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## Crop Residues in Wheat-Oilseed Rape Rotation System: a Pivotal, Shifting Platform for Microbial Meetings

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1 **Title:** Crop residues in wheat-oilseed rape rotation system: a pivotal, shifting platform for  
2 microbial meetings

3

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13

## 14 **Abstract**

15 Crop residues are a crucial ecological niche with a major biological impact on agricultural  
16 ecosystems. In this study we used a combined diachronic and synchronic field experiment  
17 based on wheat-oilseed rape rotations to test the hypothesis that plant is a structuring factor of  
18 microbial communities in crop residues, and that this effect decreases over time with their  
19 likely progressive degradation and colonization by other microorganisms. We characterized an  
20 entire fungal and bacterial community associated with 150 wheat and oilseed rape residue  
21 samples at a plurennial scale by metabarcoding. The impact of plant species on the residue  
22 microbiota decreased over time and our data revealed turnover, with the replacement of  
23 oligotrophs, often plant-specific genera (such as pathogens) by copiotrophs, belonging to  
24 more generalist genera. Within a single cropping season, the plant-specific genera and species  
25 were gradually replaced by taxa that are likely to originate from the soil. These changes

26 occurred more rapidly for bacteria than for fungi, known to degrade complex compounds.  
27 Overall, our findings suggest that crop residues constitute a key fully-fledged microbial  
28 ecosystem. Taking into account this ecosystem, that has been neglected for too long, is  
29 essential, not only to improve the quantitative management of residues, the presence of which  
30 can be detrimental to crop health, but also to identify groups of beneficial micro-organisms.  
31 Our findings are of particular importance, because the wheat-oilseed rape rotation, in which  
32 no-till practices are frequent, is particularly widespread in the European arable cropping  
33 systems.

#### 34 **Keywords**

35 community succession, microbial diversity, oilseed rape, residue microbiota, wheat

## 36 **Background**

37           Crop residues are an essential living element of agricultural soils. Smil [1] stressed that  
38 they “should be seen not as wastes but as providers of essential environmental services,  
39 assuring the perpetuation of productive agrosystems”. When left in the field in the period  
40 between two successive crops, rather than being buried immediately, crop residues contribute  
41 to the formation of soil organic carbon, improve soil structure, prevent erosion, filter and  
42 retain water, reduce evaporation from the soil surface, and increase the diversity and activity  
43 of micro-organisms in the ground [2]. No-till practices are becoming increasingly widespread,  
44 as they take advantage of these attributes [3]. However, such practices are often considered  
45 likely to increase the risk of disease epidemics [4–6]. Indeed, several leaf-, stem-, head-, and  
46 fruit-infecting micro-organisms, classified as “residue-borne” or “stubble-borne” pathogens,  
47 are dependent on host residues for survival during the period between successive crops and  
48 for the production of inoculum for their next attack [7, 8]. The epidemiological contribution  
49 of residues as an effective source of inoculum is well-established but difficult to quantify [e.g.  
50 9] and generalise, because the nature of survival structures depends on the biology of the  
51 species. The situation is rendered even more complex by the presence of several species  
52 reported to act as crop pathogens in plants as endophytes, without symptom development in  
53 the plant, and in the soil and plant residues as saprophytes. Taking into account the inoculum  
54 from stubble-borne pathogens and possible competition with other micro-organisms, it  
55 appears likely that the expression of a disease is the consequence of an imbalance between a  
56 potentially pathogenic species and the rest of the microbial community, rather than the  
57 consequence of the mere presence of this species [10].

58           Residues constitute a crucial ecological niche, not only for pathogenic species, but also  
59 for non-pathogenic and beneficial species. Residues can be viewed as both a fully-fledged  
60 matrix and a transient compartment, because they originate from the plant (temporal link), are

61 in close contact with the soil (spatial link) and degrade over the following cropping season, at  
62 rates depending on the plant species, the cropping practices used [11], and the year (climate  
63 effect). It remains unknown whether the succession of microbial communities in residues is  
64 driven primarily by plant tissue degradation or edaphic factors [12]. Many studies have  
65 investigated the structure of the microbial communities present during the life cycle of the  
66 plant [e.g. 13–15], but few have investigated the microbiota associated with plant residues.  
67 Several ecological studies have investigated the impact of the residue compartment on the  
68 structure of soil microbial communities [2, 16–19], but not the impact of the soil compartment  
69 on structure of the residue communities. The detritosphere, defined as the part of the soil  
70 attached to residues [12, 20, 21], is the most extensive and broad hotspot of microbial life in  
71 the soil [22]. The residue compartment and the detritosphere are located in close physical  
72 proximity but are considered by microbiologists to be separate trophic and functional niches  
73 [23]. A description of the residue communities and the specific changes in these communities  
74 over time might, therefore, help agronomists to understand the impact of cropping practices  
75 on crop productivity. Fungi and bacteria play important roles in the degradation of plant  
76 tissues in debris (cellulose, hemicellulose, lignin), but the interactions between them within  
77 the microbial community remain unclear, due to the lack of information about their origins  
78 (air-borne, soil-borne or plant-borne), their individual functions and the drivers of community  
79 structure in residues.

80 Crop rotation induces changes in the composition of the soil microbial community and  
81 usually reduces pathogen pressure [e.g. 18]. For instance, wheat yields benefit from “break  
82 crops” such as oilseed rape or other non-host crops to break the life-cycle of wheat-specific  
83 pathogens [24]. We focused here on the wheat-oilseed rape rotation, one of the most widely  
84 used cropping systems in Europe. In 2017, the areas under bread wheat and oilseed rape in  
85 France were 5.0 million ha and 1.4 million ha [25], respectively. As oilseed rape usually

86 recurs every three years in the rotation and is used almost systematically either directly before  
87 or directly after wheat, we estimate that this classical rotation is used on almost 4.2 million ha  
88 every year. Half the area occupied by these two crops is now grown without tillage, with at  
89 least some of the residues of the preceding crop left on the soil [26]. The issue addressed here  
90 is thus directly relevant to more than 2 million ha, or about one tenth of the total arable area in  
91 France.

92 In this study, we deliberately focused on crop residues as a neglected, transient, but  
93 fully-fledged half-plant/half-soil compartment without describing the soil microbial  
94 communities, considering that it has been already performed in several studies [e.g. 27, 28].  
95 We tested the specific hypothesis that plant is a structuring factor of bacterial and fungal  
96 communities in residues, and that this effect decreases over time, as contact with the soil  
97 induce progressive colonization of residues by other microorganisms. Over the last few years,  
98 high-throughput metabarcoding has become an indispensable tool for studying the ecology of  
99 such complex microbial communities [29], partly due to the difficulties in isolating fungal and  
100 bacterial species and growing them in axenic conditions. We used this approach to describe  
101 and compare changes in the microbial community of wheat and oilseed-rape residues left on  
102 the soil surface of three cultivated fields during two cropping seasons. We investigated  
103 whether the three main determinants of the diversity of fungal and bacterial communities -  
104 plant species, cropping season, and cropping system (monoculture vs. rotation, focusing on  
105 wheat residues) - affected the microbiota of crop residues.

106

## 107 **Methods**

### 108 **Experimental design**

109 *Field plots and rotations* – An extensive field experiment based on a wheat (W)-oilseed  
110 rape (O) rotation cropping system was carried out during the cropping seasons of 2015-2016

111 and 2016-2017 at the Grignon experimental station (Yvelines, France; 48°51'N, 1°58'E). This  
112 area is characterised by an oceanic climate (temperate, with no dry season and a warm  
113 summer). A combined diachronic and synchronic strategy [30] was used to investigate the  
114 dynamics of the residue microbial communities both over a two-year period on the same plot  
115 and along a chronosequence substituting spatial differences (three plots) for time differences.  
116 A first monoculture plot (WWW) was sown with the winter wheat cultivar Soissons. This plot  
117 had been cropped with wheat since 2007 and was used in previous epidemiological studies  
118 focusing on the impact of wheat debris on the development of *Septoria tritici* blotch [e.g. 31,  
119 32, 33]. Two other plots were cropped with oilseed rape cv. Alpaga and wheat cv. Soissons in  
120 rotation (OWO, adjacent to the WWW plot, and WOW, located 400 m away; Fig. 1). The size  
121 of the three plots was identical (20 m × 100 m). The OWO and WWW plots are characterized  
122 by a silty clay loam soil and plot WOW is characterized by a silty loam soil. Soil texture of  
123 the three plots is presented in Additional Table S1. The three plots were not tilled during the  
124 two cropping seasons. The wheat and oilseed rape residues were left on the soil surface after  
125 harvest. Soil was superficially disturbed to a depth of 10 cm with a disc harrow 6 weeks later  
126 (late September), leaving a large portion of residue on the surface. Crops were managed in a  
127 conventional way following local practices (nitrogen fertilization, insecticide and herbicide  
128 treatments). No fungicide was sprayed on the leaves during the study.

129 *Residue sampling* - Wheat and oilseed rape residues from the previous crop were  
130 collected over the two cropping seasons. The changes in the microbial communities during  
131 residue degradation were described on the basis of four sampling periods each year (October,  
132 December, February, and May) Sampling dates are presented in Additional Table S2. A  
133 supplementary sample was taken in July 2016, and *a posteriori* in July 2017, to characterise  
134 the plant microbiota before the residues came into contact with the soil. For each sampling  
135 period, residues samples were collected at soil surface from five points in each plot, 20 m

136 apart, along a linear transect (Fig. 1). Each sample was composed of twelve pieces of wheat  
137 residue or four pieces of oilseed rape residue. The five sampling points were located at the  
138 same place in the plots during the two years of the experiment.

139 *DNA extraction* - Residues were cut to take off remaining roots, rinsed with water to  
140 remove the soil and air-dried in laboratory conditions. They were then cut into small pieces,  
141 pooled in a 50 mL bowl and crushed with a Retsch™ Mixer Mill MM 400 for 60 seconds at  
142 30 Hz in liquid nitrogen, in a zirconium oxide blender. The crushed powder was stored in  
143 50 mL Falcon tubes at -80°C until DNA extraction. We transferred 40 mg of crushed residues  
144 to a 2.0 mL Eppendorf tube, which was stored to -80°C. Total environmental DNA (eDNA)  
145 was extracted according to the TriZol® Reagent protocol (Invitrogen, according to the  
146 manufacturer's instructions). Two independent extractions were performed per sample, giving  
147 a total of 300 eDNA samples. The two extractions were considered as technical replicates.

148

#### 149 **PCR and Illumina sequencing**

150 Fungal and bacterial community profiles were estimated by amplifying ITS1 and the  
151 v4 region of the 16S rRNA gene, respectively. Amplifications were performed with the  
152 ITS1F/ITS2 [34] and 515f/806r [35] primers. All PCRs were run in a reaction volume of 50  
153 µL, with 1x Qiagen Type-it Multiplex PCR Master Mix (Type-it® Microsatellite PCR kit Cat  
154 No./ID: 206243), 0.2 µM of each primer, 1x Q-solution® and 1 µL DNA (approximately 100  
155 ng). The PCR mixture was heated at 95°C for 5 minutes and then subjected to 35 cycles of  
156 amplification [95°C (1 min), 60°C (1 min 30 s), 72°C (1 min)] and a final extension step at  
157 72°C (10 min). PCR products were purified with Agencourt® AMPure® XP (Agencourt  
158 Bioscience Corp., Beverly, MA). A second round of amplification was performed with 5 µL of  
159 purified amplicons and primers containing the Illumina adapters and indexes. PCR mixtures  
160 were heated at 94°C for 1 min, and then subjected to 12 cycles of amplification [94°C (1



161 min), 55°C (1 min), 68°C (1 min)] and a final extension step at 68°C (10 min). PCR products  
162 were purified with Agencourt® AMPure® XP and quantified with Invitrogen QuantIT™  
163 PicoGreen®. Purified amplicons were pooled in equimolar concentrations in five independent  
164 batches, and the final concentration of each batch was determined with the qPCR NGS library  
165 quantification kit (Agilent). The five independent batches were sequenced in five independent  
166 runs with MiSeq reagent kit v3 (300bp PE).

167

### 168 **Sequence processing**

169 Fastq files were processed with DADA2 v1.6.0 [36], using the parameters described in  
170 the workflow for “Big Data: Paired-end” [37]. The only modification made relative to this  
171 protocol was a change in the truncLen argument according to the quality of the sequencing  
172 run. Each run was analysed separately. Taxonomic affiliations for amplicon sequence variants  
173 (ASV) generated with DADA2 were assigned with a naive Bayesian classifier on the RDP  
174 trainset 14 for bacteria [38] and the UNITE 7.1 database for fungi [39].

175 Only ASV detected in both technical replicates were conserved to ensure robustness  
176 [40] and were then added together. ASV classified as “Cyanobacteria/Chloroplast”, or not  
177 classified at the phylum level, were discarded from the datasets. This resulted in suppression  
178 of 1.2% of reads for fungi (4.2% of unclassified ASV), and 1.5% of reads for bacteria (4.9%  
179 of unclassified ASV and 1.3% of ASV affiliated to Cyanobacteria/Chloroplast). The  
180 remaining ASV were normalised according to the proportion of reads within each sample  
181 [41].

182

### 183 **Microbial community analyses**

184 Microbial community profiles were obtained for 100 wheat residue samples and 50  
185 oilseed rape residue samples. The alpha-diversity was estimated for each sample by

186 calculating the Shannon index [42], completed by Faith's phylogenetic diversity (PD; [43];  
187 [44]) for bacterial communities. The compositional dissimilarity between samples (beta-  
188 diversity) was estimated by the Bray-Curtis dissimilarity index.

189 Factors taken into account in the microbial community analyses were plant (wheat;  
190 oilseed rape), cropping system (monoculture; rotation), cropping season (2015-2016; 2016-  
191 2017), sampling period (July; October; December; February; May), and sampling plot  
192 (WWW; WOW; OWO; Fig. 1). We used a model to test these effects on each aforementioned  
193 index in a general way, and then conducted post-hoc contrasts to characterize the differences.  
194 A complete model combining all the factors could not have been used because the  
195 experimental design did not include an oilseed rape monoculture field plot. Of note oilseed  
196 rape monoculture is considered as an agronomic nonsense. Thus, a first model including the  
197 plant effect but not the cropping system effect (plant \* cropping season \* sampling period \*  
198 sampling plot) was applied using the data set from plots in rotation only (WOW and OWO).  
199 The effect of the cropping system (monoculture; rotation) was estimated separately using a  
200 second model (cropping system \* cropping season \* sampling period) applied on the data set  
201 from wheat residues only; the sampling plot factor was not included in this second model as it  
202 would have been confounding with the cropping system factor.

