

JGlot: A Tool to Find the Nomadic Genes that Help Microbes Adapt – geNomad

Menaka: I'm Menaka Wilhelm, your microbe-focused emcee. Today, we're spending a few minutes with JGI researchers who have worked on a new way to comb through microbial genomes for useful information.

Because everywhere you look, microbes are shaping the environment. They're processing nutrients like carbon and nitrogen, absorbing chemicals — even some that might be toxic to other organisms. And — they're making and releasing other chemicals that fuel the organisms in their ecosystems. They're doing a lot, and they owe all of these skills to their genes.

So to get new skills, they've got to get new genes. That's also happening all the time, thanks to other tidbits, like plasmids and viruses — that hop around, spreading their DNA. To help explain, here's Simon Roux. He's a staff scientist at the JGI studying viral genomics —

Simon Roux: So yeah, so I was trying to come up with a good analogy to this.

Menaka: And here it is. Think about a microbe and its core genome as <bike wheels noises> a person on a bike — they've got what they need. Wheels, pedals, brakes. Super functional.

Simon Roux: It's here, it's stable, it's doing what it's supposed to do.

Menaka: But — not necessarily fancy. Genetic tidbits like plasmids and viruses can change that.

Simon Roux: So to me, they're a bit like the bags you put on your bike, maybe in your, you know, saddle bag you have, helping you go faster and, and it's a bag so you can kind of take it out, you can give it to your friend, you can take it from your friend, whatever.

Menaka: To Simon, these genetic tidbits <honk honk> are essentially bells and whistles for microbes. They've got a name — they're mobile genetic elements, or MGEs for short, and they can be important. What's a bike ride without a bell? <bell ding>

Simon Roux: The same microbe with different MGEs will behave differently in the way they cycle carbon or nitrogen or any other nutrients, or even the way they grow or compete with other microbes. So in the end, yeah, they do have a strong influence on everything we're interested in when we think of microbes.

Menaka: MGEs are key for adaptation. Instead of waiting around to evolve, a microbe with the right MGEs can nearly instantly do stuff like adapting to a warmer climate, or gaining antibiotic resistance. So for example, we could use MGEs to help useful soil

microbes handle climate change — or, on the flip side, knowing which MGEs matter for antibiotic resistance could help us slow that down.

And even though these MGEs are super common, and influential, they're also really varied. There are viruses, and plasmids, transposons, and gene cassettes — historically, they're hard to track.

Antonio Camargo: The only unifying principle that defines MGEs is something that we can't easily predict from sequence.

Menaka: Antonio Camargo is a JGI researcher who set out to sort out these MGEs. So he's saying, basically, what many MGEs have in common is that... we don't know about them. Which makes them tricky to understand — but not impossible.

Antonio, and Simon, as part of a team led by Nikos Kyrpides — have been working on a new software tool to find these mobile genetic elements within microbial genomes. Antonio took the lead on developing this software, and they've tested it on thousands of sequences from the JGI's Integrated Microbial Genomes and Microbiomes (IMG/M) database. It's both fast and precise. And as a tool, it will let other researchers do even more.

Antonio Camargo: People can use this in health settings to find plasmids with antibiotic resistance genes. We know that antibiotic resistance spreading is a problem nowadays. People can use this to find viruses and plasmids that encode genes that can be leveraged in biotechnology for, for example, delivery of DNA pieces via conjugation nucleases that can cut DNA and do editing.

Menaka: They'll be able to identify MGEs and sort out which ones are doing what — some are very useful, some are harmful, and some do nothing at all. But they're always moving around.

Menaka: So, a little bit nomadic.

Antonio Camargo: A little bit nomadic, yeah. <Laugh>.

Menaka: And in honor of the nomadic nature of these MGEs, this tool is called geNomad, which Antonio doesn't take credit for.

Antonio Camargo: It was actually my wife. At the time, she was my girlfriend, but it was my wife that named it.

Simon Roux: Yeah, I think it's a great name and so far people have, you know, embraced it.

Menaka: As a pre-print, the work received a Community Spotlight Award from Google's Tensor Flow. And now, they've published a paper on the geNomad tool in *Nature*

*Biotechnology*. The software is freely available online. We'll link it in our episode description and show notes.

Antonio Camargo: There you can find, you know, download links to use geNomad, guides on how to use it. A link to the GitHub with the codes, and also of course, a link to the manuscript that you can read.

<music>

Menaka: That's it for this JGlota. So again, that was Simon Roux and Antonio Camargo, sharing a bit about their recent paper in Nature Biotechnology. The senior author on that paper was Nikos Kyrpides. It's linked wherever you're listening.

This episode was written and produced by me, Menaka Wilhelm. I had production help from Allison Joy, Massie Ballon, Ingrid Ockert and Graham Rutherford.

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Genome Insider is a production of the Joint Genome Institute, a user facility of the US Department of Energy Office of Science located at Lawrence Berkeley National Lab in Berkeley, California.

Thanks for tuning in – until next time!