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1 **Changes in soil organic matter and microbial communities after fine and coarse residues**  
2 **inputs from Mediterranean tree species**

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15 **Abstract**

16 Trees residues decomposition is a key step in forested ecosystems. In the context of  
17 sclerophyllous Mediterranean forests, the effects of residue quality on soil organic matter and  
18 microbial communities is still poorly documented. Using a mesocosm experiment, we  
19 explored microbial responses (enzyme activities, basal respiration, molecular fingerprints and  
20 catabolic profiles) and variations in soil chemical properties (pH, CaCO<sub>3</sub>, organic C and N  
21 contents, quality of soil organic matter *via* <sup>13</sup>C CP/MAS NMR) induced by coarse woody  
22 debris (W) or fine residues (i.e. twigs -leaves/needles, hereafter TL) from mono-specific or  
23 mixed stands of *Pinus halepensis* and *Quercus ilex*, *P. sylvestris* and *Q. pubescens*. After a  
24 nineteen-month incubation period, we found that the origin of residues (*Pinus spp.* stand,  
25 *Quercus spp.* stand or mixed stand) shaped the genetic structure of both fungal and bacterial  
26 communities. TL inputs led to higher soil N content and increased enzyme activities and  
27 bacterial biomass. Aromatic compounds and C to N ratio increased with W inputs, strongly  
28 shaped fungal communities and increased tyrosinase activity. Thus, the type of residue and  
29 the tree species identity (*Quercus spp* vs *Pinus spp*) appeared to modulate the balance  
30 between fungal and bacterial biomass and soil microbial diversity. Our results revealed that  
31 logging residues management, by modulating the type of residues remaining on forest floor,  
32 could have significant impacts on soil functioning by modifying both chemical properties  
33 (e.g. soil C/N ratio) and microbial structure and functions. These findings need to be  
34 supported by *in natura* studies since deciphering such mechanisms controlling C fluxes in  
35 forest soils has important consequences under the context of climate change.

36 **Keywords:** Logging residues; Mediterranean forests; microbial communities; mesocosm; soil  
37 organic matter.

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## 39 1. Introduction

40 Forest soils are important carbon (C) sinks: more than 70% of forest organic C is stored in  
41 soils and forested ecosystems store more than 80% of the terrestrial C (Lal, 2005). Forest  
42 adaptation and mitigation have been addressed in the scientific agenda as two important  
43 measures to cope with climate change effects. Forest managers are now facing the need to  
44 assess the role of silvicultural practices in this context. Forest type and associated  
45 management regimes are known to have an effect on the quantity of C that can be  
46 sequestered (Noormets et al., 2015). Mediterranean forests, which contribute strongly to  
47 global C sink (Allard et al., 2008), own distinct characteristics resulting from climate, fire  
48 frequency and forest management practices that largely affect the quality and quantity of plant  
49 C inputs (Muñoz-Rojas et al., 2015) with potential consequences on soil C storage.

50 Soil C stocks in forests largely result from a dynamic balance between plant inputs,  
51 transformation and stabilization of organic matter by soil microorganisms and loss of carbon  
52 by respiration (e.g. Batjes, 1996; Jandl et al., 2007; Jobbágy and Jackson, 2000; Six et al.,  
53 2002). Soil microorganisms thus play a fundamental role in forest soil C dynamics. Studies  
54 regarding organic matter (OM) decomposition have highlighted that fungi drive chemical  
55 changes occurring at the early stage of decomposition due to their ability to colonise plant  
56 residues *via* hyphae and to extensively produce extracellular ligninolytic enzymes. Bacterial  
57 communities appear to be important later in the oxidation of smaller molecules (Bani et al.,  
58 2018; Tláskal et al., 2016). Light is partly shed on mechanisms governing transformation,  
59 stabilization and mineralization of OM by microorganisms and the major role of OM quality  
60 on resulting C dynamics has been pointed out.

61 In Mediterranean ecosystems, the chemical composition of plant material is driven by  
62 strategies of resistance to climate stress (heat waves and drought events) including thick foliar  
63 cuticle, increased concentrations in tannins and emission of VOCs (Genard-Zielinski et al.,

64 2018; Vicente et al., 2018). Differences in organic matter content have been observed  
65 between Mediterranean tree species (resinous, evergreen and deciduous species), particularly  
66 in terms of nitrogen content, recalcitrant and allelopathic compounds. Salamanca et al. (1998)  
67 found that nutrient mobility differed between litters from either *Quercus spp.* and *Pinus spp.*  
68 This is supported by the study of Schwendener et al. (2005), who indicated that N release and  
69 transfer to soil strongly depend on the quality of leaves and that lignin proportion is a good  
70 predictor of decomposition in litters. Understanding the mechanisms of OM decomposition in  
71 Mediterranean forests is also complicated by the potential non-additivity effects of mixing  
72 litter from various tree species (Brunel et al., 2017). For instance, Versini et al. (2016)  
73 demonstrated that litter mixtures including several species are decomposed at different rates  
74 from what is expected from the dynamics of each species separately.

75 Forest management strategies further impact the type and quality of plant residues  
76 remaining on the floor after forest operations. In particular, leaf or wood residues can impact  
77 soil C dynamics since coarse wood (hereafter W) or fine residues (i.e. twigs and  
78 leaves/needles, hereafter TL) differ both physically and chemically. Higher proportions of  
79 minerals, which are known to increase OM turn-over (Freschet et al., 2013), are found in  
80 leaves, needles and twigs than in coarse wood (Ma et al., 2014). Conversely, tree organs with  
81 high contents in recalcitrant C (e.g. lignin) such as trunk and branches, are known to decay  
82 slowly (Berg and McClaugherty, 2014; Cornwell et al., 2008). However, dead coarse wood  
83 play vital roles in forest ecosystems by regulating soil temperature and water content, leading  
84 to more favorable habitats for microorganisms (Kwak et al., 2015).

85 While the interactions among microbial communities and chemical composition of fine  
86 and coarse residues have largely been studied in boreal and temperate forests (Bani et al.,  
87 2018), they remain elusive in the Mediterranean context, limiting our understanding of  
88 consequences of logging residues management on soil C dynamics in such ecosystem. Here,

89 we set up a laboratory experiment to determine how the quality of different inputs (i.e. W or  
90 TL) from four Mediterranean tree species affects OM decomposition in forest soils. We  
91 assumed i) that inputs of either coarse or fine residues would distinctively shape microbial  
92 community structures and functioning and result in different C dynamics, ii) that the relative  
93 effect of both type of residues will vary depending on fungal and bacterial communities and  
94 iii) that these modifications would also rely on the chemical prints of tree-species  
95 (broadleaves, evergreens or conifers) in admixture or not, which would indicate that the  
96 impact of litter quality on soil functioning vary depending on the forest stand of typical  
97 Mediterranean species. Mesocosms were set up with soils from mono-specific and mixed  
98 stands of *Pinus halepensis* and *Quercus ilex* on one hand and of *P. sylvestris* and *Q.*  
99 *pubescens* on the other hand and incubated for 19 months with different types of plant  
100 residues to test their influence on soil chemical and microbial properties.

