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**Application of a real-time qPCR method to measure the methanogen concentration during anaerobic digestion as an indicator of biogas production capacity.**

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# UNIVERSITÀ DEGLI STUDI DI TORINO

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2 Application of a Real-time qPCR method to evaluate methanogen load as a high-efficiency process bio-  
3 indicator for wet anaerobic co-digestion of organic wastes after different pre-treatments.

4

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14

15 **KEY WORDS:**

16 methanogen, anaerobic digestion, biogas production, renewable energy, Archea communities

17

18

19

20 **ABSTRACT:**

21 Biogas is a biofuel with a large energy value and primarily consists of methane. It is a renewable energy  
22 source and produced via anaerobic digestion of various organic materials, including waste water sludge  
23 and organic urban wastes. In reactors, anaerobic microorganisms can degrade the waste organic matter  
24 into two different products: digestate and biogas. If the microbial community is optimised, then the  
25 methane production rate could be improved, and the digestate could be used as a soil fertiliser.  
26 Methanogen is the major microbiologic group responsible for methane production. We detected the  
27 methanogen load during two wet digestion processes fed with pre-treated urban organic waste and  
28 waste water sludge. Two different pre-treatments were involved in the experimental digestions:  
29 pressure-extrusion and turbo-mixing. The applied methodology is based on Real Time quantitative PCR  
30 (RT-qPCR) using an *mcrA* target. First, we evaluated the validity of the analyses, including standard  
31 calibration, specificity, accuracy and precision. Next, we applied this method to 50 digestate samples. A  
32 positive and significant correlation between the biogas production rate and methanogen abundance was  
33 observed ( $r=0.579$ ,  $p<0.001$ ). The difference in the methanogen load between the two digestions is  
34 significant ( $F=41.190$ ,  $p<0.01$ ). Moreover, considering all the collected data and using  $0.6 \text{ m}^3/\text{Kg TVS}$  as  
35 the 'cut-off', representing an optimal production, a higher methanogen load mean was observed with  
36 the optimal production rates ( $F= 7.053$ ;  $p<0.05$ ). This suggests a role for methanogen load as diagnostic  
37 tool in digestion pre-treatment and optimisation.

38

39

## 40 1. INTRODUCTION

41 Two serious environmental and public health problems our society faces today include, first, reduction  
42 and treatment of waste, especially in high-density areas, and, second, finding an answer to the energetic  
43 request to limit use of conventional fuels (das Neves et al., 2009). In urban communities, these goals  
44 have no clear resolution, though renewable energy sources are likely a key strategy (Balat and Balat,  
45 2009). The anaerobic digestion process for organic waste combines the removal of organic pollutants,  
46 the reduction of organic waste volume, and energy conservation via biogas production (Rozzi and  
47 Remigi, 2004). Numerous organic wastes are subject to anaerobic digestion, such as wastewater sludge,  
48 pre-treated organic household waste (Bouallagui et al., 2005; Schievano et al., 2009). Biogas production  
49 is the consequence of a series of metabolic interactions among bacterial and Archeal micro-organisms  
50 (Ward et al., 2008). A particular ecosystem is present in an anaerobic reactor where several groups of  
51 microorganisms work interactively in the conversion of complex organic matter into biogas. The  
52 following four stages compose the digestion process: hydrolysis, acidogenesis, acetogenesis and  
53 methanogenesis (Lozano et al., 2009). In each step, various microorganisms are involved. During the first  
54 stage a group of micro-organisms secrete enzymes which hydrolyse polymers to monomers to convert  
55 particulate materials into dissolved materials (Whitman et al., 2006). They remove the small amounts of  
56 O<sub>2</sub> present and create anaerobic conditions. Subsequently, the acidogenic phase includes the action of a  
57 large and diverse group of fermentative bacteria, usually belonging to the Clostridia class and the  
58 Bacteroidaceaea family. These bacteria hydrolyse and ferment the organic materials and they produce  
59 organic acids, CO<sub>2</sub> and H<sub>2</sub>. Next, in the third phase, the acetogenic bacteria convert these monomers to  
60 H<sub>2</sub> and volatile fatty acids. Aceticlastic methanogens perform the final step in biogas production,  
61 primarily *Methanosarcina* in a high-acetate environment (>10<sup>-3</sup>M) and *Methanosaeta* which grows only  
62 by the aceticlastic reaction, as well as hydrogenotrophic methanogens. Methanogenesis is considered  
63 the rate-limiting step. Moreover, this phase is most vulnerable to either temperature or pH variations  
64 and toxic chemicals (Liu and Whitman, 2008b). Low methanogen activity produces an accumulation of H<sub>2</sub>

