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Application of rumen and anaerobic sludge microbes for bio harvesting from lignocellulosic biomass

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21 **Abstract**

22 This study investigated the production of biogas, volatile fatty acids (VFAs), and other
23 soluble organic from lignocellulosic biomass by two microbial communities (i.e. rumen fluid
24 and anaerobic sludge). Four types of abundant lignocellulosic biomass (i.e. wheat straw,
25 oaten hay, lurence hay and corn silage) found in Australia were used. The results show that
26 rumen microbes produced four-time higher VFAs level than that of anaerobic sludge reactors,
27 indicating the possible application of rumen microorganism for VFAs generation from
28 lignocellulosic biomass. VFA production in the rumen fluid reactors was probably due to the
29 presence of specific hydrolytic and acidogenic bacteria (e.g. *Fibrobacter* and *Prevotella*).
30 VFA production corroborated from the observation of pH drop in the rumen fluid reactors
31 indicated hydrolytic and acidogenic inhibition, suggesting the continuous extraction of VFAs
32 from the reactor. Anaerobic sludge reactors on the other hand, produced more biogas than
33 that of rumen fluid reactors. This observation was consistent with the abundance of
34 methanogens in anaerobic sludge inoculum (3.98% of total microbes) compared to rumen
35 fluid (0.11%). VFA production from lignocellulosic biomass is the building block chemical
36 for bioplastic, biohydrogen and biofuel. The results from this study provide important
37 foundation for the development of engineered systems to generate VFAs from lignocellulosic
38 biomass.

39 **Key words:** Lignocellulosic biomass; Rumen fluid; Anaerobic sludge; Volatile fatty acids,
40 Biogas; Bio harvesting.

41

42 1. Introduction

43 Lignocellulosic biomass are residues from agricultural and forestry industries with an
44 estimation of 10 billion tons annually. The conventional view of the residues is that they need
45 to be disposed of to prevent the spread of disease in the next cropping season. An alternative
46 view is that the residues, as lignocellulosic biomass, are a great reserve of carbon, the
47 keystone of energy and raw chemical production (Nanda et al., 2015; Sawatdeenarunat et al.,
48 2015). Lignocellulosic biomass has a net calorific value of up to 20 MJ/kg. However, the
49 economic value of alternate uses such as electricity generation through incineration is
50 relatively small due to high moisture content in lignocellulosic biomass. An alternative use of
51 lignocellulosic biomass will probably pave the way for the production of raw chemicals and
52 energy that currently depends on fossil resources. Harvesting processes from lignocellulosic
53 biomass have gained an upward trajectory in the last two decades; however, the recalcitrant
54 structure of lignocellulosic biomass is the main bottleneck that still requires substantial
55 research to overcome (Rouches et al., 2016; Sawatdeenarunat et al., 2015).

56 Current methods to extract raw chemicals and energy from lignocellulosic biomass have
57 low productivity (Nanda et al., 2015; Sawatdeenarunat et al., 2015). This is because the
58 chemical compositions and structure of lignocellulosic biomass (which includes cellulose,
59 hemicellulose and lignin) requires high energy or corrosive chemicals to break it down
60 (Sawatdeenarunat et al., 2015; Zabed et al., 2016). Processes that have been investigated
61 include a physical process (e.g. steam explosion and grinding); chemical process (e.g.
62 sulphuric, nitric acids, sodium hydroxide and urea soaking); and protein engineering to
63 improve the performance of existing lignocellulose-degrading enzymes (Sawatdeenarunat et
64 al., 2015; Wen et al., 2009). The physical process methods and chemical process methods are
65 limited in their effectiveness, create environmental hazards, and are energy intensive. The
66 protein engineering methods have achieved only modest results in improving lignocellulosic

67 biomass hydroxylation (Wen et al., 2009). This is mostly due to our limited understanding of
68 the mechanisms of biomass hydroxylation and the relatively low activity of currently
69 available hydrolytic enzymes.

70 Specific microbial communities from a termite gut, from the digestive tract of ruminant
71 animals and from anaerobic digester have shown the capability of degrading lignocellulosic
72 biomass. The rumen microbial community has evolved in the rumen environment for million
73 years to digest lignocellulosic biomass to produce volatile fatty acids (VFAs) and biogas. The
74 symbiotic relationship between the rumen and its microbial community has led to the
75 evolution of lignocellulosic-degrading bacteria that have not been found to proliferate
76 elsewhere. Likewise, the microbial community in 1 μ L termite gut is also specific for
77 lignocellulosic degradation. Recently, Lazuka et al. (2018) has reported that a consortium of
78 lignocellulosic-degrading bacteria can be achieved in an engineered anaerobic reactor under
79 sterile conditions. Anaerobic microbial community from the anaerobic digester has
80 demonstrated the efficiency of converting organic waste to energy (i.e. biogas) (Nghiem et
81 al., 2017; Yue et al., 2013). Research in the application of these microbial communities for
82 lignocellulosic biomass degradation has gained promising results (Sawatdeenarunat et al.,
83 2015; Takizawa et al., 2018; Wang et al., 2018; Zhang et al., 2017). Takizawa et al. (2018)
84 reported that rumen fluid pretreatment of paper sludge increased 3.4 times methane
85 production. Zhang et al. (2017) observed an enhancement of cellulose degradation due to
86 rumen microbes addition in anaerobic digestion. Therefore, microbial community sources
87 (e.g. rumen fluid and anaerobic sludge) could be used to produce VFAs and energy from
88 lignocellulosic biomass.

