Highlight: Applying the Biological Species Concept across All of Life

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Louis-Marie Bobay was not intending to redefine how we think of “species,” it all came about rather by chance.

“I was mostly focusing on gene flow, how recombination happens across bacterial strains,” says the University of Texas at Austin biologist. In the course of developing methods to quantify gene-flow and recombination across bacterial strains, he saw something.

“One day I realized when I was resampling a lot of strains because I could actually see that some strains were behaving very differently compared to the other ones,” says Bobay. “They seemed to be isolated from the other ones in terms of gene flow.”

He was working with nearly every type bacteria he could find, downloading entire sequence databases.

At the start, “I was just using those species which are very well studied,” such as E. coli and Salmonella. “But then the goal was to extend [the method] to every genome that has been sequenced.”

The results of his nearly 2-year analysis was recently published in Genome Biology Evolution in a paper titled “Biological species are universal across Life’s domains” (Bobay and Ochman 2017).

In it, Bobay and his co-author, Howard Ochman, propose a remarkable new view of bacterial species. They can be lumped, he believes, into communities that regularly swap genes, much as other species, such as plants and animals, are grouped by interbreeding individuals that are reproductively isolated from other groups.

Although Bacteria and Archaea reproduce asexually (via cloning), they can transfer and exchange genes though homologous recombination. “Here we show that barriers to homologous gene exchange define biological species in prokaryotes with the same efficacy as in sexual eukaryotes,” write Bobay and Ochman.

The suggestion is a remarkable and unifying idea: the way we define “species” in sexually reproducing eukaryotes can be extended to the entire tree of life. Naturally, as with all things in biology, it is not exactly that simple.

To start, there is more than one way to think of a species. Competing with the “biological species concept” is the “cladistic species concept,” the “cohesion species concept” and more than a half dozen other “species concepts.” And, of course, bacteria and archaea are not sexually reproducing, so at best the biological species concept can only be applied to them with modifications.

“The paper makes bold statements,” says Jesse Shapiro, an evolutionary genomics at the University of Montreal, “about things that apply across the tree of life, but nothing is universal.” That said, he believes Bobay and Ochman hedge themselves wisely.

“I think this is a very useful approach. I think it should be applied with some caution, but I think the authors appreciate that,” says Shapiro, who has floated related ideas, but was not involved in the current work.

Bobay’s method for analyzing bacterial genomes is appealing to researchers because it is genome-based, says Shapiro. “It can be applied in high-throughput, standard way, which doesn’t require specialized knowledge of each individual species.”

Bobay arrived at his method by resampling strains that are considered one species to see if the traces of gene flow would be different.

“So imagine you have 50 genomes of a species,” explains Bobay. “Instead of just analyzing 50 genomes together, I decided to randomly take 40 or 35 and recalculate the recombination rates across these different groups that are randomly chosen.”

He found that in a lot of species the amount of gene flow was very consistent in no matter what sample he would take. “And then I realized that in some of the species, whatever I would sample would have a very strong impact on the amount of gene flow and some [others] were at the point where the levels of gene flow was near zero,” says Bobay.

“That made me realize that in doing this resampling procedure we could actually try to identify strains that are not recombining [by homologous exchange] with the other ones.
and therefore they are basically sexually isolated just like in animals and plants.”

The question arises: how do bacteria speciate in the first place if they reproduce clonally? The work of Bobay and Ochman sheds light on this issue as well. Some researchers have suggested that divergence could happen when sequences within a population become too different (as a result of lack of recombination).

“Simulations have shown that the levels of difference needed for recombination to stop would have to be very, very divergent,” says Bobay, and it is unlikely that strains of different species are going to reach that level of divergence while recombining. “And our work really confirms that,” he says, “we really don’t see any correlations between the level of genome divergence and the recombination rates [in species].”

Bacterial speciation, then, is not likely to happen spontaneously. It suggests something is needed to trigger speciation: selection, for instance, or geographical barriers.

The method has already attracted the attention of some in the taxonomic community, who are trying to build pipelines to better analyze Bacteria and Archaea. This way of identifying microbes could also have an application in public health, where researchers must identify food or medial pathogens.

“Typically, if you have an epidemic of a pathogen blooming in a hospital, people generally try to identify what strain it is and what species it is,” says Bobay, “and I think that processing these data could be more relevant in this framework, as the current method basically relies on a few gene markers.”

With it becoming ever cheaper to sequence entire genomes, why not be more accurate?

Shapiro also sees wide ranging potential applications: “I think [this will be interesting] also for microbial and evolutionary biologist.”

Say a researcher finds evidence for a split in something she thought was a single species.

“I think it’s a great starting point to ask questions,” says Shapiro. Is there an ecological basis for a difference? What is causing the barrier to gene flow? It opens up new areas for research.”

**Literature Cited**

Bobay LM, Ochman H. 2017. Biological species are universal across Life’s domains. Genome Biol Evol. 9(3):491–501.

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