65 and short chain fatty acids with a consequent decrease in pH. Therefore, enhancing methanogenesis is a  
66 promising method for improving anaerobic reactor performance. There are three primary useful  
67 substrates for methanogens. Acetate is the predominant intermediate in the anaerobic food chain, and  
68 as much as two-thirds of biologically generated methane is produced from this molecule (Liu and  
69 Whitman, 2008a). Although every pathway begins differently, they all end with the same step, the  
70 reaction of methyl-coenzyme M (HS-CoM) with a second thiol coenzyme (coenzyme B) that forms  
71 methane and a mixed disulphide between coenzyme M and coenzyme B. This reaction is catalysed by  
72 methyl-coenzyme M reductase (Mcr), thus, Mcr is the key enzyme in methanogenesis (Friedrich, 2005).  
73 In its active site, this enzyme contains a unique prosthetic group, which is a nickel (Ni) porphinoid  
74 referred to as coenzyme F430 (Hedderich and Whitman, 2006). As HS-CoM has been found in all  
75 methanogens examined, it has been proposed as a sensitive biomarker for quantitative and qualitative  
76 methanogen identification in different anaerobic environments. Mcr is exclusive to methanogens, with  
77 the exception of methane-oxidising Archaea (Knittel and Boetius, 2009; Whitman et al., 2006), and  
78 specific primers have been developed for the Mcr  $\alpha$ -subunit gene sequence (*mcrA*) (Franke-Whittle et  
79 al., 2009; Luton et al., 2002; Steinberg and Regan, 2008). *McrA* analysis can be used either in conjunction  
80 with or independently of the *16S rRNA* gene (Bergmann et al., 2010a; Bergmann et al., 2010b; Cardinali-  
81 Rezende et al., 2009; Nettmann et al., 2008); this gene is absent in all non-methanogens, with the  
82 exception of the anaerobic methane-oxidizing Archea (Steinberg and Regan, 2008). The aim for the work  
83 herein was to apply a recently proposed methodology for determining methanogen abundance using  
84 Real-Time quantitative PCR (RT-qPCR) targeting the *mcrA* gene to evaluate methanogen load during the  
85 digestion process and identify its correlation with the biogas production efficiency. The purpose is to  
86 develop a useful Archea bio-indicator for process performance. The analyses involved two different  
87 digestion sessions that differed only in pre-treatment of the organic material input. We observed  
88 methanogen modulation during the digestions referring to the recorded methane production rate.  
89

## 90 2. METHODS AND MATERIALS

### 91 2.1 Digestion processes

92 Two pilot reactors were fed with a pre-treated organic fraction of municipal solid waste (OFMSW) and  
93 waste-water sludge. The pre-treatment methods used in this study included a pressure-extrusion (A)  
94 and a turbo-mixing (B) system. In method A, a specially designed extruder press separates the input  
95 waste into two fractions: dry, which is sent to thermal conversion, and semi-solid. The municipal waste,  
96 fed into the extruder press, is exposed to high pressure (280 bar) in a perforated extrusion chamber that  
97 results in a fluid organic portion (food residues, various putrescible fractions). The organic fluid is  
98 pushed out by the difference in pressure between the interior and exterior of the chamber, yielding a  
99 more homogeneous sample. This is a consequence from separating the more mechanically resistant  
100 portions (paper residues, cellulose tissues, wood and lignin parts, etc.). The pressure-extruded OFMSW,  
101 obtained using the previously described procedure, was then diluted with waste-water sludge (1:3). In  
102 contrast, method B (the turbo-mixing system) is a wet process that operates with a TS content lower  
103 than 8%. Mixing and treating occur via a rotating plate, with hummers at the bottom of the turbo-mixing  
104 chamber that, rotating at high velocity, induces the suspension to shear and crush. After 20 minutes of  
105 mixing, the turbo-mixer was empty and a vessel was filled with the mixture, where density separated  
106 the contents. The particles that weigh more than water precipitate to the bottom, where they are taken  
107 up using a screw and collected in an external vessel. The same procedure was applied to the particles  
108 that weigh less than water and float on the surface. The remaining suspension is the organic fraction,  
109 which is pumped to a storage basin after a passage through a shredding pump. In this case, the OFMSW  
110 was directly turbo-mixed with waste water sludge. Full control of the final TS content suspension is  
111 impossible in the turbo-mixing system. The primary physical-chemical characteristics for each type of  
112 feed used herein, immediately prior to the reactor, are shown in Table 1.

