

Speciation and historical Migration pattern interaction: examples from *Pinus nigra* and *Pinus sylvestris* phylogeography

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Abstract

Here, from macrophylogeographic *mtDNA* empirical data, we proposed a scenario of the evolution and speciation of two important forest trees, European Black Pine and Scotch Pine, and their multiple subspecies and varieties. Molecular clock simulations revealed that *INDELs* variability in the *Pinus* mitochondrial genome is relatively old, i.e., from the Pliocene-Miocene epoch, and related to historical tectonic continental fluctuations rather than climate change on a large geographic scale. Special attention is paid to the relationships between different speciation models and historical migration patterns and between peripheral and central populations. Species evolution involves the mixing of different speciation modes rather than only one of them, and one speciation mode has different results/effects on different DNA types (e.g., mitochondrial vs. chloroplast

vs. nuclear DNA). The misbalance between different meta-population *census size* vs. effective population size contributions for asymmetric migration pattern is a result of different genotypes (and sub-phylogenetic lines) responding to selection pressing and *adaptive evolution*.

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