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1	Carbon nanotubes alter agrosystem multifunctionality
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10	
11	Abstract
12	Since the discovery of the potential of carbon nanotubes (CNTs) in agriculture to improve crop yield,
13	many studies have been conducted to understand which effects CNTs could have on agrosystem
14	components. However, to date, very little is known about their impacts on ecosystem functions such
15	as biogeochemical cycles or primary production and consequently on the multifunctionality of
16	agrosystems. In this study, we aimed at understanding the impact of CNTs in microcosms including
17	soil bacteria and a crop plant (maize) with a special focus on H_2O , C and N cycles as well as crop
18	nutrition and resistance. After a 6-week exposure, bacterial concentration was increased by 82% in
19	soils exposed to 10 mg.kg ⁻¹ ; in parallel, the organic matter decomposition rate was also significantly
20	enhanced. An increase of nitrifier abundance was quantified with archaeal amoA gene copy numbers
21	reaching +144% in soils exposed to 10 mg.kg ⁻¹ of CNTs. Maize exposed to 0.1 mg.kg ⁻¹ of CNTs had in
22	average 34%, 18% and 12% lower chlorophyll, tannin and phenolic compounds, respectively but no
23	impact was detected on the biomass production. Maize plants were water-stressed after exposure to
24	10 mg.kg ⁻¹ of CNTs with a significant 17% increase of the dry matter compared to unexposed maize.

25 CNT exposure also led to a significant decrease of H_2O flux in the system. As a result, the 26 multifunctionality of the agrosystem was significantly decreased at 0.1 mg.kg⁻¹. Structural equation 27 modeling suggested that CNT impact on bacteria population in general, and on bacteria implied in 28 denitrification and CO₂ emission were the main factors influencing the multifunctionality index.

29 **1. Introduction**

Nanotechnology feeds the hopes of several research domains due to its many potential applications. 30 31 Indeed, nanotechnology could be an important lever to the convergence of knowledge and 32 technology for the benefit of the society and could represent an opportunity for progress in the twenty-first century¹. To develop nanotechnology, the production and use of nanomaterials have 33 increased over the years². Among nanomaterials, particular attention from industries is focused on 34 carbon nanotubes (CNTs) because of their remarkable physical, electronic and chemical properties ³, 35 and mainly because they can combine several of them. Consequently, CNTs are now found in 36 products such as electronics, tires or sport equipment ⁴, and subsequently end up into the 37 environment during their journey from production to recycling ⁵. In addition, they tend to 38 accumulate in sewage sludge used as fertilizer in agriculture 5 and modelling predicts that 39 concentration of carbonaceous nanomaterials in biosolids could reach up to 10 mg.kg⁻¹ while in 40 natural soil it could be up to 0.01 mg.kg^{-1 6}. Furthermore, CNTs might be used as nano-fertilizer as 41 42 their application on plants (for biofuel applications) and crops leads to increased yield according to 43 several studies ^{7,8}. Thus, their concentration in ecosystems, in particular in agrosystems, will possibly 44 increase in the future and their effects on this type of ecosystems need to be further examined in 45 order to ensure a sustainable use of CNTs.

According to the literature, CNTs can be taken up by plants^{7,9,10} and have contrasted impacts on 46 plants ⁷. They can act on plants from the germination stage with an activation of this process ¹¹⁻¹⁴. 47 48 Furthermore, upon exposure, plant growth was reported to either increase, decrease, or even unmodified (based on root systems, biomass production, and number of flowers and fruits)^{8,15}. When 49 50 toxicity was detected, it was mostly associated with an overproduction of reactive oxygen species (ROS), antioxidant enzymatic activities, necrotic lesions of cells and leaf tissues as well as root and 51 leaf morphological changes, decreased chlorophyll, and programmed cell death ^{16–19}. These divergent 52 results might be related with the influence of confounding factors which have been understudied so 53