113 We compared the analytical results obtained from feed samples pre-treated with methods A (pressure-  
114 extrusion) and B (turbo-mixing). OFMSW pre-treated with press-extrusion has a higher percentage of

115 volatile solids that may possibly transform into biogas in feed pre-treated with method B where the  
116 organic matter value is lower. Further, the C/N ratio for the feed mixtures was evaluated. It has been  
117 shown that optimum values for the carbon-to-nitrogen (C/N) ratio are within the 20 to 70 range for the  
118 anaerobic digestion process (Burton and Turner, 2003), but even lower values (12 to 16) have also been  
119 reported (Mshandete et al., 2004) and, recently, more widely studied (Mata-Alvarez et al., 2011). The  
120 C/N values herein were better after pre-treatment A than pre-treatment B.

121 Anaerobic co-digestion was examined using a reactor, illustrated in Figure 1, with a 15 L volume capacity  
122 and a 10 L working volume. The temperature was mesophilic and maintained at  $38\pm 2^{\circ}\text{C}$  using a water  
123 recirculation system connected to a thermostatic valve. The biogas produced was collected and  
124 measured in a calibrated gasometer, and a mixing system with the re-circulated biogas from the  
125 anaerobic digestion process was used. The reactors were equipped with two openings, one at the top  
126 for feeding and one below to collect effluent discharge. Every day, 500 ml of digestate was removed  
127 from each reactor before an additional 500 ml of fresh feed was added. The reactors were operated at a  
128 constant organic load rate of  $4.5\pm 0.3$  kg TVS / $\text{m}^3\cdot\text{day}$  for OFMSW pressure-extrusion and  $1.7\pm 0.5$  kg TVS  
129 / $\text{m}^3\cdot\text{day}$ , as a mean value, for the OFMSW pulper pre-treatment. The pre-treatments were examined  
130 over two 20-day consecutive hydraulic retention time periods for each organic loading rate. The first  
131 period would ensure the highest replacement parts of the waste material inside the reactors, and in the  
132 second 20 days, we analysed the process under stable conditions, as all the feed had replaced the  
133 inoculum content.

134 Every 2 days, representative samples from the anaerobic reactor effluent were analysed. The following  
135 parameters were analysed three times per week in accordance with Standard Methods (APHA, 1995):  
136 pH, total solids (TS), total volatile solids (TVS), alkalinity, acidity, N, and total carbon. Daily biogas  
137 production was measured using a liquid displacement system connected to the digester. The biogas  
138 volume was corrected using standard temperature and pressure conditions. The biogas composition  
139 (methane and carbon dioxide percentages) was analysed once per week using a portable analyser and



140 confirmed via gas chromatography. For methanogen analysis, the samples were collected three times  
141 per week in a 50 ml sterile tube and frozen at -20°C until extraction. More than 80 digest effluent  
142 samples were collected from more than a year of digestion operations beginning March 2009.

143

## 144 **2.2 DNA extraction and purification**

145 The digestate aliquots were thawed at 4°C overnight and centrifuged at 3000 g for 20 minutes; the  
146 supernatant was then removed, and the semi-dry aliquots were used for the following steps. The total  
147 DNA was extracted from 0.25 g of particulate matter (residue humidity was 31±5%) using the PowerSoil  
148 DNA Isolation Kit followed by UltraClean Soil DNA Kit (MoBio Laboratories). The DNA quantity extracted  
149 was 3.51±1.53 ng/μl (mean), and its quality was evaluated using gel electrophoresis before the chain  
150 reaction. Only the samples over 1 ng/μl and of sufficient DNA quality, tested by gel electrophoresis,  
151 were used for the following step. Lower quantity or a bad quality of the DNA makes the successive  
152 quantification difficult so this kind of DNA quality cut-off was applied. 50 samples were sufficient in  
153 distinct DNA quantity and quality.

