Novel ecological insights and functional roles during anaerobic digestion of saccharides unveiled by genome-centric metagenomics

In typical anaerobic digestion (AD) systems, the microbial functional assertion is hampered by synchronised versatile metabolism required for heterogeneous substrates degradation. Thus, the intricate methanogenic process from organic compounds remains an enigma after decades of empirical operation. In this study, simplified AD microbial communities were obtained with substrate specifications and continuous reactor operation. Genome-centric metagenomic approach was followed to holistically investigate the metabolic pathways of the AD and the microbial synergistic networks. In total, 63 metagenome assembled genomes (MAGs) were assembled from 8 metagenomes acquired in specific methanogenic niches. The metabolic pathways were reconstructed from the annotated genes and their dynamicity under experimental conditions. The results show that the methanogenic niches nourish unique metabolism beyond current knowledge acquired from cultivation-based methods. A novel glucose mineralization model without acetate formation was proposed and asserted in a pair of syntrophs: Clostridiaceae sp. and Methanoculleus thermophilus. Moreover, the catabolic pathway was elucidated in uncharacterized syntrophic acetate oxidizers, Synergistaceae spp. A remarkable evolutionary insight is the discovery that electron transport and energy conservation mechanisms impose selective pressure on syntrophic partners. Overall, the functional roles of the individual microbes tightly rely on the catabolic pathways and cannot always be physiologically defined in accordance with conventional four-step AD concept. The substrate-specific systems provided a traceable microbial community to dissecting the AD process. The genome-centric metagenomics successfully constructed genomes of microbes that have not been previously isolated and illustrated metabolic pathways that beyond the current knowledge of AD process. This study provides new perspectives to unravel the AD microbial ecology and suggests more attention should be paid on uncharacterized metabolism specifically harboured by AD microbial communities.

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