89 The study aims to investigate the production of VFAs and biogas as well as soluble
90 chemical oxygen demand from lignocellulosic biomass by rumen fluid and anaerobic sludge
91 microbial communities. The production rate was investigated in a biomethane potential assay

92 that provided conditions simulating anaerobic digestion process. 16S rRNA gene-based
 93 community was employed to reveal the microbial community composition in rumen fluid and
 94 anaerobic sludge. The results of microbial community analysis provided support evidence to
 95 the different observation in production rate between two communities. Results from this
 96 study provided preliminary background for the development of an engineered system to
 97 generate VFAs from lignocellulosic biomass.

98 2. Materials and methods

99 2.1 Lignocellulosic biomass and inoculum sources

100 Four lignocellulosic materials namely wheat straw (WS), lurence hay (LH), oaten hay
 101 (OH) and corn silage (CS) were obtained from a local pet store. These are some of the most
 102 abundant lignocellulosic biomass in Australia. They were washed with Milli-Q water and
 103 dried at 60 °C for 24 h. Then, they were milled and sieved through a 600- μ m pore size sieve
 104 (Fig 1a). The resultant was characterized for moisture, volatile solid (VS) and ash content and
 105 stored in a zip bag at room temperature until use. The VS contents of all four lignocellulosic
 106 materials were above 90% (Table 1). The lignocellulosic biomasses have substantial levels
 107 of COD (500-1000 kg COD/kg biomass). Therefore, these materials have high potential as
 108 feedstocks for anaerobic digestion.

109 **Table 1:** Characteristics of lignocellulosic biomass (mean \pm standard deviation from 3
 110 samples).

Materials	Moisture (%)	VS (%)	Ash (%)	COD (kg/kg)
Wheat straw (WS)	2.8 \pm 0.5	92.5 \pm 0.0	4.7 \pm 0.5	846.5 \pm 168.9
Lurence hay (LH)	4.9 \pm 0.5	91.3 \pm 0.2	3.8 \pm 0.6	1014 \pm 33.6
Oaten hay (OH)	4.2 \pm 1.1	94.6 \pm 0.2	1.7 \pm 0.9	531 \pm 8.5
Corn silage (CS)	4.4 \pm 0.7	95.3 \pm 0.5	0.3 \pm 0.2	738.5 \pm 112.4

111 Rumen fluid and anaerobic sludge were two inoculum sources (Table 2). The former was
 112 collected from a 12-year old fistulated cow after 2 hours feeding. Rumen fluid was strained
 113 through two layers of cheesecloth to remove any coarse materials, and then stored in
 114 insulated thermos bottles that had been pre-heated with warm water to maintain a temperature
 115 of approximately 39 °C during transportation to the laboratory. Anaerobic sludge was
 116 obtained from a full-scale anaerobic digester at the wastewater treatment plant in NSW,
 117 Australia. Anaerobic sludge was stored in pre-heated insulated thermos bottles during
 118 transportation and used within four hours of collection.

119 **Table 2:** Key properties of inoculum (mean \pm standard deviation of 3 measurements).

	Rumen fluid	Digested sludge
TS (%)	2.2 \pm 0.2	1.6 \pm 0.2
VS (%)	1.8 \pm 0.1	1.1 \pm 0.2
pH	7.0 \pm 0.0	7.3 \pm 0.0
Total COD (g/L)	14.8 \pm 1.7	1.8 \pm 0.5

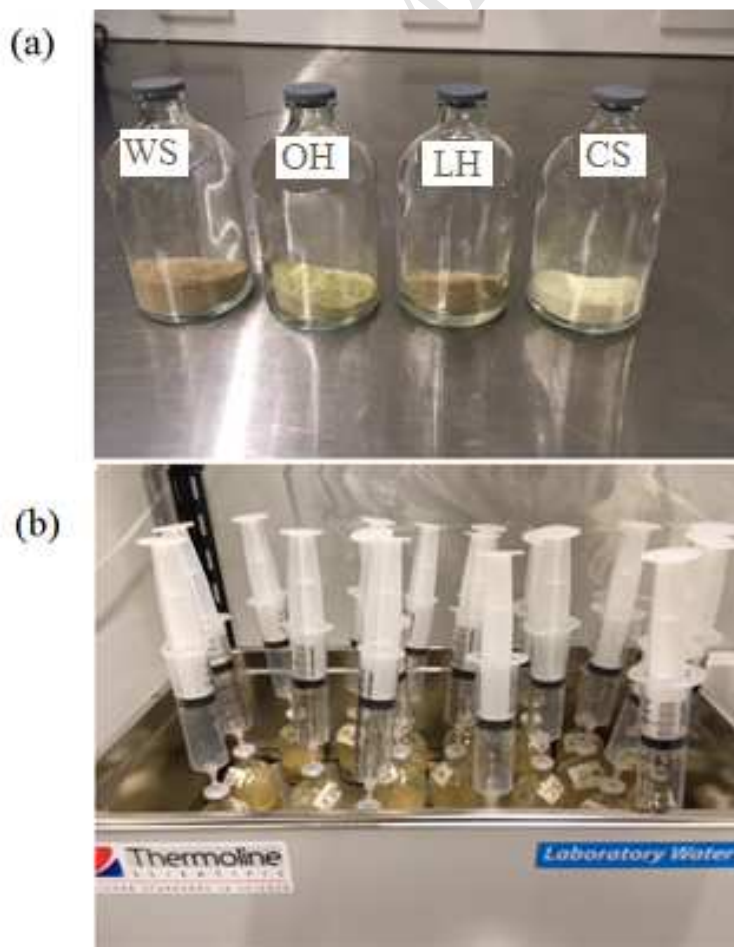
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121 2.2 Biochemical methane potential assay

