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A core microbiome across six types of anaerobic digestion reactors aiming to extract biomethane out of organic wastes

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Microorganisms play a critical role in a biogas-producing system (BPS). Many BPSs have a microbiome consisting of balanced proportions of archaea and bacteria. It has been reported that a BPS microbiome's functionality usually relied on its functional redundancy, particularly among the hydrolysers and fermenters. However, different conclusions have also been drawn based on single types of BPSs, especially from the ones under strong selective pressures, e.g. high temperature, high salinity, or recalcitrant substrates. The reasons behind remain unknown. A question that has long puzzled the academy is if functional redundancy always rules anaerobic digestion communities? Here we document a systematic study of the microbiome-functionality nexus based on 138 samples out of twenty well-profiled lab-scale BPSs in four major configurations running for up to two years. Pyrosequencing and qPCR were applied to support the microbial assembly analysis. Combined, these data sets comprise a total richness of 698 genera. Although various methanogens dominate different BPSs communities, it is striking to note a core bacterial microbiome prevailing in all BPS types, i.e. *Bacillus*, *Clostridium*, *Bacteroides*, *Eubacterium*, *Cytophaga*, *Anaerophaga* and *Syntrophomonas*. Their total relative abundance shows a correlation with the BPSs performance ($R^2=0.323\pm 0.132$, $p=0.321\pm 0.089$) that is even comparable to the correlation between the performance and archaeal 16S ribosomal RNA genes ($R^2=0.332\pm 0.181$, $p=0.021\pm 0.023$). Microbiome divergence appears on a large scale, expanding from different reactor configurations with the same mother seed to a millimetre level within a biofilm. The BPSs communities are neither functionally plastic nor functionally redundant. In other words, a high variety in communities usually exhibits a strong difference in performances.

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