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1 **Insights into microbial community structure and diversity in oil palm waste**
2 **compost**

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26 **Abstract**

27 Empty fruit bunch (EFB) and palm oil mill effluent (POME) are the major wastes generated by the oil
28 palm industry in Malaysia. The practice of EFB and POME digester sludge co-composting has shown
29 positive results, both in mitigating otherwise environmentally damaging waste streams and in producing
30 a useful product (compost) from these streams. In this study, the bacterial ecosystems of 12 week-old
31 EFB-POME co-compost and POME biogas sludge from Felda Maokil, Johor were analysed using 16S
32 metagenome sequencing. Over 10 phyla were detected with Chloroflexi being the predominant phylum,
33 representing approximately 53% of compost and 23% of the POME microbiome reads. The main
34 bacterial lineage found in compost and POME was Anaerolinaceae (Chloroflexi) with 30% and 18% of
35 the total gene fragments, respectively. The significant differences between compost and POME
36 communities were abundances of *Syntrophobacter*, *Sulfuricurvum*, and *Coprococcus*. No methanogens
37 were identified due to the bias of general 16S primers to eubacteria. The preponderance of anaerobic
38 species in the compost, and high abundance of secondary metabolite fermenting bacteria is due to an
39 extended composting time, with anaerobic collapse of the pile in the tropical heat. Predictive functional
40 profiles of the metagenomes using 16S rRNA marker genes suggest the presence of enzymes involved
41 in polysaccharide degradation such as glucoamylase, endoglucanase, arabinofuranosidase, all of which
42 were strongly active in POME. Eubacterial species associated with cellulytic methanogenesis were
43 present in both samples.

44

45 **Keyword** Oil palm empty fruit bunch. Palm oil mill effluent. Compost. Metagenomics. Microbial
46 diversity.

47

48 **1.0 Introduction**

49 **The Malaysian** oil palm industry **is** growing rapidly and Malaysia has become the second largest
50 producer of palm oil after Indonesia (MPOB 2017). Approximately 5.74 Mha of Malaysia's land area
51 was covered with oil palm plantations in 2016 (MPOB 2017) which produced 17,320,000 tonnes of
52 palm oil. This in turn generated a large amount of oil palm derived waste. The oil palm industry
53 produces millions of tonnes of oil palm biomass, especially empty fruit bunch (EFB). There is 1 kg of

54 biomass, such as empty fruit bunch (EFB), palm kernel shell (PKS) and mesocarp fibre (MF), generated
55 for each kg of oil palm extracted (Sulaiman et al. 2011). Conversion of organic waste such as EFB into
56 usable horticultural by-products has been found to be the most efficient way to reuse this raw waste
57 material (Siddiquee et al. 2017).

58 EFB and palm oil mill effluent (POME) are the most abundant waste produced in oil palm
59 mills. At present, EFB and POME have been used as raw materials for co-composting and the resulting
60 co-compost has been used in the oil palm plantations at Felda Maokil. In this case, POME was used to
61 provide moisture to the compost. Composting is one of the most efficient solutions for sustainable
62 management of organic waste, it is an aerobic process that effectively converts cellulosic organic waste
63 into a nutrient-rich organic amendment for agricultural application (Neher et al. 2013). The conversion
64 of organic waste to compost is carried out by a successive microbial community combining both
65 mesophilic and thermophilic activities (Krishnan et al. 2017). However, the microbial community of
66 end product compost in the tropics has not been well characterized.

67 Understanding the microbial diversity of compost systems is important in order to produce high
68 quality compost and determine its effectiveness (Krishnan et al. 2017). Most studies that have explored
69 this rich ecosystem have utilized culture-based methods (Ryckeboer et al. 2003; Ahmad et al. 2007;
70 Vishan et al. 2017). But, culture-based methods are only useful for identifying less than 1% of the total
71 microbial diversity, as the majority of microorganisms are unculturable under standard media and
72 aerobic growth conditions (Handelsman 2004; Ito et al. 2018). The advent of Next-Generation
73 Sequencing (NGS) and metagenomics has opened an avenue to perform comprehensive studies to
74 characterize the total microbial diversity using a culture-independent method. Metagenomics is an
75 alternative that has been widely applied over the last few years (Fernández-Arrojo et al. 2010).

76 Metagenomics refers to the direct isolation of DNA from an environmental sample
77 (Handelsman 2004). There are two different approaches, amplicon sequencing and shotgun
78 metagenomics (Escobar-Zepeda et al. 2015). Amplicon sequencing targets specific regions of DNA
79 from communities by amplifying specific regions using taxonomical informative primer targets such as
80 intergenic transcribed spacers (ITS) and the large ribosomal subunit (LSU) for eukaryotes and the 16S
81 rRNA gene for prokaryotes (Sharpton 2014). Shotgun metagenomics randomly sequences all DNA

82 from a community, which produces a less biased assessment of species abundance but at greater cost.
83 Metagenomics has been commonly used in large and complex samples containing organisms from
84 different life domains or where less bias is required. 16S amplicon sequencing, or metaprofiling
85 (Escobar-Zepeda et al. 2015), is currently the most cost-effective method for DNA library preparation
86 in conjunction with sequencing by platforms such as the Illumina MiSeq. This approach has been widely
87 utilized, not only for studying resident microbiota in wastewater and compost (Krishnan et al. 2017;
88 Wang et al. 2016), but also for studying soil samples (Yan et al. 2016), hot springs (Chan et al. 2015),
89 termite gut (Chew et al. 2018), faecal samples (Costea et al. 2017) and many others.

90 In the present study, the microbial community of the EFB-POME co-compost and POME
91 biogas sludge has been studied using the culture independent 16S amplicon sequencing approach.
92 Metagenomes from the EFB-POME co-compost and POME were directly isolated from the samples
93 without any microorganism cultivation. The V3-V4 regions of prokaryotic 16S rRNA genes were
94 amplified from the metagenome and directly sequenced using Illumina's MiSeq platform. The detailed
95 information on the microbial residents will support further research to improve the duration of the
96 composting process and the quality of final compost by addition of specified microbial species.

