

A brief introduction of studies and methods for a speciation model with gene flow

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ABSTRACT

The studies of speciation used to focus on the morphology, reproductive behavior, genetics, or biogeographic patterns of species. With the recent development of molecular biology, we now have much more powerful and useful tools to study speciation in addition to traditional means. In the last decade or so, gene flows among population were no longer considered as obstacles for speciating processes. When the view of units of speciation shifting from the whole-genome to individual genes, speciation and gene flow appear to be able to coexist. Many studies have identified the speciation gene that caused species to diverge. At the same time, advanced computer programs were employed to estimate important parameters of population genetics, including effective population size (N_e), divergence time (t), and migration rate (m), and to help infer the amount of gene flow during speciation. The view of speciation with gene flow has shifted from whether or not it can happen to how did it works, and what were the underlying mechanisms. Nevertheless, the field still need more empirical data to assess whether this mode of speciation can be applied to non-model organisms and wild populations in general.

Keywords: Species concept, speciation gene, effective population size, divergence time, migration rate, IM