

# Explosion in number of known life forms

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A total of 7280 bacterial and 623 archaeal genomes were obtained. Credit: University of Queensland

A remarkable effort from University of Queensland researchers has helped increase the number of known genomes by almost 10 per cent.

UQ School of Chemistry and Molecular Biosciences ARC Future Fellow Professor Gene Tyson said researchers obtained 7280 bacterial and 623 archaeal genomes (genetic materials from microorganisms) from [environmental samples](#).

That represents an almost 10 per cent increase on the 80,000 genomes currently in [genome](#) repositories.

"The real value of these genomes is that many are evolutionarily distinct from previously recovered genomes," said Professor Tyson, Deputy Director of the Australian Centre for Ecogenomics (ACE).

"They increase the evolutionary diversity spanned by both bacterial and archaeal genome trees by over 30 per cent, and are the first representatives within 17 bacterial and three archaeal phyla."

Professor Tyson said much microbial diversity remained to be discovered, with the majority of microbes seen under the microscope not being amenable to being grown under laboratory conditions.

"Less than one per cent can be cultured, due to challenging factors including slow growth rates, fastidious growth requirements, and the need to cross-feed off other species," he said.

However, recent advances in sequencing technology and computational techniques allowed microbial genomes to be recovered directly from environmental samples, bypassing the need for laboratory cultivation.

"The approximately 8000 genomes recovered move us closer to a comprehensive genomic representation of the microbial world, but also show that much remains to be discovered," he said.

ACE co-researcher Dr Donovan Parks said for the first time, science had the required tools to make substantial inroads into the vast diversity of phylogenetic and metabolic life.

"We anticipate that processing of environmental samples deposited in other public repositories will add tens of thousands of additional [microbial genomes](#) to the tree of life," he said.

"Numerous studies have been reported during the completion of this

research which have dozens or hundreds of evolutionarily diverse genomes from varying environments.

"The tools for obtaining genomes from environmental samples are continually improving and we expect that reprocessing the samples considered in this study will result in the recovery of additional genomes."

"Constructing a comprehensive genomic repository of [microbial diversity](#) lays the foundation for furthering our understanding of the role of microorganisms in critical biogeochemical and industrial processes."

The study, which also involves ACE researchers Director Professor Phil Hugenholtz, Dr Christian Rinke, Dr Maria Chuvochina, Pierre-Alain Chaumeil, Dr Ben Woodcroft and Dr Paul Evans, was published in *Nature Microbiology* .

**More information:** Donovan H. Parks et al, Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life, *Nature Microbiology* (2017). [DOI: 10.1038/s41564-017-0012-7](https://doi.org/10.1038/s41564-017-0012-7)

Provided by University of Queensland

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