97 **2.0 Materials and Methods**

98 **2.1 Collection of samples**

99 The 12 weeks-old EFB-POME co-compost and POME were obtained from Felda Maokil,
100 Labis, Johor (2°17'09.6"N 102°59'37.7"E). A 1 m height compost pile was made with the ratio of 40
101 ton EFB: 120 ton POME, turned over every 3 days to provide aeration. The composting was done by
102 first laying down the EFB on the ground, followed by the addition of POME to the EFB pile at three
103 day intervals to maintain a final moisture content of 65-75% as it is a solid state aerobic fermentation
104 process. A total of 1kg of 12 weeks-old compost was randomly sampled at a depth of 0.5 m inside the
105 compost pile. For POME, 2 litres was collected directly from the anaerobic digester (AD) effluent. The
106 POME and compost samples were collected in sterile containers and stored at 4 °C for further studies.

107 **2.2 Total DNA extraction**

108 Extraction of total DNA from EFB-POME co-compost was done with a modified Griffiths
109 protocol using NucleoSpin® Soil kit (Griffiths et al. 2000; Alessi et al. 2017), while the total DNA from

110 POME was extracted using NucleoSpin® Soil kit (Macherey-Nagel, Germany) based on the
111 manufacturer's protocol (Verma and Satyanarayana 2011). The detailed methods are outlined below.

112 2.2.1 Method 1: Modified Griffiths protocol

113 Half a gram of EFB-POME co-compost was transferred into a microcentrifuge tube containing
114 1 g of garnet beads (OMNI International, USA), 500 μ L SL2 lysis buffer (Macherey-Nagel, Germany),
115 500 μ L 10% CTAB, 100 μ L 1mg/mL lysozyme and 214.3 μ L enhancer SX (Macherey-Nagel,
116 Germany). After mixing, the samples were disrupted using Bead Ruptor 4 (OMNI International, USA)
117 for 3 minutes at level 3. The aqueous phase was mixed with inhibitor removal solution SL3 buffer
118 (Macherey-Nagel, Germany) and incubated at 4 °C for 5 min before centrifuging using a NucleoSpin®
119 Inhibitor Removal column (Macherey-Nagel, Germany) to remove any impurities like humic acid and
120 other PCR inhibitors. Following this, equal volumes of phenol: chloroform (1:1) was added to the eluted
121 aqueous phase and separated by centrifugation for 5 minutes at $13,300 \times g$. One-tenth volume of ice-
122 cold sodium acetate and 3 volumes of ice-cold absolute ethanol was added to the aqueous layer before
123 incubating at -80°C for 2 hours to precipitate the DNA. The resulting pellet was washed twice with
124 ice-cold 75% ethanol (Alessi et al. 2017) and the pellet was resuspended in 50 μ L TE buffer. The DNA
125 was stored at -20 °C for further use.

126 2.2.2 Method 2: NucleoSpin® Soil kit

127 Two mL of POME was centrifuged at $4,500 \times g$ for 10 minutes and the resulting pellets were
128 transferred into a microcentrifuge containing 1 g of garnet beads (OMNI International). 300 μ L SL2
129 buffer (Macherey-Nagel, Germany), 150 μ L enhancer SX (Macherey-Nagel, Germany) and 100 μ L 1
130 mg/mL lysozyme was added to the pellet. The pellet was homogenized for 3 minutes at level 3 using
131 Bead Ruptor 4 (OMNI International). 100 μ L 1 mg/mL lysozyme was added to the homogenate and
132 incubated at 37 °C for 30 minutes. The inhibitor removal solution and column were used to remove any
133 impurities like humic acids or other PCR inhibitors. The binding solution was added to the supernatant
134 before loading onto the spin column. The column was centrifuged to bind the DNA to the column and
135 the column was washed twice with wash buffer provided in the kit. The DNA was finally eluted with
136 the elution buffer and stored at -20 °C.

137

138 2.3 DNA yield and purity determination

139 DNA concentration and quality of the total DNA extracts were determined using NanoDrop™
140 Lite spectrophotometer (Thermo Scientific, Wilmington, DE, USA) and 1% w/v agarose gel
141 electrophoresis, respectively.

142 2.4 16S metagenomics library preparation, sequencing and data analysis

143 The 16S rRNA metagenome libraries were generated using purified total DNA as the template
144 in the polymerase chain reactions (PCR). The V3–V4 region of the 16S rRNA genes were amplified
145 using S-D-Bact-0341-b-S-17, 5'-TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCTACGG
146 GNGGCWGCAG-3' and S-D-Bact-0785-a-A-21, 5'-GTCTCGTGGGCTCGGAGATGTGTATAAG
147 AGACAGGACTACHVGGGTATCTAATCC-3'). The underlined oligonucleotide are the Illumina
148 adapter overhang sequences, while the non-underlined sequences are locus-specific sequences which
149 were designed according to a reported primer pair (Klindworth et al. 2013) targeting conserved regions
150 within the V3 and V4 domains of prokaryotic 16S rRNA genes. The metagenome library was then pair-
151 end sequenced on the Illumina MiSeq platform (San Diego, CA, USA) using MiSeq Reagent Kit (v3)
152 for the longest length set to 2 x 300 base pairs (bp).

153 2.5 Bioinformatics analysis

154 The resulting sequencing data were analysed using **the** Mothur software package version 1.41.1
155 (Schloss et al. 2009). Firstly, the read pairs were merged to assemble them into contigs and contigs
156 exhibiting any ambiguous positions were subsequently removed. The sequences were then aligned to
157 the SILVA reference database (Release 132). Upon removal of unaligned sequences, the remaining
158 sequences were further filtered, dereplicated and de-noised before removal of chimeras. Sequences were
159 then classified based on **the** Greengenes database using naïve Bayesian classifier with bootstrap cut-off
160 of 80% before removal of sequences classified **as** unrelated lineages. Finally, the sequences were split
161 into bins based on taxonomy and clustered into OTUs using the *cluster.split* command.