122 Biochemical methane potential assay was conducted using a set of test rigs similar to that
 123 used by Nghiem et al., (2014). The test rigs contained fermentation bottles, a water bath, and
 124 a biogas collection gallery. The fermentation bottles were made of glass with 100 mL active
 125 volume. Each bottle was equipped with a rubber stopper and aluminium cap. The water bath
 126 was Model TWB-20D Thermoline Scientific Pty Ltd and the biogas collection gallery
 127 included a 50-mL syringe connected with the needle via an inter lock. Biogas production was
 128 recorded daily following the change of syringe piston position on the graduated syringe.

129 Rumen fluid and anaerobic sludge (50 mL) were inoculated with 1.5 g lignocellulosic
130 biomass equivalent to 3% w/v into a 100-mL fermentation glass bottle that was pre-flushed
131 with N₂ gas. The bottles were flushed again with N₂ gas and immediately sealed with a
132 rubber stopper to maintain anaerobic condition. The fermentation bottles were submerged in
133 a water bath to maintain a constant temperature of 39 ± 1 °C and 35 ± 1 °C for rumen fluid
134 and anaerobic sludge fermentation, respectively (Fig 1b).

135 The fermentation process was conducted for 7 days with rumen fluid and anaerobic sludge
136 inocula, respectively. For each lignocellulosic material, six fermentation bottles were
137 prepared. Two bottles were taken for soluble COD and total organic acids (as acetate)
138 analysis every two days. Another set of bottles was prepared with only either inoculum or
139 lignocellulosic materials as the controls. Fermentation bottles were mixed manually three
140 times each day.



141

142 **Figure 1:** Four selected lignocellulosic biomass: WH = wheat straw; OH = oaten hay; CS =
143 corn silage; LH = lurence hay (a) and a photograph of biomethane potential setup (b).

144 2.3 Analytical methods

145 Moisture, volatile solid (VS) and ash content of lignocellulosic biomass were determined
146 according to Standard Methods 1684. Briefly, five gram of lignocellulosic biomass was
147 transferred into a ceramic bowl and dried at 100 °C for 24 h. The ceramic bowl was then
148 allowed to cool to room temperature in a desiccating glass chamber. The weight of ceramic
149 bowl and material was recorded. Then the ceramic bowl was heated to 550 °C in a furnace for
150 15 min. The residual weight was recorded and used to calculate moisture, VS and ash
151 content.

152 Total COD and soluble COD concentration were measured by using digestion vials (Hach,
153 Australia) and Hach DR3900 spectrophotometer program number 435 COD HR, following
154 the US-EPA Standard Method 5220 D.

155 Total organic acids (TOA) as acetate (mg/L) were measured following US-EPA Standard
156 Method 5560C, including acidification, distillation and titration. Fermented broth (3 mL)
157 from each fermentation bottle was diluted into 200 mL with Milli-Q water. Then 5 mL of
158 98% H₂SO₄ was mixed into samples. The sample was distilled using the Vapodest 300
159 (Gerhardt Germany) with set up program of heating power 80% and distillate time of 8 min.
160 The final sample was titrated using an Auto Titrator 885 (Metrohm Australia). TOA
161 concentration was calculated using the following equation:

$$\text{Total organic acid } \left(\frac{\text{mg}}{\text{L}}\right) = \frac{(\text{mL NaOH sample} - \text{mL NaOH blank}) \times N \times 60000}{\text{mL sample} \times 0.6}$$

162 Where: N= normality of NaOH and 0.6 is the recovery factor (60%).

163 2.4 Microbial community analysis

164 Rumen microbial community results were obtained from Duarte et al. (2017), who
165 sampled rumen fluid from the same fistulated cow. Anaerobic sludge microbial community
166 samples were collected before the inoculation process. Anaerobic sludge was mixed with
167 100% ethanol (1:1 v/v) to preserve the cells. Detail sample preparation procedure is available
168 elsewhere (Nguyen et al., 2019a). Briefly, samples were stored in an ice bag during transport
169 and immediately transferred to - 20 °C freezer upon arrival to the laboratory. Genomic DNA
170 was extracted using DNeasy PowerSoil Pro Kit (QIAGEN Pty Ltd, Australia) following the
171 manufacturer's instruction. The integrity, purity and concentration of the extracted DNA
172 were determined by a spectrophotometer (Nanodrop ND2300). The mass of DNA in each
173 sample was always more than 10 µg and the concentration was normalized to 50 ng/µL using
174 DNA/RNA free water. Samples were stored at - 20 °C until DNA sequencing.

