

# Estimation of isolation times in the *Drosophila simulans* complex

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The *Drosophila simulans* species complex continues to serve as an important model system for the study of new species formation. The complex is comprised of the cosmopolitan species, *D. simulans*, and two island endemics, *D. mauritiana* and *D. sechellia*. A substantial amount of effort has gone into reconstructing the natural history of the complex, in part to infer the context in which functional divergence among the species has arisen. In this regard, a key parameter to be estimated is the initial isolation time ( $t$ ) of each island species.

In a study published on June 17, 2008 in *PLoS ONE*, Dr. Richard Kliman and colleague Shannon McDermott provide evidence that both island species were isolated at about the same time, estimated at ~250,000 years ago. They also show that the difference in divergence patterns of genes in regions of low and higher recombination can be reconciled by allowing a modestly larger effective population size for the ancestral population than for extant *D. simulans*.

"Essentially, this is about the formation of island species from mainland ancestors. We are particularly interested in the time that these isolation events occurred. Our approach is to estimate the key parameter, time in the past of initial isolation, from patterns of DNA sequence variation at several genes," says Dr. Richard Kliman, associate professor of biological sciences at Cedar Crest College. "The genes that we study show an unusual pattern of variation among species: those in parts of the genome characterized by low recombination appear to have become isolated more recently than those in the rest of the genome. This could

mean that the low recombination genes were able to move between species after initial isolation. However, we show that this explanation is not necessary. If the effective population size of the current mainland species (*Drosophila simulans*) is just a little bit lower than that of the ancestral mainland population, the levels of variation at the two classes of genes can be reconciled."

New DNA sequence variation data for 17 loci corroborate the prior observation from 13 loci that DNA sequence divergence is reduced in genes of low recombination. Two models are presented to estimate  $t$  and other relevant parameters (substitution rate correction factors in lineages leading to the island species and, in the case of the 4-parameter model, the ratio of ancestral to extant effective population size) from the multilocus DNA sequence data.

Loci in regions of low recombination have lower divergence within the complex than do other loci, yet divergence from *D. melanogaster* is similar for both classes. This might reflect gene flow of the low-recombination loci subsequent to initial isolation, but it might also reflect differential effects of changing population size on the two recombination classes of loci when the low-recombination loci are subject to genetic hitchhiking or pseudohitchhiking.

"This 2-parameter model is of potential utility to researchers working on non-model organisms. DNA sequence data at multiple genes are required from the island – or otherwise long-term isolated – species of interest, its closest mainland ancestor and a third species that is closely related to both (although the island and mainland species must be more closely related to each other than either is to the third species)," says Kliman.

"Also, with the number of researchers studying the functional divergence that contributes to speciation (specifically, to decreased fitness of hybrid offspring), getting accurate estimates of isolation times for the

*Drosophila simulans* complex will allow researchers to estimate the rate at which functional divergence accumulated."

Citation: McDermott SR, Kliman RM (2008) Estimation of Isolation Times of the Island Species in the *Drosophila simulans* Complex from Multilocus DNA Sequence Data. PLoS ONE 3(6): e2442.

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