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Impact of no-tillage versus conventional maize plantation on soil mesofauna with and without the use of a lambda-cyhalothrin based insecticide: a Terrestrial Model Ecosystem experiment

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Highlights of the manuscript entitled “Impact of no-tillage versus conventional maize plantation on soil mesofauna with and without the use of a lambda-cyhalothrin based insecticide: a Terrestrial Model Ecosystem experiment”.

Highlights

1. Different cropping systems influence differently soil fauna communities
2. Herbicide in no-tillage system affected only collembolans but they recovered
3. Mites did not fully recover from insecticide especially in tillage treatments
4. Collembola were generally more resilient to insecticide than mites
5. Enchytraeids were the least sensitive to the soil managements tested

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Abstract

Different soil management in crop cultures like maize can produce a variety of effects on soil fauna. Conventional cropping includes soil tillage, promoting organic matter losses and destruction of soil structure, whereas no-tillage cropping includes a herbicide application which can potentially affect soil fauna. In both management systems, insecticides are often used, such as pyrethroid insecticides, to prevent insect pests. Understanding the impact of these different cropping systems in their different phases on soil mesofauna and investigating the ability of soil communities to recover may provide important information to select cropping strategies which are more protective of soil biodiversity. With this aim, a terrestrial model ecosystem experiment was performed over eighty-nine days. The test treatments, all including maize, were: undisturbed soil; conventional tillage; conventional tillage with insecticide; no-tillage soil with herbicide; no-tillage soil with herbicide and insecticide. In each TME, soil samples from 0-5 and 5-10 cm of the top layer were collected from which collembolans and mites were identified to species, genus or subfamily level, and enchytraeid abundance was determined. Soil tillage did not affect soil communities, but insecticide application did. For collembolans and enchytraeids, the impact of the insecticide was independent of soil management, but for mites, insecticide impact was longer in conventional tillage than in no-tillage system. Changes on collembolan abundance, in general, did not promote changes in mean community trait values and functional diversity. Data suggest that no-tillage management is more protective to soil fauna than conventional tillage.

Key words: Functional diversity; cropping systems; pyrethroid insecticide; soil communities

Different soil managements

Conventional tillage +/- insecticide

No-tillage +/- insecticide

insecticide
impact
<
in No-tillage
for mites

46 **1. Introduction**

47 Maize is the third largest planted crop in the world, after wheat and rice, and is the most widely
48 produced crop on the planet. Maize is grown in more than 165 countries with a total production of
49 more than one billion metric tons around the world in 2013 (www.croptrust.org). Historically, this
50 crop has had the large improvements of grain yield over the last years, as a result of genetic
51 enhancement and the adoption of more appropriate agronomic practices (Baker et al. 2007). For maize
52 cultivation, no-tillage and conventional tillage are the most used systems. These two cropping systems
53 include management practices that impact soil systems differently. No-tillage cropping, while
54 preserving soil structure (as soil is not ploughed), usually includes the use of a non-residual herbicide
55 (like herbicides with glyphosate as active ingredient; a.i.), to eliminate weeds (it is recognized by
56 practice that no-tillage to be viable, weeds have to be controlled; Baker et al. 2007). On the other
57 hand, conventional cropping includes soil tillage (instead of herbicide) destroying soil structure and
58 promoting organic matter losses. Apart from the known effects of tillage on soil conditions (e.g. an
59 increase in temperature of the top soil layer; Shen et al., 2018), several studies have argued that no-
60 tillage systems lead to an increase in organic carbon stocks of agricultural soils compared to
61 conventional tillage (Luo et al., 2010; Virto et al., 2012). Some countries are even encouraging the
62 implementation of no-tillage systems in croplands to reduce greenhouse gas emissions (Corbeels et
63 al., 2016). Independently of the cropping system, pyrethroid insecticides (based on pyrethroids like
64 lambda-cyhalothrin as a.i.) are often applied to prevent agricultural pests. This type of synthetic
65 insecticides is extensively used worldwide for agricultural pest control on maize crops and other
66 plants, like sorghum and sugarcane (Croft and Whalon, 1982). However, the excessive use of
67 insecticides integrated in cultivation systems (e.g. no-tillage and conventional tillage) may be harmful
68 to soil biota, modify soil functions and, consequently, affect ecosystem (Palmquist et al., 2012).

69 Soil mesofauna, predominantly dominated by mite, collembolan and enchytraeid
70 communities, plays an important role in soil systems, namely in the provision of ecosystem services
71 like organic matter decomposition and turn-over (contributing to humus production), nutrient cycling

72 and in the formation of soil aggregates. Given the crucial role of these communities in maintaining
73 ecosystem functions, the diversity, abundance and vertical spatial distribution of these communities
74 are biological indicators of soil quality (Parisi et al., 2005). Some studies have been conducted to
75 evaluate the effects of different soil management systems (e.g. no-tillage and conventional tillage) on
76 soil communities of maize crops, evidencing that soil tillage usually promotes a decrease in the
77 number of arthropods and other groups of soil invertebrates like spiders and hymenopteran parasitoids
78 (Rodrigues et al., 2006), whereas no-tillage systems improve soil properties like soil organic carbon
79 and nitrogen content and soil compaction (Tabaglio et al., 2009). There is a trade-off between
80 efficiency in soil management (that may imply intensive practices and the use of agrochemicals) and
81 maintenance of environmental quality, which depends on the long-term sustainability of crop
82 production (Reicosky and Saxton, 2007). Therefore, it is important to understand how the most
83 abundant groups of soil invertebrates (mites, collembolans and enchytraeids) can cope with and
84 recover from each disturbing event in the different cropping systems, in order to optimize cropping
85 strategies to protect soil fauna. Laboratory experiments with intact soil cores (which include the
86 original soil communities), where soil management may be simulated at a small scale as in terrestrial
87 model ecosystems (TMEs) experiments (Moser et al., 2004; Knacker et al., 2004), may provide useful
88 and new information on this subject.

89 Here we report a TME experiment that compared the effects of four different and commonly
90 used varieties of maize cropping systems and an undisturbed scenario (control) on natural soil
91 invertebrate communities over a time-span of eighty-nine days. TMEs were collected in an
92 agricultural field and manipulated in the laboratory to simulate the following maize cropping systems:
93 conventional tillage, conventional tillage with insecticide, no-tillage, and no-tillage with insecticide.
94 Measured endpoints were taxonomic diversity and abundance of collembolans, mites and total
95 enchytraeid abundance.

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99 **2. Materials and methods**

100 *2.1. TMEs extraction*

101 Fifty-seven intact soil cores (TMEs - 16.5 cm of diameter and 40 cm of height) were collected
102 in an agricultural field free of pesticides application for more than five years. The agricultural field is
103 located in the suburban limits of Penacova Municipality (centre North of Portugal), in a small village
104 called São Mamede (40°14'56"N and 8°19'29"W). Chemical, physical and biological properties of
105 soil are presented in Table 1. The area was kept uncultivated and freely colonized by weeds since its
106 last tillage performed six months before TME collection. Immediately prior to TME collection, weeds
107 at the soil surface were harvested. Extraction of TMEs was performed following the methods
108 described by Knacker et al. (2004). Soil cores were maintained in carts with a temperature of 12 ± 2
109 °C and inside of a greenhouse with a temperature of $23 \pm 5^\circ\text{C}$, a relative air humidity between 50 and
110 80% and a photoperiod of 16:8 light:dark with a light intensity over the day period of 8,000 to 12,000
111 lux (see Knacker et al., 2004 for details on the TME approach). Before starting the test, TMEs were
112 acclimated to experimental conditions and irrigated with artificial rain water (Velthorst, 1993) up to
113 three times per week (100 ml per irrigation in each TME) over three weeks. Weeds were allowed to
114 grow during this period.

115

116 *2.2. Experimental design*

117 We designed our study to determine the effects of no-tillage and conventional tillage
118 management systems with and without the use of a pyrethroid insecticide on soil fauna communities
119 (collembolans, mites and enchytraeids) and included four treatments and a control. The test treatments
120 were: conventional tillage without insecticide application (CT), conventional tillage with insecticide
121 application (CTI), no-tillage without insecticide application (NT) and no-tillage with insecticide
122 application (NTI). The control (C) was irrigated undisturbed soil. Previously germinated maize seeds
123 were used in all treatments, including controls, to simulate soil conditions in a maize crop.

124 TMEs with different test treatments were randomly distributed among four carts and irrigated
125 (independently of the treatment) with 100 mL of artificial rain (Velthorst, 1993) every two days over
126 the course of the experiment. Soil samples were collected destructively from TMEs over the 12 weeks
127 duration of the experiment. The time schedule for the experiment is summarized in Table 2 and is
128 described as follows: Five TMEs were sampled at the beginning of the test period (day 0; D0
129 sampling) to characterize the initial soil community. After 12 days, the herbicide Montana® (with
130 glyphosate as a.i. at 360 g L⁻¹ and 36.0%, mass fraction) was applied to 20 TMEs (TMEs of NT and
131 NTI treatments) through a 100 mL solution (with 71.5 mg of glyphosate L⁻¹) per TME corresponding
132 to 9.3 L of herbicide ha⁻¹, approximately the dosage recommended by the manufacturer. This
133 chemical was applied to the soil surface by spraying and resulting weed residues (from weeds that
134 grew over the three-week TME incubation period) were left on the soil surface for the duration of the
135 experiment. On the same day and in another 20 TMEs, a superficial soil tillage was simulated mixing
136 the soil intensively with the aid of a shovel to a depth of 10 cm (CT and CTI). After four days (total
137 days 16), 12 TMEs (4 undisturbed – C, 4 with herbicide – NT and 4 with tillage – CT) were sampled
138 (D16 sampling) to evaluate the effect of herbicide and soil tillage on soil communities. The next day,
139 one maize plant (previously germinated in separated vessels over 7 days in a growth chamber at 24
140 °C) was planted in each of the remaining TMEs. Sixteen days after maize plantation (total days 33),
141 the insecticide Judo® (composed by 100 g L⁻¹ of lambda-cyhalothrin as a.i.) was applied to the leaves
142 of maize plants from 16 TMEs (8 TMEs with herbicide applied – NTI; and 8 TMEs with the soil
143 tilled - CTI). In each of these TMEs, 20 mL of insecticide solution (with 2.137 mg of lambda-
144 cyhalothrin L⁻¹) was applied, corresponding to 200 mL of insecticide ha⁻¹, the recommended dose for
145 maize cultivation (20 g a.i. ha⁻¹). After four weeks (total days 61), a total of 20 TMEs (4 TMEs from
146 each test treatment – C, CT, CTI, NT and NTI), were destructively sampled (D61 sampling) to
147 evaluate the effects of insecticide application on the different soil managements. The last 20 TMEs
148 (4 TMEs from each test treatment - C, CT, CTI, NT and NTI) were destructively sampled after another

149 4 weeks (total days 89) to evaluate the potential recovery of soil communities under each cropping
150 system.

151 At each sampling date, two soil cores (5 cm diameter, 10 cm depth) were collected from each
152 TME. Each core was subdivided into an upper and a lower layer (0-5 cm and 5-10 cm, respectively)
153 to evaluate the vertical distribution of soil organisms in the two soil profiles. One of the soil cores
154 was used for mite and springtail extraction over 10 days using a MacFadyen extractor with an
155 extraction temperature of 45°C. The individuals were fixed in approximately 10 ml of an 80% ethanol
156 solution. The extracted mites and collembolans were identified using a phase-contrast microscope to
157 the genus and when possible to the species level using specific literature for mites (Moraes and
158 Flechtmann, 2008; Krantz and Walter, 2009) and collembolans (references of identification keys
159 presented in supplementary data). Additionally, five collembolan morphological traits (ocelli,
160 antenna, furca, pigmentation and the presence of hairs and scales) were evaluated to build a life-form
161 trait score, which serves as a proxy of the degree of adaptation to the different soil profiles
162 (Vandewalle et al., 2010). Through this method, species are classified on a scale from 0 to 20, where
163 higher values reflect higher adaptation to deeper soil profiles. This classification was adapted from
164 Vandewalle et al. (2010), following scores used by Reis et al. (2016). Soil samples of the second soil
165 core collected in each TME were used for enchytraeid extraction using the wet funnel method with
166 heating (O'Connor, 1962). The extraction time was 5 hours, with a final surface temperature of 45°C.

