Effectivity and stability in farm scale biogas plants - correlation to microbial community structure

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Background

Biogas at farm site is highly interesting and important as this allows the farmers to simultaneously treat organic waste fractions, produce energy and a valuable fertilizer as well as to reduce methane emissions from manure storage. With a biogas plant the farmer can also be self-sufficient on energy and contribute to the development of a sustainable and climate neural agriculture. In Sweden, biogas production at farm site is not yet well established and the majority of plants have been in operation for just a few years. To support the development in this field Swedish Rural Economy and Agricultural Society in collaboration with the institute of Agricultural and Environmental Engineering, JTI, performed an evaluation project between 2010 and 2014 (Eliasson, 2015). Here, different farm scale biogas plants were sampled, analysed and evaluated. The results showed that many plants operated at low efficiency, making it difficult to obtain investments paid back. Several reasons were identified; one was a non-optimized process with low gas production efficiency. One parameter of critical importance in order to achieve a well-functioning, stable and efficient biogas production process is the microbial community in the process. Biogas production requires a complex community of microorganisms often operating in close association with each other. If one or several groups are disturbed for one or another reason, such as suboptimal operating conditions, the result will be wash out of microbial components followed by decreased degradation and gas yields, instability and sometimes a complete process failure.

The aim of the project was to investigate and describe the microbial population structure in a selected number of biogas plants and to correlate this data with data from the operation and performance, including substrate composition, gas production, ammonia level, degree of degradation etc. The overall goal was to identify parameters having strong impact on the community structure and to identify microbial components correlating with high gas yields and stable performance. Such information will aid in the development of optimized operational management of farm based biogas plants.

Materials and methods

In total 13 biogas plants at farm scale (Table 1) were chosen for analysis regarding the composition of the microbiological community structure. All these plants were participating in the Swedish evaluation project investigating the performance, energy efficiency and economy of specifically farm scale biogas production (Eliasson, 2015). During this evaluation, data regarding the composition of substrate and digestate, process performance, digester design, gas production and quality were collected and this data, as well as samples were used in the present study (Eliasson et al., manuscript; Levén et al., manuscript). The plants selected for the present study were different concerning substrate and operational parameters as well as the construction of the plants. Most plants had one main digester and an unheated post-treatment digester, but a few plants had only one main digester (no 4, 5 and 12). Samples to be used for chemical as well as microbiological analyses were taken from the main digester, except for plant 9, 22, 23 and 25, which were sampled in the post treatment

digester. For the microbiological analysis, each plant was sampled at three times points distributed over one year. The samples were stored at -20°C until analysis

Triplicate DNA extractions were made from each sample and sampling point using a commercial extraction kit (MP Biomedicals, Santa Ana, Ca, USA). The gene sequences from constituent microorganisms were amplified by PCR with primers specific for both Bacteria and Achaea, which includes also the methanogens. The obtained products were sequenced with Illumina MiSeq at the Science for Life Laboratory/NGI (Solna, Sweden). The amplicons of sequencing data was processed and analyzed as described by Müller and co-workers (2015). The diversity analyses were calculated according to Chao1, Shannon, and Simpson index, in total giving information about species richness as well as the evenness of the community. Phylogenetic distances between samples as determined by unweighted UniFrac principal coordinate analysis (PCoA) for bacteria and archaea were computed and plotted.

To illustrate correlations between Bacteria or Archaea and operational parameters such as temperature (°C), hydraulic retention time (HRT, days), organic loading rate (OLR, g VS/L day), pH, NH_4-N (kg/ton), NH_3 (kg/ton), C/N quota, CH_4 (%), specific methane production (SMP, Nm^3/ton VS day), volume of gas produced, degree of degradation (D_D, %), degree of nitrogen mineralization (%, D_M), volatile fatty acids (VFA, g/L) and part of manure in the substrate (%), principal component analysis (PCA) were used. All input data were expressed as mean values of the whole sampling period of the evaluations project, except for the relative abundance of Bacteria and Archaea, NH_4-N, NH_3, C/N quota and VFA with values specific for each sampling point.

