Introduction and rationale
Genetic diversity and population structure of P. vivax parasites can predict the origin and spread of novel variants within a population enabling population specific malaria control measures. The aim of our study was to determine the genetic diversity and population structure of P. vivax patient isolates collected from Sri Lanka, Myanmar and Ethiopia.

Methodology
425 P. vivax isolates collected from Sri Lanka (between 2003 and 2008), Myanmar (2007) and Ethiopia (between 2006 and 2008) were genotyped using 12 highly polymorphic microsatellite markers. The 12 markers were PCR-amplified using oligonucleotide primers with the forward primer labeled with fluorescent dyes. The PCR products were size fractionated by capillary gel electrophoresis. The single or predominant allele at each locus was considered for 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 (HE) and standardized index of association (ISA) used to test for multilocus linkage disequilibrium. STRUCTURE software was used to test for clustering of haplotypes according to geographic origins and ancestry of the isolates.

Results
All three parasite populations were highly polymorphic with 3-44 alleles per locus. Almost 65% were multiple-clone infections. Mean genetic diversity (HE) was: 0.7517 (Ethiopia), 0.8450 (Myanmar) and 0.8610 (Sri Lanka). Significant linkage disequilibrium was maintained. Population structure revealed two clusters (Asian and African) according to geography and ancestry. Strong clustering of outbreak isolates from Sri Lanka and Ethiopia was observed. Predictive power of ancestry using 2/3rds of isolates as a model identified 78.2% of isolates accurately as being African or Asian.
Conclusion
Microsatellite analysis appears to be a useful tool for mapping short-term outbreaks of malaria and for predicting ancestry.

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