

# TWO-PHASE ANAEROBIC DIGESTION OF WASTEWATER WITH HIGH SALINITY

## 1. DESCRIPTION OF THE TWO-PHASE ANAEROBIC DIGESTION SYSTEM

A two-stage anaerobic system (acidogenic + methanogenic phase) was operated in continuous mode at lab scale with 2.5L working volume in each EGSB reactor. Briefly, the acidogenic phase was fed with diluted wastewater resulting in a fermented broth which was consequently diluted and fed to the methanogenic phase (Figure 1). Both reactors were inoculated with anaerobic granular sludge harvested from a one phase anaerobic digestion system treating brewery wastewater. Certain variables were controlled or measured online such as Temperature ( $30 \circ C$ ), pH, redox, volume of gas produced and biogas composition.



**Figure 1 – Top:** Schematic representation of the two-phase anaerobic digestion system. 1 – Influent tank; 2, 8,9 - feeding pumps; 3 – Gas solid liquid separator; 4 – recirculation pumps; 5 – pH and redox sensors holder; 6 – Outlet; 7 – storage tank; 10 – Water for dilution; 11-  $CH_4$  and  $CO_2$  sensors: AR – acidogenic reactor; MR – methanogenic reactor. **Bottom:** Picture of the lab scale AD set up.





In addition, samples were taken regularly to assess process performance. For this, COD, sugars, proteins, VFA's+ethanol+lactate,  $NH_4^+$ +PO4<sup>2-</sup>, TSS and VSS (as an indication of biomass), Ca<sup>+</sup>, Na<sup>+</sup>, K<sup>+</sup>, Cl<sup>-</sup>, SO4<sup>2-</sup> were analysed. Samples for microbiological analysis were also taken and stored.

Furthermore, batch tests were performed to evaluate the effect of different parameters on the acidification degree and on the biomethane production potential.

# 2. WASTEWATER CHARACTERIZATION

The wastewater used in the present work corresponds to the wastewater originated from raw hide storage throughout a period. After reception, each wastewater sample was characterized as seen in table 1. The characteristics varied between each lot of wastewater received, particularly regarding COD, protein and sodium contents. Dilutions must be made taking into account not only the inhibition of sodium, but also the COD and protein concentrations as the biomass treating this wastewater must have sufficient substrate to thrive.



WW reception date	16/01/2017	02/03/2017	21/03/2017	06/09/2017
pH	7.78	n.d.	7.58	6.70
Conductivity (mS)	149.80	n.d.	132.10	79.20
COD total (g/L)	11.35	1.00	8.70	n.d.
COD soluble (g/L)	7.95	0.67	6.32	5.52
Proteins (g/L)	4.55	n.d.	3.38	1.04
Sugar (g/L)	0.03	n.d.	0.06	n.d.
Total VFA (gCOD/L)	2.02	n.d.	1.21	1.98
<b>Cl-</b> (g/L)	132.11	n.d.	103.20	45.87
Ca+ (mg/L)	944.60	n.d.	123.00	0.11
Na+ (g/L)	88.84	n.d.	51.90	42.70
K+ (g/L)	n.d.	n.d.	0.72	0.37
$SO_4^{2-}(g/L)$	5.54	n.d.	n.d.	n.d.
<b>P-PO</b> <sub>4</sub> (mg/L)	70.53	n.d.	68.40	63.20
N-NH <sub>3</sub> (mg/L)	189.69	n.d.	147.60	322.50
TSS (g/L)	30.80	n.d.	24.40	13.60
VSS (g/L)	2.38	n.d.	1.6	1.15

**Table 1** – Characteristics of the wastewater received

n.d. not determined or under detection limit

# 3. PERFORMANCE OF THE ACIDOGENIC PHASE

#### 3.1 Effect of salinity and pH on Acidogenesis – batch tests

Batch tests were performed to assess the acidogenic biodegradability of the wastewater at different pH (5.5, 7.0 and 8.0) and by using different dilutions to achieve different salinities (0.97-57.42 g Na+/L) at pH 7.0.

### a. Methodology

500mL bottles were used, inoculated with 20% of non-adapted anaerobic granular biomass which was incubated at 30°C prior to the experiments in order to consume all endogenous substrate. All the different conditions (table 2) were tested in triplicate. F, I and L were negative control groups, i.e., only water and buffer were added to the granules. G was a positive control, i.e., no wastewater was added and casein was added as substrate. All batch tests were performed at 30°C and had duration of approximately 30 days.



