

Researchers overturn wisdom regarding efficacy of next-generation DNA techniques

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DNA double helix. Credit: public domain

Metagenomics enables us to investigate microbial ecology at a much larger scale than ever before and sheds light upon the previously invisible diversity of microscopic life. A new study appearing in *Scientific Reports* reveals that a favored method for measuring microbial biodiversity is not as accurate as previously thought.

The article, titled "Large-scale differences in [microbial biodiversity](#) discovery between 16S amplicon and shotgun sequencing," is the

collaboration of an international team of researchers, including Dr. Mercer R. Brugler of City Tech, City University of New York (CUNY).

Modern metagenomic environmental DNA studies are almost completely reliant on [next-generation sequencing](#) (NGS), making evaluation of methods critical. The researchers compared two NGS techniques - amplicon and shotgun - on water samples across four of Brazil's major river floodplain systems (Amazon, Araguaia, Paraná, and Pantanal). Less than 50% of phyla identified via amplicon sequencing were recovered from shotgun sequencing, fundamentally challenging the dogma that shotgun recovers more diversity than amplicon-based approaches. Amplicon sequencing also revealed ~27% more families. Overall, the amplicon data were more robust across both biodiversity and community ecology analyses at different taxonomic scales.

This work doubles the sampling size of similar studies, and novelly integrates environmental data (e.g., pH, temperature, nutrients) from each site, revealing divergent correlations depending on which data are used. While myriad variants on NGS techniques and bioinformatic pipelines are available, the results point to core differences that have not been highlighted in any studies to date. Given the low number of taxa identified when coupling shotgun data with clade-based taxonomic algorithms, previous studies that quantified biodiversity using such bioinformatic tools should be viewed cautiously or re-analyzed. Nonetheless, shotgun has complementary advantages that should be weighed when designing projects.

The results of this study will have repercussions for previous analyses of microbial [biodiversity](#) that used shotgun data and for how microbial DNA is sequenced and/or analyzed from this point forward.

More information: Michael Tessler et al. Large-scale differences in microbial biodiversity discovery between 16S amplicon and shotgun

sequencing, *Scientific Reports* (2017). DOI:
10.1038/s41598-017-06665-3

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