## 101 **2. Material and methods**

### 102 *2.1 Soil sampling*

103 Forest soil sampling was conducted in spring 2013 in South-Eastern France (Provence-  
104 Alpes Côte d'Azur), an area characterized by frequent and intense droughts and heat waves  
105 typical of the Mediterranean climate. Mean annual temperature and mean annual precipitation  
106 characterizing the region are respectively 11.3°C and 799mm (worldclim data). We focused on  
107 the most represented forest stands of the two bioclimatic areas (meso-Mediterranean and supra-  
108 Mediterranean areas) found in this region: monospecific and mixed stands (60/40) of *Pinus*  
109 *halepensis* / *Quercus ilex*, and *Pinus sylvestris* / *Quercus pubescens*, respectively (*Qi*, *Ph*, *Qi-Ph*,  
110 *Qp*, *Ps*, *Qp-Ps*). We selected 3 plots (20m x 20m) for each of the six forest stands (18 plots)  
111 with similar management (60 ± 10 years-old, no harvest/clear cutting since 35 years), and soil  
112 carbonate pedofeatures. To avoid the “home-field” advantage (Ayres et al., 2009; Chomel et  
113 al., 2015), soils used for mesocosms were collected from the 0-to-10-cm layer of the eighteen

114 natural forests from which the plant materials were collected. In each of the eighteen forest  
115 plots, we sampled ten subsamples of A horizon soils (0-10 cm) which were pooled and sieved  
116 (4 mm mesh) to set up mesocosms. The chemical characteristics of soils (calcaric Cambisol,  
117 Blum et al., 2018) are given in Table 1. Two physico-chemical characteristics of soils varied  
118 with forest stand: alkyl C contents of soils from *Pinus halepensis* stands were lower than  
119 those from mixed *P. halepensis* and *Q. ilex* stands ( $21.0 \pm 0.1$  vs.  $26.5 \pm 0.7$  respectively,  $F=4.6$   
120  $p=0.01$ ) and pH was more acid ( $pH = 5.20 \pm 0.79$ ,  $F=8.47$ ,  $p<0.005$ ) in soil from *Q. pubescens*  
121 stands than pH from other soils (pH around 7).

## 122 2.2 Experimental set up

123 Mesocosms were prepared by weighing 700 g (dry mass equivalent) of 4 mm-sieved  
124 soil in pots of 15 cm mean diameter and 20 cm in depth. Plant materials were collected from  
125 *Pinus halepensis* (*Ph*), *Quercus ilex* (*Qi*), *Pinus sylvestris* (*Ps*) and *Quercus pubescens* (*Qp*).  
126 Coarse branches (4 to 10 cm diameter) were separated from twigs (<0.5 cm diameter)  
127 supporting leaves/needles. After 3 weeks of drying at ambient temperature, each type of  
128 residues was crushed and sieved at 2 cm to increase their decomposability and mimic residues  
129 from forest harvesting operations. To test the influence of different residues (W and TL), each  
130 soil was amended with the species-specific residues that corresponded to its stand of origin.  
131 Mesocosms without residues were used as controls. Dried residue samples were analysed for  
132 total carbon content to homogenise carbon input in each soil i.e. 35 g C.kg<sup>-1</sup> soil DW  
133 (Hakkila, 1991; Thiffault et al., 2011; Wall, 2008). Since a higher decomposition was  
134 expected when residues are incorporated to soil (Nicolardot et al., 2007), we mixed plant  
135 material with the top part of soils (0-10cm). The 54 mesocosms were then incubated for 19  
136 months from March 2013 to October 2014 at room temperature (oscillation from 27°C in  
137 summer to 17°C in winter). Mesocosms were watered twice a week to maintain constant soil  
138 humidity to 60% of the water holding capacities. The water holding capacity of soils was

139 determined by the amount of water held in the saturated soil sample vs. the dry weight of the  
140 sample. At the end of the incubation, soils were sieved at 2 mm before being analyzed. For  
141 each mesocosm, a sub-sample of each mesocosm was stored at 4°C before microbial activity  
142 measurements, a second one at -20°C for molecular analyses and a third one was dried at  
143 60°C before physico-chemical analyses.

### 144 *2.3 Soil chemical characterization*

145 The pH of soil samples was determined in distilled water and in a KCl solution (2 M)  
146 after a 45 min equilibration. For each soil, total C and N contents were measured using a C/N  
147 elementary analyzer (Flash EA 1112 Thermo Scientific series). Soil carbonate (CaCO<sub>3</sub>) was  
148 quantified by acid dissolution (HCl 4N) followed by the volumetric analysis of the released  
149 carbon dioxide (Chaney et al., 1982). The percentage of carbon in CaCO<sub>3</sub> was calculated as  
150 follows: % C-CaCO<sub>3</sub> = 11.991 / 100 x % CaCO<sub>3</sub>. Then organic carbon was calculated as the  
151 difference between total C content and carbonate C content. The OM was characterized with  
152 solid-state <sup>13</sup>C NMR spectroscopy using cross-polarization and magic angle spinning (CP-  
153 MAS <sup>13</sup>CNMR). This method enables the linkages between emitted spectra and the structure  
154 of C compounds and their relative quantity. The solid state <sup>13</sup>C NMR spectra were obtained  
155 on a Bruker Avance 400MHz NMR spectrometer operating at a <sup>13</sup>C resonance frequency of  
156 106 MHz and a Bruker double-bearing probe. 80 mg of dry ground soil was placed in a  
157 zirconium dioxide rotor of 4 mm outer diameter and spun at a magic angle spinning (MAS)  
158 rate of 10 kHz. The cross-polarization (CP) technique (Schaefer and Stejskal, 1976) was  
159 applied with a ramped 1H-pulse starting at 100% power and decreasing to 50% during the  
160 contact time (i.e. 2 ms) to avoid Hartmanne Hahn mismatches (Cook et al., 1996; Peersen et  
161 al., 1993). To improve the resolution, a dipolar decoupling GT8 pulse sequence (Gerbaud et  
162 al., 2003) was applied during the acquisition time. To obtain a good signal-to-noise ratio in  
163 the <sup>13</sup>C CPMAS experiment, 12 000 scans were accumulated using a delay of 2.5 s. The <sup>13</sup>C



164 chemical shifts were referenced to tetramethylsilane (at 0 ppm) and calibrated with a glycine  
165 carboxyl signal set at 176.5 ppm. Each spectrum was integrated using Dmfit software  
166 (Massiot et al., 2002) to determine the relative intensity of each chemical region. The relative  
167 distribution of carbon groups in different structures was determined by integrating the signal  
168 intensities over defined chemical shift windows. The <sup>13</sup>C CP/MAS NMR spectra were divided  
169 according to Mathers and Xu (2003) into 4 regions: alkyl-C (0-45 ppm), O-alkyl-C (45-112  
170 ppm), aromatic-C (112-160 ppm) and carboxyl-C (160-185 ppm). To describe organic matter  
171 quality, the following ratios of humification (HR<sub>1</sub> and 2) and aromaticity ratio (AR) were  
172 calculated according to Baldock and Preston (1995): AR= aromatic C/ (alkyl C+ O-alkyl C+  
173 aromatic C), HR<sub>1</sub>=alkyl C/ carboxyl C and HR<sub>2</sub>= alkyl C/ O-alkyl C.

#### 174 *2.4 Soil microbial activities*

175 Catabolic-level physiological profiles (CLPP) were analysed using BIOLOG®  
176 Ecoplates (BIOLOG Inc., Hayward, CA) using a procedure adapted from Garland and Mills  
177 (1991). Briefly, the bacterial suspension was prepared by homogenizing 5 g (dry weight  
178 equivalent) of soil with 100 ml of sterile 0.1% sodium pyrophosphate (pH 7.0). This  
179 suspension was agitated 2 hours on a rotary shaker (80rpm) and centrifuged 6 min at 500g. A  
180 1/50 dilution (in 0.85% NaCl) was used to inoculate the plates (150 µl per well). Plates were  
181 incubated for up to 5 days at 25°C and the absorbance was measured twice a day (Infinite  
182 Tecan) at 590 nm. The average well colour development (AWCD) of each internal replicate  
183 block of 31 wells in each plate was calculated at each reading to determine the incubation  
184 time corresponding to AWCD = 0.3. The absorbance value at t<sub>0.3</sub> in each well was then  
185 normalized. To assess microbial catabolic diversity and evenness, a Shannon (H') and  
186 Simpson (D) diversity indexes were calculated as follow:  $H' = - \sum p_i (\ln * p_i)$  and  $D = 1 / \sum p_i^2$   
187 where p<sub>i</sub> is the ratio of the OD on each substrate (OD<sub>i</sub>) to the sum of OD on all substrates  
188  $\sum OD$ .