162 The functional composition of EFB-POME compost and POME digester sludge was analysed
163 using **the** Phylogenetic Investigation of Communities by Reconstruction of Unobserved States
164 (PICRUSt) bioinformatics software package (Langille et al. 2013). Firstly, PICRUSt analysis was done
165 by picking OTUs against the August 2013 Greengenes database release of gg_13_8_99 that contained

166 202,421 bacterial and archaeal sequences (McDonald et al. 2012). The OTU counts were normalized
167 and used for metagenome functional predictions with KEGG orthologs (KO). The output was further
168 analysed using the Statistical Analysis of Metagenome Profiles (STAMP) software package (Parks et
169 al. 2014).

170 **2.6 Data accessibility**

171 The raw sequencing data was deposited in the Sequence Read Archive (SRA) of the National
172 Centre for Biotechnology Information (NCBI) database under accession numbers SRR8181848 and
173 SRR8186815 for EFB-POME co-compost and POME, respectively.

174 **3.0 Results and Discussion**

175 **3.1 Microbial diversity analysis of EFB-POME co-compost and POME**

176 EFB-POME co-compost and POME were analysed for their microbial diversity using Illumina
177 MiSeq sequencing of V3-V4 region of the 16S rRNA genes. A total of 72,657 and 92,677 sequence
178 reads were generated from total DNA extracts of EFB-POME co-compost and POME, respectively.
179 After quality filtering and read merging, EFB-POME compost and POME generated 1,272 and 10,705
180 contigs, respectively. POME showed a higher number of OTUs, which indicates that POME has a
181 higher bacterial diversity compared to EFB-POME co-compost. Diversity coverage for each sample
182 was analysed using rarefaction analysis. The rarefaction curve illustrated in Fig.1 was calculated at 3%
183 dissimilarity. Rarefaction analysis shows the samples had reached saturation for genus level and higher
184 taxonomic level. The coverage for mature EFB-POME co-compost was 100%, while for POME was
185 99.4% with Simpson indices of 113.77 and 69, respectively.

186 The most abundant phylum present in both samples was Chloroflexi, which constituted 23% of
187 the total gene fragment abundance in POME and 53% in EFB-POME co-compost (Fig.2A). The
188 remaining phyla present in POME were Firmicutes (19%), Bacteroidetes (16%), Proteobacteria (16%)
189 and Synergistetes (3%), while in EFB-POME co-compost the phyla were Bacteroidetes (15%),
190 Firmicutes (12%), Proteobacteria (7%) and Actinobacteria (3%). According to Chandna et al. (2013),
191 the number of microbial species in early stages of composting depends on the initial substrate used and
192 the prevailing environmental conditions during the composting process, especially the temperature.
193 Composting can be divided into several phases based on the temperature. These include mesophilic,

194 thermophilic and maturing phases, during which different bacterial populations thrive. Chandna et al.
195 (2013) found that Firmicutes are abundant during mesophilic phase and decrease in the maturation
196 phase, while Actinobacteria are stable during mesophilic and thermophilic phases. Neher et al. (2013)
197 found Bacteroidetes dominated at the end of the thermophilic phase, whereas Proteobacteria was
198 dominant after the thermophilic phase. The predominance of anaerobes in the compost sample are
199 strongly suggestive of a secondary fermentation of the pile after collapse of all air spaces and exhaustion
200 of oxygen throughout the mass. The compost method was similar to that developed by Raabe at
201 Berkeley, which takes 18 days in a Mediterranean climate (Raabe 1981). After 84 days in the tropics,
202 the compost has further fermented. The 16S data for the EFB-POME compost is a glimpse of the
203 microbial structure of this mature compost post aerobic composting.

204 The major family that was observed in both samples was Anaerolinaceae, which represents
205 18% abundance in POME and 30% abundance in EFB-POME co-compost as shown in Fig.2B. These
206 OTUs represent a diversity of species, rather than a single dominant species. The other five major
207 families observed in POME were Syntrophaceae (9%), Syntrophomonadaceae (5%),
208 Porphyromonadaceae (5%), Tissierellaceae (3%), and Synergistaceae (3%), while in EFB-POME co-
209 compost, the other major families were Porphyromonadaceae (7%), Lachnospiraceae (3%),
210 Helicobacteraceae (2%), Ruminococcaceae (2%), and Tissierellaceae (2%).

211 The most abundant genus observed in POME was *Syntrophus*, which accounted for 9% of the
212 total gene fragments (Fig.2C). The remaining genus observed in POME include *Syntrophomonas* (5%),
213 *Sedimentibacter* (3%), *Gracilibacter* (3%), *Solibacillus* (3%). Most of the bacteria found in POME
214 digester sludge were anaerobic as methanogenesis is an anaerobic process. In a previous study by
215 Krishnan et al. (2017), *Parabacteroides*, *Levilinea*, *Smithella*, *Prolixibacter* and *Bellilinea* were
216 identified as the common genera found in POME. *Bellilinea* was also found in DNA extracts from
217 POME in the present study. However, this genus represented a small majority, which only accounted
218 for 1% of the community. In the EFB-POME co-compost, on the other hand, *Coprococcus* was
219 identified as the most common genera accounting for 3% of the gene fragments, followed by
220 *Sulfuricuvum* (2%), *Sedimentibacter* (2%) and *Proteiniphilium* (2%). *Coprococcus* are anaerobic
221 bacteria and a major bacterial taxa in the rumen microbiota of some ruminants (Jia et al. 2016). The

222 bacteria from **the** *Coprococcus* family are commonly involved in the degradation of cellulosic materials
223 (Moore et al. 2011) and can be found enriched in xylan based cultures (Jia et al. 2016) which are often
224 found in anaerobic cellulose digestion. Apart from these genera, *Steroidobacter*, *Nitriliruptor*,
225 *Anaeomyxobacter*, *Filomicrobium* and *Truepera* were also found inside lignocellulose biomass
226 compost by Krishnan et al. (2017).

