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1 **Microbial communities from different soil types respond**
2 **differently to organic waste input**

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21

22 **Abstract**

23 Using organic waste products (OWP) in agriculture has been reported to impact both the
24 activity and composition of soil microbial communities. However, little information is
25 available on how the response of a soil microbial community to a given OWP may depend on
26 the physicochemical and microbial properties of the soil receiving the input. Here, we
27 performed a microcosm experiment to compare the effect of 2 different OWPs (GWS: co-
28 compost of Green Wastes and Sewage sludge or FYM: FarmYard Manure), each applied to 5
29 different soils, on the activity, abundance and diversity of the soil microbial communities.
30 Soils were selected to represent a range of physicochemical and climatic characteristics. CO₂
31 and N₂O emissions, microbial biomass and taxonomic diversity were monitored for 28 days
32 following OWP input. The five soils presented different prokaryotic and fungal communities
33 structures before OWP application. During the 28 days of incubation, those control soils
34 (without OWP) harboring the highest organic matter contents released the greatest CO₂ and
35 N₂O emissions, and had the highest soil microbial biomass. The impact of organic
36 amendments on soil activity and microbial diversity differed with the nature of the OWP.
37 FYM application increased CO₂ emissions 2-fold and delayed N₂O emissions compared to
38 GWS. Major changes in prokaryotic genetic structures were also observed when GWS was
39 applied. The effect of OWPs was dependent on soil type and the five soils exhibited distinct
40 patterns of CO₂ and N₂O emission after a given input. This accorded with the fact that the
41 structure and composition of the microbial communities harbored by each soil type responded
42 differently to a given OWP application. To conclude, our results show that different soil
43 types, harboring distinct microbial community structures, responded differently to OWP
44 application, leading to different patterns and rates of greenhouse gas emissions. This response
45 was also OWP-dependent.

46 **Keywords:** soil microbes; soils incubation; CO₂; N₂O; high throughput sequencing approach.

47

48 1. Introduction

49 Organic waste products (OWP) resulting from human activities (*e.g.*, sewage sludge,
50 municipal solid waste composts or farmyard manure) are being increasingly applied to soils
51 because they facilitate the recycling of nutrients and improve soil fertility. Indeed, organic
52 amendment is known to enhance (i) physical soil fertility by improving soil porosity,
53 aggregation and structure stability, bulk density and water holding capacity (Abiven et al.,
54 2009; Annabi et al., 2011; Eden et al., 2017) and (ii) chemical fertility through pH regulation,
55 as well as increased CEC and availability of nutrients (Diacono and Montemurro, 2010;
56 Chalhoub et al., 2013). Organic amendment also improves the biological components of soil,
57 especially the soil microbial communities. Application of organic materials led to an increase
58 of soil microbial biomass (Ros et al., 2006; Chaudhry et al., 2012; Francioli et al., 2016) and
59 changes in prokaryotic and fungal community structures (Ros et al., 2006; Chaudhry et al.,
60 2012; Francioli et al., 2016; Sadet-Bourgeteau et al., 2018). The effect of OWP on soil
61 microbial communities may depend on: (i) the duration of repeated OWP application, (ii) the
62 rate of OWP applied, (iii) the delay between OWP application and soil sampling, (iv) the
63 quality of the different OWP applied and (v) the soil type (Pérez-Piqueres et al., 2006; Sadet-
64 Bourgeteau et al., 2018). In parallel to these microbial changes, several incubation studies
65 revealed an increase of CO₂, N₂O and CH₄ emissions (Saison et al., 2006; Pezzolla et al.,
66 2013; Pezzolla et al., 2015; Ho et al., 2017). Thus, the use of organic materials on agricultural
67 soils may also have unwanted side effects, such as increased greenhouse gas (GHG)
68 production.

69 Soil microorganisms (prokaryote and fungi) are key actors in ecosystem processes (Wagg
70 et al., 2014; Werling et al., 2014). Changes in the microbial community and biotic interactions
71 may therefore affect the processes mediated by soil microbes, with consequences on GHG
72 emission. In order to maximize the benefits of OWP by reducing soil GHG emissions, it is
73 therefore important to better characterize the impact of amendments on soil microbial

74 community composition and activity. Most studies have focused on the importance of the
75 quality of the applied OWP and very few have taken the importance of soil type into
76 consideration. However, soil type is the main driver of soil microbial abundance and diversity
77 (Dequiedt et al., 2011; Thomson et al., 2015).

78 Ho et al. (2017) and Pezzolla et al. (2013) investigated the impact of different organic
79 materials on several soil types and GHG emission in laboratory incubation experiments.
80 Pezzolla et al. (2013) assessed the effect of OWPs on soil microbial community response by
81 using Phospholipid Fatty Acid Analysis (PLFA) analysis, and CO₂ emission only. Ho et al.
82 (2017) targeted the soil bacterial community using high throughput sequencing techniques
83 (16S rRNA gene), and measured both CO₂ and N₂O emissions. According to these authors,
84 the CO₂ and N₂O emission patterns and rates were amendment-dependent even though the
85 soils possessed different physicochemical parameters, textures and bacterial community
86 compositions and structures. To our knowledge, these two studies are the only ones to have
87 examined the impact of different organic materials on several soil types and GHG emission in
88 the same experiment. However, only two different soil types were assessed, and different
89 methodological tools (PLFA vs 16S rRNA gene Ion Torrent amplicon sequencing) were used
90 in each study which makes general conclusions difficult.

91 The objective of the present study was to assess the effect of the application of different
92 types of organic material on five different soil microbial communities. Based on previous
93 studies, we hypothesized that whatever the soil microbial community considered, the respond
94 was amendment dependent. This work was performed using a laboratory microcosm
95 experiment involving the application of two different types of organic amendments to five
96 soils each containing different microbial communities. The soils were sampled from five field
97 sites representing contrasted pedo-climatic conditions (especially soil type and climate). The
98 sampled plots had never received any organic amendments. The organic amendments applied
99 to the microcosms differed mainly in their organic matter content and stability. One of the

100 novel point of this work was to assess in the same experiment the responses of prokaryotic
101 and fungal communities to these organic amendments by a high throughput sequencing
102 approach respectively targeting the 16S and 18S ribosomal genes. This approach is
103 appropriate to characterize the vast microbial diversity of soil and monitor microbial
104 communities' composition changes after amendment. Soil CO₂ and N₂O emission were also
105 measured in parallel.

106

107 **2. Materials and methods**

108 *2.1. Soils and Organic waste products*

109 The soil samples used in this experiment were collected in March 2015 from the
110 ploughed horizon (0-20 cm) of five french long-term observatories belonging to the SOERE-
111 PRO-network ([http://www6.inra.fr/valor-pro/SOERE-PRO-Presentation-de-l-
112 observatoire/SOERE-PRO-Les-sites](http://www6.inra.fr/valor-pro/SOERE-PRO-Presentation-de-l-observatoire/SOERE-PRO-Les-sites)): QualiAgro (Qa; at Feucherolles), PROspective (Co; at
113 Colmar), Efele (Ef; at Rennes), Couhins (Ch; at Bordeaux) and La Bouzule (LB; at Nancy).
114 Choice of using these sites were to characterize the agronomic value of regular organic
115 residue application and their environmental impacts, in a long-term field experiments. The
116 main soils properties are given in Table 1.

