). Reduction in cost makes genotyping of parasite isolates a feasible tool for surveillance in the ongoing malaria elimination programme.

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