

Genetic basis for *Anopheles arabiensis* refractoriness to *Plasmodium falciparum* in rice cultivating zones in central and western Kenya

ABSTRACT

Introduction and rationale:

Anopheles gambiae complex mosquitoes are amongst the most important vectors of malaria in sub-tropical Africa. Agricultural irrigation schemes have been reported to be highly infested with *Anopheles* mosquitoes. In areas of rice agriculture *Anopheles arabiensis* which is a member of the *Anopheles gambiae complex* is predominant mosquito species. *Anopheles arabiensis* is widely distributed in Kenya due to its ability to adapt to diverse ecological settings, including semi-arid areas. Refractoriness to the malaria parasites has been known to naturally occur in *Anopheles* mosquitoes. Determining the genetic basis of refractoriness in *Anopheles arabiensis* is a critical step towards the development of a refractory strain for eventual release into the wild for the control of malaria.

Objectives

General Objectives:

To investigate genetic basis of refractoriness in *anopheles arabiensis*

Specific Objectives

1. To determine refractoriness development of *plasmodium falciparum* in *anopheles arabiensis*
2. To determine Qualitative Trait Loci (QTLs) controlling refractoriness to *Plasmodium falciparum* in *Anopheles arabiensis*

Methodology:

Selection for refractoriness and susceptible phenotypes of *Anopheles arabiensis* will be carried out through artificial membrane feeding with blood infected malaria parasites and the oocysts counted by microscopic examination. Large numbers of micro satellite loci have been isolated in *Anopheles gambiae* and these have been found to amplify satisfactorily in *Anopheles arabiensis*. QTL mapping will be used to identify markers linked gene associated with the refractoriness to malaria parasites.