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Additional Information

1 **Understanding the performance of an AnMBR treating urban wastewater and food waste via**
2 **model simulation and characterization of the microbial population dynamics.**

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4
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10

11 **Abstract**

12 An anaerobic membrane bioreactor (AnMBR) pilot plant treating kitchen food waste (FW) jointly with urban
13 wastewater was run for 536 days. Different operational conditions were tested varying the sludge retention time (SRT),
14 the hydraulic retention time (HRT) and the penetration factor (PF) of food waste disposers. COD removal efficiency
15 exceeded 90% in all tested conditions. The joint treatment resulted in an almost 3-fold increase in methane production
16 (at 70 days of SRT, 24 hours HRT and 80% PF) in comparison with the treatment of urban wastewater only.
17 Mathematical model simulations and Illumina technology were used to obtain in-depth information of this outstanding
18 process performance. Both the PF and SRT factors increased influent biodegradability. The experimental results were
19 accurately reproduced via model simulations modifying only the influent biodegradability. The high SRT and the
20 presence of ground FW in the influent resulted in higher hydrolytic activity. Not only did the *Archaea* population
21 increase 3-fold but *Levilinea* genera was also significantly raised. Three new genera characterised by anaerobic
22 fermentation of amino acids (*Leptolinea*, *Aminomonas* and *Aminobacterium*) were among the ten most abundant of the
23 total sequences identified during the joint treatment, indicating an improvement in the hydrolysis step of anaerobic
24 degradation. Influent biodegradability remained at high values when FW addition stopped.

25

26 **Keywords** AnMBR, food waste, resource recovery, simulation.

27

28 **INTRODUCTION**

29 Both wastewater (WW) and municipal solid waste (MSW) from household activities are constantly
30 growing due to the ever-expanding worldwide population. Both wastes cause severe environmental

31 problems, such as contamination of soil, aquatic ecosystems, and air [1, 2]. To protect the
32 environment, stricter regulations have been imposed, such as European Directive 1999/31/CE,
33 which demands a considerable reduction in the organic waste sent to landfills in EU countries, or
34 European Directive 91/271/EEC, which requires specific pollutant concentrations to be met in
35 discharges from urban WWTPs.

36

37 Most urban wastewater is now treated via aerobic processes in wastewater treatment plants
38 (WWTP) due to the fact that in most developed countries WW is characterized by low organic
39 matter concentrations [3, 4, 5], which drastically limits the energy recovery potential through
40 anaerobic processes. Aerobic-based wastewater treatment schemes are energy intensive, produce
41 significant quantities of sludge and do not recover the potential resources available in wastewater
42 [6]. In these treatment systems the aeration of the reaction tank for microbial degradation of organic
43 matter consumes a huge amount of energy [7] and can require more than 60% of the total energy
44 consumption of a municipal WWTPs [8]. Moreover, the higher the organic content of the influent,
45 the higher the aeration costs [9]. However, anaerobic treatment schemes can recover energy by
46 converting organic matter into methane-rich biogas, besides having other appealing advantages such
47 as low sludge production, higher pathogen reduction and the possibility of recovering nutrients for
48 reuse in agriculture [10].

49

50 The organic matter content of WW is greatly increased by the widespread use of household food
51 waste disposers, as was shown in [11] and [12]. However, to take full advantage of this extra
52 organic matter for energy production, the current aerobic process schemes used in WWTPs should
53 be modified towards more sustainable wastewater treatments such as anaerobic processes
54 (beneficial from an economic, social and environmental points of view). At the present time there is
55 a paradigm shift in which wastewater is no longer considered a waste but a valuable source of raw
56 materials (such as water, energy, nutrients, etc.). This is in line with European Directive

57 2008/98/CE, which encourages the recovery of resources from household waste and other materials
58 in order to conserve natural resources. The use of anaerobic membrane bioreactors (AnMBR) in
59 WWTPs is thus an evident option. This technology decouples hydraulic retention time (HRT) from
60 sludge retention time (SRT), allowing the application of anaerobic digestion in low strength
61 wastewater treatment, such as typical urban wastewater [13]. Without decoupling SRT from HRT,
62 impractical reactor volumes would be required to operate the biological process at the required SRT
63 to meet the pollutant removal limits (due to the slow growth rate of anaerobic microorganisms).
64 Using membrane technology also provides an almost pathogen-free effluent (of special interest for
65 WW reuse) and high microbial diversity within the biological reactor, since the microorganisms are
66 not lost with the effluent (in contrast to the secondary settler of a conventional WWTP, in which
67 solids are always present in the clarified effluent).

68

69 The feasibility of AnMBR technology for the joint treatment of food waste (FW) and urban
70 wastewater has already been demonstrated in [14] and [15]. However, an in-depth insight into the
71 process has not yet been obtained via model simulation, so that few relevant findings on the
72 microbiology of this novel treatment are available. The aim of this work was thus to determine how
73 the different operational conditions can be simulated via a conventional mathematical model in
74 order to compare the simulation results with the experimental data and so determine the effects of
75 the joint treatment of FW and urban wastewater by anaerobic membrane technology.