154

## 155 **2.3 RT-qPCR analysis**

156 After DNA extraction and purification, total methanogen was quantified using methanogen-specific  
157 short primers for an *mcrA* sequence described by Steinberg and Regan (Steinberg and Regan, 2008) and  
158 synthesised by ThermoBiopolymer. For the reactions, we used a standard super-mix (Bio-Rad SsoFast™  
159 EvaGreen SuperMix), the RT-PCR Chromo4 (Bio-Rad) and the Opticon Monitor 3 Software. The reaction  
160 conditions were previously described (Steinberg and Regan, 2008). The standard reference was a  
161 *Methanosarcina acetivorans* *mcrA* sequence of approximately 470 base pairs (Lueders et al.,  
162 2001) included in a pCR21 vector (Invitrogen) supplied by L.M. Steinberg and J.M. Regan of the  
163 Pennsylvania State University. This plasmid was amplified by transforming *Escherichia coli* Top10 cells  
164 according to the manufacturer's instruction. The transformed cells were selected on LB agar in presence

165 of ampicillin, and the plasmid was extracted using a plasmid DNA purification kit (NucleoSpin Plasmid,  
166 Macherey-Nagel). The standard curve had six points (figure 2) and was calculated using the threshold  
167 cycle method; for the highest yield, 2,3 ng of plasmid was amplified ( $\sim 4.5 \cdot 10^8$  plasmid copies). Between  
168 each standard curve point there is a 1:10 dilution. The standards and samples were tested in triplicate.  
169 The triplicate value was accepted only if the coefficient of variation was below 20%. The correlation  
170 coefficient was considered sufficient if above 0.990. PCR efficiency was 97%, and the resolution limit for  
171 the method was  $4.5 \cdot 10^3$  copies of *mcrA*. We used in the sample amplification 2  $\mu$ l of a 1:10 dilution for  
172 each DNA extract. This quantity was evaluated as the best among various tested quantities for a  
173 standard curve and with an acceptable PCR efficiency. The 1:10 dilution limited the effect of inhibiting  
174 substances present in this type of sample. Figure 3 shows the quantification precision obtained,  
175 beginning with the same two samples re-extracted 10-fold. This test illustrated that the sampling  
176 procedure does not affect the final analysis. The variation coefficient was below 10% for sample 1 and  
177 below 20% for sample 2. The 50 samples were sufficient in DNA quantity and quality.

178

#### 179 **2.4 Statistics**

180 Statistical analyses were performed using the SPSS Package, version 17.0 for Windows. A Pearson  
181 correlation coefficient was used to assess the relationship between the variables. A T-test of  
182 independent variables was used in the mean evaluations. The differences and correlations were  
183 considered significant at  $p < 0.05$  and highly significant at  $p < 0.01$ .

184

### 185 **3. RESULTS AND DISCUSSION**

186 Table 2 shows the primary process-control factors that were monitored, such as biogas production  
187 parameters, solid reduction data and acidity values. Pre-treatment A not only yields more relevant  
188 quantities of biogas, but the biogas production was also double the value observed in treatment B. Thus,  
189 treatment A provides better input preparation likely due to a reduction in particle size, increasing the

190 available specific surface and enhancing the contact surface between bacteria. This was further  
191 confirmed via a %TVS reduction. The digestion process fed with pre-treatment A material performs  
192 better with respect to pre-treatment B, despite the unfavourable input pH (table 1).

193 The correlation between methanogen abundance and biogas production is positive and statistically  
194 significant ( $p < 0.01$ ), as shown in figure 4. This correlation holds both considering all the collected data  
195 (first and second digestions) and separating the two data sets. As a measure of the correlation, Pearson's  
196 rho is 0.579 ( $p < 0.01$ ). In figure 4, the correlations are expressed for each collected data set. Further, the  
197 single digestion showed a positive and significant correlation between methanogen quantification and  
198 biogas production rate.

