

Research team finds almost a million potential sources of next-gen antibiotics in the natural world

June 5 2024



Associate Professor Luis Pedro Coelho has used machine learning to explore the global microbiome to find almost a million antimicrobial peptides which could be used as antibiotics. Credit: QUT

Research [published](#) in the journal *Cell* by a team including Queensland University of Technology (QUT) computational biologist Associate Professor Luis Pedro Coelho has used machine learning to identify 863,498 promising antimicrobial peptides—small molecules that can kill or inhibit the growth of infectious microbes.

The findings of the study come with a renewed global focus on combating antimicrobial resistance (AMR) as humanity contends with the growing number of superbugs resistant to current drugs.

"There is an urgent need for new methods for antibiotic discovery," Professor Coelho, a researcher at the QUT Center for Microbiome Research, said. The center studies the structure and function of microbial communities from around the globe.

"It is one of the top public health threats, killing 1.27 million people each year."

Without intervention, it is estimated that AMR could cause up to 10 million deaths per year by 2050.

"Using [artificial intelligence](#) to understand and harness the power of the global microbiome will hopefully drive innovative research for better public health outcomes," he said.

The team verified the machine predictions by testing 100 laboratory-made peptides against clinically significant pathogens. They found 79 disrupted bacterial membranes and 63 specifically targeted [antibiotic-resistant bacteria](#) such as *Staphylococcus aureus* and *Escherichia coli*.

"Moreover, some peptides helped to eliminate infections in mice; two in particular reduced bacteria by up to four orders of magnitude," Professor Coelho said.

In a preclinical model, tested on infected mice, treatment with these peptides produced results similar to the effects of polymyxin B—a commercially available antibiotic which is used to treat meningitis, pneumonia, sepsis and [urinary tract infections](#).

More than 60,000 metagenomes (a collection of genomes within a specific environment), which together contained the [genetic makeup](#) of over one million organisms, were analyzed to get these results. They came from sources across the globe, including marine and soil environments, and human and animal guts.

The resulting [AMPSphere](#)—a comprehensive database comprising these novel peptides—has been published as a publicly available, open-access resource for new antibiotic discovery.

Professor Coelho's research was conducted as part of his ARC Future Fellowship through the QUT School of Biomedical Science, in collaboration with the Cesar de la Fuente laboratory at the University of Pennsylvania, Fudan University, the European Molecular Biology Laboratory and APC Microbiome Ireland.

More information: Discovery of antimicrobial peptides in the global microbiome with machine learning, *Cell* (2024). [DOI: 10.1016/j.cell.2024.05.013](#).
[www.cell.com/cell/fulltext/S0092-8674\(24\)00522-1](http://www.cell.com/cell/fulltext/S0092-8674(24)00522-1)

Provided by Queensland University of Technology

Citation: Research team finds almost a million potential sources of next-gen antibiotics in the natural world (2024, June 5) retrieved 23 June 2024 from

<https://medicalxpress.com/news/2024-06-team-million-potential-sources-gen.html>

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