175 The variable regions (V3-V4) on the 16S rRNA gene of extracted DNA were amplified using
176 the universal primers Pro341F (5'-CCTACGGGNBGCASCAG-3') and Pro805R (5'-
177 GACTACNVGGGTATCTAATCC-3') (Takahashi et al., 2014). The amplified fragments
178 were sequenced on the Illumina MiSeq sequencing platform at the Australian Genome
179 Research Facility, Australia. Raw paired-end (2×300 bp) 16S rRNA gene sequence data were
180 analyzed according to the Quantitative Insights into Microbial Ecology (QIIME2) pipeline
181 (Caporaso et al., 2010). In brief, raw sequences were denoised using DADA2 with the
182 following parameters: trim left-f = 17, trim left-r = 20, trunc-len-f = 280, trunc-len-r = 220,
183 and all other parameters at their default setting. The sequences were clustered into
184 representative OTUs based on a 97% nucleotide identity cut-off. The 16S rRNA gene
185 sequencing generated 120,000 to 450,000 sequences per sample after pre-processing. The
186 taxonomical assignment was performed against MiDAS database version 2.1 (McIlroy et al.,

187 2017). The 16S rRNA gene sequences were deposited in GenBank with the accession
188 numbers PRJNA507317.

189 **3. Results and discussion**

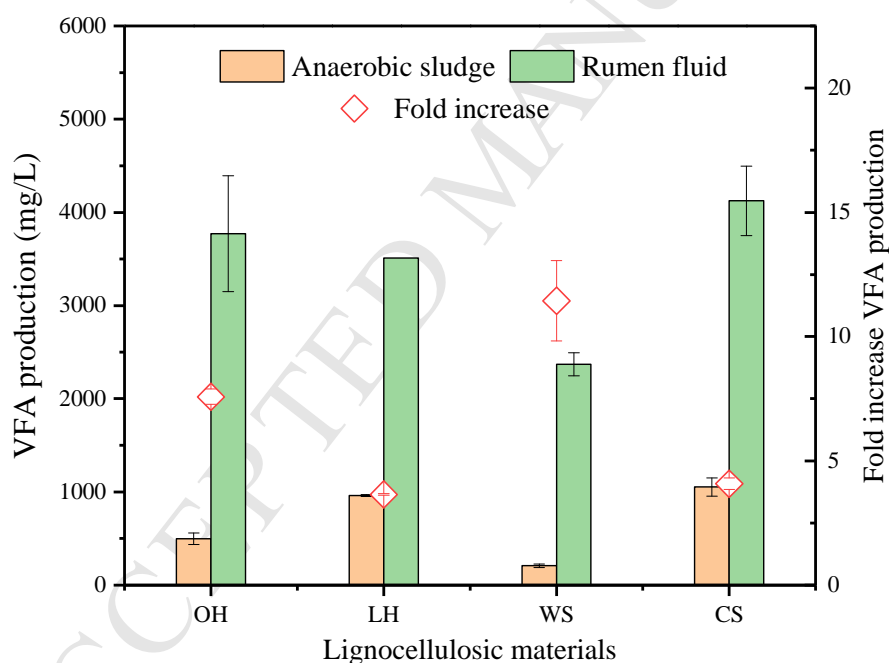
190 3.1 Volatile fatty acid production

191 Rumen fluid is a potential source of microorganisms for bio harvesting of volatile fatty
192 acids (VFAs) from lignocellulosic biomass. The rumen fluid reactors generated significantly
193 higher total volatile fatty acid (VFA) levels than that of the anaerobic sludge reactor (Fig 2).
194 An average 100 mg VFA per g of lignocellulosic biomass was produced after two days of
195 inoculation with rumen fluid, whereas this value was 23 in the reactors with anaerobic sludge
196 (an estimated of four times higher). VFAs (i.e. acetic, propionic and butyric acid) are the
197 products of hydrolytic and acidogenic steps during the fermentation process. The level of
198 VFAs indicate the efficiency of hydrolytic and acidogenic process. Results suggest that
199 rumen fluid microorganisms can hydrolyses lignocellulosic biomass for production of VFAs.
200 VFAs are building blocks for biodegradable plastics and biofuel. The market for VFAs is
201 growing with an annual demand growth rate of 7.4% (Atasoy et al., 2018). The global
202 demand for VFAs (i.e. acetic, butyric, and propionic) is predicted to be about 18 million tons
203 by 2023 (Atasoy et al., 2018; Reddy et al., 2018). The VFAs generation during the incubation
204 of rumen microorganism with lignocellulosic biomass suggest an alternative source to offset
205 the future VFA demand that currently relies on fossil resources.