76

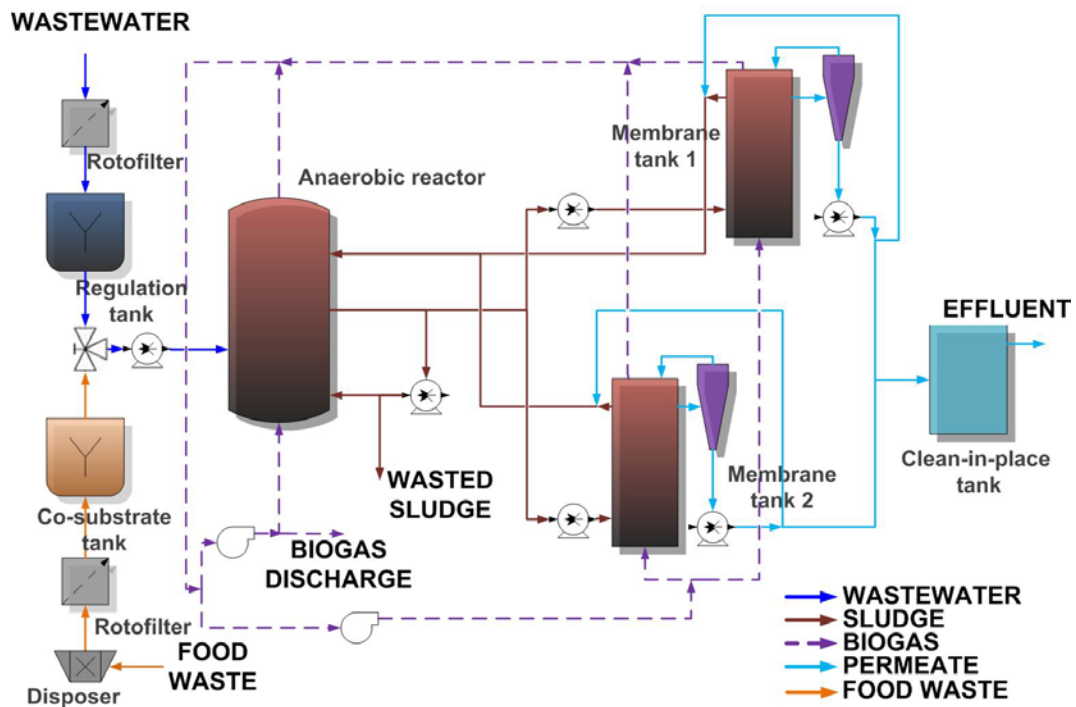
77 **MATERIALS AND METHODS**

78

79 *Pilot plant*

80 The experimental data given in this paper were collected in the AnMBR pilot plant in the Carraixet
81 WWTP (Alboraya, Valencia-Spain). The influent of the pilot plant comes from the pre-treatment of
82 the full-scale Carraixet WWTP after screening and removal of grit and grease. The process flow

83 diagram of the pilot plant is shown in Figure 1. The Food Waste (FW) consisted of leftovers from
 84 restaurants on the campus of the Universitat Politècnica de València (Valencia, Spain). The
 85 substrate was weighed and stored in bags at 4°C the day before experimental use. A commercial
 86 food waste disposer and a 0.5 mm opening size rotofilter were used for the pre-treatment of the FW,
 87 which was stored in a co-substrate tank of 0.180 m³. A three-way valve alternated wastewater and
 88 FW inputs to the anaerobic reactor (1.3 m³). The FW fraction was supplied according to the
 89 Penetration Factor (PF, or the percentage of households using food waste disposers) as laid down in
 90 the experimental plan. The plant was equipped with two 0.02 um pore size ultrafiltration
 91 membranes submerged in separate tanks. A detailed description of the pilot plant, feeding
 92 procedure, influent characterization and process results can be seen in Moñino et al. [15, 16].



93

94 **Figure 1.** Process flow diagram of the AnMBR pilot plant.

95 ***Operating conditions***

96 Six different operational periods were planned, covering a total of 536 days of experiments in the
 97 pilot plant. The main operating conditions of each period are shown in Table 1. As can be seen in
 98 this table, in four periods (P2 to P5), the AnMBR treated both FW and wastewater at different PF
 99 levels (40 and 80%). These two percentages were chosen to consider the effects of different

100 numbers of households using food waste disposers. In the first and last periods only wastewater was
 101 treated. Period 1 was prior to the joint treatment and Period 6 was after FW addition, when a new
 102 pseudo steady-state was reached. The data used for the process-modelling was the average process
 103 variables from the pseudo steady-state periods. These periods were determined after checking
 104 negligible COD accumulation in the COD mass-balance, together with the stabilization of both the
 105 reactor solids concentration and methane production.

106

107 **Table 1.** Operational conditions tested in the AnMBR pilot plant.

	P1	P2	P3	P4	P5	P6
SRT (d)	40±2	41±3	Extended*	70±11	69±6	70±2
T (°C)	25±2	28±1	28±1	28±1	27±1	28±3
HRT (h)	30±4	18±4	26±3	22±6	24±6	22±4
PF (%)**	0	40±4	40±3	40±4	80±7	0
Duration of the period (d)	31	105	148	125	61	66
Number of days in pseudo steady-state (d)	20	30	25*	40	30	25

108 * In period 3 (P3), only the sludge required for the daily laboratory analysis was harvested (this period was labelled 'extended SRT').

