

## Exploring active microbial community of anaerobic digestion systems by 454 pyrosequencing

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Biotransforming organic waste into energy has been regarded as one of the promising technologies to combat energy crisis in the future. In this study, we queried the highly active functional population in the anaerobic digestion system with various potential substrates (food waste, cellulose, xylan) by integrating the sludge DNA and RNA of subculture from the substrates. Using barcoded 454-pyrosequencing, we analyzed and compared the bacterial and archaeal 16S rRNA genes of one digester sludge (DNA) sample and three subcultures (cDNA) by giving three individual substrates to the digester sludge in order to identify the active members in digesting organic wastes to biomethane. A total of 19K bacterial and 13K archaeal effective sequences were assigned to taxonomy from phylum to genera levels, providing insights into the microbial community structure and further correlating the community members to the performance of the subculture. The principal coordinates' analyses on the basis of UniFrac of OTUs revealed that there are significant differences among the digester sludge and digestion culture samples. Cellulose and xylan culture community are more closer to each compared to food waste culture, even though it still has a slight difference between cellulose and xylan culture. Overall, the phylogenetic information based on DNA and RNA provides a comprehensive and systematic view of the anaerobic microbial community within the digestion systems.

### Biography

Lu Xiao Ying has obtained his PhD in Civil Engineering from the University of Hong Kong, Hong Kong. She is currently an Assistant Professor of the Faculty of Science and Technology, Technological and Higher Education Institute of Hong Kong (THEi). She is specialized in environmental microbiology, bioenergy production from solid waste and advanced materials development in energy and environment.

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