206 Anaerobic hydrolysis and acidogenesis of lignocellulosic biomass by rumen microbes
207 caused a decline in pH (Table S1). The pH of the reactor dropped from 7.0 to 5.6 after four
208 days incubation. This observation is in consistent with the high level of VFAs production.
209 Extending the incubation period to 6 days resulted in no further pH drop. Therefore, it is
210 inferred that hydrolytic and acidogenic processes were inhibited by high level of VFAs

211 accumulation. Likewise, the VFA concentration profiles along incubation times showed no
212 significantly different after two days incubation with rumen microbes (Fig S1). This study
213 suggests that pH is a detrimental factor to hydrolytic and acidogenic processes. This result is
214 in consistent with the observation that rumen microbes are inhibited at pH below 5.5 (Zhang
215 et al., 2017). On the other hand, hydrolysis and acidogenesis are possible the rate limiting
216 steps in the anaerobic sludge reactor. In consistent with the low level of VFAs production, pH
217 of the reactor was relatively stable (Table S1). In conclusion, VFAs produced from rumen
218 microbe fermentation should be collected from the reactor or on a regular basis.

219



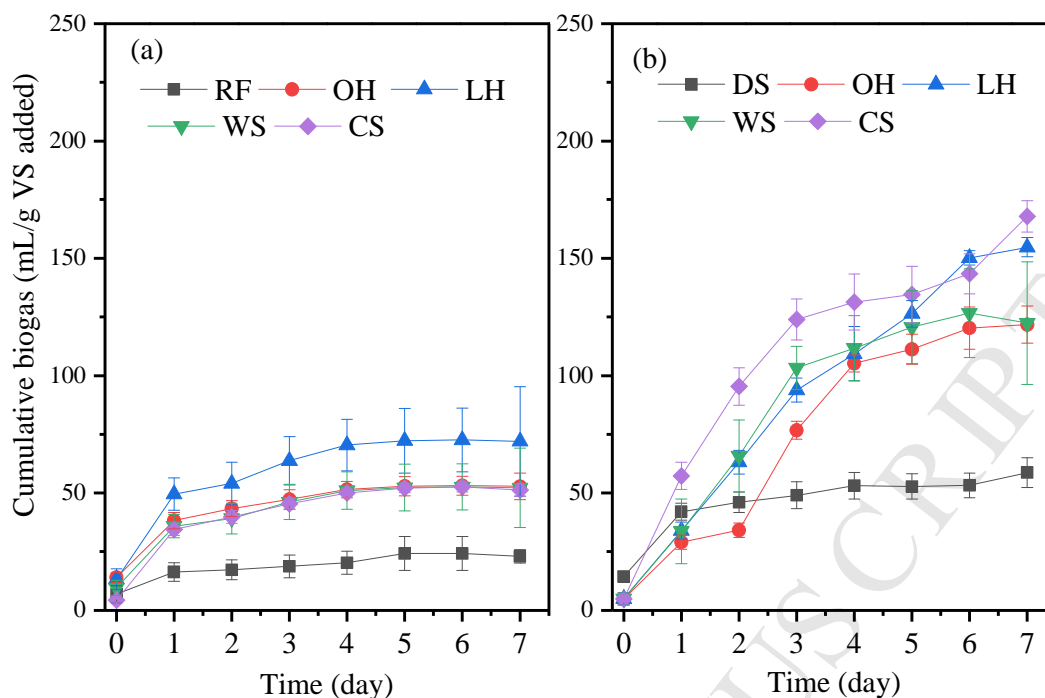
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221 **Figure 2:** Volatile fatty acid production from anaerobic digestion of lignocellulosic biomass
222 by rumen fluid and digested sludge inocula. Data was recorded after four days incubation.
223 Value and error bars are mean and standard deviation ($n = 4$).

224 3.2 Biogas production

225 BMP results indicated a higher biogas production from the anaerobic sludge than from
226 rumen fluid reactor (Fig. 3). At the end of the incubation period (i.e. 7 days), the BMP bottles
227 with anaerobic sludge produced an average 2.5 times higher biogas than the rumen fluid
228 reactors. Biogas production is a direct indicator of methanogenesis in the anaerobic digestion
229 process. Many studies have demonstrated the positive correlation between biogas production
230 and the abundance of methanogens (Hao et al., 2016; Nguyen et al., 2019a; Tale et al., 2011).
231 Results from this study suggest that methanogenesis is a limiting step in the rumen fluid
232 reactor. That is because of the low abundance of methanogens in the rumen fluid (Patra et al.,
233 2017). Methanogens are often outcompeted by hydrolytic and acidogenic microbes in
234 ruminant microbiota. VFAs compounds, which are substrate for methanogens, are
235 continuously adsorbed in the rumen of host animals (Patra et al., 2017). Another notable
236 observation is the accumulation of VFAs and drop in pH in rumen fluid reactor (Section 3.1).
237 Methanogens are slow-growing microbes and sensitive to pH environment. These conditions
238 indicate an onset of the inhibition for the methanogenesis process (Nguyen et al., 2019b).

239 Anaerobic sludge reactors produced 120 to 170 mL biogas per g VS added of
240 lignocellulosic biomass (Fig. 3). These values are lower than that typically obtained from the
241 anaerobic digestion of municipal solid waste, waste activated sludge and organic wastes
242 (Nghiem et al., 2014; Nguyen et al., 2019a). This result is likely due to the limitation in
243 hydrolysis and acidogenesis of lignocellulosic biomass by anaerobic sludge microbes.
244 Overall, rumen fluid microbes can be used for the production of VFAs, whereas anaerobic
245 sludge can be used for biogas production. The complementary effect of these two inocula
246 presents a potential solution for bio harvesting from lignocellulosic biomass.