Results and discussion

Performance and operating condition data

The majority of plants investigated operated at a mesophilic temperature range (36-40 °C), but two plants (no 22 and 24) used thermophilic temperature (52-55 °C). All plants used manure (cattle or/and pig) as main substrate in combination with various amounts of different co-substrates, with the highest proportion of co-substrate in plant 22 (75 %) and the lowest in plant 4, 5, 9, 23 and 24 (0-4 %). The organic loading rate (OLR) varied between 1.3 and 3.9 g VS/L day and the hydraulic retention time (HRT) between 19 and 63 days. The performance in regard to methane production, degree of degradation and nitrogen mineralization also varied among the plants, but they all had stable process performance with low levels of volatile fatty acids <1 g/L, with one exception, plant 24. This plant was a thermophilic plant with pig manure as main substrate (97 %, VS based) and high ammonia levels (430-480 mg/L). The proportion of methane in the produced biogas ranged from 54 to 66 %. As expected, plants treating protein rich and fatty materials in co-digestion with manure (plant 22, 24 and 25) had the highest methane concentration in the gas, 63, 64 and 66 % respectively. The specific methane production varied between 119 and 422 L/kg VS day and the degree of degradation (TS and VS reduction) between 34 and 90 %. The highest values were found in plant 22 and 14 (422 and 343 L/kg VS day; 90 % and 85 %). These plants used energy rich co-substrate such as slaughterhouse waste, candy and corn starch, which affected the gas production positively. Plant 4, 5 and 13, using mainly cattle manure as a substrate, had the lowest values for specific methane production (168, 163 and 119 L/kg VS day) as well as degree of degradation (45 %, 39 % and 34 %). The highest degree of nitrogen mineralization was shown in plant 22 (52 %) operating at thermophilic temperature and the lowest in the mesophilic plant no 14 (5 %). In line with this, the level of free ammonia ranged from 30 to 500 mg/L, with the lowest values in plant 14 (30 mg/L) and the highest in the thermophilic plants no 22 and 24 (380-500 mg/L).

Diversity index

Analysis of archaeal and bacterial communities by Illumina MiSeq sequencing resulted in around 5.1 million sequences in total after quality check and filtering, ranging from 75 000 to 300 919 sequences per sample. The estimated coverage, based on the species richness and Chao 1 index, of the total microbial communities (both Bacteria and Archaea) ranged from 75-84 % (Table 1). Plants with high ammonia levels (340-500 mg/L NH_3) and thermophilic temperature (52-55°C) showed the lowest levels of species richness, i.e. the number of different microorganisms (1471-1725), and community evenness (Simpson index; 0.89-0.92). The Shannon diversity index was also low in these plants. This strong effect of temperature on the microbial diversity in biogas processes has previously been reported by e.g. Sun et al. (2015) and Li et al., (2015). In addition, ammonia is known to have a strong influence the bacterial diversity, with decreasing values with increasing ammonia level (Müller et al., 2015). Among the mesophilic plants low species richness was seen for plant 14 and 25, with values of 1708 and 1391, respectively, levels similar to the thermophilic biogas plants. The similarity between plant no 25 and the thermophilic plants in this regard was likely caused by the high ammonia levels, enhance by operational temperature set to the higher mesophilic range (40 °C). Furthermore, Welch's t-test revealed that plants digesting cattle manure as main substrate had a comparably higher diversity, measured as the number of OTU (P<0.01), the Simpson index (P<0.0001) and Shannon index (P<0.0001), compared to plants using pig manure as main substrate (Table 1).

Table 1. Summary of Chao1, OTUs, coverage, Shannon and Simpson index in 13 farm-scale biogas plants in Sweden treating cattle manure (4-15) and pig manure (20-27) as the main substrate, respectively. Two plants had thermophilic process temperature (22 and 24). The calculations were based on both bacterial and archaeal sequences.