109 Operating at this high SRT made it almost impossible to achieve a true pseudo steady-state. For this reason, the last 25 days of the
 110 period, in which a relatively stable solid, COD and biogas production was observed, were used to calculate the average process
 111 variables for the mathematical model simulation.

112 ** PF is the percentage of households that use food waste disposers.

113

114 *Analytical Methods*

115 Influent, effluent and AnMBR reactor samples were collected twice a week to monitor the evolution
 116 of the biological process. Volatile Solids (VS), COD, sulphide and sulphate concentrations were
 117 determined according to Standard Methods [17]. Methane production was recorded and dissolved
 118 methane in the effluent was calculated by Henry's Law, as described in [18]. Specific methanogenic
 119 activity (SMA) tests were carried out for each period using the Automatic Methane Potential Test
 120 System (AMPTS) [Bioprocess Control, Sweden] and performed as described in [19].

121

122 *Microbial community analysis*

123 Sludge samples were stored at -20°C and prepared for nucleic acid extraction. For this purpose, the
124 E.Z.N.A Soil DNA Kit (Omega-Biotek) was used following the protocol provided by the
125 manufacturer. The quality and quantity of the nucleic material extracted was determined in a
126 Nanodrop 2000 spectrophotometer (Thermo Scientific) and Qubit 3.0 fluorometer (Life
127 Technologies), respectively. From the extracted DNA samples, 0.2 ng/μL was used for the
128 construction of libraries with universal prokaryotic indexed primers targeting the v4 hyper-variable
129 region of the 16S rDNA [20]. Finally, amplicon sequencing was performed in a MiSeq sequencer
130 within a 2x300 paired-end run by the genomic department of *Fundación para el Fomento de la*
131 *Investigación Sanitaria y Biomédica de la Comunidad Valenciana* (FISABIO) in Valencia (Spain).

132
133 The data retrieved from Illumina sequencing was processed for barcode and index removal and then
134 quality trimmed with default parameters of the prinseq-pl algorithm [18]. After joining the filtered
135 reads with fastq-join [19], non-chimeric sequences were phylogenetically classified at genus level
136 within the Ribosomal Database Project Classifier (default parameters). The results were exported to
137 the multimedia and interactive Krona tool [20].

138

139 **RESULTS AND DISCUSSION**

140 The experimental results from the AnMBR pilot plant (included in Table 2) showed an exceptional
141 increase of methane production, by up to 3-fold, at 70 days of SRT, 24 hours HRT and 80% PF,
142 compared with the treatment of urban WW only (148.7 vs 51.2 L_{CH4}/Kg COD removed). This
143 increase is attributed to the higher biodegradability of the FW (in comparison with urban WW)
144 together with the process operation at high SRT (70 days). The higher the SRT the higher the
145 hydrolysis and degradation of slowly biodegradable organic compounds as a result of the extended
146 contact time between the pollutants and the microorganisms. Both factors also helped to reduce
147 sludge production (from 0.614 kg VS / kg removed COD in P1 to 0.142 in P5), which is currently
148 of special interest due to the stricter environmental constraints on WWTP sludge disposal. The

149 lowest sludge production (0.015 kg VS / kg removed COD) was observed during AnMBR operation
 150 at extended SRT (P3), but under normal operating conditions 0.142 kg VS / kg removed COD could
 151 be a representative and achievable reference value. COD and TS legal requirements were achieved
 152 in the effluent of the AnMBR plant thanks to the use of the ultrafiltration membranes. COD
 153 removal efficiency exceeded 90% in all the tested conditions. The VFA concentration was always
 154 lower than the detection limit (10 mg HAc/L), indicating that no process imbalance occurred.
 155 Conversely, effluent nutrient concentrations (N and P) exceeded the regulation limits. This effluent
 156 could thus be either directly used for agricultural irrigation (note that the ultrafiltration membranes
 157 also provide the required disinfection level) or could be given a tertiary treatment to meet the
 158 stricter nutrient requirements imposed by the legislation. Indeed, the nutrient concentration in the
 159 effluent was higher than in the influent of the AnMBR pilot-plant due to the hydrolysis of the
 160 organic matter. In Table 2 it can be seen that N and P effluent concentrations were similar in all the
 161 operating conditions with and without FW addition, showing the relatively similar nutrient
 162 composition of the FW and WW.

163

164 **Table 2.** Summary of the main experimental results from the AnMBR pilot plant. The data shown are the average
 165 values from each pseudo steady-state period.

