

The genomic basis of adaptations, the differences between species, and the mechanisms of speciation

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How do new species arise, and how quickly does this happen?
Evolutionary biologist Professor Axel Meyer from the University of

Konstanz and his team have come one decisive step closer to answering fundamental questions in biology. Upon evaluation of an extensive data set collected during extensive research on extremely young species of cichlids in crater lakes in Nicaragua, empirical evidence suggests that the evolutionary divergence of a population in the same geographical area into a new species is more likely to occur when many genes across the genome are involved in producing species-distinguishing characteristics. Additionally, new species can emerge within only a few hundred years. This contradicts the hitherto established theory that speciation is a slow process and that ecologically important interspecies differences with simple, genetically locally limited architecture are more likely to result in the formation of a new species than those on a so-called polygenic basis are. Ultimately, it is about the question that Darwin already asked: What is a species, and how and why do new species arise? The results of this large-scale multidisciplinary study have been published in the scientific journal *Nature*.

Which genes, and how many of them are involved in speciation?

In genetics, the question of emergence of [new species](#) translates into: What is the pattern of changes in the [genome](#) that leads to the emergence of new species? What happens genetically during the continuum from initially no differences within a population up to the completed speciation of reproductively separate species? Since his [doctoral thesis](#) in the 1980s at the University of California, in Berkeley, U.S., and since the end of the 1990s at the University of Konstanz, Axel Meyer has been researching the question of which and how many genes or genetic loci—i.e. regions on the genome—are involved in the development of adaptations and new species. Here, the focus is on the study of very young species of cichlids, often only a few hundred generations old, living in crater lakes in Nicaragua. Although all these fishes descended

from the same older original populations in the two large lakes of Nicaragua, Lake Managua and Lake Nicaragua, there are [fish populations](#) or even small species complexes of several species in each of the crater lakes that live exclusively in the respective [lake](#), with specific phenotypic differences that are sometimes found in very similar fashion in several lakes, i.e. seem to have developed independently several times.

Multiple phenotypes in the same crater lake

There are fishes with pronounced lips and others without lips, gold-colored and black and white fishes, fishes that differ from others by having particularly slender bodies or certain delicate or robust tooth shapes. These phenotypes originated within the crater lakes, thus in the same [geographical area](#) (sympatric speciation), without external barriers such as rivers or mountains favoring this by limiting gene flow by gene exchange through reproduction. Thus, this is not allopatric speciation.

The variations regarding the lips, color, body and tooth shape of the fishes are genetically rooted in the original population, as Axel Meyer and his team (especially Dr. Andreas Kautt, Dr. Claudius Kratochwil and Dr. Alexander Nater) were able to show after analyzing complete genomes of a total of almost 500 fishes from each of the small lakes. Thus, these represent not independently originated new mutations, but rather the sorting and selective choosing of the same original gene variants, which have re-assorted themselves in the individual lakes. Previously, it was unclear whether these are new species that have individually evolved through adaptation to new ecological conditions. In fact, the phenotypically different populations in the lakes also prefer to mate among themselves.

Many genes have a large effect

For Ernst Mayr, who helped to develop the biological species concept, this would be an indication that this is a species in its own right.

However, the new results of genome sequencing suggest otherwise. After the sequencing of more than 450 piscine genomes, crossbreeding experiments and genome-wide association (GWA), it was found that the conspicuous differences, such as lip size and color, in the genomes of these populations are determined by only one or two locally very limited genome regions via Mendelian inheritance. Fish with the same type of lips or color reproduce almost exclusively with each other. These genes did not lead to genome-wide genetic differences as would be expected between species. In contrast, surprisingly, the other sympatric species with the phenotypically far less conspicuous differences in body shape and special tooth shape showed much greater genome-wide genetic differences.

This means that many genes at many positions in the genome each make a small contribution to genetic differentiation with the effects effectively adding up over the entire genome and leading to the emergence of new species. The number of mutations in the entire genome between these young species is 10 times higher than in the physically very different polymorphisms of the large-lipped or golden versus black and white striped fishes, for example, that do not represent unique species.

The combined effect of many genes thus has a stronger effect on the development of new species. "This is not what we expected. It also contradicts large parts of the theory according to which individual loci with a great effect on the appearance of species, such as pronounced lips or colouration, should cause new species to develop more quickly," said Axel Meyer. And, it is especially surprising here, where the loci impact both the ecology and the choice of partners. "At least according to the criterion of the average difference in the entire genome, fishes with such conspicuous phenotypical differences are nevertheless not different species, but are at the level of mere polymorphisms (diversity) on the

speciation continuum."

Crater lakes constitute a natural experiment

The geographical situation makes the crater lakes a kind of natural experiment. The original [fish](#) populations originate from two much older neighboring lakes, to which there is no connection. This chain of crater lakes has been colonized by the fish populations independently of each other. When and how specimens from the original population got into each of the seven smaller lakes can only be calculated by simulation.

It took place, however, somewhere between just a few hundred and a few thousand generations ago, and there were not very many fish that colonized the crater lakes. The emergence of new [species](#) can thus, as demonstrated here, take place much faster than previously thought. Meyer compares the lakes with Petri dishes, all inoculated with the same initial genetic situation, which evolve independently over generations: "There are very few systems in the world, such as the Galapagos Islands or the [crater lakes](#) in Nicaragua, that are a natural experiment for evolutionary research."

More information: Contrasting signatures of genomic divergence during sympatric speciation, *Nature* (2020). [DOI: 10.1038/s41586-020-2845-0](#), www.nature.com/articles/s41586-020-2845-0

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