Researchers demonstrate adaptive potential of hybridization in mosquito species

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Researchers from LSTM have exploited a natural experiment created by insecticidal pressure to determine how the most important malaria vectors - *A. gambiae s.s.* and *A. coluzzii* – respond rapidly to environmental change.

Working with genome analysis specialists from the Wellcome Trust Sanger Institute and field entomologists in Ghana, LSTM researchers sequenced the genomes of individual wild mosquitoes of each species from southern Ghana. The results, published in *Nature Communications*, reveal that transfer of a major insecticide resistance mutation (kdr) resulted in replacement of over 3 million surrounding DNA bases (1.5% of the genome) of *A. coluzzii*, with that of *A. gambiae s.s.* This is especially significant because the two species are very closely related and the region replaced is one of relatively few areas of their genomes that are substantially different. Surprisingly, this apparently huge genomic disruption has had no detectable impact on reproductive isolation with hybridisation rates between the species in Ghana remaining low and stable despite a dramatic rise in frequency of the kdr mutation in *A. coluzzii*.

Dr David Weetman, co-first author and LSTM Lecturer in Population Genomics, said: "Our work demonstrates amazing flexibility in the genomes of closely related species. The genomic section replaced is not only huge but was previously considered a major 'speciation island'; a probable location for genes driving reproductive isolation between the species. The findings not only call into question the general importance

of 'speciation islands', but also importantly show that these closely-related mosquito species, can evolve largely separately but then interchange genetic variation to allow rapid adaptation to human-driven environmental changes.".

The two species, which co-occur throughout much of West and Central Africa, exhibit behavioural and ecological differences. *Anopheles coluzzii* is thought to be able to exploit relatively stable agricultural breeding sites, which can extend malaria transmission far into the dry season. *A. gambiae s.s.* has traditionally been the more insecticide resistant, but, with transfer of insecticide resistance mutations, this is changing. In addition to concerns for vector control, this presented a near-unique opportunity to investigate the popular theory that new species form through the development of pockets of divergence in the genome containing speciation genes. Driven by technological advances and early work on the *Anopheles gambiae* species pair, this has become a rapidly-growing area of research in evolutionary biology.

LSTM's Professor Martin Donnelly, senior author of the study, said: "Through our collaboration with the Wellcome Trust Sanger Institute we are learning how to use *Anopheles* genomic information to address questions of immense evolutionary and public health importance. This paper is just a foretaste of the studies that the vector community will be able to perform as the *Anopheles gambiae* 1000 Genome data sets become available (see http://www.malariagen.net/projects/vector/ag1000g)."

"This is a wonderful example of how new technologies for genome sequence analysis can elucidate specific biological questions in the field," says Professor Dominic Kwiatkowski, Head of the Malaria Programme at the Wellcome Trust Sanger Institute, whose team have worked closely with LSTM on this project.

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