

## **PfEMP1 DBL $\alpha$ Sequence Tags in Genomic DNA of *P. falciparum* Field Isolates from Two Malaria Endemic Sites in Kenya**

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### **Abstract**

#### **Background**

Malaria caused by *Plasmodium falciparum* remains a major cause of childhood morbidity and mortality in sub-Saharan Africa. PfEMP1 protein, coded for by a family of about sixty variant *var* genes, is a parasite protein found on infected erythrocyte membrane. PfEMP1 protein mediates cytoadherence of infected erythrocytes on endothelial cells which may lead to severe symptoms of malaria. Although PCR amplification of the whole gene is difficult due to high variability, primers targeting the DBL $\alpha$  domain have been designed and used to study *pfemp1* genes. This objective of this study was to establish the distribution of DBL $\alpha$  sequence tags in isolates of *Plasmodium falciparum* from two malaria endemic sites in Kenya.

#### **Methods**

DNA extracted from field isolates collected from Mbita (Western Kenya) and Tiwi (Coastal region) was used to isolate and amplify DBL $\alpha$  domain sequence tags of *pfemp1* by PCR. PCR products were sequenced by 454 next generation sequencing. After assembly, the translated protein sequences (GenBank KP085750-KP087726) were then aligned in Mega 5.2 and classified into cys/PoLV groups based on the number of cysteine residues and the motifs at PoLV1 and PoLV2 within the sequence tag. Six sequence groups were found in sequences from both endemic sites. Group 4 sequences were the most prevalent (57.35% and 57.07% in isolates from Mbita and Tiwi respectively) in the isolates from both sites. Sequence tags from Tiwi had a higher proportion of cys2 (group 1 and 2) than sequences from Mbita although individual group 2 sequence tags were slightly higher in Mbita tags. Similarly the proportion of

groups 5 and 6 sequence tags was higher in sequence tags from Tiwi than those from Mbita.

### **Conclusion**

In conclusion, the frequency of the different cyc/PoLV groups of DBL $\alpha$  sequence tags at both endemic sites follow almost similar pattern with group four sequence tags being the majority among the sequence tags isolated from patient isolates from both study sites. However, in the absence of expression data, the impact of this genomic distribution pattern on malaria pathology remains unknown.

Key Words: Malaria, PfEMP1, cys/PoLV, DBL $\alpha$ , var, Sequence tags

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