189           Microbial biomass (MB) was estimated using Substrate-Induced Respiration (SIR). 10  
190 g (dry weight equivalent) of standardized samples at 60% of WHC were placed in 117 ml  
191 flushed-air glass jars and amended with a powder of talc and glucose (1000  $\mu\text{g C g}^{-1}$  soil).  
192 After ninety minutes, 1 ml of air was sampled with a syringe and injected into a gas  
193 chromatograph (Chrompack CHROM 3 – CP 9001) to determine  $\text{CO}_2$  production. The gas  
194 chromatograph was equipped with a thermal conductivity detector and a packed column  
195 (Porapak). The carrier gas helium flow was regulated at 60  $\text{ml h}^{-1}$ .  $\text{CO}_2$  concentration of  
196 flushed air was subtracted from the  $\text{CO}_2$  concentration of each sample and resulting values  
197 were adjusted to 22°C according to Ideal Gas Laws using  $Q_{10} = 2$ . SIR rates were converted  
198 into MB using equations given by Beare et al., (1990). Basal respiration was estimated using  
199 the same method to calculate the metabolic quotient  $q\text{CO}_2$  (the ratio of basal respiration to  
200 microbial biomass), which is a sensitive ecophysiological indicator of soil stress induced by  
201 environmental conditions (Anderson, 2003).

202           To determine the catabolic potential of microbial communities, four extracellular  
203 enzyme activities (EEA) involved in soil organic carbon and nitrogen cycles were assessed:  
204 tyrosinase, cellulase, urease and protease activities. Enzyme activities were expressed as  
205  $\mu\text{moles}$  of reaction products released per minute (U) per gram of dry soil ( $\text{U g}^{-1}$  DS). All the  
206 experiments were performed in triplicate for each soil sample. Tyrosinase activity was  
207 assessed according to the modified method of Saiya-Cork et al. (2002). 2 ml of 25 mM L-  
208 DOPA solution (L-3,4-dihydroxyphenylalanine) in potassium phosphate buffer (50 mM, pH  
209 6.5) were added to 0.4 g of soil (fresh weight), mixed and incubated for 30 min, in darkness at  
210 25°C. The mixture was centrifuged for 3 minutes at 12 000 g before absorption was measured  
211 at 590 nm. Cellulase activity was assayed using CarboxyMethylCellulose (CMC) 1% in 2 mL  
212 of sodium acetate buffer (50 mM, pH 6) added to 0.5 g of soil (fresh weight) incubated for 4 h  
213 at 50°C. Glucose was quantified according to the Somogyi-Nelson method and absorption

214 was read at 870 nm (Farnet et al., 2010). Protease activity was measured using 5 g of soil  
215 (fresh weight) in 5 mL of casein at 2% in TrisHCl buffer (50 mM, pH 8.1). The mixture was  
216 incubated for 3 hours at 50°C and then the reaction was stopped with 5 mL of Trichloroacetic  
217 acid solution (at 15%) and the mixture centrifuged (2min, 12 000g). Aromatic amino acids  
218 were detected using Folin reagent (33%) at 700 nm (Ladd and Butler, 1972). Tyrosine was  
219 used as standard. Urease activity was assessed using 0.5 g of soil (fresh weight) in 2mL of  
220 urea solution (80 mM) in a sodium phosphate buffer (50 mM, pH 6). The mixture was  
221 incubated for 2h at 37°C and then centrifuged (2 min, 12 000 g). Ammonium was revealed in  
222 microplates using an adapted Mulvaney method (1996): 15µL of EDTA solution, 60 µL of  
223 Na-salicylate solution and 30 µL of hypochlorite solution were added to 30 µL of the  
224 supernatant. After 45 min, mixture absorption was measured at 667 nm.

## 225 *2.5 Fungal and bacterial abundances*

226 To further describe fungal and bacterial communities, DNA was extracted from 0.25 g  
227 of frozen sample, using the PowerSoil DNA Isolation Kit (MoBio, USA) according to the  
228 manufacturer's instructions. The quality of DNA extractions was checked by electrophoresis  
229 on 1% agarose gels stained with GelRed (Molecular Probes, USA) using a Gel Doc image  
230 analyser (BioRad,USA). The DNA concentration was quantified using Quant-iT™ dsDNA  
231 High-Sensitivity Assay Kit (Invitrogen, Canada). All DNA extracts were then diluted to 0.5  
232 ng mL for subsequent analysis. Copy numbers of bacterial and fungal small subunit ribosomal  
233 genes were assessed by quantitative PCR (qPCR) with a StepOne™ Real-time PCR (Applied  
234 BioSystem, USA) targeting the 16S rRNA gene for bacteria and the internal transcribed  
235 spacer (ITS) gene for fungi. The primers used in the amplifications were 341F 5'-  
236 CCTACGGGAGGCAGCAG-3' and 534R 5'-ATTACCGCGGCTGCTGGCA-3' in the  
237 bacterial assay, and ITS3 5'-GCATCGATGAAGAACGCAGC-3' and ITS4 5'-  
238 TCCTCCGCTTATTGATATGC-3' in the fungal assay. The qPCR have been performed as

239 described in (Changey et al., 2018). The results were analyzed using StepOne V 2.2.2  
240 software.

## 241 *2.6 Bacterial and fungal community structures*

242 The effect of the different residues on the structure of bacterial and fungal  
243 communities were analysed using a terminal restriction fragment length polymorphism (T-  
244 RFLP) and automated ribosomal intergenic spacer analysis (ARISA), respectively, as  
245 described in Moni et al. (2015). Bacterial 16S rRNA gene was amplified using primers 63F  
246 (5'-CAGGCCTAACACATGCAAGTC-3') fluorescently labelled at the 5' end with FAM dye  
247 and 1389R (5'-ACGGGCGGTGTGTACAAG-3') (Marchesi et al., 1998). Fungal internal  
248 transcribed spacers (ITS) were amplified using primers ITS1F (5'-  
249 CTTGGTCATTTAGAGGAAGTAA-3') (Gardes and Bruns, 1993) fluorescently labelled at  
250 the 5' end with Yakima Yellow® dye and ITS4 (5'-TCCTCCGCTTATTGATATGC-3').  
251 PCR were performed using Biorad T100 thermal cycler, with 2 µL of diluted DNA template  
252 (0,5 ng.µL<sup>-1</sup>) in a total volume of 15 µL (Master Mix Kit, Qiagen) and 0.05 mM of each  
253 primer. Amplification, quality check and sequencing processes were performed according to  
254 Moni et al., 2015. Fragments and amplicons were binned with 0.5bp interval and only peaks  
255 height  $\geq$  50 fluorescence units were considered in the analysis. Fragments between 50 and 500  
256 bp and amplicons between 500 and 800 bp were included in T-RFLP and for ARISA analysis,  
257 respectively. As measures of alpha diversity, we calculated the OTU richness and the  
258 Shannon index, H'(Shannon, 1948).

