

The Effect of Spatial Population Structure on Levels of Genetic Variation

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ABSTRACT

A vast amount of genetic variation is a striking hallmark of natural populations, and is vital to the adaptation and long-term survival of a species. Just why this variation is there, however, is unclear: the two most prominent theories, selectionism and neutralism, appear to predict patterns of variation inconsistent with those observed in nature. Harvard geneticist Richard Lewontin has called this mismatch between theory and observation “the paradox of variation” and argued that it is the central problem in population genetics. Selectionist explanations have a number of theoretical difficulties. For instance, using computer simulations of single-population constant-viability selection models, Lewontin *et al.* showed that with more than about 5 alleles, the proportion of random combinations of fitnesses preserving polymorphisms was minuscule. This result was interpreted as implying that this standard form of selection (and maybe selection, in general) could not maintain the large numbers of alleles often found in natural populations. Subsequently, however, Spencer and Marks published a series of papers challenging this interpretation. Also using computer simulations, they showed that including recurrent mutation to new alleles in models of selection based on constant viability differences produced patterns of variation much closer to natural ones. Most importantly, it was easy to find selection schemes (i.e., sets of fitness values) that maintained high levels of variation. None of this modeling took account of any spatial structure in the simulated population, however. Here we examine a simple two-deme population with bidirectional migration between the demes, in which constant-viability selection acts independently in the two demes. We show that (i) the proportion of random fitnesses maintaining all alleles in this model is substantially greater than the proportion in the unstructured population model of Lewontin *et al.* and (ii) incorporating recurrent mutation into the model (analogously to the approach of Spencer & Marks) increases the number of alleles in the population for low migration rates but decrease this number for high rates, compared to both the structured model without mutation (result i above) and the unstructured model with mutation (the original Spencer & Marks result).

Keywords and phrases: population genetics, natural selection, subdivided population, genetic polymorphism, simulation model