117 For each observatory, a composite soil sample was made from a pool of five sub-samples
118 (Ø 7 cm) in the diagonal section of plots that never received organic waste products. Samples
119 were then mixed and homogenized by passing them through a 4 mm sieve to remove above-
120 ground plant debris, roots and stones. A portion of each soil was air-dried at room
121 temperature for physico-chemical analysis. Particle size distribution, pH, soil organic matter,
122 soil organic carbon, soil total nitrogen (N), soil C/N ratio, Olsen P and Cation Exchange
123 Capacity (CEC), were determined by the Soil Analysis Laboratory at INRA Arras, France
124 (<http://www.lille.inra.fr/las>; Table 1). The rest of the sieved soils, was used for incubation.

125 The organic amendments used in the experiment included a farmyard manure (FYM) and
126 a compost issued from the co-composting of green wastes with sewage sludge (GWS). pH,
127 organic carbon, phosphorus and total N contents were determined for each of these two
128 organic waste products (OWP). Before analysis, the organic amendments were dried and
129 ground to 1 mm. The total N and organic C contents were measured by elemental analysis
130 (NA 1500, Fison Instrument, San Carlos, CA, USA) after additional grinding to 200 μm
131 (Retsch SM 2000, Haan, Germany). The mean OWP characteristics measured are represented
132 in Table 2. The index of residual organic carbon (I_{ROC}) that represents the proportion of
133 organic matter potentially incorporated into soil organic matter after OWP application
134 (Lashermes et al., 2009) was also determined (Table 2).

135

136 *2.2. Microcosms set up and Incubation*

137 The experimental design consisted of a factorial arrangement with five soils (Qa, Co, Ef,
138 Ch and LB), two amendments (a farmyard manure (FYM) and a co-compost of sewage
139 sludge, green wastes and wood chips (GWS)) plus unamended control for each soil (CON).
140 For each treatment, a series of 9 sterile plasma flasks (150 mL) were filled with 30 g of dried
141 and sieved soil to allow for 3 destructive samplings at 0 (d0), 7 (d7) and 28 (d28) days of
142 incubation. These microcosms were supplemented with sterile water to attain 60 % soil water-
143 holding capacity. After 2 weeks of pre-incubation (20°C), FYM or GWS were thoroughly
144 mixed with soil samples in their dry form (5 and 6.9 mg g^{-1} of soil respectively). The
145 sampling time d0 was considered immediately after amendment. The rest of plasma flasks
146 were then incubated for 7 and 28 days in the dark at 20°C and always 60 % water-holding
147 capacity to ensure good biomass activation. Every week, plasma flasks were aerated by
148 flushing with air and at the same time, the water content was adjusted to correct for any soil
149 moisture lost through evaporation. At d0, d7 and d28, for each treatment, soil from
150 corresponding plasma flasks were sacrificed for molecular analyses. After sampling, each

151 sample was lyophilized and stored at -40 °C until use for molecular analyses based on soil
152 DNA extraction.

153

154 *2.3. CO₂ and N₂O emissions*

155 At 0, 3, 7, 14, 21 and 28 days of incubation, the gaseous phase was sampled in 10 mL
156 pre-vacuumed airtight flasks exetainers, to measure the CO₂ and N₂O concentrations using an
157 Agilent 7890B GC coupled to an automatic sampler (Agilent HS7697A Headspace). The
158 concentrations were measured on a thermal conductivity detector for CO₂ and on a plasma
159 emission detector (LDeTek) for N₂O. The GC system was calibrated using multipoint CO₂ and
160 N₂O gas standards prepared by a GasMix (Alytech, France). Since the microcosms were
161 hermetically-sealed and aerated by flushing with air at each sampling date, the concentrations
162 measured corresponded to the CO₂ and N₂O accumulated in the microcosm headspace
163 between two sampling dates.

164

165 *2.4. DNA Extraction and purification*

166 Microbial DNA was extracted from 1 g (dry weight) of soil from the 135 microcosms,
167 GWS (n=3) or FYM (n=3), using a single procedure standardized by the GenoSol platform
168 (INRA, Dijon, France, www.dijon.inra.fr/plateforme_genosol) (Terrat et al., 2012). Since a
169 highly positive linear relationship has been shown between soil DNA recovery and C-biomass
170 measurement (Marstorp et al., 2000; Dequiedt et al., 2011), DNA concentrations of crude
171 extracts were determined by electrophoresis in 1% agarose gel stained with ethidium bromide
172 using a calf thymus DNA standard curve, and used as estimates of microbial biomass
173 (Dequiedt et al., 2011). After quantification, nucleic acids were separated from the residual
174 impurities, particularly humic substances, by centrifuging through two types of minicolumn.
175 Aliquots (100 µL) of crude DNA extract were first loaded onto polyvinyl polypyrrolidone

176 minicolumns (BIORAD, Marne-la-Coquette, France) and centrifuged at $1000 \times g$ for 4 min at
177 10°C . The eluates were then purified using the GeneClean turbo kit (Mp Biomedicals,
178 Illkirch, France) (Ranjard et al., 2003). Purified DNA concentrations were finally measured
179 using the Quantifluor (Promega, Lyon, France) staining kit, according to the manufacturer's
180 instructions.

181

182 *2.5. High throughput sequencing of 16S and 18S rRNA gene*

183 For prokaryotic (bacterial-archaeal) diversity, a 440-base 16S rRNA gene fragment was
184 amplified from each DNA sample with the following primers: F479 (5'-CAG CMG CYG
185 CNG TAA NAC-3') and R888 (5'-CCG YCA ATT CMT TTR AGT-3') as previously
186 described (Tardy et al., 2014). For each sample, 5 ng of DNA were used for a 25 μL PCR
187 conducted under the following conditions: 94°C for 2 min, 35 cycles of 30 s at 94°C , 52°C
188 for 30 s and 72°C for 1 min, followed by 7 min at 72°C .

189 For fungal diversity, a 350-base 18S rRNA gene fragment was amplified from each DNA
190 sample with the following primers: FF390 (5'-CGA TAA CGA ACG AGA CCT-3') and FR1
191 (5'-ANC CAT TCA ATC GGT ANT-3') (Chemidlin Prévost-Bouré et al., 2011). For each
192 sample, 5 ng of DNA were used for a 25 μL PCR conducted under the following conditions:
193 94°C for 3 min, 35 cycles of 30 s at 94°C , 52°C for 1 min and 72°C for 1 min, followed by
194 5 min at 72°C . Prokaryotic and fungal PCR products were purified using the Agencourt®
195 AMPure® XP kit (Beckman Coulter, Italy, Milano) and quantified with the Quantifluor
196 (Promega, Lyon, France) staining kit according to the manufacturer's instructions.

197 A second PCR was performed with the purified PCR products (7.5 ng of DNA for
198 bacteria and archaea, and 5 ng of DNA for fungi), with 10-bp multiplex identifiers added to
199 the 5' end of the primers for the specific identification of each sample and the prevention of
200 PCR biases. For bacteria and archaea, the second PCR conditions were the same as previously

201 described but with only seven cycles. For fungi, the second PCR conditions were optimized,
202 with the number of cycles being reduced to seven and the denaturation step processed at 94
203 °C during 1 min. PCR products were purified with the MinElute PCR purification kit (Qiagen
204 NV) and quantified with the Quantifluor (Promega, Lyon, France) staining kit according to
205 the manufacturer's instructions. Equal amounts of each sample were pooled and then cleaned
206 with the SPRI (Solid Phase Reverse Immobilization Method) using the Agencourt®
207 AMPure® XP kit (Beckman Coulter, Italy, Milano). The pooled samples was finally
208 sequenced with a MiSeq Illumina instrument (Illumina Inc, San Diego, CA) operating with
209 V3 chemistry and producing 250 bp paired-reads.

