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Taxonomic structure of the microbial community of an industrial biogas plant feeding on a complex organic mixture

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Biomethane production is based on the metabolic activity of methanogenic archaea fed by various bacteria through syntrophic relations. The task of this work was to analyze the taxonomic composition of eubacteria in the microbial community of biogas plant "Luchki" (LLC "AltEnergO") in the North of the Belgorod region. The fermented mass included pig farming manure drains, corn silage, meat waste, sugar-beet pulp, etc. Fermentation was carried out at 39 °C. The first test analyzed the ratio of bacteria to archaea. It was shown that at the early stage of fermentation the fraction of archaea was 3.9% and 2.9% at the late stage. The second test analyzed the taxonomic composition of the bacterial community at the level of phyla and classes in percent. Taxon-specific pairs of primers based on the literature data were used to detect microorganisms of phyla Firmicutes, Actinobacteria, Bacteroidetes, Deferribacteres, candidatus Saccharibacteria, Verrucomicrobia, Tenericutes and three classes of phylum Proteobacteria: Beta-, Gamma- and Epsilonproteobacteria. System of bioreactors of biogas plant "Luchki" includes several zones, where primary and late fermentation stages occur. Analysis of the taxonomic structure of the bacterial component of the community in the zone of primary fermentation showed the next content of different taxa (Fig.1A): Firmicutes 60%, Bacteroidetes 14%, Gammaproteobacteria 9.1%, candidatus Saccharibacteria 0.36%, Betaproteobacteria 0.13%, Actinobacteria 0.01% and 16% of the rest. In the late fermentation zone (Fig.1B), during substrate depletion, the dominance of Firmicutes phylum became even more pronounced and amounted to 78%, while the content of Bacteroidetes was 12%, Gammaproteobacteria 2.8%, Betaproteobacteria 0.02% and 7.1% others. Candidatus Saccharibacteria and Actinobacteria phyla were stopped being detected. Thus, at the late stage of fermentation, the diversity of bacteria in the biogas plant is reduced, which reflects a significant degree in depletion of substrates processed by bacterial microflora and the narrowing of available ecological niches.

Recent Publications

1. Bacchetti De Gregoris T B, Aldred N, Clare A S and Burgess J G (2011) Improvement of phylum and class specific primers for real-time PCR quantification of bacterial taxa. *Journal of Microbiological Methods* 86: 351–356.
2. Enzmann F, Mayer F, Rother M and Holtmann D (2018) Methanogens: biochemical background and biotechnological applications. *AMB Express* 8:1.
3. Pampillón-González L, Ortiz-Cornejo N L, Luna-Guido M, Dendooven L and Navarro-Noya Y E (2017) Archaeal and bacterial community structure in an anaerobic digestion reactor (Lagoon Type) used for biogas production at a pig farm. *J. Mol. Microbiol. Biotechnol.* 27:306-317.
4. Sun L, Liu T, Müller B and Schnürer A (2016) The microbial community structure in industrial biogas plants influences the degradation rate of straw and cellulose in batch tests. *Biotech. Biofuels* 9:128.
5. Yang Y.W., Chen M.K., Yang B.Y., Huang X.J., Zhang X.R., He L.Q., Zhang J., Hua Z.C. (2015) Use of 16S rRNA Gene-targeted group-specific primers for real-time PCR analysis of predominant bacteria in mouse feces. *Applied and Environmental Microbiology*. 81:6749-6756.

Biography

Viktoriia A Iatsenko develops molecular methods to study the taxonomic structure of complex microbial communities using taxon-specific RT PCR. Her research is focused primarily on the application in industries using microbial consortia in particular and on the production of biogas from mixtures of organic waste.

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