

## Phylogeography

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The science of phylogeography is concerned with the principles and processes governing the geographic distributions of genealogical lineages, especially those at the intraspecific level. The word itself was coined in 1987, but the discipline's intellectual development began early in the century with studies of the population dynamics of surname turnover in human societies. The statistical and mathematical sides of phylogeography have developed in recent years into what is now termed coalescent theory, which addresses how, as functions of population demography, lineages trace back in time through extended pedigrees to common ancestors.

On the empirical side, phylogeographic analyses have been motivated primarily by molecular genetic appraisals of animal mitochondrial DNA (mtDNA). Because this molecule evolves rapidly and is maternally inherited without recombination, it provides a chronicle of matrilineal relationships within and among related species. Thus, phylogenetic analyses of mtDNA variants can be used to estimate the extended matrilineal component of an organismal pedigree in much the same way that family surnames in many human societies traditionally record patrilineal histories. Unlike surnames, however, the mitochondrial genetic archives extend much farther back in time and in principle can be recovered from nearly any multicellular animal species. For technical reasons,

comparable studies in plants often focus on another cytoplasmic genome – chloroplast DNA (cpDNA) – rather than mtDNA. A future challenge for the field of phylogeography centers on developing comparable genealogical methods for autosomal genes, a task made more difficult by a slow evolutionary pace for many nuclear DNA sequences and by the likelihood of historical intragenic recombination.

Comparative studies in molecular phylogeography have revealed the following: (1) Most species are composed of geographic populations whose members occupy recognizable phylogenetic branches in a matrilineal tree; (2) exceptional cases (in which phylogeographic population structure is minimal or nonexistent) usually involve highly vagile organisms, and/or species that have occupied historically continuous ranges; (3) historical population separations can range from temporally shallow to deep; and (4) pronounced phylogenetic gaps often observed between regional populations usually appear to have resulted from long-term biogeographic barriers to gene flow. Molecular phylogeographic patterns also are highly relevant to conservation biology and to an understanding of speciation processes.

In broad terms, the most important contributions of phylogeography to evolutionary analysis have been to: (1) emphasize the historical, nonequilibrium aspects of microevolutionary change, (2) clarify the tight connections between population demography and genealogy, and (3) build empirical and conceptual bridges between the nominally separate fields of population genetics and phylogenetic biology.

### Further Reading

Avise JC (1999) *Phylogeography: The History and Formation of Species*. Cambridge, MA: Harvard University Press.

**See also: 1016, 0995**