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FOCUS

PROJECT

How Common is Speciation in the Face of Gene Flow?

One of the oldest and most controversial debates in evolutionary biology concerns whether populations can diverge to form new species under conditions where there is interbreeding between the populations (i. e., gene flow in sympatry or parapatry). Theoretical models have shown that speciation in the face of gene flow is possible, and a few relatively well-accepted examples from nature now exist. The critical question - how common speciation with gene flow is - has not been systematically evaluated. The answer to this question determines whether this process is an important component of the origins of species diversity on earth. I propose to apply standardized population-genetic analyses to a large and unbiased sample of published DNA sequences from numerous pairs of sister species to objectively test how common speciation with gene flow is. Additionally, I will estimate the magnitude of gene flow that occurs during speciation.

Recommended Reading

Nosil, P., S. P. Egan and D. J. Funk. 2008. "Heterogeneous genomic differentiation between walking-stick ecotypes: 'isolation by adaptation' and multiple roles for divergent selection." Evolution 62: 316-336.

Nosil, P. 2007. "Divergent host-plant adaptation and reproductive isolation between ecotypes of Timema cristinae." Am. Nat. 169: 151-162.

Nosil, P., B. J. Crespi and C. P. Sandoval. 2003. "Reproductive isolation driven by the combined effects of ecological adaptation and reinforcement." Proc. R. Soc. Lond. B. 270: 1911-1918.

COLLOQUIUM, 20.01.2009

Natural selection and the (incomplete) formation of new species

Natural selection is a central mechanism of evolutionary change within species. Recent years have seen renewed efforts to test the degree to which natural selection is also responsible for the formation of new species (i.e. speciation). Under such a scenario: (1) populations living in different ecological environments (e.g. desert versus forest habitats) undergo divergent evolutionary change via natural selection, to better adapt them to their respective environments and (2) these same evolutionary changes also result in the populations evolving into separate species. For example, adaptation to different environments might cause differences between populations in the way individuals tend to look, smell, and behave. In turn, these differences might cause individuals from different populations to dislike mating with one another. Thus, the populations cease to interbreed, thereby diverging into separate species because of the changes that occurred via natural selection.

I review recent support for this 'ecological speciation' hypothesis, from case studies as well as from a comparative analysis of over 500 species pairs of plants and animals. However, although natural selection appears to commonly promote the speciation process, it does not always complete it. For example, adaptation to different environments often causes some mating incompatibility between populations, but not to the extent that distinct species are created. I review an example of such 'incomplete' speciation in walking-stick insects. I close by outlining two hypotheses for why natural selection varies in the degree to which it promotes speciation. These hypotheses consider the fact that natural selection can vary in how strong it is, and in how many characteristics of an organism ('traits') it affects. Under a 'stronger selection' hypothesis, the completion of speciation can occur when natural selection acts on just one or a few characteristics of an organism, so long as natural selection on those characteristics is very strong. Under a 'multifarious selection' hypothesis, the completeness of speciation is positively related to the number of different characteristics of organisms that are affected by selection.

In essence, are distinct new species created via large evolutionary change in one or a few characteristics (e.g. a large differences in body size alone), or smaller changes in many different characteristics (e.g. smaller differences in body size and color and behavior and smell)? I describe recent advances in addressing this question that use manipulative experiments and genome-wide molecular DNA methods. These data may allow a more complete understanding of how the formation of new species unfolds, from beginning to end.

Nosil, Patrik (London,2013)

Sexual dimorphism dominates divergent host plant use in stick insect trophic morphology

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1665013435

Nosil, Patrik (London,2012)

Establishment of new mutations under divergence and genome hitchhiking

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1683950690

Nosil, Patrik (London,2012)

Genomic divergence during speciation : causes and consequences

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1683949102

Nosil, Patrik (Oxford,2012)

Ecological speciation

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=717994678

Oxford series in ecology and evolution

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=717994678

Nosil, Patrik (New York, NY,2011)

Ecological divergence and the origins of intrinsic postmating isolation with gene flow

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1687132682

Nosil, Patrik (Amsterdam [u.a.],2011)

The genes underlying the process of speciation

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1049264436

Nosil, Patrik (2011)

Adaptive chromosomal divergence driven by mixed geographic mode of evolution

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1049263324

Nosil, Patrik (2010)

The role of gene expression in ecological speciation

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1665051396

Nosil, Patrik (2010)

The efficacy of divergence hitchhiking in generating genomic islands during ecological speciation

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1049264770

Nosil, Patrik (2010)

Widespread genomic divergence during sympatric speciation

https://kxp.k10plus.de/DB=9.663/PPNSET?PPN=1046028057