

## Mapping of DBL $\alpha$ Sequence Tags of Field Isolates from Two Malaria Endemic Sites in Kenya

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### Abstract

*Plasmodium falciparum* Erythrocyte Membrane Protein 1 (PfEMP1) found on the surface of infected erythrocytes (IEs) mediate antigenic variation during *P. falciparum* infection enabling the parasite evade host immune responses and prolong infection. These molecules mediate binding of IEs to host endothelial cells and uninfected erythrocytes. Cytoadhesion of IE to host cells leads to sequestration in tissues and PfEMP1 is thought to play an important role in parasite virulence. Here we analysed 1725 sequence tags sampled from the DBL $\alpha$  region of PfEMP1 encoding “*var*” genes from 27 patients in two different geographical regions in Kenya, Mbita in Western Kenya and Twiga on the Kenyan coast. The objective of this study was to construct a network to assess the extent of shared position specific polymorphic blocks (PSPBs) in sequences isolated from genomic DNA of field isolates from the two malaria endemic sites in Kenya. Sequences from Mbita study site and those from Tiwi largely clustered into separate giant networks with only a limited number of sequences from the two sites linking to each other. This observation suggests that the parasite populations from the two endemic sites could be genetically varied and that PfEMP1 sequencing could be a useful tool of understanding the genetics of parasite populations. Thus the network approach of studying relationships between DBL $\alpha$  sequences is a useful tool of uncovering the genetic structure of parasite populations circulating in different malaria endemic regions.

**Keywords:** PfEMP1, Networks, Position Specific Polymorphic Groups, DBL $\alpha$ , Malaria, *P. falciparum*

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