

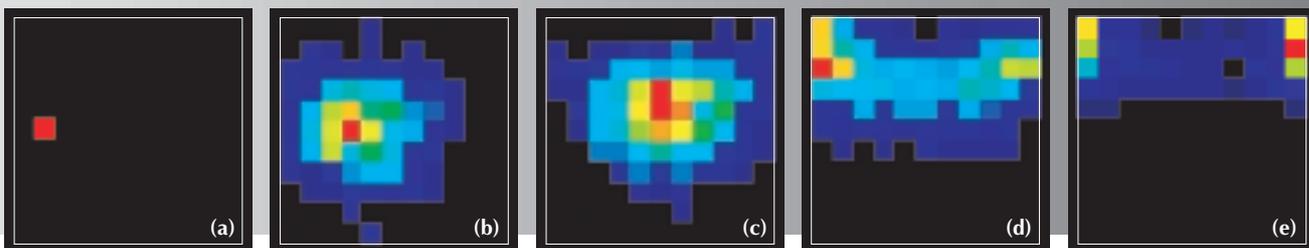
Adaptive Speciation

Conventional wisdom holds that new species primarily arise from a common ancestor when populations become isolated geographically—a process known as allopatric (“other homeland”) speciation. Yet empirical evidence, based on recent studies of various species of plants and animals, indicates that new species can also occur as a result of sympatric (“same homeland”) speciation, where subpopulations that no longer look alike or mate with each other appear within a single geographic habitat.

Research by IIASA’s ADN project has strengthened the theoretical foundation for sympatric speciation by incorporating population genetics and mating mechanisms into ecological models. ADN’s models show that situations in which individuals must compete for resources can often select against the predominant type and lead to selective mating. When individuals mate primarily with others like themselves, a sexually reproducing population can split into two subspecies. Over multiple generations, these subspecies cease to mate with each other, and their genetic makeup diverges. Such evolutionary branching can occur either if the mating choice depends on a trait directly related to fitness in the environment, such as body size or temperature preference, or if it is based on a selectively neutral trait, such as coloration or courtship behavior. In the former case (see figure below), however, scientists predict that speciation will proceed more rapidly.

The recent paper “On the Origin of Species by Sympatric Speciation,” by Ulf Dieckmann and Michael Doebeli (*Nature* **400**; 22 July, 1999) attracted considerable attention among geneticists and ecologists. ADN’s 1999 workshop, held at IIASA, focused on “The Formation of Biodiversity through Adaptive Speciation”; the papers presented at the meeting will serve as the basis of the fifth volume in the *Cambridge Studies in Adaptive Dynamics* series. For a complete list of ADN publications on this topic, visit the IIASA ADN Web page www.iiasa.ac.at/Research/ADN/Speciation.html.

ADN’s findings hold for wide ranges of competitive interactions and have also been demonstrated to apply to all other fundamental types of ecological interaction. Other researchers confirm that ADN’s approach solves problems that have undercut other models of disruptive selection. These results could change the way scientists view the generation of biodiversity by speciation processes—a topic still vigorously debated 140 years after Charles Darwin’s groundbreaking treatise *On the Origin of Species* appeared in 1859.



Evolutionary branching can lead to sympatric speciation in sexual populations. Loci in this individual-based multi-locus model are diploid, diallelic, and additive, and recombine freely. The five figures show the evolution of the frequency distribution of phenotypes (from high to low: red, orange, yellow, green, cyan, blue, black) for two metric traits: an ecological character (horizontal) and a second character that determines type and degree of assortative mating (vertical: upper half = assortative; lower half = disassortative). (a) Evolution starts from a randomly mating population; (b) directional selection drives the population toward an evolutionary branching point located at the center of the horizontal axis; (c) disruptive selection at the branching point induces increased degrees of assortative mating; (d) after this increase, disruptive selection can split the phenotypic distribution into two branches; ultimately (e) gene flow between the two branches essentially ceases.