far such as plant species ²⁰ or soil type ²¹. Additionally, CNTs can also influence gas exchanges of 54 plants with their environment. For example, CNT exposure at 250 mg.L⁻¹ increased carbon (C) 55 assimilation rate of Zea mays and also decreased stomatal conductance and transpiration rate 56 possibly as a result of H₂O use modulation ²². The same results were observed on Orthosiphon 57 stamineus with a decrease in transpiration rate, stomatal conductance and net photosynthesis 58 following a dose-dependent relationship with the increase of CNT concentration (0, 700, 1400 and 59 2100 mg.L⁻¹)²³. Plants were also water-stressed as demonstrated by the positive correlation between 60 water use efficiency and CNT concentration ²³. At lower concentrations (25 mg.L⁻¹ and 54 mg.L⁻¹), no 61 62 effects of CNT exposure were observed on Arabidopsis thaliana on ambient photosynthetic rate, stomatal conductance, transpiration, intrinsic water use efficiency and instantaneous water use 63 efficiency ²⁴. It is also worth mentioning that these reported studies were performed in hydroponics 64 65 which is not a realistic exposure scenario for agrosystems; usually not taking into account interactions with other biotic and abiotic components of the environment. 66

In parallel, interactions of CNTs with micro-organisms have also been investigated. Microscopy observations have evidenced that CNTs can interact with bacterial cell membranes; they can disrupt integrity of the membrane structure by oxidative stress and/or physical damage ^{25–28}. In addition, most studies have reported a decrease in soil microbial activity following exposure to CNTs and a loss of viability ^{28–32}. Furthermore, CNT and other carbon nanomaterial application can also cause changes in microbial community structure ^{29,32–34}. Finally, microbial functions such as organic matter decomposition, nitrogen (N) cycle and CO₂ fixation could be modified ^{35–38}.

From this brief overview of the literature, we can see that if the impact of CNTs in single-organism exposure condition has been studied so far, very little has been done at the ecosystem scale ^{39,40}. However, having a functional overview of contaminant impacts at this scale is of tremendous importance as plant/soil micro-organism interactions drive multiple processes and functions supporting ecosystem services such as food production ⁴¹. In particular, aboveground-belowground

interactions drive biogeochemical cycles (C, N, P) through several processes such as photosynthesis, mineralisation, nitrogen fixation, nitrification, denitrification, among others. One way to tackle this gap of knowledge is the use of multifunctionality index as developed in ecology ^{42–44}. This score provides an easily interpretable measure of the ability of different entities composing an ecosystem (bacteria and plants, for example) to sustain multiple functions simultaneously by gathering the selected functions in an index ⁴⁵.

85 The objective of this study was thus to investigate the impacts of CNTs at both the organism (crop plant) or community (micro-organisms) scales and at the microcosm scale by implementing a 86 87 multifunctionality score. More specifically, after exposure to CNTs their toxicity was assessed on (1) 88 the abundance of microbial communities and in particular those related to the N cycle by quantifying 89 marker genes by qPCR, (2) the organic matter decomposition process using tea bags, (3) the plant 90 growth (height, biomass, foliar surface area, dry matter content), (4) the plant physiology 91 (photosynthetic pigment and secondary metabolite concentrations by spectrophotometry and plant 92 mineral nutrition) and (5) the greenhouse gas exchanges of the system (CO_2 , H_2O , CH_4). From these 93 different variables, the impact of CNTs on ecosystem functioning was determined by an integrative 94 approach based on multifunctionality scores and, structural equation modeling was used to better 95 understand the relationships among the different drivers and multifunctionality.

96

97 2. Material and methods

98 2.1. CNT synthesis and characterization

CNTs were synthesized at the Interuniversity Center of Materials Research and Engineering (CIRIMAT,
 Toulouse University). More information is available in Supporting Information.

101 CNTs were characterized using transmission electron microscopy (JEOL 1400F, operated at 120 kV,), 102 Raman spectroscopy (Labram HR 800 Yvon Jobin equipped with a He laser at 633 nm) and BET

103 method (on freeze-dried samples). They were oxidized multiwalled CNTs (MWCNTs) with length 104 varying from 1 to 20 μ m, an average diameter of 22.5 ± 5.0 nm (Figure S1) and a specific surface area 105 of 60 m².g⁻¹. CNTs were suspended in deionised water at 100 mg.L⁻¹ and homogenized for 15 min in 106 an ultrasonic bath before use.