Plant	Chao1	Observed species (OTU)	Shannon	Simpson	Coverage (%)
4	2566±213	2128±194	7.38±0.21	0.97±0.02	83
5	2504±190	2102±132	7.32±0.17	0.97±0.01	84
9	2787±208	2233±136	7.55±0.19	0.98±0.01	80
12	3084±228	2580±259	7.84±0.34	0.98±0.01	84
13	3085±90	2549±117	7.89±0.06	0.98±0.003	83
14	2283±47	1708±39	6.86±0.29	0.97±0.01	75
15	3047±80	2538±129	7.94±0.24	0.98±0.004	83
20	2961±180	2302±135	6.81±0.14	0.95±0.01	78
22	2052±223	1537±173	6.04±0.21	0.92±0.02	75
23	2743±233	2160±169	7.13±0.15	0.97±0.01	79
24	1912±179	1471±95	5.80±0.31	0.89±0.03	77
25	1794±217	1391±166	6.39±0.34	0.94±0.02	78
27	3080±84	2504±15	7.30±0.11	0.97±0.01	81

In general, a high diversity is suggested to result in a potential for multiple options for degradation of a certain compound and thus give the process a high functional capacity. High diversity is also assumed to results in a possibility for the community to adapt to new and also suboptimal conditions (De Vrieze et al., 2013; Vanworterghem et al., 2014). A high level of evenness, i.e. equal abundance of different species present, has also been shown to be of importance for functionality under selective stress and also to correlate with high methanogenic activity (Werner et al., 2011; De Vrieze et al. 2013). However, high microbial

diversity is not always critical for functional and stable operation (if no changes in operational strategies) (Haruta el al 2002; Sun et al., 2015; Westerholm et al., 2015). Thus the comparably lower diversity found for some of the plants in the present study might not be of critical importance for the functionality of these plants. The flexibility/dynamics of the community might instead be a more important factor for process performance (Dearman et al., 2006).

Factors affecting the microbial community structure

The sequence analysis and preceding statistical analysis showed that the microbial community structure in the three samples taken during one year at each of the 13 farm scale biogas plants grouped well together, which shows that the microbial communities were relatively similar and stable over the investigated time period (Figure 1). Some differences were seen between samples from the same plant, possibly explained by variations in the operation caused by e.g. technical problems (plant 12, 15 and 20), uneven load of substrate (plant 14 and 20), and substrate and technical changes (plant 13 and 27). Still there was a clear difference between the different plants suggesting that the communities were shaped by the operating conditions at each plant site. Factors know to impact on the microbial community structure include, temperature, organic loading rate, hydraulic retention time, substrate composition and rector configuration.
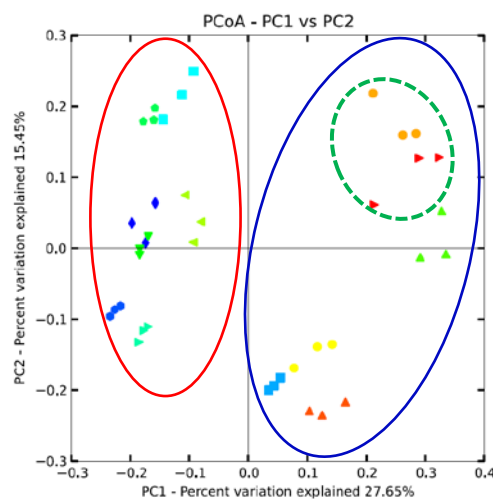

Figure 1. Phylogenetic distances between samples as determined by unweighted UniFrac principal coordinate analysis (PCoA) for bacteria and archaea. Samples with the same color and shape originate from the same plant taken at three different time points during one year. Red circle = cattle manure as main substrate; blue circle = pig manure as main substrate; Green striped circle = thermophilic plants.