227 The overall population in compost is illustrated in Fig.3A. The most common phyla found in
228 the EFB-POME co-compost was Chloroflexi (53% of the total gene fragments) and this phyla was
229 represented 100% of the total Chloroflexi by Anaerolinaceae family. The second most abundant phyla
230 was Bacteroidetes, which accounted for 15% of the total 16S rRNA gene fragments. The major family
231 in Bacteroidetes was Porphyromonadaceae comprising 47.5% of the total Bacteroidetes. *Petrimonas*
232 and *Proteiniphilum* were identified which represent 9.2% and 32.2% of the total Porphyromonadaceae
233 gene fragments. The remaining family in the Bacteroidetes was unclassified with 52.5% of the total
234 Bacteroidetes gene fragments. The third major phyla in compost was Firmicutes accounting for 12% of
235 the total gene fragments. Fig.3B shows that the major order was Clostridiales, which amounts to 89%
236 of the total Firmicutes gene fragments. The remaining were Bacillales and unclassified Firmicutes with
237 2.7% and 8.3%, respectively. Clostridiales were represented commonly by the family of
238 Lachnospiraceae (24.6% of the total Clostridiales gene fragments) followed by Tissierellaceae (23.8%),
239 Ruminococcaceae (23%), Syntrophomonadaceae (7.7%), Gracilibacteraceae (3.8%), Christenellaceae
240 (2.3%) and Clostridiaceae (1.5%) as shown in Fig.3B.

241 The overall bacterial population of POME **are** shown in Fig.4A. Similar to EFB-POME co-
242 compost, Cloroflexi was also identified as the dominant phyla (23% of the total gene fragments) which
243 was 100% represented (of the total Cloroflexi gene fragments) by **the** Anearolinaceae family.
244 Anearolinaceae **dominates** the population of POME and EFB-POME co-compost. Anearolinaceae is
245 anaerobic and involved in methanogenesis. This family of bacteria is indigenous in many environments
246 rich in oil and hydrocarbon (Liang et al. 2015) and associated with the anaerobic degradation of oil-
247 related compounds (Sutton et al. 2013). Anaerolinaceae has been reported as the predominant species
248 isolated from anaerobic digester systems and has a fermentative metabolism, utilizing carbohydrates
249 and proteinaceous carbon sources under anaerobic conditions (McIlroy et al. 2017; Sun et al. 2016;

250 Yamada et al. 2006). The absence of the archaean methanogens in the data is due to the known poor
 251 ability of the standard 16S primers to amplify these organisms (Klindworth et al. 2013). As all known
 252 methanogens are archaea, methanogenic archaea ecosystems are only served by specific 16S primers
 253 such as S-D-Arch-0349-a-S-17 and S-D-Arch-0786-a-A-20 primer pair (Fischer et al. 2016). The
 254 second common phyla identified in the POME population was Firmicutes with 12% of the total gene
 255 fragments (Fig.4B). The major order observed from this phylum was Clostridiales with 77.3% of the
 256 total Firmicutes gene fragments. The family of Syntrophomonadaceae was the most dominant,
 257 accounting for 31.7% of the total Clostridiales gene fragments. The remaining families observed were
 258 Gracilibacteraceae (22.5%), Tissierellaceae (21.7%), Ruminococcaceae (5.7%), Clostridiaceae (5.7%)
 259 and Lachnospiraceae (3.1%) as shown in Fig.4B. The family of bacteria found in Clostridiales were
 260 similar to the community found in co-compost, with slight variations in abundances as many bacteria
 261 in this family are thermotolerant and are to survive the composting process.

262 3.2 Comparative analysis of EFB-POME co-compost and POME bacterial communities

263 Sequence data sets retrieved from EFB-POME co-compost and POME digester sludge were
 264 compared. Fig.5 compared the relative abundance of the 12 major genus represented in both EFB-
 265 POME compost and POME. There were fewer bacterial genera in POME than during the composting
 266 process. The dominant bacteria in the compost were *Syntrophobacter*, *Sulfuricurvum* and *Coprococcus*.
 267 There is limited evidence that these bacteria are able to produce compost, and in fact are anaerobes.
 268 These organisms likely represent the secondary fermentation of the compost, once the pile had collapsed
 269 and oxygen and easily metabolisable carbon had been exhausted. Their fermentative abilities are
 270 directed to metabolites likely present after thermophilic composting of woody biomass. Bacteria that
 271 did not survive aerobic composting but were found in the POME sludge were *Petrimonas*, *Syntrophus*,
 272 *Treponema*, *Bellilinea*, *Solibacillus*, *Clostridium*, *Gracilibacter*, *Syntrophomonas*, and *Acholeplasma*.
 273 Most of these bacteria are anaerobes and facultative anaerobes as POME is an anaerobic digester
 274 effluent.

275 In this study, *Sulfuricurvum* was identified as the predominant bacteria in the mature compost.
 276 *Sulfuricurvum* is chemolithoautotrophic and a sulphur-oxidizing bacterium, capable of thriving under
 277 microaerobic and anaerobic conditions (Kodama and Watanabe 2004). The condition inside the EFB-

278 POME compost is facultative anaerobic which is therefore, favourable for the growth of *Sulfuricurvum*.
279 *Sulfuricurvum* has previously been identified in contaminated soil (Liu et al. 2015), river sediments (Liu
280 et al. 2018), underground crude-oil storage (Kodama and Watanabe 2004) and wastewater sludge
281 (Hatamoto et al. 2011). The presence of a chemolithoautotroph demonstrates how limited the nutrients
282 were and how mature the compost was. Liu et al. (2015) reported that the abundance of *Sulfuricurvum*
283 increases with higher moisture, since high moisture content is associated with low redox potential and
284 anaerobic environments (Brockett et al. 2012).

