

# GENOMIC OPTIMISATION OF HYDROLYSIS IN BIOGAS PRODUCTION

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## Introduction

Biogas, due to its high content of methane (60-70%) might be a good source of environmental-friendly renewable energy (Yadvika et al. 2004; Berglund and Börjesson 2006).

Biogas production is conducted by complex microbial community characterized by some relationships amongst it that influence methane yields in anaerobic digesters (Yadvika et al. 2004). The microbial community structure can be changed by high amounts of some compounds produced during the process, for instance – hydrogen. Low hydrogen concentrations can be maintained by hydrogenotrophic methanogens (considered as methanogens causing low methane yields) and connected with the promotion of for example hydrogen-producing bacteria activity (Weiland 2010; Li et al. 2011; Ziganshin et al. 2011).

The hypothesis of the project is the assumption that some kind of syntrophy exists between particular candidate division hydrogen-producing bacteria and hydrogenotrophic methanogens whose activity are connected with low methane yields. Thus, the candidate division bacteria could act as a biomarker of low methane production in anaerobic digesters.

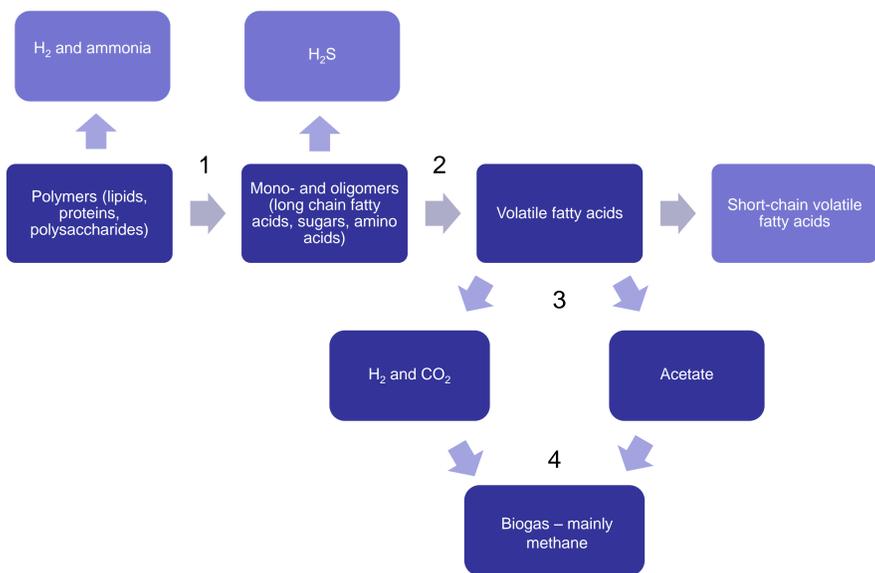
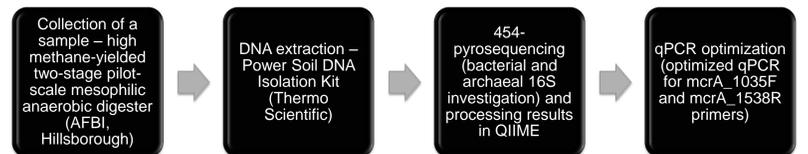


Fig. 1. Diagram showing the biogas production process. Designation: 1 – hydrolysis, 2 – acidogenesis, 3 – acetogenesis, 4 – methanogenesis

## Methods



## Results

454-pyrosequencing of the sample revealed that the most abundant group of bacteria was *Firmicutes* (especially order *Clostridiales*). The most dominant Archaea were *Euryarchaeota* (especially order *Methanosarcinales*). More detailed results are showed below.

Optimisation of some qPCRs are conducting resulting in optimised reaction with mcrA\_1035F and mcrA\_1538R archaeal primers.

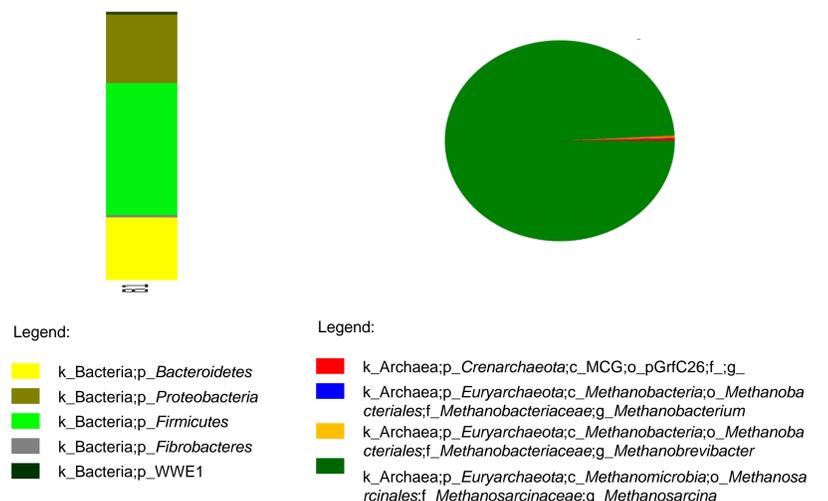


Fig. 2. The chart showing the abundance of bacteria phyla in the AFBI's sample

Fig. 3. Pie chart indicating the proportion between different species of Archaea in the sample from AFBI

## Aims

The investigation of possible syntrophy between candidate division hydrogen-producing bacteria and hydrogenotrophic methanogens and its influence on methane yields by using metagenomic tools

The development of robust metagenomic technique (targeting the biomarker – candidate division bacteria) to monitor methane yields in anaerobic digesters

The study on the possible shifts in microbial community as a result of various reactor performance – especially in terms of feedstock

## Conclusions

The results indicate that the most abundant Archaea in the digester is *Methanosarcina* which is classified as aceticlastic methanogen group. The predominance of such methanogens with simultaneous absence of particular candidate division bacteria in the digester characterized by high methane production is in agreement with our hypothesis. In contrast, hydrogenotrophic methanogens predominance with the presence of particular candidate division hydrogen-producing bacteria would be connected with non-optimal digester performance. However, the hypothesis still needs confirmation by investigating samples from other reactors.

### References:

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