	P1	P2	P3	P4	P5	P6
TSS reactor (g/L)	16.58±2	16.25±2	28.94±3	15.48±2	14.41±2	12.83±1
% SSV reactor	69.18±4	68.98±5	68.38±4	70.21±5	69.67±4	69.75±5
Sludge production (kg SV/ Kg COD removed)	0.614	0.316	0.015	0.179	0.142	0.245
Effluent COD (mg/L)	49±3	51.6±4	22.7±2	54.3±5	51.9±5	25.7±3
Effluent AGV (mg HAc/L)	<LD	<LD	<LD	<LD	<LD	<LD
N-NH ₄ effluent (mg/L)	49.6 ± 11.1	40.8 ± 5.5	69.6 ± 11.1	69.6 ± 7.7	53.5 ± 4.8	44.5 ± 5.7
P-PO ₄ effluent (mg/L)	5.6 ± 0.8	5.0 ± 0.5	7.9 ± 1.3	7.6 ± 1.1	7.9 ± 0.4	5.4 ± 0.8
CH ₄ (L/d)	18.2±3	83.7±6	201.7±12	244.1±14	333.7±15	98.8±7
(L/kg COD removed)	51.2±20.4	80.4±22.5	121.1±24.1	114.9±58.5	148.7±57.2	93.9±40.7
SMA (mL CH ₄ / g VS d)	10±2	10±2	36±3	49±3	51±4	43±3

166 *In period 3 (P3), only the sludge required for the daily laboratory analysis was harvested (*extended SRT)

167 ** PF is the percentage of households that use food waste disposers.

168 <LD Lower than the detection limit (10 mg HAc/L).

169

170 Model simulations were performed to reproduce each pseudo steady-state, based on the plant-wide
 171 Biological Nutrient Removal Model No. 2 (BNRM2) proposed in [25] and including the sulphate
 172 reducing bacteria (SRB) model proposed in [26]. For this purpose the average values were used of
 173 all the variables measured (influent, anaerobic reactor and effluent) during each pseudo steady-state.
 174 Table 3 gives the main influent variables used for the simulation of each period.

175

176 **Table 3.** Characterization of the influent during each pseudo steady-state period. These influent variable values were
 177 used in the model simulations.

Parameter	P1	P2	P3	P4	P5	P6
Total COD (mg/L)	612 ± 64	11512 ± 1023	6283 ± 947	6558 ± 850	11553 ± 1102	606 ± 52
Soluble COD (mg/L)	102 ± 22	3690 ± 339	1619 ± 194	1868 ± 150	3395 ± 353	94 ± 8
Total Nitrogen (mg/L)	58.5 ± 4.5	197.6 ± 11	128.0 ± 7	92.0 ± 6	198.4 ± 13	55.0 ± 4.0
Soluble Nitrogen (mg/L)	43.0 ± 4.3	115.9 ± 6	68.0 ± 5	59.0 ± 4.2	116.3 ± 6	41.0 ± 3
N-NH ₄ (mg/L)	35.6 ± 4	28.7 ± 3	49.8 ± 2.7	40.9 ± 2.7	40.8 ± 3	40.0 ± 2.5
P-PO ₄ (mg/L)	3.9 ± 0.9	11.9 ± 2.5	10.9 ± 2.8	10.3 ± 3.2	11.0 ± 3.5	3.8 ± 0.6
S-SO ₄ (mg/L)	98.0 ± 5.3	331.9 ± 15.4	340.7 ± 15.8	357.6 ± 29.7	373.3 ± 67.6	114.0 ± 9.7
Alkalinity (mg CaCO ₃ / L)	246 ± 32	301 ± 35	307 ± 30	302 ± 27	252 ± 30	300 ± 28
VFA(mg HAc/ L)	< LD	612 ± 35	522 ± 30	360 ± 25	722 ± 57	18 ± 5

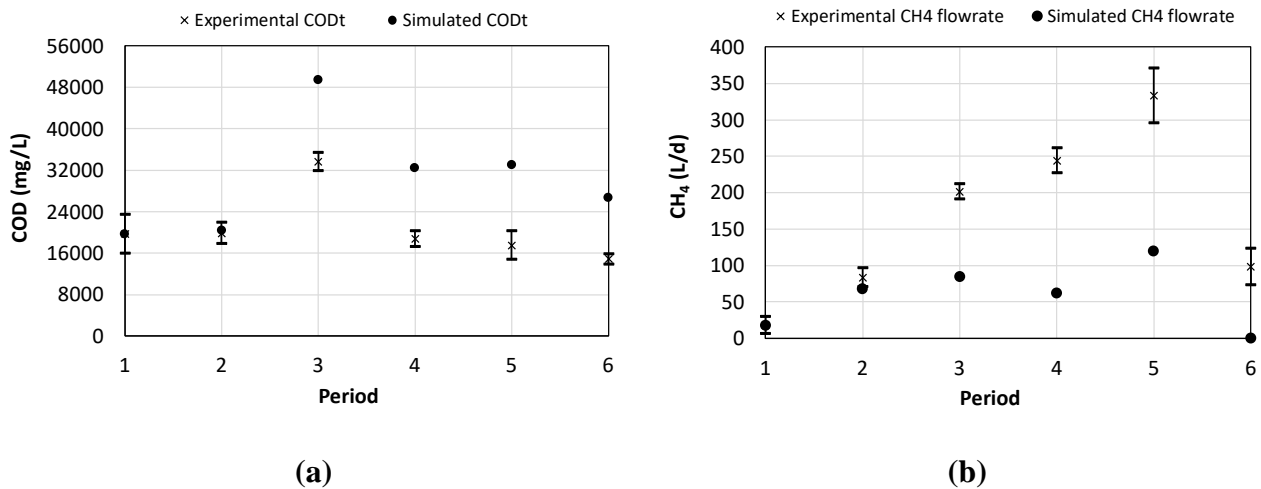
178 <LD Lower than the detection limit (10 mg HAc/L).