	рН	COD (g/L)	[Na+] (g/L)
Α		6.89	57.42±2.48
В		5.66	48.26±1.66
С		4.35	36.05±1.06
D	7.0	2.18	19.88±2.13
Ε		0.87	9.79±1.79
F		0.00	$0.97 \pm 0.06$
G		6.75	1.00
Н	5 5	6.89	54.32±0.30
Ι	5.5	0.00	0.23±0.02
J	<u>۹</u>	6.89	58.03±2.90
K	0.0	0.00	0.22±0.02

Table 1	– nH	COD	and sodium	concentrations	applied to	each a	acidogenic	hatch test
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Samples were taken daily to analyse the production of fermentation products, monitoring the lag, exponential and stationary phase of each treatment. In addition, VSS/TSS, nutrients ( $NH_4^+$  and  $PO_4^{3-}$ ), COD and protein were measured at the start and end of each treatment.

Based on the analysis performed, several parameters were calculated, such as acidification degree (DA) (Equation 1) and the specific acidification rate (SAR) (Equation 2).

The DA (%) was determined using the following equation:

$$DA = \frac{[FP]}{[COD_{total}]} \times 100$$
 Equation 1

where, [FP] corresponds to the sum of the concentration of VFAs, lactate and ethanol at the end of each treatment and  $[COD_{total}]$  corresponds the total COD at the start of treatment.

The SAR (gFP/(gCOD.gVSS.day)) was determined using the following equation:

$$SAR = \frac{FP_{final} - FP_{initial}}{[COD_{total}].[VSS].\Delta t}$$
 Equation 2

where  $FP_{final}$  and  $FP_{initial}$  is the FP concentration during stationary and lag phase, respectively,  $[COD_{total}]$  corresponds the total COD concentration at the start of each treatment, [VSS] is the concentration of VSS and  $\Delta t$  is the time duration of the exponential phase.

#### b. Results

Sodium had a visible effect on the performance of the acidogenic community (Figure 2). However, when diluting the wastewater the COD was simultaneously decreased and as such, also the COD concentrations played an important role in the performance. Interestingly, at lower sodium concentrations (< 30 g/L) both SAR and DA were the lowest which could be due to the lower COD concentrations (< 3g/L), i.e., less bioavailable substrate for the conversions. The best SAR (0.0038±.0006 gFP/(gCOD.gVSS.day)) and DA (78.45±8.02%) were obtained at 36 gNa<sup>+</sup>/L and initial COD of 4.35 g/L. Nevertheless, high DA was obtained even at sodium concentrations close to 60 g/L (70.75±1.00%). Higher sodium concentrations seem to impact mainly the rate, i.e., longer residence times are needed when working at high sodium concentrations.

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Comparing to the SAR obtained for the positive control, group G,  $(0.0228\pm0.0083 \text{ gFP/(gCOD.gVSS.day)})$  the group with highest sodium (~60 gNa<sup>+</sup>/L) tested presented 66% inhibition. These values are better than those obtained by Lefebre et al., (2007), where 85% inhibition of acidogenesis was obtained at NaCl concentrations above 60 g/L, i.e., 23.6 gNa<sup>+</sup>/L, using ethanol as substrate.



Figure 2 – Effect of sodium and COD concentrations on the specific acidification rate (SAR) and acidification degrees (DA).

The increase of salinity (and increase of COD) seems to have clear impact on the profile of the FP (Figure 3). Higher salinities led to higher concentrations of acetate and butyrate. Isovalerate remained stable when sodium concentrations were above 30 g/L but increased at concentrations below 20 g/L. The enrichment in acetate at higher salinities (and higher COD) is very favourable for the methanogenesis, as methanogenic microorganisms utilize acetate as main substrate.



**Figure 3** – Effect of sodium on the profile of the fermentation products (A – 57.42±2.48 gNa<sup>+</sup>/L; B – 48.26±1.66 gNa<sup>+</sup>/L; C - 36.05±1.06 gNa<sup>+</sup>/L; D - 19.88±2.13 gNa<sup>+</sup>/L; E - 9.79±1.79 gNa<sup>+</sup>/L).



pH also had a visible effect on the acidogenesis performance (Figure 4). However, the results obtained are not straightforward. While SAR increased with the increase of pH, reaching its maximum  $(0.022\pm0.001)$  at pH 8.0, the DA was higher  $(70.75\pm1.00\%)$  at pH 7.0. On one hand, higher pH seems to speed up the acidification process by a factor of 2.8 (higher SAR). On the other hand, the higher DA at pH 7.0 might be an indication that, given enough time, more substrate can be converted to fermentation products. In addition, the wastewater had a good buffering capacity at neutral pH. Thus, and keeping in mind the costs involved for pH control, pH 7.0 is suggested for the acidogenic phase.



Figure 4 - Effect of pH on the specific acidification rate and acidification degrees.

