Understanding the genomic signature of coevolution

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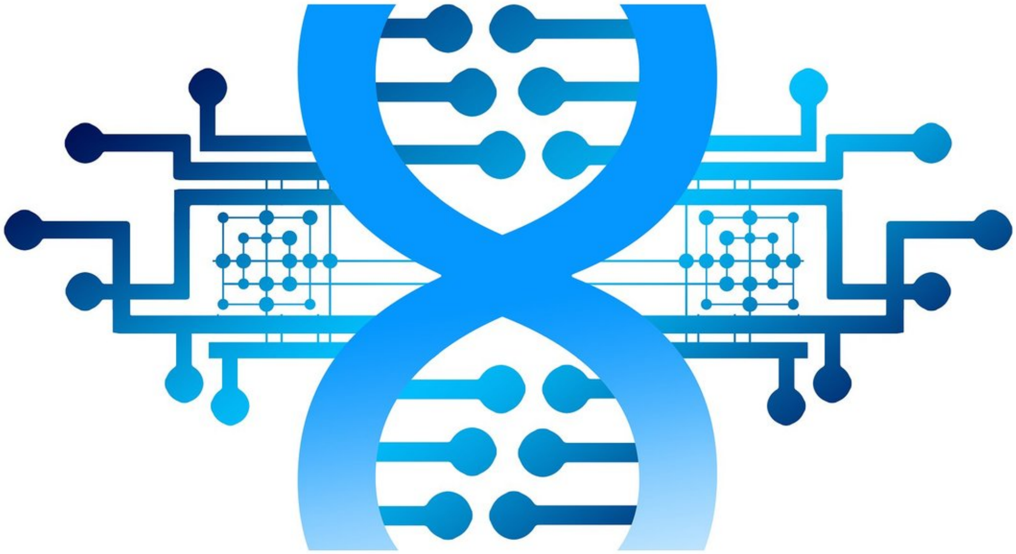

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An international team of researchers including limnologists from the University of Konstanz shows that rapid genomic changes during antagonistic species interactions are shaped by the reciprocal effects of ecology and evolution.

In a recent study entitled "The feedback between selection and demography shapes genomic diversity during coevolution," which is due for publication in *Science Advances* on 2 October 2019, researchers from Germany, Switzerland, China and the United Kingdom demonstrate that molecular evolution during species interactions is shaped by both eco-evolutionary feedback dynamics and interspecific differences in how genetic diversity is generated and maintained.

"Species interactions and coevolution are integral to ecological communities," explains Professor Lutz Becks, Professor of Limnology at the University of Konstanz and main author of the study alongside Dr. Philine Feulner from the Swiss Federal Institute of Aquatic Science and Technology. "Recent experimental studies on molecular evolution in host-virus systems show that coevolution has a significant impact on molecular evolution, host adaptation and diversification as well as speciation. The idea that host and virus adapt to each other by turns has been taken for a well-established fact for a long time," explains Lutz Becks. "Typically, after one round of resistance evolution—i.e. the point in time when the host evolves resistance to the parasite through a mutation and the parasite cannot infect and reproduce anymore—you would expect that the host population consists of only the resistant type. As mutations are rare, we always assumed that there is a long period after the resistance evolution during which there is not much diversity at all. However, what we have found in this study is that things are much more complicated than that. Diversity does in fact make a rather striking comeback within a very short period of time."

The researchers believe this to be due to the interplay between changes in selection—once the host has evolved resistance to the virus, the virus can no longer exert selection pressure—and population growth. Each new mutation after resistance evolution, even if it does not have an effect, increases in frequency because the host population at the same time rapidly expands in size, which in turn generates sustainable diversity. "This is new," says Lutz Becks. "We were really surprised by the speed of these processes and by how well we were able to track them."

The approach adopted in this study can best be described as experimental evolution, as Lutz Becks elaborates: "We create certain conditions by introducing microorganisms to an experimental environment and then study how properties of individuals within the populations change over time. By doing this, we are able to not only study one point in time, but to track the entire process over an extended period of time and even go back in order to compare different states with each other. In other words, we can confront a past state of the host with a virus state of the future, which provides us a fantastic opportunity for identifying evolutionary changes such as resistance evolution in the host or a counter adaptation in the virus." The experiment carried out for this study involved approximately 100 generations of hosts over a period of 100 days, allowing the researchers to track genomic, phenotypic and population size changes of the host and virus populations by gaining temporally resolved information on both.

The model system used involved Chlorella variabilis algae (host) and the giant virus Paramecium bursaria Chlorella virus 1 (PBCV-1), both of which reproduce exclusively asexually. Lutz Becks: "Typically, what one does is to take a sample, look at how much or little diversity there is and then interpret the results according to one of the well-established patterns for coevolution, which are traditionally placed on a spectrum between two extremes: the so-called "Arms Race dynamics' and the "Fluctuating-Selection dynamics'". For the purposes of their study, the researchers investigated a number of time points: "Looking at a point in time shortly after resistance evolution, there shouldn't be anything happening until the virus counter adapts. However, what we observed was that there was a lot of activity within the host population, involving the build-up of a much higher diversity than anticipated." By linking these changes in genetic diversity to changes in population size and the resistance and infectivity evolution, the researchers were able to prove that the build-up of diversity was the result of an eco-evolutionary feedback, where rapid evolution and ecological changes directly affect each other.

However, as the study also clearly demonstrates, the same cannot be said for the virus, for which the researchers observed the expected pattern of low diversity after a round of infectiveness evolution. They believe that this has to do with the organisms themselves, as Lutz Becks explains: "The host has a relatively large genome of 46 Megabase pairs (Mbp), which is probably much more flexible than the smaller genome of the virus, which is estimated to consist of only 330 Kilobase pairs (kbp). Size counts insofar as any mutation in the virus can have a negative impact, which means that it will not become prevalent." This suggests that differences in genome architecture result in distinctly different dynamics of molecular evolution between these two coevolving species.

The researchers expect that a wider recognition of the various ways by which ecological and evolutionary change can affect each other will be essential to unlocking the genomic signature of evolution during species interactions and to understanding the mode, pace and predictability of evolution in natural communities.

More information: Cas Retel et al. The feedback between selection and demography shapes genomic diversity during coevolution. *Science Advances*, 2 October 2019.
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Provided by University of Konstanz

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