



Genetic diversity and the dynamics of metapopulations

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Summary

Habitat fragmentation has important consequences for the genetics and dynamics of populations. As such, ideas concerning the effects of fragmentation have become an important part of conservation biology, often under the name of metapopulation biology. A metapopulation is a group of subpopulations that live in discrete habitat patches, but may be connected by dispersal. While much work on metapopulations has looked at genetics and dynamics separately, there is a growing body of literature examining the relationship between these two aspects of metapopulation biology. In this study I examined how patterns of genetic diversity can be used to gain insights into various aspects of metapopulation dynamics.

The thesis can essentially be divided into two sections. In the first section I considered the relationship between the rate at which individuals enter a population, and their impact in terms of gene flow. In particular, I addressed one of the assumptions involved when using genetic diversity data to infer immigration rates between habitat patches: that immigrants have the same fitness as population residents. For this I performed a laboratory experiment, using *Drosophila melanogaster*, to measure the genetic contribution of single male immigrants to small, inbred populations. Genetic contribution was assessed by measuring the relative frequency of immigrant marker alleles. When immigrants were outbred, the mean frequency of the immigrant allele was significantly higher than its initial frequency, as early as one generation after immigration. There was no significant change in allele frequency for populations receiving inbred immigrants. The increase in allele frequency for outbred immigrants was attributed to an initial outbred vigour fitness advantage of immigrant males over resident males experiencing inbreeding depression. Furthermore, hybrid vigour of immigrant progeny and the rare male effect did not have a statistically significant role in the fitness advantage of the immigrant allele. These results, based initially on parametric analyses, were also supported by randomisation tests and bootstrap analyses.

The results of this experiment add to our understanding of the complex relationship between the rate at which immigrants arrive into a population and their impact in terms of gene flow. This work also has implications for understanding the rescue effect, whereby immigrants may

rescue extant populations from extinction. In particular, this study suggests that large, outbred populations may be valuable for their contribution to the genetic diversity of small, inbred populations.

In the second section of the thesis I explored the value of using genetic diversity data to make qualitative "rules of thumb" decisions when managing the dynamics of metapopulations. In particular, I examined whether ranking patches based on genetic diversity provides a good estimate of the relative value of those patches in terms of their contribution to metapopulation persistence. The logic behind this approach is that the same features that make a patch valuable for metapopulation persistence also tend to increase the genetic diversity of the subpopulation occupying that patch. Thus, a large, centrally located patch is expected to (1) be valuable for maintaining metapopulation persistence, and (2) support a genetically diverse subpopulation. I explored this potential link between genetic diversity and relative patch value using an individual-based computer simulation model for two taxa with very different life history properties: owls and rodents. The model was run over a number of scenarios: three-patch and eight-patch metapopulations, with and without catastrophes, with sex-biased and unbiased dispersal, and over a range of dispersal rates. For each scenario, the relative value of two patches to the metapopulation was assessed by measuring the effect of patch removal on the metapopulation's 100-year extinction probability, as determined by simulation. The question was whether a measure of the relative genetic diversity for the two patches could reliably identify which of the two was most valuable for metapopulation persistence. The probability of correctly ranking patches was then estimated by simulation, based on a number of measures of nuclear and mitochondrial DNA diversity.

In some scenarios, genetic diversity provided very good predictions of relative patch value, with a greater than 90% chance of correctly ranking the two patches in question. However, in other scenarios this predictive accuracy was as low as (or sometimes lower than) the null hypothesis of 50% (equivalent to randomly assigning relative patch value). Importantly, this variation in predictive accuracy appears to be related to how different two patches are in value; the greater the difference in value between two patches, the higher the probability that we will rank them correctly using genetic diversity. This pattern suggests that biologists could make statements about the probability of correctly ranking patches as a function of the difference in patch value.

A relatively tight, positive relationship between relative patch value and the predictive accuracy of genetic rankings was found for owl metapopulations whose genetic diversity (mean number of alleles per locus) was sampled 40 years after the system was fragmented. It appears that with earlier samples there was too little time for the subpopulations to diverge in genetic diversity, while with later samples there was too great a chance that one or more of the patches would be unoccupied. Unfortunately it was not possible to explore the link between relative patch value and predictive accuracy of genetic rankings for rodent metapopulations beyond 10 years after fragmentation, as too many metapopulations contained unoccupied habitat patches. This limitation is attributable to the higher extinction probabilities of rodent metapopulations compared to owl metapopulations, which, in turn, is a reflection of the highly stochastic nature of rodent population dynamics. As such, one avenue for further study would be to model rodent metapopulations with larger, more extinction-resistant subpopulations. In summary, this second section of the thesis suggests that genetic diversity may, in some circumstances, provide a useful way of assessing the relative value of the various patches in metapopulations.