

Comparative analysis of methanogenic communities in different laboratory-scale anaerobic digesters

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Abstract

© 2016 Ayrat M. Ziganshin et al. Comparative analysis of methanogenic archaea compositions and dynamics in 11 laboratory-scale continuous stirred tank reactors fed with different agricultural materials (chicken manure, cattle manure, maize straw, maize silage, distillers grains, and Jatropha press cake) was carried out by analysis of the methyl coenzyme-M reductase -subunit (mcrA) gene. Various taxa within Methanomicrobiales, Methanobacteriaceae, Methanosarcinaceae, Methanosaetaceae, and Methanomassiliicoccales were detected in the biogas reactors but in different proportions depending on the substrate type utilized as well as various process parameters. Improved coverage and higher taxonomic resolution of methanogens were obtained compared to a previous 16S rRNA gene based study of the same reactors. Some members of the genus *Methanoculleus* positively correlated with the relative methane content, whereas opposite correlations were found for *Methanobacterium*. Specific biogas production was found to be significantly correlating with Methanosarcinaceae. Statistical analysis also disclosed that some members of the genus *Methanoculleus* positively correlated with the ammonia level, whereas the prevalence of *Methanocorpusculum*, *Methanobacterium*, and *Methanosaeta* was negatively correlated with this parameter. These results suggest that the application of methanogenic archaea adapted to specific feedstock might enhance the anaerobic digestion of such waste materials in full-scale biogas reactors.

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