203 Shannon index was calculated for both bacterial and fungal communities with the  
204 ggpubr package in R [45] and Faith's phylogenetic diversity was calculated for bacterial  
205 communities with the picante package [46]. The effect of each factor on the Shannon index  
206 was assessed with two complementary ANOVA. A Kruskal-Wallis test also performed to  
207 assess significant differences in microbial diversity with time for each cropping season and  
208 sampling plot. Wilcoxon pairwise tests were also performed to compare the effects of  
209 sampling periods. Divergences were considered significant if  $p < 0.05$ .

210 The effect of each factor on the Bray-Curtis dissimilarity index was assessed with two  
211 complementary PERMANOVA using the `adonis2` function of the `vegan` R package (version  
212 2.4-4 [47] with “margin” option, used to determine the effect of each term in the model,  
213 including all other variables, to avoid sequential effects. They were visualized by  
214 multidimensional scaling (MDS) on the Bray-Curtis dissimilarity index with the `phyloseq`  
215 package in R (version 1.22.3 [48] and completed for bacterial communities by incorporating  
216 phylogenetic distances using the UniFrac distance matrix. After the aggregation of ASV for  
217 each sampling condition “sampling period/cropping year \* crop within a rotation”, the  
218 `betapart` R package [49] was used to determine whether temporal changes in community  
219 composition were due to turnover (i.e. replacement of ASV between two sampling periods) or  
220 nestedness (gain or loss of ASV between two sampling periods). The effect of the plant on the  
221 microbial communities associated with residues during degradation was also assessed with  
222 PERMANOVA on each sampling period, for each cropping season.

223 The genus composition of fungal and bacterial communities was analysed with a  
224 cladogram based on genus names. Only genera observed in three biological samples harvested  
225 on the same plot were incorporated into the cladogram. A cladogram representing the number  
226 of ASV for each genus, read percentage, occurrence and distribution for each sample, was  
227 constructed with the Interactive Tree Of Life (iTOL [50]) online tool for phylogenetic trees.

228 To illustrate taxonomic changes over time, especially between plant-derived  
229 communities and communities involved later in the colonization of the residues, we focused  
230 on seasonal shifts (increase, decrease or stability) in the relative abundance of a selection of  
231 some fungal and bacterial genera and tested their statistical significance (Wilcoxon tests  
232 between sampling periods).

233

## 234 **Results**

235 The bacterial and fungal communities associated with wheat (W) and oilseed rape (O) crop  
236 residues were characterised on three plots: the wheat monoculture (WWW), and two oilseed  
237 rape-wheat rotation plots (WOW and OWO) (Fig. 1). We assessed the composition of these  
238 microbial communities four times per year, during two consecutive cropping seasons (in  
239 October, December, February, and May). An additional time point (in July) was also included  
240 for identification of the micro-organisms present on the plant before contact with the soil. The  
241 analysis of raw sequence datasets for the 150 samples of wheat and oilseed rape residues  
242 collected over the two cropping seasons resulted in the grouping of 14,287,970 bacterial and  
243 9,898,487 fungal reads into 2,726 bacterial and 1,189 fungal amplicon sequence variants  
244 (ASV). ASV not detected in both technical replicates (5.4% of bacterial reads and 1.5% of  
245 fungal reads) were removed from the datasets. Total number of reads remaining after ASV  
246 filtering is presented in Additional Table S3.

247

#### 248 **Alpha diversity of microbial communities**

249 Diversity dynamics, assessed by calculating the Shannon index, differed between the  
250 two cropping seasons and between fungi and bacteria. The diversity was significantly  
251 impacted by most of factors, including cropping system (monoculture; rotation) for wheat  
252 residues (Table 1; Fig. 2). Oilseed rape residues supported less fungal diversity and as much  
253 bacterial diversity than wheat residues in rotation. In addition, the diversity was significantly  
254 higher in wheat grown in monoculture than in wheat grown in rotation for both bacteria and  
255 fungi.

256 Fungal diversity increased over time in 2015-2016, whereas the differences between  
257 the samples in 2016-2017 did not reflect a gradual increase as the minimum was reached in  
258 December. Bacterial diversity followed a quite similar trend with however a significant  
259 decreased from February to May, more pronounced for wheat residues than for oilseed rape

260 residues during the first cropping season; this trend was also illustrated by the Faith's  
261 phylogenetic diversity (Additional Figure S1). The climatic conditions during residue  
262 degradation (Additional Table S4) or differences in initial diversity on the plant before harvest  
263 may explain the less marked trends observed between the two cropping seasons.

264

### 265 **Comparison of microbial communities associated with residues (beta diversity)**

266 We analysed the effects of plant, cropping system, cropping season, and sampling  
267 period on communities using the Bray-Curtis dissimilarity index and PERMANOVA. There  
268 was remarkably little heterogeneity between the five samples collected in the same sampling  
269 plots (Fig. 3) and the number of biological samples was, therefore, sufficient to assess  
270 differences due to the variables of interest (i.e. plant cropping season, sampling period, and  
271 cropping system). This result was confirmed by the structure of bacterial communities  
272 visualized by incorporating phylogenetic distances using the UniFrac distance matrix  
273 (Additional Fig. S2).

274 *The structure of bacterial and fungal communities is influenced by plant species and*  
275 *cropping system* – Oilseed rape and wheat residues presented different sets of ASV, for both  
276 bacterial and fungal communities (Fig. 3). Plant species was the main factor explaining  
277 differences between the communities, accounting for 38.4% for fungi and 26.6% of the  
278 variance for bacteria, as established with PERMANOVA (Table 2). For wheat, the cropping  
279 system (rotation; monoculture) accounted for 10.5% of the variance for fungal community  
280 composition and 6.6% of the variance for bacterial community composition.

281 The percentage of variance explained by the plant decreased over time for fungal  
282 community structure (e.g. from 75% in October 2016 to 40% in May), while for bacteria the  
283 decrease of the percentage of variance explained by the plant was less pronounced (from 65%

284 to 50%). The percentages of variance associated with the plant for each date are presented in  
285 Additional Table S5.

286 *Community structures change over time* – Cropping season was the main temporal  
287 factor underlying changes in community structure, accounting for 11.8% of the variance for  
288 bacteria when considering only the plots in rotation (or 24.8% when considering only the  
289 wheat residues without sampling plot effect), and 13.1% of the variance for fungi when  
290 considering only the plots in rotation (or 29.2% when considering the wheat residues without  
291 sampling plot effect; Table 2). Sampling period had also a significant impact on community  
292 composition, accounting for 14.9% of the variance for bacteria when considering only the  
293 plots in rotation (or 20.4% when considering only the wheat residues without sampling plot  
294 effect), and 6.8% of the variance for fungi when considering only the plots in rotation (or  
295 12.3% when considering the wheat residues without sampling plot effect). Theoretically,  
296 changes in ASV composition result from turnover (replacement of ASV between two  
297 sampling periods) and nestedness (gain or loss of ASV between two sampling periods [49]).  
298 We found that the dissimilarity between sampling periods was smaller for bacterial than for  
299 fungal ASV structure. By decomposing the dissimilarity between sampling periods, we found  
300 that, for fungi, 94% ( $\pm 5\%$ ) of dissimilarity was explained by turnover for oilseed rape, 89%  
301 ( $\pm 15\%$ ) for wheat in monoculture, and 80% ( $\pm 13\%$ ) for wheat in rotation. For bacteria, 69%  
302 ( $\pm 17\%$ ) of dissimilarity was explained by turnover for oilseed rape, 61% ( $\pm 19\%$ ) for wheat in  
303 monoculture, and 80% ( $\pm 16\%$ ) for wheat in rotation. Decomposition of dissimilarity between  
304 sampling periods is presented in Additional Table S6.

305

### 306 **Changes in communities, by genus**

307 We characterised potential taxonomic differences in communities over time by  
308 analysing wheat and oilseed rape residues separately. ASV were aggregated together at genus

309 level, resulting in 84 fungal and 184 bacterial genera for wheat, and 63 fungal and 186  
310 bacterial genera for oilseed rape. For the sake of clarity, most 60 genera of fungi and bacteria  
311 were presented in Fig. 4 and Fig. 5, respectively. All the detected genera and their evolution  
312 over time were presented in Additional Fig. S3, S4, S5 and S6. For both plant species, we  
313 identified genera that disappeared or displayed a significant decrease in relative abundance  
314 over time. The seasonal shifts of some genera and their significance are presented in  
315 Additional Fig. S6. Among these genera, some are known to be associated with plants, such  
316 as *Alternaria*, *Acremonium* [14, 51, 52], *Cryptococcus* [53], *Sarocladium* [54] and  
317 *Cladosporium* [13, 51–54].

318 Some of the fungal species detected on wheat, such as *Oculimacula yallundae* (all  
319 ASV of *Oculimacula* genera), *Zymoseptoria tritici* and *Pyrenophora tritici-repentis*, (Fig. 4,  
320 Additional Fig. S3) are known to be pathogenic. Some of the species detected on oilseed rape,  
321 such as *Verticillium* spp., *Leptosphaeria maculans* (= *Plenodomus maculans*) and  
322 *Leptosphaeria biglobosa* (= *Plenodomus biglobosa*), are also known to be pathogenic.  
323 Strikingly, *L. maculans* and *L. biglobosa* predominated over the other taxa. *Verticillium*  
324 *longisporum*, *V. dahlia* and *V. albo-atrum* were mostly detected during the second sampling  
325 year (Fig. 4, Additional Fig. S4). As samples were collected in two different fields, it was not  
326 possible to determine whether the occurrence of *Verticillium* spp., a soil-borne pathogen  
327 complex causing *Verticillium* wilt [55], was affected more by year or by the soil  
328 contamination. *Acremonium*, *Clonostachys* and *Alternaria* genera, which have also been  
329 described as associated with plants [56], were detected in the early sampling periods. Their  
330 relative abundances decreased over time (Additional Fig. S7). Most of the genera that were  
331 not present at early sampling points and with relative abundances increasing over time (e.g.  
332 *Coprinellus*, *Psathyrella*, *Torula*, *Tetracladium*, and *Exophiala*) were common to wheat and

333 oilseed rape residues (Fig. 4). These genera can thus be considered as probably derived  
334 primarily from the surrounding soil.

335 For bacteria, the difference in the genera detected between the two plants species was  
336 less marked than for fungi, as 146 genera were common to wheat and oilseed rape residues  
337 (Fig. 5). These 146 genera corresponded to the 98.7% most prevalent reads for wheat and  
338 97.5% most prevalent genus reads for oilseed rape. *Proteobacteria* was the predominant  
339 phylum the first year. The most prevalent proteobacterial subgroup was *Alphaproteobacteria*,  
340 with a high prevalence of *Rhizobiales* and *Sphingomonadales*. *Rhizobium* and *Neorhizobium*,  
341 two major genera from *Rhizobiales*, decreased in abundance between October and May in  
342 both wheat and oilseed rape (Additional Fig. S7). *Sphingomonadales* genera were much more  
343 abundant on wheat than on oilseed rape, especially *Sphingomonas* (Fig. 5). *Bacteroidetes*  
344 genera, including *Pedobacter* in particular, were frequently detected and their prevalences  
345 tended to be stable for oilseed rape residues, and to decrease for wheat residues (Additional  
346 Fig. S7). In parallel, an increase in *Actinobacteria*, particularly *Nocarioides*, was observed.  
347 Major differences between July and October were observed for oilseed rape, consistent with  
348 the beta-diversity analysis, in which the percentage dissimilarity between July and October  
349 was high, due to both species extinction and turnover. *Gammaproteobacteria* were highly  
350 abundant on oilseed rape in July. Their frequency then decreased rapidly from October to  
351 May, due largely to the decrease in *Pseudomonas* (Fig. 5, Additional Fig. S7). In parallel, we  
352 observed an increase in the levels of *Alphaproteobacteria*, especially *Rhizobium* and  
353 *Sphingomonas*, between July and October. A small decrease in levels of  
354 *Gammaproteobacteria* was observed between July and October for wheat in rotation, whereas  
355 the percentage of reads associated with this class increased between July and December for  
356 wheat in monoculture, due largely to the decrease in *Pantoea* and *Enterobacteria* (Fig. 5,



357 Additional Fig. S7). The abundance of *Bacteroidetes*, especially *Pedobacter* and  
358 *Flavobacterium*, also increased between July and October.

359

## 360 **Discussion**

361 Most studies on crop residues have focused on their impact on soil microbial  
362 communities [16], and the rare studies investigating the impact of soil on residue communities  
363 focused exclusively on bacteria [27, 28] or fungi [57]. Most of these studies were conducted  
364 on residues from a single year. Bastian et al. [12] established an extensive description of the  
365 species present in the soil, detritosphere and wheat residues, using sterilised residues and soil  
366 in a microcosm. In this study, we showed, under natural conditions, that three main factors  
367 (plant species, cropping season, rotation) simultaneously influence the composition of both  
368 fungal and bacterial communities present on residues. This study is the first to investigate the  
369 total fungal and bacterial communities associated with wheat and oilseed rape residues by a  
370 metabarcoding approach over two consecutive years. The very low variability of the  
371 communities for the five replicates is remarkable and shows that our strategy would be  
372 appropriate for comparing the effects of different treatments on microbial communities.

373

374 **Crop residues should be viewed as a shifting platform for microbial meeting**  
375 **strongly affected by plant species**

376 Oilseed rape and wheat residues contained different sets of micro-organisms before  
377 soil contact and during the firsts sampling periods after harvest. Similar results were  
378 previously obtained for the bacterial communities of buried crop residues [28]. Consistent  
379 with the findings of this previous study, the divergence between wheat and oilseed rape  
380 bacterial communities was probably due to differences in the chemical compounds present in  
381 the plants. The rapid change in the community observed at early stages of residue degradation

382 for oilseed rape may be explained by the modification of simple compounds (sugars, starch,  
383 etc.), whereas wheat is composed of more complex compounds (lignin) and is, therefore,  
384 broken down less quickly, resulting in a slower change in the microbial community [28].  
385 Overall, the change in bacterial community composition highlights turnover between  
386 copiotrophs and oligotrophs. Although copiotrophy and oligotrophy are physiological traits,  
387 several attempts have been made to classify microorganisms as oligotrophs and copiotrophs  
388 based on phylogeny [58]. According to this generalization, bacterial and fungal taxa whose  
389 relative abundances are significantly decreased during succession belong mainly to  
390 copiotroph. These taxa include for instance *Alternaria*, *Cladosporium*, *Massilia* and  
391 *Pseudomonas* (Additional file: Fig. S5). In contrast, the relative abundances of oligotrophic  
392 taxa such as *Coprinellus* or *Nocardiodes* increased during residues degradation, which could  
393 be indicative of the superior abilities of these micro-organisms to degrade complex polymers.