210

211 *2.6. Bioinformatic analysis of 16S and 18S rRNA gene sequences*

212 Bioinformatic analyses were done using the GnS-PIPE, which was initially developed by
213 the Genosol platform (INRA, Dijon, France) (Terrat et al., 2012). Data from soils and OWP
214 were treated independently. First, all the 16S and 18S raw reads were sorted according to the
215 multiplex identifier sequences. The raw reads were then filtered and deleted based on their
216 length, their number of ambiguities (Ns), and their primer(s) sequence(s). More precisely, all
217 raw sequences were checked and discarded if: (i) they contained any ambiguous base (Ns),
218 (ii) if their length was less than 350 nucleotides for 16S reads or 300 nucleotides for 18S
219 reads, (iii) if the exact primer sequences were not found (for the distal primer, the sequence
220 can be shorter than the complete primer sequence, but without ambiguities). A PERL program
221 was then applied for rigorous dereplication (i.e. clustering of strictly identical sequences). The
222 dereplicated reads were then aligned using Infernal alignment (Cole et al., 2009), and
223 clustered into operational taxonomic units (OTU) using a PERL program that groups rare
224 reads to abundant ones, and does not count differences in homopolymer lengths with a
225 threshold of 95% of sequence similarity. A filtering step was then carried out to check all
226 singleton (reads detected only once and not clustered, which might be artifacts, such as PCR

227 chimeras) based on the quality of their taxonomic assignments. Finally, in order to compare
228 the datasets efficiently and avoid biased community comparisons, the reads retained were
229 homogenized by random selection (soils: 9 600 and 8 420 reads for 16S and 18S rRNA gene
230 sequences, respectively; Organic Waste Products (OWP): 5 080 and 8 420 reads for 16S and
231 18S rRNA gene sequences, respectively).

232 The retained high-quality reads were used for: (i) taxonomy-independent analyses,
233 determining several biodiversity indexes (Shannon, richness and evenness) using the OTU
234 dataset and defining global OTU matrices, and (ii) taxonomy-based analysis using similarity
235 approaches against dedicated reference databases from SILVA (Quast et al., 2012). The raw
236 data sets are available in the EBI database system under project accession number
237 PRJEB31513.

238

239 2.7. Statistical analyses

240 All statistical analyses were achieved with R studio (RStudio, Version 0.98.501, RStudio
241 Inc., Boston, Massachusetts, USA) with the free statistics software R (R version 3.0.2). A
242 three-way analysis of variance (ANOVA) was used to compare the CO₂ and N₂O cumulative
243 fluxes and microbial community indicators. The statistical model included soil type, OWP
244 type, incubation time, soil type × OWP type and soil type × OWP type × incubation time. For
245 all parameters, all significant effects were assessed by Tukey's Honestly Significant
246 Difference (HSD) *post hoc* test ($P < 0.05$). All the variables were tested for normality using
247 Shapiro-Wilk test. The prokaryotic and fungal communities from all samples were also
248 compared by using taxonomical abundance matrix. Principal Component Analysis (PCA) was
249 then used to graphically depict any differences in the microbial structure at phylum level
250 between the samples. For each sample, the coordinates of both principal axes were analyzed
251 by calculating the Euclidean distance (Eudist) between the treatment and the corresponding
252 controls for each incubation time and OWP type. This genetic distance was interpreted as the

253 magnitude of genetic structure modifications induced by OWP application and was calculated
254 as follows. Magnitude of modifications, example of calculation for one OWP type and each
255 incubation time = [Average of Inter Eudist (treated microcosms/control microcosms)]-
256 [((Average of Intra Eudist treated microcosms) + (Average of Intra Eudist control
257 microcosms))/2] (Bressan et al., 2008).

258

259 **3. Results**

260 *3.1. CO₂ emissions*

261 Variations in the cumulative emissions of CO₂ in unamended and amended soils are
262 shown in Fig. 1. Basal respiration differed significantly between the five control soils, the
263 greatest cumulative emissions of CO₂ being observed with LB (94.1 μg C g⁻¹ of soil), and the
264 lowest with Co (34.2 μg C g⁻¹ of soil, *P* < 0.001). Addition of organic amendment (GWS or
265 FYM) resulted in greater cumulative emissions of CO₂ in all five soils with respect to the
266 unamended controls (Fig.1, *P* < 0.001). Regardless of the soil, GWS application led to lower
267 cumulative emissions of CO₂ (on average 156.9 μg C g⁻¹ of soil) than FYM (on average 304.8
268 μg C g⁻¹ of soil, *P* < 0.001), particularly at the end of incubation (from day 14 to 28). In
269 amended soils (GWS or FYM), the cumulative emissions of CO₂ also differed according to
270 the soil type, greater values being observed for soil from Ch (188.1 and 369.7 μg C g⁻¹ of soil
271 for GWS and FYM respectively) and the lowest values being observed for soil from Co
272 (104.9 and 217.1 μg C g⁻¹ of soil for GWS and FYM respectively, *P* < 0.001).

273

274 *3.2. N₂O emissions*

275 Variations in the cumulative emissions of N₂O in unamended and amended soils are
276 reported in Fig. 2. Only control soil from LB, Ch and Ef soils showed a significant N₂O
277 release throughout the incubation period (from 0 to 3.7 ng N g⁻¹ of soil in average, *P*<0.001).

278 The addition of organic amendment (GWS or FYM) resulted in greater cumulative emissions
279 of N₂O in all five soils with respect to unamended controls ($P < 0.001$). Regardless of the
280 soil, GWS and FYM application induced equivalent cumulative emissions of N₂O (23.6 and
281 26.4 ng N g⁻¹ of soil respectively). GWS led to more rapid N₂O emission (until day 3) than
282 FYM. In amended soils, the cumulative emissions of N₂O differed according to the site
283 considered. For GWS, the highest cumulative emissions of N₂O were observed for Co (35.9
284 ng N g⁻¹ of soil, $P < 0.001$). LB and Ef soils emitted significantly less (~1.3 fold) N₂O than
285 Co (23.7 and 30.3 ng N g⁻¹ of soil respectively). Still compared to Co soil, Qa emitted ~2 fold
286 less (17.5 ng N g⁻¹ of soil, $P < 0.001$) and Ch ~4 fold less (10.3 ng N g⁻¹ of soil, $P < 0.001$).
287 The soil emission classification after FYM application differed from that observed with GWS,
288 the lowest emission rates of N₂O being observed for Co and Qa soils (4.5 and 16.2 ng N g⁻¹ of
289 soil respectively). Ch emitted ~5 fold more N₂O (22.1 ng N g⁻¹ of soil, $P < 0.001$) than Co.
290 Soils Ef and LB emitted ~10 fold more N₂O than Co (52.2 and 36.9 ng N g⁻¹ of soil
291 respectively, $P < 0.001$).

