

## Genetic maps for malaria vectors

Hilary Ranson<sup>1</sup>, Mark Benedict,<sup>2</sup> Maureen Coetzee<sup>3</sup>, Janet Hemingway<sup>1</sup>, John Morgan<sup>1</sup>, Patricia Penilla<sup>4</sup>, Patricia Pignatelli<sup>1</sup>, Charles Wondji<sup>1</sup>

<sup>1</sup> Liverpool School of Tropical Medicine, Liverpool, UK

<sup>2</sup> Center for Disease Control, Chamblee, USA

<sup>3</sup> National Institute for Communicable Diseases, Johannesburg, South Africa

<sup>4</sup> Instituto Nacional de Salud Publica, Tapachula, Mexico

The sequencing of the genomes of disease vectors is providing vast datasets that facilitate the identification of genes controlling traits with relevance to vector control. However, for complex traits involving multiple loci, identifying these loci, and predicting their contribution to the final phenotype, can be a major challenge. We have used genetic mapping to identify quantitative trait loci (QTL) associated with insecticide resistance in *Anopheles gambiae*. As the genome sequence has been determined for this species, we were able to search for candidate genes within the QTL regions and screen each of these for their role in insecticide resistance. Several genes causing insecticide resistance in laboratory strains of *A. gambiae* have been identified in this manner and these are now being investigated directly in field populations.

Genetic maps are being constructed for two additional malaria vectors, *Anopheles funestus* and *Anopheles albimanus*. For *A. funestus* we have resolved four linkage groups that correspond to chromosomes X, 2, 3R and 3L. The resolution of this map is being increased by the addition of new microsatellite markers, identified in sequences from the *A. funestus* BAC library, and single nucleotide polymorphisms, identified by sequencing genes that have been physically mapped to the *A. funestus* genome. In collaboration with National Institute for Communicable Diseases, Johannesburg, South Africa, we hope to be able to use this map to identify QTL associated with pyrethroid resistance in *A. funestus* from Mozambique.

A microsatellite-based genetic map is also in progress for *A. albimanus*. To date, three linkage groups have been resolved which have been anchored to the three chromosomes of *A. albimanus* by linkage to chromosomally defined morphological markers. The majority of markers so far are located on chromosome two and additional markers are needed to improve the resolution on chromosome three and the X chromosome. Nevertheless this preliminary genetic map will be of value for population genetic studies in this species.