

Anaerobic Digestion Batch Study of Taxonomic Variations in Microbial Communities during Adaptation of Consortium to Different Lignocellulosic Substrates Using Targeted Sequencing

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Abstract : Anaerobic digestion has been widely used for production of methane from different biowastes. However, the complexity of microbial communities involved in the process is poorly understood. The performance of biogas production process concerning the process productivity is closely coupled to its microbial community structure and syntrophic interactions amongst the community members. The present study aims at understanding taxonomic variations occurring in any starter inoculum when acclimatised to different lignocellulosic biomass (LBM) feedstocks relating to time of digestion. The work underlines use of high throughput Next Generation Sequencing (NGS) for validating the changes in taxonomic patterns of microbial communities. Biomethane Potential (BMP) batches were set up with different pretreated and non-pretreated LBM residues using the same microbial consortium and samples were withdrawn for studying the changes in microbial community in terms of its structure and predominance with respect to changes in metabolic profile of the process. DNA of samples withdrawn at different time intervals with reference to performance changes of the digestion process, was extracted followed by its 16S rRNA amplicon sequencing analysis using Illumina Platform. Biomethane potential and substrate consumption was monitored using Gas Chromatography(GC) and reduction in COD (Chemical Oxygen Demand) respectively. Taxonomic analysis by QIIME server data revealed that microbial community structure changes with different substrates as well as at different time intervals. It was observed that biomethane potential of each substrate was relatively similar but, the time required for substrate utilization and its conversion to biomethane was different for different substrates. This could be attributed to the nature of substrate and consequently the discrepancy between the dominance of microbial communities with regards to different substrate and at different phases of anaerobic digestion process. Knowledge of microbial communities involved would allow a rational substrate specific consortium design which will help to reduce consortium adaptation period and enhance the substrate utilisation resulting in improved efficacy of biogas process.

Keywords : amplicon sequencing, biomethane potential, community predominance, taxonomic analysis

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