# Nucleotide Sequence Polymorphism in Region I of The Gene Encoding Erythrocyte Binding-Like Protein, *Ebl-1* In Kenyan *Plasmodium falciparum* Field Isolates

By
Abdirahman Issak Abdi

B.Sc (UoN)

A research thesis submitted in partial fulfilment for the requirement of the award of Masters of Science in Biochemistry of the University of Nairobi.

Department of Biochemistry

**School of Medicine,**
University of Nairobi

# DECLARATION

I**, Abdirahman Abdi** do hereby declare that this thesis is my original work and has not been presented for the award of a degree elsewhere.

Supervisors**:**

**Dr. W.D Bulimo** Date

---

Department of Biochemistry

University of Nairobi

**Dr. Githui Elijah Kem** Date

---

Department of Molecular Genetics

National Museums of Kenya

**Dr. P.P.M Wambua**. Date

---

Department of Biochemistry

University of Nairobi

**Chairman**, Department of Biochemistry, Date

---

School of Medicine, University of Nairobi

# ABSTRACT

Malaria is a major health challenge facing Africa where it kills one child every 30 seconds. A vaccine is the ideal long-term solution for resource poor countries but there is as yet no effective vaccine. Several merozoite surface proteins have been proposed as vaccine candidates and highly polymorphic regions have been observed within the genes coding for these proteins. The erythrocyte binding protein family, of which *ebl-1* is a member, encodes antigenic surface proteins that normally become recognised by the host immune system, and polymorphism observed in these genes is likely driven by immune pressure. This study investigated the level of polymorphism in region I of the *ebl-1* gene using the molecular population genetics approach.

*Plasmodium falciparum*-infected blood samples were obtained from four malaria endemic regions of Kenya. These were Kilifi, Kisumu, Embu and Busia from which 23, 6, 5 and 3 samples were collected respectively. Total genomic DNA was extracted from these samples and gene-specific primers were used to amplify region I of the *ebl-1* gene. The nucleotide sequences of the amplified products were obtained.

Several neutrality tests were applied on the DNA sequences of region I of the *ebl-1* gene from 37 field isolates. All the tests revealed that region I is under positive Darwinian selection acting to promote diversity at the amino acid level. These results suggest that region I of the *ebl-1* is under positive selection, presumably exerted by the host immune system. However, a 5 nucleotides frame shift insertion observed in the majority of the field isolates (84%), which, effectively knock-out the gene, suggests that this gene may not be an appropriate vaccine candidate.