## 259 *2.7 Statistical analyses*

260 Statistical analyses were performed with R version 3.0.0 (R Development Core Team,  
261 2007). The statistical significance of the forest stand influences on the initial soil properties  
262 was determined by one-way analysis of variance (ANOVA) and the Tukey HSD test was used  
263 to distinguish significant differences between treatments. When the dataset remains non-

264 parametric after transformations, the GLM test with the appropriate model and link function  
265 was used to compare data between treatments, i.e. stands of origin and residues' types  
266 (Crawley, 2012). Residue quality was described by principal component analysis (PCA). PCA  
267 was performed on a covariance matrix to observe the variations induced by the organ (wood  
268 or twigs/leaves) and stand origin of each residue, and the proportion of variance explained by  
269 each principal component was calculated (Factominer package, Lê et al., 2008). For microbial  
270 genetic fingerprinting, between class analysis (ade4 package, Dray and Dufour, 2007) were  
271 performed on PCA using each tree residues as data matrix and stand origin as class. The  
272 differences among stand origin were tested using the Monte Carlo Permutation Test. The  
273 similarity of Euclidian distances matrices obtained with or without organic input was  
274 determined using a Mantel test performed on  $10^5$  permutations.

275         Differences in organic matter quality and in microbial parameters induced by the types  
276 of residues were observed by comparing differences between each mesocosm and their  
277 control (without residues) after 19 months. Values of chemical markers obtained from  
278 amended soils were subtracted to the corresponding control to find out variations in OM  
279 quality and quantity potentially induced by the residue inputs. Variations were tested using a  
280 t-test. Analyses of variance were also performed to determine effects of the types (W or TL),  
281 the stand origin ( $Q_i$ ,  $Ph$ ,  $Q_i-Ph$ ,  $Q_p$ ,  $Ps$ ,  $Q_p-Ps$ ) of residues and of their interaction. Post-hoc  
282 tests were realised to identify such differences.

283         We used a non-parametric method of multivariate analysis of variance based on  
284 pairwise distances (PERMANOVA) to detect influence of the type and the stand origin of  
285 residues on the CLPPs, EEAs and genetic composition of fungal and bacterial communities.  
286 Then differences induced by the stand origin or type of residues were determined as described  
287 above using two-way analyses of variance. The importance of the OM quality of residues  
288 (organic C, carboxyl C, alkyl C, O-alkyl C, aromatic C, pH, and total N and the ratio AR,

289 HR1, HR2 and the C to N ratio) in determining CLPP, EEAs patterns, bacterial and fungal  
290 composition of soils was evaluated by variation partitioning using db-RDA on Bray-Curtis  
291 distance matrices (Vegan package, Dixon, 2003). The significance of explanations was  
292 determined by ANOVA of the partial RDA test using 999 permutations. Then, relationships  
293 between soil microbial and chemical variables were analyzed by Pearson linear regression  
294 models and reported when significant ( $P < 0.05$  and  $r > |0.4|$ ).

295

### 296 3. Results

#### 297 3.1 Effect of plant residues addition on soil organic matter

298 Differences in the chemical patterns of plant residues were described depending on the  
299 forest stand (*P. halepensis*, *Q. ilex*, *P.halepensis/Q. ilex*, *P. sylvestris*, *Q. pubescens*,  
300 *P.sylvestris/Q. pubescens*) and the type of residues (i.e. wood vs twigs and leaves/needles).  
301 Figure 1 A and B shows a factorial map from PCA based on the first two axes that accounted  
302 for 87.96% of variance. Residues composed of wood (W) and of twigs and leaves/needles  
303 (TL) were clearly separated on the first axis (51.61%). TL residues were positively correlated  
304 to the C fraction relevant to cutin compounds (i.e. the alkyl C fraction and COOH), HR2  
305 (alkyl-C/O-alkyl-C) and N content, while wood residues were associated to polysaccharide  
306 signal (O-alkyl-C) and C to N ratio. The second axis (36.35%) described differences  
307 associated with the tree species depending on the plant material: few differences were found  
308 for W while discrimination between TL was clearly observed. Total C content and recalcitrant  
309 compounds (aromaticity ratio and alkyl-C/COOH i.e. lipids) were strongly associated to *Pinus*  
310 *spp.* TL and pH was positively correlated to *Quercus spp* TL.

311 Both W and TL inputs indeed induced a significant increase in soil organic C (Fig.  
312 2.A) but both did not result in significant variations in the recalcitrant fraction of OM i.e.  
313 aromatic C (Fig. 2.D). On the other hand, certain soil chemical properties varied depending on

314 W or TL inputs. TL inputs increased soil N content (Fig. 2.B) but did not result in a decreased  
315 C/N ratio (Fig. 2.C). W inputs increased polysaccharide content (O-alkyl C fraction, Fig. 2.E)  
316 and reduced lipid content (alkyl C fraction, Fig. 2.F). Consequently, a decrease in alkyl C to  
317 O-alkyl C ratio was observed in W amended soils, which was not found in TL amended soils  
318 (Fig. 2.G). Thus, TL and W addition resulted in different soil chemical variations compared to  
319 controls: an increase in N availability was found in soils amended with TL, while an increase  
320 in more labile C sources was observed in W amended soils. It has to be noted that W addition  
321 also led to an increase in pH compared to control (Fig. 2.H).

322         Depending on the tree species origin of residues, variations in carboxyl C fraction of  
323 OM (and thus in alkyl C to carboxyl C ratio) was observed: it decreased after addition of  
324 residues from *Qi*, *Ph* and *Qp-Ps* mixture compared to what was observed with *Qp* residues  
325 (Fig. 3.A). Consequently, in soils amended with *Qi*, *Ph* and the *Qp-Ps* mixture, a higher alkyl  
326 C to carboxyl C ratio linked to longer alkyl chains (lipids) were found, while in *Qp* amended  
327 soils, a low alkyl C to carboxyl C ratio indicated the production of short-chain acids  
328 potentially linked to a more intense mineralization (Fig. 3.B). No effect of the interaction  
329 between species origin and type of tree residues was found on soil organic matter  
330 characteristics. This is a result of importance since it shows that the effects of the type of tree  
331 residues on soil chemical properties were not driven by tree species.

### 332 *3.2 Soil microbial abundance, structure and activities*

333         No variation in fungal nor bacterial biomass (assessed via qPCR of ITS or 16S rDNA,  
334 respectively) or in active biomass (*via* substrate-induced respiration) was found after addition  
335 of plant residues whatever their type (W *vs* TL) or origin (tree species), data not shown. On  
336 the other hand, the main factor shaping bacterial and fungal community structures was the  
337 origin of the tree organ as shown by the between class analysis performed using T-RFLP and  
338 ARISA fingerprints (Fig. 4) and the Monte Carlo test (simulated  $P < 0.001$ ). When using T-

339 RFLP subset data separately for control, C, TL and W treatments, the degrees of similarity  
340 (Mantel r coefficients) obtained between treatments C and TL and between treatments C and  
341 W were 0.76 ( $P < 0.001$ ) and 0.71 ( $P < 0.001$ ), respectively. This result indicates that treatments  
342 TL and W induced similar effects on bacterial community structure. When using ARISA  
343 subset data separately for C, TL and W treatments, the degrees of similarity (Mantel r  
344 coefficients) obtained between treatments C and TL and between treatments C and W were  
345 0.49 ( $P < 0.001$ ) and 0.31 ( $P < 0.001$ ), respectively. This result indicates that treatment W  
346 induced a stronger effect on the fungal community structure than treatment TL.

347 We further determined to what extent the type of tree residues, W and TL, influenced  
348 microbial markers using variance partitioning analyses on CLPP, EEAs and the genetic  
349 structure of fungal and bacterial communities (ARISA and T-RFLP respectively). Results  
350 from db-RDA, and their significances (using ANOVA-like permutation test) are shown in  
351 Figure 5 and Table 2 respectively. The amount of variation explained by the type of tree organ  
352 on bacterial properties (both CLPP and T-RFLP) ranged from 24% to 41% for W and from  
353 20% to 34% for TL, but the only significant effect was observed for W residues on CLPP (W  
354 explained 41 % of the variance in CLPP). Variations in fungal community structure were  
355 explained by both W (36%) and TL (34%).

