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INVESTIGATION OF THE MICROBIAL COMMUNITY IN BIOGAS PLANTS BY METAPROTEOME ANALYSIS

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Abstract

Optimization of biogas plants requires a deeper knowledge about the microbial communities and their metabolism. In contrast to genetic, metabolic or cultivation- based analytical techniques, the investigation of the microbial proteome (metaproteome) is expected to detect actual biological activity and microbial interactions.

Metaproteome analysis of biogas plant samples is challenging because samples contain high amount of impurities and are very complex. Furthermore, the identification of proteins is hindered due to limited availability of relevant genome sequence data.

For removal of sample impurities phenol extraction showed the best results. To reduce sample complexity SDS-PAGE and 2D-PAGE coupled to LC-MS/MS were applied to biogas plant samples. Finally, proteins were identified by database search against NCBI and a metagenome, as well as by *de novo* sequencing.

Up to 100 microbial proteins were identified including hydrolytic enzymes such as peptide hydrolases and enzymes of methanogenesis such as methyl-coenzyme M reductase and F420-dependent methylenetetrahydromethanopterin dehydrogenase. Surprisingly, plant proteins originating from the substrate maize such as photosystem type II and ribulose-1, 5-bisphosphate carboxylase/oxygenase were detected.

Results show that metaproteome analysis of biogas plant samples can give valuable functional information about complex microbial communities. More comprehensive studies could be used to identify predictive biomarkers for process monitoring and control.