285 *Syntrophobacter* was also found in a higher relative abundance in EFB-POME compost
286 compared to POME. *Syntrophobacter* has the ability to degrade propionate, which is usually isolated
287 from methanogenic ecosystems (Boone and Bryant 1980), characteristic of the POME sludge. In
288 anaerobic digestion, the acetogenesis stage is predominantly acetogenic bacteria such as
289 *Syntrophobacter*, which converts fermentation products with more than two carbon atoms, alcohols and
290 aromatics fatty acids into acetate and hydrogen (Kangle et al. 2012). In this stage, the bacteria convert
291 products from the first phase (hydrolysis) to butyric acid, propionic acid, ethanol, acetic acid, carbon
292 dioxide and hydrogen (Nalo et al. 2014).

293 3.3 Predicted functional metagenome profiles

294 Metagenome functional prediction was carried out using Phylogenetic Investigation of
295 Communities by Reconstruction of Unobserved States (PICRUSt) analysis based on the Greengenes
296 16S rRNA database and KO. A bar graph was plotted to compare the abundance of the metabolic
297 features between the two samples as shown in Fig.6. From the result of this study, energy metabolism
298 was found to be highly represented in POME and compost community. The subfunctions in energy
299 metabolism included carbon fixation pathways in prokaryote, oxidative phosphorylation, nitrogen
300 metabolism, sulphur metabolism and methane metabolism. The proportion of sequences for the energy
301 metabolism is higher in POME sample compared to compost, as the secondary fermentation of the
302 compost in anaerobic conditions is relatively energy limited. For the xenobiotics biodegradation and
303 metabolism, the subfunctions benzoates degradation, bisphenol degradation, drug metabolism by
304 cytochrome P450, naphthalene degradation and polycyclic aromatic hydrocarbon degradation were
305 observed to have higher sequence proportion in the compost community compared to the POME

306 community. These functional classes are explained by secondary fermentation of the remaining
307 recalcitrant substrates in the now anoxic pile.

308 Carbohydrate metabolism such as nucleotide sugar, fructose and mannose, starch and sucrose
309 and butanoate were observed to be **slightly** higher in proportion in the POME community compared to
310 compost **due to** active anaerobic processing of the oil palm products **in POME**. The degradation of
311 cellulose and hemicellulose during the composting process can produce carbohydrates (Toledo et al.
312 2017). Those compounds are easily degradable substances, which are preferentially degraded by aerobic
313 eubacteria. Carbohydrate metabolism plays an important role in degradation of hemicellulose and
314 cellulose during the composting process (Wei et al. 2018). Furthermore, amino acids are sources of
315 energy and carbon for bacterial metabolism produced throughout the composting process (López-
316 González et al. 2015). Wu et al. (2017) suggest that a higher abundancy of bacteria with **active** amino
317 acid metabolism increases humic substance synthesis.

318 In order to determine the potential roles of microbial communities in the decomposition of plant
319 polymers, carbon degradation enzymes were identified and their presence is illustrated in Fig.7. The
320 enzymes include genes encoding alpha-amylase, glucoamylase and neopullulanase for starch
321 degradation; beta-glucanase, endoglucanase, and beta-glucosidase for cellulose degradation;
322 arabinofuranosidase and xylanase for hemicellulose degradation; and lastly, beta-hexosaminidase,
323 chitinase, and peptidoglycan hydrolase involved in degradation of chitins derived from fungal
324 decomposition of the plant mass. Apart from that, genes related **to** chemotaxis was also more abundant
325 in the POME sample as this was a liquid culture.

326 Due to the poor amplification of archaean 16S sequences however, methanogenesis is only
327 observed in a limited way in both samples. Limitations of 16S primers targeting the V3-V4 domains
328 are clear in this study, where the primary fermentation **was** not observed. To overcome this limitation
329 and obtain an unbiased view of the archaean diversity, shotgun **metagenomics** sequencing could be
330 employed.

331

332 **Conflict of interest**

333 On behalf of all authors, the corresponding author states that there is no conflict of interest.

334 **References**

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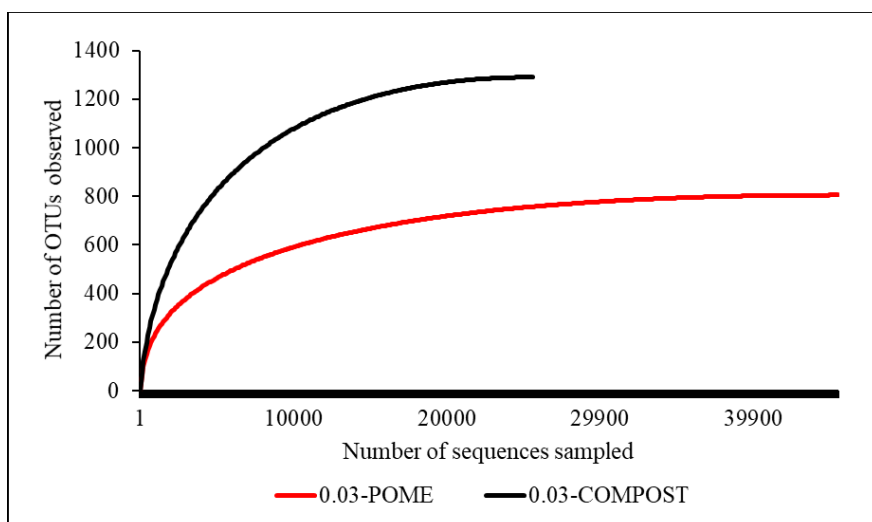