In all investigated biogas digesters, representatives of Bacteria dominated the microbial community and the Archaea represented only between 0.04 and 13.3 %. The phylum *Euryarchaeota* (81.3-100 % of the total number of Archaea) dominated the archaeal community, followed by a minor fraction of the phyla *Crenarchaeota* and *Parvarchaeota* (up to 16.1% and 14.8 %, respectively). This dominance of *Euryarchaeota,* which comprise all known methanogens, has been seen before in different biogas plants (Ziganshin et al. 2013; Sun et al., 2015). For the bacterial community the phylum *Firmicutes* showed the highest relative abundance in all plants (37.6-92.4 %), which is conforming previous results (Kröber et al. 2009; Wirth et al., 2012; Ziganshin et al., 2013; St Pierre and Wright, 2014; Tuan et al., 2014; Moset et al., 2015; De Vrieze et al., 2015; Li et al., 2015; Sun et al., 2015). The predominance of *Bacteroidetes* (in mesophilic plants, 1.7-37.9 %) and presence of e.g. *Actinobacteria*, *Cloacimonetes* (previously WWE1) and *Synergistetes* at lower levels were

also in line with several previous investigations of anaerobic digesters treating various substrates (Ziganshin et al., 2013; St Pierre and Wright, 2014; Li et al., 2015; Sun et al., 2015). The dominance of bacteria belonging to *Firmcutes* and *Bacteriodetes* is probably due to their ability to degrade a wide range of complex organic macro-molecules, such as proteins and carbohydrates including cellulose (Lynd et al., 2002; Wiegel et al., 2005; Robert et al., 2007; Hatamoto et al., 2014; Naas et al., 2014). Furthermore, bacterial members of *Synergistetes* are suggested to play an important role in the acetate production (Li et al., 2015)

Cattle manure versus pig manure

Previous studies comparing the microbial community structure in biogas plants reveal substrate composition as a strong regulating parameter (Sundberg et al. 2013; Ziganshin et al. 2013; Zhang et al. 2014). In line with these previous studies one of the most influential factors determining the microbial community composition in present study was the substrate. Based on the substrate two separate clusters were obtained, one comprising plants using swine manure as the main substrate and one with plants treating cattle manure (Figure 1).

When cattle manure was used as main substrate for biogas production *Methanosarcina* from the order *Methanosarcinales* was the most dominant archaeal genus. This dominance of *Methanosarcina* is in line with previous studies of cattle manure based digesters (Goberna et al., 2010; St-Pierre and Wright, 2013, Sun et al 2015; Moset et al 2015). In the swine manure based digesters *Methanobacteriales* were instead present at the highest relative abundance. This result is also in agreement with earlier studies, showing high abundance of *Methanobacteriales* when using swine manure as a substrate (Song et al., 2010; Zhu et al., 2011 Tuan et al., 2014). The composition of the methanogenic community in plant 14, 15 and 27 differed compared with the rest of the plants within respective group, i.e. cattle and pig manure digesters. Possibly this results was caused by the comparably higher level of co-digestion substrate in these plants, resulting in different substrate composition, but also changes of process parameters.

Methanosarcina is one of two known acetate utilizing methanogens, but can also use hydrogen and carbon dioxide as well as methanol for methanogenesis, unlike the other acetotrophic methanogen *Methanosaeta*, which only uses acetate. These features, which enhance its competitive ability, have been suggested as the explanation for the presence of this methanogen in many biogas reactors (De Vrieze *et al*., 2012). High abundance of *Methanosarcina* has been suggested to be caused by its relatively high growth rate and ability to tolerate conditions inhibitory to other methanogens (De Vrieze *et al*., 2012). The high abundance of *Methanobacteriales* in the biogas plants using pig manure suggests that hydrogen is the main substrate for methanogenesis. Methanogens within this order can produce methane from formate, methanol, H_2 and CO_2. The dominance of this methanogen might be correlating to the comparably higher levels of ammonia in the pig manure digesters, known to inhibit acetate utilizing methanogens and results in methanogenesis mainly via bacterial acetate oxidation followed by methanogens from hydrogen.

The dominant bacterial phylum in all digesters was *Firmicutes,* with a higher abundance in digesters using pig manure as main substrate compared to cattle manure digesters. The opposite was observed for *Bacteroidetes*, which was observed at higher abundance when cattle manure was used as main substrate. In addition, the substrate, e.g. pig or cattle manure, influenced the taxonomic composition and the relative abundance of different microbial group within the *Firmicutes* and *Bacteroidetes*. A clear example of such a difference was seen within the phylum *Firmicutes* and the order *Clostridiales*. Within this order, *Clostridiaceae* was identified as the major family in all plants. However, within this family, *Clostridium* was

the dominant known genus in cattle manure digesters, but when using pig manure as substrate an unknown genus was instead predominant. In addition, a higher abundance of the families *Porphyromonadaceae* and *Marinilabiacea* within the phylum *Bacteroidetes* were found in cattle manure digesters.