179

180 In the first approach to modelling the AnMBR process performance, the default values for all the
 181 stoichiometric and kinetic parameters from the BNRM2 model proposed in [25] and for the SRB
 182 extension of [26] were used in the simulations of the six pseudo steady-state periods. Figure 2
 183 shows the experimental and simulated total COD in the AnMBR and average methane production.
 184 As can be clearly seen in Figure 2, there are considerable discrepancies between the experimental
 185 values and the simulated results in Periods 3 to 6, where changes were made to either the influent
 186 composition (due to FW addition) or SRT. The mathematical model predicted higher COD
 187 accumulation in the anaerobic reactor (percentage error for the simulated data ranged from 46% to

188 88% in Periods P₃ to P₆) and lower methane production reactor (percentage error for this variable
 189 ranged from - 58 % to -100 % in Periods P₃ to P₆).

190



191 **Figure 2.** Experimental versus simulated variables in each pseudo steady-state period prior to model calibration: (a)
 192 AnMBR Total COD (b) Methane production. Note that the 95% interval confidence limits have been included in the
 193 experimental values. These confidence limits are calculated as the $[\text{average} \pm t_{n-1, \alpha/2} (s/n^{0.5})]$, where s is the standard
 194 deviation, n the number of values of the variable considered and α the significance level used to compute the confidence
 195 level: in this case 0.05.

196

197 These discrepancies between the experimental and simulated data suggest a clear difference
 198 between the COD biodegradability predicted by the model and the experimental biodegradation
 199 observed in the reactor. High biodegradability is directly related to high COD degradation (thus,
 200 resulting in low COD accumulation) and high methane production. To address these differences, the
 201 anaerobic biodegradability of the influent particulate organic matter was therefore chosen as the
 202 calibration parameter. Table 4 shows the initial values of this parameter for each pseudo steady-
 203 state (experimentally obtained by means of the classical BOD and COD determinations in the
 204 influent, and used in the initial set of simulations) together with the calibrated values obtained via
 205 computational analysis to produce the best fit between the experimental data of the process
 206 behaviour and the model simulations.

207

208 **Table 4.** Biodegradability of the influent particulate organic matter obtained experimentally and computationally (to get
209 the best fit between the experimental data of the process behaviour and model simulations).

	P1	P2	P3	P4	P5	P6
SRT (d)	40±2	41±3	Extended*	70±11	69±6	70±2
PF (%)**	0	40±4	40±3	40±4	80±7	0
Initial biodegradability***	44.8	50.1	49.6	49.5	49.2	44.8
Calibrated biodegradability	44.8	52.8	70.8	80.1	86.1	77.5

210 The biodegradability of the influent particulate organic matter is calculated as $X_s/(X_s+X_i)$, where X_s is the particulate biodegradable
211 organic matter and X_i the particulate inert organic matter.

212 *In period 3 (P3), only the sludge required for the daily laboratory analysis was harvested ('extended SRT')

213 ** PF is the percentage of households that use food waste disposers.

214 *** The initial biodegradability was experimentally obtained by means of classical BOD and COD determinations in the influent.

215

216 Using the calibrated values of the anaerobic biodegradability of the influent particulate organic
217 matter, a good agreement was seen between the experimentally measured variables of the process
218 and the simulated results (see Table 5). This was the only parameter modified to achieve an
219 accurate fit. It is worth highlighting that the calibrated biodegradability reached values of up to
220 86%, which is even higher than the experimental anaerobic biodegradability of the FW obtained in
221 [16] (73% (252 ± 11 mL CH_4 / g COD). It therefore seems that the introduction of FW (rich in
222 biodegradable organic matter) and operating at high SRT values result in clearly increased organic
223 matter biodegradation, which could reflect either greater activity of the existing microbial
224 population or a change in the microbial consortia towards a more efficient and hydrolytic species.
225 The fact that this effect remained when FW was no longer added is of special relevance. To get a
226 deeper insight into these microbiological aspects, the microbial population was analysed by
227 Illumina high-throughput sequencing of the 16S rRNA gene.

228 As pointed out by Kim *et al.* [23], results are required on the characterization of the microbial
229 community structure in a pilot-plant and full-scale anaerobic digestion systems during the treatment
230 of food waste.

231

232

233 **Table 5.** Experimental from the AnMBR pilot-plant versus Simulated results from the calibrated model.