167

168 2.3. Statistical analysis

169 The abundance of mites, collembolans and enchytraeids was estimated as the number of
170 individuals of each family/species per square meter in each treatment and sampling date. To
171 investigate the effects of the CT and NT managements and insecticide application (CTI and NTI) on
172 the abundance of mites, collembolans and enchytraeids, a Poisson generalised linear mixed model
173 (GLMM) with the log link function was performed for each group of organisms (mites, collembolans
174 and enchytraeids). In each GLMM, the abundance of each group of organisms was used as response

variable, treatment (C, CT, CTI, NT and NTI), soil layer (0-5 cm and 5-10 cm of depth) and sampling date (D0, D16, D61 and D89) as explanatory variables and soil layer nested in soil core as random factor. The collinearity between explanatory variables was checked through the estimation of the variation inflation factor. The significance of explanatory variables and its interaction was verified through the *p*-values of single term deletion tables. Model validation was performed by evaluating normality and homogeneity of data and independence of the explanatory variables. Differences between test treatments within the same soil layer (0-5 or 5-10 cm of depth) and between soil layers within the same treatment (C, CT, CTI, NT or NTI) were analysed through a multiple comparison test on planned contrasts. The traits and morphological attributes of collembolan groups were also used to evaluate the effect of soil managements. Data gathered from the analysis of collembolan morphological traits of replicates per treatment were used to estimate two indices: the community trait weighted mean (mT) and the average functional diversity (FD) as described by Chelinho et al. (2014) and Vandewalle et al. (2010), respectively. The mT was estimated as an average for a given trait weighted by species abundance, according to the formula:

$$mT = \sum_{i=1}^S P_i X_i$$

where P_i is the proportion of the *i*-th species and X_i the trait value of the *i*-th species in a sample. For each category, the relative abundance of a particular group (or modality) is calculated by the index. Functional diversity (FD) was estimated by Rao's Q index using R version 3.4.3 (R Core Team, 2017) with package FD (Laliberté and Legendre, 2010; Laliberté et al., 2014).

Soil samples without collembolans were not considered for calculating these indices. The effects of soil management and insecticide application on mT and FD was assessed by linear mixed models (LMMs) with normal distribution. In these LMMs the same response and explanatory variables and random factor used in the GLMM for abundance data analyses were considered. Differences between treatments within and between soil layers were analysed as performed for organisms abundance data. Before statistical analyses, outlier values were identified using the

200 Grubbs/Dixon outlier test (Sachs, 2002) and removed from the analysis. Multiple comparison *p* values
201 of GLMM and LMM are shown as supplementary data (Tables S5 - S7, S9 and S10). These statistical
202 analyses were performed using R version 3.4.3 (R Core Team, 2017) with packages drc (Ritz et al.,
203 2015), car (Fox and Weisberg, 2011), lme4 (Bates et al., 2015) and MASS (Venables and Ripley,
204 2002).

205 Additionally, the effect of soil management on soil mite and collembolan communities over
206 time was assessed through principal response curve (PRC) analyses (Van den Brink and Ter Braak,
207 1999) from abundance data. This method tests community changes over time between treatments and
208 controls and also provides the species weight which indicates how closely the response of each
209 individual taxon matches overall community response (for information about the statistical model
210 behind PRC see Van den Brink and Ter Braak, 1999). This analysis was carried out using CANOCO
211 4.5 (Microcomputer Power, Ithaca, USA) and SPSS 15 (SPSS Inc., Chicago, USA). Statistical
212 differences between canonical coefficients of test treatments within the same sampling time were
213 analysed through one-way ANOVAs followed by Dunnett's *post-hoc* test using Statistica 7.0.

214

215 **3. Results and Discussion**

216 The initial soil community (D0 sampling) had a high abundance of microarthropods and
217 enchytraeids (Table 3 and S1). In the top 5 cm soil layer, samples had eight (out of eleven) of the
218 total mite species and all eleven collembolan species were found (Table S1). In D0 samplings
219 collembolan communities of the top layer had a mT value lower (although not significantly different)
220 compared to the 5-10 cm layer, despite the similar FD found in both layers. This was a tendency that
221 was found in the majority of samplings (Tables 4 and S8). Collembola species with morphological
222 traits more adapted to the surface and with lower mT (i.e. high pigmentation and mobility) were more
223 present in the 0-5 cm layer, whilst species more adapted to deeper soil layers (i.e. low pigmentation
224 and mobility) with higher mT scores were more abundant in the 5-10 cm layer.

225 Soil tillage (CT) did not significantly affect Collembola and mite abundances on the second
226 sampling date (D16) when compared to control treatments (C) in both the top 5 cm and the 5-10 cm
227 soil layers (Table 3, S5 and S6). For mites, these results were confirmed in the PRC analysis in the
228 top 5 cm layer (Fig. 1), but for the 5-10 cm layer, the PRC analysis was not significant ($p>0.05$; graph
229 not shown). For Collembola, PRC analysis of the top 5 cm layer found that canonical coefficients
230 significantly increased with soil tillage at D16, while in 5-10 cm layer they did not change
231 significantly (Fig. 2). Apparently, soil tillage does not negatively affect mites and collembolans and
232 may even promote the increase of abundance of certain collembolan species in surface soil layers.

233 Since the seventies, it is known that moldboard plowing is detrimental to soil fauna (including
234 mites and collembolans; Edwards and Lofty, 1975) and subsequent studies have confirmed this effect
235 (e.g. Neave and Fox, 1998; Rodriguez et al., 2006). On the other hand, Loring et al. (1981) reported
236 that populations of mites and collembolans increased or remained unaffected after chisel plow tillage
237 (mechanical disturbance but at lower depth than moldboard plowing) compared to moldboard
238 plowing or no-till management. This implies that the impact on mesofauna populations from
239 mechanical disturbances may depend on the intensity/depth of soil tillage. In fact, the 10 cm depth
240 soil tillage adopted in CT treatment is closer to a chisel plow tillage than moldboard plowing (usually
241 up to 30 cm in depth). However, this contradicts the data reported by Van Capelle et al. (2012) where,
242 in German arable soils, both mite and collembolan densities decreased with reduced tillage intensity.
243 Also, according to Rodriguez et al. (2006), specific groups of mites can be more abundant or are not
244 affected in tilled soil due to their high resistance to drought conditions. In fact, mite abundance found
245 in samples of D16 of 5 cm top layers of CT was higher (although not significantly different) compared
246 to C predominantly due to the increase in abundance of *Tyrolichus casei* and a species from the
247 Rhodacaridae family (Table S2). *T. casei* belongs to the Astigmata suborder, which is known to
248 comprise species with physiological mechanisms to prevent water loss (Wharton and Furumizo,
249 1977).

250 In the CT samples, while the abundance and FD of collembolans (Tables 3 and 4, respectively)
251 did not differ from the other treatments, their mT was lower than other treatments (although only
252 significantly lower compared to NT) in the 5-10 cm soil layer (Tables 4 and S9). This lower mT was
253 the result of the increase in abundance of *Isotomurus* sp. in the deeper soil layers of the CT treatment.
254 This species has one of the lowest trait scores (Table S8) and the appearance of individuals from this
255 species compensated the losses of individuals from other species with higher trait score value (e.g.
256 *Hemisotoma thermophila*). This resulted in a similar abundance but reduced the mT value of samples
257 from CT, compared to C and NT. It could be that tillage reduces soil compaction, increasing light
258 penetration and the incorporation of litter at deeper soil layers, thus promoting the increase in
259 abundance of species (like *Isotomurus* sp.) with traits adapted to the soil surface.

260 Soil tillage did not change enchytraeid abundance in any of the soil layers sampled in D16
261 and the top 5 cm soil layer was the most abundant only in C treatment (Tables 3 and S7). These results
262 do not agree with several previous studies (House and Parmelee, 1985; Parmelee et al., 1990; Postma-
263 Blaauw et al., 2012; Domínguez and Bedano, 2016) that have reported greater densities of
264 enchytraeids in no-tillage systems than in conventional tillage systems. However, the literature lacks
265 consensus on this matter, which suggests that the effect of soil tillage on enchytraeid communities is
266 site/community specific. For instance, there is a study reporting no influence of soil tillage on
267 enchytraeid abundance (Yokota, 2002), which agrees with our data, and others reporting higher
268 abundances in conventional tillage systems compared to no-till systems (Manetti et al., 2010; Van
269 Capelle et al., 2012). Pelosi and Römcke (2016) have argued that enchytraeids may benefit from soil
270 tillage as this practice increases the incorporation of crop residues in deeper soil layers leading to an
271 increase in food sources. Furthermore, soil tillage may promote bacterial growth (which favours
272 bacterial-feeding enchytraeids) and an increase in pore spaces in soil, which favours enchytraeid
273 growth. However, this behaviour was not observed in the present study and the abundance of both
274 soil layers remained unaffected by soil tillage.

Herbicide application, similar to tillage, did not affect mite abundance, as evidenced by the canonical coefficients of PRC analyses (Fig. 1 and 2), but promoted a reduction of collembolan abundance in the top 5 cm soil layer that was statistically significant only compared to CT (Tables 3 and S6). The herbicide application reduced the abundance of collembolans in the top 5 cm layer, which made the abundances of both soil layers (0- 5 and 5- 10 cm) statistically similar. In terms of FD, no significant effects were observed in both soil layers (Tables 4 and S10). On the other hand, the herbicide application promoted an increase of mT in the 5-10 cm soil layer (significant only compared to CT), but mT was not affected in top 5 cm layer in comparison to C samples for the same soil layer (Tables 4 and S9). In the top 5 cm layer of NT, the decrease in collembolan abundance (significant only compared to CT) was caused mostly by the reduction of *H. thermophila*, *Isotomodes* sp. and *Protaphorura* cf. *armata* (Table S2). Apparently, these individuals (characterized by high trait score values; Table S8) were sensitive to herbicide application resulting in a reduction in abundance, but they also appear to have avoided the top 5 cm layer by migrating to deeper layers. The avoidance behaviour of these species is also reflected in the increase of mT value in the 5-10 cm layer of NT. However, this avoidance behaviour was not sufficient to significantly increase collembolan abundance in the 5-10 cm layer compared to the other treatments (Tables 3 and S6). Despite changes in mT values, FD was not affected most probably due to functional redundancy of the species (Tables 4 and S10).

Glyphosate is known to affect collembolan populations, and Mohammed et al. (2017) previously reported the complete elimination of collembolan populations in glyphosate treated plots fourteen days after its application. These authors also reported a decrease in mite communities, contradicting the results observed in the present study. The lowest dose used by the authors (1.4 ml of herbicide m⁻²) was higher than the dose of 0.93 mL m⁻² applied in the present study, but when modelling exposure, concentrations are comparable. According to EPPO (2003) and assuming the DT50 value (at 30°C and 60% water-holding capacity of soil following Bento et al. (2016)), a soil depth of 10 cm (with uniform distribution of the herbicide over soil layer) and a 1.5 g cm⁻³ soil density,

301 the dose used by Mohammed et al. (2017) was 0.69 mg kg⁻¹. Following the same assumptions, the
302 dose applied in the present study was 1.21 mg kg⁻¹. On the other hand, our results are not in agreement
303 with previous studies that have affirmed that the use of herbicides based on glyphosate do not affect
304 collembolan populations from agricultural areas (Blitzer et al., 2002; Vilma et al., 2007) or even
305 stimulate their abundance, negatively affecting mite populations (Damgaard et al., 2016). Taking into
306 consideration literature data from laboratory ecotoxicological tests with standard invertebrate species
307 to glyphosate, reported information has been highly variable. While studies conducted by Santos et
308 al. (2010, 2012) reported EC50 values for the collembolan *Folsomia candida* of 0.33 to 0.54 mg
309 glyphosate kg⁻¹ of soil (using the same commercial formulation used in the present study), more
310 recent data has found no effects at an application dose of 472.8 mg a.i. kg⁻¹ (no information is given
311 concerning the commercial formulation used) for *F. candida* and the mite *Hypoaspis aculeifer* (Mérey
312 et al., 2016). Considering that the herbicide applied in the present study corresponded to a
313 concentration of 2.24 mg a.i. kg⁻¹ (assuming no compost degradation and a soil density of 1.5 g cm⁻³
314 and an equal distribution of the herbicide at the top 10 cm soil layer), the decrease of collembolan
315 abundance found in the top layer of NT treatment of the present study is supported by the data reported
316 in Santos et al. (2010, 2012).

317 Regarding enchytraeids, no effects were observed at any of the sampled soil layers. Effects of
318 glyphosate on enchytraeid communities are not known but previous studies have reported no
319 significant toxic effects of glyphosate on other oligochaete species, both under field (Dalby et al.,
320 1995) and laboratory conditions (Santos et al., 2012).