Fig. 1

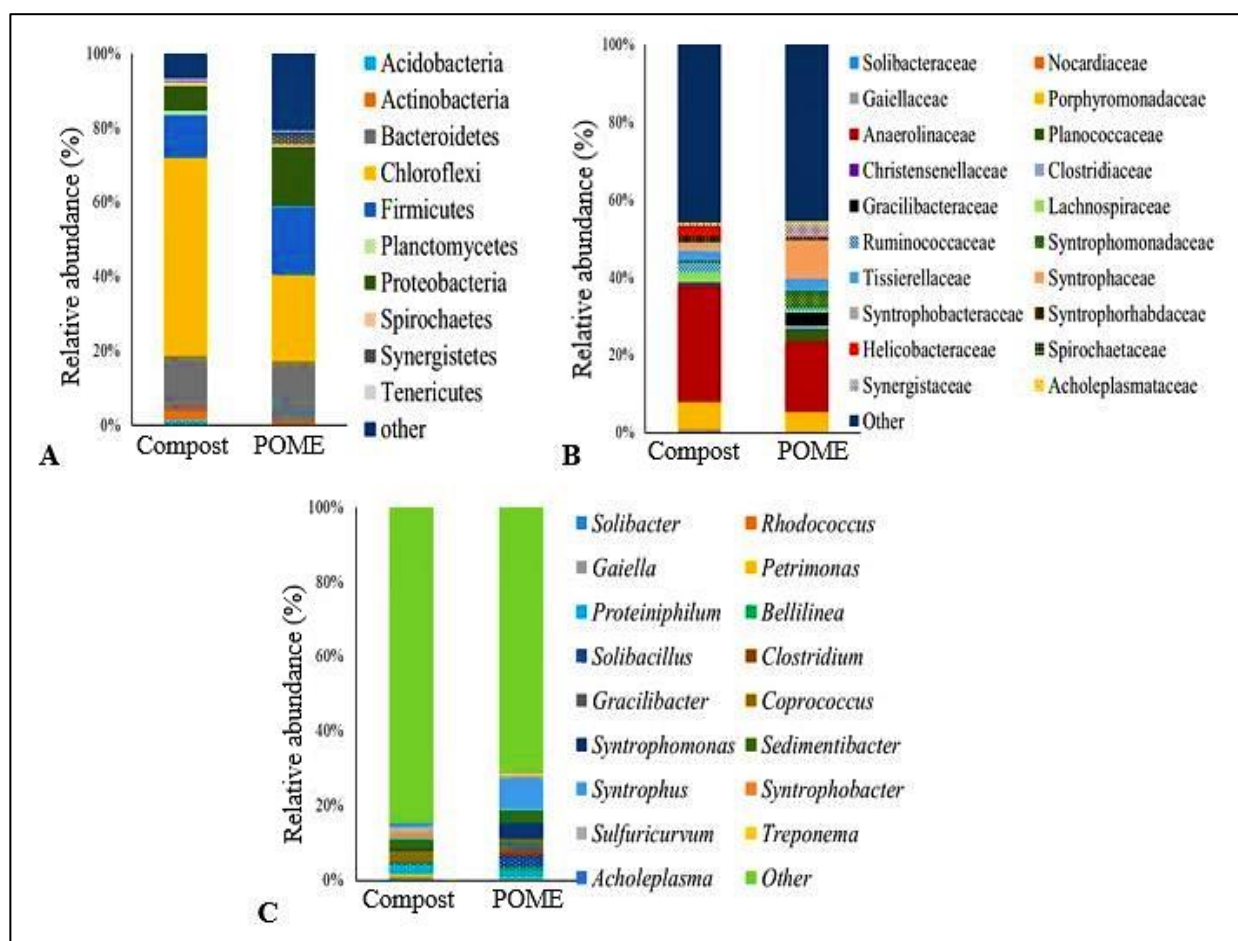


Fig. 2

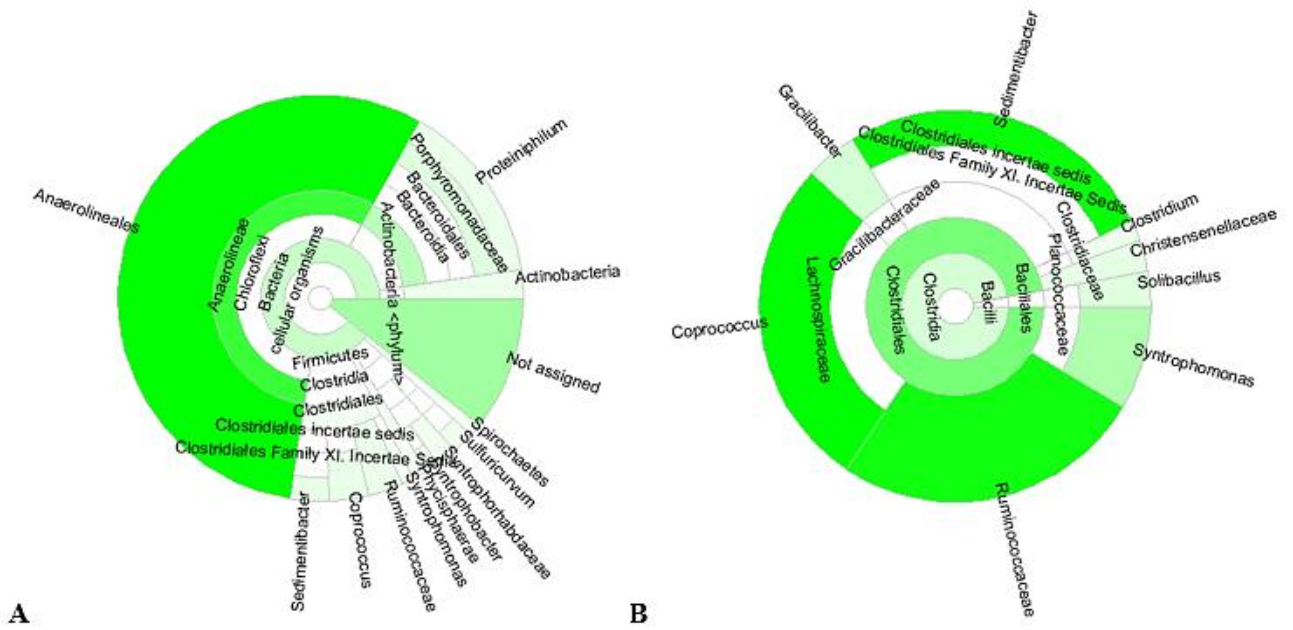


Fig. 3