	Period 1		Period 2		Period 3		Period 4		Period 5		Period 6			
	Exp.	Sim.	Exp.	Sim.	Exp.	Sim.	Exp.	Sim.	Exp.	Sim.	Exp.	Sim.		
AnMBR Effluent	COD _{sol} mgCOD/L	49.0	60.0	51.6	64.7	22.7	34.2	54.3	48.7	51.9	44.6	25.7	24.6	
	CH ₄ mg/L	46.1	50.2	45.6	58.0	55.5	55.6	54.3	57.8	60.1	56.6	52.9	60.9	
	VFA mgCOD/L	0	1.8	2.6	1.7	0	1.2	0	1.3	0	1.4	0	1.3	
	N-NH ₄ mgN/L	49.6	41.4	40.8	30.3	70.1	56.8	69.1	70.4	53.5	53.6	44.6	47.9	
	P-PO ₄ mgP/L	5.6	4.4	5.0	5.3	8.2	6.9	7.6	5.6	7.9	8.7	5.4	4.5	
	S-SO ₄ mgS/L	6.7	3.3	8.4	3.0	6.5	0	11.4	0	11.5	0.0	9.3	0.8	
	S-HS mgS/L	93.2	96.4	89.2	90.1	95.0	118.4	97.0	124.2	98.8	123.1	92.6	114.7	
	Mixed Liquor AnMBR	COD _{total} mgCOD/L	19730	19629.4	19903	19690.2	33650	33463.7	18798	18376.3	17557	17730.4	14880	14962.8
		TSS mg/L	16581	16530.3	16254	16398.5	28943.1	28923.5	15483.7	15516.8	14417	14541.7	12831	12868.9
		VSS mg/L	11476	11417.4	11215	11346	19788	19819	10873	10892	10048	10142.4	8956	8989.1
NVSS mg/L		5105	5112.9	5039	5052.5	9155.1	9104.5	4610.7	4624.8	4369	4399.3	3875	3879.8	
pH		6.6	6.8	6.9	6.8	6.7	6.7	6.6	6.8	6.6	6.7	6.8	6.8	
Gas		CH ₄ Flowrate L/d	18.2	18.2	83.7	83.0	201.7	196.2	244.1	243.8	333.7	327.7	98.8	95.6
	Sludge production (Kg SV/KgCOD)	0.614	0.598	0.316	0.347	0.015	0.017	0.179	0.184	0.142	0.155	0.245	0.217	

234

235 The microbial population in the AnMBR was found to be highly diverse in terms of the different
236 Bacteria and Archaea genera detected. Figure 3 gives the composition at phylum taxonomic level of
237 the communities found in all periods in the form of krona graphs. Figure 4 contains a heatmap
238 quantifying the changes in microbial communities between each two consecutive periods (i.e., from
239 Period 1 to Period 2, from Period 2 to Period 3, and so on). The heatmap is a plot of a data matrix in
240 which the individual values are represented as colours and was used to visually highlight the
241 relevant changes in the microbial genera (increases and decreases) through the color gradient, as
242 well as those genera that do not change appreciably. The main change in the microbial population
243 was detected in the relative abundance of the *Anaerolineaceae* family, belonging to *Chloroflexi*
244 phylum. Four representative genera from this family were found among the most abundant in all the
245 periods: *Levilinea*, *Bellilinea*, *Longilinea* and *Leptolinea*, *Levilinea* being dominant (Table 6 and
246 Figure 4). Another phylum whose relative abundance increased in Periods 4 and 5 was