107

108 **2.2. Soil characterization and contamination**

109 The experiment was performed with a sandy soil (LUFA-Speyer 2.1) sieved to 2 mm with 86.0% of sand, 12.6% of loam and 1.4% of clay. It contained 0.58 wt. % of organic carbon, 0.04 wt. % of 110 111 nitrogen, with a pH of 5.0 \pm 0.1 (H₂O extraction according to NF ISO 10390:2004), a water retention capacity of 30g/100g and a cation exchange capacity of 2.9 ± 0.2 meq. $100g^{-1}$. More details on soil 112 113 characteristics are available in supporting information (Table S1). Soils were contaminated by the addition of the required volume of CNT suspension to reach a final concentration of 0.1 or 10 mg.kg⁻¹ 114 115 dry soil while maintaining the water holding capacity at 25%; the first concentration being close to environmentally predicted concentrations ⁶ and the second one representing a worst-case scenario 116 (use of nano-fertilizer, for instance). They were then mixed manually for 10 min every day for a week 117 118 to ensure that CNTs were homogeneously distributed in the soil.

119

120 2.3. Microcosm set-up

Three hundred grams of soil were distributed in each microcosm (L = 45 cm, D = 10 cm). A tea-bag (©Lipton green tea sencha, 1.13 ± 0.32 g) was introduced after the addition of 50 g of soil in each microcosm to study organic matter decomposition. Prior to introduction, tea bags were infused in water at 90°C to remove tea molecules which could have induced bias in microbial community behaviour, dried at 70°C during 48 h and weighted. One seed of *Zea mays* L. subsp. mays was added, plants were watered *ad libitum*. For each condition (CNT concentration of 0, 0.1 and 10 mg.kg⁻¹), microcosms were replicated five times with a total of 15 microcosms. The experiment lasted for 6
weeks in an environmental chamber with controlled parameters (10 h/14 h day/night cycle,
24°/18 °C and a hygrometry rate of 85%).

130

131 **2.4.** Bacterial abundance, functional genes and litter decomposition

132 The bacterial abundance (16S rRNA) and the abundance of selected genes indicators for N cycling (nitrification and denitrification) were analysed by qPCR ⁴⁶. To summarize, after DNA isolation from 133 contaminated soil using the extraction DNeasy PowerSoil kit ©QIAGEN, the total abundance of soil 134 135 bacteria was measured by targeting the universal 16S rRNA gene. The following genes related to N 136 cycle were quantified: ammonia monooxygenase A gene (amoA) of ammonia oxidizing archaea (AOA) 137 and ammonia oxidizing bacteria (AOB), nitrite reductase (nirK) and nitrous oxide reductase (nosZ) genes. The same experimental procedure as described in Vijayaraj et al.⁴⁷ was used. Results were 138 139 expressed relative to the initial gene abundances at the beginning of the experiment to account for 140 initial variability among microcosms (Figure S2; absolute results after exposure are also available in 141 Figure S3).

142 To study litter decomposition (C cycle), tea bags were removed and weighted after the 6 weeks of 143 exposure which permitted to calculate a decomposition average rate as follows:

Decomposition rate = $\frac{Mi - Mf}{Duration of exposure}$

where Mi and Mf represent the initial and final mass (mg dry weight) of the tea bag and the durationof exposure is expressed in days.

146

147 **2.5. Plant morphology and metabolism**

148 Upon exposure, indicators of the C cycle and biomass production were gathered through the determination of the effective quantum yield of maize plants (Diving-Pam underwater fluorometer, 149 Walz, United Kingdom), the height, the fresh and dry biomasses and the leaf surface area (using 150 Image J software). Part of the leaf biomass was oven-dried (60°C until constant weight) to determine 151 152 elemental concentrations by ICP-AES (see section 2.7). The remaining biomass was used fresh for 153 methanol-based extraction to quantify photosynthetic pigments (chlorophyll a and b) and secondary metabolites *i.e.* total phenolic compounds, flavonoids and tannins as described in Leroy et al. ⁴⁸ More 154 155 details on the phytotoxicity markers are available in SI.

156

157 **2.6. Greenhouse gas exchange measurements and analysis**

When plants were sufficiently high (*i.e.* sixth week), H_2O , CO_2 and CH_4 exchanges were recorded every second for 3 minutes. To do so, an airtight flux chamber (V = 0.06 m³) was connected to a trace gas analyser (LI-7810, ©LI-COR inc, United States).

