

# Whole-genome sequence of the fruit fly *Drosophila mauritiana*

December 17 2012

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Credit: Biodiversity Institute of Ontario

In the twentieth century the sequencing of an entire genome of a higher (eukaryotic) organism was a truly exceptional event – by the end of the year 2000, only four such sequences were available. Since then, technological advances have put whole-genome sequencing within the reach of many more groups and new sequences have appeared at regular intervals. Viola Nolte in the group of Christian Schlötterer at the University of Veterinary Medicine, Vienna has just published the first whole-genome sequence of a eukaryote to be determined at this university. The results are published in the current issue of the journal *Genome Research* and reveal intriguing details about the evolution of the species.

The species in question is the fruit fly [Drosophila](#) *mauritiana*, a close relative of the well known (and previously sequenced) *Drosophila*

*melanogaster* that swarms around our fruit bowls in summer. Nolte and colleagues now present a complete [genomic sequence](#), annotating it to indicate the various genes it contains. The information will naturally be extremely useful to all those who are working on this organism.

But the present study goes much, much further. Schlötterer's group has recently developed powerful analytic methods for measuring the genetic variability of populations. In contrast to its widespread cousin, *Drosophila mauritiana* is only found on the island of Mauritius and it might be expected that the species' highly restricted distribution would lead to a relatively low rate of variability. Surprisingly, however, Nolte and her colleagues found that its genome is highly diverse, with polymorphisms ([genetic variation](#)) present across the [chromosomes](#). Interestingly, the polymorphisms are not evenly distributed throughout the genome. Instead, the researchers observed that within the highly variable regions there are two large areas where the sequence is much more highly conserved. Such "troughs in variability" are thought to be the result of selective sweeps: newly arising mutations confer so great a selective advantage on the flies in question that they spread rapidly through the population until they become "fixed", or present in essentially all individuals.

One of the classical tenets of genetics is that when a parent carries two different versions of a gene at a particular locus, each of the so-called alleles has an equal probability of being passed to the next generation. Recently, however, it has become clear that certain genes are able to "cheat" and ensure that they are preferentially transmitted to the offspring. The simplest model involves two genes close together, of which one encodes a poison to which the other confers resistance. The poison kills all the gametes that do not contain the resistance gene, effectively ensuring the rapid spread of the allele in question through the genome. Might the two "troughs in variability" in the *Drosophila mauritiana* genome have arisen from an intragenomic conflict of this

kind? It is hard to answer this question with certainty. However, one of the two troughs that Nolte identified contains the so-called Odysseus gene, which has previously been suggested to be involved in genomic conflict in the closely related *Drosophila simulans*. The other might relate to a second system characterized in *Drosophila simulans*.

The fact that two areas of the *Drosophila mauritiana* genome vary considerably less than surrounding regions suggests that some of the genes present have recently been involved in intragenomic conflicts. And these may indirectly help ensure the species' identity. As Schlötterer explains, "the biggest challenge for a newly separated species is to avoid being subsumed back into the species from which it derived. The weapons used in intragenomic conflicts also work against hybrids with related species so we can speculate that they act as a type of 'speciation gene'. It will be intriguing to study whether this has been the case for the Mauritius [fruit flies](#)."

**More information:** The paper "Genome-wide Patterns of Natural Variation Reveal Strong Selective Sweeps and Ongoing Genomic Conflict in *Drosophila mauritiana*" by Viola Nolte, Ram Vinay Pandey, Robert Kofler and Christian Schlötterer is published in the online version of the journal *Genome Research* ( [doi:10.1101/gr.139873.112](https://doi.org/10.1101/gr.139873.112) ). The printed version of the paper will appear in the journal's January 2013 issue.

Provided by University of Veterinary Medicine -- Vienna

Citation: Whole-genome sequence of the fruit fly *Drosophila mauritiana* (2012, December 17) retrieved 6 May 2024 from <https://phys.org/news/2012-12-whole-genome-sequence-fruit-drosophila-mauritiana.html>

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