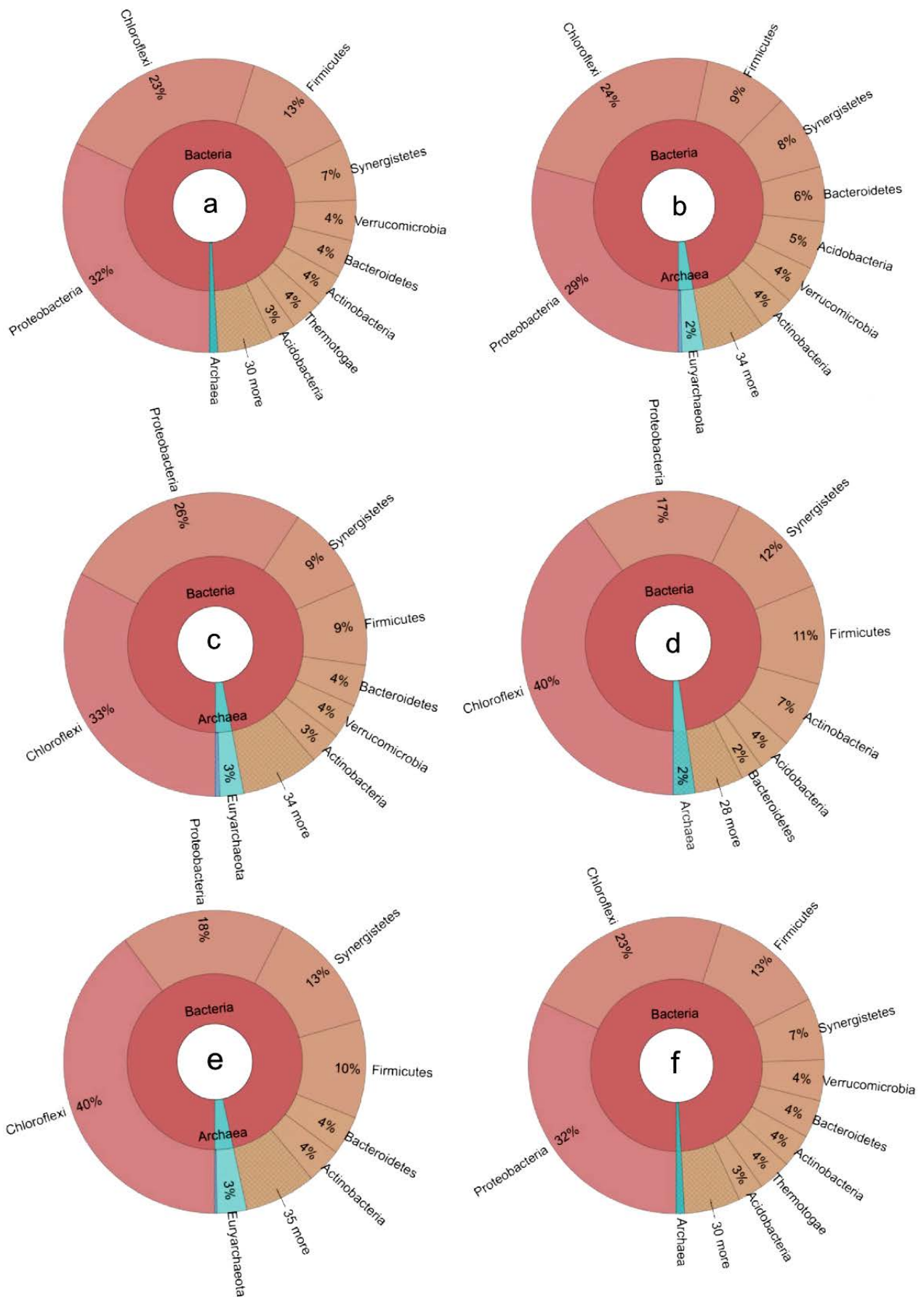
247 *Synergistetes*. The change found inside this phylum was related to the higher relative abundance of
 248 *Aminomonas* and *Aminobacterium* in these periods. The relative abundance of these three genera
 249 increased as the hydrolytic capacity of the system was enhanced, thus denoting the positive effect of
 250 operating at high SRT for FW degradation in the AnMBR. Finally, as can be seen in Table 6, there
 251 was a remarkable relative abundance of *Methanosaeta* in Periods 4 and 5.

252

253 **Table 6.** Relative abundances of the dominant genera detected in the AnMBR microbial community

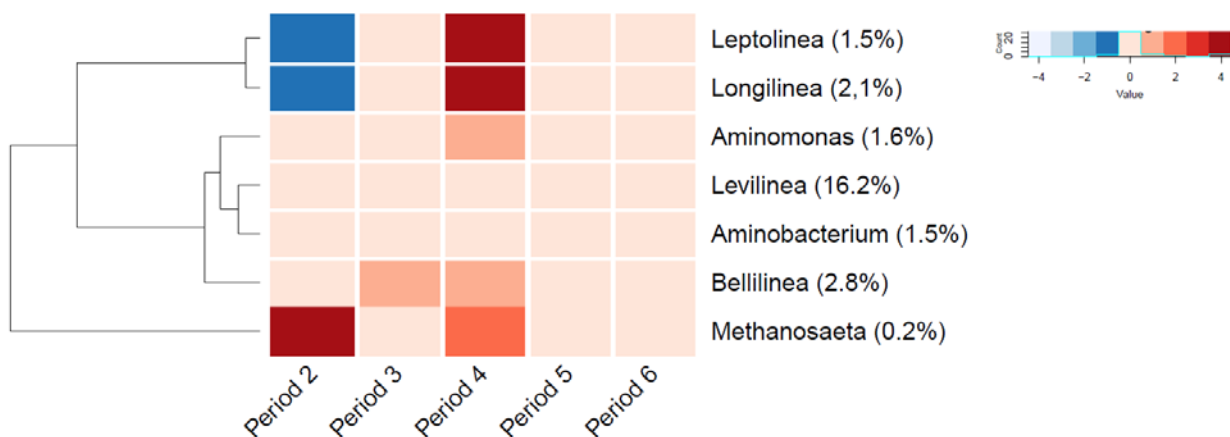
Dominant genera	P1	P2	P3	P4	P5	P6
<i>Bacteria; Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; Levilinea</i>	16.2	20.0	27.2	25.8	25.7	20.4
<i>Bacteria; Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; Bellilinea</i>	2.8	1.8	3.4	6.2	6.0	4.5
<i>Bacteria; Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; Longilinea</i>	2.1	0.8	0.9	4.6	4.2	3.4
<i>Bacteria; Chloroflexi; Anaerolineae; Anaerolineales; Anaerolineaceae; Leptolinea</i>	1.5	0.4	0.5	2.6	2.7	2.2
<i>Bacteria; Synergistetes; Synergistia; Synergistales; Synergistaceae; Aminomonas</i>	1.6	2.3	3.4	5.5	7.2	4.2
<i>Bacteria; Synergistetes; Synergistia; Synergistales; Synergistaceae; Aminobacterium</i>	1.5	n.d.	n.d.	2.3	2.7	1.7
<i>Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosaetaceae; Methanosaeta</i>	0.2	1.1	0.7	1.9	2.7	2.5

254



255

256 **Figure 3.** Composition of the microbial communities in Periods 1 (a), 2 (b), 3 (c), 4 (d), 5 (e) and 6 (f) at phylum
 257 taxonomic level. A digital version of these krona plots can be found in the online version of this manuscript.