Temperature and ammonia level

Among the many parameters that impact on the microbial community structure in a biogas process, temperature (mesophilic vs thermophilic) and ammonia concentration have in many studies been shown to have strong effect (Levén et al., 2007; Westerholm et al., 2011a, 2011b; Ziganshin et al., 2013; De Vrieze at al., 2015; Li et al 2015; Moset et al., 2015). Moset et al. (2015) suggested that temperature has a higher impact on the microbial composition in the digesters than the initial microbial composition in the manure or the HRT. De Vrieze et al. (2015) investigated in total 29 different full-scale anaerobic digesters and in-depth analysis of operational and environmental parameters and bacterial community structure showed three potential clusters, determined by total ammonia concentration, free ammonia concentration and temperature. In line with previous studies the microbial community in the thermophilic biogas plants investigated in this study formed a separate cluster (Figure 1). However, one mesophilic plant (no 25) had a similar phylogenetic composition as the thermophilic biogas plants (Figure 1; light green triangle within the blue circle). This plant operated at a slightly higher mesophilic temperature range (40 °C). However, the community structure in plant 25 was most likely strongly influenced by the ammonia level, being more similar to the thermophilic plants, rather than the temperature. Ammonium is released during the degradation of protein and in the biogas process exists in equilibrium with ammonia. This equilibrium shifts toward ammonia with increasing pH and temperature. As a consequence thermophilic plants typically have a comparably higher level of ammonia and thus the influence of this compound on the community is sometimes difficult to separate from the effect of temperature per se. In contrast, the community structure in plant 23 (Figure 1; orange triangle within the blue circle), which also had temperature set to 40 °C, was closer to the mesophilic plants. This plant had problems keeping the temperature at this high level, possibly explaining the difference compared to plant 25.

For Archaea, *Methanobacteriales* is known to positively correlate to temperature (De Vrieze et al., 2015). In line with this, the relative abundance of the genus *Methanosphaera* (mainly plant 22) and *Methanothermobacter*, both belonging to the order *Methanobacteriales* was high in the thermophilic digesters in this study. *Methanosphaera* has earlier been identified in cattle manure (Sun et al., 2015) as well as in a mesophilic digester using a variety of substrates (Song et al., 2015) and a thermophilic digester treating pig wastewater (Weiss et al., 2008). *Methanothermobacter* has previously been shown to positively correlate to temperature (Li et al. 2015) and was first found in a thermophilic anaerobic digester using swine manure as only substrate (Tuan et al., 2014). Further analysis of the archaeal community in the present study revealed that the order *Methanomicrobiales* and the genus *Methanoculleus sp* in particular correlated to high ammonia (Figure 2a). The highest relative abundance was found in thermophilic plants with high ammonia levels. The presence of this hydrogen-utilizing methanogen in high ammonia digesters at both mesophilic and thermophilic temperature has been reported before and has been suggested to be a result of a comparably higher ammonia tolerance combined with a high hydrogen consuming efficiency (Moestedt et al., 2015; Westerholm et al., 2015). Furthermore, temperature has a strong effect on the pathway for methanogeneis, with a shift from aceticlastic to hydrogenotrophic methanogenesis above 40 °C (Conrad et al., 2009; Rui et al., 2011).