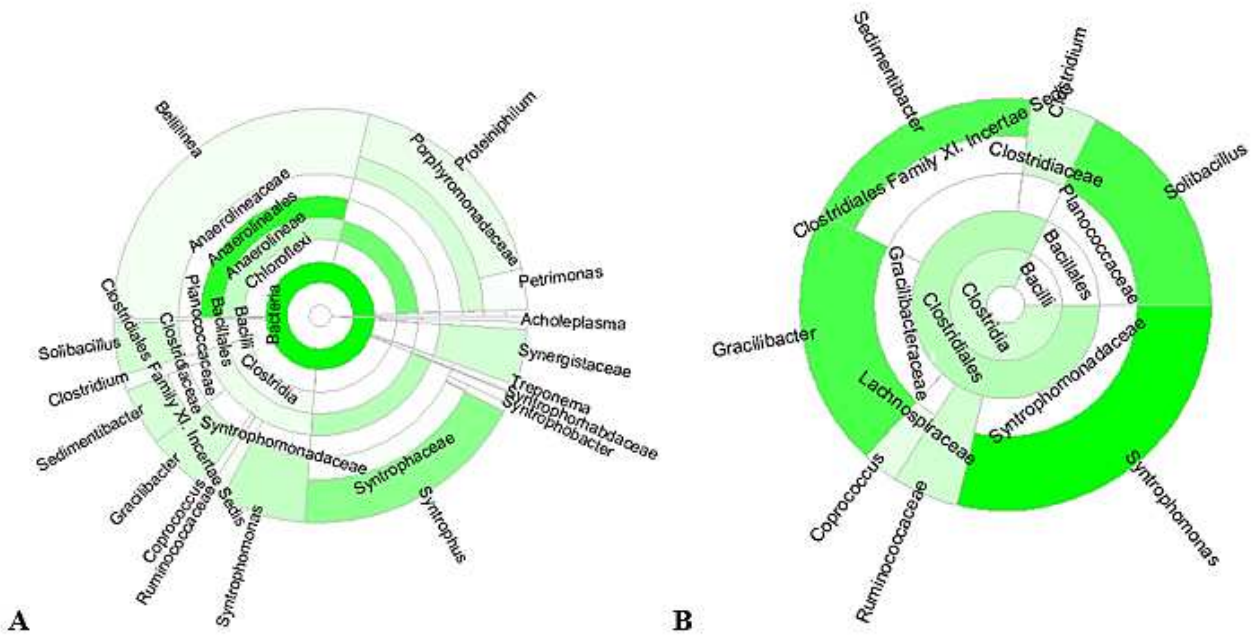


Fig. 4

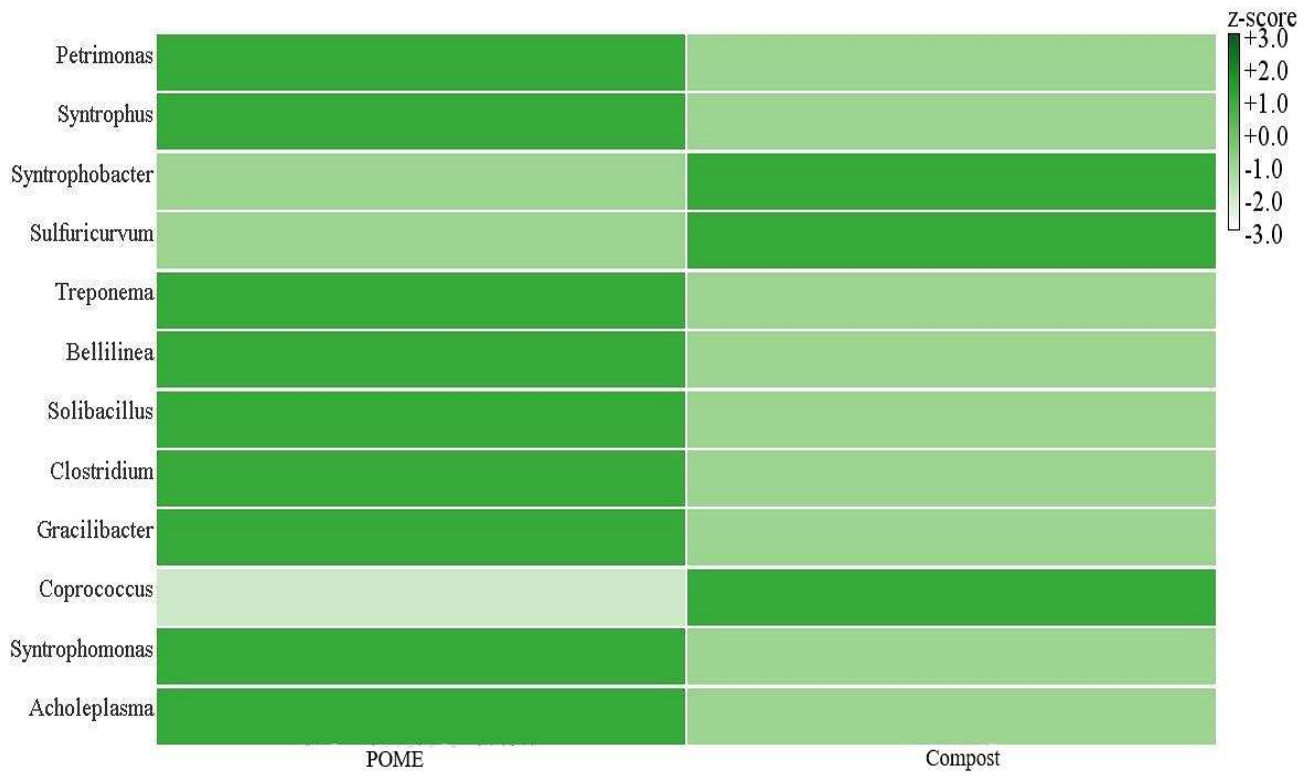


Fig.5

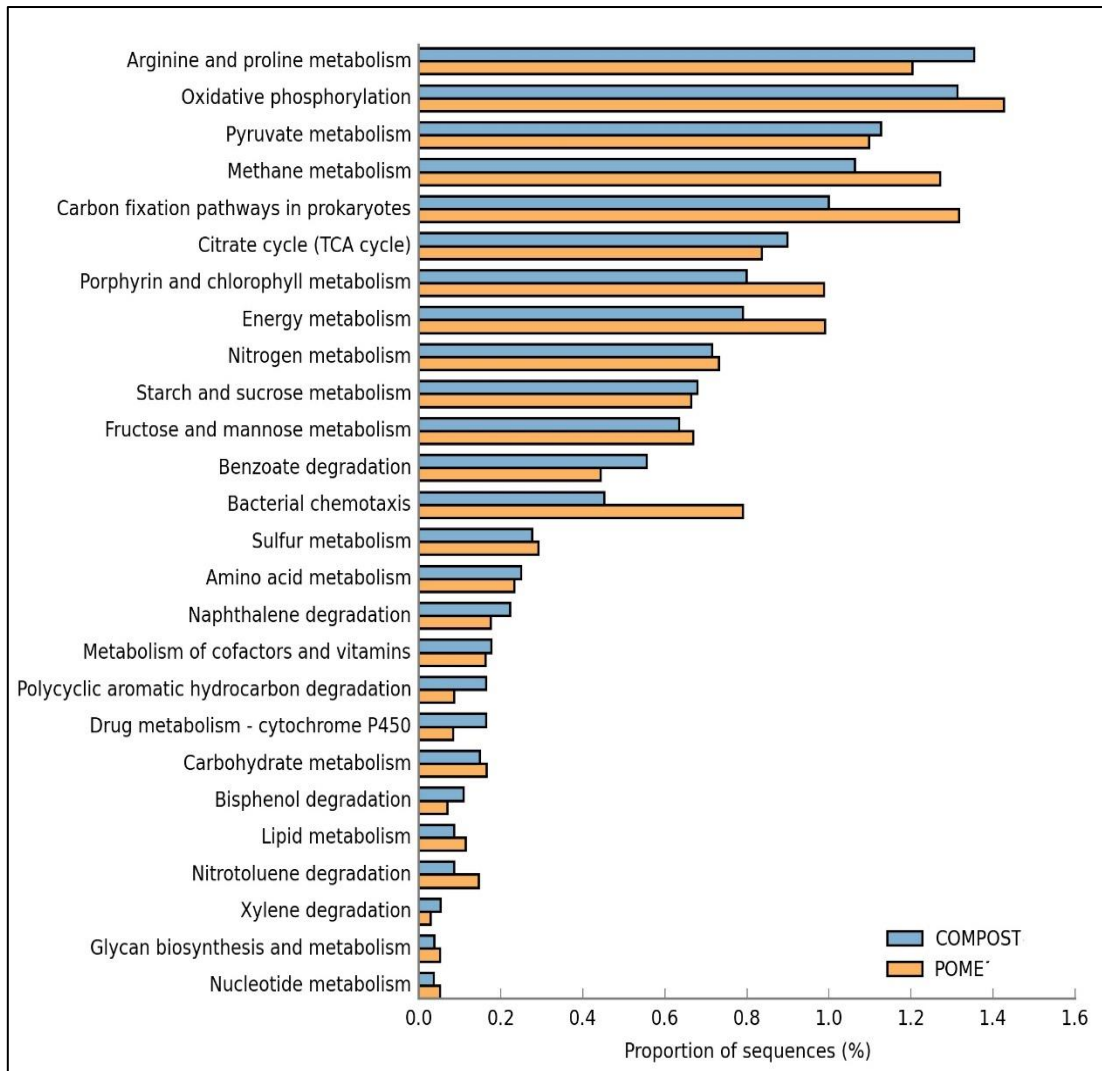