Although to a lesser extent than sodium concentrations pH also had an effect in the FP profile (Figure 5). More acidic pH resulted in higher percentage of butyrate and lower percentage of isovalerate. No obvious difference in the FP profile can be seen between pH 7.0 and 8.0.



Figure 5 - Effect of pH on the profile of the fermentation products (A – pH 7.0; H – pH 5.5; J – pH 8.0)



# 4. CONCLUSIONS

The development of anaerobic digestion technologies for SALTGAE project to treat waste/wastewater containing high salinity has implied the following steps:

- Optimization of acidogenic reactor at lab-scale
- Optimization of methanogenic reactor at lab-scale
- Optimization of solid phase anaerobic digestion at lab-scale
- Optimization of CO<sub>2</sub> recovery

As a conclusion of the work done on the optimization of the acidogenic phase, tests showed that the anaerobic microorganisms in the granules used were capable of converting the organic matter present in the pickling wastewater to fermented product even at sodium concentrations as high as 57 gNa<sup>+</sup>/L. At pH 6.5, an acidification degree up to  $80.66\pm19.21\%$  was reached at an OLR of 1.24 gCOD/L.d. To our knowledge, such a high salinity was never reported in anaerobic granular bioreactors. The system proved to be robust and can operate efficiently under dynamic feeding with no apparent destruction of granules.

Regarding the optimization of the methanogenic phase, the methanogenic community needed longer time to adjust to the high salinity conditions. Adapting the microbial culture to increasing amounts of sodium proved to be successful (low inhibition) and the methanogenic community was capable of coping with feedstock with sodium concentration of 14 gNa<sup>+</sup>/L, producing 0.49  $LCH_4/d$ .

The limit values for sodium in two phase anaerobic granular filters were set based on laboratory experiment to avoid inhibition in mesophilic anaerobic treatment:

- Acidogenic reactor: a sodium concentration of maximally 50 g Na+/L
- Methanogenic reactor: a sodium concentration of maximally 20 g Na+/L

The test in continuous operation has been demonstrated at larger, pilot scale, with successful gradually adaptation of microbial culture in the granules to high salinity. The sodium concentration in the Acidogenic reactor has been up to 38.7 g Na+/L and in the Methanogenic reactor up to 25.1 g Na+/L.



## REFERENCES

	References
01	Lefebvre O., Quentin, S., Torrijos, M., Godon, J.J., Delgenès, J.P., Moletta, R., 2007. Impact of increasing NaCl concentrations on the performance and community composition of two anaerobic reactors. <i>Appl. Microbiol Biotechnol</i> . 75:61-69
02	Lim, S.J., Kim T.H., 2014. Applicability and trends of anaerobic granular sludge treatment processes. <i>Biomass and Bioenergy</i> . 60, 189-202.
03	Costa, J.C., Mesquita, D.P., Amaral, A.L., Alves, M.M., Ferreira, E.C., 2013. Quantitative image analysis for the characterization of microbial aggregates in biological wastewater treatment: a review. <i>Envrion Sci Pollut Res</i> . 20:5887-5912
04	Amann, R.I., Binder, B.J., Olson, R.J., Chisholm, S.W., Devereux, R., Stahl, D.A., 1990. Combination of 16S rRNA-targeted oligonucleotide probes with flow cytometry for analyzing mixed microbial populations. <i>Appl. Environ. Microbiol.</i> 56:1919–1925.
05	Amann RI. 1995. In situ identification of microorganisms by whole cell hybridization with rRNA-targeted nucleic acid probes. In: Akkermans ADL, van Elsas JD, de Bruijn FJ (eds). Molecular Microbial Ecology Manual. Kluwer Academic Publications: Dordrecht, Holland, pp 1–15.
06	Angenent, L.T., Sung, S., Raskin, L. 2004. Formation of granules and Methanosaeta fibres in an anaerobic migrating blanket reactor (AMBR). <i>Environ. Microbiol.</i> 6: 315–322.
07	Chen, S., Q. He. 2015. Persistence of Methanosaeta populations in anaerobic digestion during process instability. <i>Journal of Industrial Microbiology and Biotechnology</i> . In press. DOI: 10.1007/s10295-015-1632-7.
08	Crocetti, G., Murto, M., Björnsson, L. 2006. An update and optimisation of oligonucleotide probes targeting methanogenic Archaea for use in fluorescence in situ hybridisation (FISH). <i>Journal of microbiological methods</i> . 65:194-201.
09	Daims, H., Brühl, A., Amann, R., Schleifer, KH., Wagner, M., 1999. The Domain- specific Probe EUB338 is Insufficient for the Detection of all Bacteria: Development and Evaluation of a more Comprehensive Probe Set. <i>Syst. Appl. Microbiol.</i> 22:434–444.
10	Daims, H., Lucker, S., Wagner, M., 2006. Daime, a novel image analysis program for microbial ecology and biofilm research. <i>Environ. Microbiol.</i> 8:200-213.
11	Greuter D, Loy A, Horn M, Rattei T. 2016. probeBase —an online resource for rRNA- targeted oligonucleotide probes and primers: new features 2016. <i>Nucleic Acids Res.</i> 10.1093/nar/gkv1232.
12	Hallberg, K.B., Coupland, K., Kimura, S., Johnson, D.B. 2006. Macroscopic streamer growths in acidic, metal-rich mine waters in north wales consist of novel and remarkably simple bacterial communities. <i>App. Environ. Microbiol.</i> 72:2022-30.
13	Ito, T., Yoshiguchi, K., Ariesyady, H.D., Okabe, S. 2012Identification and quantification of key microbial trophic groups of methanogenic glucose degradation in an anaerobic digester sludge. <i>Bioresource Technology</i> . 123: 599–607.
14	Loy, A., Lehner, A., Lee, N., Adamczyk, J., Meier, H., Ernst, J., Schleifer, K.H., Wagner, M., 2002. Oligonucleotide microarray for 16S rRNA gene-based detection of all recognized lineages of sulfate-reducing prokaryotes in the environment. <i>Applied and Environmental Microbiology</i> . 68: 5064–5081.
15	Ma, K., Liu, X.L., Dong, X.Z., 2005. Methanobacterium beijingense sp. nov., a novel methanogen isolated from anaerobic digesters. <i>International Journal of Systematic and Evolutionary Microbiology</i> . 55 (1): 325–329.
16	Manz, W., Amann, R., Ludwig, W., Wagner, M., Schleifer, KH., 1992. Phylogenetic Oligodeoxynucleotide Probes for the Major Subclasses of Proteobacteria: Problems and Solutions. <i>Syst. Appl. Microbiol.</i> 15:593–600.