199 Even if biomolecular methodology for methanogen analyses during anaerobic processes became  
200 nowadays diffused, this is one of first studies to analyse and correlate methanogen load with the biogas  
201 production during full digestion sessions. Further, this are very few studies that monitored by such  
202 biological method different process and that observed a significant correlation using a *mcrA*-based PCR  
203 method. Although, anaerobic methanotrophs that are phylogenetically related to methanogens have an  
204 Mcr-like protein that catalyses methane oxidation (Nunoura et al., 2008), the abundance of this  
205 microbial population is likely negligible with respect to the methanogen community, as deduced from  
206 the scarcity of methanotroph products such as  $N_2$  and  $HS^-$  (Balat and Balat, 2009).

207 Figure 5 shows a marked and statistically significant difference between the methanogen load present in  
208 the digester feed from pre-treated A and pre-treated B organics. This trend is similar to biogas  
209 production (table 2), even if only the methanogen load difference is statistically significant ( $p < 0.01$ ).

210 Setting a 'cut-off' for optimal production generated an additional measure of correlated activity. As also  
211 observed in the literature, production rate ranged between 0.3 to 0.8  $m^3$  biogas/kg TVS in base of  
212 various parameters such as input characteristics, process temperature, organic load, and so on. Optimal  
213 production can be defined as 0.6  $m^3$  biogas/kg TVS (Cuetos et al., 2009; Gomez et al., 2006). Shown in  
214 figure 5, the methanogen load is lower in the samples with sub-optimal production rates compared with

215 optimal samples (T-test,  $p < 0.05$ ).

216 However, we would also discuss in this paper whether, overall, the data support methanogen  
217 abundance, determined with the previously described RT-qPCR method, decrease as a biomarker for  
218 methanogenesis efficiency. The stability parameters typically measured when monitoring digestions,  
219 such as pH, alkalinity and acidity of the mixture as well as split volatile fatty acid concentration in the  
220 reactor, were not sufficient early predictors during this process. A variation of these parameters  
221 correlates with a contemporaneous decrease in production. In this instance, corrective steps to support  
222 a productive balance in the reactor are ineffective. As shown in figure 6, prediction may only be relevant  
223 at certain times during the process, such as between the 3<sup>rd</sup> and 17<sup>th</sup> of April, 8<sup>th</sup> and 15<sup>th</sup> of May and  
224 22<sup>nd</sup> and 29<sup>th</sup> of May. On certain days, we observed a decrease in the *mcrA* copies just before a decrease  
225 in the specific biogas production rate; however, this event was not regular during the digestion process.  
226 Recent studies show that methanogen population dynamics and community structures can vary during  
227 the digestion processes (Lee et al., 2009a; Lee et al., 2009b; Yu et al., 2006), as can volatile fatty acid  
228 concentrations (Wang et al., 2009). All of these studies discussed the microbial communities' capacity  
229 for responding to changes in anaerobic environments, such as altered feeding (Kovacik et al., 2010) and  
230 different temperature (Sasaki et al., 2011), among others.

231

232

#### 233 **4. CONCLUSIONS**

234 Despite the environmental complexities inherent in the work herein, we conducted a representative  
235 sampling procedure and a valid DNA extraction. The results show proper quantitation for the majority of  
236 the collected samples (63%). The experiments conducted during the digestion process in the reactors  
237 demonstrate a good method for determining methanogen concentration with respect to the biogas  
238 production. The hypothesis, that methanogen community abundance and composition are strictly  
239 related to the methane production, is confirmed.

240 In the last few years, the research community has enhanced our knowledge regarding Archea  
241 microorganisms from both an ecological standpoint (Leigh et al., 2011; Liu and Whitman, 2008b) and a  
242 human health perspective (Johnston et al., 2010). The economic costs are really onerous for these  
243 analyses (Kalia and Purohit, 2008) moreover the proposed PCR method herein is a useful tool for  
244 studying methanogen populations and their modulation related to biogas production rate (Lee et al.,  
245 2009a; Patil et al., 2010), even if the results herein cannot yet provide a clear activity prediction.  
246 McrA gene-based methods could be even more diffused methods (Zhu et al., 2011), also relating with  
247 digestion performance (Bialek et al., 2011) and feeding matrices, which currently pose a relevant  
248 concern for waste management and public health (Cardinali-Rezende et al., 2009). A fundamental step  
249 includes analysis of, at least, the different families of methanogens to identify a better early bio-  
250 indicator among the total methanogen population (Steinberg and Regan, 2009; Vavilin et al., 2008).  
251 From these studies, an alarm threshold for micro-organism levels could be a useful, fundamental  
252 process-control parameter but the introduction of this analysis must be economically sustainable.  
253 Prediction ability with respect to biogas loss over several days might also be interesting from an  
254 economic standpoint. The problems related with arrested methanogenesis are one of the largest  
255 obstacles to anaerobic digestion diffusion. In the approach proposed herein, it is essential to examine  
256 the community composition and the genus contribution to optimise the digestion process and maximise  
257 CH<sub>4</sub> yield.