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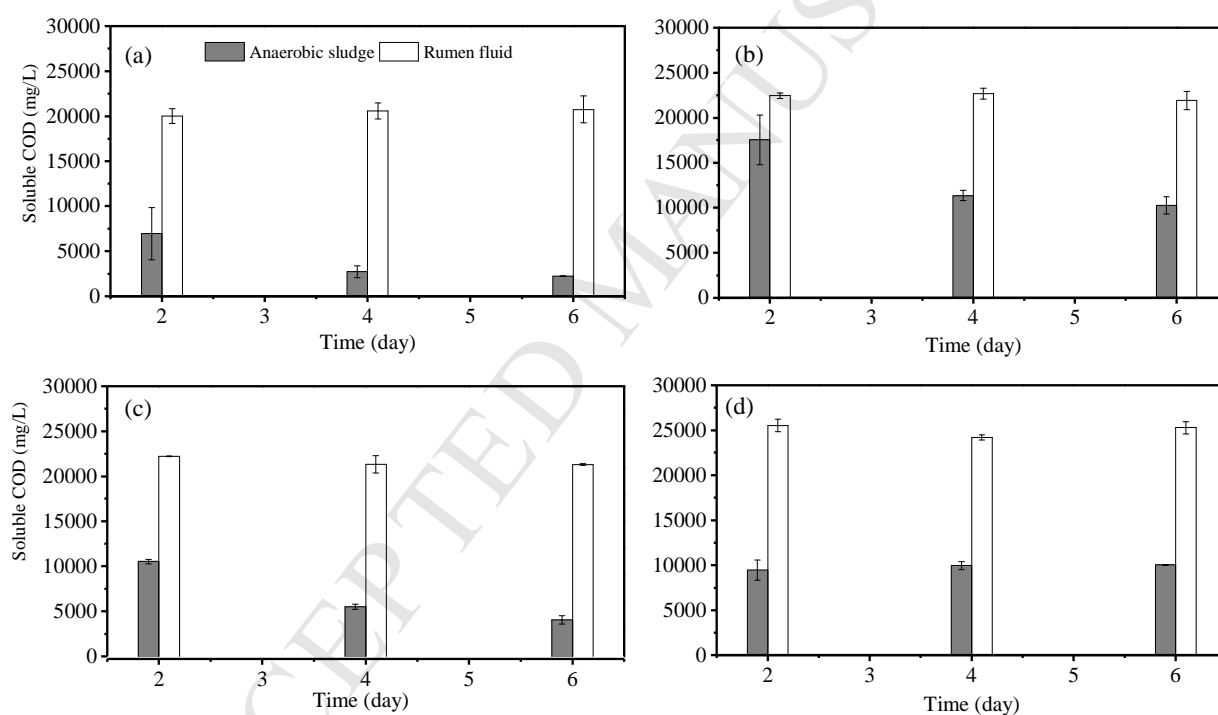
248 **Figure 3:** Cumulative biogas production (mL/g VS added) plotted against time from
 249 anaerobic digestion of lignocellulosic biomass by rumen fluid (a) and digested sludge (b)
 250 inocula. Value and error bars are mean and standard deviation ($n = 4$).

251 3.3 Soluble chemical oxygen demand

252 Rumen fluid and anaerobic sludge inoculum have an impact on soluble COD production
 253 from lignocellulosic biomass fermentation (Fig. 4). Lignocellulosic biomass is insoluble. The
 254 control reactor (i.e. contain lignocellulosic biomass only) has negligible amount of sCOD.
 255 Therefore, any increase in sCOD is mainly due to the biological conversion of lignocellulosic
 256 biomass. The rumen fluid reactors produced 227 (OH), 251 (LH), 187 (WS) and 340 (CS) mg
 257 sCOD/g VS added, whereas the anaerobic sludge reactors produced 135 (OH), 32 (LH), 56
 258 (WS) and 256 (CS) mg sCOD/g VS added.

259 The levels of sCOD depend on the methanogenic microbes. According to the COD
 260 balance calculation, Xie et al., (2017) estimated about 50% conversion of input COD to
 261 biogas. Therefore, the activity of methanogens could negatively correlate with sCOD

262 concentration. In the rumen fluid reactors, the sCOD concentration was high after two days of
 263 inoculation and remained stable towards the end of incubation period (Fig. 4). On the other
 264 hand, in the anaerobic sludge reactors, the sCOD concentration gradually decreased from day
 265 2 to day 6 (Fig. 4). Furthermore, the ratio of sCOD and VFA from rumen fluid reactors (ca.
 266 1.88 [OH], 2.14 [LH], 2.36 [WS], and 2.48 [CS]) was much lower than those of the anaerobic
 267 sludge reactors (ca. 7.5 [OH], 10.37 [LH], 8.0 [WS], and 7.11 [CS]). This observation
 268 indicated two scenarios (i) sCOD was converted to VFAs in the rumen fluid reactors and (ii)
 269 sCOD was converted to VFAs and biogas in the anaerobic sludge.



270
271

272 **Figure 4:** Soluble COD production from anaerobic digestion of lignocellulosic biomass by
 273 rumen fluid and digested sludge inocula: (a) control sets with inocula only or lignocellulosic
 274 biomass only (a) and tested sets inoculated with WS (b), LH (c), OH (d) and CS (e). Value
 275 and error bars are mean and standard deviation ($n = 4$).