### 356 *3.3 Relationships between soil organic matter properties and microbial communities*

357 To better understand how the type of tree residues in litter modified soil microbial  
358 communities, we determined the Pearson correlation coefficients between microbial markers  
359 and soil physico-chemical properties (Table 3). Most enzyme activities were positively  
360 correlated to organic C and/or total N amount. More particularly N content, which was higher  
361 in TL amended soils (Fig 2.B), was positively correlated with cellulase, protease, and urease  
362 activities, thus enhancing enzymes involved in mineralization of the labile fraction of organic  
363 matter and N cycle. Lignocellulolytic activities (cellulase and tyrosinase) and urease activities



364 were also positively correlated to organic C amount that increased in both W and TL amended  
365 soils (Fig 2.A). Similarly, tyrosinase was also positively correlated to C/N ratio, which was  
366 higher in W and TL amended soils (Fig 2.C).

367 The active microbial biomass (assessed *via* SIR) and the bacterial biomass (determined  
368 *via* the 16S copy numbers) were positively correlated to both organic C and total N contents.  
369 It has to be noted that a significant relationship was found between active microbial biomass  
370 and bacterial biomass ( $r=0.55$ ,  $P<0.001$ , data not shown) and not between active microbial  
371 biomass and fungal biomass, which suggests that fungal communities were weakly involved  
372 in SIR measurement. C/N ratio increased with tyrosinase activities and the Fungi to Bacteria  
373 ratio. This result is corroborated with the correlation linking tyrosinase activities to the fungal  
374 biomass ( $r=0.64$ ,  $p>0.001$ , data not shown). The active microbial biomass was negatively  
375 correlated to pH and a pH increase was found in W amended soils (Fig 2.H): together, such  
376 results suggest that W inputs are likely to down regulate the active microbial biomass (and  
377 thus particularly bacteria).

378 Our results also pointed out that an increase in carboxyl C was associated to a decrease  
379 in catabolic diversity ( $H'$ ) and in the relative fungal biomass (assessed *via* the fungi to  
380 bacteria ratio) but positively associated to fungal richness. We also observed an increase in  
381 fungal diversity associated with the alkyl C fraction of organic matter (OM). Since our  
382 previous results highlighted that modification in the carboxyl C fraction of OM was linked to  
383 tree species origin of residues (more -COOH in *Pinus spp.* residues) and that the alkyl fraction  
384 also differed between soil origin, this result indicates that tree species chemical 'print' could  
385 affect soil processes through both microbial catabolic potential and fungal population shaping.

## 386 4. Discussion

### 387 4.1 Changes in soil chemical characteristics induced by tree residues

388 After a 19 month incubation period, we observed higher C content in soils amended by  
389 both fine (TL) and coarse (W) residues compared to non-amended soils, attesting the  
390 decomposition of residues and transfer of degradation products from plant materials to soil.  
391 Plant residues are obviously supposed to be degraded more slowly *in natura via* litter decay.  
392 In our experiment, we crushed and sieved plant residues before mixing them into the top soil  
393 of mesocosms under controlled humidity over time (60% humidity). We expected this process  
394 to enhance plant decay rate by increasing the surface available for microbial colonization (Ma  
395 et al., 2014) and thus microbial activities. The standardized quantity of C inputs across  
396 treatment can explained similar level of C increase in all amended soils.

397 On the other hand, it is noteworthy that fine and coarse residues led to a different soil  
398 OM quality. After wood addition, higher soil C quality was found as shown by a lower alkyl  
399 C to O-alkyl C ratio, while addition of fine residues did not lead to modification in C quality,  
400 as described by NMR data, but in higher N content. Tree mineral nutrients are known to be  
401 mainly stored in leaves and in smallest twigs (Ma et al, 2014). Higher N content in fine  
402 residues and higher C/N ratio and O-alkyl C in wood residues were found back as a ‘chemical  
403 print’ in soil. OM turnover is known to be strongly regulated by C and N stoichiometry, and  
404 many studies showed that C/N was a strong predictor of decomposition of wood and leaves  
405 (Jackson et al., 2013; Sundqvist et al., 2011). Thus, our study demonstrated that, under our  
406 experimental conditions, coarse or fine residues modified C/N, a major factor regulating  
407 microbial activities and thus OM turnover in soil. The contrasting effects of fine and coarse  
408 residues suggest a major role of such residue as drivers of soil properties (Freschet et al.,  
409 2013). Concerning the aromatic fraction of soils, no variation after residue addition has been  
410 observed and the weak ‘print’ of lignin from plant residues on soil chemical properties is

411 probably linked to a slower degradation of such recalcitrant compounds (Kalbitz et al., 2006).  
412 At the early stage of decomposition, polysaccharides are preferentially used over lignin (Berg  
413 and McClaugherty, 2014).

414 Tree species origin of residues modified alkyl C to carboxyl C ratio which is a  
415 chemical marker of decomposition : a low ratio indicates intense mineralization leading to  
416 short-chain acids (Mourik et al., 1998; Preston et al., 2002). A low ratio was found after  
417 addition of *Q. pubescens* residues only. Thus, *Q. pubescens*, the only deciduous species  
418 considered, produced residues which favored OM turnover compared to the other tree  
419 residues tested. Polyakova and Billor (2007) studied the impact of deciduous tree species on  
420 litter quality and decomposition processes in pine stands and found that deciduous species,  
421 more than evergreen, favored decomposition because of higher mineral content and easily-  
422 degradable OM amount.

423 The type of residues (i.e. wood or twigs with leaves or needles) modified more  
424 strongly soil OM quality than tree species origin. Interestingly, no modification in soil  
425 chemical properties associated to fine or coarse residues depended on the tree species (no  
426 effect of interaction). This result is sustained by the study of Pietsch et al. (2014), who  
427 demonstrated the importance of wood and leaf residue decomposability as ‘after-life’ effects  
428 of plant traits, which could potentially lead to variations in OM turn-over rates. These  
429 observations are substantial since they suggest that the type of residues is likely to modify  
430 differently C and N cycling, and moreover that their impacts on soil chemical properties are  
431 similar whatever the forest stands considered (pure or mixed stands, coniferous, deciduous or  
432 evergreen species).

#### 433 *4.2 Fine and coarse residues shape catabolic and genetic structures of microbial communities*

434 Microbial community fingerprinting (ARISA and T-RLFP) showed that the coarse or  
435 fine residues clearly shaped fungal communities, while it did not significantly explain

436 variations in bacterial community structure. Moreover, the origin of the residues (tree species)  
437 also modified the genetic structure of fungal communities and not that of bacteria. The  
438 particular sensitivity of fungal communities to residues addition is probably associated to the  
439 potential of mycelia to actively colonize plant residues in bulk soil. Mycelium growth rates in  
440 laboratory mesocosm can reach up to 8 mm per day (Donnelly et al., 2004). Thus, fungi are  
441 able to produce propagule networks which ramify at the interface between soil and residues,  
442 making nutrient resources available over wide surfaces (Boddy et al., 2009). Conversely,  
443 bacteria are connected to their immediate surroundings, i.e. micro-niches with soil-pore size  
444 (Vos et al., 2013), with very specific conditions (i.e. pH, conductivity), which differ from the  
445 average properties of their environmental matrix (Urbanová et al., 2011). This lack of  
446 connectivity is probably enhanced in our mesocosms where no mesofauna can favor OM  
447 circulation.

