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Genetic diversity of *Plasmodium falciparum* isolates based on MSP-1 and MSP-2 genes from Kolla-Shele area, Arbaminch Zuria district, southwest Ethiopia

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Background: The genetic diversity of *Plasmodium falciparum* has been extensively studied in various countries. However, limited data are available from Ethiopia. This study was conducted to evaluate the extent of genetic diversity of *P. falciparum* in Kolla-Shele in the southwest of Ethiopia.

Methods: A total of 88 isolates from patients with uncomplicated *P. falciparum* attending Kolla-Shele Health Centre was collected from September to December 2008. After extraction of DNA by Chelex® method, the samples were genotyped by using nested-PCR of *MSP1* (block 2) and *MSP2* (block 3) including their allelic families: K1, MAD20, RO33 and FC27, 3D7/IC1, respectively.

Results: Allelic variation in both *MSP1* and *MSP2* were identified in the 88 blood samples. For MSP1 67% (59/88) and MSP2 44% (39/88) were observed. K1 was the predominant msp1 allelic family observed in 33.9% (20/59) of the samples followed by RO33 and MAD20. Of the *MSP2* allelic family 3D7/IC1 showed higher frequency (21.5%) compared to FC27 (10.3%). A total of twenty-three alleles were detected; of which, eleven were from MSP2 and twelve from *MSP2* genes. Fifty-nine percent of isolates had multiple genotypes and the overall mean multiplicity of infection was 1.8 (95% CI: 1.48-2.04). The heterozygosity index was 0.79 and 0.54 for *MSP1* and *MSP2*, respectively. There was no statically significant difference in the multiplicity of infection by either age or parasite density ($p>0.05$).

Conclusion: This genetic diversity study showed the presence of five allelic types in the study area with dominance K1 in the MSP1 family and 3D7/IC1 in the MSP2 family. Multiple infections were observed in nearly 60% of the samples.

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Divergences in gene repertoire among the reference *Prevotella* genomes derived from distinct body sites of human

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In a human body, the distinct body-sites form unique niches for the resident microbiota. There has been an increasing amount of literature on the habitat-specific variations in the microbiome composition at the phylum, genus or species levels, not much information is available on the variations, at the genome/sub-genome levels of a specific microbial community across different niches. This report aims to explore, as a case study, the habitat-driven changes in the gene repertoire of 28 *Prevotella* reference genomes derived from different body-sites. Pan-genome analysis of *Prevotella* has yielded 24885 distinct gene families. Among these, 456 forms are the conserved core, 7263 are accessory genes and 17166 are singletons. The study reveals exclusive presence of 11798, 3673, 3348 and 934 gene families and exclusive absence of 17, 221, 115 and 645 gene families in *Prevotella* genomes derived from oral cavity, gut, urogenital-tract and skin, respectively. Distribution of functional COG categories differs appreciably among the niche-specific genes. Accessory and singletons show high frequencies of signal transduction mechanisms category in skin and gut isolates, while defense mechanisms category is over-represented among singletons of the urogenital-tract and some oral isolates. These observations clearly point towards the niche-specific modulation in genetic make-ups of microbiome components. Plausible metabolic/physiological implications of such niche-specific gene repertoire are now being investigated in an attempt to have an insight into the host-microbiome interactions at different body-sites. A novel computational pipeline for pan-genome analysis of microbial organisms has also been developed in course of this study.

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