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Exploring the Microbial Symphony - Unveiling the Dynamics of Biogas-Producing Communities

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Research on biogas-producing microbial communities focuses on uncovering the correlations and dependencies between process parameters and community compositions to optimize process stability and biogas output. The tremendous advances in High-Throughput (HT) sequencing technologies have shifted the study of microbiomes predominantly to metagenome research methods. Thousands of Metagenomically Assembled Genomes (MAGs) have been compiled from biogas microbiomes using metagenome assembly and binning approaches. Deep sequencing of biogas microbiomes has made it possible to reconstruct genomes from community members and predict how these communities adapt to specific conditions at the species level. In this context, MAG-based metabolic reconstruction has provided insights into the genetically determined metabolic potential of the previously less understood genus *Limnochordia*, which is predicted to be metabolically versatile and ubiquitously active in many pathways of the biogas process chain. Interestingly, *Limnochordia* appears resilient to varying process conditions, making it a compelling candidate for production applications as shown in this study. However, in most cases, physiological experiments to confirm metabolic predictions are not feasible, as isolates for many MAGs are unavailable. Therefore, culturomics is essential to determine the phenotypes of microorganisms represented by MAGs, complementing the functional profiling of microbiome members.

Consent

Yes

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