292

293 3.3. Microbial biomass

294 The dynamics of the microbial biomass during incubation of unamended and amended
295 soils are shown in Fig. 3. The microbial biomass in control soils generally remained constant
296 throughout the incubation ($P > 0.05$). The LB soil had the highest biomass (on average 73.6
297 µg DNA g⁻¹ of dry soil) and Ch the lowest (on average 16.9 µg DNA g⁻¹ of dry soil; $P <$
298 0.001). The biomass values for Co, Qa and Ef soils were similar and significantly lower than
299 LB, and greater than Ch (on average 29.8 µg DNA g⁻¹ of dry soil; $P < 0.001$). Addition of
300 GWS or FYM enhanced the microbial biomass only in LB soil, from 7 days of incubation
301 (106.7 and 123.7 µg DNA g⁻¹ of dry soil respectively; $P < 0.001$). A significantly greater
302 amount of microbial biomass was observed when FYM was applied on LB soil with respect
303 to GWS (123.7 and 106.6 µg DNA g⁻¹ of dry soil respectively; $P < 0.001$).

305 *3.4. Prokaryotic and fungal diversity indices*

306 The dynamics of the microbial diversity indices during incubation of unamended and
307 amended soils are shown in Fig. 4. In general, the control soils did not show any variations in
308 prokaryotic and fungal diversity indices (richness and Shannon) throughout the study period.
309 Only the control soils from LB showed, at 28 days of incubation, an increase in fungal
310 richness and microbial Shannon indices ($P < 0.001$). The effect of organic amendment on
311 microbial diversity indices was dependent on the soil and the type of amendment. Thus, the
312 addition of GWS led to a decrease of prokaryotic richness and Shannon index in Qa soil after
313 7 days of incubation ($P < 0.001$), and an increase of the prokaryotic Shannon index in LB soil
314 after 28 days of incubation ($P < 0.001$). Concerning fungal diversity indices, the addition of
315 GWS led to a decrease of richness and Shannon index in Co and Ch soils ($P < 0.001$), after 7
316 days of incubation, but an increase of richness in Ef soil ($P < 0.001$). The addition of FYM
317 increased the prokaryotic richness in Ch soil and the fungal richness in Co soil after 7 days of
318 incubation ($P < 0.001$). For Co soil, from day 7 to 28, the fungal Shannon index decreased to
319 reach, at the end of incubation, a value lower than that observed before the application ($P <$
320 0.001). This suggests that the fungal community from Co soil would be resilient 28 days after
321 FYM application. The addition of FYM also led to a decrease of the fungal Shannon index in
322 Ef soil throughout the entire incubation ($P < 0.001$).

323

324 *3.5. Prokaryotic and fungal community structures and taxonomic composition*

325 Principal Component Analysis (PCA) achieved on phyla taxonomical abundance matrix
326 revealed that before the OWP application, the microbial community structures in the five soils
327 differed significantly from each other (Supplementary Fig. S1A and B). The addition of GWS
328 or FYM induced, from 7 days of incubation, a change in the prokaryotic and fungal (Fig. 5A
329 and B, Supplementary Fig. 1A and 1B) community structure in all the soils. Same results

330 were obtained on genera taxonomical abundance matrix (data not shown). OWP (FYM or
331 GWS) application impacted prokaryotic community structure whatever the sampling site, as
332 evidenced by the Euclidian distances calculated at D7 and 28 (Fig. 5). However, the
333 amplitude of the modifications depended on the type of OWP applied, with major changes
334 observed when GWS, rather than FYM, was used (Fig. 5). The prokaryotic genetic structures
335 seemed to be more impacted in Ch than in the other soils, 28 days after OWP application
336 (FYM or GWS) ($P < 0.05$). Analysis of the taxonomic composition, following FYM
337 application to Ch soil, revealed that the observed changes in prokaryotic genetic structures
338 were mainly due to an increase in the relative abundance of *Firmicutes* and a decrease of
339 *Acidobacteria* and *Planctomycetes* groups ($P < 0.05$). GWS led only to a decrease of the
340 *Planctomycetes* group in that soil. Twenty-eight days after GWS application, the prokaryotic
341 genetic structure showed resilience in the Ef, LB and Qa soils, but not in the Ch and Co soils
342 (Fig. 5). This was also observed after FYM amendment, but only in Co soil (Fig. 5). OWP
343 (FYM or GWS) application also impacted the fungal community structure whatever the
344 sampling site (Fig. 5). Fungal genetic structure changes were due to a decrease of
345 *Chytridiomycota* in Ef soil 28 days after FYM application ($P < 0.05$). FYM input also led to
346 an increase of *Glomeromycota* in Ch soil 28 days after application ($P < 0.05$). A decrease of
347 *Chytridiomycota* was observed in LB soil 28 days after GWS application ($P < 0.05$). Twenty-
348 eight days after GWS application, the fungal genetic structure in Ch, Co and Qa soils showed
349 resilience (Fig. 5). This was not observed after amendment with FYM (Fig. 5). Interestingly,
350 in the present study, the prokaryotic and fungal communities appeared more resilient after
351 GWS application than after FYM application.

352

353 4. Discussion

354 The addition of OWP (FYM or GWS) led to a rapid increase of CO₂ emission in all the
355 soil samples tested. This confirmed the role of labile C (provided by OWP) in inducing a

356 rapid increase of soil microbial respiration after amendment application. Among the different
357 soil types studied, those with the greatest basal respiration (Ch, LB and Ef) were also the
358 greatest emitters when OWPs were applied. Soil CO₂ emissions were not correlated with any
359 of the soil physicochemical characteristics measured in the present study. From 14 days of
360 incubation, and whatever the type of soil considered, CO₂ emission was ~50 % greater in soils
361 amended with FYM than in those amended with GWS. As previously observed by Brenzinger
362 et al. (2018), this could be explained by the quality of OWP applied. In the present study, the
363 different OWP varied in their organic matter quality. FYM was characterized by a lower
364 potential ability to increase soil stable pool of exogenous organic matter - total organic
365 carbon, as shown by its smaller I_{ROC} (66.6 %), compared to GWS (77.6 %) (Lashermes et al.,
366 2009). This suggests that FYM was subjected to a greater biodegradability of organic carbon
367 and a greater CO₂ emission compared to GWS.

368 The addition of OWP (FYM or GWS) led to an increase of N₂O emission. Twenty-eight
369 days after application, both OWP led to equivalent cumulative emissions of N₂O. However,
370 the trend of N₂O emission differed according to the amendment applied. Indeed, whatever the
371 type of soil considered, the application of GWS led to earlier N₂O emission with ~50 % of the
372 total N₂O emission observed after 3 days of incubation. After the same period of incubation,
373 FYM application had induced only 10 % of the total N₂O emission. Increased N₂O emission
374 from soil is commonly reported after organic fertilization (Shah et al., 2016; Ho et al., 2017);
375 however, the effect of the type of OWP amendment on the kinetics of N₂O emission is poorly
376 documented (Shah et al., 2016). According to Shah et al. (2016), the kinetics of N₂O emission
377 would depend on the C/N ratio of the applied OWP. More precisely, a high C/N ratio means
378 that N will be exhausted before the C has been digested by the bacteria as an energy source,
379 hence leading to a lower N₂O emission. Conversely, a low C/N ratio results in high NH₄⁺
380 concentrations and finally a greater emission of N₂O (Shah et al., 2016). Thus, the lower C/N
381 ratio measured for GWS (13.2 ± 0.5), as compared to FYM (18.1 ± 0.1), could explain the
382 earlier N₂O emission observed with this amendment.