394 The initial fungal communities were structured mostly by the presence of species  
395 originating from the plant, several of which were highly specialised on the host plant. These  
396 species were gradually replaced by more generalist species, which colonised the residues of  
397 both plants. Most of these generalists, such as *Exophiala*, *Coprinellus* and *Torula*, are known  
398 to be soil-born [59, 60], or involved in degradation, such as *Copriopsis* [61]. The host-  
399 specific fungi identified in our study included a large number of ascomycetes known to be  
400 foliar pathogens (*O. yallundae*, *Fusarium* sp. and *Gibberella* sp., *Z. tritici*, *P. tritici-repentis*,  
401 *Parastagonospora nodorum*, *Monographella nivalis*, *L. biglobosa* and *L. maculans*). The  
402 lifestyles of some pathogens are well-documented, as for *Z. tritici*, *P. tritici-repentis* and *L.*  
403 *maculans*. The decrease with time in levels of *Z. tritici* and other pathogens in wheat residues  
404 contrasts with the persistence of *L. maculans* and *L. biglobosa* in oilseed rape residues. These  
405 three pathogens are all known to reproduce sexually on the residues of their host plant [31,  
406 62], but the life cycle of *L. maculans* is characterised by systemic host colonisation through

407 intracellular growth in xylem vessels [63], whereas the development of *Z. tritici* is localised  
408 and exclusively extracellular [64]. Oilseed rape residues thus provide *L. maculans* with  
409 greater protection than is provided to *Z. tritici* by wheat residues. This likely explains  
410 differences in the persistence of the two pathogens and in the temporal dynamics of ascospore  
411 release: over up to two years for *L. maculans* [65, 66] but only a few months for *Z. tritici* [31,  
412 67]. The predominance of *L. maculans* on oilseed rape residues was not surprising given that  
413 the oilseed rape cultivar Alpage is known to be susceptible to *L. maculans*, but the high  
414 abundance of *L. biglobosa* was much more remarkable. One surprising finding of our study  
415 was the constant association of *L. maculans* with *L. biglobosa* on residues. Indeed, *L.*  
416 *biglobosa* is known to be more associated with upper-stem lesions [68], and its presence in  
417 large amounts on residues has never before been reported.

418 Our findings are consistent with current epidemiological knowledge of emblematic  
419 wheat and oilseed rape diseases, but they highlight our lack of knowledge concerning the  
420 lifestyles of many other fungal pathogens present on residues. A key point to be taken into  
421 account is that the trophic status of many species known to be principally pathogenic or non-  
422 pathogenic is not definitive [69]. For instance, *Alternaria infectoria* is sometimes described as  
423 a pathogen of wheat [13, 70], sometimes as an endophyte [71], and has even been tested as a  
424 potential biocontrol agent against *Fusarium pseudograminearum* on wheat [72]. Crop  
425 residues, half-plant/half-soil, should be the focus of future studies aiming to disentangle the  
426 succession of microbial species with different lifestyles and to characterise their relative  
427 impacts on the development of currently minor, but potentially threatening diseases.

428

429 **The residue microbiota should be analysed in a dynamic manner, both within and**  
430 **between years**

431 The results of our study highlight the importance of conducting multi-year studies  
432 focusing on ecological dynamics both within and between years in natural conditions. Year  
433 had a strong effect on both bacterial and fungal communities. Fluctuations of climatic  
434 conditions (temperature, rainfall, wind) have a major impact on pathogenesis (disease triangle  
435 concept [73]) and on the saprophytic survival of plant pathogens during interepidemic periods  
436 [74]. The two years of our study were marked by similar means of 10-day mean temperatures,  
437 but large differences in rainfall: mean 10-day cumulative rainfall in the first year was almost  
438 twice that in the second (Additional Table S5). The colonisation of residues by late colonisers  
439 may be affected by such climatic differences: in wheat, most prevalent degrading fungi (like  
440 *Coprinellus*, *Psathyrella*, *Coprinopsis*) were almost absent in the second year of the study.  
441 There was also considerable dissimilarity between the bacterial communities associated with  
442 each of the two years. For example, genus *Enterobacter*, which was highly abundant in the  
443 second year, was barely detectable in the first year.

444

#### 445 **Crop rotation has little impact on residue microbial communities**

446 Oilseed rape is never grown in monoculture, so the effect of crop rotation was assessed  
447 only for wheat. The effect of rotation on residue microbial communities was much smaller  
448 than the effect of year (cropping season). It was more marked for fungi, for which diversity  
449 was greater in monoculture than in rotation. The use of a rotation may prevent the most  
450 strongly specialised species, in this case fungi, from becoming established, regardless of their  
451 pathogenicity. This finding is consistent with the greater development of some diseases in  
452 monoculture conditions, which promote the maintenance of pathogens through the local  
453 presence of primary inoculum. For instance, the presence of *P. tritici-repentis*, agent of tan  
454 spot disease, in the wheat monoculture plot and its absence from wheat-oilseed rape plots is

455 consistent with epidemiological knowledge indicating that this disease can be controlled by  
456 leaving a sufficient interval between consecutive wheat crops in the same field [75].

457

458 **Lesson to be learned from the residue microbial communities for the sustainable**  
459 **management of debris-borne diseases: a delicate balance between pathogenic and**  
460 **beneficial micro-organisms**

461 The maintenance of crop residues at the surface of the cultivated soil increases the  
462 microbial diversity of the soil and, in some ways, helps to maintain good functional  
463 homeostasis [76]. However, conservation practices tend to increase the risk of foliar diseases  
464 [4–6]. Most disease management strategies focus on epidemic periods, during which the  
465 pathogen and its host are in direct contact. Interepidemic periods are also crucial for pathogen  
466 development, although during these periods the primary inoculum is not directly in contact  
467 with the new crop whilst not present in the field. Indeed, by carrying the sexual reproduction  
468 of several fungal pathogens, residues contribute to the generation and transmission of new  
469 virulent isolates potentially overcoming resistance genes, during monocyclic epidemics, as  
470 described for oilseed rape canker caused by *L. maculans* [77], but also polycyclic epidemics,  
471 as described for Septoria tritici blotch caused by *Z. tritici* [78].

472 However, the results of our study suggest that residues should not only be considered as  
473 a substrate for pathogens and a potential source of inoculum. Indeed, we detected several  
474 fungi identified as beneficial or even biocontrol agents in previous studies, such as  
475 *Clonostachys rosea*, *Aureobasidium pullulans*, *Chaetomium globosum* and *Cryptococcus* spp.  
476 *C. rosea*, which was detected in both oilseed rape and wheat residues, has been reported to  
477 limit the sexual and asexual reproduction of *Didymella rabiei* on chickpea residues by  
478 mycoparasitism [79]. It has also been reported to be effective against *Fusarium culmorum* on  
479 wheat plants, through antibiosis during the epidemic period [80], and on wheat residues,

480 through antagonism during the interepidemic period [81]. *Cladosporium* sp., which were  
481 abundant in our study, have also been reported to inhibit the development of *P. tritici-repentis*  
482 on wheat plants [82] and of *Fusarium* sp. on wheat residues [81]. The presence of these  
483 fungal species on wheat and oilseed rape residues is of potential interest for future analyses of  
484 interactions. Due to the use of a low-resolution marker for bacterial characterisation, we were  
485 unable to identify similarly the bacteria potentially interacting with pathogenic fungi. For  
486 instance, the presence of *Pseudomonas* spp. suggests possible interactions both with other  
487 microbial species and with the host plant [83], but the nature of the potential interactions is  
488 indeterminate: species of the *Pseudomonas fluorescens* group are known to be beneficial to  
489 plants, whereas *Pseudomonas syringae* and *Pseudomonas aeruginosa* are known to be  
490 pathogens of plants and even humans.

491 Although our study reveals the presence of genera or species reported in the literature as  
492 biocontrol agents, it has not yet shown any interaction between them and the pathogens. This  
493 experimental study (sampling effort, residue treatments, etc.) was not designed to characterize  
494 such interactions. A strategy involving the inference of microbial interaction networks from  
495 metabarcoding datasets might help to identify the species beneficial against pathogens,  
496 through competition, antagonism or parasitism. This however requires a more analytical,  
497 comparative experimental approach, that goes beyond the only description of shifts in natural  
498 communities composition: for example, using different “treatments” in a broad sense (e.g.  
499 artificial inoculation with a species or a group of species, change of biotic or abiotic  
500 environmental conditions, etc.) in order to modify interaction networks and so highlight the  
501 impact of some groups of micro-organisms on the whole community or a given species.

502

## 503 **Conclusion**

504 This study shows that crop residues, which can be seen as half-plant/half-soil transient  
505 compartment, constitute a pivotal fully-fledged microbial ecosystem that has received much  
506 less attention than the phyllosphere and rhizosphere to date. This study therefore fills a gap in  
507 knowledge of the communities present on crop residues under natural conditions. It confirms  
508 that the microbiote of crop residues should be taken into account in the management of  
509 residue-borne diseases. Taking into account this ecosystem is essential, not only to improve  
510 the quantitative management of crop residues, but also to identify groups of beneficial micro-  
511 organisms naturally present. The beneficial elements of the microbial community should be  
512 preserved, or even selected, characterised and used as biological control agents against the  
513 pathogens that complete their life cycle on the residues. These results are particularly  
514 important in that wheat-oilseed rape rotations are among the most widespread arable cropping  
515 systems in France and Europe.

516

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531

### 532 **Availability of data and materials**

533 The raw sequencing data is available from the European Nucleotide Archive (ENA) under the  
534 study accession PRJEB27255 (Sample SAMEA4723701 to SAMEA4724326). We provide  
535 the command-line script for data analysis and all necessary input files as Additional File 2.

536

### 537 **Authors' contributions**

538 LK, FS, VL, MHB, MB conceived the study, participated in its design, and wrote the  
539 manuscript. LK conducted the experiments and analysed the data. FS and VL supervised the  
540 project. All authors read and approved the final manuscript.

541

### 542 **Ethics approval and consent to participate**

543 Not applicable

544

### 545 **Consent for publication**

546 Not applicable

547

### 548 **Competing interests**

549 The authors declare that they have no competing interests.

550

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789

## 790 **Figure and table captions**

791

792 **Figure 1** - Experimental layout of the experiment. (A) Plots (WWW, WOW and OWO) used  
793 during the two cropping seasons of the experiment at the INRA Grignon experimental station  
794 (Yvelines, France). WWW: plot cropped with winter wheat since 2007. WOW and OWO:  
795 plots cropped with a wheat-oilseed rape rotation since 2014. Wheat straw and oilseed rape  
796 debris were chopped at harvest and a large portion of residue was then left on the surface. The

797 dashed line indicates the sampling transect. **(B)** Oilseed rape residues in a plot cropped with  
798 wheat (OWO or WOW). **(C)** Wheat residues in a plot cropped with oilseed rape (WOW or  
799 OWO). **(D)** Wheat residues in the wheat monoculture crop (WWW).

800 **Figure 2** - Fungal **(A)** and bacterial **(B)** diversity in plants (July) and residues (October;  
801 December; February; May), as assessed with the Shannon index, according to sampling  
802 period, the crop within a rotation (oilseed rape in WOW and OWO; wheat in WWW; wheat in  
803 WOW and OWO) and the cropping season (2015-2016; 2016-2017). Each box represents the  
804 distribution of Shannon index for five sampling points. Kruskal-Wallis tests were performed  
805 for each “crop within a rotation \* cropping season” combination (*p*-values are given under  
806 each graph). Wilcoxon tests between sampling periods were performed when the Kruskal-  
807 Wallis test revealed significant differences. Samples not sharing letters are significantly  
808 different.

809 **Figure 3** - Structure of the fungal **(A)** and bacterial **(B)** communities present in oilseed rape  
810 and wheat residues, according to compositional dissimilarity (Bray-Curtis dissimilarity  
811 index), after multidimensional scaling (MDS). The two MDS were performed on the overall  
812 dataset and faceted according to the sampling period. Each point represents one sample  
813 corresponding to a cropping season (shape: 2015-2016; 2016-2017; 2017-2018) and crop  
814 within a rotation (colour: oilseed rape in rotation, i.e. in WOW and OWO; wheat  
815 monoculture, i.e. in WWW; wheat in rotation, i.e. in WOW and OWO).

816 **Figure 4** – Distribution of the 60 most prevalent fungal genera detected in wheat residues in  
817 the five samples for each sampling date. Unclassified genera were removed from the  
818 visualisation.

819 **Figure 5** – Distribution of the 60 most prevalent bacterial genera detected in wheat residues in  
820 the five samples for each sampling date. Unclassified genera were removed from the  
821 visualisation.

822 **Table 1** - Results of the ANOVA performed to assess the effects of plant (wheat; oilseed rape),  
823 cropping season (2015-2016; 2016-2017), sampling period (July, October; December;  
824 February; May) and sampling plot on the Shannon index of the fungal and bacterial  
825 communities present in oilseed rape and wheat residues from the plots in rotation (OWO;  
826 WOW). The effect of the cropping system (monoculture; rotation) was estimated separately  
827 with a second ANOVA performed on the wheat residue samples dataset only (wheat in  
828 monoculture, i.e. in WWW; wheat in rotation, i.e. in WOW and in OWO).

829 **Table 2** - Results of the PERMANOVA performed to assess the effects of plant (wheat;  
830 oilseed rape), cropping season (2015-2016; 2016-2017), sampling period (July; October;  
831 December; February; May) and sampling plot on the Bray-Curtis dissimilarity index of the  
832 fungal and bacterial communities present in oilseed rape and wheat residues from the plots in  
833 rotation (OWO; WOW). The effect of the cropping system (monoculture; rotation) was  
834 estimated separately with a second PERMANOVA performed on the wheat residue samples  
835 data set only (wheat in monoculture, i.e. in WWW; wheat in rotation, i.e. in WOW and in  
836 OWO). PERMANOVAs were performed using the adonis2 function with “margin” option.