448         While the limitations of BIOLOG methodology for the characterization of whole  
449 communities are well known, CLPP remain useful to analyse the dynamic of copiotrophic  
450 bacteria from the soil (Lladó and Baldrian, 2017). Here, variance in CLPP was significantly  
451 explained by the quality of coarse residues (wood). Fanin et al. (2014) examined the effects of  
452 litter with different chemical prints on CLPP and highlighted that the catabolic potential of  
453 communities was influenced by residue quality and particularly by the C, N, and P  
454 stoichiometry. Higher labile C fraction content (O-alkyl) was found in wood residues, and  
455 thus the availability of labile carbon substrate may have favored fast-growing decomposers  
456 such as copiotrophic bacteria and consequently modified the functional structure of microbial  
457 communities.

#### 458 *4.3 Coarse or fine residues modulate microbial enzymes involved in C and N cycling*

459         The strong correlation observed between N content and urease, protease and cellulase  
460 suggest that nitrogen was the major factor stimulating extracellular enzyme activities involved

461 in mineralization of labile fraction, but did not affect lignin-modifying enzyme (tyrosinase).  
462 Cellulase is secreted by a large number of microorganisms, but only a small number are able  
463 to produce lignin-modifying enzyme (e.g. white-rot basidiomycetes and xylacarious  
464 ascomycetes) (Carreiro et al., 2000). Thus, this difference in enzyme response could be  
465 related to the changes in microbial community structure described above. More precisely, N  
466 content was related to the active microbial biomass, here mainly referring to bacterial  
467 communities. Conversely, fungal communities and their activities seemed favored by high  
468 C/N and more precisely the potential of aromatic compound transformation (tyrosinase) and  
469 the balance between fungal and bacterial biomass. Since C/N was higher in soils amended  
470 with wood than with fine residues, coarse residues may facilitate the settlement of fungal  
471 populations and their lignocellulolytic activities. Moreover, as described by the positive  
472 relation between alkyl C content and fungal diversity, the reduction in alkyl C observed in  
473 wood amended soils may affect fungal equitability by selecting specific taxa. Our results are  
474 supported by the microcosm experiment of Kooijman et al. (2016), who demonstrated, using  
475 selective inhibition of either bacterial or fungal communities, a higher N demand by bacteria  
476 than by fungi. Thus, it is noteworthy that coarse or fine residues modified differently the  
477 structures and functions of bacterial and fungal communities.

478 In their meta-analysis, Chen et al. (2018) showed that soil N addition reduced  
479 phenoloxidase activities and that this N-induced enzyme repression was associated with  
480 increases in soil C. This is consistent with our result as we found that the proportion of N (via  
481 C/N ratio) was negatively associated to lignin-modifying enzyme. Moreover, we found deep  
482 modification in enzyme activities and soil microbial properties (including soil respiration SR,  
483 which represents one of the largest C fluxes from terrestrial ecosystems to the atmosphere)  
484 related to OM quality variation due to the type of residues. Since lignin and cellulose are the  
485 two most abundant organic resources derived from plants, differences induced by the type of

486 residues on C-releasing activities of soil microbes and their C-acquiring enzymes have  
487 potential to deeply modify soil C and N cycling.

## 488 **5. Conclusion**

489 Our study revealed that, under laboratory conditions, coarse or fine residues differently  
490 shaped soil microbial communities. It is noteworthy that in a more natural setting, the material  
491 would fall on the surface of the soil and work its way into the soil over time. Thus, the rate of  
492 OM decomposition and resulting effects on microbial communities and soil C and N cycling  
493 would occur on a longer time step which would differ between residues sizes. However, our  
494 findings remain of importance since we show that the type of residues modulates soil  
495 microbial responses to plant residues, prevailing over the species origin of residues.  
496 Moreover, C/N ratio (characterizing the chemical print of fine inputs) appeared to strongly  
497 control the balance between fungal and bacteria biomass. This is particularly noteworthy since  
498 fungal communities are supposed to be k-strategists which favor humification and soil C  
499 storage. Tree residues can thus be considered as important drivers of soil microbial  
500 functioning and *in natura*, the type and amount of such residues can be modified by  
501 silvicultural practices. This should be considered to enhance carbon sequestration in forest  
502 soils under the context of climate change.

