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Isolation of Bacterial Species with Potential Capacity for Siloxane Removal in Biogas Upgrading

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Abstract : Volatile methylsiloxanes (VMS) are a group of manmade silicone compounds widely used in household and industrial applications that end up on the biogas produced through the anaerobic digestion of organic matter in landfills and wastewater treatment plants. The presence of VMS during the biogas energy conversion can cause damage on the engines, reducing the efficiency of this renewable energy source. Non regenerative adsorption onto activated carbon is the most widely used technology to remove siloxanes from biogas, while new trends point out that biotechnology offers a low-cost and environmentally friendly alternative to conventional technologies. The first objective of this research was to enrich, isolate and identify bacterial species able to grow using siloxane molecules as a sole carbon source: anoxic wastewater sludge was used as initial inoculum in liquid anoxic enrichments, adding D4 (as representative siloxane compound) previously adsorbed on activated carbon. After several months of acclimatization, liquid enrichments were plated onto solid media containing D4 and thirty-four bacterial isolates were obtained. 16S rRNA gene sequencing allowed the identification of strains belonging to the following species: Ciceribacter lividus, Alicycliphilus denitrificans, Pseudomonas aeruginosa and Pseudomonas citronellolis which are described to be capable to degrade toxic volatile organic compounds. Kinetic assays with 8 representative strains revealed higher cell growth in the presence of D4 compared to the control. Our second objective was to characterize the community composition and diversity of the microbial community present in the enrichments and to elucidate whether the isolated strains were representative members of the community or not. DNA samples were extracted, the 16S rRNA gene was amplified (515F & 806R primer pair), and the microbiome analyzed from sequences obtained with a MiSeq PE250 platform. Results showed that the retrieved isolates only represented a minor fraction of the microorganisms present in the enrichment samples, which were represented by Alpha, Beta, and Gamma proteobacteria as dominant groups in the category class thus suggesting that other microbial species and/or consortia may be important for D4 biodegradation. These results highlight the need of additional protocols for the isolation of relevant D4 degraders. Currently, we are developing molecular tools targeting key genes involved in siloxane biodegradation to identify and quantify the capacity of the isolates to metabolize D4 in batch cultures supplied with a synthetic gas stream of air containing 60 mg m^{-3} of D4 together with other volatile organic compounds found in the biogas mixture (i.e. toluene, hexane and limonene). The isolates were used as inoculum in a biotrickling filter containing lava rocks and activated carbon to assess their capacity for siloxane removal. Preliminary results of biotrickling filter performance showed 35% of siloxane biodegradation in a contact time of 14 minutes, denoting that biological siloxane removal is a promising technology for biogas upgrading.

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