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Comparative Phylogeography of Four Hawaiian Damselfly Species



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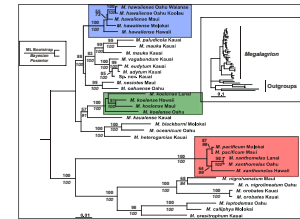
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The question:

Dominant processes in Hawaiian biogeography and phylogeography can be inferred from phylogenies, and include 1) **progression** from old islands to young, 2) adaptive **radiation** within islands, 3) **unresolved** and **stochastic** phylogenies, which indicate recent colonization events and/or frequent interisland dispersal, and 4) **back dispersal** up the island chain^{1,2}. For any specific taxon, these patterns may be the result of a dynamic tension between 3 classes of factors, more or less respectively: 1) the geological history of the Hawaiian Islands, 2) the immediate environment with the resources and interactions it presents, and 3) the characteristics of the individual organisms themselves (e.g., dispersal ability). Of course, there is a great deal of overlap between these classes, and their influence on a particular taxon can be qualitatively plotted on a triangular continuum (see below). Here, we use this dynamic framework to compare phylogeographic patterns of 245 individuals from 4 widespread species of Hawaiian damselfly.

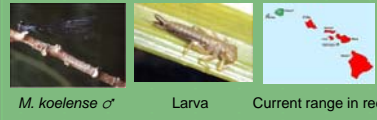
The players:



Tree based on nuclear (~1000 bp) and mt. DNA (~1300 bp)

Megalagrion koelense

- Larvae live in plant leaf axils
- Long thought to be at least 3 species, recently synonymized
- 51 indi.'s sequenced, mt COII gene



Megalagrion hawaiiense

- Larvae live on waterfalls and seeps
- Described as at least two species
- High morphological variation across range
- 37 indi.'s sequenced, mt COII gene



M. xanthomelas & *M. pacificum*

- Larvae live in streams, ponds, pools
- Two closely related species
- Some populations endangered
- 157 indi.'s sequenced, mt COII gene



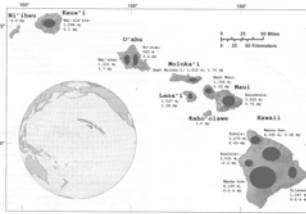
¹Wagner and Funk. 1995. Hawaiian Biogeography. Smithsonian Inst. Press.

²Roderick and Gillespie. 1998. Speciation and phylogeography of Hawaiian terrestrial arthropods. Molecular Ecology 7:519-531.

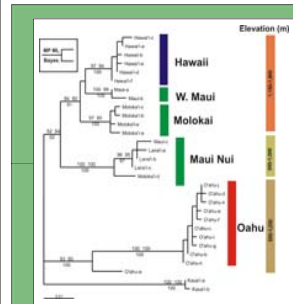
The data:

About 660 bp of the mitochondrial COII gene sequenced from 245 individual damselflies, representing every island where these four species now occur. Analyzed with Maximum Parsimony (MP) and Maximum Likelihood (ML) heuristic and bootstrap searches, and Bayesian analysis.

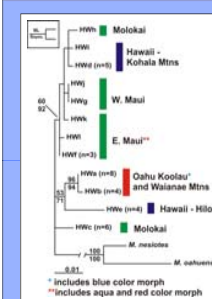
The stage:



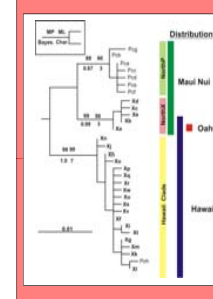
The Hawaiian Islands formed sequentially as the Pacific tectonic plate drifted over a stationary hotspot. The islands are arranged linearly by age. Molokai, Lanai, Maui, and Kahoolawe connect to form the super-island of Maui Nui during periods of low sea stands (i.e., glacial maxima). Maui Nui was once connected to Oahu (about 2 mya), but never to Hawaii.



- Contrary to known historical island connections, the largest genetic divergence is between Oahu and Maui Nui/Hawaii
- A strongly supported clade is correlated with altitude and may merit species status



- Virtually no geographic/genetic correlation suggesting extensive dispersal between islands
- Most clades are from one island
- Haplotypes shared by individuals with highly varied color and genital morphologies

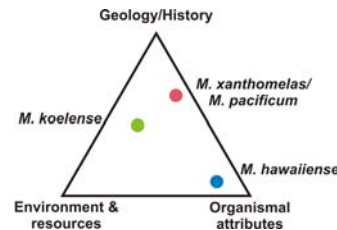


- In accordance with known historical island connections, the largest genetic divergence is between Oahu/Maui Nui and Hawaii
- Very little dispersal across ocean channels
- Low genetic diversity on Maui Nui suggests repeated bottlenecks as range varied with sea level change

The conclusions:

Although these 4 species are closely related, very different factors have dictated their phylogeographic histories. We have attempted to summarize the interplay between these factors for each group using the triangular continuum at right. It is significant that closely related taxa show such historical variation, suggesting that our desire for universal rules of community assembly should be tempered by the particular.

One could argue that these species are highly vagile compared to other Hawaiian taxa studied phylogeographically (e.g. snails¹, spiders², and *Drosophila*³), and thus merit plotting closer to the organismal pole. This illustrates that this continuum approach is qualitative and subjective, and works best within, rather than between studies. Nevertheless, valuable insights can be gained from its use.



Megalagrion koelense

- Poor dispersers living at higher elevations
- Their distribution is mainly influenced by their ecology (elevational needs) and the physical barriers between islands
- Should probably be split into 2 or more species

Megalagrion hawaiiense

- Use a variety of water habitats and appear to cross ocean barriers between islands fairly easily
- Distribution appears to be mainly influenced by their good dispersal abilities and their flexibility in habitat selection

M. xanthomelas & *M. pacificum*

- Disperse well within islands, but not between
- Genetic patterns most closely mirror geological record
- Hawaii Island population is very divergent, suggesting incipient speciation

¹Holland and Hadfield. 2002. Islands within islands: phylogeography and conservation genetics of the endangered Hawaiian tree snail *Achatinella mustelina*. Molecular Ecology 11:365-375. ²Roderick and Gillespie. See above. ³Piano et al. 1997. Phylogeny of the island populations of the Hawaiian *Drosophila grimshawi* complex: evidence from combined data. Mol. Phylo. and Evol. 7:173-184.