Fig. 6

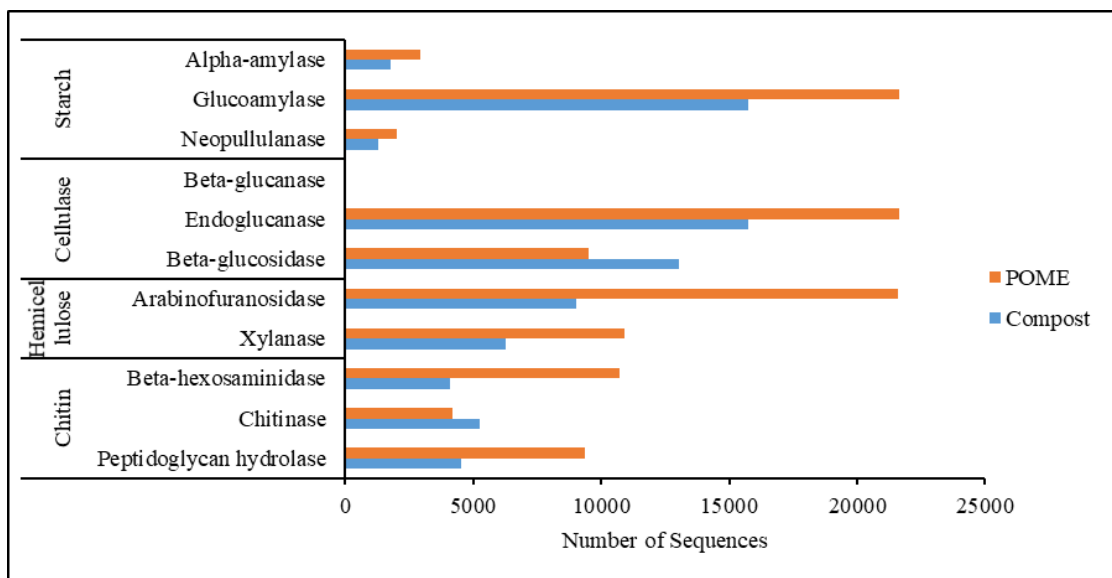


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