For Bacteria, *Firmicutes* (37.6-92.4 %), *Bacteroidetes* (1.7-37.9 %), *Actinobacteria* (0.6-8.9 %) and *Cloacimonetes* (previously WWE1; up to 10.1 %) were found to be the predominant phyla in the mesophilic biogas plants. In the plants operating at thermophilic temperature *Firmicutes* (73.7-87.5 %), *Synergistetes* (1.7-12.7 %) and *Actinobacteria* (1.1-3.7 %) were the three most dominant phyla. Furthermore, analysis of the bacterial community identified the highest quota of *Firmicutes/Bacteriodes* in the thermophilic digesters followed by digesters running at 40°C. Such high quota has been observed previously in digesters operating at high temperature (Levén et al 2007; Li et al. 2015; Smith et al. 2014; Moset et al 2015; Sun et al 2015). In the thermophilic digesters, members belonging to the class *Clostridia* within the phylum *Firmicutes* were more abundant compared to mesophilic digesters. This effect of temperature on the presence of *Clostridia* has previously been found both in digesters treating organic household waste (Levén et al., 2007) and cattle manure (Sun et al., 2013, 2015; Moset et al., 2015) and is possibly due to heat activation of the spore-forming *Clostridia* (Mead, 1992). Moreover, in the PCA plot a positive correlation was shown between *Firmicutes* and the free ammonia concentrations (Figure 2b). This high relative abundance of *Firmicutes* at high ammonia levels is consistent with