837 **Additional files**

838

839 **List of supplementary figures:**

840 **Figure S1** - Bacterial diversity in plants (July) and residues (October, December, February,  
841 May), as assessed with the Faith's Phylogenetic Diversity index (PD).

842 **Figure S2** - Structure of the bacterial communities present in oilseed rape and wheat residues  
843 visualized by incorporating phylogenetic distances using the UniFrac distance matrix.

844 **Figure S3** - Distribution of the most prevalent fungal genera detected in wheat residues.

845 **Figure S4** - Distribution of the most prevalent fungal genera detected in oilseed rape residues.

846 **Figure S5** - Distribution of the most prevalent bacterial genera detected in wheat residues.

847 **Figure S6** - Distribution of the most prevalent bacterial genera detected in oilseed rape  
848 residues.

849 **Figure S7** - Seasonal shift in the relative abundance of a selection of fungal and bacterial  
850 genera present on wheat and oilseed rape residues.

851

852 **List of supplementary tables:**

853 **Table S1** - Soil texture of the three plots.

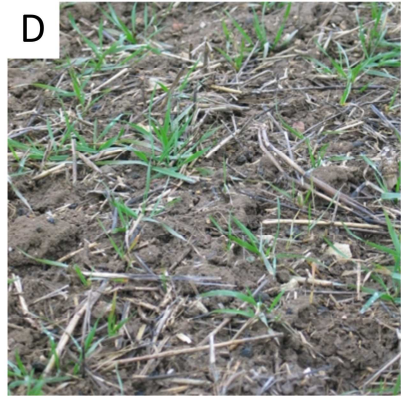
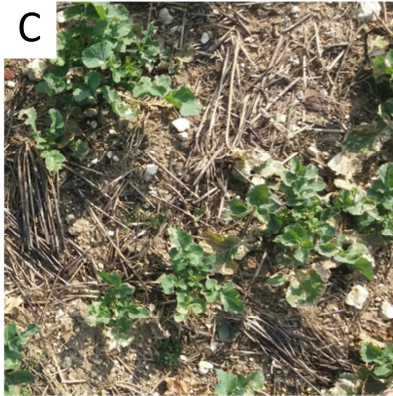
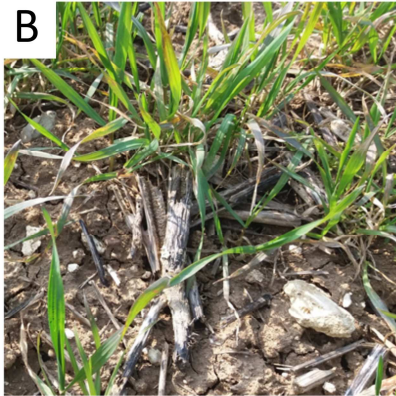
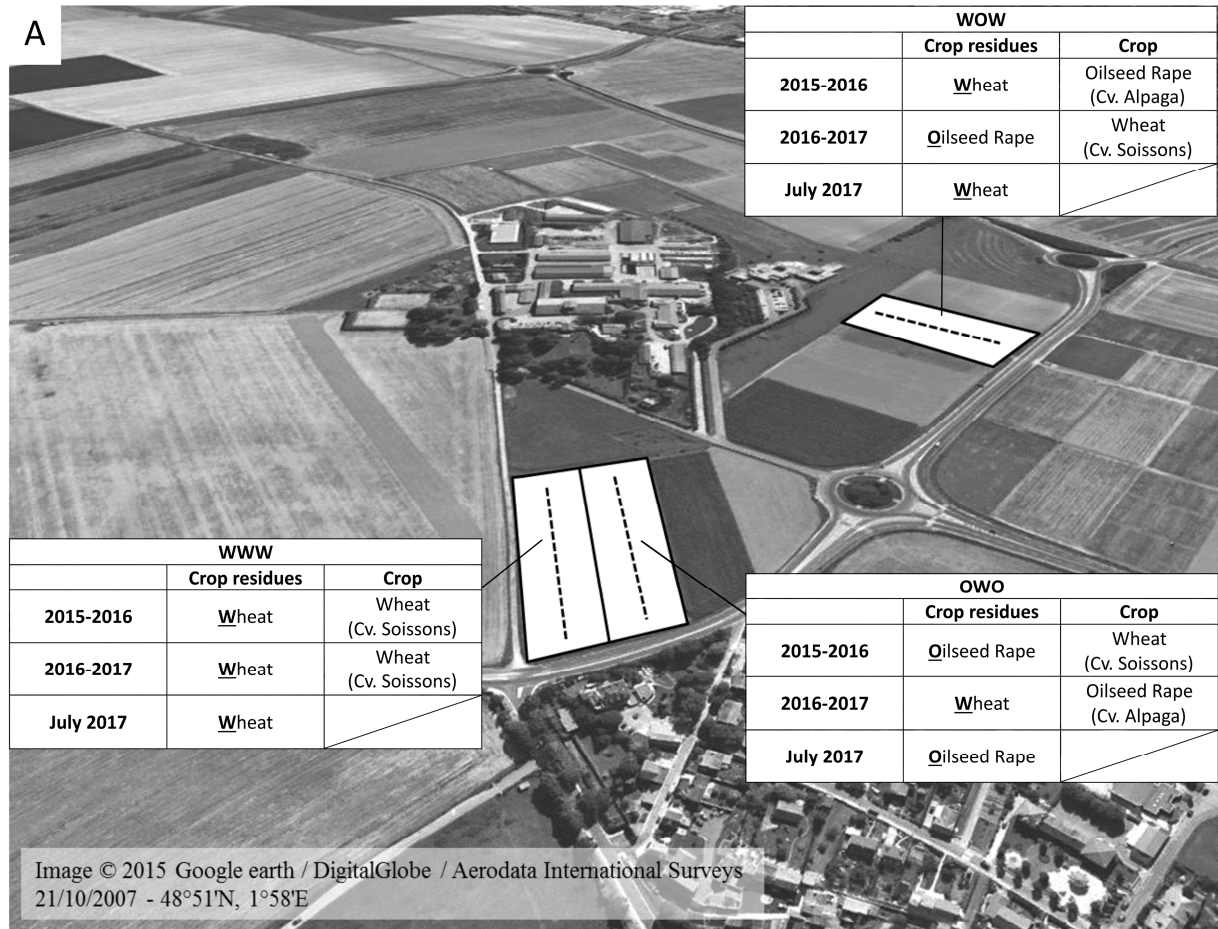
854 **Table S2** - Sampling dates of wheat and oilseed rape plants (July) and residues (October,  
855 December, February and May) for each cropping season.

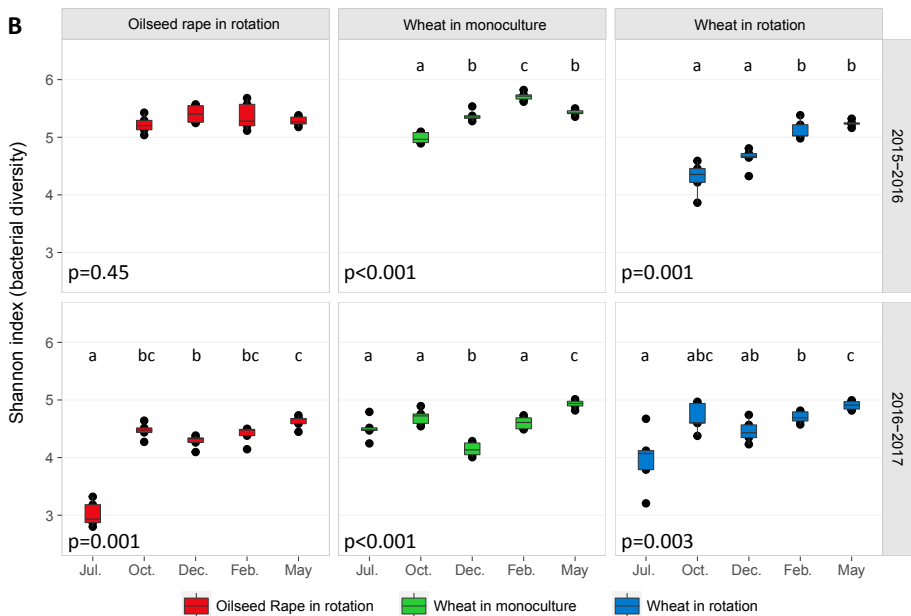
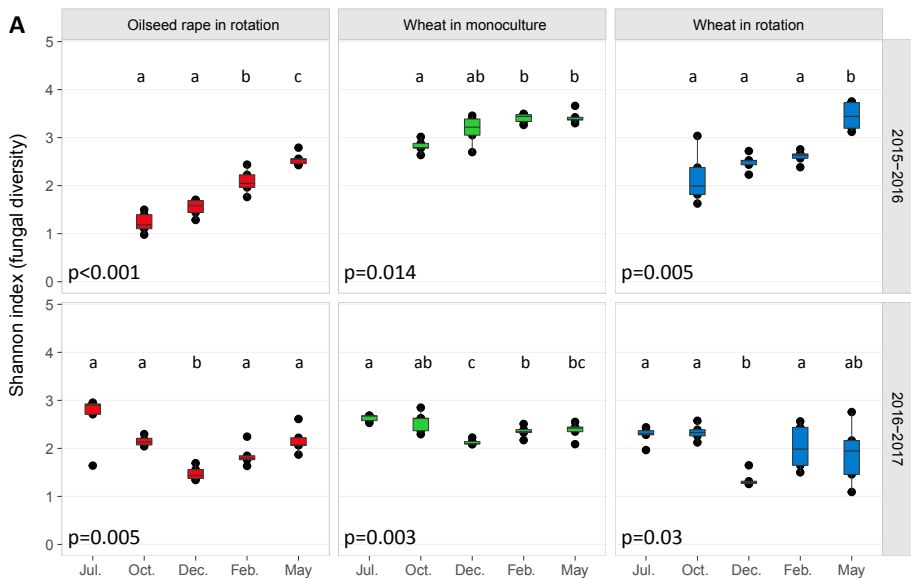
856 **Table S3** - Total number of reads and percentage (in brackets) remaining after ASV filtering.

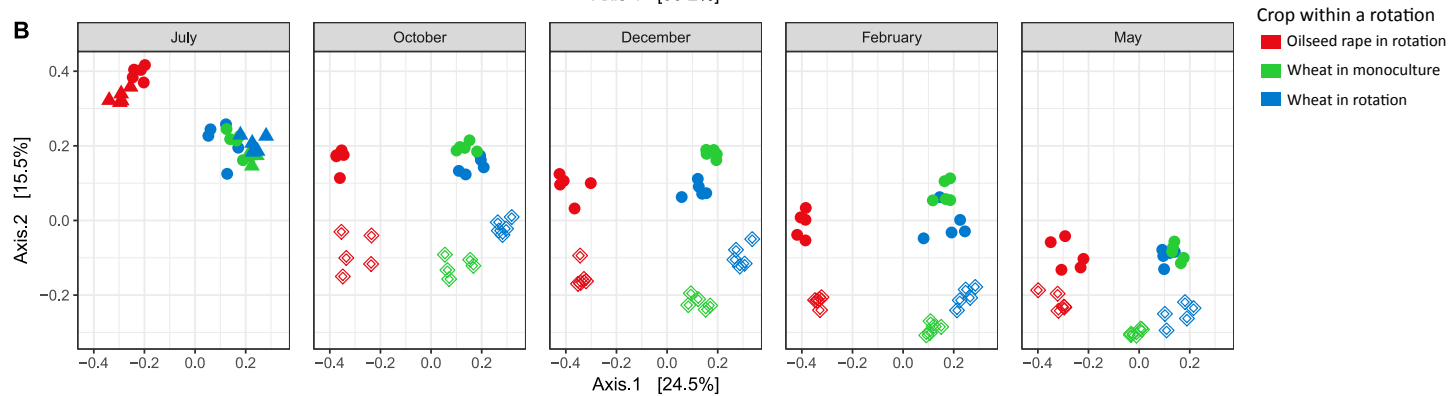
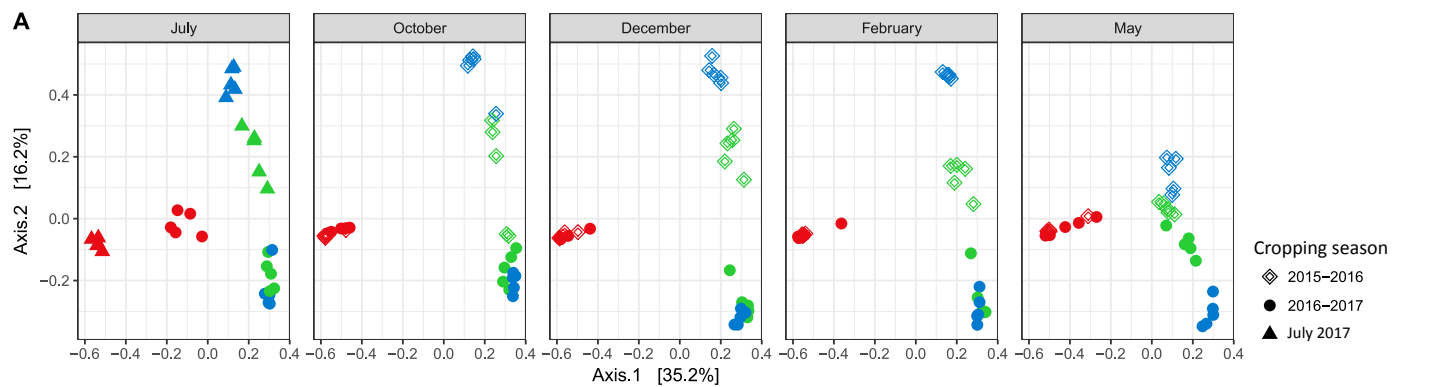
857 **Table S4** - Summary of meteorological data (temperature, rainfall) for the INRA Grignon  
858 experimental station (Yvelines, France).

859 **Table S5** - Plant effect (wheat vs. oilseed rape) on community dispersion.

860 **Table S6** - Decomposition of dissimilarity due to temporal changes in fungal (F) and bacterial  
861 (B) community.

