

MECHANISMS OF GENETIC DIFFERENTIATION AMONG CONSPECIFIC POPULATIONS

Summary

The process of genetic differentiation among conspecific populations constitutes the first stage of speciation, and its understanding is crucial for the advance of evolutionary studies. However, the underlying ecological mechanisms controlling gene flow between populations are still poorly known. According to the classical population genetic theory, genetic differentiation among populations results from spatial isolation due to physical barriers to dispersal. In the absence of such barriers in contemporary distribution of a species, genetic differentiation among populations was usually explained by past fragmentation of a species range, e.g. as a result of isolation in different refugia during the Pleistocene glaciations. In many extant species of animals and plants, distinct evolutionary lineages have non-overlapping geographical distributions, and the time of their splitting is often estimated at several million years, suggesting their long-term geographical separation. However, genetic studies on remains of Pleistocene mammals revealed that the correlation between phylogenetic relationships and geographical distribution does not necessarily imply long-term genetic isolation. The distribution of lineages was shown to dynamically change over time due to lo-

cal extinctions and reinvasions. In some cases, range boundaries between genetically distinct populations were surprisingly stable despite lineage shifts, suggesting that they could have been shaped by ecological barriers that were relatively constant through time. Consistently, recent studies on extant populations of highly mobile animals with wide continuous ranges revealed cryptic genetic structure in the absence of physical barriers to dispersal, which may be shaped by ecological factors.

This suggests that ecological speciation may play an important role in the process of formation of new species. Studies on the role of ecological factors in population differentiation have been constrained by limited knowledge of the relationship between phenotype and genotype. However, recent advances in molecular biology opened the possibility of studying genome-wide variability in natural populations, enabling identification of the genetic background of traits influencing fitness. The synthesis of population ecology and population genetics seems to become possible, and it may be expected to lead to a fast advance in evolutionary biology in the nearest future.