Developing microbial monitoring methods for anaerobic biological processes

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INTODUCTION

In anaerobic digestion, the changes that occur in the treatment and energy production process is highly dependent on the activity and interactions of microbial communities. To achieve optimum efficiency in anaerobic digestion processes, require a greater understanding of the fundamental relationships between bacterial populations in the biomass with respect to the different anaerobic digestion systems. A basic understanding of microbial diversity and interactions is needed to develop predictive models to better manage and engineer anaerobic digesters. The common questions that arise when trying to study microorganisms in a given microbiome irrespective of their life style are; (1) what kind of microorganisms are present; (2) how abundant are they; (3) how do their activities influence other organisms and (4) how does the microbiome influence the structure and function of the microorganisms present. To answer these questions, different molecular methods ranging from culture-dependent methods to culture independent-techniques have been used. Culture dependent methods have been used to monitor changes in anaerobic digestion processes. However, they provide limited information about the total microbial community (encompassing < 1% of the diversity) with respect to changes that occur. The application of culture-independent techniques has overcome these limitations and recently revealed a new and improved view of the microbial world. The implementation of these techniques as the method of choice to investigate microbial communities in anaerobic digestion processes is expected to be used routinely in the near future as the prices for the analysis are dropping.

TECHNOLOGICAL CHALLENGES

Currently, the monitoring of anaerobic digestion processes such as anaerobic digestion and dark fermentation is based mainly on chemical analyses. Changes in the anaerobic treatment and energy production efficiency depend highly on the microbial communities, but the chemical variables only show changes that have already occurred. Recent advances in genomics and sequencing technologies have paved way for discovering and comprehensively characterizing the enormous microbial diversity to understanding their interactions with biotic and abiotic factors. A laboratory scale experiment will be conducted to study biohydrogen production by dark fermentation with thermophilic microorganisms. High-throughput sequencing will be implemented to study the active microbial communities at different levels. Mathematical modelling will also be implemented as a predictive tool and for process optimization.

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