17	Manz, W., Amann R., Ludwig W., Wagner M., and Schleifer K.H. 1996. Application of a suite of 16S rRNA-specific oligonucleotide probes designed to investigate bacteria of the phylum cytophaga-flavobacter-bacteroides in the natural environment. <i>Microbiology</i> . 142: 1097-1106.
18	Oehmen, A., Zeng, R.J., Saunders, A.M., Blackall, L.L., Keller, J., Yuan, Z., 2006. Anaerobic and aerobic metabolism of glycogen-accumulating organisms selected with propionate as the sole carbon source. <i>Microbiology</i> 152: 2767–2778.
19	Raskin, L., Stromley, J.M., Rittmann, B.E., Stahl, D.A. 1994. Group-specific 16S rRNA hybridization probes to describe natural communities of methanogens. <i>Applied and Environmental Microbiology</i> . 60: 1232–1240.
20	Stahl, D. A., B. Flesher, H. R. Mansfield, and L. Montgomery. 1988. Use of phylogenetically based hybridization probes for studies of ruminal microbial ecology. <i>Applied and Environmental Microbiology</i> . 54:1079-1084.
21	Smith, K. S., Ingram-Smith, C. 2007. Methanosaeta, the forgotten methanogen? Trends in Microbiology 15:150-155.
22	Wu, W., Jain, M., Zeikus, J. 1996. Formation of fatty acid-degrading, anaerobic granules by defined species. <i>Applied and Environmental Microbiology</i> 62 (6): 2037–2044.
23	Neves, L.A., Crespo, J.G., Coelhoso, I.M., 2010. Gas permeation studies in supported ionic liquid membranes. J. Memb. Sci. 357, 160–170.
24	Feijani, E.A., Tavasoli, A., Mahdavi, H., 2015. Improving Gas Separation Performance of Poly(vinylidene fluoride) Based Mixed Matrix Membranes Containing Metal–Organic Frameworks by Chemical Modification. <i>Ind. Eng. Chem. Res.</i> 54, 12124–12134.
25	Dorosti, F., Omidkhah, M., Abedini, R., 2014. Fabrication and characterization of Matrimid/MIL-53 mixed matrix membrane for CO <sub>2</sub> /CH <sub>4</sub> separation. <i>Chem. Eng. Res. Des.</i> 92, 2439–2448.
26	Perez, E. V., Balkus, K.J., Ferraris, J.P., Musselman, I.H., 2009. Mixed-matrix membranes containing MOF-5 for gas separations. <i>J. Memb. Sci.</i> 328, 165–173.
27	Robeson, L.M., 2008. The upper bound revisited. J. Memb. Sci. 320, 390-400.