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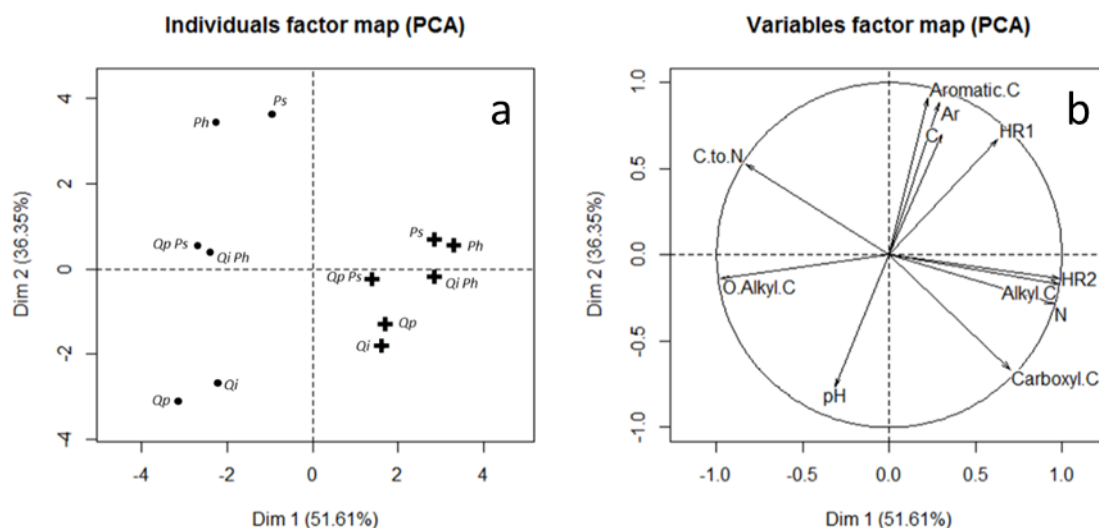
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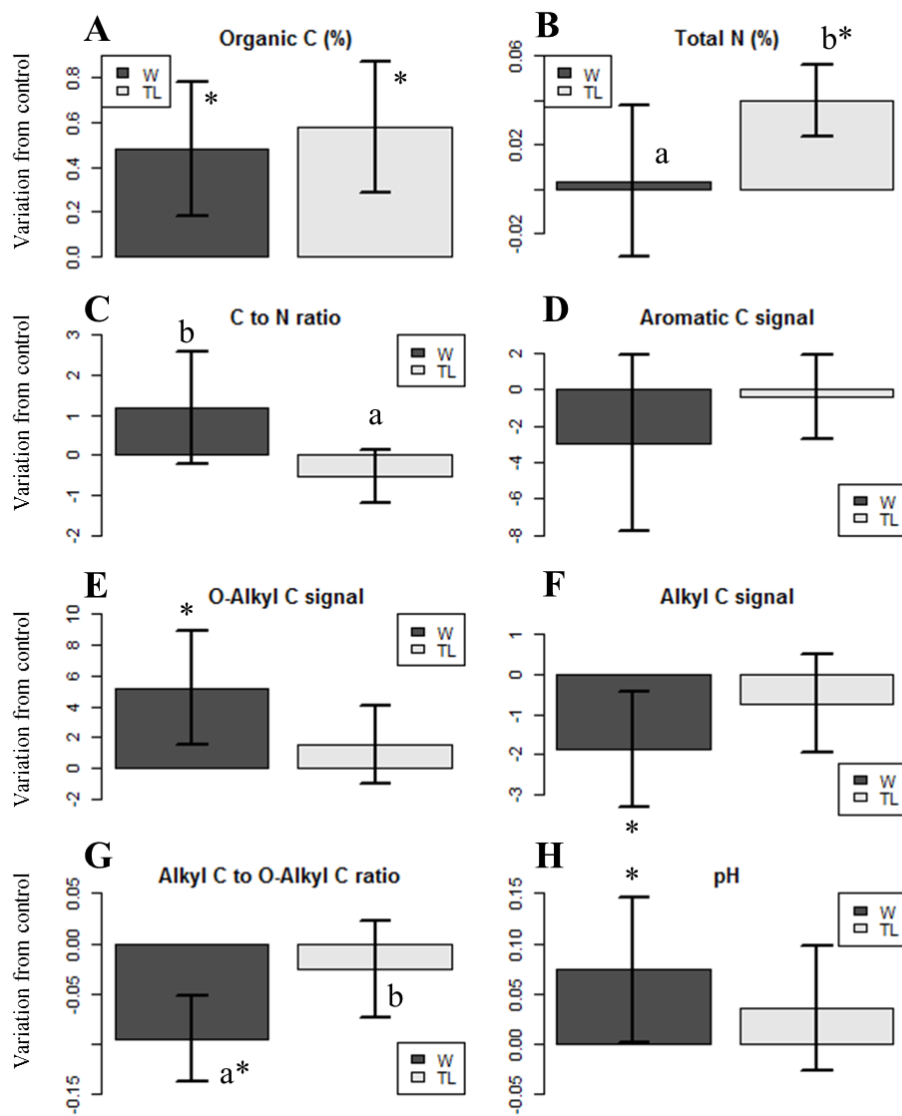
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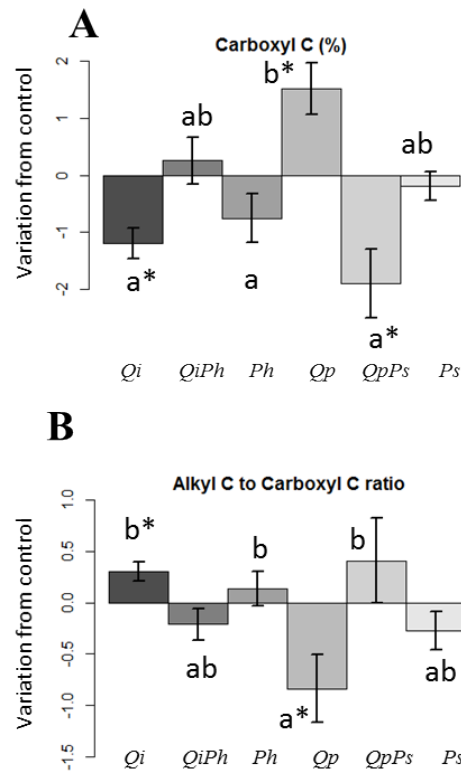
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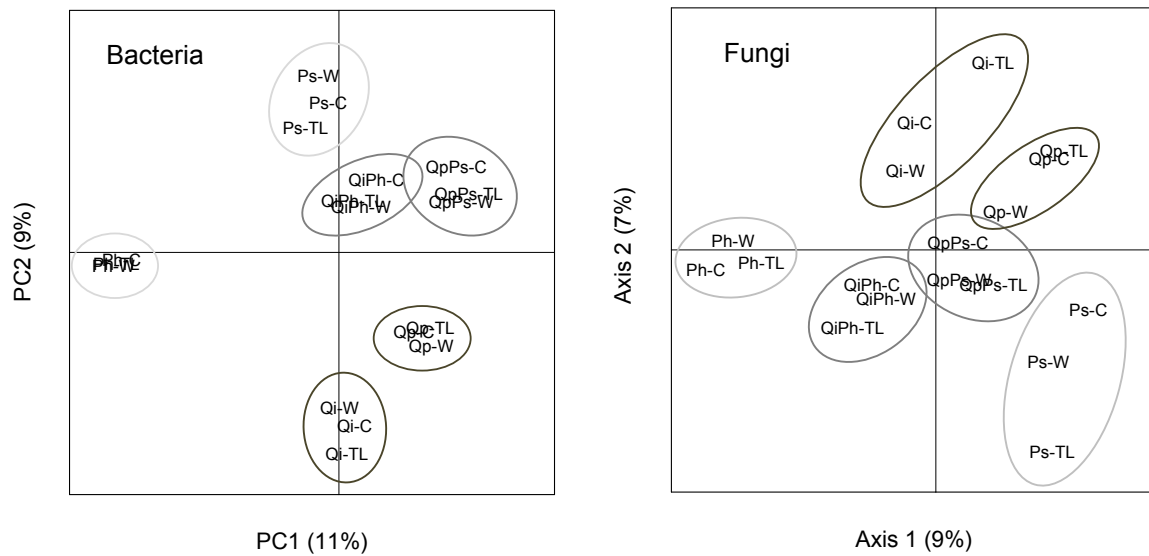
**Figure 1:** Scores (a) and loadings (b) plots of the Principal Component Analysis calculated on the chemical properties of plant residues. Tree-species and the type of input: (+) stands for Twigs and Leaves/needles (TL), and (•) for Wood (W), (*Qi*) *Quercus ilex*. (*Ph*) *Pinus halepensis*. (*Qp*) *Quercus pubescens* and (*Ps*) *Pinus sylvestris*. HR1 stands for Alkyl C to Carboxyl C ratio and HR2 for Alkyl C to O-Alkyl C ratio.



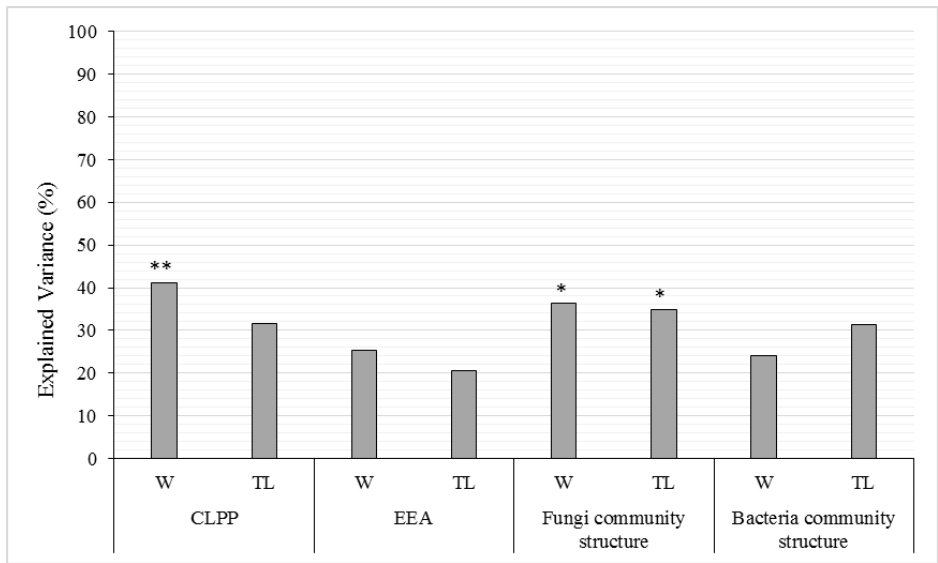
**Figure 2:** Variations in soil OM quality: (A) Organic C (%), (B) Total N %, (C) C to N ratio, (D) Aromatic-C signal, (E) O-alkyl-C signal, (F) Alkyl-C signal, (G) Alkyl-C to O-Alkyl-C ratio, (H) pH after 19-month incubation depending on the different residues (W, wood, TL, Twigs and leaves/needles). Significant differences are indicated by different letters. Differences compared to the control soils are indicated by (\*).