383 Interestingly, an effect of soil type on N₂O emission was also observed. Soil with the
384 highest pH before amendment (Co; pH=8.51) emitted the greatest amount of N₂O after
385 amendment with GWS, but the lowest after amendment with FYM. As previously mentioned,
386 the cumulative emissions of N₂O from other soil types were equivalent after GWS and FYM
387 applications. According to the literature, the relationship between soil pH and denitrification
388 remains unclear. In the present study, soil pH had not been measured throughout the
389 incubation. However, based on previous study (Shah et al. 2016), for a same soil type, the
390 dynamic of soil pH would be different according to the quality of OWP applied. Some authors
391 indicated that the N₂O fraction could be larger at low soil pH (Focht, 1974; Goodroad and
392 Keeney, 1984; Eaton and Patriquin, 1989; Brumme and Beese, 1992; Thomas et al., 1994),
393 whereas others reported lower N₂O emissions in acidic compared to neutral or slightly
394 alkaline soils (Šimek and Cooper, 2002). Thus, it is difficult to explain the effect of soil type
395 on N₂O emission as being determined by soil pH and other interpretations are needed.

396 In the present work, before the amendments, the prokaryotic and fungal community
397 structures and compositions of the five soils were distinctly different (Supplementary Fig.
398 S2). Moreover, as previously observed by Ho et al. (2017), the application of OWP led to
399 changes in the microbial community that were dependent on the soil type and the quality of
400 OWP applied (Fig. 5 and Supplementary Fig. S1). Nitrous oxide (N₂O) is mainly generated
401 *via* microbial processes of nitrification and denitrification in soils (Pajares and Bohannan,
402 2016). Thus, as proposed by Ho et al. (2015), we hypothesized that, in the case of Co soil,
403 GWS application stimulated the soil-borne microbes involved in denitrification (resulting in
404 earlier N₂O emission), whereas FYM favored those involved in the nitrification process
405 (leading to later N₂O emission). The effect of OWP quality on N₂O emission was not so
406 marked for the other soil types probably due to the differences between the soil-borne
407 microbial communities.

408 From 7 to 28 days of incubation, and only in LB soil, the addition of OWP (FYM or
409 GWS) led to a ~40 % increase in microbial biomass. Previous soil incubation studies had
410 already highlighted an increase in microbial biomass within 10 days after the addition of
411 OWP (Saison et al., 2006; Pezzolla et al., 2013; Pezzolla et al., 2015). However, in the present
412 study, OWP had an effect on microbial biomass in only one soil (LB), which is surprising. As
413 proposed by Marschner et al. (2003), this could be due to the higher organic carbon content
414 (17.9 g kg^{-1}) of LB soil before OWP application. Indeed, the organic carbon content is known
415 to determine the response of microbial communities to external inputs, soils with higher
416 organic carbon being more prone to an increase in microbial biomass and changes in the
417 microbial community (Marschner et al., 2003). Further studies also reported a correlated
418 increase of soil CO_2 emission and microbial biomass in the first days after OWP application
419 (Saison et al., 2006; Pezzolla et al., 2013). This was not observed in the present study, except
420 for the LB soil. As proposed by other studies, this suggests that the modifications in activity
421 highlighted would more likely be due to a modification in microbial community structure and
422 composition, rather than in its size (Zogg et al., 1997; Zhang et al., 2005).

423 No overall tendency was observed regarding the effect of OWP on soil microbial diversity
424 indices. However, changes in microbial richness and diversity occurred depending both on
425 the type of soil and OWP. The effects of OWP on microbial diversity reported in the literature
426 are often ambiguous, mainly due to great variations between the experimental systems and
427 management definitions (Chaudhry et al., 2012; Hartmann et al., 2015; Chen et al., 2016;
428 Sadet-Bourgeteau et al., 2018). As reported by several authors (Saison et al., 2006; Pezzolla et
429 al., 2013; Pezzolla et al., 2015; Federici et al., 2017), OWP addition (GWS or FYM) led to a
430 rapid shift in microbial community structure, in all soils, within 7 days. The observed changes
431 in microbial structure were dependent on the soil type and the quality of OWP applied. It
432 cannot be excluded that these early changes might be due to microorganisms present in the
433 organic materials applied (Supplementary Fig. S3). This hypothesis is reinforced by the
434 different microbial genera composition present in unamended soils and OWPs

435 (Supplementary Fig. S2 and S3). However, as mentioned by Saison et al. (2006), the OWP
436 microbiota added to soil is rapidly outcompeted by the soil-derived microorganisms and its
437 effect on community structure is likely to be marginal. In addition, as proposed by Ho et al.
438 (2016), the changes in microbial community structure observed in the present study is more
439 likely due to the stimulation of soil-borne microbes by chemical composition of OWP
440 applied than microbes present in the organic materials applied. The early shift in structure
441 of the soil microbial community seems in close agreement with the initial increase of
442 microbial respiration observed immediately after applying the amendments and could be
443 ascribed to the stimulation of microbial populations with great ability to rapidly metabolize
444 the labile organic C provided by OWP (Blagodatskaya et al., 2007). This was corroborated by
445 the fact that, in the present study, the application of FYM led to a stimulation of *Firmicutes* in
446 Ch soil and also the highest CO₂ emission. Carbon additions appear to strongly stimulate
447 organisms within the *Firmicutes* clades (Cleveland et al., 2007). The dominance of organisms
448 within the *Firmicutes* groups, and their relative increase in abundance in response to C
449 additions, suggested that members of these groups quickly respond to the addition of organic
450 material to the soil, leading to rapid increases in soil respiration (Cleveland et al., 2007). In
451 parallel, the decrease of *Acidobacteria* and *Planctomycetes*, suggested that these organisms
452 exhibit poor competitiveness and colonization ability, which could explain their decrease in
453 the present experiment. The impact on these *phyla* generally becomes apparent 3 days after
454 amendment and has already been highlighted in previous studies of the impact of digestate
455 application on soil microbial communities (Fierer et al., 2007; Cruz-Martínez et al., 2009;
456 Pezzolla et al., 2015). Interestingly, contrary to FYM, the addition of GWS to soils only led to
457 a decrease in *Planctomycetes* 3 to 28 days after the application. As mentioned above, the lack
458 of increase in the proportion of *Firmicutes* in GWS-amended soils may help to explain the
459 lower CO₂ emissions, as compared to FYM.

460 The fungal community also responded by a decrease of *Chytridiomycota* 28 days after
461 FYM or GWS application, and an increase in *Glomeromycota* 28 days after FYM application.

462 *Chytridiomycota* have been recovered as saprophytes and can degrade polymers from a
463 variety of plant and animal debris (Czeczuga and Mazalska, 2000; Czeczuga et al., 2005).
464 This fungal phylum is probably included within the group of k-strategists, which could
465 explain its decrease in the present experiment. It has been reported in the literature that 4
466 months after the last application, OWP tended to increase *Basidiomycota*, one of the main soil
467 decomposers (Ma et al., 2013; Weber et al., 2013) and to decrease *Glomeromycota* (Chen et
468 al., 2016; Sadet-Bourgeteau et al., 2018). This did not occur in the present study, where no
469 effect on *Basidiomycota* was apparent and an increase of *Glomeromycota* was observed 28
470 days after OWP application. As mentioned in a previous study, this emphasizes the
471 importance of taking the delay between OWP application and soil sampling into account
472 when studying the effect of OWP on the soil microbial community (Sadet-Bourgeteau et al.,
473 2018).