161 Net ecosystem exchange of CO_2 (NEE) was measured using a transparent chamber and a LED light 162 while ecosystem CO_2 respiration (RECO) was measured using a darkened chamber. Gross primary 163 productivity (GPP: CO_2 uptake as a result of photosynthesis), was calculated as the difference 164 between NEE and RECO.

The slope of gas concentration was calculated and used to determine CO_2 flux rates (µmol.m⁻².h⁻¹). using R software and the "flux" ⁴⁹ and "gasfluxes" ⁵⁰ packages. For NEE, calculations used an exponential nonlinear function to calculate the change in the concentration in the chamber over time f⁵¹. RECO was calculated using linear regression of gas concentrations in the chamber over time. The same was done with H₂O and CH₄ to obtain fluxes in presence of light and in the dark. Positive values for the CO₂ and CH₄ fluxes indicate C release from the system while negative values indicate C uptake by the mesocosm. 172

173 **2.7. Sample preparation and chemical analysis by ICP-AES**

Plant samples were digested using 1 ml of a mix of HNO₃ and HCl (3:1 v/v) and 1 ml of H₂O₂ in a close vessel in a microwave system (MARS 2, ©CEM corporation, USA: ramp time: 20-25 min; holding time: 10 min; temperature: 190 °C). Digested samples were then diluted in 5% HNO₃ before analysis on an ICP-AES (ARCOS FHX22, ©AMETEK Spectral, United States) along with control samples (blanks with only chemicals and standard reference material NIST SRM 1570a: Trace Elements in Spinach Leaves).

180

181 **2.8. Statistical analyses**

182 For statistical analyses, 1-way ANOVAs were performed on the toxicity endpoints to test the effects of the addition of CNTs. The normality, independence and homoscedasticity of the residues were 183 184 checked using Shapiro, Durbin-Watson and Breusch-Pagan tests, respectively. Data were 185 transformed to log or square root if one of the three conditions of validity was not met. A non-186 parametric Kruskal-Wallis test was performed in the case of failed transformations. All statistical 187 analyses were performed on RStudio software (version 3.4.1). Principal component analyses (PCA) 188 were performed on the elemental concentrations in plants to assess the impact of CNTs on plant 189 nutrition.

Different functions with corresponding indicators were selected to be representative of the two main types of functions provided by agroecosystems: ecological functions and nutritional functions⁵². Ecological functions of agroecosystems include fluxes of energy and nutrients such as primary production, decomposition, and biological fixation by plants. These functions are basic ecosystem processes but are key to defining the global functioning of the system. As an extension of these basic functions, nutritional functions have to be measured alongside their ecological counterparts as 196 agroecosystems' primary goal is food production. Nutritional functions encompass a broad suite of 197 functions such as crop production, nutrient quality or resistance to environmental stress. In our case, 198 we gathered the functions and variables as follows: N cycle including both nitrification (with amoA-199 AOA and amoA-AOB gene abundances as indicators) and denitrification (nirK, nosZ), C cycle including 200 litter decomposition, ecosystem respiration, methane emission, and gross primary production 201 (related to bacterial abundance, quantum yield, chlorophyll, crop biomass), H₂O cycle (plant dry 202 matter content), plant nutrition (Z-score based on all elements quantified by ICP-AES), and plant resistance (total phenolic compounds and tannins). Using the packages "dplyr" ⁵³ and "tidyverse" ⁵⁴ 203 as well as the code library "mulitidiv"⁵⁵, the data were standardized and implemented in a unique Z-204 205 score, an index representing the multifunctionality of the ecosystem (Allan et al., 2015, Delgado-206 Baquerizo et al., 2016). A negative Z-score indicates a low multifunctionality and a positive Z-score a 207 high multifunctionality of the considered agrosystem.

208 We then combined CNTs, the multifunctionality of the agrosystem and its drivers to determine which 209 function was influenced most by CNTs and then drove a change in the multifunctionality of the agrosystem. Specifically, we constructed a structural equation model (SEM) using the package 210 "lavaan" ⁵⁶, which draws from a hypothesis-driven *a priori* model based on agrosystem theory and 211 212 accounting for our expectation that individual agrosystem functions may respond either positively or 213 negatively to CNTs, and therefore differently influence agrosystem multifunctionality. We considered 214 all available variables to investigate how individual indicators of each function related to agrosystem 215 multifunctionality (that is the full model). Then, the full model was simplified by step-wise exclusion of variables with non-significant weights and/or significant collinearity, as estimated by AIC and chi-216 217 squared statistics, until a minimal adequate model showing specific linkages remained ⁵⁷. We 218 diagnosed model fits using chi-squared statistics (P > 0.05), root-mean-square error of approximation 219 index (RMSEA ≤0.1), standardized root-mean-square residual index (SRMR ≤0.1) and comparative fit indices (CFI \geq 0.95), and included variables and paths in the final model based on chi-squared 220 221 statistics (P < 0.05) and AIC values of the model.

