

Population Genetics Project #3

Due 15 May 2001

Damselflies in the genus *Megalagrion* are endemic to the Hawaiian islands. As part of his dissertation research Steve Jordan has collected nucleotide sequence data from mitochondrial genes of the widespread *M. xanthomelas*. He's identified two classes of haplotypes, *xantho* (x1–x23 in the data you'll be analyzing), and *pacificum* (p1–p8), and he has data on the frequency of each haplotype from 12 populations. Your task is to use **Arlequin** and **nucleodi**¹ to analyze the pattern of genetic differentiation among these populations and to use that pattern to say what you can about the history of divergence among these populations. The types of questions you'll want to address will include:²

1. Is there evidence for natural selection on nucleotide sequence diversity in any of the population samples? If so, how might it affect phylogeographic analyses, which assume that population divergence is a result of drift, mutation, and limited migration?
2. Is there an identifiable pattern of historical relationships among populations, i.e., do some populations clearly have more recent historical connections than others?
3. Do the haplotype classes Steve identified, *xantho* and *pacificum*, identify populations with unique evolutionary histories?
4. If there are identifiable patterns of historical relationships among the populations, what kind of biogeographical story do they tell? Does it appear, for example, that the oldest lineages are found on the oldest islands?³ Are populations on the same island more closely related to one another than they are to populations on different islands?

There are two data files available on the course web site. **xantho.arp** is in **Arlequin** format and includes everything you'll need for an AMOVA analysis, except the population structure specification.⁴ **xantho.txt** is in **nucleodi** format and is ready for the analysis.

Note on running nucleodi: If you run **nucleodi** on the machines in the EEB computer lab, I recommend copying **nucleodi.exe** from 'c:\Program Files\EEB348\nucleo' to a directory under your personal folder. You'll then need to go to a DOS prompt, **cd** to that directory, and run the analysis in that directory (**nucleodi xantho.txt > xantho.out**).⁵

¹The primitive program I showed you in class on Friday.

²This list isn't exhaustive. Other questions may occur to you. You should answer them if they do. If you don't know how to answer them, you should at least mention what they are.

³I'll get a map with population locations up on the course web site by Wednesday or Thursday.

⁴I ran the data with a population structure specification that Steve provided, and everything worked just fine.

⁵**xantho.txt** is, of course, the input file. **xantho.out** is the output file. You can name it anything you want as long as you keep the part before the period 8 characters or shorter and the part after the period 3 characters or shorter. I wrote this program a long time ago, and it hasn't been modernized.