474 Despite the above-described overall response of soils to OWP application, in the present
475 work, the microbial communities of some soils responded differently. This concurs with
476 observations by Pérez-Piqueres et al. (2006) that the changes in microbial community
477 structure induced by amendments were related both to the soil and to the type of OWP used.
478 The particular behavior of the prokaryotic community in response to OWP application in the
479 Ch soil could be related to the soil's physico-chemical characteristics. Indeed, Ch soil has a
480 sandy loam texture, unlike the other soils in the present study (silty clay loam or silty loam
481 texture). In a recent study, Ho et al. (2017) highlighted that the composition of the bacterial
482 community from sandy loam soil responded differently to a same type of OWP application
483 than a bacterial community from clay soil. Thus, we suggest that, contrary to the other soils in
484 this study, the sandy loam texture of Ch soil would be an important determinant of its
485 microbial community composition, and lead to a different impact of the amendment on soil
486 prokaryotic community composition. As previously observed by Procter et al. (2014), the
487 effect of OWP on the fungal community was also soil type-dependent. Some of the microbial
488 communities impacted by OWP application, tended to revert to their initial structure (before

489 amendment). This resilience was dependent on soil type, and globally more marked after
490 GWS input. This accords with reports by Saison et al. (2006) that the resilience of the soil
491 microbial community was OWP-quality dependent.

492

493 **5. Conclusions**

494 The present study indicated that soils with different physico-chemical properties and
495 microbial community structures responded differently to organic fertilization. This response
496 appeared to depend on the type of OWP and suggests that GHG emission could be modulated
497 by spreading specific types of amendment on specific types of soil. Further analyses are
498 needed to best determine which type of amendment should be applied to which type of soil in
499 order to limit soil GHG emission.

500

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508

Table 1

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Soil physico-chemical parameters from control plots of different Long-Term observatories

| Item | Long-Term Observatories | | | | |
|--|--------------------------------------|--------------------------|--------------------------------|--------------------------------|----------------------------------|
| | QualiAgro (Qa) | PROspective (Co) | EFELE (Ef) | La Bouzule (LB) | Couhins (Ch) |
| Location | Feucherolles North West of France | Colmar Est of France | Rennes North West of France | Nancy North Est of France | Bordeaux South West of France |
| Geographical coordinates | 48°53'49"N, 1°58'21"E | 48°03'33"N, 7°19'41"E | 48°05'35.9"N, 1°48'53.1"W | 48°44'23.64"N, 6°19'20.16"E | 44°45'06.45"N, 0°33'34.37"W |
| Clay (<2 µm) g kg ⁻¹ | 199 | 243 | 181 | 359 | 83 |
| Fine silt (2/20 µm) g kg ⁻¹ | 263 | 292 | 241 | 398 | 45 |
| Coarse silt (20/20 µm) g kg ⁻¹ | 442 | 353 | 423 | 127 | 21 |
| Fine sand (50/200 µm) g kg ⁻¹ | 87 | 69 | 103 | 44 | 64 |
| Coarse sand (200/2000 µm) g kg ⁻¹ | 9 | 43 | 52 | 72 | 787 |
| Organic Carbon g kg ⁻¹ | 9.11 | 13.4 | 11.3 | 17.9 | 9.33 |
| Total N g kg ⁻¹ | 0.87 | 1.18 | 1.17 | 1.76 | 0.64 |
| C/N | 10.4 | 11.4 | 9.64 | 10.2 | 14.6 |
| Organic Matter g kg ⁻¹ | 15.8 | 23.1 | 19.6 | 31 | 16.1 |
| pH | 6.88 | 8.51 | 6.4 | 6.93 | 6.06 |
| CEC cmol+kg ⁻¹ | 8.26 | 10.8 | 6.79 | 14.3 | 2.78 |
| P ₂ O ₅ g 100g ⁻¹ | 0.13 | 0.23 | 0.25 | 0.35 | 0.06 |

510 **Table 2**

511 Main characteristics of the different organic waste products (OWP) used

| Treatment | | FYM | GWS |
|---------------------------------------|----------------------------------|--------------|-------------|
| Dry Matter (DM [†]) | % | 33.9 ± 0.7 | 67.2 ± 1.3 |
| Organic Carbon | g.kg ⁻¹ DM | 355 ± 14 | 257 ± 2 |
| Total N | g.kg ⁻¹ DM | 19.7 ± 0.6 | 22.5 ± 0.5 |
| P ₂ O ₅ (Olsen) | g.kg ⁻¹ DM | 2.6 ± 0.1 | 0.8 ± 0.1 |
| C:N | | 18.1 ± 0.1 | 13.2 ± 0.5 |
| pH (water) | | 8.8 ± 0.3 | 7.7 ± 0.1 |
| I _{ROC} [‡] | (% organic C) | 66.6 ± 7.5 | 77.6 ± 9.3 |
| Microbial Biomass | μg of DNA.g ⁻¹ of OWP | 515.5 ± 87.0 | 54.9 ± 19.1 |

512 [†]DM: Dry Matter; FYM: farmyard manure; GWS: green wastes with sewage sludge513 [‡]I_{ROC}: index of residual organic carbon

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522 **Fig 1.** The dynamics of cumulative emission of CO₂ from five different types of soils
523 (QualiAgro (Qa), PROspective (Co), Efele (Ef), Couhins (Ch) and La Bouzule (LB))
524 amended or not (control) with two different organic materials (FYM: farmyard manure or
525 GWS: green wastes with sewage sludge).

526 **Fig. 2.** The dynamics of cumulative emission of N₂O from five different types of soils
527 (QualiAgro (Qa), PROspective (Co), Efele (Ef), Couhins (Ch) and La Bouzule (LB))
528 amended or not (control) with two different organic materials (FYM: farmyard manure or
529 GWS: green wastes with sewage sludge).

530 **Fig. 3.** The dynamics of microbial biomass from five different types of soils (QualiAgro (Qa),
531 PROspective (Co), Efele (Ef), Couhins (Ch) and La Bouzule (LB)) amended or not (control)
532 with two different organic materials (FYM: farmyard manure or GWS: green wastes with
533 sewage sludge).

534 **Fig. 4.** The dynamics of Prokaryotic (A) and fungal (B) diversity indices from five different
535 types of soils (QualiAgro (Qa), PROspective (Co), Efele (Ef), Couhins (Ch) and La Bouzule
536 (LB)) amended or not (control) with two different organic materials (FYM: farmyard manure
537 or GWS: green wastes with sewage sludge).

538 **Fig. 5.** Magnitude of the prokaryotic and fungal genetic structure of five different types of
539 soils (QualiAgro (Qa), PROspective (Co), Efele (Ef), Couhins (Ch) and La Bouzule (LB))
540 modifications during 28 days after amendment with two different organic materials: (A)
541 farmyard manure or (B) green wastes with sewage sludge.

542 **Supplementary Figure S1**

543 Principal Component Analysis of the evolution of microbial community composition over
544 time (A: Prokaryote and B: Fungi) of five different types of soils (QualiAgro (Qa),
545 PROspective (Co), Efele (Ef), Couhins (Ch) and La Bouzule (LB)) amended or not (CON)
546 with two different organic materials (FYM: farmyard manure or GWS: green wastes with
547 sewage sludge).

548 **Supplementary Figure S2**

549 Relative abundances of prokaryotic (A) and fungal (B) *phyla* and prokaryotic (A') and fungal
550 (B') *genera* in the different sampling sites (QualiAgro (Qa), PROspective (Co), Efele (Ef),
551 Couhins (Ch) and La Bouzule (LB)) before the application of organic waste products (T0).

552 **Supplementary Figure S3**

553 Relative abundances of prokaryotic (A) and fungal (B) *phyla* and prokaryotic (A') and fungal
554 (B') *genera* in the two organic waste products applied on soils (GWS and FYM).