previous reports (De Vrieze et al., 2015; Müller et al., 2015). Moreover, *Synergistetes* and *Actinobacteria* can be found at both mesophilic and thermophilic temperature (Weiss et al., 2009; Ziganshin et al., 2013; St Pierre and Wright, 2014; Tuan et al., 2014; Li et al., 2015; Sun et al., 2015). In agreement with previous result (Li et al. 2015), the phylum *Thermotogae* also revealed positive correlation with process temperature (Figure 2b). In addition, the mesophilic plant 14 showed high levels of this phylum but with the difference from the thermophilic plants that the dominating genus was represented by *Kosmotoga* instead of S1 (the only genus found in the thermophilic plants).
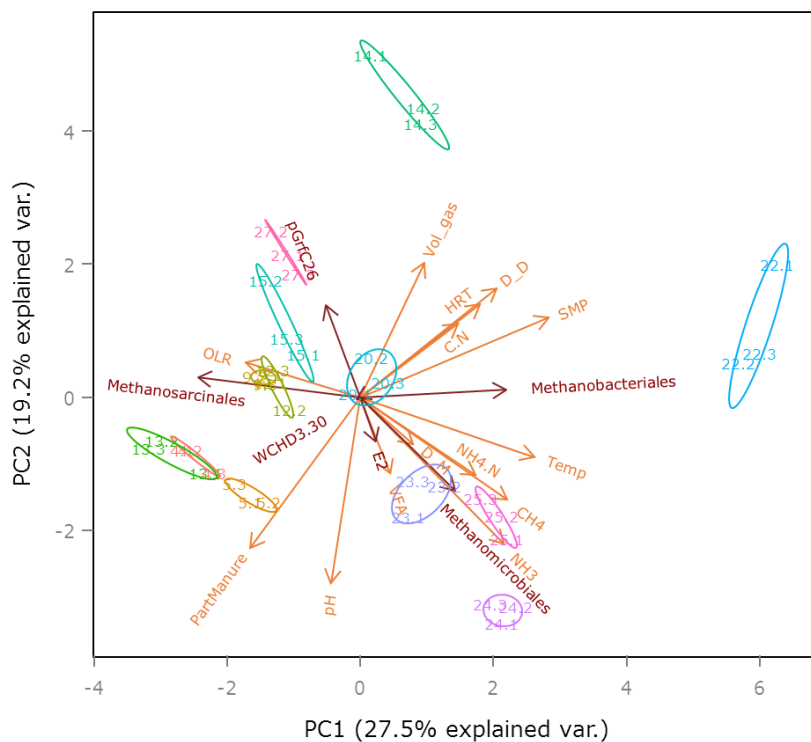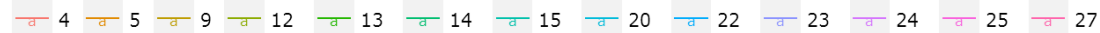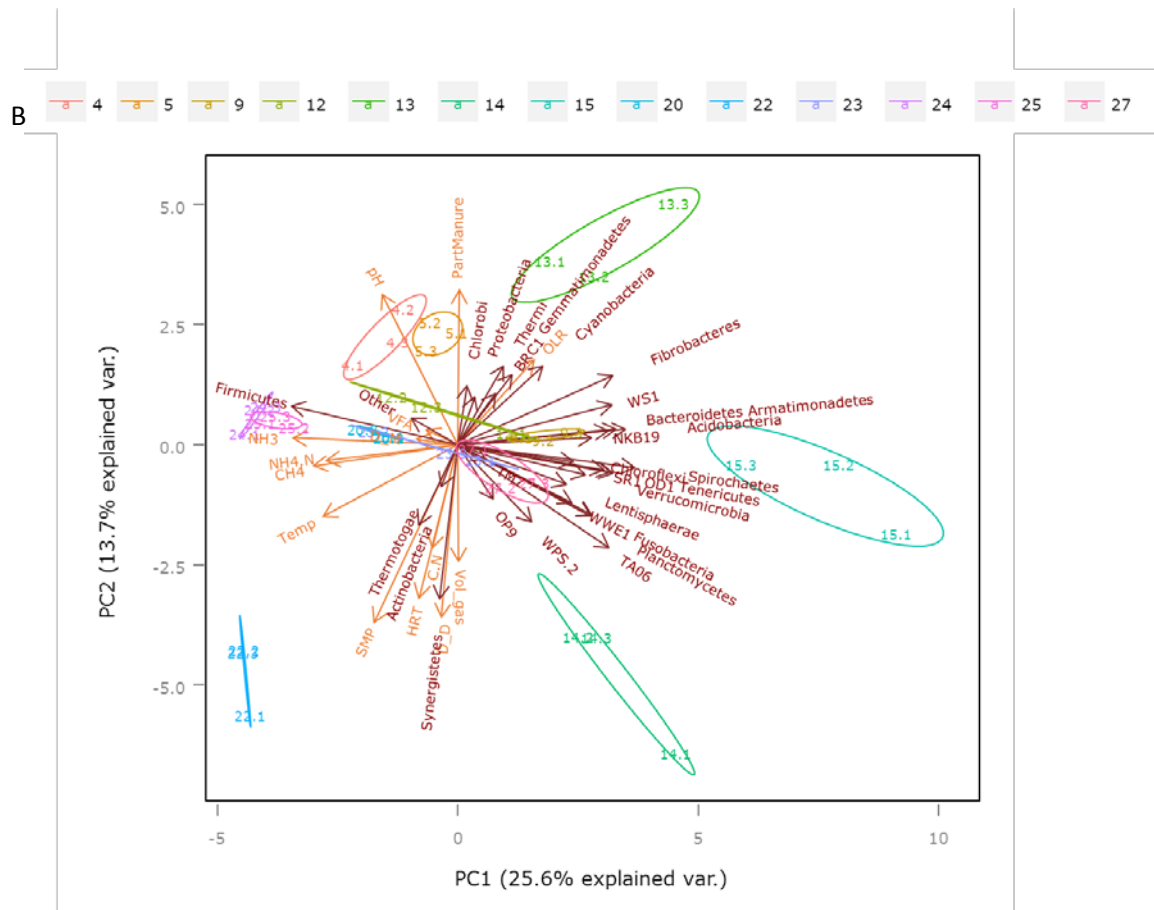
Figure 2. PCA of (a) the archaea at order level and (b) the bacteria at phyla level and correlations to different process and operational parameters. CH_4: methane content (%), NH_3: free ammonia (mg/L), NH_4-N: ammonium nitrogen (g/L), HRT: hydraulic retetion time (days), OLR: organic loading rate (gVS/L day), D_D: degree of degradation (%), D_M: degree of nitrogen mineralization (%), C/N: carbon and nitrogen quoata (total C and N), SMP: Specific methane production (Nm3/ton VS day), Vol_gas: volume of gas produced (L), VFA: volatile fatty acids (g/L), PartManure: part of manure in the substrate (%, VS based).