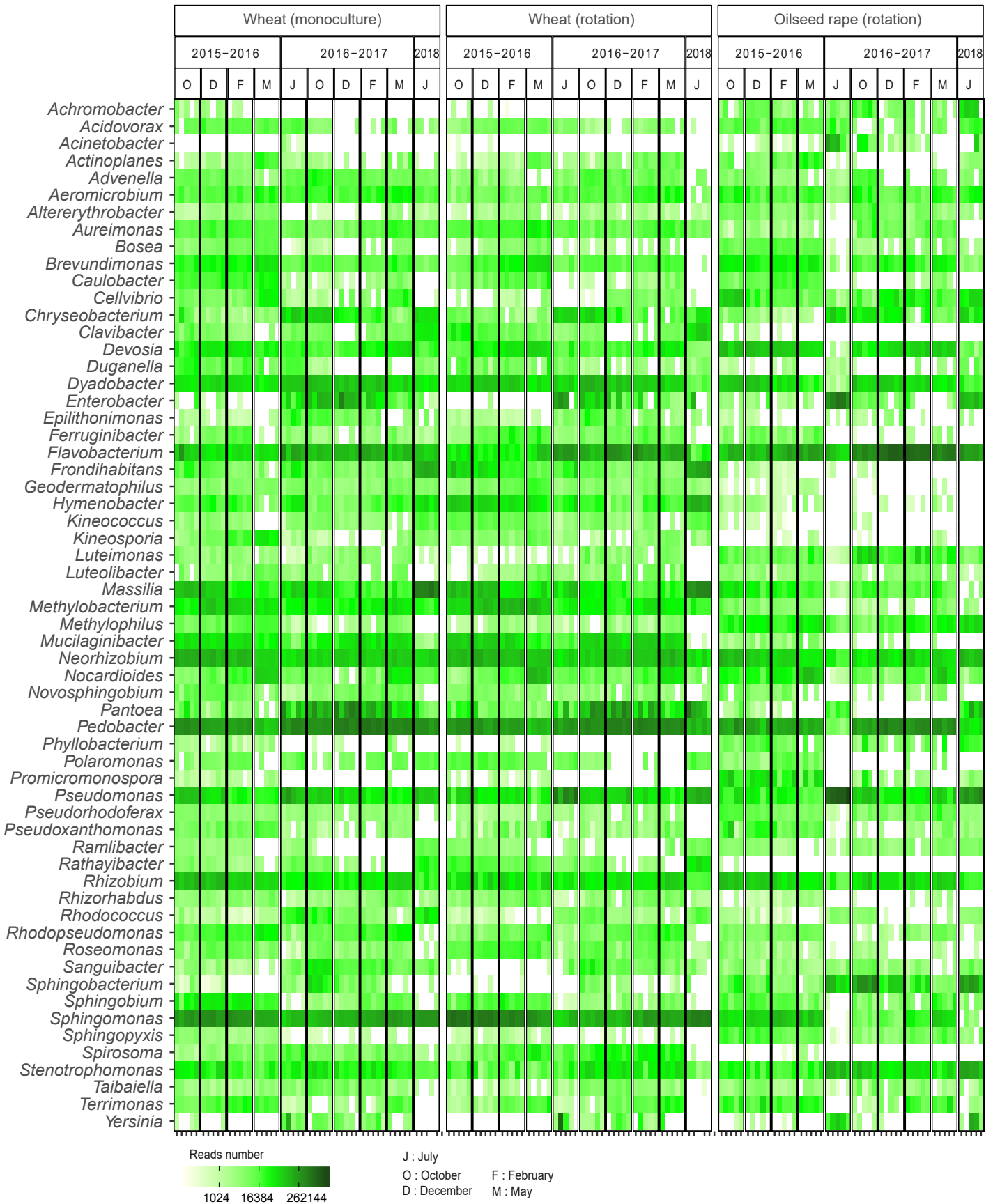












**Table 1** - Results of the ANOVA performed to assess the effects of plant (wheat; oilseed rape), cropping season (2015-2016; 2016-2017), sampling period (July, October; December; February; May) and sampling plot on the Shannon index of the fungal and bacterial communities present in oilseed rape and wheat residues from the plots in rotation (OWO; WOW). The effect of the cropping system (monoculture; rotation) was estimated separately with a second ANOVA performed on the wheat residue samples dataset only (wheat in monoculture, i.e. in WWW; wheat in rotation, i.e. in WOW and in OWO).

		Fungi		Bacteria	
Tested factors		F value	<i>p</i> -value	F value	<i>p</i> -value
Plots in rotation	Plant	22.42	< 0.001	0.33	0.567
	Cropping season	14.19	< 0.001	35.28	< 0.001
	Sampling period	14.25	< 0.001	37.73	< 0.001
	Sampling plot	31.06	< 0.001	61.57	< 0.001
Wheat residues	Cropping system	46.42	< 0.001	23.66	< 0.001
	Cropping season	51.43	< 0.001	33.34	< 0.001
	Sampling period	6.72	< 0.001	13.89	< 0.001

**Table 2** - Results of the PERMANOVA performed to assess the effects of plant (wheat; oilseed rape), cropping season (2015-2016; 2016-2017), sampling period (July; October; December; February; May) and sampling plot on the Bray-Curtis dissimilarity index of the fungal and bacterial communities present in oilseed rape and wheat residues from the plots in rotation (OWO; WOW). The effect of the cropping system (monoculture; rotation) was estimated separately with a second PERMANOVA performed on the wheat residue samples data set only (wheat in monoculture, i.e. in WWW; wheat in rotation, i.e. in WOW and in OWO). PERMANOVAs were performed using the `adonis2` function with “margin” option.

Data set	Factors	Fungi		Bacteria	
		R <sup>2</sup>	<i>p</i> -value	R <sup>2</sup>	<i>p</i> -value
Plots in rotation	Plant	0.384	< 0.001	0.266	< 0.001
	Cropping season	0.131	< 0.001	0.118	< 0.001
	Sampling period	0.068	< 0.001	0.149	< 0.001
	Sampling plot	0.100	< 0.001	0.053	< 0.001
Wheat residues	Cropping system	0.105	< 0.001	0.066	< 0.001
	Cropping season	0.292	< 0.001	0.248	< 0.001
	Sampling period	0.123	< 0.001	0.204	< 0.001

Figure S1 - Bacterial diversity in plants (July) and residues (October, December, February, May), as assessed with the Faith's Phylogenetic Diversity index (PD), according to sampling period, the crop within a rotation (oilseed rape in OWO or WOW, wheat in WWW, wheat in WOW or OWO) and the cropping season (2015-2016, 2016-2017). Each box represents the distribution of PD for five sampling points. Kruskal-Wallis tests were performed for each "crop within a rotation \* cropping season" combination (p-values are given under each graph). Wilcoxon tests between sampling periods were performed when the Kruskal-Wallis test revealed significant differences. Samples not sharing letters are significantly different.

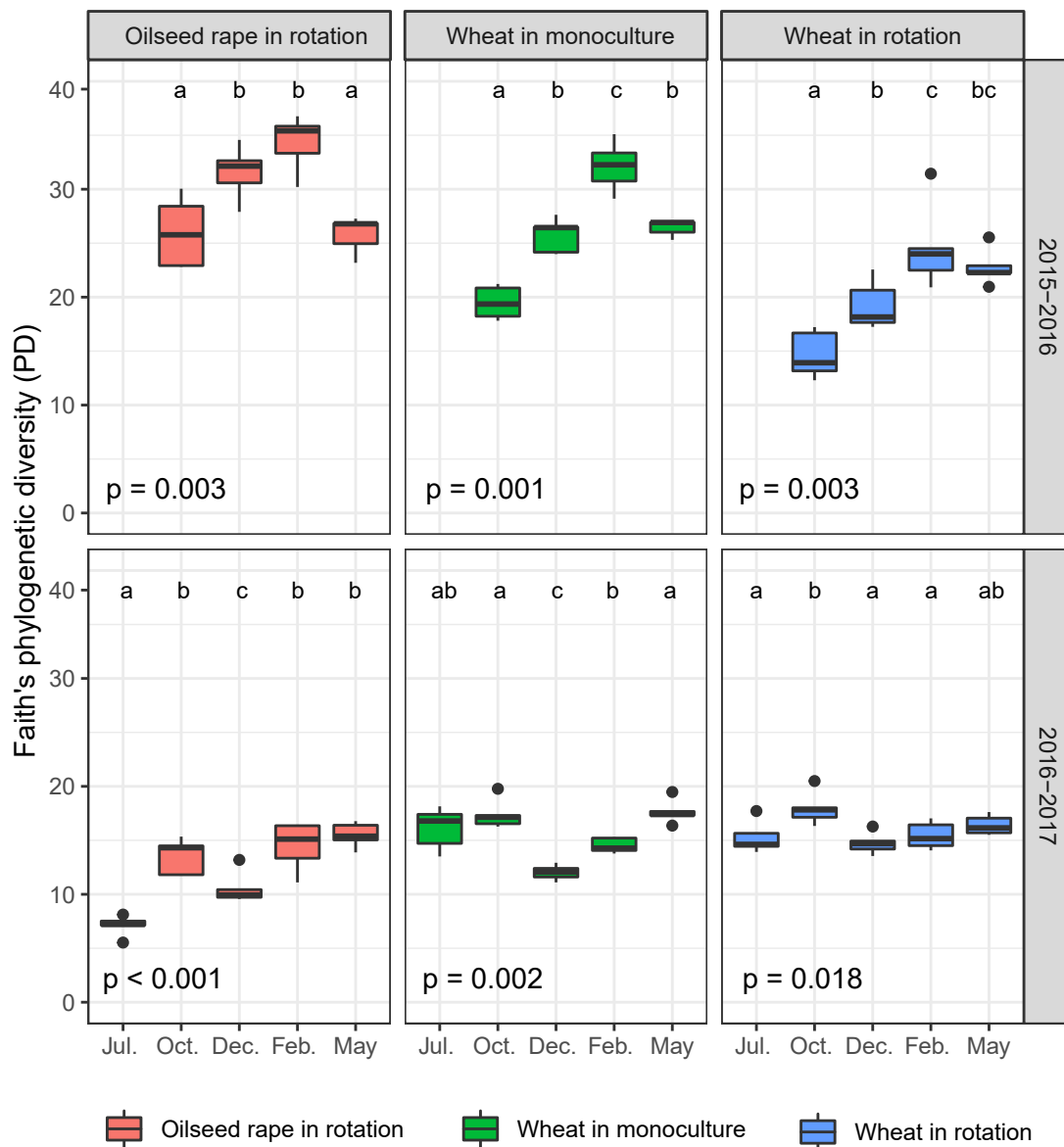
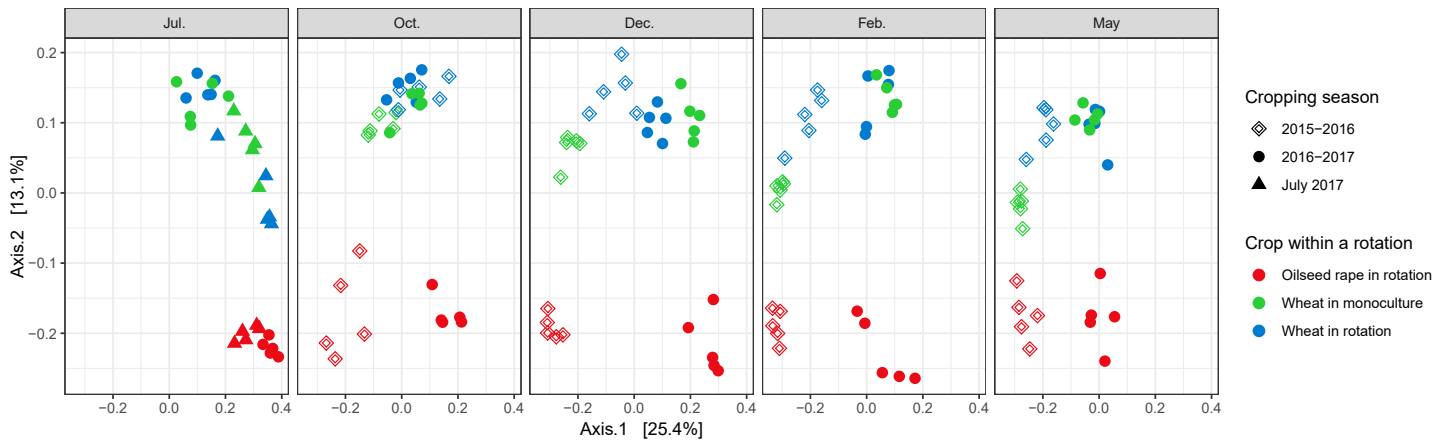
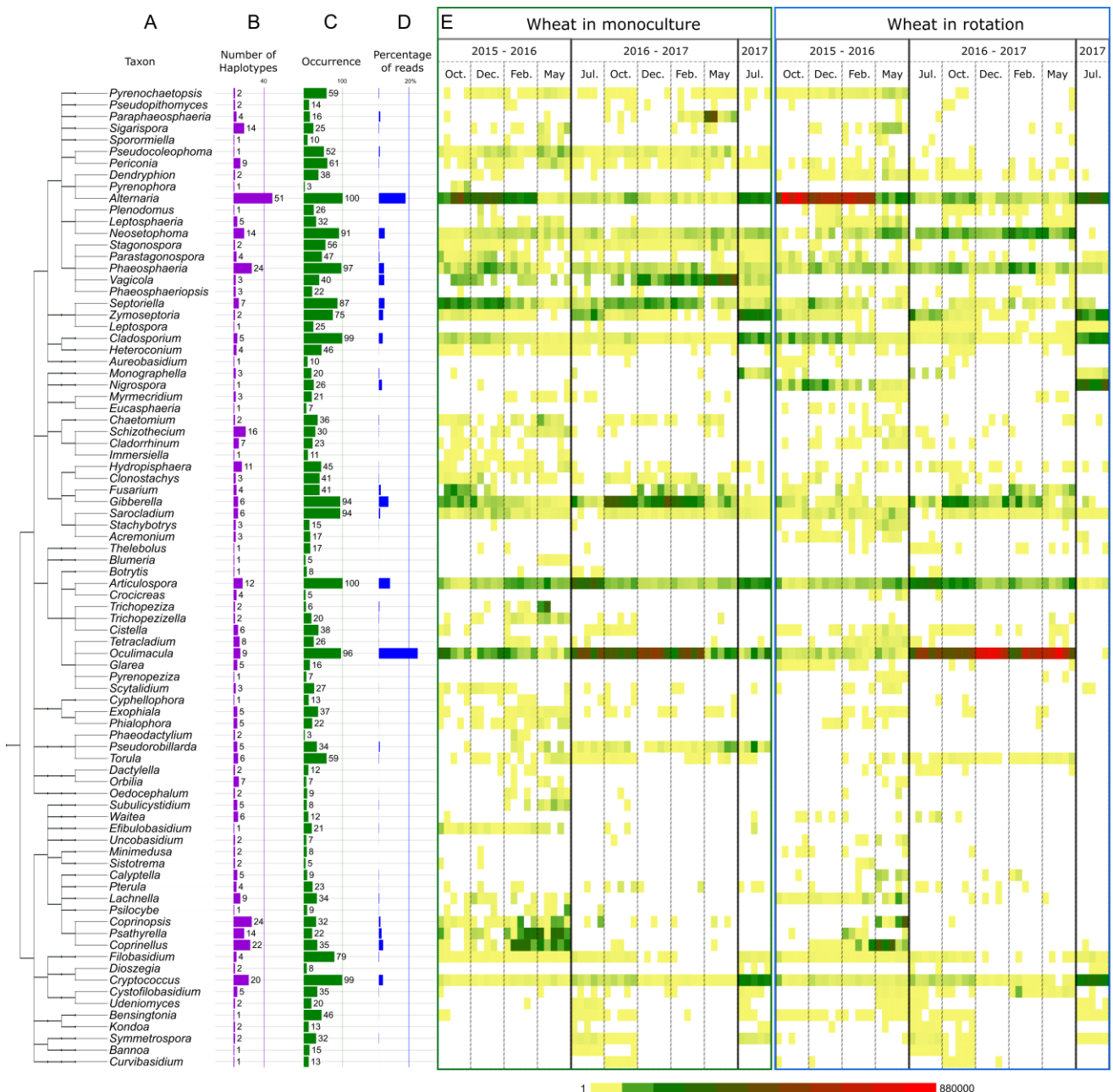


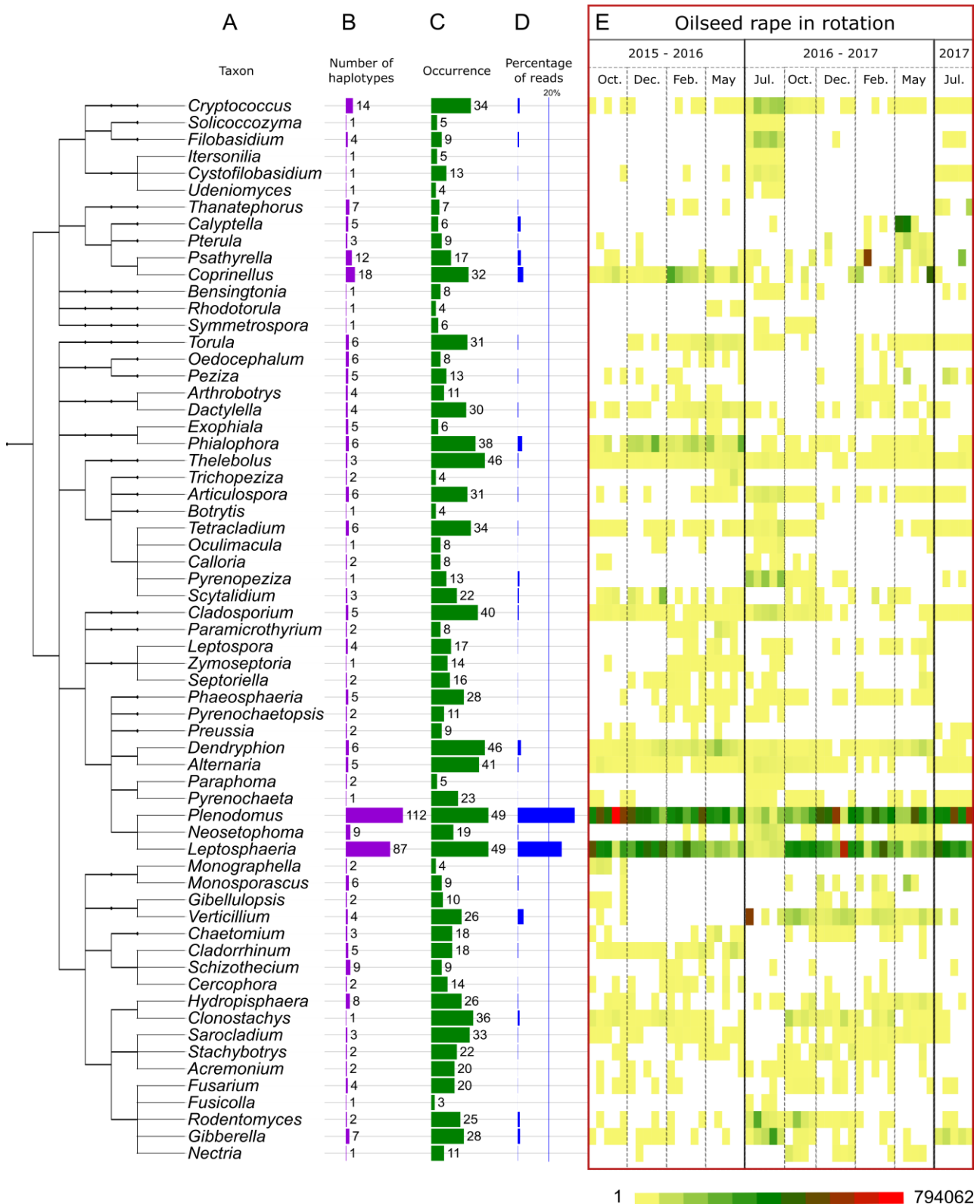
Figure S2 - Structure of the bacterial communities present in oilseed rape and wheat residues visualized by incorporating phylogenetic distances using the UniFrac distance matrix. MDS were performed on the overall dataset and faceted according to the sampling period. Each point represents one sample corresponding to a cropping season (shape: 2015-2016; 2016-2017; 2017-2018) and crop within a rotation (colour: oilseed rape in rotation, i.e. in WOW and OWO; wheat monoculture, i.e. in WWW; wheat in rotation, i.e. in WOW and OWO).



**Figure S3** - Distribution of the most prevalent fungal genera detected in wheat residues. **(A)** Cladogram of the most prevalent genera. Genera were filtered according to their occurrence (at least three times in the five sampling points for each “crop within a rotation \* cropping season \* sampling period” combination). Unclassified genera were removed from the tree. **(B)** Number of ASV of each genus. **(C)** Occurrence of each ASV in the 100 samples of wheat residues. **(D)** Percentage of reads for each genus. **(E)** Distribution of each genus in the five samples per date (increasing number of reads shown on a scale running from yellow to red).

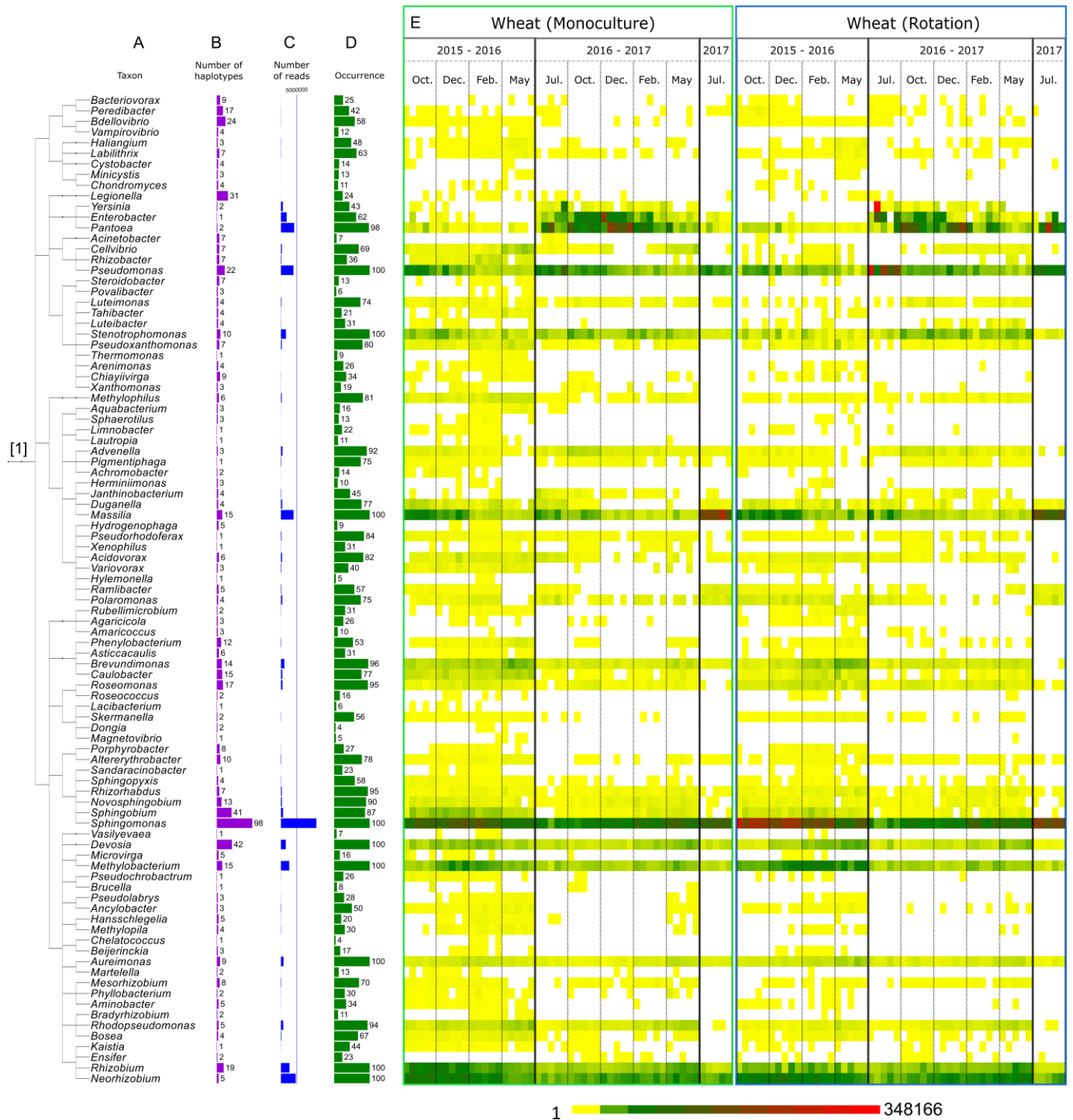


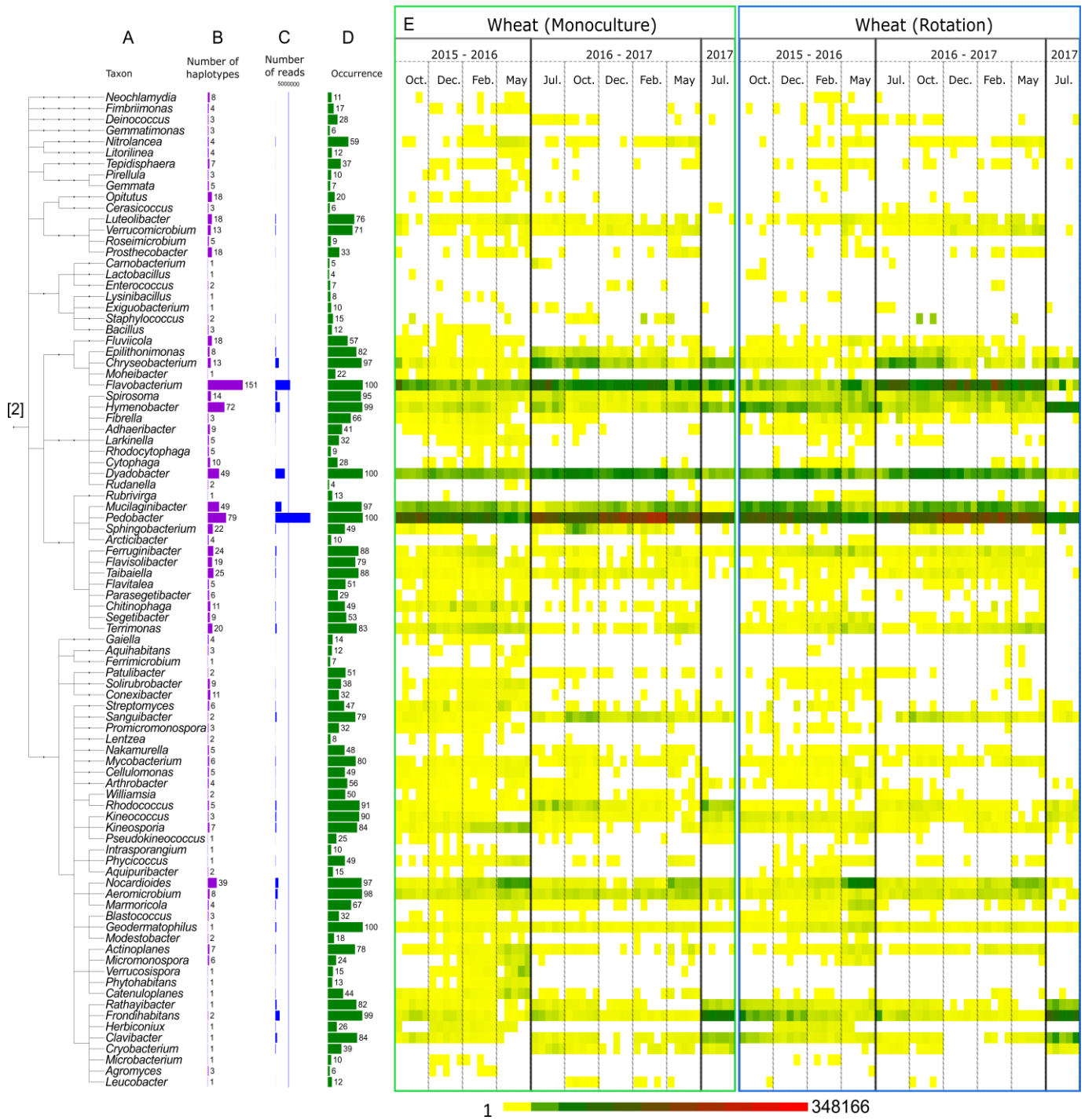
**Figure S4** - Distribution of the most prevalent fungal genera detected in oilseed rape residues. **(A)** Cladogram of the most prevalent genera. Genera were filtered according to their occurrence (at least three times in the five sampling points for each “crop within a rotation \* cropping season \* sampling period”) combination. Unclassified genera were removed from the tree. **(B)** Number of ASV for each genus. **(C)** Occurrence of each ASV in the 50 samples of oilseed rape residues. **(D)** Percentage of reads for each genus. **(E)** Distribution of each genus in the five samples per date (increasing number of reads shown on a scale from yellow to red).



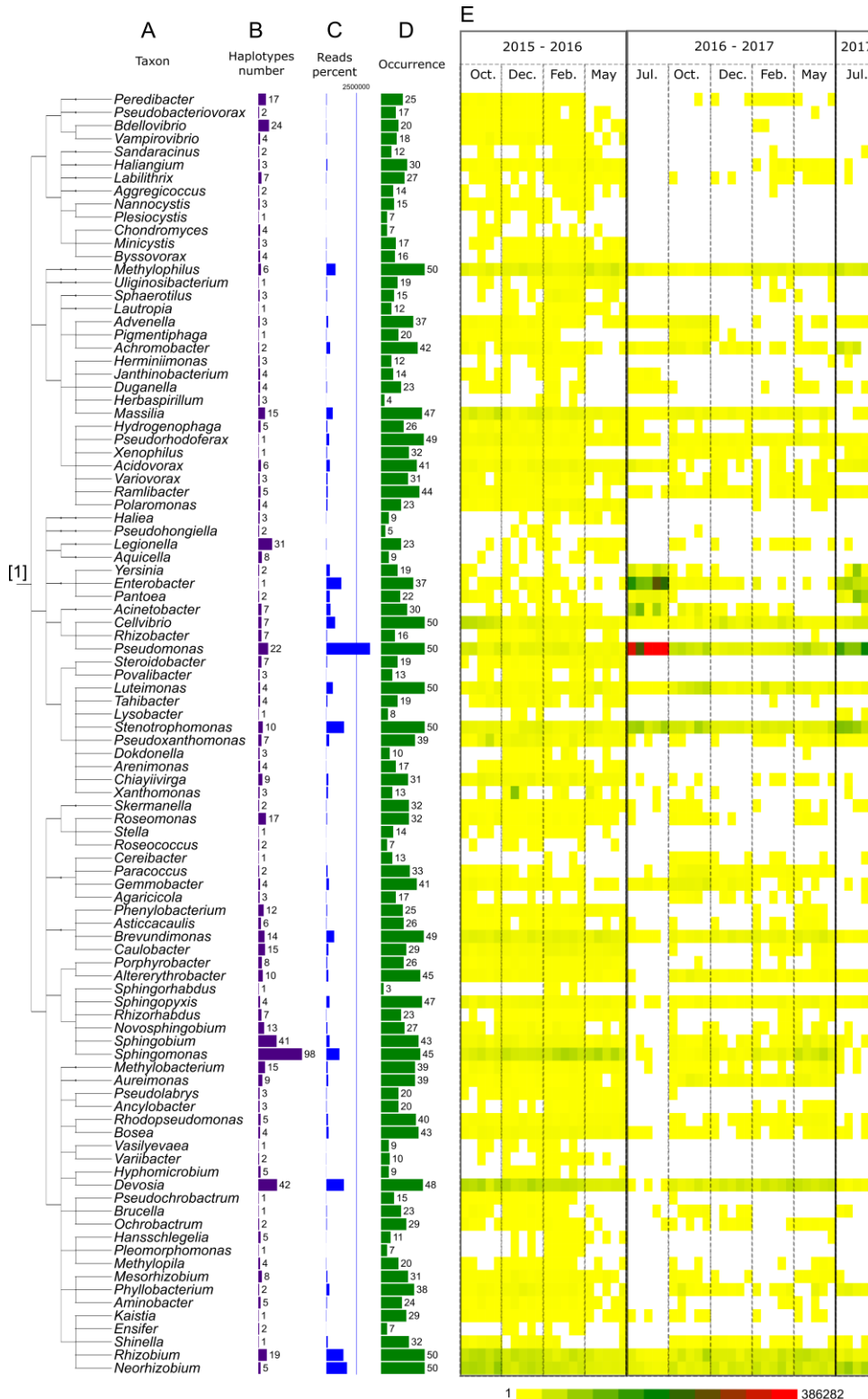


**Figure S5** - Distribution of the most prevalent bacterial genera detected in wheat residues. **(A)** Cladogram of the most prevalent genera. Genera were filtered according to their occurrence (at least three times in five sampling points for each “crop within rotation \* cropping season \* sampling period” combination). Unclassified genera were removed from the tree. **(B)** Number of ASV for each genus. **(C)** Occurrence of each ASV in the 100 samples of wheat residues. **(D)** Number of reads for each genus. **(E)** Distribution of each genus in the five samples per date (increasing numbers of reads on a scale running from yellow to red). Due to the number of genera, the plot is separated in [1] proteo- and [2] other bacteria.





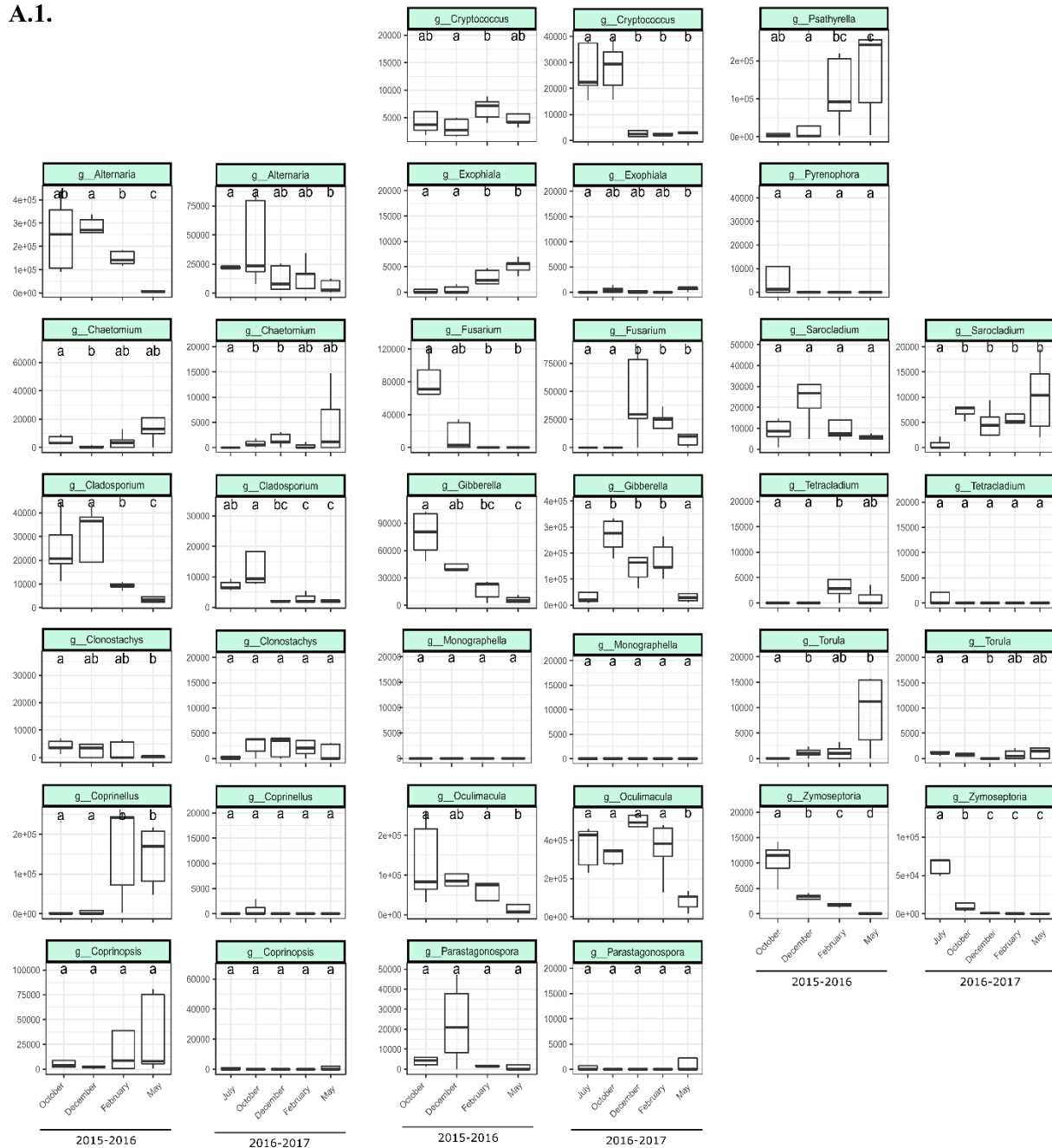
**Figure S6** - Distribution of the most prevalent bacterial genera detected in oilseed rape residues. **(A)** Cladogram of most prevalent genera. Genera were filtered according to their occurrence (at least three times in five sampling points for each “crop within rotation \* cropping season \* sampling period” combination). Unclassified genera were removed from the tree. **(B)** Number of ASV for each genus. **(C)** Occurrence of each ASV in the 49 samples of oilseed rape residues. **(D)** Number of reads for each genus. **(E)** Distribution of each genus in the five samples per date (increasing number of reads shown on a scale running from yellow to red). Due to the number of genera, the plot is separated in [1] proteo- and [2] other bacteria.



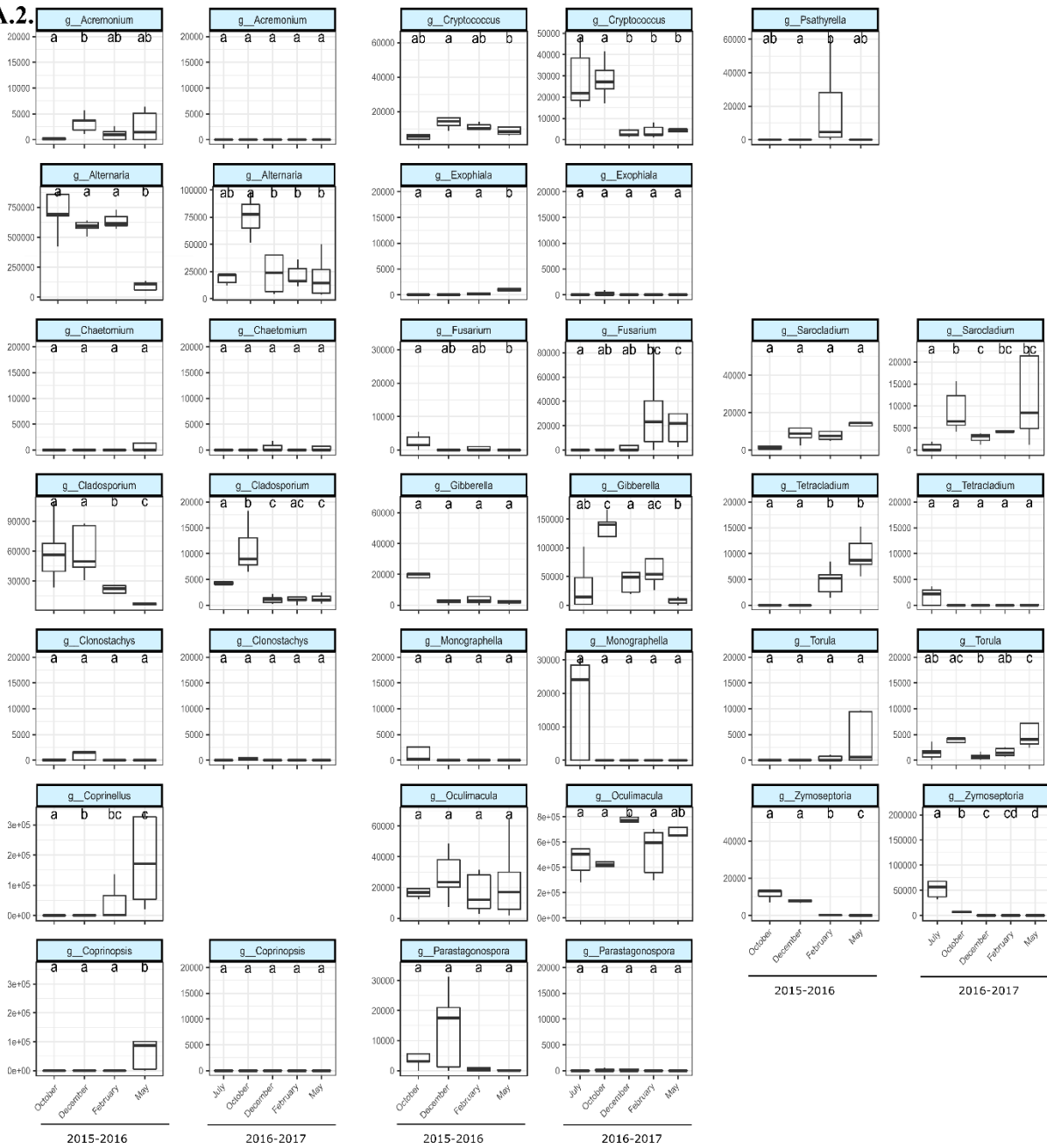


**Figure S7** - Seasonal shift in the relative abundance of a selection of fungal (**A**) and bacterial (**B**) genera present on wheat and oilseed rape residues according to the system (wheat monoculture [1], wheat in rotation [2], oilseed rape in rotation [3]) and the cropping season (2015-2016, 2016-2017). Due to the plant impact (wheat and oilseed rape) in the fungal community, the fungal genera used here as examples are different for the two plants, unlike the case of the bacterial community. Each box represents the distribution of genera relative abundance for the five sampling points. Samples not sharing letters are significantly different (Wilcoxon tests between sampling periods).

**A.1.**



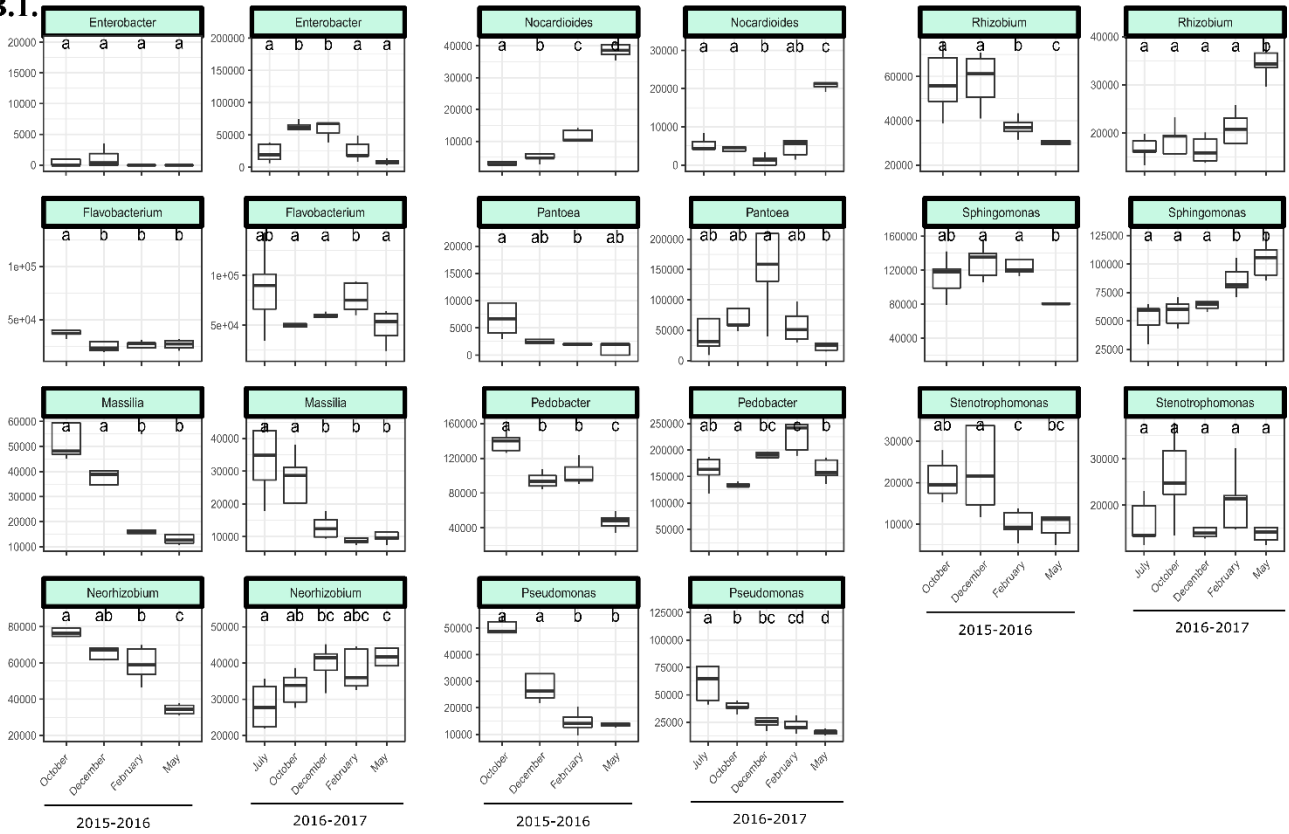
A.2.



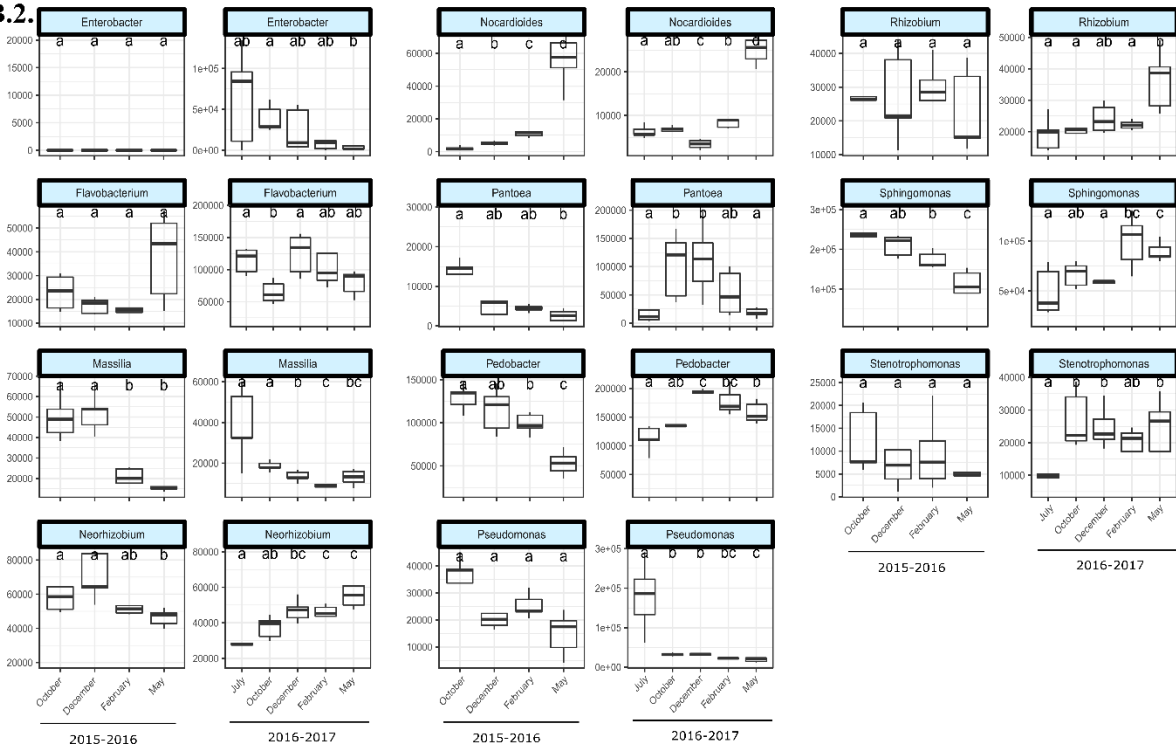
**A.3.**



### B.1.

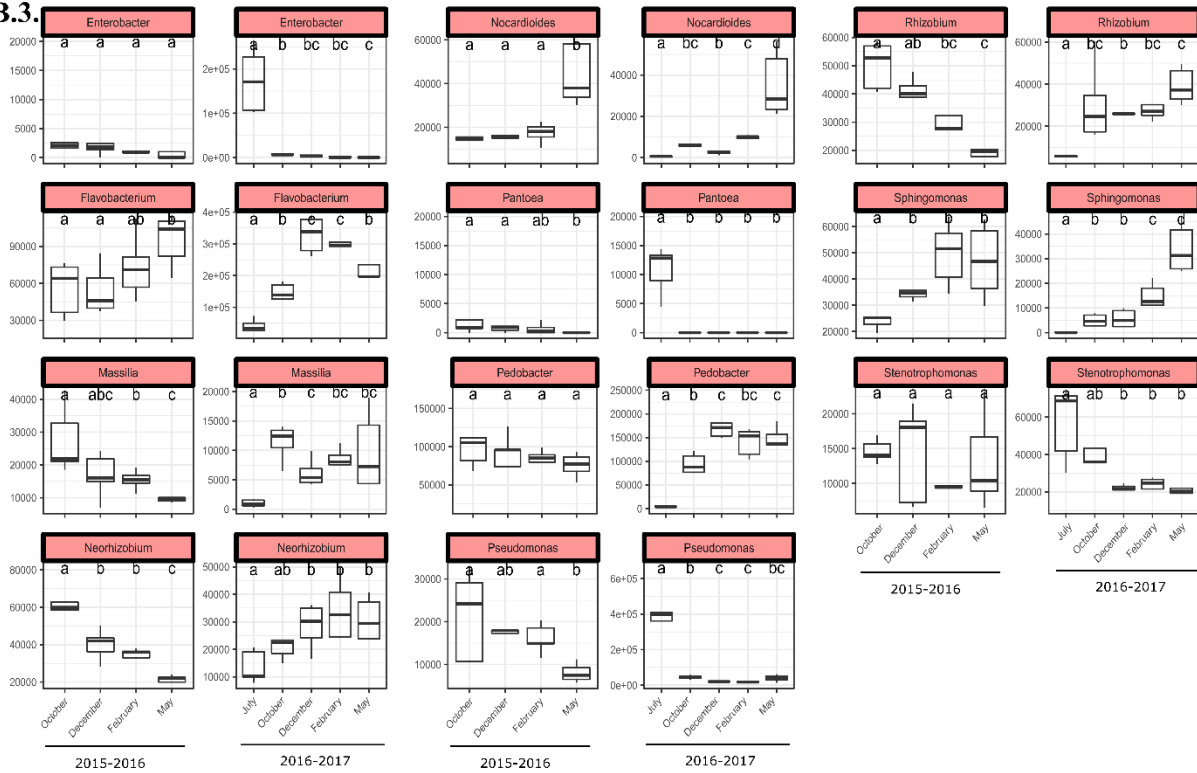


### B.2.





**B.3.**



**Table S1** - Soil texture of the three plots (WWW, OWO and WOW).

	WWW, OWO	WOW
Clay (%)	27.4	18.2
Silt (%)	53.2	61.2
Sand (%)	18.8	20.4

**Table S2** - Sampling dates of wheat and oilseed rape plants (July) and residues (October, December, February, and May) for each cropping season.

Cropping season	July	October	December	February	May
2015-2016	/	23.10.2015	04.12.2015	26.02.2016	19.05.2016
2016-2017	11.07.2016	17.10.2016	05.12.2016	06.02.2016	15.05.2017
2017-2018	07.07.2017	/	/	/	/

**Table S3** - Total number of reads and percentage (in brackets) remaining after ASV filtering.

	After DADA2	After replicate suppression	After taxon suppression
Bacterial reads	14,287,970	13,509,461 (94.6%)	13,228,976 (92.6%)
Fungal reads	9,898,487	9,753,628 (98.5%)	9,628,995 (97.3%)
Bacterial haplotypes	19,235	2,905	2,726
Fungal haplotypes	3,587	1,241	1,189

**Table S4** - Summary of meteorological data (temperature, rainfall) for the INRA Grignon experimental station (Yvelines, France), obtained from the CLIMATIK INRA database ([https://intranet.inra.fr/climatik\\_v2/](https://intranet.inra.fr/climatik_v2/)) from July 1<sup>st</sup> to May 31<sup>st</sup> of the following year, for the cropping seasons 2015-2016 and 2016-2017.

	10-day mean temperature (°C)		10-day cumulative rainfall (mm)	
	2015-2016	2016-2017	2015-2016	2016-2017
Mean	11.2	10.8	22.6	12.3
Minimum	2.0	0.9	0	0
Maximum	21.8	21.4	131	55

**Table S5** - Plant effect (wheat vs. oilseed rape) on community dispersion. This effect was tested by applying the adonis function of the vegan R package to the Bray-Curtis dissimilarity index (PERMANOVA). *P*-values (not shown) were all < 0.02.

	Fungi				Bacteria			
	All	2015-2016	2016-2017	2017	All	2015-2016	2016-2017	2017
July	0.372	/	0.611	0.755	0.423	/	0.540	0.696
October	0.495	0.612	0.755	/	0.367	0.520	0.659	/
December	0.486	0.688	0.691	/	0.370	0.573	0.641	/
February	0.429	0.541	0.651	/	0.409	0.643	0.611	/
May	0.273	0.337	0.401	/	0.315	0.435	0.508	/

**Table S6** - Decomposition of dissimilarity due to temporal changes in fungal (F) and bacterial (B) community composition. Total dissimilarity is broken down into turnover (replacement of ASV) and nestedness (gain or loss of ASV).

Crop within a rotation	Season	Sampling period compared	Total dissimilarity		Turnover		Nestedness	
			F	B	F	B	F	B
Oilseed rape	2015-2016	Oct. - Dec.	0.622	0.318	0.618	0.219	0.005	0.099
Oilseed rape	2015-2016	Dec. - Feb.	0.650	0.321	0.577	0.290	0.073	0.031
Oilseed rape	2015-2016	Feb. - May	0.591	0.390	0.565	0.202	0.027	0.188
Oilseed rape	2016-2017	Jul. - Oct.	0.652	0.554	0.648	0.250	0.004	0.304
Oilseed rape	2016-2017	Oct. - Dec.	0.620	0.353	0.549	0.217	0.071	0.136
Oilseed rape	2016-2017	Dec. - Feb.	0.585	0.353	0.516	0.276	0.068	0.077
Oilseed rape	2016-2017	Feb. - May	0.529	0.384	0.529	0.342	0.000	0.042
Wheat in monoculture	2015-2016	Oct. - Dec.	0.427	0.330	0.425	0.142	0.002	0.188
Wheat in monoculture	2015-2016	Dec. - Feb.	0.444	0.294	0.416	0.190	0.028	0.104
Wheat in monoculture	2015-2016	Feb. - May	0.444	0.458	0.424	0.255	0.020	0.203
Wheat in monoculture	2016-2017	Jul. - Oct.	0.438	0.346	0.424	0.300	0.014	0.046
Wheat in monoculture	2016-2017	Oct. - Dec.	0.463	0.330	0.257	0.113	0.207	0.217
Wheat in monoculture	2016-2017	Dec. - Feb.	0.386	0.248	0.311	0.200	0.075	0.048
Wheat in monoculture	2016-2017	Feb. - May	0.344	0.332	0.341	0.213	0.004	0.120
Wheat in rotation	2015-2016	Oct. - Dec.	0.425	0.317	0.409	0.157	0.016	0.160
Wheat in rotation	2015-2016	Dec. - Feb.	0.472	0.266	0.370	0.185	0.102	0.081
Wheat in rotation	2015-2016	Feb. - May	0.505	0.347	0.432	0.311	0.073	0.035
Wheat in rotation	2016-2017	Jul. - Oct.	0.498	0.313	0.427	0.272	0.071	0.041
Wheat in rotation	2016-2017	Oct. - Dec.	0.541	0.287	0.292	0.214	0.249	0.073
Wheat in rotation	2016-2017	Dec. - Feb.	0.350	0.284	0.292	0.284	0.059	0.000
Wheat in rotation	2016-2017	Feb. - May	0.424	0.334	0.329	0.287	0.095	0.047
Mean			0.496	0.341	0.436	0.234	0.060	0.107