276 3.4 Microbial community in rumen fluid and anaerobic sludge inocula

277 The first difference between rumen fluid and anaerobic sludge microbial community is the
278 presence of bacteria in the phylum of *Fibrobacteres* (Table 2). The abundance of the phylum
279 *Fibrobacteres* in the rumen fluid (i.e. 8.8%) was significantly higher than that in the
280 anaerobic sludge inoculum (i.e. 0.06%). Bacteria in the phylum of *Fibrobacteres* are the
281 major rumen microbes, allowing for the degradation of plant-based cellulose in ruminant
282 animals. For example, the genus of *Fibrobacter* is specific hydrolytic bacteria that have genes
283 encoding for enzymes cellulases and xylanases. *Fibrobacter succinogenes*, which is one of
284 two cultivated species in the phylum of *Fibrobacter*, degrades effectively crystalline
285 cellulose. Its genome contains high number of genes that were classified into 31 identified
286 cellulases (Suen et al., 2011). This species also encodes hemicellulose-degrading enzymes to
287 remove hemicelluloses for other enzymes to attach on cellulose. These enzymes are highly
288 specific for hydrolysis (i.e. cellulolysis) of lignocellulosic biomass (i.e. 30-60% cellulose, 10-
289 25% lignin and 8-40% hemicellulose).

290 The second difference is the presence of bacteria in the *Prevotellaceae* family in the
291 rumen fluid inoculum (Table 2). In this family, *Prevotella* was dominant in rumen microbiota
292 (Duarte et al., 2017). Baba et al. (2017) observed that species in the *Prevotella* family
293 presented at 50.5% of total microbial abundance in the rumen fluid of cattle. Member of the
294 *Prevotella* family such as *P. brevis*, *P. ruminicola* and *P. bryantii* produce cellulolytic
295 enzymes such as CMCase and xylanases. The *Prevotella* species function synergistically with
296 other cellulolytic organisms to contribute to the ruminal fibrolytic activity. In contrast,
297 *Prevotellaceae* were present at very low abundance in anaerobic sludge (Table 2). The
298 presence of *Fibrobacter* and *Prevotella* at high abundance and their cellulolytic functions
299 probably explain for the generation of soluble COD and VFAs in the reactor inoculated with
300 rumen fluid and lignocellulosic biomass.

301 Another possible difference between rumen fluid and anaerobic sludge inoculum is the
302 presence of flagellate protozoa and fungi in the rumen fluid. The number of protozoa in the
303 rumen fluid inoculum was 6×10^4 cells/mL (Figure S2). Endogenous and protozoal enzymes
304 could act independently or synergistically with bacterial enzymes to breakdown
305 lignocellulosic biomass in the rumen. For example, ruminal protozoan *Polyplastron*
306 *multivesiculatum* comprise a family of 22 carbohydrate-binding module (CBM) that binds
307 strongly to various crystallinities cellulose (Devillard et al., 2003). Fungi are unique among
308 rumen microorganism in which they penetrate the cuticle of plant cells. With high levels of
309 cellulases and hemicellulases, rumen fungi hydrolyse or solubilize the entire plant cell wall.
310 However, the potential of rumen protozoa and fungi to degrade more recalcitrant plant walls
311 is not always achieved in the rumen. Future study is recommended to investigate the
312 proliferation of rumen protozoa and fungi in anaerobic digestion of lignocellulosic biomass.

313 The compositions and relative abundance of methanogenic communities in the rumen fluid
314 were different from the anaerobic sludge inoculum (Table 2). Three genera including
315 *Methanobacterium*, *Methanobrevibacter* and *Methanomicrobium* were present at the relative
316 abundance of less than 0.1%. These genera have been described as hydrogenotrophic rumen
317 methanogens. This is consistent with the physiology of the rumen. Volatile fatty acid, CO₂
318 and H₂ are formed during hydrolysis and fermentation of plant polymers in the rumen. While
319 the ruminant consumes VFAs, CO₂ and H₂ are used by rumen methanogens to produce
320 methane. These methanogens via hydrogenotrophic pathway function as hydrogen sink and
321 thus support the activity of hydrolytic and fermentative bacteria. Consistently,
322 hydrogenotrophic methanogens have been observed in many rumen microbial community
323 studies (Agematu et al., 2017; Bayané & Guiot, 2011; Patra et al., 2017). On the other hand,
324 aceticlastic methanogens dominated the methanogenic community in the anaerobic sludge
325 (Table 2). The genus of *Methanosaeta* is strictly aceticlastic methanogens, presented at

326 3.16% of total microorganism population. This is consistent with the high abundance of the
327 genera *Methanosaeta* in most of the anaerobic digestion process (Nguyen et al., 2019b). The
328 genus of *Methanosaeta* is strictly aceticlastic methanogens. Chen et al. (2015) reported the
329 robustness of *Methanosaeta* genus at high levels of acetate in anaerobic digestion (44 mM).
330 Overall, the relative abundance of methanogens in anaerobic sludge was significantly higher
331 than that of rumen fluid, explaining for the high biogas production and no accumulation of
332 VFAs in reactor inoculated with anaerobic sludge.