258 **Figure 4.** Heatmap quantifying the changes in microbial communities from one period to another. Numbers in
 259 parenthesis indicate the relative abundance of the genus in Period 1.

260

261 The significant change in the performance of the AnMBR previously described in terms of methane
 262 production and influent biodegradability was also observed in the AnMBR microbial community,
 263 which shifted towards a more hydrolytic population. This was mainly composed of six genera
 264 which are considered the FW-degrading core of the system. The fold changes detected for each of
 265 these six genera besides the main methanogen (*Methanosaeta*) are shown in the heatmap plot
 266 (Figure 4). Enchained metabolic reactions take place in anaerobic digestion processes and are
 267 overdriven by different microorganisms. In the present study, the *Chloroflexi* phylum could have
 268 been responsible for the improvement of the hydrolysis and fermentative stages, as no solids were
 269 accumulated in the system, but were converted into methane enriched biogas at high rates. As
 270 reported by other authors, *Anaerolineaceae* members belonging to the *Chloroflexi* phylum, such as
 271 *Levilinea*, *Bellilinea*, *Longilinea* and *Leptolinea* have high diverse metabolism capacities but have
 272 been poorly described until now. Their crucial role in the degradation of complex polysaccharides
 273 has recently been reported by culture-independent analysis [27]. After the hydrolysis of FW from
 274 the AnMBR influent, different fermentative genera belonging to the *Anaerolineaceae* family
 275 therefore facilitated the conversion of more simplex organic compounds into lactate, hydrogen and
 276 mainly acetate. Also, the degradation of the protein content present in this influent was mainly
 277 attributed to the *Synergistetes* phylum, as several amino acid fermenters have been described and

278 affiliated with this taxon [28]. This assumed metabolic potential has also been suggested in other
279 studies that analyzed the microbial diversity in mesophilic anaerobic digesters [29, 30]. Finally, the
280 well described acetoclastic methanogenic capacity of the *Methanosaeta* genus could be attributed to
281 the high SMA values determined in Periods 4 and 5. The higher relative abundance and presumably
282 higher activity and abundance of the fermentative microorganisms found in the digester explain the
283 higher SMA values registered. The rapid conversion of organic compounds from FW into acetate
284 compounds therefore boosted the metabolism of the dominant methanogen found in the system *i.e.*,
285 *Methanosaeta*. The specific method of this microorganism of breaking acetate up into methane leads
286 to high values of methane production, thus having a positive and highlighting effect over the
287 previously mentioned, which were five times the SMA values. Furthermore, as acetate was
288 expeditiously converted into methane, no VFA accumulation was observed during the whole
289 experimental period (Table 2).

290

291 The dominant composition of the microbial community established in the AnMBR between Periods
292 4 and 5 was found to have a remarkable potential for the biomethanization of the organic matter in
293 the influent. This community was not only observed in the periods in which FW was added to the
294 influent, but was also detected in Period 6, when FW was no longer being added (Table 6 and
295 Figure 4). These results therefore indicate the acclimatization of the biomass to influent during
296 long-term operations and the consequent change in composition and microbial activity from the
297 starting community characterized in Period 1. Thanks to the persistence of the genera that boosted
298 the conversion of organic matter into methane during Periods 4 and 5, the biodegradability values
299 remained over 75% at the end of the experimental period. The role of this microbial-degrading
300 community as hydrolytic microorganisms had a positive effect on the AnMBR performance.

301

302 **CONCLUSIONS**

303 In this work, the simulation results perfectly matched the experimental data from an AnMBR pilot-
304 plant scale and modified only the anaerobic biodegradability of the influent particulate organic
305 matter. An increase in influent biodegradability occurred when either the FW load or the SRT was
306 raised. This result can be attributed to higher hydrolytic activity within the AnMBR, which was
307 confirmed experimentally via Illumina technology. Adding FW and increasing SRT led to changes
308 in the microbial population within the AnMBR. Hydrolytic and fermentative bacteria were favoured
309 and their activity gave rise to a considerable increase in biodegradation of influent organic matter.
310 The evidence for this is the higher methane production (from 51.2 to 148.7 L_{CH₄}/kg COD removed),
311 higher SMA (from 10 to 51 mL CH₄ / g VS day) and lower sludge production (from 0.614 to 0.142
312 kg VSS / kg COD removed). The FW-degrading microbial population (dominated by
313 *Anaerolineaceae*, *Synergistaceae* and *Methanosarcinaceae*) was not only established during the
314 joint treatment period but also remained in the AnMBR when it again treated wastewater only.
315 Process stability was observed under all the tested experimental conditions, with negligible VFA
316 concentration in the anaerobic reactor and no signals of any type of inhibition.

317

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321

322 **References**

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