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224 3. Results

225

226 3.1. Microbial responses to CNT exposure

In soils exposed to 10 mg.kg⁻¹ of CNT, 16S rRNA and *amoA*-AOA gene abundances exhibited significant differences ($p_{ARN 16S} < 0.01$ and $p_{amoaA-AOA} < 0.01$, Figure 1A), with a 82% and 144% increase in comparison to the control at the end of the experiment ranging from 3.87.10¹¹ to 5.02.10¹¹ cells.g⁻¹ for 16S rRNA and from 2.04.10² to 3.68.10² cells.g⁻¹ for *amoA*-AOA gene while no difference was detected at 0.1 mg.kg⁻¹. Also, no significant difference was found for *nosZ*, *nirK* and *amoA*-AOB gene copies with on average 4.05.10¹⁰, 2.37.10⁶ and 1.5.10⁶ cells.g⁻¹ across conditions, respectively ($p_{nosZ} =$ 0.76, $p_{nirK} = 0.39$, $p_{amoA-AOB} = 0.13$).

Decomposition rate of the litter was faster in soils exposed to 10 mg.kg⁻¹ of CNT compared to the other conditions ($p_{litter decomposition} < 0.01$) with on average 9.1 mg.j⁻¹ vs. 7.8 mg.j⁻¹ (Figure 1B).

236

237

238 **3.2. Crop plant response to CNT exposure**

At the end of exposure, the proportion of dry weight was higher for plants exposed to 10 mg.kg⁻¹ of CNT with on average +17.4% compared to control plants ($p_{DW/FW} < 0.01$, Figure 2A). No significant difference was found on the other growth parameters tested: height, fresh weight (FW) and leaf area with on average 54.23 cm, 3.54 g and 126.34 cm², respectively whatever the condition ($p_{height} = 0.7$, $p_{FW} = 0.6$, $p_{leaf area} = 0.5$; Figure 2 B-C-D).

At the metabolic level, no difference on the quantum yield was detected between maize grown on control soils and those exposed to CNTs ($p_{quantum yield} = 0.3$, Figure 3A). However, the concentration of total chlorophyll was on average 34% and 9% lower in maize exposed to 0.1 and 10 of mg.kg⁻¹ CNT than in maize in control condition ($p_{Chlorophyll} < 0.01$, Figure 3B). Furthermore, phenolic compounds decreased by 15% when exposed to 0.1 mg.kg⁻¹ of CNT compared to control condition ($p_{phenolic compounds}$ < 0.01, Figure 3C). Similarly, maize exposed to the two CNT concentrations (0.1 and 10 mg.kg⁻¹) decreased by 18% their tannin content in leaves compared to control soils ($p_{tannin} = 0.01$, Figure 3D).

251 CNT exposure impacted significantly plant mineral nutrition. Indeed, the PCA on maize leaf elemental 252 composition (Ca, Cu, Fe, Mg, Mn, Na, P, S, Zn) after exposure suggested that plants exposed to 253 0.1 mg.kg⁻¹ CNT were depleted in Fe but enriched in P, K while plants exposed to 10 mg.kg⁻¹ were 254 enriched mainly in S; both exposure concentrations led to plant enrichment in Mg and Zn (Figure 3E, 255 Table S2).

