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Microbial community dynamics during a successful acclimation process to extremely high ammonia levels in continuous anaerobic digester

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High ammonia concentrations ($> 3 \text{ g NH}_4^+ \text{-N L}^{-1}$), released during anaerobic digestion (AD) of nitrogen-rich substrates, could result in reactor performance instability or even failure (Yenigün & Demirel, 2013). Acclimatized anaerobic communities to high ammonia levels can offer a solution to this problem. Thus, investigation of microbial community dynamics during the acclimation process and characterization of the ammonia-tolerant consortia, can both provide fundamental insight and offer practical engineering solutions to this challenge in the future (Appels et al., 2011). Therefore, in this study, 16S rRNA sequencing was applied to explore the community changes during a successful acclimation process in a mesophilic continuous reactor with a stepwise total ammonia increase ($0.5 \text{ g NH}_4^+ \text{-N L}^{-1}$ each step) up to $10 \text{ g NH}_4^+ \text{-N L}^{-1}$.

Throughout the experimental period, the reactor performance (i.e. methane production, VFA and pH) was stable and within the optimal range of normal anaerobic digestion. 16S rRNA sequencing results showed that a clear microbiome change happened during this process, resulting in narrowed microbial community adapted to high ammonia toxicity. Furthermore, compared to low ammonia levels, *Clostridium ultunense* (syntrophic acetate oxidizing bacteria) and *Methanoculleus spp.* increased significantly in abundance at ammonia levels above $7 \text{ g NH}_4^+ \text{-N L}^{-1}$, indicating an enhanced hydrogenotrophic methanogenic pathway. Interestingly, the most abundant methanogens at the highest ammonia levels were the well-known aceticlastic methanogens- *Methanosarcina spp.*, with more than 60% of the archaea abundance. Overall, the results demonstrated that by evolving to a specialized community composition, anaerobic digestion could happen under extremely high ammonia levels.

Reference:

Appels, L., Lauwers, J., Degrève, J., Helsen, L., Lievens, B., Willems, K., Van Impe, J., Dewil, R. 2011. Anaerobic digestion in global bio-energy production: Potential and research challenges. *Renewable and Sustainable Energy Reviews*, **15**(9), 4295-4301.
Yenigün, O., Demirel, B. 2013. Ammonia inhibition in anaerobic digestion: A review. *Process Biochemistry*, **48**(5-6), 901-911.

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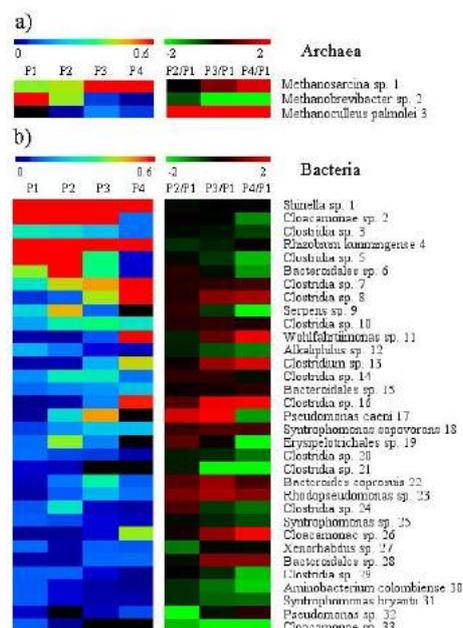


Fig. 1. Relative abundance (%) (left) and the corresponding folds change (right) for the interesting a) archaea and b) bacteria.