321 Insecticide application significantly decreased the abundances of mites in the top 5 cm soil
322 layer (Table 3) of both conventional tillage (CTI) and no-tillage systems (NTI) when compared to
323 their respective treatments without insecticide application (CT and NT) in the D61 samples (49 days
324 after tillage/herbicide and 28 days after insecticide application, Table S5). For Collembola, insecticide
325 application also led to a decrease in abundance in CTI and NTI compared to CT and NT but this
326 decrease was only statistically significant in NTI (Table S6). In the 5-10 cm soil layer, mite abundance

only decreased in CTI compared to CT (but not significantly) and collembolan abundance increased in CTI and NTI compared to CT and NT, respectively (Tables 3, S5 and S6). In the PRC analysis, for mites in the top 5 cm soil layer of D61 samples, the canonical coefficient for CT treatment is significantly lower than control as well as canonical coefficients of CTI and NTI treatments (Fig. 1). For collembolan communities, in the top 5 cm layer, the canonical coefficients of CTI and NTI were significantly lower than in the control, while that of NT was significantly higher compared to the control. In the 5-10 cm layer, PRC analyses corroborated the changes in abundance of collembolan communities observed in Table 3, and canonical coefficients of CTI and NTI were significantly higher than control (Fig. 2). The decrease of mite abundance observed in the top 5 cm layer of both CTI and NTI treatments and in the 5-10 cm layer of CTI (Table 3) agrees with previous studies that report noxious effects of synthetic pyrethroid insecticides on mite communities (Croft et al., 1982; Huusela-Veistola et al., 1994). On the other hand, the decrease of collembolan abundance in the top layer of CTI and NTI (significant only for NTI) are not in agreement with previous studies that have reported increases in collembolan abundances in the presence of other pyrethroid insecticides (Holopainen and Rikala, 1995; Frampton et al., 2007). However, it is known that insecticides with pyrethroids (e.g. lambda-cyhalothrin) affect nerve impulse transmission in insects, acting on voltage-sensitive sodium channels (Palmquist et al., 2012), which could explain the collembolan community response observed in the present study. The decrease of collembolan abundance in the top layer of NTI was not followed by changes in mT or FD (Tables 4, S9 and S10). Similarly, increases of collembolan abundance observed in CTI and NTI treatments in the 5-10 cm layer occurred without significant changes in the mT and FD values (Tables 4, S9 and S10). The only significant change observed was the mT of CT in 5-10 cm layer. This change was related to the disappearance of species of low to median trait score (e.g. *H. thermophila*) which promoted the increase of the mT value. The decrease of collembolan abundance observed in the top 5 cm layer of CTI and NTI was followed by an increase in collembolan abundance in the 5-10 cm layer of the same treatments. Collembolan species which were present in CT and NT in the top soil layer occurred at much lower abundance in

353 CTI and NTI but increased in abundance in deeper soil layers, which did not occur in CT and NT.
354 This demonstrates a vertical avoidance behaviour of Collembola from the soil surface, where higher
355 insecticide concentrations are expected, down to deeper layers, reducing their exposure. In contrast
356 to the tillage treatments, here the migration of Collembola to a deeper soil layer did not affect the mT
357 values. This suggests that the repellent effect of the insecticide was not species-specific. Such
358 avoidance behaviour was also observed by Zortéa et al. (2015) for another pyrethroid insecticide
359 (cypermethrin) but for the collembolan *F. candida*.

360 Regarding the enchytraeid community, its abundance did not significantly change with
361 insecticide application in any soil layer and treatment (Tables 3 and S7). In fact, enchytraeid
362 abundance in the top 5 cm layer (where insecticide concentration is expected to be higher) remained
363 statistically similar to that in the 5-10 cm layer of the CTI and NTI treatments. To our knowledge, the
364 only study available in the literature evaluating the effect of lambda-cyhalothrin to enchytraeids was
365 conducted by Bandow et al. (2013). These authors reported 21-day EC50 values between 1.33 and
366 4.75 mg kg⁻¹ for the species *Enchytraeus bigeminus*. Taking into account that, in the present study,
367 the concentration of lambda-cyhalothrin in soil could not be higher than 0.0133 mg a.i. kg⁻¹ (assuming
368 no degradation of the pyrethroid, a soil density of 1.5 g cm⁻³ and an equal distribution of the compound
369 in the top 10 cm soil layer), the pyrethroid was in soil at a concentration at least one hundred times
370 lower than the lowest EC50 value reported by Bandow et al. (2013). This fact supports the absence
371 of effects observed in enchytraeid communities of treatments with insecticide (NTI and CTI). On the
372 other hand, the sensitivity of the enchytraeid *Enchytraeus crypticus* to other synthetic pyrethroids
373 (namely alpha-cypermethrin) has been reported as more sensitive than the collembolan *F. candida*
374 and the earthworm *Eisenia fetida* (Hartnik et al., 2008). In this case, these results do not agree with
375 the data obtained in the present study which showed higher sensitivity of Collembola community to
376 the insecticide than enchytraeid community.

377 The last sampling date (D89) revealed that, in both soil layers, abundance of mite communities
378 recovered in most of the treatments, except in CTI (Table 3). In CTI, mite abundance in the top 5 cm

layer was significantly lower than in the control (C) but not significantly different than CT (Tables 3 and S5). On the other hand, the PRC analysis in the top 5 cm layer showed canonical coefficients significantly lower than the control in CT, CTI and NTI. When compared to D61, all treatments show a recovery trend to control levels (Fig. 1). This suggests that mite communities affected by conventional tillage (CT) and insecticide application (CTI and NTI) can recover from these disturbances but while this process is under way, a larger timescale than the one used in the TME experiment is required (>56 days). This ability to recover may be explained by the fact that the mite community was dominated by *T. casei* mites (the species with the highest b_k value in PRC from the top 5 cm layer; Fig. 1). This species belongs to the Astigmata group whose mites are known to be relatively resilient to drought conditions (Wharton and Furumizo, 1977) and synthetic insecticides (like Carbofuran; Broadbent and Tomlin, 1982). This resilience is mostly related to their high fecundity, fast development and high reproductive rate (Norton, 1994). *T. casei*, together with the species from the Rhodacaridae family, were the most abundant species in the test treatments. Species of Rhodacaridae belong to the Mesostigmata suborder that includes predominantly mites which predate nematodes, collembolans, other soft-bodied mites and small insects (Karg, 1978; Walter et al., 1988) and some are omnivores, feeding on fungi and animal prey (Walter and Lindquist, 1989). These mites are usually numerically dominant in soil and are known to respond more sensitively and rapidly to environmental changes in soil than other species due to their high metabolism, high fecundity and short life cycle (Koehler, 1999). In contrast, species of the genus *Oribatida* were the most abundant in D0 and D16 for all test treatments in general and started to decrease in D61 samples presenting its lowest appearance in D89 samplings, especially in treatments with conventional tillage (CT and CTI), where these mites practically disappeared. This agrees with the lower metabolic rates, slow development and low fecundity of mite species belonging to the Oribatida suborder that are known as species whose populations rapidly decline when their habitat is disturbed (Lebrun and van Straalen, 1995). This fact has given strength to the use of species from this suborder to detect environmental degradation (Lebrun and van Straalen, 1995). Overall it appears that, especially in

405 treatments with conventional tillage (CT and CTI), there is a shift in the mite communities from
406 species belonging to groups which are less adaptable to environmental change (Oribatida) in the
407 initial samples, to species more adapted to environmental fluctuations and disturbances in the later
408 samples as a response to stress (Mesostigmata and Astigmata).

409 The last sampling (D89) demonstrated that collembolan communities recovered in all
410 treatments in the top 5 cm layer. No statistical differences were found between treatments (Tables 3
411 and S6). In the 5-10 cm layer, collembolan abundance of CTI treatment was significantly higher than
412 all treatments without insecticide (C, CT and NT; Tables 3 and S6). PRC analysis corroborates the
413 abundances data found in D89 samples of the top 5 cm layer and demonstrates a recovery of
414 collembolan communities in all treatments. In the 5-10 cm layer, PRC analysis canonical coefficients
415 for CTI and NTI were significantly higher than control (Fig. 2). Despite some differences in
416 abundance, mT and FD were not statistically different between treatments, except for CTI in the top
417 5 cm layer where mT was significantly lower than that of C and NT (Tables 4 and S9). This mT
418 decrease was mainly due to the disappearance of species of the genus *Proisotomodes* (with a trait
419 score of 10, Table S8).

420 The higher collembolan abundance found in the 5-10 cm layer of samples in CTI and NTI
421 treatments at D89 and D61, respectively, was mainly due to the increased abundance of *H.*
422 *thermophila* (the species with the highest b_k value in PRC from the 5-10 cm layer of Fig. 2).
423 Apparently, this species is resistant to soil disturbance: Fiera (2009) reported *H. thermophila* as the
424 most abundant species in a highly polluted site. The high abundance of Collembola in this study can
425 be attributed to species such as *H. thermophila* with ability to resist the presence of pollutants. Other
426 studies have also reported high abundance of this species in contaminated sites (Sterzynska and
427 Kuznetsova, 1997; Fountain and Hopkin, 2004).

428 Concerning enchytraeids, their abundances remained unchanged among treatments and
429 remained in the same order of magnitude in both layers. Enchytraeid data collected throughout the
430 test period suggests that this community was more resistant than mites and collembolans.

431

432 **4. Conclusions**

433 Concerning the soil managements evaluated, the highest impact was found after the
434 insecticide application. This impact was not influenced by soil management (conventional tillage or
435 no-tillage) for collembolan and enchytraeid communities, but was longer in the conventional tillage
436 treatment for mite communities. This fact suggests that no-tillage management is more protective to
437 soil fauna communities, than conventional tillage, by improving their resilience against insecticide
438 application. Apparently, the disturbance provoked by soil tillage (destruction of soil structure)
439 amplifies the effect of the insecticide to mites that are less impacted in the no-tillage system despite
440 the herbicide application. These findings suggest that synergistic effects between soil disturbances
441 (either physical or chemical) may result in a higher impact to soil fauna.

442

443

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647 **Figure captions:**

648

649

650 **Fig. 1.** Principal response curve (PRC) and respective species weights (b_k) of mites collected in the
651 top 5 cm soil layer. See the text for sampling and treatment code meanings. * Significant differences
652 compared to control of the same sampling time ($p \leq 0.05$). PRC explains 73.7% of the total variance
653 observed, from which 24.2% is explained by time and 49.5% by treatments; $F=13.74$, $p=0.002$.

654

655 **Fig. 2.** Principal response curves and respective species weight (b_k) of collembolans collected in the
656 top 5 cm and 5-10 cm soil layers (first and second graph, respectively). See the text for sampling
657 and treatment codes meaning. * Significant differences compared to control of the same sampling
658 time ($p \leq 0.05$). First PRC explains 77.2% of the total variance observed, from which 26% is
659 explained by time and 51.2% by treatments, $F=13.226$, $p=0.002$; and second PRC explains 82,7%
660 of the total variance of, from which 47.7% is explained by time and 35% by treatments, $F=54.035$,
661 $p=0.002$.

662

664 **Table 1.** Chemical, physical and biological characterization of field soil used in the TME experiment.

Chemical properties							Texture			Mesofauna	
pH (H ₂ O)	pH (KCl)	OM (%)	P ₂ O ₅ (mg kg ⁻¹)	K ₂ O (mg kg ⁻¹)	N(M) (mg kg ⁻¹)	N(T) (mg kg ⁻¹)	Sand (%)	Silt (%)	Clay (%)	0-5 cm Σ = 124	5-10 cm Σ = 76
5.2	3.5	6.0	>200	116	21	4872	51.37	35.02	13.61	62 ± 29	38 ± 3

665 OM (organic matter) conducted by Walkey-Black method; P₂O₅ (phosphorus) and K₂O (potassium) both modified Egner-Rhien extracts; N(M) mineral nitrogen N(T) total nitrogen;
666 Σ : total number of collembolans, mites and enchytraeids in a cylinder with 5 cm of diameter and 10 cm of height, average ± SD (standard deviation, *n* = 3).

667

668

669 **Table 2.** Summary of the test schedule used in a TME experiment simulating maize crops using undisturbed soil (C), conventional tillage system (CT),
670 conventional tillage system with insecticide (CTI), no-tillage system (NT) and no-tillage system with insecticide (NTI). Four TMEs were destructively
671 sampled in each soil sampling per each treatment (except for soil sampling of day 0 where five TMEs were sampled).

672

Day	Test treatment				
	C	CT	CTI	NT	NTI
0	Soil sampling	-	-	-	-
12	-	Soil tillage	Soil tillage	Herbicide application	Herbicide application
16	Soil sampling	Soil sampling	-	Soil sampling	-
17	Maize planting	Maize planting	Maize planting	Maize planting	Maize planting
33	-	-	Insecticide application	-	Insecticide application
61	Soil sampling	Soil sampling	Soil sampling	Soil sampling	Soil sampling
89	Soil sampling	Soil sampling	Soil sampling	Soil sampling	Soil sampling

Table 3. Average abundance ($\pm$ SD, $n = 5$ to 4) of mites, collembolans and enchytraeids found in soil samples (values extrapolated to individuals per square meter) from the top 0-5 and 5-10 cm layer in different sampling times (D0, D16, D61 and D89) and under different soil managements (C, CT, CTI, NT and NTI) in a TME experiment. See the text for sampling and treatment codes.

	D0	D16	D61	D89
<i>Mites</i>				
0 - 5 cm				
C	8467 $\pm$ 2121 A	8799 $\pm$ 1406 Aa	8547 $\pm$ 3262 Aa	12243 $\pm$ 2163 Aa
CT	-	11350 $\pm$ 2056 Aa	5103 $\pm$ 2734 Aab	8290 $\pm$ 1687 Aab
CTI	-	-	1019 $\pm$ 0 Ac	4463 $\pm$ 2332 Abc
NT	-	9313 $\pm$ 2444 Aa	11734 $\pm$ 3252 Aa	15308 $\pm$ 6276 Aa
NTI	-	-	2678 $\pm$ 2710 Abc	9313 $\pm$ 5126 Aac
5 - 10 cm				
C	4593 $\pm$ 3439 A	4977 $\pm$ 1785 Aa	2808 $\pm$ 2299 Ba	3953 $\pm$ 2547 Ba
CT	-	5612 $\pm$ 4981 Aa	4210 $\pm$ 1276 Aa	4463 $\pm$ 2897 Aa
CTI	-	-	1019 $\pm$ 720 Aa	3701 $\pm$ 5056 Aa
NT	-	4463 $\pm$ 1972 Aa	2935 $\pm$ 1406 Ba	2935 $\pm$ 967 Ba
NTI	-	-	2808 $\pm$ 883 Aa	1785 $\pm$ 1584 Ba
<i>Collembolans</i>				
0 - 5 cm				
C	8467 $\pm$ 4556 A	9313 $\pm$ 2332 Aab	7271 $\pm$ 3238 Aabc	6121 $\pm$ 2734 Aa
CT	-	16327 $\pm$ 3972 Aa	6762 $\pm$ 1925 Aabc	9692 $\pm$ 930 Aa
CTI	-	-	3187 $\pm$ 1131 Aac	5355 $\pm$ 1692 Aa
NT	-	4210 $\pm$ 2612 Ab	13776 $\pm$ 5369 Ab	11481 $\pm$ 883 Aa
NTI	-	-	3061 $\pm$ 589 Ac	10206 $\pm$ 4785 Aa
5 - 10 cm				
C	1734 $\pm$ 1378 B	892 $\pm$ 640 Ba	766 $\pm$ 883 Ba	1402 $\pm$ 1579 Ba
CT	-	766 $\pm$ 883 Ba	766 $\pm$ 659 Ba	1533 $\pm$ 589 Ba
CTI	-	-	5869 $\pm$ 509 Ab	6762 $\pm$ 3262 Abc
NT	-	1785 $\pm$ 1584 Aa	2168 $\pm$ 1738 Bab	1402 $\pm$ 869 Ba
NTI	-	-	16070 $\pm$ 3369 Bc	3953 $\pm$ 1341 Aac
<i>Enchytraeids</i>				
0 - 5 cm				
C	29079 $\pm$ 8290 A	28701 $\pm$ 11112 Aa	11224 $\pm$ 5220 Aa	7654 $\pm$ 11047 Aa
CT	-	29210 $\pm$ 7304 Aa	27168 $\pm$ 17220 Aa	6888 $\pm$ 5986 Aa
CTI	-	-	18112 $\pm$ 10692 Aa	10967 $\pm$ 7411 Aa
NT	-	25509 $\pm$ 6304 Aa	11991 $\pm$ 2262 Aa	13009 $\pm$ 10276 Aa
NTI	-	-	28827 $\pm$ 13808 Aa	20154 $\pm$ 12598 Aa
5 - 10 cm				
C	9897 $\pm$ 2411 A	7397 $\pm$ 6645 Ba	8547 $\pm$ 4682 Aa	2551 $\pm$ 2855 Aa
CT	-	13519 $\pm$ 16028 Aa	9056 $\pm$ 7266 Aa	4593 $\pm$ 2000 Aa
CTI	-	-	6378 $\pm$ 3369 Aa	5103 $\pm$ 2318 Aa
NT	-	8290 $\pm$ 2294 Aa	14925 $\pm$ 14505 Aa	4210 $\pm$ 5093 Aa
NTI	-	-	8290 $\pm$ 4336 Aa	8290 $\pm$ 2294 Aa

Different lowercase letters indicate statistical differences of treatments (C, CT, CTI, NT or NTI) within the same depths (top 0-5 or 5-10 cm layer) and sampling dates (D0, D16, D61 or D89); and different capital letters indicate statistical differences within treatments between depths (differences analysed through single term deletion tables followed by multiple comparison of planned contrasts, $p \leq 0.05$; see Tables S5-S7 for p values).

682
683 **Table 4.** Mean community trait values (mT) and average functional diversity (FD) of collembolan
684 communities in the top 5 cm and 5-10 cm layers in different sampling times (D0, D16, D61 and D89)
685 and under different soil managements (C, CT, CTI, NT and NTI) in a TME experiment. See the text
686 for sampling and treatment codes.

	D0	D16	D61	D89
<i>mT</i>				
0 - 5 cm				
C	10.95 ± 1.06 A	9.89 ± 0.50 Aa	9.65 ± 1.15 Aa	9.65 ± 1.27 Aa
CT	-	8.39 ± 0.91 Aa	9.68 ± 1.21 Aa	9.31 ± 1.15 Aab
CTI	-	-	8.66 ± 2.69 Aa	5.94 ± 1.90 Ab
NT	-	8.76 ± 1.54 Aa	9.96 ± 4.04 Aa	9.47 ± 0.91 Aa
NTI	-	-	8.17 ± 1.89 Aa	8.41 ± 1.56 Aab
5 - 10 cm				
C	12.80 ± 0.98 A	10.56 ± 1.07 Aab	10.67 ± 3.06 Aa	11.30 ± 3.72 Aa
CT	-	6.67 ± 3.77 Aa	16.44 ± 2.69 Bb	11.00 ± 2.58 Aa
CTI	-	-	9.38 ± 0.61 Aa	10.72 ± 0.80 Ba
NT	-	12.70 ± 1.48 Bb	10.83 ± 2.13 Aa	10.07 ± 0.44 Aa
NTI	-	-	9.18 ± 1.31 Aa	8.80 ± 0.92 Aa
<i>FD</i>				
0 - 5 cm				
C	0.05 ± 0.03 A	0.08 ± 0.06 Aa	0.10 ± 0.04 Aa	0.09 ± 0.02 Aa
CT	-	0.08 ± 0.03 Aa	0.13 ± 0.02 Aa	0.07 ± 0.03 Aa
CTI	-	-	0.07 ± 0.05 Aa	0.05 ± 0.06 Aa
NT	-	0.06 ± 0.07 Aa	0.08 ± 0.02 Aa	0.09 ± 0.01 Aa
NTI	-	-	0.08 ± 0.06 Aa	0.06 ± 0.03 Aa
5 - 10 cm				
C	0.04 ± 0.03 A	0.01 ± 0.02 Aa	0.03 ± 0.05 Aa	0.02 ± 0.04 Aa
CT	-	0.04 ± 0.05 Aa	0.02 ± 0.03 Ba	0.07 ± 0.08 Aa
CTI	-	-	0.10 ± 0.03 Aa	0.07 ± 0.04 Aa
NT	-	0.03 ± 0.03 Aa	0.02 ± 0.04 Aa	0.00 ± 0.01 Aa
NTI	-	-	0.06 ± 0.04 Aa	0.00 ± 0.01 Aa

687 Different lowercase letters indicate statistical differences of treatments (C, CT, CTI, NT or NTI) within the same depths
688 (top 0-5 or 5-10 cm layer) and sampling dates (D0, D16, D61 or D89); and different capital letters indicate statistical
689 differences within treatments between depths (differences analysed through single term deletion tables followed by
690 multiple comparison of planned contrasts, $p \leq 0.05$; see Tables S9 and S10 for p values).
691

Fig. 1.

Fig. 2.

Impact of no-tillage versus conventional maize plantation on soil mesofauna with and without the use of a lambda-cyhalothrin based insecticide: a Terrestrial Model Ecosystem experiment

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Supplementary data:

List of bibliographic references of the identification keys used in Collembolan identifications:

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Table S1. Mean number ($\pm$ standard deviation; $n = 5$) of individuals of mites and collembolan families and subfamilies/species found in soil samples collected in TMEs (values extrapolated to individuals per square meter), at the beginning of the experiment (D0; before soil tillage or herbicide applications).

Samplings		D0	
Treatments		Initial	
Family/group	Subfamily/Species	0 – 5 cm	5 – 10 cm
Mites			
Acaridae	<i>Tyrolichus casei</i>	813 $\pm$ 927	103 $\pm$ 228
Ascidae	<i>Asca</i> sp.	0	617 $\pm$ 427
Ascidae	<i>Protogamasellus mica</i>	0	206 $\pm$ 279
Cunaxidae	Cunaxoidinae	0	206 $\pm$ 279
Ologamasidae	<i>Ologamasus</i> sp.	411 $\pm$ 427	0
Ologamasidae	<i>Neogamasellevans</i> sp.	103 $\pm$ 228	206 $\pm$ 456
Oribatida	<i>Oribatida</i> spp.	3570 $\pm$ 510	1019 $\pm$ 1767
Oribatida	<i>Brachypylina</i> sp.	813 $\pm$ 854	0
Rhagidiidae	sp.	308 $\pm$ 279	0
Rhodacaridae	sp.	2346 $\pm$ 927	2140 $\pm$ 2265
Uropodidae	sp.	103 $\pm$ 228	103 $\pm$ 228
Collembolans			
Entomobryid	<i>Pseudosinella</i> sp.	206 $\pm$ 456	0
Entomobryid	<i>Lepidocyrtus</i> sp.	103 $\pm$ 228	0
Entomobryid	<i>Heteromurus</i> sp.	308 $\pm$ 685	0
Isotomid	<i>Isotomodes</i> sp.	2654 $\pm$ 1106	617 $\pm$ 838
Isotomid	<i>Isotomurus</i> sp.	308 $\pm$ 685	0
Isotomid	<i>Hemisotoma thermophile</i>	411 $\pm$ 427	0
Isotomid	<i>Proisotomodes</i> sp.	411 $\pm$ 427	0
Onychiurid	<i>Protaphorura</i> cf. <i>armata</i>	1019 $\pm$ 807	514 $\pm$ 510
Podurid	<i>Brachystomella parvula</i>	1019 $\pm$ 1082	103 $\pm$ 228
Podurid	<i>Ceratophysella</i> sp.	1635 $\pm$ 757	514 $\pm$ 722
Sminthuridid	<i>Sphaeridia pumilis</i>	411 $\pm$ 427	0

Table S2. Mean number ($\pm$ standard deviation; $n = 4$) of individuals of mites and collembolan families and subfamilies/species found in soil samples collected in TMEs (values extrapolated to individuals per square meter), submitted to different treatments (C, CT and NT), four days after simulated soil tillage or herbicide application (D16). Meaning of treatment codes: C – undisturbed soil; CT – simulated conventional tillage; NT – no-tillage.

Samplings		D16					
Treatments		C		CT		NT	
Family/group	Subfamily/Species	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm
Mites							
Acaridae	<i>Tyrolichus casei</i>	1145 $\pm$ 871	0	2547 $\pm$ 1718	1273 $\pm$ 659	2545 $\pm$ 1250	642 $\pm$ 642
Ascidae	<i>Asca</i> sp.	642 $\pm$ 488	257 $\pm$ 295	1016 $\pm$ 833	257 $\pm$ 510	0	0
Ascidae	<i>Protogamasellus mica</i>	888 $\pm$ 765	257 $\pm$ 295	0	0	0	0
Cunaxidae	Cunaxoidinae	0	385 $\pm$ 488	385 $\pm$ 488	257 $\pm$ 510	771 $\pm$ 659	128 $\pm$ 255
Ologamasidae	<i>Ologamasus</i> sp.	514 $\pm$ 722	128 $\pm$ 255	514 $\pm$ 722	0	128 $\pm$ 255	128 $\pm$ 255
Ologamasidae	<i>Neogamasellevans</i> sp.	0	514 $\pm$ 1020	257 $\pm$ 510	0	0	0
Oribatida	<i>Oribatida</i> spp.	1787 $\pm$ 510	514 $\pm$ 417	2173 $\pm$ 1131	2418 $\pm$ 3849	2301 $\pm$ 1586	771 $\pm$ 977
Oribatida	<i>Brachypylina</i> sp.	1145 $\pm$ 1342	0	888 $\pm$ 642	0	1016 $\pm$ 417	385 $\pm$ 765
Rhagidiidae	sp.	514 $\pm$ 417	0	0	257 $\pm$ 510	0	0
Rhodacaridae	sp.	2044 $\pm$ 1502	2932 $\pm$ 1926	3575 $\pm$ 1767	1145 $\pm$ 871	2547 $\pm$ 1718	2418 $\pm$ 1342
Uropodidae	sp.	128 $\pm$ 255	0	0	0	0	0
Collembolans							
Entomobryid	<i>Pseudosinella</i> sp.	0	0	128 $\pm$ 255	0	0	0
Entomobryid	<i>Lepidocyrtus</i> sp.	0	0	0	0	0	0
Entomobryid	<i>Heteromurus</i> sp.	257 $\pm$ 295	0	1787 $\pm$ 659	0	385 $\pm$ 488	0
Isotomid	<i>Isotomodes</i> sp.	1530 $\pm$ 1102	128 $\pm$ 128	2301 $\pm$ 884	257 $\pm$ 255	128 $\pm$ 255	1145 $\pm$ 871
Isotomid	<i>Isotomurus</i> sp.	888 $\pm$ 1786	0	3318 $\pm$ 1932	514 $\pm$ 510	771 $\pm$ 977	0
Isotomid	<i>Hemisotoma thermophila</i>	1016 $\pm$ 417	128 $\pm$ 128	1016 $\pm$ 1718	0	888 $\pm$ 1052	257 $\pm$ 255
Isotomid	<i>Proisotomodes</i> sp.	1530 $\pm$ 1954	0	2932 $\pm$ 871	0	642 $\pm$ 488	0
Onychiurid	<i>Protaphorura</i> cf. <i>armata</i>	1145 $\pm$ 765	0	1145 $\pm$ 488	0	257 $\pm$ 510	385 $\pm$ 383
Podurid	<i>Brachystomella parvula</i>	771 $\pm$ 1531	0	1016 $\pm$ 932	0	385 $\pm$ 765	0
Podurid	<i>Ceratophysella</i> sp.	1016 $\pm$ 1718	514 $\pm$ 510	888 $\pm$ 1206	0	514 $\pm$ 722	0
Sminthuridid	<i>Sphaeridia pumilis</i>	1145 $\pm$ 1052	128 $\pm$ 128	1787 $\pm$ 1586	0	257 $\pm$ 295	0

Table S3. Mean number ($\pm$ standard deviation; $n = 4$) of individuals of mites and collembolan families and subfamilies/species found in soil samples collected in TMEs (values extrapolated to individuals per square meter), submitted to different treatments (C, CT, CTI, NT and NTI), twenty-eight days after the insecticide application in CTI and NTI (D61). Meaning of treatment codes: C – undisturbed soil; NT – no-tillage; NTI – no-tillage with insecticide application; CT – simulated conventional tillage; CTI – simulated conventional tillage with insecticide application.

Samplings		D61									
Treatments		C		CT		CTI		NT		NTI	
Family/group	Subfamily/Species	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm
Mites											
Acaridae	<i>Tyrolichus casei</i>	4334 $\pm$ 2517	385 $\pm$ 488	257 $\pm$ 510	888 $\pm$ 871	128 $\pm$ 255	128 $\pm$ 255	3061 $\pm$ 2204	0	385 $\pm$ 488	1273 $\pm$ 659
Ascidae	<i>Asca</i> sp.	0	0	0	0	0	0	385 $\pm$ 488	128 $\pm$ 255	128 $\pm$ 255	0
Ascidae	<i>Protogamasellus mica</i>	0	0	0	0	0	0	257 $\pm$ 510	0	0	0
Cunaxidae	Cunaxoidinae	128 $\pm$ 255	0	257 $\pm$ 295	385 $\pm$ 488	0	0	128 $\pm$ 255	0	0	0
Ologamasidae	<i>Ologamasus</i> sp.	257 $\pm$ 295	128 $\pm$ 255	0	0	0	0	771 $\pm$ 510	128 $\pm$ 255	385 $\pm$ 488	128 $\pm$ 255
Ologamasidae	<i>Neogamasellus</i> sp.	128 $\pm$ 255	257 $\pm$ 510	385 $\pm$ 765	0	257 $\pm$ 510	128 $\pm$ 255	514 $\pm$ 722	0	0	0
Oribatida	<i>Oribatida</i> spp.	1016 $\pm$ 1382	514 $\pm$ 1020	514 $\pm$ 1020	385 $\pm$ 488	0	0	1530 $\pm$ 2732	1145 $\pm$ 966	257 $\pm$ 295	385 $\pm$ 255
Oribatida	<i>Brachypylna</i> sp.	888 $\pm$ 1206	128 $\pm$ 255	642 $\pm$ 255	0	0	128 $\pm$ 255	1273 $\pm$ 1531	0	888 $\pm$ 1786	128 $\pm$ 255
Rhagidiidae	sp.	128 $\pm$ 255	0	0	0	0	0	888 $\pm$ 871	128 $\pm$ 255	0	257 $\pm$ 295
Rhodacaridae	sp.	1530 $\pm$ 1102	1145 $\pm$ 255	2675 $\pm$ 1276	2547 $\pm$ 1102	385 $\pm$ 488	385 $\pm$ 488	2675 $\pm$ 966	1402 $\pm$ 1131	642 $\pm$ 255	642 $\pm$ 488
Uropodidae	sp.	128 $\pm$ 255	257 $\pm$ 510	385 $\pm$ 765	0	257 $\pm$ 510	257 $\pm$ 295	257 $\pm$ 295	0	0	0
Collembolans											
Entomobryid	<i>Pseudosinella</i> sp.	888 $\pm$ 1131	0	0	0	385 $\pm$ 488	0	257 $\pm$ 510	128 $\pm$ 255	0	0
Entomobryid	<i>Lepidocyrtus</i> sp.	0	0	0	0	0	0	0	0	0	0
Entomobryid	<i>Heteromurus</i> sp.	1016 $\pm$ 1178	0	1530 $\pm$ 722	0	0	771 $\pm$ 659	4206 $\pm$ 4215	128 $\pm$ 255	128 $\pm$ 255	1016 $\pm$ 833
Isotomid	<i>Isotomodes</i> sp.	257 $\pm$ 295	0	888 $\pm$ 488	128 $\pm$ 255	0	0	642 $\pm$ 1276	0	0	385 $\pm$ 488
Isotomid	<i>Isotomurus</i> sp.	514 $\pm$ 417	0	385 $\pm$ 765	0	771 $\pm$ 977	0	888 $\pm$ 1206	0	1016 $\pm$ 417	0
Isotomid	<i>Hemisotoma thermophila</i>	1273 $\pm$ 1350	128 $\pm$ 255	888 $\pm$ 1052	0	0	1659 $\pm$ 255	514 $\pm$ 417	0	642 $\pm$ 642	7395 $\pm$ 1473
Isotomid	<i>Proisotomodes</i> sp.	1145 $\pm$ 1342	257 $\pm$ 510	257 $\pm$ 295	0	128 $\pm$ 255	385 $\pm$ 765	2932 $\pm$ 2139	128 $\pm$ 255	0	1273 $\pm$ 884
Onychuirid	<i>Protaphorura</i> cf. <i>armata</i>	1402 $\pm$ 1052	257 $\pm$ 510	1530 $\pm$ 833	514 $\pm$ 417	385 $\pm$ 488	1016 $\pm$ 417	2173 $\pm$ 1686	257 $\pm$ 510	385 $\pm$ 488	1787 $\pm$ 1586
Podurid	<i>Brachystomella parvula</i>	385 $\pm$ 488	0	514 $\pm$ 722	0	514 $\pm$ 417	0	257 $\pm$ 510	257 $\pm$ 510	0	128 $\pm$ 255
Podurid	<i>Ceratophysella</i> sp.	257 $\pm$ 510	128 $\pm$ 255	257 $\pm$ 510	128 $\pm$ 255	128 $\pm$ 255	1016 $\pm$ 589	1145 $\pm$ 765	1273 $\pm$ 1350	888 $\pm$ 765	2173 $\pm$ 1465
Sminthuridid	<i>Sphaeridia pumilis</i>	128 $\pm$ 255	0	514 $\pm$ 417	0	888 $\pm$ 488	1016 $\pm$ 417	771 $\pm$ 659	0	0	1916 $\pm$ 1276

Table S4. Mean number ($\pm$ standard deviation; $n = 4$) of individuals of mites and collembolan families and subfamilies/species found in soil samples collected in TMEs (values extrapolated to individuals per square meter), submitted to different treatments (C, CT, CTI, NT and NTI), fifty-six days after the insecticide application in CTI and NTI (D89). Meaning of treatment codes: C – undisturbed soil; NT – no-tillage; NTI – no-tillage with insecticide application; CT – simulated conventional tillage; CTI – simulated conventional tillage with insecticide application.

Samplings		D89									
Treatments		C		CT		CTI		NT		NTI	
Family/group	Subfamily/Species	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm	0 – 5 cm	5 – 10 cm
Mites											
Acaridae	<i>Tyrolichus casei</i>	4591 $\pm$ 1502	1016 $\pm$ 2041	2932 $\pm$ 1579	1273 $\pm$ 884	2301 $\pm$ 510	1916 $\pm$ 3495	7523 $\pm$ 2837	514 $\pm$ 417	2044 $\pm$ 1250	128 $\pm$ 255
Ascidae	<i>Asca</i> sp.	128 $\pm$ 255	385 $\pm$ 765	514 $\pm$ 417	128 $\pm$ 255	0	0	128 $\pm$ 255	771 $\pm$ 659	771 $\pm$ 884	0
Ascidae	<i>Protogamasellus mica</i>	0	0	0	0	0	0	385 $\pm$ 765	0	514 $\pm$ 722	0
Cunaxidae	Cunaxoidinae	128 $\pm$ 255	0	1016 $\pm$ 722	0	0	128 $\pm$ 255		0	0	0
Ologamasidae	<i>Ologamasus</i> sp.	1016 $\pm$ 932	0	1016 $\pm$ 417	0	385 $\pm$ 255	257 $\pm$ 510	642 $\pm$ 255	128 $\pm$ 255	257 $\pm$ 510	128 $\pm$ 255
Ologamasidae	<i>Neogamasellevans</i> sp.	385 $\pm$ 488	0	128 $\pm$ 255	0	0	0	257 $\pm$ 510	0	385 $\pm$ 765	0
Oribatida	<i>Oribatida</i> spp.	1659 $\pm$ 1736	257 $\pm$ 510	0	128 $\pm$ 255	0	0	1787 $\pm$ 1350	128 $\pm$ 255	1658 $\pm$ 642	257 $\pm$ 295
Oribatida	<i>Brachypylina</i> sp.	514 $\pm$ 417	0	385 $\pm$ 765	0	0	0	642 $\pm$ 1276	128 $\pm$ 255	1016 $\pm$ 722	0
Rhagidiidae	sp.	257 $\pm$ 295	0	0	514 $\pm$ 417	771 $\pm$ 884	0	888 $\pm$ 1465	0	514 $\pm$ 722	128 $\pm$ 255
Rhodacaridae	sp.	3318 $\pm$ 2263	1916 $\pm$ 488	2301 $\pm$ 510	2418 $\pm$ 1633	1016 $\pm$ 1102	1402 $\pm$ 1276	2675 $\pm$ 966	1273 $\pm$ 295	1787 $\pm$ 1692	1016 $\pm$ 1382
Uropodidae	sp.	257 $\pm$ 510	385 $\pm$ 765	0	0	0	0	385 $\pm$ 488	0	385 $\pm$ 765	128 $\pm$ 255
Collembolans											
Entomobryid	<i>Pseudosinella</i> sp.	257 $\pm$ 510	0	0	0	0	0	385 $\pm$ 765	0	257 $\pm$ 510	0
Entomobryid	<i>Lepidocyrtus</i> sp.	385 $\pm$ 765	0	0	0	0	0	257 $\pm$ 295	0	385 $\pm$ 765	0
Entomobryid	<i>Heteromurus</i> sp.	257 $\pm$ 510	0	888 $\pm$ 488	0	2044 $\pm$ 932	128 $\pm$ 255	888 $\pm$ 488	0	771 $\pm$ 884	0
Isotomid	<i>Isotomodes</i> sp.	257 $\pm$ 295	257 $\pm$ 510	257 $\pm$ 510	0	128 $\pm$ 255	0	128 $\pm$ 255	257 $\pm$ 295	128 $\pm$ 255	257 $\pm$ 510
Isotomid	<i>Isotomurus</i> sp.	128 $\pm$ 255	0	514 $\pm$ 722	0	1530 $\pm$ 1767	0	642 $\pm$ 966	0	1273 $\pm$ 1586	0
Isotomid	<i>Hemisotoma thermophila</i>	1916 $\pm$ 642	128 $\pm$ 255	4206 $\pm$ 1131	128 $\pm$ 255	514 $\pm$ 1020	2418 $\pm$ 871	2675 $\pm$ 488	257 $\pm$ 510	3061 $\pm$ 1954	2418 $\pm$ 2098
Isotomid	<i>Proisotomodes</i> sp.	385 $\pm$ 488	0	1402 $\pm$ 1342	128 $\pm$ 255	0	1016 $\pm$ 722	1530 $\pm$ 1102	0	385 $\pm$ 765	0
Onychiurid	<i>Protaphorura</i> cf. <i>armata</i>	1016 $\pm$ 722	257 $\pm$ 510	1273 $\pm$ 884	385 $\pm$ 488	257 $\pm$ 510	1273 $\pm$ 884	1787 $\pm$ 659	0	642 $\pm$ 642	0
Podurid	<i>Brachystomella parvula</i>	385 $\pm$ 488	0	771 $\pm$ 659	0	385 $\pm$ 255	888 $\pm$ 1206	1145 $\pm$ 1971	257 $\pm$ 510	771 $\pm$ 977	128 $\pm$ 255
Podurid	<i>Ceratophysella</i> sp.	888 $\pm$ 1206	771 $\pm$ 1215	128 $\pm$ 255	642 $\pm$ 488	385 $\pm$ 488	1016 $\pm$ 1102	1016 $\pm$ 932	642 $\pm$ 488	1787 $\pm$ 1350	1016 $\pm$ 1178
Sminthuridid	<i>Sphaeridia pumilis</i>	257 $\pm$ 295	0	257 $\pm$ 510	257 $\pm$ 295	128 $\pm$ 255	0	1016 $\pm$ 833	0	771 $\pm$ 977	128 $\pm$ 255

Table S5 – Multiple comparisons of GLMM on planned contrasts using mite abundances of samples collected as response variable (see the manuscript for details on GLMM). The differences analysed were between treatments within the same soil layer (Top means 0 to 5-cm top layer; Deep means 5 to 10-cm top layer) and the same sampling (D0, D16, D61 or D89) and between soil layers within the same treatment (C, CT, CTI, NT or NTI, see the manuscript for details on test treatment code meanings) and the same Sampling. Significance codes - * means $p \leq 0.05$; ** means $p \leq 0.01$; *** means $p \leq 0.001$.

Linear Hypotheses:	Estimate	Std. Error	z value	Pr(> z)
<i>C-TopD0 vs C-DeepD0</i>	0.722534	0.285102	2.534	0.3903
<i>C-TopD16 vs C-DeepD16</i>	0.587595	0.313549	1.874	0.8978
<i>CT-TopD16 vs CT-DeepD16</i>	0.855012	0.307588	2.780	0.2250
<i>NT-TopD16 vs NT-DeepD16</i>	0.758991	0.317104	2.394	0.5071
<i>C-TopD16 vs CT-TopD16</i>	-0.259996	0.289082	-0.899	1.0000
<i>C-TopD16 vs NT-TopD16</i>	-0.052650	0.293441	-0.179	1.0000
<i>CT-TopD16 vs NT-TopD16</i>	0.207347	0.287762	0.721	1.0000
<i>C-DeepD16 vs CT-DeepD16</i>	0.007421	0.330396	0.022	1.0000
<i>C-DeepD16 vs NT-DeepD16</i>	0.118746	0.335749	0.354	1.0000
<i>CT-DeepD16 vs NT-DeepD16</i>	0.111325	0.334883	0.332	1.0000
<i>C-TopD61 vs C-DeepD61</i>	1.142374	0.346473	3.297	0.0492 *
<i>CT-TopD61 vs CT-DeepD61</i>	0.171645	0.337794	0.508	1.0000
<i>CTI-TopD61 vs CTI-DeepD61</i>	0.006428	0.554988	0.012	1.0000
<i>NT-TopD61 vs NT-DeepD61</i>	1.403810	0.335855	4.180	<0.01 **
<i>NTI-TopD61 vs NTI-DeepD61</i>	-0.095495	0.391437	-0.244	1.0000
<i>C-TopD61 vs CT-TopD61</i>	0.530442	0.314577	1.686	0.9638
<i>C-TopD61 vs CTI-TopD61</i>	2.127633	0.445112	4.780	<0.01 ***
<i>C-TopD61 vs NT-TopD61</i>	-0.330323	0.290208	-1.138	0.9999
<i>C-TopD61 vs NTI-TopD61</i>	1.205995	0.350711	3.439	0.0301 *
<i>CT-TopD61 vs CTI-TopD61</i>	1.597191	0.456667	3.497	0.0243 *
<i>CT-TopD61 vs NT-TopD61</i>	-0.860765	0.307723	-2.797	0.2144
<i>CT-TopD61 vs NTI-TopD61</i>	0.675553	0.365122	1.850	0.9091
<i>CTI-TopD61 vs NT-TopD61</i>	-2.457956	0.440285	-5.583	<0.01 ***
<i>CTI-TopD61 vs NTI-TopD61</i>	-0.921638	0.482207	-1.911	0.8787
<i>NT-TopD61 vs NTI-TopD61</i>	1.536318	0.344652	4.458	<0.01 ***
<i>C-DeepD61 vs CT-DeepD61</i>	-0.440288	0.367681	-1.197	0.9997
<i>C-DeepD61 vs CTI-DeepD61</i>	0.991686	0.479436	2.068	0.7797
<i>C-DeepD61 vs NT-DeepD61</i>	-0.068888	0.385417	-0.179	1.0000
<i>C-DeepD61 vs NTI-DeepD61</i>	-0.031874	0.387658	-0.082	1.0000
<i>CT-DeepD61 vs CTI-DeepD61</i>	1.431974	0.462143	3.099	0.0921
<i>CT-DeepD61 vs NT-DeepD61</i>	0.371400	0.363617	1.021	1.0000
<i>CT-DeepD61 vs NTI-DeepD61</i>	0.408414	0.365938	1.116	0.9999
<i>CTI-DeepD61 vs NT-DeepD61</i>	-1.060574	0.476402	-2.226	0.6533
<i>CTI-DeepD61 vs NTI-DeepD61</i>	-1.023560	0.478199	-2.140	0.7231
<i>NT-DeepD61 vs NTI-DeepD61</i>	0.037014	0.383823	0.096	1.0000
<i>C-TopD89 vs C-DeepD89</i>	1.173626	0.318832	3.681	0.0125 *
<i>CT-TopD89 vs CT-DeepD89</i>	0.661205	0.321010	2.060	0.7861
<i>CTI-TopD89 vs CTI-DeepD89</i>	0.305234	0.356421	0.856	1.0000
<i>NT-TopD89 vs NT-DeepD89</i>	1.643582	0.331988	4.951	<0.01 ***
<i>NTI-TopD89 vs NTI-DeepD89</i>	1.649246	0.380595	4.333	<0.01 ***
<i>C-TopD89 vs CT-TopD89</i>	0.394698	0.289401	1.364	0.9975
<i>C-TopD89 vs CTI-TopD89</i>	1.041200	0.312400	3.333	0.0430 *
<i>C-TopD89 vs NT-TopD89</i>	-0.195724	0.277562	-0.705	1.0000
<i>C-TopD89 vs NTI-TopD89</i>	0.319249	0.287878	1.109	0.9999
<i>CT-TopD89 vs CTI-TopD89</i>	0.646502	0.320281	2.019	0.8144
<i>CT-TopD89 vs NT-TopD89</i>	-0.590422	0.286418	-2.061	0.7842
<i>CT-TopD89 vs NTI-TopD89</i>	-0.075449	0.296415	-0.255	1.0000
<i>CTI-TopD89 vs NT-TopD89</i>	-1.236925	0.309588	-3.995	<0.01 **
<i>CTI-TopD89 vs NTI-TopD89</i>	-0.721951	0.318786	-2.265	0.6192
<i>NT-TopD89 vs NTI-TopD89</i>	0.514973	0.284833	1.808	0.9267
<i>C-DeepD89 vs CT-DeepD89</i>	-0.117722	0.347474	-0.339	1.0000
<i>C-DeepD89 vs CTI-DeepD89</i>	0.172809	0.361759	0.478	1.0000

<i>C-DeepD89 vs NT-DeepD89</i>	0.274232	0.367086	0.747	1.0000
<i>C-DeepD89 vs NTI-DeepD89</i>	0.794870	0.404380	1.966	0.8482
<i>CT-DeepD89 vs CTI-DeepD89</i>	0.290532	0.356729	0.814	1.0000
<i>CT-DeepD89 vs NT-DeepD89</i>	0.391955	0.362163	1.082	0.9999
<i>CT-DeepD89 vs NTI-DeepD89</i>	0.912592	0.399909	2.282	0.6051
<i>CTI-DeepD89 vs NT-DeepD89</i>	0.101423	0.376247	0.270	1.0000
<i>CTI-DeepD89 vs NTI-DeepD89</i>	0.622061	0.412259	1.509	0.9902
<i>NT-DeepD89 vs NTI-DeepD89</i>	0.520638	0.417093	1.248	0.9993

Table S6 – Multiple comparisons of GLMM on planned contrasts using Collembola abundances of samples collected as response variable (see the manuscript for details on GLMM). The differences analysed were between treatments within the same soil layer (Top means 0 to 5-cm top layer; Deep means 5 to 10-cm top layer) and the same sampling (D0, D16, D61 or D89) and between soil layers within the same treatment (C, CT, CTI, NT or NTI, see the manuscript for details on test treatment code meanings) and the same Sampling. Significance codes - * means $p \leq 0.05$; ** means $p \leq 0.01$; *** means $p \leq 0.001$.

Linear Hypotheses:	Estimate	Std. Error	z value	Pr(> z)
<i>C-TopD0 vs C-DeepD0</i>	1.622401	0.340974	4.758	<0.01 ***
<i>C-TopD16 vs C-DeepD16</i>	2.365462	0.459373	5.149	<0.01 ***
<i>CT-TopD16 vs CT-DeepD16</i>	3.105477	0.478830	6.486	<0.01 ***
<i>NT-TopD16 vs NT-DeepD16</i>	0.864714	0.397459	2.176	0.6879
<i>C-TopD16 vs CT-TopD16</i>	-0.565402	0.275334	-2.054	0.7846
<i>C-TopD16 vs NT-TopD16</i>	0.843881	0.315046	2.679	0.2801
<i>CT-TopD16 vs NT-TopD16</i>	1.409283	0.305489	4.613	<0.01 ***
<i>C-DeepD16 vs CT-DeepD16</i>	0.174613	0.603460	0.289	1.0000
<i>C-DeepD16 vs NT-DeepD16</i>	-0.656867	0.519414	-1.265	0.9991
<i>CT-DeepD16 vs NT-DeepD16</i>	-0.831480	0.541918	-1.534	0.9872
<i>C-TopD61 vs C-DeepD61</i>	2.257980	0.489211	4.616	<0.01 ***
<i>CT-TopD61 vs CT-DeepD61</i>	2.196769	0.489981	4.483	<0.01 ***
<i>CTI-TopD61 vs CTI-DeepD61</i>	-0.624531	0.340630	-1.833	0.9128
<i>NT-TopD61 vs NT-DeepD61</i>	1.859747	0.351514	5.291	<0.01 ***
<i>NTI-TopD61 vs NTI-DeepD61</i>	-1.670555	0.322205	-5.185	<0.01 ***
<i>C-TopD61 vs CT-TopD61</i>	0.056696	0.302064	0.188	1.0000
<i>C-TopD61 vs CTI-TopD61</i>	0.814984	0.335225	2.431	0.4682
<i>C-TopD61 vs NT-TopD61</i>	0.638412	0.286168	-2.231	0.6420
<i>C-TopD61 vs NTI-TopD61</i>	0.850840	0.337448	2.521	0.3944
<i>CT-TopD61 vs CTI-TopD61</i>	0.758288	0.336687	2.252	0.6236
<i>CT-TopD61 vs NT-TopD61</i>	-0.695108	0.287872	-2.415	0.4822
<i>CT-TopD61 vs NTI-TopD61</i>	0.794144	0.338886	2.343	0.5444
<i>CTI-TopD61 vs NT-TopD61</i>	-1.453396	0.322507	-4.507	<0.01 ***
<i>CTI-TopD61 vs NTI-TopD61</i>	0.035856	0.368766	0.097	1.0000
<i>NT-TopD61 vs NTI-TopD61</i>	1.489252	0.324811	4.585	<0.01 ***
<i>C-DeepD61 vs CT-DeepD61</i>	-0.004515	0.622959	-0.007	1.0000
<i>C-DeepD61 vs CTI-DeepD61</i>	-2.067527	0.493003	-4.194	<0.01 **
<i>C-DeepD61 vs NT-DeepD61</i>	-1.036645	0.529992	-1.956	0.8491
<i>C-DeepD61 vs NTI-DeepD61</i>	-3.077695	0.478932	-6.426	<0.01 ***
<i>CT-DeepD61 vs CTI-DeepD61</i>	-2.063012	0.492716	-4.187	<0.01 **
<i>CT-DeepD61 vs NT-DeepD61</i>	-1.032130	0.529770	-1.948	0.8544
<i>CT-DeepD61 vs NTI-DeepD61</i>	-3.073180	0.478633	-6.421	<0.01 ***
<i>CTI-DeepD61 vs NT-DeepD61</i>	1.030882	0.368286	2.799	0.2079
<i>CTI-DeepD61 vs NTI-DeepD61</i>	-1.010168	0.289528	-3.489	0.0249 *
<i>NT-DeepD61 vs NTI-DeepD61</i>	-2.041050	0.349228	-5.844	<0.01 ***
<i>C-TopD89 vs C-DeepD89</i>	1.492024	0.409265	3.646	0.0142 *
<i>CT-TopD89 vs CT-DeepD89</i>	1.870183	0.388217	4.817	<0.01 ***
<i>CTI-TopD89 vs CTI-DeepD89</i>	-0.216829	0.312432	-0.694	1.0000
<i>NT-TopD89 vs NT-DeepD89</i>	2.133743	0.395548	5.394	<0.01 ***
<i>NTI-TopD89 vs NTI-DeepD89</i>	0.924800	0.315899	2.928	0.1492
<i>C-TopD89 vs CT-TopD89</i>	-0.487682	0.297696	-1.638	0.9722
<i>C-TopD89 vs CTI-TopD89</i>	0.122128	0.315400	0.387	1.0000
<i>C-TopD89 vs NT-TopD89</i>	-0.659172	0.294230	-2.240	0.6331
<i>C-TopD89 vs NTI-TopD89</i>	-0.496748	0.297753	-1.668	0.9661
<i>CT-TopD89 vs CTI-TopD89</i>	0.609810	0.302130	2.018	0.8085
<i>CT-TopD89 vs NT-TopD89</i>	-0.171490	0.279856	-0.613	1.0000
<i>CT-TopD89 vs NTI-TopD89</i>	-0.009066	0.283762	-0.032	1.0000
<i>CTI-TopD89 vs NT-TopD89</i>	-0.781300	0.298712	-2.616	0.3241
<i>CTI-TopD89 vs NTI-TopD89</i>	-0.618876	0.302253	-2.048	0.7886
<i>NT-TopD89 vs NTI-TopD89</i>	0.162423	0.280127	0.580	1.0000
<i>C-DeepD89 vs CT-DeepD89</i>	-0.109523	0.479118	-0.229	1.0000
<i>C-DeepD89 vs CTI-DeepD89</i>	-1.586725	0.406969	-3.899	<0.01 **

<i>C-DeepD89 vs NT-DeepD89</i>	-0.017452	0.487118	-0.036	1.0000
<i>C-DeepD89 vs NTI-DeepD89</i>	-1.063972	0.422676	-2.517	0.3969
<i>CT-DeepD89 vs CTI-DeepD89</i>	-1.477202	0.396230	-3.728	0.0103 *
<i>CT-DeepD89 vs NT-DeepD89</i>	0.092071	0.478231	0.193	1.0000
<i>CT-DeepD89 vs NTI-DeepD89</i>	-0.954449	0.412307	-2.315	0.5683
<i>CTI-DeepD89 vs NT-DeepD89</i>	1.569272	0.405914	3.866	<0.01 **
<i>CTI-DeepD89 vs NTI-DeepD89</i>	0.522752	0.325657	1.605	0.9778
<i>NT-DeepD89 vs NTI-DeepD89</i>	-1.046520	0.421630	-2.482	0.4264

Table S7 – Multiple comparisons of GLMM on planned contrasts using Enchytraeid abundances of samples collected as response variable (see the manuscript for details on GLMM). The differences analysed were between treatments within the same soil layer (Top means 0 to 5-cm top layer; Deep means 5 to 10-cm top layer) and the same sampling (D0, D16, D61 or D89) and between soil layers within the same treatment (C, CT, CTI, NT or NTI, see the manuscript for details on test treatment code meanings) and the same Sampling. Significance codes - * means $p \leq 0.05$; ** means $p \leq 0.01$; *** means $p \leq 0.001$.

Linear Hypotheses:	Estimate	Std. Error	z value	Pr(> z)
<i>C-TopD0 vs C-DeepD0</i>	1.06882	0.38462	2.779	0.2276
<i>C-TopD16 vs C-DeepD16</i>	1.49804	0.44136	3.394	0.0367 *
<i>CT-TopD16 vs CT-DeepD16</i>	1.19560	0.43181	2.769	0.2336
<i>NT-TopD16 vs NT-DeepD16</i>	1.13654	0.43388	2.619	0.3314
<i>C-TopD16 vs CT-TopD16</i>	-0.05561	0.42063	-0.132	1.0000
<i>C-TopD16 vs NT-TopD16</i>	0.07921	0.42139	0.188	1.0000
<i>CT-TopD16 vs NT-TopD16</i>	0.13482	0.42080	0.320	1.0000
<i>C-DeepD16 vs CT-DeepD16</i>	-0.35805	0.45180	-0.793	1.0000
<i>C-DeepD16 vs NT-DeepD16</i>	-0.28229	0.45331	-0.623	1.0000
<i>CT-DeepD16 vs NT-DeepD16</i>	0.07577	0.44455	0.170	1.0000
<i>C-TopD61 vs C-DeepD61</i>	0.29357	0.44429	0.661	1.0000
<i>CT-TopD61 vs CT-DeepD61</i>	1.20321	0.43978	2.736	0.2526
<i>CTI-TopD61 vs CTI-DeepD61</i>	0.99317	0.44623	2.226	0.6573
<i>NT-TopD61 vs NT-DeepD61</i>	0.02933	0.43736	0.067	1.0000
<i>NTI-TopD61 vs NTI-DeepD61</i>	1.24514	0.43595	2.856	0.1856
<i>C-TopD61 vs CT-TopD61</i>	-0.84068	0.43142	-1.949	0.8621
<i>C-TopD61 vs CTI-TopD61</i>	-0.41135	0.43539	-0.945	1.0000
<i>C-TopD61 vs NT-TopsD61</i>	-0.12520	0.43721	-0.286	1.0000
<i>C-TopD61 vs NTI-TopD61</i>	-0.93257	0.43081	-2.165	0.7086
<i>CT-TopD61 vs CTI-TopD61</i>	0.42933	0.42731	1.005	1.0000
<i>CT-TopD61 vs NT-TopD61</i>	0.71548	0.42915	1.667	0.9689
<i>CT-TopD61 vs NTI-TopD61</i>	-0.09189	0.42263	-0.217	1.0000
<i>CTI-TopD61 vs NT-TopD61</i>	0.28616	0.43316	0.661	1.0000
<i>CTI-TopD61 vs NTI-TopD61</i>	-0.52121	0.42670	-1.221	0.9996
<i>NT-TopD61 vs NTI-TopD61</i>	-0.80737	0.42854	-1.884	0.8949
<i>C-DeepD61 vs CT-DeepD61</i>	0.06895	0.45232	0.152	1.0000
<i>C-DeepD61 vs CTI-DeepD61</i>	0.28825	0.45492	0.634	1.0000
<i>C-DeepD61 vs NT-DeepD61</i>	-0.38944	0.44438	-0.876	1.0000
<i>C-DeepD61 vs NTI-DeepD61</i>	0.01900	0.44927	0.042	1.0000
<i>CT-DeepD61 vs CTI-DeepD61</i>	0.21929	0.45809	0.479	1.0000
<i>CT-DeepD61 vs NT-DeepD61</i>	-0.45840	0.44756	-1.024	1.0000
<i>CT-DeepD61 vs NTI-DeepD61</i>	-0.04996	0.45252	-0.110	1.0000
<i>CTI-DeepD61 vs NT-DeepD61</i>	-0.67769	0.45027	-1.505	0.9908
<i>CTI-DeepD61 vs NTI-DeepD61</i>	-0.26925	0.45510	-0.592	1.0000
<i>NT-DeepD61 vs NTI-DeepD61</i>	0.40844	0.44457	0.919	1.0000
<i>C-TopD89 vs C-DeepD89</i>	0.80136	0.51321	1.561	0.9854
<i>CT-TopD89 vs CT-DeepD89</i>	0.27184	0.47077	0.577	1.0000
<i>CTI-TopD89 vs CTI-DeepD89</i>	0.59118	0.46115	1.282	0.9990
<i>NT-TopD89 vs NT-DeepD89</i>	1.14135	0.47624	2.397	0.5094
<i>NTI-TopD89 vs NTI-DeepD89</i>	0.78602	0.43770	1.796	0.9327
<i>C-TopD89 vs CT-TopD89</i>	-0.22806	0.47569	-0.479	1.0000
<i>C-TopD89 vs CTI-TopD89</i>	-0.65434	0.46852	-1.397	0.9967
<i>C-TopD89 vs NT-TopsD89</i>	-0.77912	0.46685	-1.669	0.9685
<i>C-TopD89 vs NTI-TopD89</i>	-1.37195	0.45884	-2.990	0.1294
<i>CT-TopD89 vs CTI-TopD89</i>	-0.42629	0.45839	-0.930	1.0000
<i>CT-TopD89 vs NT-TopD89</i>	-0.55106	0.45658	-1.207	0.9996
<i>CT-TopD89 vs NTI-TopD89</i>	-1.14390	0.44742	-2.557	0.3766
<i>CTI-TopD89 vs NT-TopD89</i>	-0.12477	0.44946	-0.278	1.0000
<i>CTI-TopD89 vs NTI-TopD89</i>	-0.71761	0.44057	-1.629	0.9758
<i>NT-TopD89 vs NTI-TopD89</i>	-0.59284	0.43864	-1.352	0.9979
<i>C-DeepD89 vs CT-DeepD89</i>	-0.75757	0.50978	-1.486	0.9922
<i>C-DeepD89 vs CTI-DeepD89</i>	-0.86452	0.50699	-1.705	0.9602

<i>C-DeepD89 vs NT-DeepD89</i>	-0.43912	0.52197	-0.841	1.0000
<i>C-DeepD89 vs NTI-DeepD89</i>	-1.38729	0.49643	-2.795	0.2183
<i>CT-DeepD89 vs CTI-DeepD89</i>	-0.10695	0.47311	-0.226	1.0000
<i>CT-DeepD89 vs NT-DeepD89</i>	0.31845	0.49027	0.650	1.0000
<i>CT-DeepD89 vs NTI-DeepD89</i>	-0.62972	0.46159	-1.364	0.9976
<i>CTI-DeepD89 vs NT-DeepD89</i>	0.42540	0.48736	0.873	1.0000
<i>CTI-DeepD89 vs NTI-DeepD89</i>	-0.52277	0.45844	-1.140	0.9999
<i>NT-DeepD89 vs NTI-DeepD89</i>	-0.94817	0.47633	-1.991	0.8353

Table S8. Individual and total trait values and respective life-form group according to the vertical stratification in soil (from surface to deep layers: epigeic, hemiedaphic or euedaphic) of each collembolan species found in soil samples collected over the TME experiment. Meaning of individual trait values: ocelli (absent = 4, present = 0); antenna (size up to half of the body length = 4, size between half and the total body length = 2, size higher than the body length = 0); furca (absent = 4, reduced or short = 2, fully developed = 0); hairs/scales (absent = 4, present = 0); pigmentation (absent = 4, coloured but no patterns = 2, coloured and with patterns = 0).

Species	Traits					Total	Life-form
	Ocelli	Antenna	Furca	Hairs/Scales	Pigmentation		
<i>Isotomurus</i> sp.	0	2	0	0	2	4	Epigeic
<i>Lepidocyrtus</i> sp.	0	2	0	0	2	4	Epigeic
<i>Heteromurus</i> sp.	0	2	0	0	2	4	Epigeic
<i>Sphaeridia pumilis</i>	0	2	2	0	2	6	Epigeic
<i>Hemisotoma thermophila</i>	0	2	0	4	2	8	Hemiedaphic
<i>Proisotomodes</i> sp.	0	2	0	4	4	10	Hemiedaphic
<i>Pseudosinella</i>	0	2	0	4	4	10	Hemiedaphic
<i>Brachystomella parvula</i>	0	2	2	4	2	10	Hemiedaphic
<i>Ceratophysella</i> sp.	0	2	2	4	2	10	Hemiedaphic
<i>Isotomodes</i> sp.	0	2	2	4	4	12	Hemiedaphic
<i>Protaphorura</i> cf. <i>armata</i>	4	2	4	4	4	18	Edaphic

Table S9 – Multiple comparisons of LMM on planned contrasts using Collembola community mT of samples collected as response variable (see the manuscript for details on LMM). The differences analysed were between treatments within the same soil layer (Top means 0 to 5-cm top layer; Deep means 5 to 10-cm top layer) and the same sampling (D0, D16, D61 or D89) and between soil layers within the same treatment (C, CT, CTI, NT or NTI, see the manuscript for details on test treatment code meanings) and the same Sampling. Significance codes - * means $p \leq 0.05$; ** means $p \leq 0.01$; *** means $p \leq 0.001$.

Linear Hypotheses:	Estimate	Std. Error	z value	Pr(> z)
<i>C-TopD0 vs C-DeepD0</i>	-1.82529	1.02399	-1.783	0.9372
<i>C-TopD16 vs C-DeepD16</i>	-0.59146	1.15867	-0.510	1.0000
<i>CT-TopD16 vs CT-DeepD16</i>	1.72983	1.31079	1.320	0.9985
<i>NT-TopD16 vs NT-DeepD16</i>	-3.91495	1.15612	-3.386	0.0369 *
<i>C-TopD16 vs CT-TopD16</i>	1.53883	1.07071	1.437	0.9950
<i>C-TopD16 vs NT-TopD16</i>	1.17046	1.07065	1.093	0.9999
<i>CT-TopD16 vs NT-TopD16</i>	-0.36837	1.07051	-0.344	1.0000
<i>C-DeepD16 vs CT-DeepD16</i>	3.86012	1.38427	2.789	0.2214
<i>C-DeepD16 vs NT-DeepD16</i>	-2.15304	1.23879	-1.738	0.9513
<i>CT-DeepD16 vs NT-DeepD16</i>	-6.01315	1.38131	-4.353	<0.01 ***
<i>C-TopD61 vs C-DeepD61</i>	-1.14290	1.15617	-0.989	1.0000
<i>CT-TopD61 vs CT-DeepD61</i>	-6.76383	1.15642	-5.849	<0.01 ***
<i>CTI-TopD61 vs CTI-DeepD61</i>	-0.70911	1.07064	-0.662	1.0000
<i>NT-TopD61 vs NT-DeepD61</i>	-0.85195	1.07064	-0.796	1.0000
<i>NTI-TopD61 vs NTI-DeepD61</i>	-1.00669	1.07064	-0.940	1.0000
<i>C-TopD61 vs CT-TopD61</i>	-0.03564	1.07016	-0.033	1.0000
<i>C-TopD61 vs CTI-TopD61</i>	0.99397	1.07016	0.929	1.0000
<i>C-TopD61 vs NT-TopD61</i>	-0.30941	1.07016	-0.289	1.0000
<i>C-TopD61 vs NTI-TopD61</i>	1.48199	1.07016	1.385	0.9970
<i>CT-TopD61 vs CTI-TopD61</i>	1.02961	1.07056	0.962	1.0000
<i>CT-TopD61 vs NT-TopD61</i>	-0.27377	1.07056	-0.256	1.0000
<i>CT-TopD61 vs NTI-TopD61</i>	1.51763	1.07056	1.418	0.9959
<i>CTI-TopD61 vs NT-TopD61</i>	-1.30338	1.07056	-1.217	0.9996
<i>CTI-TopD61 vs NTI-TopD61</i>	0.48802	1.07056	0.456	1.0000
<i>NT-TopD61 vs NTI-TopD61</i>	1.79140	1.07056	1.673	0.9676
<i>C-DeepD61 vs CT-DeepD61</i>	-5.65657	1.23658	-4.574	<0.01 ***
<i>C-DeepD61 vs CTI-DeepD61</i>	1.42776	1.15625	1.235	0.9995
<i>C-DeepD61 vs NT-DeepD61</i>	-0.01845	1.15625	-0.016	1.0000
<i>C-DeepD61 vs NTI-DeepD61</i>	1.61821	1.15625	1.400	0.9965
<i>CT-DeepD61 vs CTI-DeepD61</i>	7.08433	1.15635	6.126	<0.01 ***
<i>CT-DeepD61 vs NT-DeepD61</i>	5.63812	1.15635	4.876	<0.01 ***
<i>CT-DeepD61 vs NTI-DeepD61</i>	7.27478	1.15635	6.291	<0.01 ***
<i>CTI-DeepD61 vs NT-DeepD61</i>	-1.44622	1.07056	-1.351	0.9979
<i>CTI-DeepD61 vs NTI-DeepD61</i>	0.19045	1.07056	0.178	1.0000
<i>NT-DeepD61 vs NTI-DeepD61</i>	1.63666	1.07056	1.529	0.9888
<i>C-TopD89 vs C-DeepD89</i>	-1.79452	1.15562	-1.553	0.9864
<i>CT-TopD89 vs CT-DeepD89</i>	-1.68536	1.07064	-1.574	0.9839
<i>CTI-TopD89 vs CTI-DeepD89</i>	-4.76824	1.07064	-4.454	<0.01 ***
<i>NT-TopD89 vs NT-DeepD89</i>	-0.56647	1.07064	-0.529	1.0000
<i>NTI-TopD89 vs NTI-DeepD89</i>	-0.37602	1.07064	-0.351	1.0000
<i>C-TopD89 vs CT-TopD89</i>	0.32094	1.07016	0.300	1.0000
<i>C-TopD89 vs CTI-TopD89</i>	3.69545	1.07016	3.453	0.0290 *
<i>C-TopD89 vs NT-TopD89</i>	0.16025	1.07016	0.150	1.0000
<i>C-TopD89 vs NTI-TopD89</i>	1.22557	1.07016	1.145	0.9998
<i>CT-TopD89 vs CTI-TopD89</i>	3.37450	1.07056	3.152	0.0796
<i>CT-TopD89 vs NT-TopD89</i>	-0.16069	1.07056	-0.150	1.0000
<i>CT-TopD89 vs NTI-TopD89</i>	0.90463	1.07056	0.845	1.0000
<i>CTI-TopD89 vs NT-TopD89</i>	-3.53519	1.07056	-3.302	0.0486 *
<i>CTI-TopD89 vs NTI-TopD89</i>	-2.46987	1.07056	-2.307	0.5865
<i>NT-TopD89 vs NTI-TopD89</i>	1.06532	1.07056	0.995	1.0000
<i>C-DeepD89 vs CT-DeepD89</i>	0.43011	1.15572	0.372	1.0000
<i>C-DeepD89 vs CTI-DeepD89</i>	0.72174	1.15572	0.624	1.0000

<i>C-DeepD89 vs NT-DeepD89</i>	1.38830	1.15572	1.201	0.9997
<i>C-DeepD89 vs NTI-DeepD89</i>	2.64407	1.15572	2.288	0.6038
<i>CT-DeepD89 vs CTI-DeepD89</i>	0.29162	1.07056	0.272	1.0000
<i>CT-DeepD89 vs NT-DeepD89</i>	0.95819	1.07056	0.895	1.0000
<i>CT-DeepD89 vs NTI-DeepD89</i>	2.21396	1.07056	2.068	0.7831
<i>CTI-DeepD89 vs NT-DeepD89</i>	0.66657	1.07056	0.623	1.0000
<i>CTI-DeepD89 vs NTI-DeepD89</i>	1.92234	1.07056	1.796	0.9323
<i>NT-DeepD89 vs NTI-DeepD89</i>	1.25577	1.07056	1.173	0.9998

Table S10 - Multiple comparisons of LMM on planned contrasts using Collembola FD of samples collected as response variable (see the manuscript for details on LMM). The differences analysed were between treatments within the same soil layer (Top means 0 to 5-cm top layer; Deep means 5 to 10-cm top layer) and the same sampling (D0, D16, D61 or D89) and between soil layers within the same treatment (C, CT, CTI, NT or NTI, see the manuscript for details on test treatment code meanings) and the same Sampling. Significance codes - * means $p \leq 0.05$; ** means $p \leq 0.01$; *** means $p \leq 0.001$.

Linear Hypotheses:	Estimate	Std. Error	z value	Pr(> z)
<i>C-TopD0 vs C-DeepD0</i>	0.0138546	0.0311613	0.445	1.0000
<i>C-TopD16 vs C-DeepD16</i>	0.0714740	0.0334729	2.135	0.7252
<i>CT-TopD16 vs CT-DeepD16</i>	0.0488980	0.0359786	1.359	0.9973
<i>NT-TopD16 vs NT-DeepD16</i>	0.0367983	0.0333909	1.102	0.9999
<i>C-TopD16 vs CT-TopD16</i>	0.0002871	0.0232255	0.012	1.0000
<i>C-TopD16 vs NT-TopD16</i>	0.0176443	0.0232240	0.760	1.0000
<i>CT-TopD16 vs NT-TopD16</i>	0.0173572	0.0232304	0.747	1.0000
<i>C-DeepD16 vs CT-DeepD16</i>	-0.0222889	0.0300109	-0.743	1.0000
<i>C-DeepD16 vs NT-DeepD16</i>	-0.0170315	0.0268442	-0.634	1.0000
<i>CT-DeepD16 vs NT-DeepD16</i>	0.0052574	0.0299704	0.175	1.0000
<i>C-TopD61 vs C-DeepD61</i>	0.0751454	0.0335503	2.240	0.6387
<i>CT-TopD61 vs CT-DeepD61</i>	0.1157362	0.0333901	3.466	0.0277 *
<i>CTI-TopD61 vs CTI-DeepD61</i>	-0.0286242	0.0320171	-0.894	1.0000
<i>NT-TopD61 vs NT-DeepD61</i>	0.0553348	0.0320171	1.728	0.9504
<i>NTI-TopD61 vs NTI-DeepD61</i>	0.0226270	0.0320171	0.707	1.0000
<i>C-TopD61 vs CT-TopD61</i>	-0.0330593	0.0232254	-1.423	0.9949
<i>C-TopD61 vs CTI-TopD61</i>	0.0341223	0.0232254	1.469	0.9923
<i>C-TopD61 vs NT-TopD61</i>	0.0220161	0.0232254	0.948	1.0000
<i>C-TopD61 vs NTI-TopD61</i>	0.0214338	0.0232254	0.923	1.0000
<i>CT-TopD61 vs CTI-TopD61</i>	0.0671816	0.0232210	2.893	0.1669
<i>CT-TopD61 vs NT-TopD61</i>	0.0550754	0.0232210	2.372	0.5251
<i>CT-TopD61 vs NTI-TopD61</i>	0.0544931	0.0232210	2.347	0.5457
<i>CTI-TopD61 vs NT-TopD61</i>	-0.0121062	0.0232210	-0.521	1.0000
<i>CTI-TopD61 vs NTI-TopD61</i>	-0.0126885	0.0232210	-0.546	1.0000
<i>NT-TopD61 vs NTI-TopD61</i>	-0.0005823	0.0232210	-0.025	1.0000
<i>C-DeepD61 vs CT-DeepD61</i>	0.0075315	0.0268892	0.280	1.0000
<i>C-DeepD61 vs CTI-DeepD61</i>	-0.0696473	0.0251648	-2.768	0.2314
<i>C-DeepD61 vs NT-DeepD61</i>	0.0022056	0.0251648	0.088	1.0000
<i>C-DeepD61 vs NTI-DeepD61</i>	-0.0310846	0.0251648	-1.235	0.9993
<i>CT-DeepD61 vs CTI-DeepD61</i>	-0.0771787	0.0250816	-3.077	0.0993
<i>CT-DeepD61 vs NT-DeepD61</i>	-0.0053259	0.0250816	-0.212	1.0000
<i>CT-DeepD61 vs NTI-DeepD61</i>	-0.0386161	0.0250816	-1.540	0.9862
<i>CTI-DeepD61 vs NT-DeepD61</i>	0.0718528	0.0232231	3.094	0.0945
<i>CTI-DeepD61 vs NTI-DeepD61</i>	0.0385627	0.0232231	1.661	0.9673
<i>NT-DeepD61 vs NTI-DeepD61</i>	-0.0332902	0.0232231	-1.433	0.9944
<i>C-TopD89 vs C-DeepD89</i>	0.0638326	0.0334962	1.906	0.8791
<i>CT-TopD89 vs CT-DeepD89</i>	0.0034980	0.0320171	0.109	1.0000
<i>CTI-TopD89 vs CTI-DeepD89</i>	-0.0176490	0.0320171	-0.551	1.0000
<i>NT-TopD89 vs NT-DeepD89</i>	0.0861081	0.0320171	2.689	0.2798
<i>NTI-TopD89 vs NTI-DeepD89</i>	0.0564402	0.0320171	1.763	0.9399
<i>C-TopD89 vs CT-TopD89</i>	0.0117429	0.0232254	0.506	1.0000
<i>C-TopD89 vs CTI-TopD89</i>	0.0359553	0.0232254	1.548	0.9853
<i>C-TopD89 vs NT-TopD89</i>	-0.0008536	0.0232254	-0.037	1.0000
<i>C-TopD89 vs NTI-TopD89</i>	0.0281246	0.0232254	1.211	0.9995
<i>CT-TopD89 vs CTI-TopD89</i>	0.0242123	0.0232210	1.043	1.0000
<i>CT-TopD89 vs NT-TopD89</i>	-0.0125965	0.0232210	-0.542	1.0000
<i>CT-TopD89 vs NTI-TopD89</i>	0.0163816	0.0232210	0.705	1.0000
<i>CTI-TopD89 vs NT-TopD89</i>	-0.0368089	0.0232210	-1.585	0.9805
<i>CTI-TopD89 vs NTI-TopD89</i>	-0.0078307	0.0232210	-0.337	1.0000
<i>NT-TopD89 vs NTI-TopD89</i>	0.0289782	0.0232210	1.248	0.9992
<i>C-DeepD89 vs CT-DeepD89</i>	-0.0485917	0.0251170	-1.935	0.8633
<i>C-DeepD89 vs CTI-DeepD89</i>	-0.0455263	0.0251170	-1.813	0.9218

<i>C-DeepD89 vs NT-DeepD89</i>	0.0214219	0.0251170	0.853	1.0000
<i>C-DeepD89 vs NTI-DeepD89</i>	0.0207322	0.0251170	0.825	1.0000
<i>CT-DeepD89 vs CTI-DeepD89</i>	0.0030654	0.0232231	0.132	1.0000
<i>CT-DeepD89 vs NT-DeepD89</i>	0.0700136	0.0232231	3.015	0.1196
<i>CT-DeepD89 vs NTI-DeepD89</i>	0.0693239	0.0232231	2.985	0.1296
<i>CTI-DeepD89 vs NT-DeepD89</i>	0.0669482	0.0232231	2.883	0.1726
<i>CTI-DeepD89 vs NTI-DeepD89</i>	0.0662585	0.0232231	2.853	0.1861
<i>NT-DeepD89 vs NTI-DeepD89</i>	-0.0006897	0.0232231	-0.030	1.0000