555

556 **References**

- 557 Abiven, S., Menasseri, S., Chenu, C., 2009. The effects of organic inputs over time on soil
558 aggregate stability—A literature analysis. *Soil Biol. Biochem.* 41, 1-12.
- 559 Annabi, M., Le Bissonnais, Y., Le Villio-Poitrenaud, M., Houot, S., 2011. Improvement of
560 soil aggregate stability by repeated applications of organic amendments to a cultivated silty
561 loam soil. *Agr. Ecosyst. Environ.* 144, 382-389.
- 562 Blagodatskaya, E., Blagodatsky, S., Anderson, T.-H., Kuzyakov, Y., 2007. Priming effects in
563 Chernozem induced by glucose and N in relation to microbial growth strategies. *Appl Soil
564 Ecol.* 37, 95-105.
- 565 Brenzinger, K., Drost, S.M., Korthals, G., Bodelier, P.L.E., 2018. Organic Residue
566 Amendments to Modulate Greenhouse Gas Emissions From Agricultural Soils. *Front.
567 Microbiol.* 9, 1-16.
- 568 Bressan, M., Mougél, C., Dequiedt, S., Maron, P.A., Lemanceau, P., Ranjard, L., 2008.
569 Response of soil bacterial community structure to successive perturbations of different types
570 and intensities. *Environ. Microbiol.* 10, 2184-2187.
- 571 Brumme, R., Beese, F., 1992. Effects of liming and nitrogen fertilization on emissions of CO₂
572 and N₂O from a temperate forest. *J. Geophys. Res-Atmos.* 97, 12851-12858.
- 573 Chalhoub, M., Garnier, P., Coquet, Y., Mary, B., Lafolie, F., Houot, S., 2013. Increased
574 nitrogen availability in soil after repeated compost applications: Use of the PASTIS model to
575 separate short and long-term effects. *Soil Biol. Biochem.* 65, 144-157.
- 576 Chaudhry, V., Rehman, A., Mishra, A., Chauhan, P., Nautiyal, C., 2012. Changes in Bacterial
577 Community Structure of Agricultural Land Due to Long-Term Organic and Chemical
578 Amendments. *Microb Ecol.* 64, 450-460.
- 579 Chemidlin Prévost-Bouré, N., Christen, R., Dequiedt, S., Mougél, C., Lelièvre, M., Jolivet,
580 C., Shahbazkia, H.R., Guillou, L., Arrouays, D., Ranjard, L., 2011. Validation and
581 Application of a PCR Primer Set to Quantify Fungal Communities in the Soil Environment by
582 Real-Time Quantitative PCR. *PLOS ONE.* 6, e24166.

583 Chen, C., Zhang, J., Lu, M., Qin, C., Chen, Y., Yang, L., Huang, Q., Wang, J., Shen, Z., Shen,
584 Q., 2016. Microbial communities of an arable soil treated for 8 years with organic and
585 inorganic fertilizers. *Biol Fertil Soils*. 52, 455-467.

586 Cleveland, C.C., Nemergut, D.R., Schmidt, S.K., Townsend, A.R., 2007. Increases in soil
587 respiration following labile carbon additions linked to rapid shifts in soil microbial
588 community composition. *Biogeochemistry*. 82, 229-240.

589 Cole, J.R., Wang, Q., Cardenas, E., Fish, J., Chai, B., Farris, R.J., Kulam-Syed-Mohideen,
590 A.S., McGarrell, D.M., Marsh, T., Garrity, G.M., Tiedje, J.M., 2009. The Ribosomal
591 Database Project: improved alignments and new tools for rRNA analysis. *Nucleic Acids Res*.
592 37, D141-D145.

593 Cruz-Martínez, K., Suttle, K.B., Brodie, E.L., Power, M.E., Andersen, G.L., Banfield, J.F.,
594 2009. Despite strong seasonal responses, soil microbial consortia are more resilient to long-
595 term changes in rainfall than overlying grassland. *ISME J*. 3, 738.

596 Czczuga, B., Mazalska, B., 2000. Zoosporic aquatic fungi growing on avian excrements in
597 various types of water bodies. *Limnologica-Ecology and Management of Inland Waters*. 30,
598 323-330.

599 Czczuga, B., Mazalska, B., Godlewska, A., Muszyńska, E., 2005. Aquatic fungi growing on
600 dead fragments of submerged plants. *Limnologica*. 35, 283-297.

601 Dequiedt, S., Saby, N.P.A., Lelievre, M., Jolivet, C., Thioulouse, J., Toutain, B., Arrouays,
602 D., Bispo, A., Lemanceau, P., Ranjard, L., 2011. Biogeographical patterns of soil molecular
603 microbial biomass as influenced by soil characteristics and management. *Global Ecol*.
604 *Biogeogr*. 20, 641-652.

605 Diacono, M., Montemurro, F., 2010. Long-term effects of organic amendments on soil
606 fertility. A review. *Agron Sustain Dev*. 30, 401-422.

607 Eaton, L.J., Patriquin, D.G., 1989. Denitrification in lowbush blueberry soils. *Can. J. Soil*.
608 *Sci*. 69, 303-312.

609 Eden, M., Gerke, H.H., Houot, S., 2017. Organic waste recycling in agriculture and related
610 effects on soil water retention and plant available water: a review. *Agron Sustain Dev.* 37, 11.

611 Federici, E., Massaccesi, L., Pezzolla, D., Fidati, L., Montalbani, E., Proietti, P., Nasini, L.,
612 Regni, L., Scargetta, S., Gigliotti, G., 2017. Short-term modifications of soil microbial
613 community structure and soluble organic matter chemical composition following amendment
614 with different solid olive mill waste and their derived composts. *Appl Soil Ecol.* 119, 234-
615 241.

616 Fierer, N., Bradford, M.A., Jackson, R.B., 2007. Toward an ecological classification of soil
617 bacteria. *Ecology.* 88, 1354-1364.

618 Focht, D.D., 1974. Effect of temperature, pH, and aeration on production of nitrous-oxide and
619 gaseous nitrogen - zero-order kinetic model. *Soil Sci.* 118, 173-179.

620 Francioli, D., Schulz, E., Lentendu, G., Wubet, T., Buscot, F., Reitz, T., 2016. Mineral vs.
621 organic amendments: microbial community structure, activity and abundance of agriculturally
622 relevant microbes are driven by long-term fertilization strategies. *Front. Microbiol.* 7.

623 Goodroad, L.L., Keeney, D.R., 1984. Nitrous-oxide production in aerobic soils under varying
624 pH, temperature and water-content. *Soil Biol. Biochem.* 16, 39-43.

625 Hartmann, M., Frey, B., Mayer, J., Mäder, P., Widmer, F., 2015. Distinct soil microbial
626 diversity under long-term organic and conventional farming. *ISME J.* 9, 1177-1194.

627 Ho, A., El-Hawwary, A., Kim, S.Y., Meima-Franke, M., Bodelier, P., 2015. Manure-
628 associated stimulation of soil-borne methanogenic activity in agricultural soils. *Biol Fertil*
629 *Soils.* 51, 511-516.

630 Ho, A., Ijaz, U.Z., Janssens, T.K., Ruijs, R., Kim, S.Y., de Boer, W., Termorshuizen, A., van
631 der Putten, W.H., Bodelier, P.L., 2017. Effects of bio-based residue amendments on
632 greenhouse gas emission from agricultural soil are stronger than effects of soil type with
633 different microbial community composition. *GCB. Bioenergy.* 9, 1707-1720.