**Figure 3:** Variations in soil OM quality compared to the corresponding control soil, after amendments with debris from: (*Qi*) for *Quercus ilex*, (*Ph*) for *Pinus halepensis*, (*Qp*) for *Quercus pubescens*, (*Ps*) for *Pinus sylvestris*, and (*Qi-Ph*) and (*Qp-Ps*) for their respective mixture. Panel (A) show results for the Carboxyl C fraction, and panel (B) for the Alkyl C to Carboxyl C ratio. Significant differences between amended soils are indicated by different letters. Differences compared to control soils are indicated by (\*).



**Figure 4:** Differences in bacterial (left) and fungal (right) community structure represented by between class analysis (BCA) based on molecular profiling. Soft-grey-lined ellipses represent soils from pine stands (Ps and Ph), intermediate-grey-lined ellipses represent soils from mixed stands (QpPs and QiPh) and dark-grey-lined ellipses represent soil from oak stands (Qp and Qi). Suffix - C, -TL and - W correspond to non-amended samples (Control) or amended with twigs-leaves/needles or coarse wood respectively. Letters represent the barycenter of replicates (n=3) for each treatments. Monte Carlo test revealed significant differences among trees species (simulated  $P < 0.001$ ) for both taxa.



**Figure 5:** Variance partitioning of Catabolic Level Physiological Profile (CLPP), extracellular enzyme activities (EEAs), and fungal and bacterial community structure after addition of twigs-leaves/needles (TL) or coarse wood (W). Significance levels: P,0.05: \*; P,0.01: \*\*.



**Table 1:** Chemical properties (including solid state  $^{13}\text{C}$  NMR data) of soils at T0. Soils used to set up the experiment were collected from different forest stands: *Qi* for *Quercus ilex*, *Ph* for *Pinus halepensis*, *Qp* for *Quercus pubescens* and *Ps* for *Pinus sylvestris*. Values are the mean  $\pm$  standard deviation (n=18). Mean differences between control and amended soils were determined by Tuckey tests. Different letters indicate significant differences (P<0.05).

	<i>Ph</i>	<i>Qi Ph</i>	<i>Qi</i>	<i>Ps</i>	<i>Qp Ps</i>	<i>Qp</i>
<b>Organic C %</b>	4.62 ( $\pm$ 1.14)	6.84 ( $\pm$ 0.59)	9.67 ( $\pm$ 1.03)	8.04 ( $\pm$ 5.47)	7.83 ( $\pm$ 3.88)	5.18 ( $\pm$ 0.70)
<b>Total N %</b>	0.262 ( $\pm$ 0.12)	0.417( $\pm$ 0.10)	0.537 ( $\pm$ 0.12)	0.394 ( $\pm$ 0.26)	0.406 ( $\pm$ 0.24)	0.327 ( $\pm$ 0.05)
<b>C to N ratio</b>	17.4 ( $\pm$ 2.9)	17.1 ( $\pm$ 3.4)	18.9 ( $\pm$ 4.9)	22.7 ( $\pm$ 8.1)	21.1 ( $\pm$ 4.2)	15.8 ( $\pm$ 1.1)
<b>Alkyl C %</b>	21.0 ( $\pm$ 0.1) <sup>a</sup>	26.5 ( $\pm$ 0.7) <sup>b</sup>	23.4 ( $\pm$ 0.7) <sup>ab</sup>	24.0 ( $\pm$ 0.5) <sup>ab</sup>	21.9 ( $\pm$ 1.6) <sup>ab</sup>	24.5 ( $\pm$ 2.9) <sup>ab</sup>
<b>O-Alkyl C %</b>	45.4 ( $\pm$ 5.1)	41.8 ( $\pm$ 4.0)	46.3 ( $\pm$ 1.7)	50.3 ( $\pm$ 0.9)	48.7 ( $\pm$ 2.8)	45.1 ( $\pm$ 1.7)
<b>Carboxyl C %</b>	10.0 ( $\pm$ 2.6)	7.4 ( $\pm$ 1.2)	10.3 ( $\pm$ 1.1)	6.9 ( $\pm$ 0.4)	7.3 ( $\pm$ 1.6)	11.7 ( $\pm$ 3.4)
<b>Aromatic C %</b>	23.4 ( $\pm$ 5.5)	24.1 ( $\pm$ 5.2)	19.8 ( $\pm$ 1.3)	18.7 ( $\pm$ 1.2)	21.8 ( $\pm$ 5.5)	18.6 ( $\pm$ 2.4)
<b>CaCO<sub>3</sub></b>	3.55 ( $\pm$ 1.17)	2.33 ( $\pm$ 1.31)	0.37 ( $\pm$ 0.53)	1.50 ( $\pm$ 1.48)	0.84 ( $\pm$ 1.01)	1.09 ( $\pm$ 1.89)
<b>pH</b>	7.41 ( $\pm$ 0.22) <sup>b</sup>	7.02 ( $\pm$ 0.19) <sup>b</sup>	6.96 ( $\pm$ 0.33) <sup>b</sup>	6.73 ( $\pm$ 0.57) <sup>b</sup>	6.96 ( $\pm$ 0.11) <sup>b</sup>	5.20 ( $\pm$ 0.79) <sup>a</sup>

**Table 2:** Effect of the chemical properties of W and TL residues (considering N, C, C to N ratio, aromatic C, alkyl C O-alkyl C, carboxyl C, Ar, HR1, HR2 and pH) on CLPP, EEA patterns, and bacterial and fungal community structure (finger prints). Significance of the effects were determined by ANOVA on RDA model with (significance levels are indicated as follow: P<0.05: \*; P<0.01: \*\*).

Dataset	CLPP		EEA		Fungal community structure		Bacterial community structure	
	W	TL	W	TL	W	TL	W	TL
<b>% Var</b>	41.06	31.55	25.41	20.52	36.26	34.85	24.06	31.47
<b>F</b>	1.6721	1.1063	0.8174	0.6198	1.3652	1.2884	0.7605	1.1023
<b>P</b>	0.002**	0.37	0.6	0.828	0.019*	0.049 *	0.877	0.338

**Table 3:** Correlation coefficients (r) between soil chemical and microbiological parameters as determined by Pearson's Test. (significance levels are indicated as follow: \*P <0.05. \*\*P <0.01 and \*\*\*P <0.001, n=54).

	Total N (%)	Organic C (%)	C/N	pH H <sub>2</sub> O	Carboxyl C	Alkyl C
Catabolic Diversity (H')	ns	ns	ns	ns	-0.41*	ns
Protease Activity	0.45*	ns	ns	ns	ns	ns
Cellulase Activity	0.47**	0.70***	ns	ns	ns	ns
Urease Activity	0.59***	0.59**	ns	ns	ns	ns
Tyrosinase Activity	ns	0.53**	0.42*	ns	ns	ns
Active Microbial Biomass	0.79***	0.73***	ns	-0.42*	ns	ns
Bacterial Biomass (16S copy number)		0.71***	ns	ns	ns	ns
Fungal Biomass (ITS copy number)	ns	0.66***	ns	ns	ns	ns
Fungi to Bacteria ratio	-0.53**	ns	0.56**	ns	-0.55**	ns
Fungal composition (H')	ns	ns	ns	ns	ns	0.42*
Fungal Richness (number of ITS amplicons)	ns	ns	ns	ns	0.46*	ns
Bacterial composition (H')	ns	ns	ns	ns	ns	ns
Bacterial Richness (number of T-RFs)	ns	ns	ns	ns	ns	ns

## Declaration of interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: