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► **To cite this version:**

Sandrine S. Salmon, Tom Vittier, Sébastien Barot, Jean-François Ponge, Farida Ben Assoula, et al.. Responses of Collembola communities to mixtures of wheat varieties: a trait-based approach. *Pedobiologia*, 2021, 87-88, pp.150755. 10.1016/j.pedobi.2021.150755 . hal-03315374

**HAL Id: hal-03315374**

**<https://hal.science/hal-03315374>**

Submitted on 5 Aug 2021

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1 Ref.: Ms. No. PEDOBI-D-20-00086

2 **Responses of Collembola communities to mixtures of wheat varieties: a**  
3 **trait-based approach**

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13

14 **Highlights**

15 Mixtures of wheat varieties did not increase abundance and richness of Collembola

16 Wheat traits explained 13% of species assemblages of Collembola

17 Wheat traits explained 11% of trait assemblages of Collembola

18 Wheat sensitivity to fungal diseases explained 4.7% of trait assemblages of Collembola

19 Soil features explained 10.8% of species assemblages of Collembola

20 **ABSTRACT**

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21 The genetic diversity of cultivated crops has decreased continuously since the beginning of  
22 the 20<sup>th</sup> century, because of the gradual replacement of genetically heterogeneous traditional  
23 varieties by new genetically homogenous varieties, grown in monospecific stands. The  
24 resulting agro-ecosystems are now considered as unsustainable. Increasing within-field  
25 genetic crop diversity by using a mixture of varieties could increase the sustainability of these  
26 agro-ecosystems. This could also potentially increase non-crop biodiversity. In the present  
27 study we used an experimental approach to test whether the number of wheat varieties  
28 (genetic diversity), the number of functional groups (functional diversity), the composition of  
29 functional groups and wheat traits influence (1) species richness and abundance of  
30 Collembola, and (2) species and trait assemblages of Collembola. A total of 104 plots were  
31 seeded with either monocultures or mixtures of 2, 4 and 8 wheat varieties. Soil cores were  
32 collected in each plot to extract Collembola and measure soil features. The number of wheat  
33 varieties and the functional wheat diversity did not influence the abundance and species  
34 richness of Collembola. The sensitivity of wheat to septoria leaf blotch was positively related  
35 to the abundance and species richness of Collembola, while specific root length was  
36 positively related to collembolan species richness. Wheat traits related to sensitivity to fungal  
37 diseases, (more especially septoria leaf blotch) and characteristics of aerial parts and roots  
38 impacted collembolan species and trait assemblages, but these effects were weak. Soil  
39 features, especially the proportion of coarse silt, were also influential. Our study did not show  
40 a favorable impact of wheat genetic diversity on soil Collembola, which might result from  
41 their low abundance. Nevertheless, it suggests correlations between some variety traits and  
42 the species richness and abundance of Collembola.

43 *Keywords:* crop management practices; genetic diversity; arthropod communities; wheat  
44 variety mixture; functional diversity; plant functional traits

## 45 **1. Introduction**

46 Most current cropping systems are based on the use of a small number of species,  
47 usually grown in monospecific stands (Litrice et al., 2015). Within-field genetic diversity has  
48 decreased since the beginning of the 20<sup>th</sup> century through the gradual replacement of  
49 genetically-heterogeneous traditional varieties with genetically-homogeneous varieties, often  
50 selected for higher yield or higher resistance to certain diseases (Bonnin et al., 2014).  
51 However, it is increasingly accepted that this mode of production is fragile and unsustainable:  
52 genetically poor farming systems can resist pests and maintain high yields only through the  
53 use of chemical inputs (e.g. nitrogen and phosphorus mineral fertilizers), and through the  
54 intensive use of pesticides that tend to decrease non-crop biodiversity (Tooker and Frank,  
55 2012). A profound questioning of the modes of agricultural production thus became  
56 necessary. Favoring inter- and intraspecific crop diversity could be a promising alternative as  
57 part of sustainable agriculture (Barot et al., 2017a; Crutsinger et al., 2006; Loeuille et al.,  
58 2013).

59 Many studies showed that increasing plant species richness improved ecosystem  
60 functioning, e.g. increased nutrient retention or biomass production and stabilization of crop  
61 production (Prieto et al., 2015; Tooker and Frank, 2012). Plant diversity also increases the  
62 resistance of ecosystem productivity to climate extremes, which is an advantage in the context  
63 of global change (Isbell et al., 2015). Functional crop diversity (i.e. diversity of crop  
64 characteristics or traits) can even provide more ecosystem services than species richness per  
65 se, such as increases in yield or aboveground biomass nitrogen (Finney and Kaye, 2017).  
66 These favorable effects of biodiversity are partly explained by functional complementarity  
67 attributed to niche partitioning (Loreau and Hector, 2001). Another mechanism may explain  
68 the positive effect of crop diversity on ecosystem functions: the “sampling effect” (Barot et  
69 al., 2017a), i.e. the natural selection of species within a diverse community (compared to a

70 community poorer in species), increases the likelihood of communities to host productive  
71 species in given local conditions (soil properties, climate...). For instance, Prieto et al (2015)  
72 showed that multispecies assemblages of plants were more productive than monocultures  
73 when subjected to drought, and that the number of genotypes per species present increased the  
74 temporal stability of production under both drought and non-drought conditions. This led us  
75 to hypothesize that mixing crop varieties would lead to the same positive effects as increased  
76 species diversity, and through the same mechanisms (Barot et al., 2017b; Borg et al., 2018;  
77 Prieto et al., 2015).

78 Biodiversity in one trophic group may also impact biodiversity in other trophic groups  
79 through vertical, i.e. inter-trophic levels effects (Duffy et al., 2007). For example, the  
80 diversity of arthropods often increases with plant species richness (Castagneyrol and Jactel,  
81 2012). Plant species richness and plant functional diversity have also often been shown to  
82 benefit growth, density and diversity of soil organisms (Eisenhauer et al., 2011; Milcu et al.,  
83 2006), presumably by improving quality or diversity of belowground resources. Nevertheless,  
84 a number of studies showed no strong, or controversial, effects of plant diversity per se on soil  
85 fauna (Wardle et al. 2003, Milcu et al. 2006, Korboulewsky et al. 2016), which highlights the  
86 lack of consistency in results so far obtained.

87 Intraspecific genetic diversity could lead to the same types of effect. For example the  
88 positive impact of plant genetic diversity (variety mixtures) on the diversity of arthropods has  
89 been shown in forests (Tovar-Sánchez et al., 2015) and agricultural crop systems (Crutsinger  
90 et al., 2006; McArt et al., 2012). It is hypothesized that, by increasing crop genetic and  
91 phenotypic diversity, the number of available resources increases, which in turn has a positive  
92 impact on the diversity of fauna (Abrams, 1983). Besides providing various food resources,  
93 mixtures of crop varieties could also provide different micro-habitats that can similarly shape  
94 richer arthropod communities. Moreover, experiments on variety mixtures have shown that

95 intraspecific diversity can increase the abundance of natural enemies of insect pests and thus  
96 could be used as a plant disease management technique (Chateil et al., 2013; Zhu et al., 2000).

97         Collembola are an arthropod group known to be impacted by plant community  
98 composition and diversity (Chateil et al., 2013; Eisenhauer et al., 2011). They are among the  
99 most widespread and abundant groups of terrestrial arthropods and they impact ecosystem  
100 functioning by their high number (Hopkin, 1997). One of the main roles of Collembola is the  
101 regulation and dispersal of decomposer microorganisms (fungi and bacteria) which are  
102 responsible for the recycling of nutrients taken up by plants (de Vries et al., 2013). By  
103 consuming plant fungal pathogens, Collembola can limit fungal diseases (Meyer-Wolfarth et  
104 al., 2017; Schrader et al., 2013). By regulating the activity and dispersal of mycorrhizal fungi,  
105 they can also they can also either promote or reduce the uptake of nutrients by cultivated  
106 plants (Warnock et al., 1982; Ngosong et al., 2014) or regulate the architecture of some plants  
107 (Endlweber and Scheu, 2007).

108         A previous study showed that wheat genetic diversity benefited collembolan species  
109 richness in cultivated fields (Chateil et al., 2013). However, this study did not test for a  
110 possible effect of the identity/quality of varieties which could interact with the effect of  
111 genetic diversity. Other studies suggested that the quality of resources (e.g. litter) that enter  
112 belowground ecosystems, depending on plant identity, had more impact on the composition or  
113 biomass of soil fauna than plant diversity (Milcu et al., 2006; Viketoft and Sohlenius, 2011).

114         In the present study, we assessed whether the number of wheat varieties (genetic  
115 diversity), the number of functional groups (functional diversity), the composition of  
116 functional groups and wheat traits influence 1) the species richness and abundance of  
117 Collembola, and (2) species and trait assemblages of Collembola. The focus on functional  
118 traits of communities (e.g. plants), in addition to species, is an approach which allows

119 addressing directly the functions fulfilled by organisms both at species and community levels  
120 (Vandewalle et al., 2010). Several studies showed that functional traits of Collembola allow  
121 better predicting environmental effects on soil collembolan communities than species do  
122 (Bokhorst et al., 2012; Salmon et al., 2014; Vanhee et al., 2017).

## 123 **2. Material and methods**

### 124 *2.1. Study site, wheat varieties and experimental design*

125 Our field experiment took place in an experimental research station in Versailles,  
126 France. Winter wheat *Triticum aestivum* was chosen because it is the main cereal crop of the  
127 region, and also because it displays a wide array of phenotypic variation among varieties. The  
128 experiment has been fully described in Dubs et al. (2018a).

129 We have followed the general approach of biodiversity-ecosystem functioning  
130 experiment as implemented in the Jena experiments (Weisser 2017) and thoughts on the  
131 implementation of functional diversity in such experiments (Ebeling 2014). Twenty-seven  
132 functional traits (above- and belowground morphological, phenological and physiological  
133 traits) have been measured in 57 varieties that have been chosen to be representative of the  
134 diversity of varieties cultivated in the Parisian basin. Hence they include both local landraces  
135 and modern elite varieties (Dubs et al., 2018a). Wheat traits were measured in the field and in  
136 greenhouses by different teams of the Wheatmix consortium in 2014 (i.e. before our  
137 experiment), except traits related to diseases that come from Arvalis and databases of two  
138 laboratories (see Table 2 of Dubs et al., 2018a ). Using a hierarchical clustering method  
139 (Ward method), these varieties have been classified on the base of 27 functional traits (yield,  
140 earliness, Specific Leaf Area, specific root length, root absorption capacity of nitrate and  
141 ammonium...) into 4 functional groups thereafter named c1, c2, c3, c4 clusters. Wheat  
142 varieties of the c1 functional group were characterized by high sensitivity to fungal diseases.

143 Functional group c2 comprised wheat varieties with short root lengths, high rate of  $\text{NO}_3^-$   
144 absorption, high relative growth rate and low sensitivity to fungal diseases. The c3 functional  
145 group was composed of varieties characterized by their slow growth but elevated  
146 aggressiveness regarding plant-plant competition, and with high rate of  $\text{NH}_4^+$  absorption  
147 capacity. Finally, the c4 functional group contained varieties with high specific root lengths,  
148 low relative growth rate and low rate of  $\text{NO}_3^-$  absorption capacity (Dubs et al. 2018a). Sixteen  
149 varieties have been selected to be used in the experiment, in order to maximize the overall  
150 functional diversity: for each cluster four varieties have been chosen avoiding varieties too far  
151 from the center of the cluster (thus varieties not representative of the cluster) and avoiding  
152 varieties that are too similar within the cluster. These 16 varieties were used to create 72  
153 combinations of varieties encompassing three levels of diversity: 24, 28, and 20 mixtures  
154 combining 2, 4 and 8 varieties, respectively (Dubs et al., 2018a). The number of functional  
155 groups also varied in each of the three levels of variety mixtures: some mixtures were  
156 functionally “homogeneous” (a single functional group) while other were heterogeneous (two  
157 or more functional groups). Thus, these mixtures have been implemented for experimental  
158 purpose, to be able to compare mixtures with different number of varieties and different levels  
159 of functional diversity. These mixtures were clearly not designed because of their particular  
160 relevance for farmers. The list of varieties, mixtures and their distribution over the 104 plots  
161 are detailed in Dubs et al. (2018a). The 72 mixtures have been seeded into 72 plots and the 16  
162 varieties have also been seeded alone, in duplicate, providing a total of 104 10.5 m x 8.0 m  
163 plots encompassing 4 levels of variety mixtures (1, 2, 4 and 8 varieties each).

164 Varieties were seeded in November 2014 after ploughing. After sowing, the mixtures  
165 of seeds from the different varieties we controlled for the spatial homogeneity of germination,  
166 which shows that all varieties germinated. The crop was grown with a target yield of 60  
167 quintal  $\text{ha}^{-1}$  (75 = French average national wheat yield in 2015). No insecticide and fungicide



168 were used except for seed coating, the same for all varieties for which CELEST (2 l t<sup>-1</sup>–  
169 Fludioxonil 25 g l<sup>-1</sup>) and SIGNAM (0.6 kg g t<sup>-1</sup>–Cypermethryne 300 g l<sup>-1</sup>) were used. One  
170 spraying of two herbicides (Archipel®, 50% Iodosulfuron and 50% Mesosulfuron; Harmony  
171 Extra®, 66 % thifensulfuron-methyl and 33% tribenuron-methyle) was performed on March  
172 14, 2015. 160 kg N ha<sup>-1</sup> was used as compared to the estimated optimal amount of 180 kg N  
173 ha<sup>-1</sup>. The fertilizer (ammonium-nitrate) was spread as follows: 40 kg N ha<sup>-1</sup> on March 5, 2015,  
174 80 kg N ha<sup>-1</sup> on April 16, 2015, 40 kg N ha<sup>-1</sup> on May 11, 2015. All plots were harvested  
175 between the last week of July and the first week of August 2015.  
176 After harvest, wheat crop residues were left in the field until last soil faunal sampling (from  
177 which springtails were extracted), in November.

178

## 179 2.2. *Collembola* sampling

180 Collembola were sampled in March (one core sample taken in the center of each plot)  
181 and November 2015 (two core samples taken in the center of each half plot) in the 104 plots.  
182 The three samples taken in each plot at two sampling dates allowed better accounting spatial  
183 and temporal plot heterogeneity. Each core sample was 5 cm in diameter and 15 cm deep,  
184 leading to a total sampled area of 59 cm<sup>2</sup> per plot. Collembola were extracted during ten days  
185 by the Berlese method (Edwards and Fletcher, 1971). The three samples of Collembola were  
186 pooled together for each plot because the density of Collembola in one sample was relatively  
187 low. They were then sorted, mounted, cleared in chloral-lactophenol and identified to species  
188 level under a light microscope (400× magnification) according to Hopkin (2007), Potapow  
189 (2001), Thibaud et al. (2004) and Bretfeld (1999). Other samples were taken in the same plots  
190 to measure soil features. A soil core (5 cm diameter, 15 cm depth) was taken in the center of  
191 each plot to measure soil water content (dry/wet weight) and pH<sub>water</sub> according to ISO 10390  
192 in March 2015. Another soil core (8 cm diameter, 15cm depth, litter excluded) was taken in

193 the center of each plot in October 2015 to measure particle size distribution (clay, fine silt,  
194 coarse silt, fine sand, coarse sand) according to NF X 31-107, total concentration in nitrogen  
195 according to ISO 13878, total concentration in organic carbon and organic matter by dry  
196 combustion according to ISO 10694, and the C/N ratio. Soil analyses were performed at the  
197 INRA Laboratory for Soil Analysis (Arras, France).

### 198 *2.3. Statistical analysis*

199 Abundances of collembolan species in the three samples taken in each plot were  
200 pooled for the calculation of abundance and species richness per plot.

201 We performed generalized linear models (GLM) to determine whether the abundance  
202 and species richness of Collembola were influenced by the number of wheat varieties, wheat  
203 functional diversity (number of functional groups), functional group composition (c1, c2, c3,  
204 or c4) and mean of wheat functional traits in variety mixtures. Given the high number of  
205 wheat traits available, we first made an a priori selection according to their potential impact  
206 on Collembola. We selected traits related to root system, plant cover, and sensitivity to fungal  
207 diseases. At least some collembolan species are known to live and feed on roots (Thimm and  
208 Larink, 1995), depend on plant cover (Heiniger et al., 2015) and feed on fungi, including  
209 pathogenic fungi (Friberg et al., 2005; Jorgensen et al., 2005; Ponge, 1988). Wheat trait  
210 measures and soil features were then standardized (thus discarding spurious effects of various  
211 units). Spearman correlation coefficients were calculated between wheat traits, soil features  
212 and geographical coordinates in order to eliminate correlated explanatory variables (Table  
213 S3). As coarse silt was highly correlated with other particle size fractions and with  
214 geographical coordinates according to a textural gradient, the latter two sets of variables were  
215 discarded from further analyses. As the impact of soil texture on soil fauna is well known,  
216 especially in conventional agroecosystems (Grossi and Brun, 1997) we preferred to keep

217 coarse silt and remove geographical coordinates. The set of soil features selected for further  
218 analyses was coarse silt, soil pH, soil water content and C/N ratio. Correlation coefficients  
219 also allowed to select the set of wheat traits used in further analyses (Table 1).

220 As the number of varieties and the number of functional groups bring redundant  
221 information about wheat diversity, they were analysed separately, like wheat traits and the  
222 composition of functional groups (groups of varieties associated according to their traits). We  
223 thus performed a first model to test the effect of wheat diversity (number of varieties), the  
224 composition of wheat functional groups (c1, c2, c3 and c4), and soil features, on species  
225 richness and abundance of Collembola, respectively. This model allowed to share the part of  
226 diversity and that of composition of functional groups (varying according to traits displayed in  
227 each functional group) in the effect of wheat on Collembola communities (Spehn et al. 2005).  
228 In the same way, we then analysed the effect of the number of functional groups (functional  
229 diversity), the set of wheat traits and soil features, on species richness and abundance of  
230 Collembola. Soil features were included in models, because the potential effect of variety  
231 mixtures on collembolan communities could be blurred or biased in the absence of reference  
232 to soil variation.

233 We then selected final models step by step, by keeping variables that significantly  
234 contributed to models and by using AIC (Spehn et al. 2005, Bolker et al. 2009). All models  
235 were diagnosed with the “DHARMA” package (Hartig, 2020) for R software: “Uniformity”  
236 (tests if the global distribution of residuals is in line with predicted values with a  
237 Kolmogorov-Smirnov test and a QQ-plot), “Outliers” (tests if there are more simulation  
238 outliers than expected), “Dispersion” (tests if the simulated dispersion is equal to the observed  
239 dispersion), “Quantiles” (fits a quantile regression or residuals against a predictor (predicted  
240 value by default), and tests if that predictor conforms to the expected quantile),

241 “Zeroinflation” (tests if there are more zeros than expected). In order to fulfil all model  
242 assumptions (especially dispersion), collembolan abundances were log-transformed.

243 At last we performed Analyses of Deviance (Type II Wald chi-square tests) on final  
244 models, with the “Anova” function of the “car” R package. Full models and codes are detailed  
245 in Tables S3 to S7).

246 Canonical correspondence analysis (CCA; Ter Braak (1986) followed by Monte Carlo  
247 permutation tests (999 permutations) was used to assess whether wheat variety traits, variety  
248 number, functional group number, functional group composition and soil features constrained  
249 collembolan species assemblages. This technique was particularly appropriate to our data  
250 because it addresses the large number of zeros which characterizes community compositional  
251 data (Legendre and Legendre, 1998) and does not try to display all variation in the data, but  
252 only the part that can be explained by the constraints. Species represented by only one  
253 individual in one sample were deleted from CCA analyses. Two first CCAs were performed  
254 following the same logic and using the same explanatory variables as for GLM, i.e. one with  
255 the number of wheat varieties, the composition of wheat functional groups (c1, c2, c3, c4) and  
256 soil features (soil water content, pH<sub>water</sub>, coarse silt, and C/N ratio), the other CCA with the  
257 number of wheat functional groups, wheat traits (see Table 1) and soil features. Soil features  
258 were included in all analyses to separate the variation of collembolan species distribution due  
259 to soil features from that due to wheat related variables. This also limited misinterpretations in  
260 the case of interactions between soil features and wheat related variables. Soil features and  
261 wheat traits were standardized prior to CCA. Then, partial CCAs (pCCA) were performed  
262 from each of the two first CCAs, to disentangle the effects of wheat diversity (number of  
263 variety or number of functional groups), wheat composition (functional group composition or  
264 traits) and soil features, on the composition of collembolan communities. Prior to partial  
265 CCAs, two partial least square regressions (CCA-PLSs; Tenenhaus, 1998) were performed

266 using the same variables as for the two first CCAs, in order to classify explanatory variables  
267 according to their contribution to the distribution of species. Variables contributing most to  
268 species distribution (with the highest Variable Importance in the Projection, VIP) were  
269 included in three partial CCAs and their effect was displayed in three graphics (Figs. 3a, b, c).

270 Two redundancy analyses (RDA; Legendre and Legendre, 1998) were performed,  
271 following the same procedure and using the same explanatory variables as for GLM and  
272 CCA, to measure the effects of 1) variety number, functional group composition and soil  
273 features, and 2) functional group number, wheat variety traits (Table 1), and soil features, on  
274 community-weighted mean traits (CWM) of Collembola. RDA was chosen because CWMs  
275 are continuous variables. CWM traits have been widely used in ecological research for  
276 summarizing different facets of functional composition and shifts in mean trait values within  
277 communities due to environmental selection for some functional traits (Ricotta and Moretti,  
278 2011). Collembolan traits were extracted from the Coltrait database (Salmon et al., 2014),  
279 then the CWM of each trait was calculated using “species x traits” and “plots x species  
280 abundance” matrices (Ricotta and Moretti, 2011). RDA is a direct gradient ordination method  
281 that constrains the position of response variables, here collembolan CWMs, by a set of  
282 environmental factors, here wheat related variables and soil features (Legendre and Legendre,  
283 1998). Using RDA to analyze the impact of diverse environmental variables on the  
284 distribution of CWMs is a common practice in trait-based approaches in ecology (Vandewalle  
285 et al., 2010). As for pCCAs, partial RDAs (pRDA) were performed to disentangle the effects  
286 of wheat diversity (variety or functional group number), wheat composition (functional group  
287 composition or traits) and soil features on collembolan CWMs. Then, further partial RDAs  
288 were performed to assess the relative importance of traits related to either sensitivity to fungal  
289 diseases, crop canopy cover or root characteristics, after removing the effects of soil features,

290 wheat diversity and of the two other types of wheat traits. RDAs were followed by Monte  
291 Carlo permutation tests (999 permutations).

292 GLMs were performed with R software (version 3.6.3, 2020), using the “glmmTMB”  
293 package (Brooks et al 2017) for GLM construction, the DHARMA package for diagnostics of  
294 models (Hartig, 2020). Analyses of Deviance on final models were performed with the “car”  
295 package (Fox, Weisberg, 2019). CWMs were calculated with the FD package (Laliberté et al.,  
296 2014) of R. CCA and RDA were performed with XLSTAT (v2013.3.05, Addinsoft, 2021).

297

### 298 **3. Results**

#### 299 *3.1. Effect of wheat varieties on abundance and species richness of Collembola*

300 A total of 1,594 individuals were found. The abundance of Collembola in the three  
301 pooled samples varied from  $10 \pm 0.53$  individuals ( $1,698 \text{ ind.m}^{-2}$ ) in plots with two varieties  
302 to  $25 \pm 3.25$  individuals ( $4,246 \text{ ind.m}^{-2}$ ) in plots with eight varieties (mean  $\pm$  standard error),  
303 but the difference was not significant (Fig. 1a, Table S5). Collembolan species richness per  
304 plot did not vary with the number of wheat varieties, averaging four species per plot (Fig. 1b,  
305 Table S4). First, models showed that variety number and functional group number did not  
306 influence the species richness and abundance of Collembola (S4 and S5, Fig.1). Two wheat  
307 traits, Specific Root Length and sensitivity to septoria leaf blotch, and the c1 functional group  
308 positively increased the species richness of Collembola but to a lesser extent than the coarse  
309 silt content (Table 2, Figs. 2b, c, S2, S3b). The sensitivity to Septoria leaf blotch also  
310 significantly increased the abundance of Collembola but its effect was twice less than that of  
311 coarse silt content (Tables 2, S7, Figs. 2a, S3a). A negative effect of the c2 functional group

312 on collembolan abundance was also detected by the first models but this effect was no longer  
313 significant (or only marginally significant) in the final model (Tables 2, S6).

314 .

### 315 *3.2. Effect of wheat varieties on species assemblages of Collembola*

316 The CCA with wheat variety number, wheat functional group composition (c1, c2, c3,  
317 c4) and soil features (soil water content, pH<sub>water</sub>, coarse silt, and C/N) showed that these  
318 variables significantly (p-value: 0.011) explained 23.3% of the variation of species  
319 distribution. Partial CCAs testing the effect of variety number and functional group  
320 composition after removing the effect of soil features showed that variety number and  
321 functional group composition significantly explained 9.4% (p-value: 0.010) of the  
322 collembolan species distribution. When variety number (1.1%, p-value 0.60) and functional  
323 group composition (6.6%, p-value: 0.13) were tested separately, their effect was not  
324 significant. The effect of soil features after removing the effect the variety number and  
325 functional group composition accounted for 8.7% (p-value: 0.006) of the collembolan species  
326 distribution.

327 The CCA with functional group number, wheat traits (Table 1) and soil features as  
328 explanatory variables showed that these variables significantly explained 27% (p-value: 0.04)  
329 of the variation of collembolan species distribution. Partial CCAs testing the effect of  
330 functional group number and wheat traits after removing the effect of soil features showed  
331 that functional group number and wheat traits significantly explained 14.5% (p-value: 0.01) of  
332 the collembolan species distribution. When the functional group number and wheat traits were  
333 tested separately, wheat traits significantly explained 13.1% (p-value 0.016) of collembolan  
334 species distribution, while the effect of functional group number was not significant (1.173%,

335 p-value: 0.659). The effect of soil features after removing the effect of wheat traits and  
336 functional group number accounted for 10.8% (p-value < 0.0001).

337 The first CCA-PLS classified the variety number, functional group composition and  
338 soil features as follow: nbvar > Co-silt > C\_N > pH > c2-0 > c2-1 > Water > c3-0 > c3-1 >  
339 c1-0 > c1-1 > c4-0 > 4-1. The second CCA-PLS classified functional group number, wheat  
340 traits and soil features as follows: GAIT1 > Co-silt > Septo > pH > C\_N > SRR > GAIT6 >  
341 nbclu > YR > Water > SRL > RD. In order to facilitate the interpretation of CCA graphs by  
342 limiting the effect of interacting factors, we performed three CCAs with the most influential  
343 variables given by the two CCA-PLSs: a first one with the number of wheat varieties and the  
344 c2 functional group (Fig. 3a), the second one with the three traits most contributing to  
345 Collembola species distribution (GAIT1, Septo, SRR, Fig. 3b) and the third CCA with the  
346 three most contributing soil features (Co-silt, pH, C/N, Fig. 3c). Figure 3a shows that species  
347 positively influenced by the number of wheat varieties were *Proisotoma minuta*, *Seira*  
348 *domestica*, *Entomobrya lanuginosa* and *Folsomides parvulus*. *P. minima* and *Folsomia*  
349 *candida* were more abundant in the c2 wheat functional group, while *Desoria tigrina*,  
350 *Isotomurus palustris* and *Megalothorax gr. incertus* were less abundant or absent from plots  
351 with the c2 functional group. Figure 3b shows that *D. tigrina*, *Seira domestica* and *Willowsia*  
352 *platani* were positively influenced by plant cover (GAIT1). *Isotomurus palustris*,  
353 *Sminthurinus elegans*, *Sminthurides signatus*, *Parisotoma notabilis* and *Megalothorax gr.*  
354 *incertus* were positively impacted by the shoot/root ratio and/or the sensitivity to septoria. At  
355 last, Figure 3c shows that *F. parvulus*, *S. signatus*, *Sminthurinus aureus*, and *P. minima* were  
356 negatively impacted by coarse silt, contrary to *P. minuta*, *F. candida*, and *Megalothorax*  
357 *minimus* which were more frequent or abundant in plots with a higher level of coarse-silt.  
358 Higher soil pH was favorable to *Heteromurus nitidus* and *I. palustris* and the C/N ratio  
359 positively influenced the distribution of *D. tigrina* and *S. domestica*.



360 *3.3. Effect of wheat varieties on trait assemblages of Collembola*

361 The RDA testing the effect of wheat variety number, functional group composition  
362 and soil features showed that these variables together significantly explained 14.1% of the  
363 variation of collembolan trait distribution (p-value: 0.004). Partial RDAs testing the effect of  
364 variety number after removing the effects of soil features and functional group composition  
365 showed no significant effect on collembolan trait distribution (0.45%, p-value: 0.78). The  
366 effect of functional group composition after removing that of soil features and variety number  
367 on collembolan trait distribution was not significant (5.1 %, p-value:0.17). Even when tested  
368 together after removing the effect of soil features, variety number and functional group  
369 composition had no significant effect. The effect of soil features after removing the effect the  
370 variety number and functional group composition accounted for 9.7% (p-value:0.004) of the  
371 variation in collembolan trait distribution.

372 The RDA with wheat functional group number, wheat traits (Table 1) and soil features  
373 showed that these variables significantly explained 19.2% (p-value: 0.004) of the variation of  
374 collembolan trait distribution. Partial RDAs testing the effect of functional group number and  
375 wheat traits after removing the effect of soil features showed that they significantly explained  
376 10.9% (p-value: 0.004) of collembolan trait distribution. When functional group number and  
377 wheat traits were tested separately, wheat traits significantly explained 10.85% (p-value  
378 0.015) of collembolan trait distribution, while the effect of functional group number was not  
379 significant (0.08%, p-value: 0.999). The effect of soil features after removing the effect of  
380 wheat traits and functional group number accounted for 8.8% (p-value: 0.002) (Fig. 4a).  
381 Further partial RDAs were achieved to disentangle the effect of three types of wheat traits  
382 linked to: 1) roots (SRL, SRR, RD), 2) plant cover (Green Area Index: GAI), 3) sensitivity to  
383 fungal diseases (Septo, YR). These partial RDAs were performed after removing the effect of  
384 soil features, functional group number and the two other types of wheat traits than that tested.

385 Traits linked to the root system (2.8%, p-value: 0.45) and plant cover (2.25 %, p-value: 0.29)  
386 had no significant effects on the distribution of collembolan traits, respectively. The  
387 sensitivity to fungal diseases (septoriose and yellow rust) significantly explained 4.7% (p-  
388 value: 0.018) of collembolan trait distribution (Fig. 4a).

389 Partial RDAs assessing the effects of the sensitivity to fungal diseases on the  
390 distribution of collembolan traits (Fig. 4a) showed that the sensitivity to septoria leaf blotch  
391 (Septo) was associated to Collembola with pigmented and spherical body, long furcula,  
392 presence of trichobothria, high ocelli number and living in superficial soil layers. Axis 2  
393 separated collembolan traits according to sensitive and insensitive varieties to yellow rust.  
394 Collembola associated to the sensitivity to yellow rust were pigmented, with high ocelli  
395 number, pseudocelli, sexual reproduction and not specialized for a soil layer depth (NS).

396 The RDA assessing the effects of soil features (Fig.4b) (after removing variety number  
397 and functional group composition) showed that they explained 9.7% ( $p = 0.004$ ) of the  
398 variation in the distribution of collembolan traits. Axis 1 separated soils with a high content of  
399 coarse silt on the positive side from soils with a low content of coarse silt and thus more clay  
400 on the negative side. Axis 2 separated soils with a neutral pH from soils that were richer in  
401 organic matter (C/N) and wetter (Water). Plots with more coarse silt accommodated species  
402 living only deeply in the soil (Eda), or in upper soil layers (Hemieda), and species living in  
403 both deep and superficial soil layers (Eda-Hemieda) while soils with less coarse silt and thus  
404 more clay accommodated epigeic species, living above the soil surface (Epi) or species  
405 without preference regarding soil layers (NS). Morphological traits supported this  
406 interpretation: characteristics of epigeic species such as spherical body, higher number of  
407 visual organs (Ocel), long legs (LegL), long furcula (FurcaL), presence of trichobothria  
408 (Tricho) and pigmentation (Pigm) of the body were associated with soils displaying less  
409 coarse silt and therefore more clay. Species with cylindrical body occurred more frequently in

410 soils with high coarse silt content. The number of Collembola that did not have a preference  
411 for soil depth (NS) was higher in average in wetter soils with a high C/N ratio.

## 412 **4. Discussion**

### 413 *4.1. Effect of wheat varieties on the abundance and species richness of Collembola*

414 The number of wheat varieties and wheat functional groups (functional wheat  
415 diversity) did not impact the abundance and species richness of Collembola, contrary to our  
416 expectation (Hypothesis 1). This result is not due to the short duration of our study since  
417 Aström and Bengtsson (2011) observed no dispersal limitation of Collembola over distances  
418 as far as 3 meters in 10 weeks. Our results support the conclusions of several studies showing  
419 little effects of plant species or functional group richness on soil biota, including Collembola  
420 (Wardle et al. 2003, Salamon et al., 2004, Milcu et al. 2006, Korboulewsky et al. 2016). The  
421 weakness of the effect of wheat genetic diversity is supported by the results of Dubs et al.  
422 (2018b) for aboveground arthropods on the same experimental parcels. Nevertheless, plant  
423 genetic and functional diversities have been shown to increase the density and/ or the  
424 diversity of many groups of invertebrates (Crawford et al., 2007; Crutsinger et al., 2006;  
425 Johnson et al., 2006; Jones et al., 2011). Moreover, Chateil et al. (2013) observed that  
426 mixtures of wheat varieties increased the species richness of Collembola compared to a single  
427 wheat variety. However, in Chateil et al. (2013) the respective effects of diversity and  
428 composition of wheat varieties could not really be disentangled. In fact, the observed increase  
429 in collembolan species richness could have resulted from the identity of wheat varieties that  
430 had been added to the single variety (used as a control) when creating variety mixtures.

431 Discrepancies among the effects of plant diversity observed in different studies on  
432 species richness of Collembola suggest that these effects are weak and/or are blurred by  
433 interactive factors. The effect of crop diversity could depend on other factors such as

434 agricultural practices (e.g. conventional vs. organic farming), surrounding landscape  
435 (Bengtsson et al., 2005; Jeanneret et al., 2003) and soil features (Heiniger et al., 2015). The  
436 favorable impact of coarse silt (its content being inversely proportional to clay content) on the  
437 abundance and species richness of Collembola is likely due to the fact that coarse silt (in  
438 comparison to clay) reduces soil compaction. Indeed, soil compaction often increases with  
439 soil tillage in conventionally cultivated crops where earthworms are scarce (Clements et al.,  
440 1991; Imhoff et al., 2016; Nuutinen, 1992). By limiting soil compaction (Håkansson and  
441 Lipiec, 2000), known to decrease the abundance of Collembola (Schrader and Lingnau,  
442 1997), a more silty texture could favor a higher abundance and species richness of  
443 Collembola. Regarding agricultural practices, our field experiment was conducted in an  
444 experimental agricultural research center so that our plots had a long history of conventional  
445 use of tillage and pesticides, which can have reduced collembolan biodiversity at start of the  
446 experiment (Cortet et al., 2002; Tsiafouli et al., 2015), limiting the response of this  
447 microarthropod group to mixtures of varieties, contrary to the field experiment by Chateil et  
448 al. (2013), which was under organic farming. This hypothesis is corroborated by the  
449 particularly low abundances of Collembola in our field experiment. Although collembolan  
450 abundances were within the range found by Cluzeau et al. (2012) and Joimel et al. (2017) in  
451 arable lands, they were in average twice to three times lower than in other conventional crop  
452 systems in Europe (Cluzeau et al., 2012; Heisler and Kaiser, 1995; Lagerlof and Andren,  
453 1991). The mean local species richness was also relatively low in all plots and was at the  
454 lowest level of the range of species richness observed by Cluzeau et al. (2012) for the same  
455 sample size.

456         We observed that the composition of the functional groups of wheat and some traits  
457 influence the species richness and abundance of Collembola. Collembolan species richness  
458 increased in plots with varieties of the c1 functional group, which was characterized by a high

459 sensitivity to fungal diseases. This effect was supported by the significant impact of two  
460 wheat traits: sensitivity to septoria leaf blotch, which was related to increase in both  
461 abundance and species richness of Collembola, and specific root length, related to increase in  
462 their species richness. However, these effects were weak, and generally twice less as the  
463 effect of soil particle size (coarse silt).

464         Although weak, the effect of wheat composition was higher than that of wheat  
465 diversity in our field experiment. Other studies on collembolan populations showed that the  
466 effect of plant functional groups was stronger than the effect of plant diversity per se (Milcu  
467 et al., 2006; Salamon et al., 2004). However, these studies dealt with functional groups of  
468 various plant species and it is the first time that this effect could be demonstrated with groups  
469 of plant varieties. Our results suggest that specific root length could contribute to increase  
470 collembolan species richness by increasing food resources for soil-dwelling species: the  
471 higher the specific root length, the thinner the roots and the shorter their lifespan (Eissenstat et  
472 al., 2000). Some collembolan species are known to feed on roots (Thimm and Larink, 1995).  
473 Moreover some Collembola, assumed to be mainly decomposers, switch their diet in the  
474 presence of plant roots, especially fine roots, and may obtain carbon and nitrogen almost  
475 exclusively from plant roots (Eerpina et al., 2017; Endlweber et al., 2009). In the same way,  
476 an increase in the sensitivity of wheat varieties to septoria leaf blotch, may increase food  
477 resources for fungal-feeding collembolan species (Friberg et al., 2005; Jorgensen et al., 2005;  
478 Ponge, 1988). The biomass of fungi and fungal-invaded area of wheat available to Collembola  
479 should increase in the more fungal-sensitive wheat varieties.

#### 480 *4.2. Effect of wheat on species and trait assemblages of Collembola*

481         Most of the species collected in our study are frequently observed in agricultural  
482 crops, e.g. *Entomobrya multifasciata*, *Folsomides parvulus*, *Heteromurus nitidus*, *Isotomurus*

483 *palustris*, *Lepidocyrtus cyaneus*, *L. lanuginosus*, *Megalothorax minimus*, *Neotullbergia*  
484 *ramiscuspis*, *Parisotoma notabilis*, *Proisotoma minuta*, *Pseudosinella alba*, *Sminthurinus*  
485 *aureus*, *Sminthurinus elegans* (Axelsen and Kristensen, 2000; Frampton et al., 2001; Fratello  
486 et al., 1985; Ponge et al., 2003; Querner and Bruckner, 2010; Rebecchi et al., 2000; Sousa et  
487 al., 2004).

488         The number of wheat varieties, the number of functional groups and functional group  
489 composition (c1, c2, c3 or c4) did not have any effects on collembolan species and trait  
490 assemblages when tested alone. The effect of variety number and functional group  
491 composition (especially c2, including varieties with low sensitivity to septoria leaf blotch)  
492 together was significant but weak as it explained 9.4% of the collembolan species distribution.  
493 The contribution of functional group composition to explain the distribution of collembolan  
494 species and traits was weak but about six times higher (about 6%) than that of variety number.  
495 As for the variety number, the effect of the functional diversity (functional group number)  
496 alone was extremely weak (about 1%) and not significant. Wheat traits contributed the most  
497 to explain the distribution of collembolan species and traits but only about 13% and 11%,  
498 respectively.

499         Wheat traits related to the sensitivity to fungal diseases and to characteristics of aerial  
500 (plant cover) and root parts impacted significantly, although weakly, the distribution of  
501 collembolan species and traits. Wheat traits related to aerial parts (plant cover) and root  
502 characteristics contributed to explain the distribution of collembolan traits but their effects  
503 were not significant when analysed separately. The sensitivity to fungal diseases, and more  
504 especially to septoria leaf blotch, were the only trait the effect of which remains significant  
505 after deleting the effect of all other variables. Among species associated to wheat varieties  
506 sensitive to septoria leaf blotch, *Parisotoma notabilis*, *Sminthurinus elegans* and  
507 *Megalothorax incertus group* are known to feed on fungi (Addison et al., 2003; Gillet and

508 Ponge, 2005). Other species found in our study, e.g. *Pseudosinella alba*, *Folsomia candida*,  
509 also known to feed on fungi, including pathogenic species (Mehl, 1996; Meyer-Wolfarth et  
510 al., 2017; Ponge and Charpentié, 1981; Ponge, 1988), were not really linked to the sensitivity  
511 of wheat varieties to septoria leaf blotch in our graphics. This discrepancy may be explained  
512 by the selective attraction of Collembola to fungi (Jorgensen et al., 2005), while the above  
513 cited experimental studies concerned fungal pathogens other than *Mycosphaerella*  
514 *graminicola* (septoria leaf blotch). *Isotomurus palustris*, another species associated to the  
515 sensitivity to septoria leaf blotch, was also less abundant in plots with wheat varieties less  
516 sensitive to septoria (c2 functional group), corroborating the influence of this wheat trait.  
517 Wheat varieties with both increased sensitivity to fungal diseases and high canopy cover,  
518 including high shoot-root ratios, favored logically Collembola living aboveground with  
519 morphological traits adapted to aerial life, e.g. with pigmented and spherical body, long  
520 furcula and high ocelli number (Salmon et al., 2014). Furthermore, the effect of canopy cover  
521 had been observed to impact collembolan populations, the abundance of which decreased  
522 indirectly with specific leaf area of oak leaves (Santonja et al., 2018). This is exemplified in  
523 our study by *Willowsia platani*, an epigeic species that was positively influenced by plant  
524 cover and is known to search for protection against light and dryness (usually under bark of  
525 trees or lichen) (Gisin, 1960).

526         However, we have to acknowledge that the effect of wheat traits on Collembola  
527 communities was very weak. The fact that wheat traits had been measured one year before our  
528 field experiment and on different sites, or come from literature, may explain at least partly the  
529 weakness of the relationships observed. In fact, a measure of each wheat trait in each plot  
530 probably could have better clarified their effect on Collembola communities. The weak effect  
531 of wheat traits may also be explained by the low abundances of Collembola in our field  
532 experiment, as discussed above.

533 Soil features explained about 10% of the variation in collembolan species and trait  
534 assemblages. Among soil features, coarse silt had the strongest impact on Collembola species  
535 and trait distribution. Species living belowground were more abundant in plots with a higher  
536 content in coarse silt while species living aboveground (with long appendices, pigmentation  
537 and air-sensitive bristles) were more abundant in plots with lower content in coarse silt (and  
538 thus more clayish and compact). This finding corroborates the role of coarse silt suggested  
539 above (section 4.1), i.e. attenuating soil compaction and allowing more euedaphic Collembola  
540 to live belowground, while in soils with less coarse silt (and thus more clayish and compact)  
541 epigeic species (here *Sminthurides signatus*, *Entomobrya* cf. *multifasciata*, *Sminthurinus*  
542 *aureus* and *aureus* group, *Lepidocyrtus cyaneus*) were probably more abundant than  
543 euedaphic species because of the reduction in the number and size of soil pores (Schrader and  
544 Lingnau, 1997).

545 The increase in wheat diversity did not foster collembolan species diversity,  
546 corroborating some previous studies failing to show an effect of plant diversity on soil fauna  
547 communities. This may be due to the fact that (1) wheat varieties most suitable to Collembola  
548 were underrepresented, (2) the overall low collembolan diversity in the experimental plots  
549 prevented an increase in local species richness with wheat diversity, and (3) soil features,  
550 especially particle size distribution (texture), impacted collembolan distribution despite our  
551 efforts (seedling randomization) to take this natural effect in account in our experimental  
552 design. Moreover, our results show that the composition of plant populations, including  
553 functional composition, has a greater impact (although low) than intraspecific plant diversity  
554 on collembolan communities. They showed significant although weak effects of the  
555 composition of wheat functional groups that likely provide more resources and/or a larger  
556 niche volume (more roots and more fungal pathogens) suitable to Collembola. This suggests  
557 that mixtures with wheat varieties having a higher specific root length could be chosen to



558 increase collembolan species richness by providing more habitat and food. Moreover, our  
559 study suggests that keeping in mixture some wheat varieties with a lower resistance to fungal  
560 diseases (e.g. by selecting other traits related to higher yield) could be compensated by the  
561 consumption of fungal pathogens by Collembola (Sabatini et al., 2000), which would  
562 contribute to increase collembolan species richness. This greater effect of the composition of  
563 wheat varieties could explain why our results, contrast with those of a previous study (Chateil  
564 et al., 2013), which showed that wheat genetic diversity increased the species richness of  
565 several groups of invertebrates, including Collembola. In fact, the field experiment of Chateil  
566 et al. (2013) encompassed a low number of wheat varieties, and the varieties added in the  
567 higher level of diversity were probably all beneficial to Collembola.

568

## 569 **5. Conclusions**

570 Our study showed no effect of genetic wheat diversity on Collembola communities  
571 and weak although significant effects of wheat variety composition and traits. In fact, soil  
572 features, especially particle size, impacted more strongly Collembola than wheat composition  
573 or diversity. Our study suggests that, at least in conventional agroecosystems, other factors  
574 such as soil features, but also perhaps the surrounding landscape or agricultural practices  
575 contribute more to structuring collembolan communities than intraspecific diversity. Studying  
576 the effect of the diversity of wheat varieties using the same experimental method (high  
577 number of varieties and four levels of diversity, respectively) but in crops grown in organic  
578 farming, and with more homogenous soil features (if possible), could allow better assessing  
579 the impact of intraspecific diversity and composition of plants on soil invertebrate  
580 communities. A measure of each functional wheat trait during the experiment would also  
581 allow to directly assess potential impacts of wheat traits on Collembola.

582 **Acknowledgements**

583           This work was supported by the ANR WHEATAMIX project, grant ANR-13-AGRO-  
584 0008 of the French National Research Agency. The authors thank all the persons who were  
585 involved in the management of the field experiment, and particularly Dr. Jérôme Enjalbert,  
586 Dr. Sébastien Saint-Jean, and Christophe Montagnier. The authors gratefully thank Pr.  
587 Emmanuelle Porcher for constructive comments and recommendations which helped to  
588 improve quality of the paper.

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825 **Table 1.** Wheat trait in mixtures of varieties and their codes used in our statistical analyses.

<b>Trait code</b>	<b>Wheat trait in mixtures of varieties</b>
SRL	Mean specific root length ( $\text{m.g}^{-1}$ )
SRR	Mean shoot/root ratio
RD	Mean root diameter (mm)
GAIT1	Mean Green Area Index in December = ratio of leaf green area to ground area
YR	Mean sensitivity to yellow rust (mean percentage of sporulating area)
Septo	Mean sensitivity to septoria leaf blotch (mean percentage of sporulating area)
GAIT6	Mean of Green Area Index in April = ratio of leaf green area to ground area

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828 **Table 2.** Analysis of Deviance Table (Type II Wald chisquare tests) (Chisquare, P-value) from final  
829 models with abundance and species richness of Collembola as response variables respectively, soil  
830 features+ variety number+ functional group composition or soil features+ functional group number+  
831 wheat traits , as explanatory variables. Only explanatory variables showing a significant effect were  
832 kept in the final model (See Tables S4 to S7 for details). See Table 1 for wheat trait codes; Co-silt: the  
833 amount of coarse silt; C1, C2: C1 and C2 functional groups of wheat.

	<b>Final model</b>	<b>Explanatory variables</b>	<b>Degrees of freedom</b>	<b>Chisquare</b>	<b>P-value</b>
Species richness	C1+Co-silt	Co-silt	1	16.4311	5.045e-05
		C1	1	7.9275	0.004869
	SRL+Septo+Co-silt	SRL	1	4.0832	0.043311
		Septo	1	7.9036	0.004934
		Co-silt	1	20.1757	7.065e-06
Abundance	C2+Co-silt	Co-silt	1	17.1698	3.418e-05
		C2	1	3.2121	0.07309
	Septo+Co-silt	Septo	1	9.7172	0.001826
		Co-silt	1	20.1981	6.982e-06

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837 **Table 3.** Names and codes of Collembola species

<b>Species name</b>	<b>Code</b>
<i>Desoria tigrina</i>	Destig
<i>Deuterosminthurus sp.</i>	Deutersp
<i>Entomobrya lanuginosa</i>	Entlan
<i>Entomobrya sp. cf multifasciata</i>	Entmul
<i>Entomobryoides purpurascens</i>	Entpur
<i>Entomobrya sp.</i>	Entsp
<i>Folsomia candida</i>	Folcan
<i>Folsomides parvulus</i>	Folpar
<i>Heteromurus nitidus</i>	Hetnit
<i>Isotomurus antennalis</i>	Isoant
<i>Isotomurus palustris</i>	Isopal
<i>Lepidocyrtus cyaneus</i>	Lepcya
<i>Lepidocyrtus lanuginosus</i>	Leplan
<i>Lepidocyrtus lignorum</i>	Leplig
<i>Megalothorax group incertus</i>	Meginc
<i>Megalothorax group minimus</i>	Megmin
<i>Mesaphorura sp.</i>	Messp
<i>Neotullbergia ramicuspis</i>	Neoram
<i>Parisotoma notabilis</i>	Parnot
<i>Proisotoma minima</i>	Promini
<i>Proisotoma minuta</i>	Prominu
<i>Pseudosinella alba</i>	Psealb
<i>Seira domestica</i>	Seidom
<i>Sminthurinus aureus</i>	Smiaur
<i>Sminthurides signatus</i>	Smisig
<i>Sminthurinus group aureus</i>	Smigraur

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<i>Sminthurinus elegans</i>	Smiele
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<i>Willowsia platani</i>	Wilpla
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842 **Table 4.** Names and codes of Collembola traits. Micro-habitats (Epi, Eda, Hemi-Eda) were attributed  
843 from micro-habitats where species are usually collected (they are not life forms deduced from  
844 morphological traits, see Salmon et al. 2014)

<b>Trait code</b>	<b>Trait name</b>
ReproPart	Parthenogenetic reproduction
ReproSex	Sexual reproduction
SpheB	Spherical body
CylB	Cylindrical body
BodyL	Body length
FurcaL	Furcula length
LegL	Leg length
AntL	Antenna length (wearing sensory organ)
Ocel	Number of ocelli (visual organ)
PAOVes	Max number of PAO vesicles (sensory organ)
Tricho	Trichobothria (sensory organ)
Scal	Scales (protective feature)
Pigm	Pigmentation (UV protection)
Psoc	Pseudocelli (defense against predators)
Epi	Micro-habitat Epigeic (above soil surface)
Eda	Micro-habitat Edaphic (soil)
Hemieda	Micro-habitat Hemiedaphic (litter)
Hemi-Eda	Micro-habitat Hemiedaphic & Edaphic (litter and soil)
NS	No specialisation for micro-habitat (depth)

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## Figure captions

849 **Fig. 1.** Box-plots of log-transformed abundance (a, decimal logarithm of the number of  
850 individuals in 3 pooled samples) and species richness (b, number of species in 3  
851 pooled samples) of Collembola for each number of wheat varieties (varnb): 1, 2, 4 and  
852 8 varieties per plot. Upper, lower and median bands of boxes, crosses and dots  
853 represent first and third quartiles, median, average, minimum and maximum values,  
854 respectively. The ends of whiskers are calculated using 1.5 times the interquartile  
855 space (distance between 1st and 3rd quartiles).

856

857 **Fig. 2.** Abundance (a, decimal logarithm of the number of individuals in 3 pooled samples)  
858 and species richness (b, number of species in 3 pooled samples) of Collembola as a  
859 function of the standardized mean sensitivity to septoria (a, b, percentage of leaf area  
860 covered by septoria), and specific root length (c) of wheat in each plot. Each dot  
861 represents one plot.

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863 **Fig. 3.** Canonical correspondence analysis (CCA) showing the distribution and assemblage of  
864 species (active variables) constrained by the number of wheat variety (nbvar) and the  
865 presence of the c2 functional group (5a), three wheat traits (5b) and three soil features  
866 (5c) along the first two canonical axes F1 and F2. Explicative variables (c2 functional  
867 group, nbvar, Septo, GAIT1, Septo, Co-silt, pH, C\_N) were the variables that  
868 impacted the most the collembolan assemblages as shown by the CCA PLS. Co-silt:  
869 Coarse silt ; C/N: soil carbon to nitrogen ratio, pH: soil pH. See Table 1 for wheat trait  
870 abbreviations and Table 3 for Collembola species name abbreviations

871 **Fig. 4.** Redundancy analysis (RDA) showing the distribution and assembly of community  
872 weighted-mean (CWM) collembolan functional traits (active variables) constrained by  
873 two wheat traits (a) and four soil features (b) along canonical axes F1 and F2. Septo:  
874 sensitivity to Septoria; YR: sensitivity to Yellow rust ; Co-silt: Coarse silt; C/N: soil  
875 carbon to nitrogen ratio; pH: soil pH; Water: soil water content. See Table1 for wheat  
876 trait abbreviations. See Table 4 for collembolan trait abbreviations, Table S1 for  
877 collembolan trait values and Salmon et al. (2014) for more details about collembolan  
878 traits.

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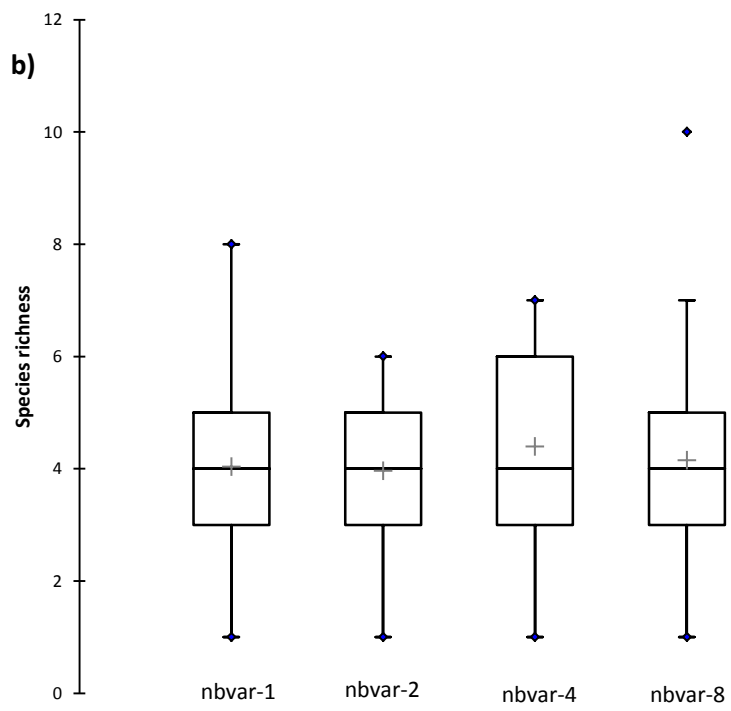
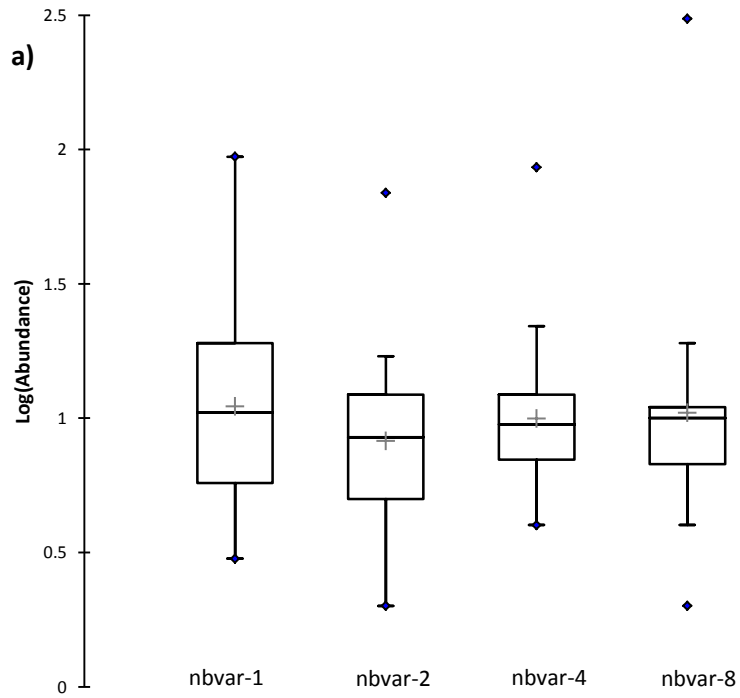
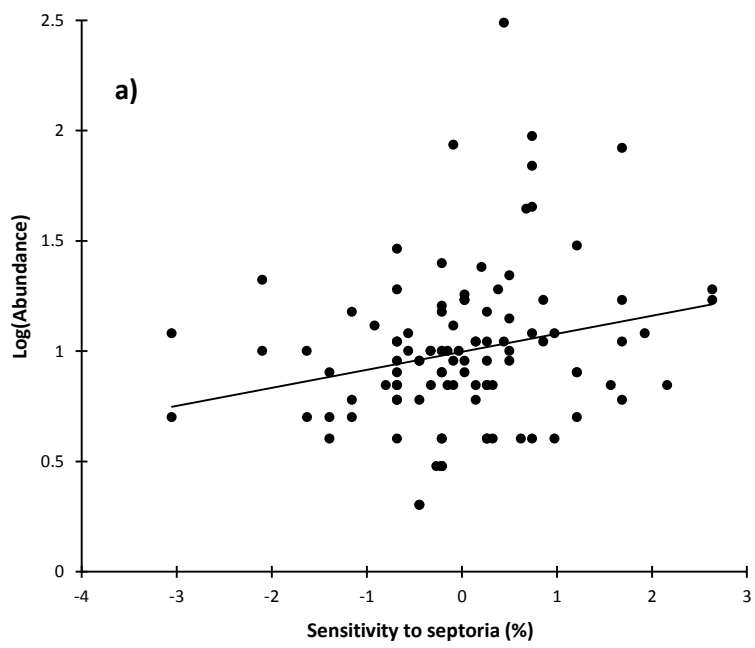
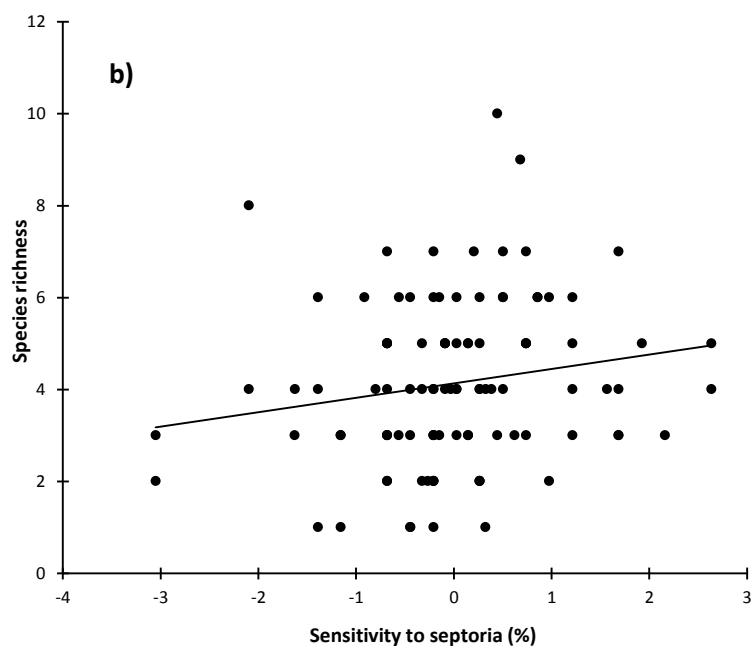


Figure 1

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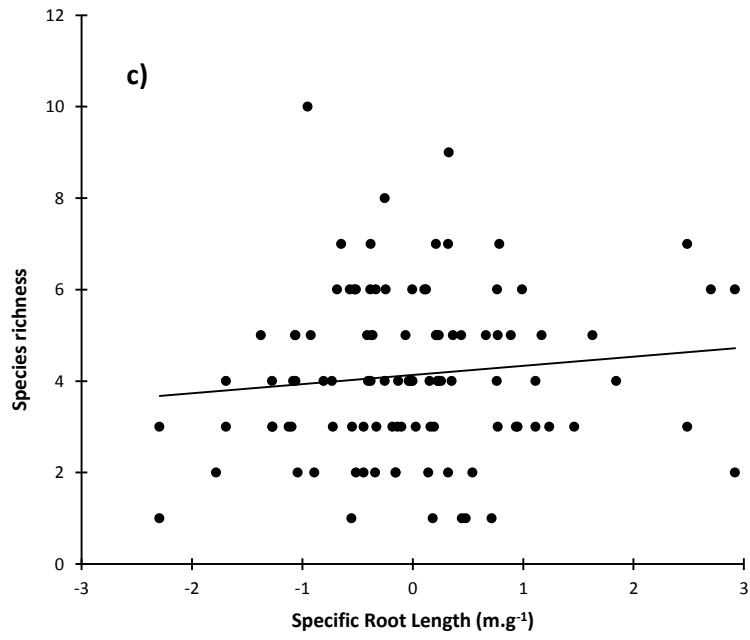


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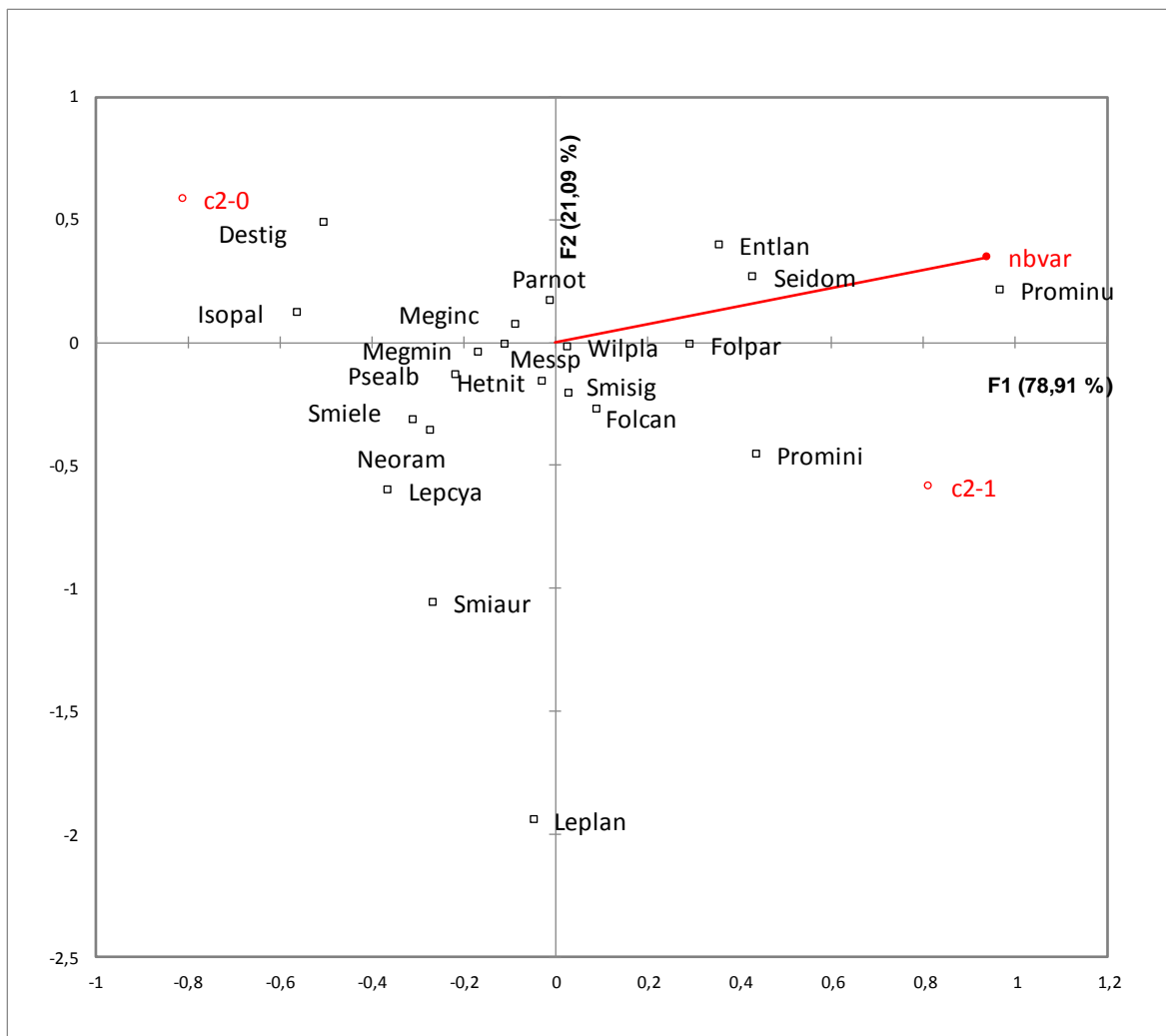


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914 Figure 2

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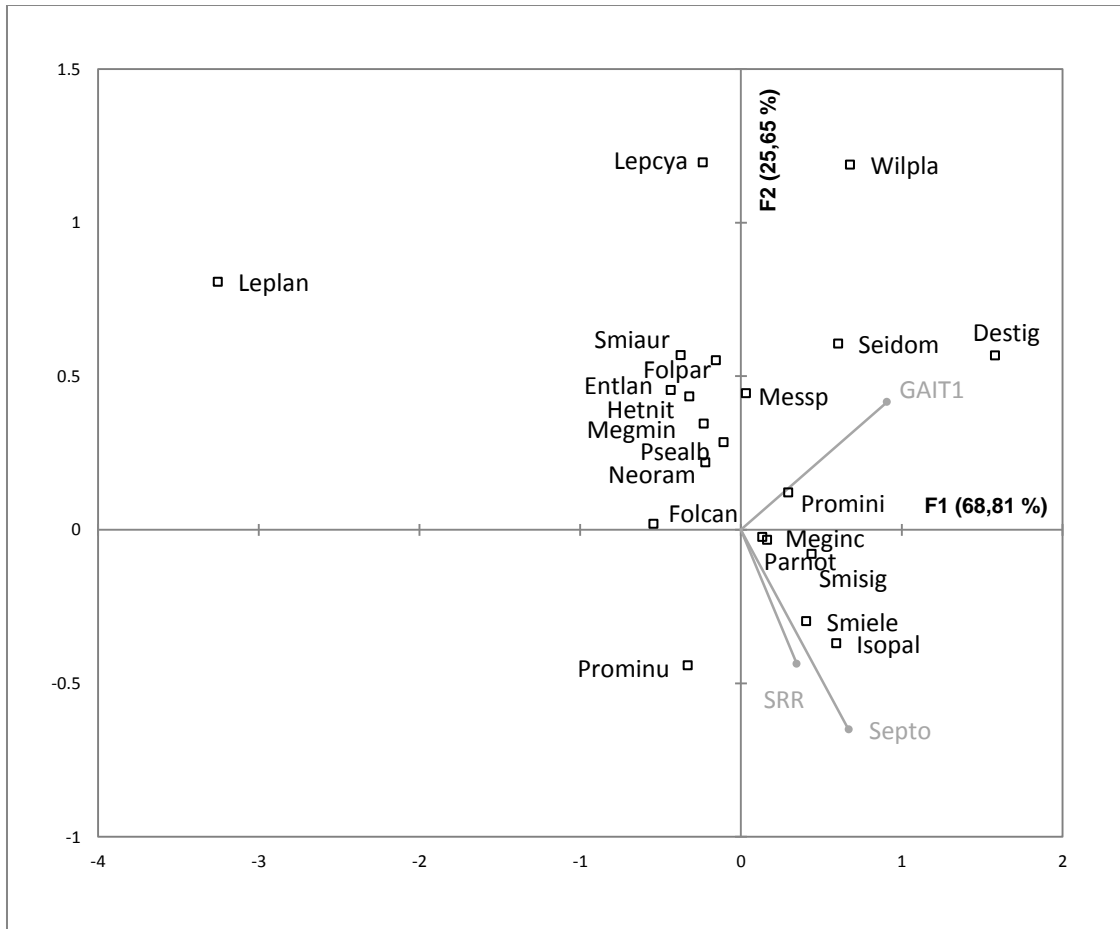
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923 Figure 3a

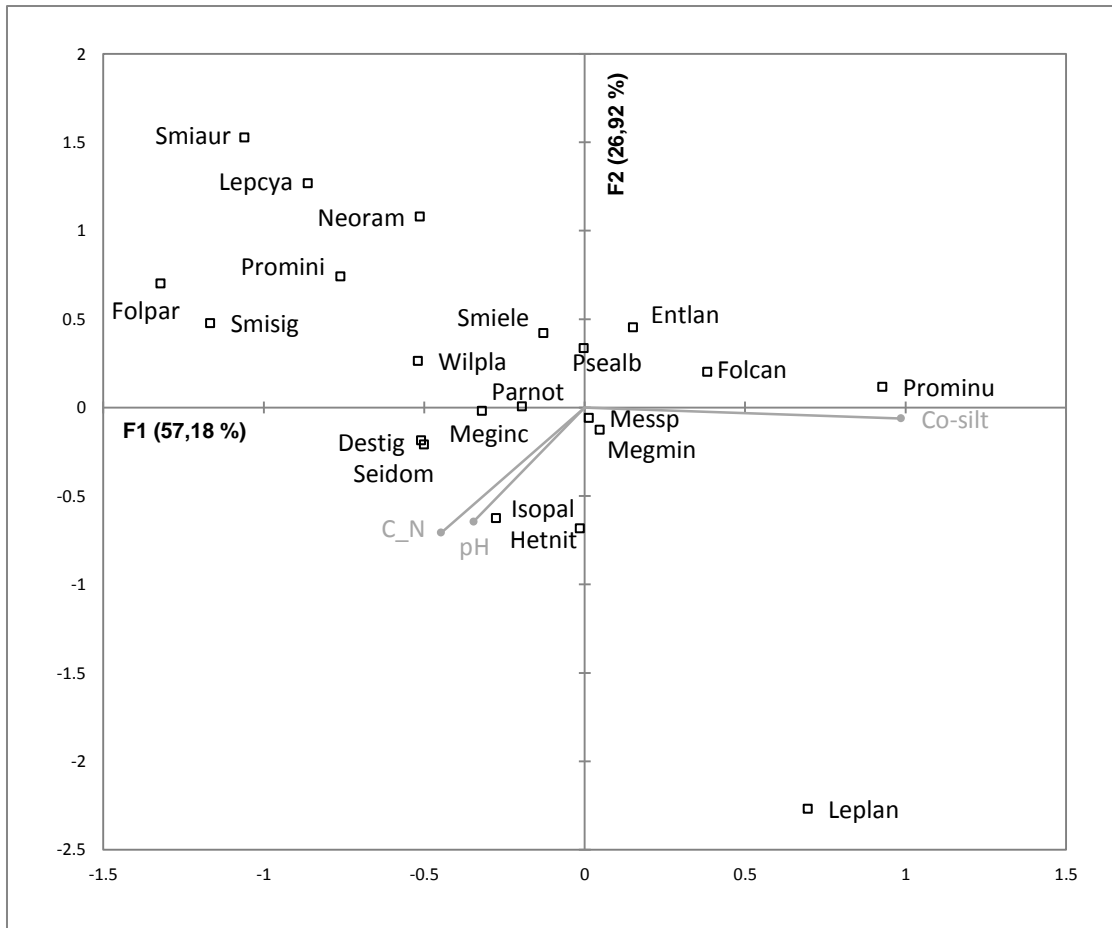
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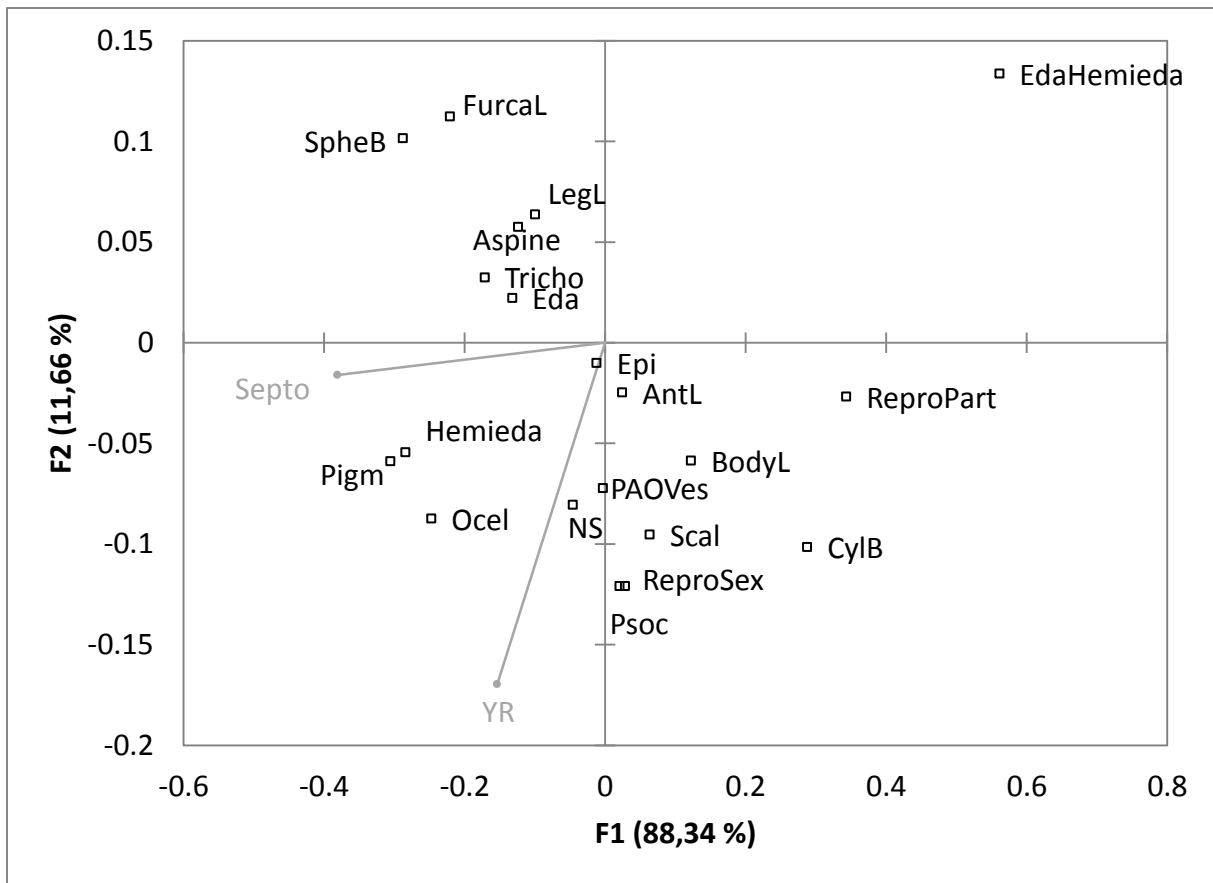
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936 Figure 3b



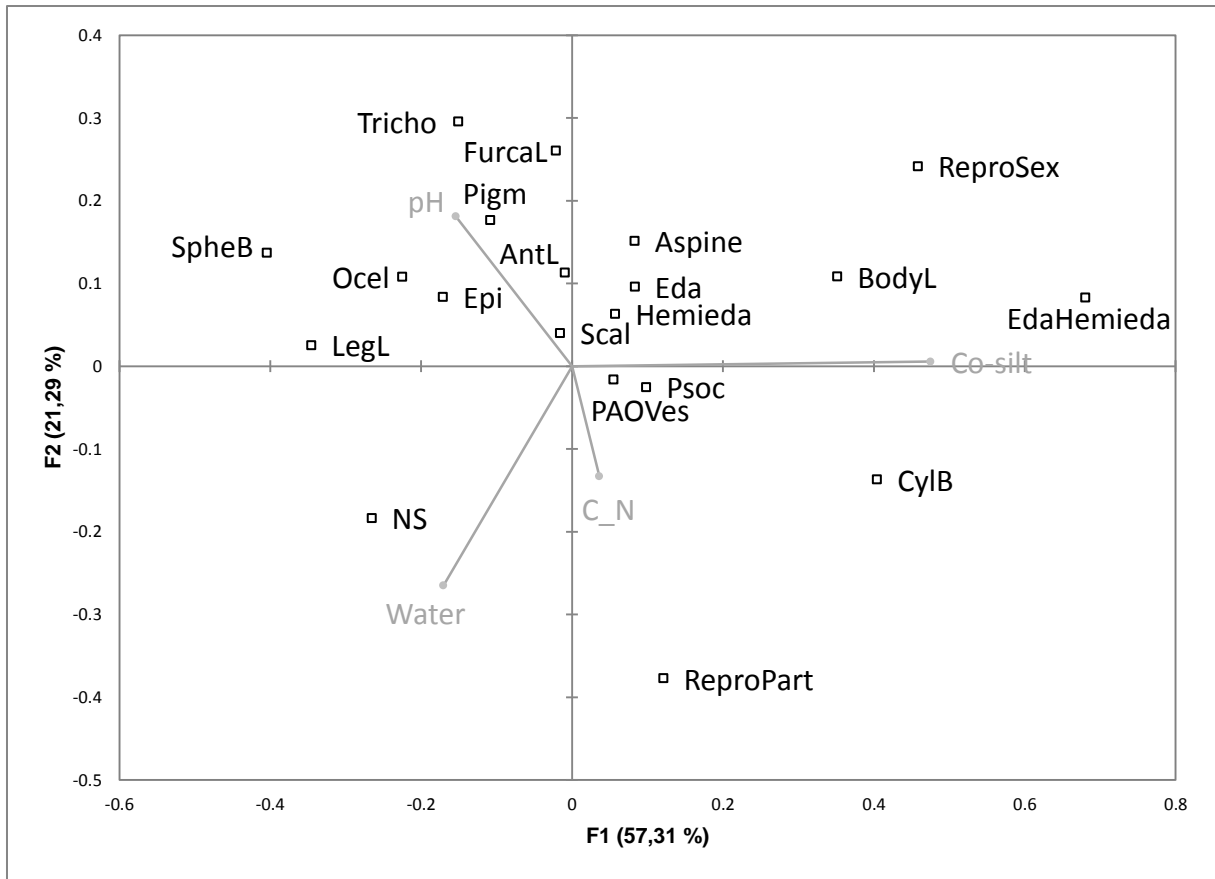
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Figure 3c



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Figure 4a



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Figure 4b

## Supplementary material

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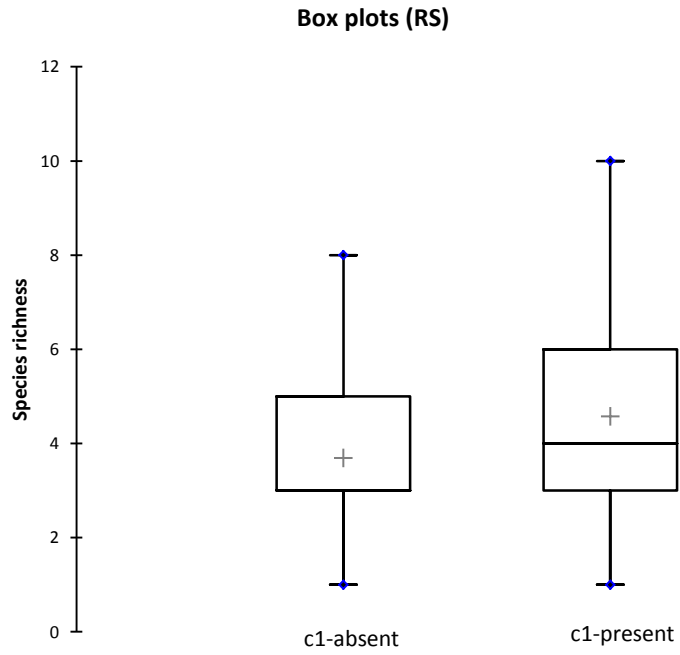
953 Figure S1 : Part of the experimental design of randomized plots in the Wheatamix project.

954 Orange : pure (1 variety) ; Pink :2 varieties ; Green :4 varieties, Yellow : 8 varieties ;

955 Red : commercial varieties, not taken into account in the present study. Grey bands : Triticale

	A	B	C	D	E	F	G
1,76 m							
10,50 m	107A 107B						
1,76 m		69	11	71	12	85	6
10,50 m							
1,76 m	15	25	79	65	63	105	31
10,50 m							
1,76 m	51	117	63	29	55	14	27
10,50 m							
1,76 m	109	81	77	49	33	115	1
10,50 m							
1,76 m	6	16	35	2	19	21	75
10,50 m							
1,76 m	57	119	53	17	9	41	3
10,50 m							
1,76 m	7	39	113	23	73	37	8
10,50 m							
1,76 m	13	4	61	87	47	10	45
10,50 m							
1,76 m	43	59	111	67	110	91	82
10,50 m							
1,76 m	64	40	80	104	46	114	93
10,50 m							
1,76 m	102	98	26	52	34	78	28
10,50 m							
1,76 m	60	62	97	99	74	106	90
10,50 m							
1,76 m	118	22	54	88	48	30	72
10,50 m							
1,76 m	68	56	32	101	24	76	66
10,50 m							
1,76 m	108	86	96	44	70	89	38
10,50 m							
1,76 m	18	103	42	112A 112B	50	36	94
10,50 m							
1,76 m	116	92	100	20	84	95	58





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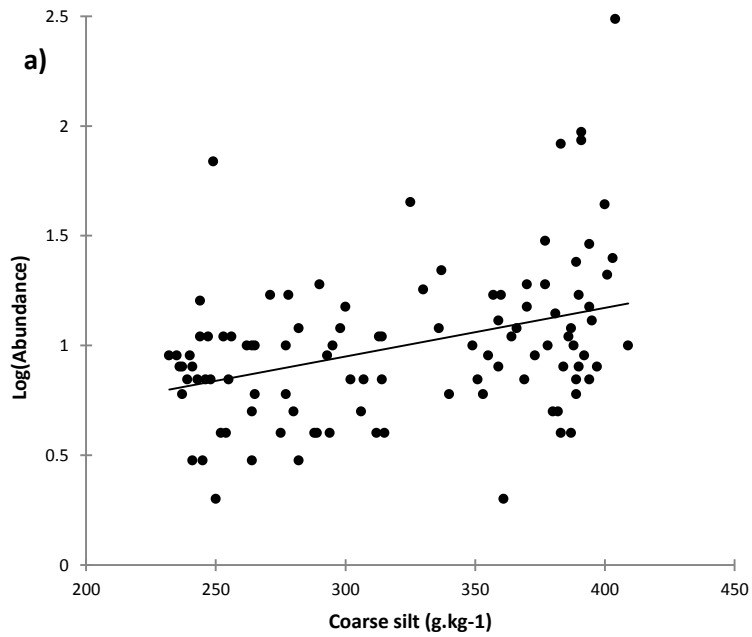
959

960 **Fig. S2.** Box-plots of species richness (number of species in 3 pooled samples) of Collembola,  
961 comparing plots without (c1-absent) and with (c1-present) the c1 functional group. See  
962 Figure 1 for the meaning of boxes, whiskers, crosses and dots.

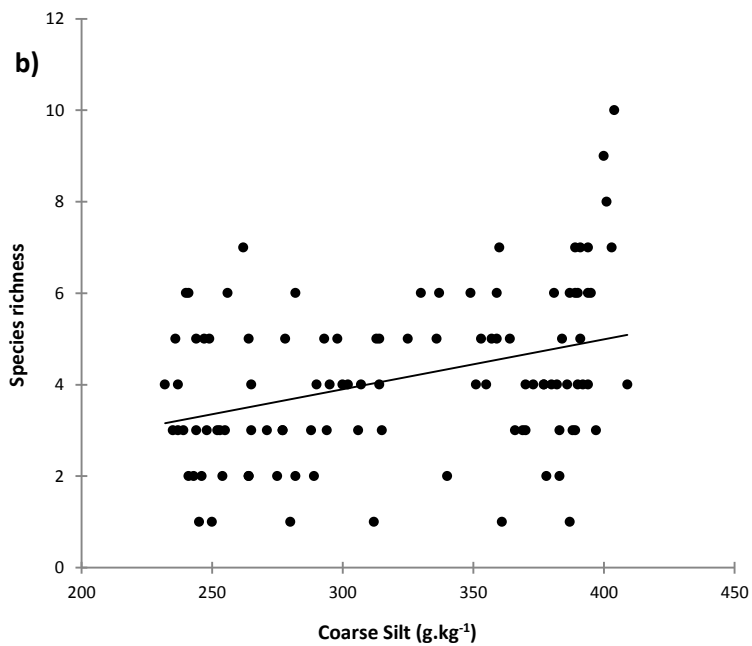
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970 **Figure S3.** Log-transformed abundance (a, decimal logarithm of the number of individuals in  
 971 3 pooled samples) and species richness (b, number of species in 3 pooled samples) of  
 972 Collembola as a function of the amount of coarse silt (20–50  $\mu\text{m}$ ) in soil. Each dot represents  
 973 one plot.



1 Table S1: Values of Collembola traits (see Table S1 and S2 for abbreviations of species and trait names)

	Repro Sex	Repro Part	CylB	SpheB	Scal	Pigm	BodyL	Ocel	FurcaL	AntL	PAO Ves	Tricho	Psoc	LegL	Aspine	Micro- Habitat
Destig	1	0	1	0	0	1	2.1	8	4	1.35	1	0	0	0.3	0	NS
Deusp	1	0	1	0	0	1	0.75	8	4	1.87	0	1	0	0.486	0	NS
Entlan	1	0	1	0	0	0	2	8	4	2.337	0	1	0	0.47	0	Epi
Entmul	1	0	1	0	0	1	1.75	8	4	2.407	0	1	0	0.46	0	Epi
Entpur	1	0	1	0	0	1	1.5	8	4	2.35	0	1	0	0.6	0	Epi
Entsp	1	0	1	0	0	0	1.975	8	4	2.7175	0	1	0	0.452	0	Epi
Folcan	1	1	1	0	0	0	1.85	0	3	1.25	1	0	0	0.28	0	Hemi- Eda
Folpar	0	1	1	0	0	0	0.9	2	2	0.9	1	0	0	0.5	0	NS
Hetnit	1	0	1	0	1	1	2.25	2	4	2	0	1	0	0.49	0	Hemi- Eda
Isoant	1	0	1	0	0	1	2.2	8	4	2	1	0	0	0.413	0	Hemieda
Isopal	1	0	1	0	0	1	2.7	8	4	2	1	1	0	0.4	0	NS
Lepcya	1	0	1	0	1	1	1.5	8	4	1.4	0	1	0	0.3925	0	Epi
Leplan	1	0	1	0	1	1	2	8	4	1.6	0	1	0	0.455	0	NS
Leplig	1	0	1	0	1	1	1.8	8	4	1.5	0	1	0	0.48	0	NS
Meginc	0	0	0	1	0	0	0.5	0	4	0.5	0	1	0	0.51	1	Eda
Megmin	0	0	1	0	0	0	0.4	0	4	0.5	0	1	0	0.5	1	Eda

Messsp	1	1	1	0	0	0	0.582	0	0	0	31.8	0	14	0.11	1	Eda
Neoram	1	0	1	0	0	0	1	0	0	0.72	60	0	14	0.14	1	Eda
Parnot	1	1	1	0	0	1	1.2	5	4	0.95	1	0	0	0.34	0	Hemieda
Promini	1	1	1	0	0	0	0.8	5	2	1.05	1	0	0	0.12	0	NS
Prominu	1	0	1	0	0	1	1.2	8	2	0.85	1	0	0	0	0	Epi
Psealb	1	0	1	0	1	0	1.05	2	4	1.8	0	1	0	0.51	0	Eda
Seidom	1	0	1	0	1	0	3	8	4	2.8	0	1	0	0	0	NS
Smiaur	1	0	0	1	0	1	1	8	4	1	0	1	0	0.6	0	Epi
Smidsig	1	0	0	1	0	1	0.3	8	4	1.57	0	1	0	0.49	0	Epi
Smigraur	1	0	0	1	0	1	0.85	8	4	1.2	0	1	0	0.6	0	Epi
Sminele	1	0	0	1	0	1	0.7	8	4	1.4	0	1	0	0.6	0	Epi
Wilpla	1	0	1	0	1	1	3	8	4	2.64	0	1	0	0.34	1	Epi

2

3

- 4 Table S2: see Excel file  
Table S2. Abundances of Collembola species in three pooled samples of 104 plots of the Wheatmix project  
nbvar: number of wheat varieties; nbclu: number of clusters (wheat functional groups)  
See table 3 for the name of Collembola species
- 5  
6  
7 Table S3: Spearman correlation coefficients between explanatory variables  
8  
9

Variables	nbvar	nbclu	SRR	RDMC	RGR	SRL	RD	GAIT1	GAIT6	Yellow-Rust	Septo	xDD	yDD	Clay	Fi-Silt	Co-Silt	Fi-Sand	Co-Sand	N	C/N	Corg	OM	wa
nbvar	<b>1</b>	<b>0,800</b>	0,180	0,120	-0,055	0,062	0,027	0,018	0,081	0,070	0,026	-0,002	0,031	-0,039	-0,094	-0,051	0,117	0,028	-0,088	0,031	-0,072	-0,076	
nbclu	<b>0,800</b>	<b>1</b>	0,126	0,108	-0,052	0,064	0,023	0,019	0,069	0,066	0,049	-0,045	0,060	-0,075	-0,068	-0,010	0,056	0,023	-0,124	0,079	-0,073	-0,075	
SRR	0,180	0,126	<b>1</b>	0,056	<b>-0,275</b>	<b>0,300</b>	<b>0,333</b>	<b>0,255</b>	0,051	0,004	0,178	<b>-0,201</b>	<b>-0,377</b>	<b>0,315</b>	-0,166	<b>-0,285</b>	<b>0,221</b>	<b>0,265</b>	<b>0,314</b>	-0,166	0,156	0,155	
RDMC	0,120	0,108	0,056	<b>1</b>	<b>0,695</b>	<b>-0,581</b>	0,052	<b>-0,235</b>	0,147	0,111	0,099	0,035	0,066	-0,024	0,081	0,070	-0,142	-0,027	-0,018	0,042	-0,018	-0,021	
RGR	-0,055	-0,052	<b>-0,275</b>	<b>0,695</b>	<b>1</b>	<b>-0,928</b>	0,009	<b>-0,206</b>	0,067	<b>0,277</b>	<b>0,303</b>	<b>0,203</b>	0,078	-0,030	0,014	0,053	-0,129	-0,002	-0,033	0,190	0,063	0,065	
SRL	0,062	0,064	<b>0,300</b>	<b>-0,581</b>	<b>-0,928</b>	<b>1</b>	0,065	<b>0,280</b>	<b>-0,204</b>	<b>-0,228</b>	<b>-0,208</b>	<b>-0,242</b>	-0,045	0,011	0,021	-0,020	0,090	-0,016	-0,012	-0,188	-0,109	-0,110	
RD	0,027	0,023	<b>0,333</b>	0,052	0,009	0,065	<b>1</b>	-0,059	-0,030	0,095	<b>0,450</b>	-0,053	-0,089	0,026	0,017	-0,024	0,033	-0,009	0,058	-0,031	0,052	0,054	
GAIT1	0,018	0,019	<b>0,255</b>	<b>-0,235</b>	<b>-0,206</b>	<b>0,280</b>	-0,059	<b>1</b>	-0,191	<b>0,473</b>	<b>0,262</b>	0,064	-0,131	0,135	<b>-0,277</b>	<b>-0,226</b>	<b>0,291</b>	<b>0,203</b>	0,108	0,005	0,111	0,113	
GAIT6	0,081	0,069	0,051	0,147	0,067	<b>-0,204</b>	-0,030	-0,191	<b>1</b>	<b>-0,450</b>	-0,036	-0,047	-0,048	0,111	-0,033	-0,064	0,014	0,069	0,053	-0,039	0,020	0,018	
Yellow-Rust	0,070	0,066	0,004	0,111	<b>0,277</b>	<b>-0,228</b>	0,095	<b>0,473</b>	<b>-0,450</b>	<b>1</b>	<b>0,486</b>	<b>0,240</b>	0,040	-0,056	-0,117	0,000	0,058	0,015	0,012	<b>0,197</b>	0,155	0,159	
Septo	0,026	0,049	0,178	0,099	<b>0,303</b>	<b>-0,208</b>	<b>0,450</b>	<b>0,262</b>	-0,036	<b>0,486</b>	<b>1</b>	0,040	-0,110	0,101	-0,154	-0,116	0,099	0,135	0,039	0,063	0,100	0,103	
xDD	-0,002	-0,045	<b>-0,201</b>	0,035	<b>0,203</b>	<b>-0,242</b>	-0,053	0,064	-0,047	<b>0,240</b>	0,040	<b>1</b>	-0,097	<b>0,212</b>	<b>-0,278</b>	<b>-0,252</b>	<b>0,224</b>	<b>0,247</b>	<b>0,314</b>	<b>0,710</b>	<b>0,646</b>	<b>0,646</b>	
yDD	0,031	0,060	<b>-0,377</b>	0,066	0,078	-0,045	-0,089	-0,131	-0,048	0,040	-0,110	-0,097	<b>1</b>	<b>-0,845</b>	<b>0,648</b>	<b>0,867</b>	<b>-0,723</b>	<b>-0,793</b>	<b>-0,823</b>	0,134	<b>-0,628</b>	<b>-0,627</b>	
Clay	-0,039	-0,075	<b>0,315</b>	-0,024	-0,030	0,011	0,026	0,135	0,111	-0,056	0,101	<b>0,212</b>	<b>-0,845</b>	<b>1</b>	<b>-0,681</b>	<b>-0,861</b>	<b>0,643</b>	<b>0,799</b>	<b>0,814</b>	-0,027	<b>0,679</b>	<b>0,679</b>	
Fi-Silt	-0,094	-0,068	-0,166	0,081	0,014	0,021	0,017	<b>-0,277</b>	-0,033	-0,117	-0,154	<b>-0,278</b>	<b>0,648</b>	<b>-0,681</b>	<b>1</b>	<b>0,833</b>	<b>-0,895</b>	<b>-0,808</b>	<b>-0,586</b>	-0,112	<b>-0,572</b>	<b>-0,570</b>	
Co-Silt	-0,051	-0,010	<b>-0,285</b>	0,070	0,053	-0,020	-0,024	<b>-0,226</b>	-0,064	0,000	-0,116	<b>-0,252</b>	<b>0,867</b>	<b>-0,861</b>	<b>0,833</b>	<b>1</b>	<b>-0,878</b>	<b>-0,935</b>	<b>-0,785</b>	0,024	<b>-0,659</b>	<b>-0,658</b>	
Fi-Sand	0,117	0,056	<b>0,221</b>	-0,142	-0,129	0,090	0,033	<b>0,291</b>	0,014	0,058	0,099	<b>0,224</b>	<b>-0,723</b>	<b>0,643</b>	<b>-0,895</b>	<b>-0,878</b>	<b>1</b>	<b>0,767</b>	<b>0,634</b>	-0,025	<b>0,535</b>	<b>0,534</b>	
Co-Sand	0,028	0,023	<b>0,265</b>	-0,027	-0,002	-0,016	-0,009	<b>0,203</b>	0,069	0,015	0,135	<b>0,247</b>	<b>-0,793</b>	<b>0,799</b>	<b>-0,808</b>	<b>-0,935</b>	<b>0,767</b>	<b>1</b>	<b>0,714</b>	0,040	<b>0,630</b>	<b>0,628</b>	
N	-0,088	-0,124	<b>0,314</b>	-0,018	-0,033	-0,012	0,058	0,108	0,053	0,012	0,039	<b>0,314</b>	<b>-0,823</b>	<b>0,814</b>	<b>-0,586</b>	<b>-0,785</b>	<b>0,634</b>	<b>0,714</b>	<b>1</b>	-0,032	<b>0,836</b>	<b>0,835</b>	
C/N	0,031	0,079	-0,166	0,042	0,190	-0,188	-0,031	0,005	-0,039	<b>0,197</b>	0,063	<b>0,710</b>	0,134	-0,027	-0,112	0,024	-0,025	0,040	-0,032	<b>1</b>	<b>0,490</b>	<b>0,490</b>	
Corg	-0,072	-0,073	0,156	-0,018	0,063	-0,109	0,052	0,111	0,020	0,155	0,100	<b>0,646</b>	<b>-0,628</b>	<b>0,679</b>	<b>-0,572</b>	<b>-0,659</b>	<b>0,535</b>	<b>0,630</b>	<b>0,836</b>	<b>0,490</b>	<b>1</b>	<b>1,000</b>	
OM	-0,076	-0,075	0,155	-0,021	0,065	-0,110	0,054	0,113	0,018	0,159	0,103	<b>0,646</b>	<b>-0,627</b>	<b>0,679</b>	<b>-0,570</b>	<b>-0,658</b>	<b>0,534</b>	<b>0,628</b>	<b>0,835</b>	<b>0,490</b>	<b>1,000</b>	<b>1</b>	
water	0,090	0,030	0,177	-0,140	<b>-0,206</b>	0,159	-0,057	0,141	-0,013	0,051	-0,011	-0,031	<b>-0,471</b>	<b>0,379</b>	-0,092	<b>-0,317</b>	<b>0,261</b>	<b>0,208</b>	<b>0,527</b>	<b>-0,247</b>	<b>0,335</b>	<b>0,337</b>	
pH	-0,041	-0,057	0,108	-0,056	0,050	-0,069	0,111	0,138	0,045	-0,003	0,071	0,138	<b>-0,201</b>	<b>0,271</b>	<b>-0,447</b>	<b>-0,350</b>	<b>0,409</b>	<b>0,326</b>	<b>0,264</b>	0,039	<b>0,276</b>	<b>0,273</b>	
c1	<b>0,401</b>	<b>0,518</b>	0,053	<b>0,457</b>	<b>0,432</b>	<b>-0,339</b>	<b>0,263</b>	0,065	0,149	<b>0,429</b>	<b>0,532</b>	0,078	0,049	-0,026	-0,033	-0,010	-0,004	0,045	-0,042	0,104	0,043	0,044	
c2	<b>0,401</b>	<b>0,518</b>	-0,018	0,123	0,166	<b>-0,357</b>	-0,123	<b>-0,452</b>	0,185	-0,098	<b>-0,233</b>	-0,018	0,053	-0,071	0,001	0,044	-0,049	-0,010	-0,029	0,045	0,001	-0,002	
c3	<b>0,401</b>	<b>0,518</b>	<b>0,219</b>	0,013	-0,174	<b>0,295</b>	-0,081	<b>0,502</b>	<b>-0,413</b>	<b>0,269</b>	-0,124	0,035	-0,050	0,001	-0,154	-0,113	0,184	0,079	0,072	0,009	0,050	0,050	
c4	<b>0,401</b>	<b>0,518</b>	-0,002	<b>-0,384</b>	<b>-0,522</b>	<b>0,525</b>	-0,012	-0,070	<b>0,212</b>	<b>-0,475</b>	-0,068	<b>-0,243</b>	0,041	-0,080	0,096	0,054	-0,033	-0,055	-0,192	-0,125	<b>-0,247</b>	<b>-0,249</b>	

10

variable codes      variable name and unity

xDD                  geographical coordinate x

yDD                  geographical coordinate y

pH                    soil pH

water	water content in soil cores(g)
Clay	clay (< 2 $\mu\text{m}$ ) (g/kg)
Fi-Silt	fine silt (2/20 $\mu\text{m}$ ) (g/kg)
Co- Silt	coarse silt (20/50 $\mu\text{m}$ ) (g/kg)
Fi- Sand	fine sand (50/200 $\mu\text{m}$ ) (g/kg)
Co-Sand	coarse sand (200/2000 $\mu\text{m}$ )
N	Total Nitrogen (g/kg)
C/N	C/N ratio
Corg	Organic Carbon (g/kg)
OM	Organic matter (g/kg)
RDMC	Mean of Root Dry Matter content (mg.g-1)
RGR	Mean of Relative Growth rate (mg.day-1)
SRL	Mean Specific Root Length (m.g-1)
RD	Mean of Root Diameter (mm)
GAIT1	Mean Green Area Index in December= ratio of leaf green area to ground area
GAIT6	Mean of Green Area Index in April= ratio of leaf green area to ground area
Yellow Rust	Mean sensitivity to Yellow Rust (mean percentage of sporulating area)
Septoria	Mean of sensitivity to Septoria leaf blotch (mean percentage of sporulating area)





12 Table S4: Results of glm on the effect of the variety number (nbvar), composition of wheat variety assemblies (C1..) and soil parameters on the  
 13 species richness of collembola (full model followed by final model, followed by Analysis of Deviance Table; intermediate model  
 14 indicated that no interaction was significant)

```

15 Mod1 <- glmmTMB (RS ~ nbvar+ c1+ c2+ c3+c4+Co-silt+C_N+eau+pH, data= datanorm, family = gaussian)
16 > summary(Mod1)
17 Family: gaussian ( identity )
18 Formula:
19 RS ~ nbvar + c1 + c2 + c3 + c4 + Co-silt + C_N +water+ pH
20 Data: datanorm
21
22      AIC      BIC  logLik deviance df.resid
23  408.7   437.8  -193.3   386.7     93
24
25
26 Dispersion estimate for gaussian family (sigma^2): 2.41
27
28 Conditional model:
29      Estimate Std. Error z value Pr(>|z|)
30 (Intercept)  3.69880    0.32645  11.330 < 2e-16 ***
31 nbvar       -0.05125    0.08364  -0.613 0.540057
32 c1           0.90900    0.34351   2.646 0.008140 **
33 c2          -0.29404    0.33605  -0.875 0.381587
34 c3          -0.06463    0.33780  -0.191 0.848278
35 c4           0.66819    0.33888   1.972 0.048635 *
36 Co-silt      0.60274    0.17530   3.438 0.000585 ***
37 C_N          0.09837    0.15733   0.625 0.531815
38 water       -0.09545    0.16650  -0.573 0.566479
39 pH           0.02284    0.16640   0.137 0.890812
40

```

```

41 Mod1 <- glmmTMB (RS~Co-silt+c1, data= datanorm, family = gaussian)
42 > summary(Mod1)
43
44 Family: gaussian ( identity )
45 Formula:      RS ~ Co-silt + c1
46 Data: datanorm
47

```

```

48      AIC      BIC  logLik deviance df.resid
49  400.7    411.3  -196.4   392.7     100
50
51
52 Dispersion estimate for gaussian family (sigma^2): 2.56
53
54 Conditional model:
55      Estimate Std. Error z value Pr(>|z|)
56 (Intercept)  3.6933    0.2217  16.660 < 2e-16 ***
57 Co-silt      0.6354    0.1568   4.054 5.05e-05 ***
58 c1           0.8827    0.3135   2.816 0.00487 **
59
60
61
62
63
64
65 > library(car)
66 > Anova(Mod1)
67 Analysis of Deviance Table (Type II wald chisquare tests)
68
69 Response: RS
70      Chisq Df Pr(>Chisq)
71 Limg 16.4311 1 5.045e-05 ***
72 c1    7.9275 1 0.004869 **
73
74

```

75

76 Table S5 : Results of glm on the effect of the functional group number of wheat (nbclu), wheat traits and soil parameters on the species richness  
 77 of Collembola (full model followed by final model, followed by Analysis of Deviance Table; intermediate model indicated that no  
 78 interaction was significant)

79

```

80 Mod1 <- glmmTMB (RS ~ nbclu+SRR+SRL+RD+GAIT1+GAIT6+YR+Septo+Co-silt+C_N+eau+pH, data= datanorm, family = gaussian)
81 > summary(Mod1)
82 Family: gaussian ( identity )
83 Formula:
84 RS ~ nbclu + SRR + SRL + RD + GAIT1 + GAIT6 + YR + Septo + Co-silt +
85 C_N +water+ pH
86 Data: datanorm
87
88      AIC      BIC  logLik deviance df.resid
89  409.3    446.3  -190.7   381.3      90
90
91
92 Dispersion estimate for gaussian family (sigma^2): 2.29
93
94 Conditional model:
95      Estimate Std. Error z value Pr(>|z|)
96 (Intercept)  3.69358    0.31809  11.612 < 2e-16 ***
97 nbclu        0.22052    0.14068   1.568 0.116989
98 SRR         -0.09037    0.19944  -0.453 0.650474
99 SRL         0.47410    0.18780   2.525 0.011584 *
100 RD          0.02947    0.21767   0.135 0.892299
101 GAIT1       -0.21507    0.20844  -1.032 0.302163
102 GAIT6       0.18229    0.19650   0.928 0.353586
103 YR         -0.04138    0.26335  -0.157 0.875141
104 Septo       0.53499    0.22318   2.397 0.016526 *
105 Co-silt     0.63010    0.17474   3.606 0.000311 ***
106 C_N        0.15544    0.15797   0.984 0.325123
107 water     -0.16827    0.16276  -1.034 0.301219

```

```

108 pH          0.01884    0.16422    0.115 0.908689
109
110

```

```

111 Mod1 <- glmTMB (RS ~ SRL + Septo + Co-silt, data= datanorm, family = gaussian)
112 summary(Mod1)

```

```

113
114 Family: gaussian (identity)
115 Formula:      RS ~ SRL + Septo + Co-silt
116 Data: datanorm
117
118      AIC      BIC  logLik deviance df.resid
119  400.6   413.8  -195.3   390.6        99
120
121

```

```

122 Dispersion estimate for gaussian family (sigma^2): 2.5
123

```

```

124 Conditional model:

```

```

125      Estimate Std. Error z value Pr(>|z|)
126 (Intercept)  4.1346     0.1552  26.645 < 2e-16 ***
127 SRL          0.3197     0.1582   2.021 0.04331 *
128 Septo       0.4467     0.1589   2.811 0.00493 **
129 Co-silt     0.7034     0.1566   4.492 7.06e-06 ***
130

```

```

131 library(car)

```

```

132 Anova(Mod1)

```

```

133 Analysis of Deviance Table (Type II wald chisquare tests)
134

```

```

135 Response: RS

```

```

136      Chisq Df Pr(>Chisq)
137 SRL    4.0832 1 0.043311 *
138 Septo  7.9036 1 0.004934 **
139 Limg  20.1757 1 7.065e-06 ***
140

```

```

141

```

142

143 Table S6: Results of glm on the effect of the variety number (nbvar), composition of wheat variety assemblies (C1..) and soil parameters on the

144 Log of Collembola abundance (full model followed by final model, followed by Analysis of Deviance Table; intermediate model

145 indicated that no interaction was significant)

```
146 Mod1 <- glmmTMB (LogAb~ nbvar+ c1+ c2+ c3+c4+Co-silt+C_N+water+pH, data= datanorm, family = gaussian)
```

```
147 summary(Mod1)
```

```
148 Family: gaussian ( identity )
```

```
149 Formula:
```

```
150 LogAb ~ nbvar + c1 + c2 + c3 + c4 + Co-silt + C_N +water+ pH
```

```
151 Data: datanorm
```

152

	AIC	BIC	logLik	deviance	df.resid
	77.9	107.0	-27.9	55.9	93

155

156

```
157 Dispersion estimate for gaussian family (sigma^2): 0.1
```

158

```
159 Conditional model:
```

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	1.02129	0.06655	15.347	< 2e-16	***
nbvar	0.01233	0.01705	0.723	0.4696	
c1	0.05521	0.07003	0.788	0.4304	
c2	-0.13935	0.06851	-2.034	0.0419	*
c3	-0.07537	0.06886	-1.094	0.2738	
c4	0.02859	0.06908	0.414	0.6790	
Co-silt	0.14121	0.03574	3.951	7.77e-05	***
C_N	0.03117	0.03207	0.972	0.3312	
water	0.02246	0.03394	0.662	0.5083	
pH	0.01312	0.03392	0.387	0.6989	

171

172

173

```
174 Mod1 <- glmmTMB (LogAb~ Co-silt+c2, data= datanorm, family = gaussian)
```

```
175 > summary(Mod1)
```

```
176 Family: gaussian ( identity )
```

```
177 Formula:          LogAb ~ Co-silt + c2
```

```

178 Data: datanorm
179
180      AIC      BIC  logLik deviance df.resid
181    68.4    79.0   -30.2    60.4     100
182
183
184 Dispersion estimate for gaussian family (sigma^2): 0.105
185
186 Conditional model:
187      Estimate Std. Error z value Pr(>|z|)
188 (Intercept)  1.05450    0.04490  23.485 < 2e-16 ***
189 Co-silt      0.13164    0.03177   4.144 3.42e-05 ***
190 c2          -0.11388    0.06354  -1.792  0.0731 .
191
192 Anova\(Mod1\)
193 Analysis of Deviance Table (Type II wald chisquare tests)
194
195 Response: LogAb
196      Chisq Df Pr(>Chisq)
197 Limg 17.1698  1  3.418e-05 ***
198 c2    3.2121  1  0.07309 .
199
200
201
202
203

```

204  
 205 Table S7 : Results of glm on the effect of the functional group number of wheat (nbclu), wheat traits and soil parameters on the Log of  
 206 Collembola abundance (full model followed by final model, followed by Analysis of Deviance Table; intermediate model indicated that  
 207 no interaction was significant)

```
208 Mod1 <- glmTMB (LogAb~ nbclu+SRR+SRL+RD+GAIT1+GAIT6+YR+Septo+Co-silt+C_N+eau+pH, data= datanorm, family = gaussian)
209 > summary(Mod1)
```

```
210 Family: gaussian ( identity )
211 Formula:
212 LogAb ~ nbclu + SRR + SRL + RD + GAIT1 + GAIT6 + YR + Septo +
213 Co-silt + C_N +water+ pH
214 Data: datanorm
```

```
215
216      AIC      BIC  logLik deviance df.resid
217 76.7    113.7   -24.4    48.7      90
```

```
218
219
220 Dispersion estimate for gaussian family (sigma^2): 0.0935
```

```
221 Conditional model:
222      Estimate Std. Error z value Pr(>|z|)
223 (Intercept)  1.022507   0.064282  15.907 < 2e-16 ***
224 nbclu        -0.012473   0.028429  -0.439  0.66084
225 SRR          -0.015933   0.040304  -0.395  0.69260
226 SRL          0.033206   0.037951   0.875  0.38159
227 RD           0.012039   0.043987   0.274  0.78432
228 GAIT1        0.008373   0.042122   0.199  0.84244
229 GAIT6       -0.005605   0.039711  -0.141  0.88775
230 YR          -0.068785   0.053220  -1.292  0.19620
231 Septo        0.132573   0.045102   2.939  0.00329 **
232 Co-silt      0.152664   0.035312   4.323  1.54e-05 ***
233 C_N          0.037322   0.031923   1.169  0.24235
234 water        0.017596   0.032892   0.535  0.59268
235 pH           0.005600   0.033188   0.169  0.86600
```

```
236
237
238
239
240
241
242
```



```

243 Mod1 <- glmmTMB (LogAb~ Septo+Co-silt, data= datanorm, family = gaussian)
244 summary(Mod1)
245 Family: gaussian ( identity )
246 Formula:      LogAb ~ Septo + Co-silt
247 Data: datanorm
248
249      AIC      BIC   logLik deviance df.resid
250  62.3    72.9   -27.2    54.3     100
251
252
253 Dispersion estimate for gaussian family (sigma^2): 0.0987
254
255 Conditional model:
256      Estimate Std. Error z value Pr(>|z|)
257 (Intercept)  0.99756    0.03081  32.38 < 2e-16 ***
258 Septo        0.09661    0.03099   3.12  0.00183 **
259 Co-silt      0.13929    0.03099   4.49  6.98e-06 ***
260
261 library(car)
262 Anova(Mod1)
263 Analysis of Deviance Table (Type II wald chisquare tests)
264
265 Response: LogAb
266      Chisq Df Pr(>Chisq)
267 Septo    9.7172 1  0.001826 **
268 Co-silt 20.1981 1  6.982e-06 ***
269
270
271
272
273

```