634 Lashermes, G., Nicolardot, B., Parnaudeau, V., Thuriès, L., Chaussod, R., Guillotin, M.L.,
635 Linères, M., Mary, B., Metzger, L., Morvan, T., Tricaud, A., Villette, C., Houot, S., 2009.

636 Indicator of potential residual carbon in soils after exogenous organic matter application. *Eur.*
637 *J. Soil Sci.* 60, 297-310.

638 Ma, A., Zhuang, X., Wu, J., Cui, M., Lv, D., Liu, C., Zhuang, G., 2013. Ascomycota
639 members dominate fungal communities during straw residue decomposition in arable soil.
640 *PLoS One.* 8, e66146.

641 Marschner, P., Kandeler, E., Marschner, B., 2003. Structure and function of the soil microbial
642 community in a long-term fertilizer experiment. *Soil Biol. Biochem.* 35, 453-461.

643 Marstorp, H., Guan, X., Gong, P., 2000. Relationship between dsDNA, chloroform labile C
644 and ergosterol in soils of different organic matter contents and pH. *Soil Biol. Biochem.* 32,
645 879-882.

646 Pajares, S., Bohannan, B.J., 2016. Ecology of nitrogen fixing, nitrifying, and denitrifying
647 microorganisms in tropical forest soils. *Front. Microbiol.* 7, 1045.

648 Pérez-Piqueres, A., Edel-Hermann, V., Alabouvette, C., Steinberg, C., 2006. Response of soil
649 microbial communities to compost amendments. *Soil Biol. Biochem.* 38, 460-470.

650 Pezzolla, D., Marconi, G., Turchetti, B., Zadra, C., Agnelli, A., Veronesi, F., Onofri, A.,
651 Benucci, G.M.N., Buzzini, P., Albertini, E., Gigliotti, G., 2015. Influence of exogenous
652 organic matter on prokaryotic and eukaryotic microbiota in an agricultural soil. A
653 multidisciplinary approach. *Soil Biol. Biochem.* 82, 9-20.

654 Pezzolla, D., Said-Pullicino, D., Raggi, L., Albertini, E., Gigliotti, G., 2013. Short-term
655 variations in labile organic C and microbial biomass activity and structure after organic
656 amendment of arable soils. *Soil Sci.* 178, 474-485.

657 Procter, A.C., Ellis, J.C., Fay, P.A., Polley, H.W., Jackson, R.B., 2014. Fungal Community
658 Responses to Past and Future Atmospheric CO₂ Differ by Soil Type. *Appl Environ Microbiol.*
659 80, 7364-7377.

660 Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., Peplies, J., Glöckner,
661 F.O., 2012. The SILVA ribosomal RNA gene database project: improved data processing and
662 web-based tools. *Nucleic Acids Res.* 41, D590-D596.

663 Ranjard, L., Lejon, D.P., Mougél, C., Schehrer, L., Merdinoglu, D., Chaussod, R., 2003.
664 Sampling strategy in molecular microbial ecology: influence of soil sample size on DNA
665 fingerprinting analysis of fungal and bacterial communities. *Environ. Microbiol.* 5, 1111-1120.
666 Ros, M., Pascual, J.A., Garcia, C., Hernandez, M.T., Insam, H., 2006. Hydrolase activities,
667 microbial biomass and bacterial community in a soil after long-term amendment with
668 different composts. *Soil Biol. Biochem.* 38, 3443-3452.
669 Sadet-Bourgeteau, S., Houot, S., Dequiedt, S., Nowak, V., Tardy, V., Terrat, S., Montenach,
670 D., Mercier, V., Karimi, B., Chemidlin Prévost-Bouré, N., Maron, P.A., 2018. Lasting effect
671 of repeated application of organic waste products on microbial communities in arable soils.
672 *Appl Soil Ecol.* 125, 278-287.
673 Saison, C., Degrange, V., Oliver, R., Millard, P., Commeaux, C., Montange, D., Le Roux, X.,
674 2006. Alteration and resilience of the soil microbial community following compost
675 amendment: effects of compost level and compost-borne microbial community. *Environ.*
676 *Microbiol.* 8, 247-257.
677 Shah, A., Lamers, M., Streck, T., 2016. N₂O and CO₂ emissions from South German arable
678 soil after amendment of manures and composts. *Environmental Earth Sciences.* 75, 427.
679 Šimek, M., Cooper, J., 2002. The influence of soil pH on denitrification: progress towards the
680 understanding of this interaction over the last 50 years. *Eur. J. Soil Sci.* 53, 345-354.
681 Tardy, V., Mathieu, O., Lévêque, J., Terrat, S., Chabbi, A., Lemanceau, P., Ranjard, L.,
682 Maron, P.-A., 2014. Stability of soil microbial structure and activity depends on microbial
683 diversity. *Env. Microbiol. Rep.* 6, 173-183.
684 Terrat, S., Christen, R., Dequiedt, S., Lelièvre, M., Nowak, V., Regnier, T., Bachar, D.,
685 Plassart, P., Wincker, P., Jolivet, C., Bispo, A., Lemanceau, P., Maron, P.A., Mougél, C.,
686 Ranjard, L., 2012. Molecular biomass and MetaTaxogenomic assessment of soil microbial
687 communities as influenced by soil DNA extraction procedure : Soil DNA extraction impact
688 on bacterial diversity. *Microb Biotechnol.* 5, 135-141.

689 Thomas, K.C., Hynes, S.H., Ingledew, W.M., 1994. Effects of particulate materials and
690 osmoprotectants on very-high-gravity ethanolic fermentation by *Saccharomyces cerevisiae*.
691 *Appl Environ Microbiol.* 60, 1519-1524.

692 Thomson, B.C., Tisserant, E., Plassart, P., Uroz, S., Griffiths, R.I., Hannula, S.E., Buée, M.,
693 Mougel, C., Ranjard, L., Van Veen, J.A., Martin, F., Bailey, M.J., Lemanceau, P., 2015. Soil
694 conditions and land use intensification effects on soil microbial communities across a range of
695 European field sites. *Soil Biol. Biochem.* 88, 403-413.

696 Wagg, C., Bender, S.F., Widmer, F., van der Heijden, M.G., 2014. Soil biodiversity and soil
697 community composition determine ecosystem multifunctionality. *PNAS.* 111, 5266-5270.

698 Weber, C.F., Vilgalys, R., Kuske, C.R., 2013. Changes in Fungal Community Composition in
699 Response to Elevated Atmospheric CO₂ and Nitrogen Fertilization Varies with Soil Horizon.
700 *Front. Microbiol.* 4, 78.

701 Werling, B.P., Dickson, T.L., Isaacs, R., Gaines, H., Gratton, C., Gross, K.L., Liere, H.,
702 Malmstrom, C.M., Meehan, T.D., Ruan, L., 2014. Perennial grasslands enhance biodiversity
703 and multiple ecosystem services in bioenergy landscapes. *PNAS.* 111, 1652-1657.

704 Zhang, W., Parker, K.M., Luo, Y., Wan, S., Wallace, L.L., Hu, S., 2005. Soil microbial
705 responses to experimental warming and clipping in a tallgrass prairie. *Glob Chang Biol.* 11,
706 266-277.

707 Zogg, G.P., Zak, D.R., Ringelberg, D.B., White, D.C., MacDonald, N.W., Pregitzer, K.S.,
708 1997. Compositional and Functional Shifts in Microbial Communities Due to Soil Warming.
709 *Soil Sci Soc Am J.* 61, 475-481.

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