333 Results from the analysis of rumen fluid and anaerobic sludge microbial community
334 compositions revealed the possible complementary between two inocula. The co-inoculation
335 of specific lignocellulolytic consortium (i.e. rumen fluid) with the high methanogenic
336 consortium (i.e. anaerobic sludge) can increase the digestion of lignocellulosic biomass for
337 biogas production. Recent studies have achieved some progress in improving anaerobic
338 digestion of cow manure by co-inoculation of cow rumen fluid and anaerobic sludge
339 (Ozbayram et al., 2018). However, knowledge into the interactions between rumen microbes
340 and anaerobic sludge microbes as well as their associations with the environmental conditions
341 (i.e. may be different from the rumen conditions) is required to fully realise the co-
342 inoculation approach. This study preliminary suggests maintaining the abundance of
343 lignocellulolytic bacteria (e.g. *Fibrobacter* and *Prevotella*) in anaerobic digestion is necessary
344 for the degradation of lignocellulosic biomass.

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349 **Table 2:** Relative abundance (%) of specific genera in rumen fluid and anaerobic sludge
 350 inocula

Genera	Relative abundance (%)		Ecological function
	Rumen fluid (<i>n</i> = 2)*	Anaerobic sludge (<i>n</i> = 4)	
Bacteria			
<i>Fibrobacter</i>	8.8	0.06	Hydrolytic
<i>Prevotellaceae</i>	35.8	0.08	Hydrolytic
<i>Firmicutes</i>	25.9	11.4	Hydrolytic, acidogenic
Methanogens			
<i>Methanobacterium</i>	0.01	0.003	Hydrogenotrophic
<i>Methanobrevibacter</i>	0.09	0.04	Hydrogenotrophic
<i>Methanomicrobium</i>	0.01	nd	Hydrogenotrophic
<i>Methanolinea</i>	nd	0.62	Aceticlastic
<i>Methanospirillum</i>	nd	0.10	Aceticlastic
<i>Methanosaeta</i>	nd	3.16	Aceticlastic
<i>Methanoculleus</i>	nd	0.05	Aceticlastic
<i>Methanosphaera</i>	nd	0.01	Aceticlastic
Total abundance (%)	0.11	3.98	

351 * Data were retrieved from Duarte et al. (2017); nd = not detected.

352 4. Conclusions

353 Lignocellulosic biomass (i.e. wheat straw, oaten hay, lurence hay and corn silage) can be
 354 used for VFAs and biogas production depending on the inoculum sources. Rumen fluid
 355 microbes demonstrated the efficiency to digest lignocellulosic biomass into VFAs (at four-

356 time higher than anaerobic sludge). This was likely due to the presence at the high abundance
357 of lignocellulolytic bacteria in the genus of *Fibrobacter* (8.8% of total microbes) and
358 *Prevotella* (35.8%). On the other hand, anaerobic sludge produced higher biogas than rumen
359 fluid reactors. Consistently, the methanogenic abundance in anaerobic sludge was at 3.98%
360 of total microbes, significantly higher than in the rumen fluid inoculum (0.11%). The results
361 of this study suggest the use of rumen fluid microbes together with a continuous extraction of
362 produced VFAs can be an alternative solution to enhance the environmental and economic
363 benefits of lignocellulosic biomass.

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465

Table 2: Key properties of inoculum (mean \pm standard deviation of 3 measurements).

	Rumen fluid	Digested sludge
TS (%)	2.2 \pm 0.2	1.6 \pm 0.2
VS (%)	1.8 \pm 0.1	1.1 \pm 0.2
pH	7.0 \pm 0.0	7.3 \pm 0.0
Total COD (g/L)	14.8 \pm 1.7	1.8 \pm 0.5

Table 3: Relative abundance (%) of specific genera in rumen fluid and anaerobic sludge inocula

Genera	Relative abundance (%)		Ecological function
	Rumen fluid (<i>n</i> = 2)*	Anaerobic sludge (<i>n</i> = 4)	
Bacteria			
<i>Fibrobacter</i>	8.8	0.06	Hydrolytic
<i>Prevotellaceae</i>	35.8	0.08	Hydrolytic
<i>Firmicutes</i>	25.9	11.4	Hydrolytic, acidogenic
Methanogens			
<i>Methanobacterium</i>	0.01	0.003	Hydrogenotrophic
<i>Methanobrevibacter</i>	0.09	0.04	Hydrogenotrophic
<i>Methanomicrobium</i>	0.01	nd	Hydrogenotrophic
<i>Methanolinea</i>	nd	0.62	Aceticlastic
<i>Methanospirillum</i>	nd	0.10	Aceticlastic
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<i>Methanosphaera</i>	nd	0.01	Aceticlastic
Total abundance (%)	0.11	3.98	

* Data were retrieved from Duarte et al. (2017); nd = not detected.

Highlight

- Rumen fluid produced 4 times more VFAs from biomass than anaerobic sludge microbes
- Lignocellulolytic bacteria (*Fibrobacter*, *Prevotella*) were abundant in rumen fluid
- Methanogenic abundance was high in anaerobic sludge inoculum
- Continuous extraction of VFAs from rumen fluid reactor is required for efficiency