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Image: Ad Konings

Answer to Darwin's question

In a paper published in "Nature", evolutionary biologist Axel Meyer from the University of Konstanz analyses almost 500 genomes and provides answers to questions concerning the genomic basis of adaptations, the differences between species, and the mechanisms of speciation

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. And, what is more, 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 today's issue (28 October 2020) of the scientific

journal *Nature* that is available online at <https://www.nature.com/articles/s41586-020-2845-0>

(<https://www.nature.com/articles/s41586-020-2845-0>).

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, USA, 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 such without lips, gold-coloured 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 favouring this by limiting gene flow by gene exchange through reproduction. This is, thus, no “allopatric speciation”.

The variations regarding the lips, colour, 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 analysing 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 out 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 – known by his contemporaries as the “Darwin of the 20th century” who helped to develop the biological species concept – this would be an indication that this is a species in its own right. (Mayr, who was Axel Meyer's mentor from Harvard University, was awarded an honorary doctorate by the University of Konstanz in 1994 before passing away in 2005). 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 colour, 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 colour 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 ten 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 studied a "natural experiment". The original fish populations originate from two much older neighbouring lakes, to which there is no connection. This chain of crater lakes has been colonised 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 colonised 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."

Funding through an ERC Advanced GrantThe extensive investigations and laborious sequencing work were made possible by an ERC Advanced Grant from the European Research Council (ERC). For his project "Comparative genomics of parallel evolution in repeated adaptive radiations", Axel Meyer received funding of 2.5 million euros from 2012 to 2017. In addition to the team from Konstanz, the publication is co-authored by Professor Eugene Myers, and his colleague Dr Martin Pippel at the Max Planck Institute of Molecular Cell Biology and Genetics in Dresden and the Center for Systems Biology Dresden.

Facts:

- Original publication: Andreas F. Kautt, Claudio F. Kratochwil, Alexander Nater, Gonzalo Machado-Schiaffino, Melisa Olave, Frederico Henning, Julian Torres-Dowdall, Andreas Härer, C. Darrin Hulsey, Paolo Franchini, Martin Pippel, Eugene W. Myers, Axel Meyer: Contrasting signatures of genomic divergence in rapidly speciating crater lake cichlid fishes, *Nature*, <https://www.nature.com/articles/s41586-020-2845-0> (<https://www.nature.com/articles/s41586-020-2845-0>).
- Speciation in the same geographical area ("sympatric speciation") more likely to occur with on a polygenic basis than on a limited genetic basis (via Mendelian inheritance).
- Funded from 2012 to 2017 by an ERC Advanced Grant of the European Research Council (ERC) ("GenAdap" #293700) with 2.5 million euros
- Funding of several sub-projects, which were also incorporated into this publication, by the German Research Foundation (DFG). **More information** (<https://gepris.dfg.de/gepris/person/1621603?context=person&task=showDetail&id=1621603&>).



Image: Ad Konings



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- ↗ [Publication](https://www.nature.com/articles/s41586-020-2845-0) (<https://www.nature.com/articles/s41586-020-2845-0>).
- ↗ [Professor Axel Meyer's website](https://www.evolutionsbiologie-uni-konstanz.com/prof-dr-axel-meyer.html) (<https://www.evolutionsbiologie-uni-konstanz.com/prof-dr-axel-meyer.html>).