258

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268

269 **FIGURE CHAPTERS**

270

271 **Figure 1** – The pilot hardware description is illustrated. The same reactor, in different six-month  
272 fermentation sessions, was used with two different feed pre-treatments.

273

274 **Figure 2** – Example of a standard curve obtained during experiment. The same curve is included in all  
275 analysis sessions, and the samples are placed within the standard points.

276

277 **Figure 3** - RT-PCR quantification of 10 different, consecutive extractions for the same two samples.  
278 Different samples collected on different days were used. Cross-shaped points represent each different  
279 extract quantification. For each set, the last point (score) represents the mean from all the analyses. For  
280 each data point, the standard deviation is shown.

281

282 **Figure 4** - Linear regression model for RT-PCR quantification samples collected from reactors and the  
283 logarithm of the target gene copies for each  $\mu\text{l}$  of DNA sample. (A) circles represent pressure-extrusion  
284 pre-treatment data,  $y=1.0303x+6.5118$  (correlation=0.418,  $p<0.05$ ); (B) rhombus represent the turbo-  
285 mixing pre-treatment data,  $y=2.5629x+4.3782$  (correlation=0.622,  $p<0.05$ ).

286

287 **Figure 5** - *McrA* abundance evaluated during the digestion process, subdivided by input material pre-  
288 treatment (T-test  $p<0.01$ ) and optimal biogas production ( $0.6 \text{ m}^3/\text{kg SV}$ ) (T-test  $p<0.05$ ).

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290 **Figure 6** - Temporal trends of *mcrA* abundance (squares) and biogas production (rhombus) during  
291 digestion of the pressure-extruded input for the reactor.

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**TABLES**

|  | <b>Pre-treatment A</b> | <b>Pre-treatment B</b> |
|--|------------------------|------------------------|
| <b>pH</b>                              | 4.4 ± 0.3              | 6.0 ± 0.7              |
| <b>Total Solids (TS) (%)</b>           | 9.9 ± 0.7              | 4.6 ± 1.1              |
| <b>Total volatile solids (TVS) (%)</b> | 8.7 ± 0.7              | 3.3 ± 1.1              |
| <b>TVS/ST (%)</b>                      | 86.8 ± 0.2             | 70.6 ± 4.9             |
| <b>Carbon (C) (%ST)</b>                | 46.0 ± 0.9             | 37.0 ± 3.4             |
| <b>Nitrogen (N) (%ST)</b>              | 3.1 ± 0.2              | 3.5 ± 0.3              |
| <b>C/N ratio</b>                       | 15.2 ± 1.1             | 10.4 ± 1.5             |

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**Table 1:** Characteristics of the pre-treated inputs from the two different methods used in the anaerobic co-digestion processes.

| <b>Parameters</b>  | <b>Pre-treatment A</b> | <b>Pre-treatment B</b> |
|--|------------------------|------------------------|
| Daily biogas production (L/die)                                      | 27.08 ± 3.01           | 4.87 ± 2.46            |
| Specific biogas production (m <sup>3</sup> /kg VS <sub>added</sub> ) | 0.64 ± 0.07            | 0.30 ± 0.13            |
| TS reduction (%)   | 64.44 ± 7.57           | 31.67 ± 6.23           |
| TVS reduction (%)  | 73.84 ± 5.87           | 38.13 ± 6.70           |
| pH   | 7.36 ± 0.34            | 6.82 ± 0.52            |
| Ac./Alc. ratio   | 0.37 ± 0.18            | 2.47 ± 2.41            |
| CH <sub>4</sub> (%)  | 60.60 ± 2.90           | 57.50 ± 6.10           |
| CO <sub>2</sub> (%)  | 37.70 ± 3.20           | 41.00 ± 6.44           |

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**Table 2:** Evaluation of relevant parameters for the co-digestion processes subdivided by pre-treated method.



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