OLR

Organic loading rate (OLR) and hydraulic retention time (HRT) have in several studies shown impact on the microbial community structure (Ziganshin et al., 2013; Moestedt et al., 2014; De Vrieze et al., 2015). In line with this a strong positive correlation was seen between the achaeal order *Methanosarcinales* and OLR in this study (Figure 2a). Moreover, the increase in abundance of the family *Methanosarcinace* (*Methanosarcina*) within *Methanosarcinales* with increasing OLR has been reported previously (De Vrieze et al., 2012; Moestedt et al., 2014). *Methanosarcina* sp. is known to be quite robust and able to handle different impairments such as high ammonia, salt and VFA concentrations as well as high OLR (De Vrieze et al., 2012). In a study where the community structure in 29 different full-scale anaerobic digesters where investigated, *Methanosarcinales,* but also *Methanobacteriales,* were shown to be positively correlated to OLR (De Vrieze et al., 2015).

Impact of process management on microbial community structure

Plants on farm scale can have different reasons for operating a biogas production system (Eliasson et al., manuscript). The main purpose of the plants can be energy production, as for plant 14. This plant co-digest cattle manure with candy residues and corn starch and convert

the biogas into electricity. Another reason for setting up a biogas plant is to contribute to the nutrient management at the farm and to reduce the use of mineral fertilizers. This was the case for plant 12, mainly digestion cattle and chicken manure. As a consequence, the digestate produced at plant no 12 has a comparably higher nutrient value, i.e. higher ammonia level, while plant 14 has a comparably higher specific methane production. These differences in operation strategies likely also affected the microbial community as ammonia at elevated levels, as mentioned above, influence both the microbial composition as well as the diversity.

Comparing these two plants, plant 12 had higher relative abundance of the bacterial phylum *Proteobacteria* and the archaeal order *Methanosarcinales* with the predominance of *Methanosarcina* whereas plant 14, with a comparably higher methane production (total and specific), had a higher abundance of sequences affiliated to the phylum *Synergistetes*, OP9, *Planctomycetes*, and the archaeal order *Methanobacteriales,* with *Methanobacterium* as the dominant genus. Using the data from all the investigated biogas plants a statistical positive correlation was also observed between *Methanobacteriales, Synergistetes*, *Thermotogae*, *Actinobacteria* and the methane production (Figure 2a). The correlation between high methane production and *Methanobacteriales* is in line with previously data, presented by De Vrieze and colleges (2015). This order has thereby also been suggested to be of important for high-rate anaerobic digestion systems. Furthermore, the abundance of representatives within the phylum *Synergistetes* has been shown to be more abundant in co-fermentation systems than in digesters with manure as the only feedstock (Li et al., 2014). Thus, the high efficient performance obtained in plant 14 may be achieved through well-established interactions between syntrophic bacteria and methanogens.

Conclusions

In overall, substrate composition, temperature and ammonia level had a clear impact on the microbial community, both in terms of diversity and structure of the microbial community. Generally, a lower diversity was observed in plants with pig manure as main substrate compared to cattle manure, possibly due to a higher concentration of ammonia and in some cases higher temperature. A correlation was found between high gas production and the presence of *Methanobacteriales* common in swine manure plants and at thermophilic temperature. A correlation was also observed for *Synergistetes* and high gas production. This phylum was negatively correlated to the proportion of manure in the present study, i.e. the abundance was higher in plants using high degree of co-digestion, a correlation also shown in other studies. This result provides information that can assist during further efforts to reach economical feasible biogas production at farm site.

Dissemination of results to the agricultural/horticultural sector

All participants engaged in this study has close contact with the sector and the knowledge can thus immediately be transferred and implemented; Karin Eliasson is an advisor at Swedish Rural Economy and Agricultural Society working with biogas plants at farm scale bringing this knowledge into practice; Anna Schnürer holds a position as an external collaboration specialist and is active in many outreach activities related to biogas production, including e.g. teaching at courses for farmers; Lotta Levén is a researcher at JTI which has close contact with farmers working with farm scale biogas plants.

Publications

Under preparation
*Microbial community structure in Swedish farm scale biogas plants - correlation to process operation and productivity, Lotta Levén, Karin Ahlberg Eliasson, Li Sun, Johan Dicksved and Anna Schnürer
*Production efficiency of Swedish farm scale biogas plants, Karin Ahlberg Eliasson, Lotta Levén, Elisabeth Nadeau and Anna Schnürer

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