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Insights on the activity of the anaerobic digestion microbiome by means of metatranscriptomic functional investigation

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Nowadays there is an urgent need of a sustainable solution for energy generation and waste resource recovery. Biogas production from Anaerobic Digestion (AD) of organic matter is an attractive technology that gained increasing attention as renewable source of energy. Anyway, the intricate set of microbial species that by their activity and abundance drives the AD process is far from being completely understood (Campanaro *et al.*, 2016). In order to produce high-value products, i.e. almost pure methane, the influence of operational parameters (e.g. temperature, pH, feedstock composition, etc.) on microbial activity needs to be addressed. A set of metatranscriptomic studies have been performed in replicate biogas reactors with the aim of correlating the microbial community structure and their changes in gene expression with the variations in process parameters. The first study investigated the transcriptional changes in a community after radical shifts of the influent feedstock determined by the addition of long chain fatty acids (LCFA). The importance of *Syntrophomonas* species was confirmed and the activation of chemotaxis genes was evidenced in several species; moreover an increased gene expression in *Methanosarcina* sp. was recorded (Treu *et al.*, 2016). Other two ongoing studies are focused on hydrogenotrophic methanogenesis and the role of syntrophic bacteria in the biogas production improvement obtained by the conversion of CO₂ into CH₄ via external hydrogen addition. Moreover, acetate accumulation and pH fluctuations were analyzed to identify the microbial key functions and correlate them with the disturbances affecting the AD process. Results shed light on the inhibitory conditions that can rise during the process, deciphering some of the metabolic pathways present in the species responsible for acetate production and accumulation.

References

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