256

257 3.3. Greenhouse gas exchange

At the 6th week of exposure, the NEE, RECO and CH₄ (in light and dark conditions) were similar 258 whatever the CNT concentration with on average 0.04 and 0.07 mg_{co2} .m⁻².h⁻¹ and -0.004 and -0.002 259 $mg_{CH4}.m^{-2}.h^{-1}$ respectively ($p_{NEE} = 0.6$, $p_{RECO} = 0.2$, $p_{CH4 \ Light} = 0.4$, $p_{CH4 \ darkness} = 0.9$ Figure 4A-B-E-F). 260 Additionally, the GPP was also similar whatever the CNT concentration with on average -0.16 261 mg_{CO2} .m⁻².h⁻¹ (p_{GPP} = 0.7, Figure S4). In contrast, the emission of H₂O in microcosms measured with 262 263 light (ie the evapotranspiration gathering both leaf transpiration and soil evaporation) was around 264 twice lower in the presence of CNTs at the two concentrations studied than in controls with on average 16.4 and 37.2 mg_{H20}.m⁻².h⁻¹, respectively ($p_{H20 \text{ light}} < 0.01$, Figure 4C). This was not the case 265 without light: the emission of H_2O was on average 10.5 mg_{H2O} .m⁻².h⁻¹ whatever the CNT 266 267 concentration ($p_{H2O dark} = 0.16$, Figure 4D).

268

269 **3.4. Multifunctionality and structural equation modeling**

270 The agrosystem multifunctionality significantly decreased from 0.18 ± 0.10 in control condition and

271 0.17 ± 0.22 at 10 mg.kg⁻¹ CNT to -0.35 ± 0.14 with the addition of 0.1 mg.kg⁻¹ (p<0.001, Figure 5A).

272 The SEM model revealed that CNT addition impacted the multifunctionality of the agrosystem mostly 273 indirectly (path = 0.193, p > 0.05; Figure 5B). In particular, multifunctionality was altered through the 274 impact of CNTs on microbial properties which impaired the C and N cycles. Indeed, CNTs directly 275 increased bacterial abundance (path = 0.420), which in turn positively influenced amoA-AOA (path = 276 0.773) and nirK (path = 0.705) gene abundances, as well as CO_2 respiration (path = 0.519) and organic 277 matter decomposition (path = 0.349) rates. Increasing nitrification (*amoA*-AOA, path = 0.888), 278 denitrification to a lower extent (*nirK* gene abundance; path = 0.285) and, CO₂ respiration (path = 279 0.552) then positively and significantly influenced agrosystem multifunctionality. CNTs also directly 280 increased the ratio between dry and fresh plant weight (path = 1.155), which in turn negatively 281 influenced methane emissions (path = -0.493) but positively influenced H₂O fluxes (path = 0.682) and 282 decomposition (path = 0.622). Additionally, CNT also directly impacted other plant parameters such 283 as plant nutrition with a positive influence on mineral content (path = 0.516) or on plant defense with a negative influence on tannins (path = -0.621) or on water cycle overall (path = -1.327). Plant 284 285 related parameters contributed to a lesser extent to the multifunctionality with either non-significant 286 paths or paths < 0.4.

287

288

289 4. Discussion

290 4.1. Impacts of CNTs on C cycle

Organic matter decomposition was 17% faster with the addition of 10 mg.kg⁻¹ of CNT compared to control microcosms. This increase was related to the increase in the relative number of universal 16S rRNA gene copies (+82%) showing an increase in bacterial density at this same condition (Figure 5B).

294 In parallel, plant photosynthesis did not seem to be impacted (slight trend of a decrease in the 295 quantum yield of exposed maize, although not significant) even though there was a significant

decrease in total chlorophyll pigments for plants exposed to CNTs. Plant growth (fresh biomass
 production and height) was also not impacted after 6 weeks of exposure.

298 In the literature, it has been reported in different articles that nanomaterials can increase organic matter decomposition process ^{58,59}. A study with similar exposure duration (56 days) highlighted the 299 300 same increase in 16S rRNA copies in the presence of CNTs (both single-walled CNTs and multi-walled CNTs, between 0.7 and 2.6% O) at 10 and 50 g.kg^{-1 60}. Although, there was no significant differences 301 in 16S RNA gene copy between the control condition and the soil exposed to 0.1 mg.kg⁻¹ CNT after 302 303 the 6 weeks of exposure; in this last condition, there was a significant decrease of gene copy 304 between the beginning and the end of exposure (T-test; p=0.041) suggesting toxicity at this lower 305 concentration. This higher toxicity of CNTs at lower concentrations has already been evidenced with similar reduction of microbial biomass after exposure to carbon nanomaterials such as graphene ^{32,61}, 306 graphene oxide ^{32,61,62} and CNTs ^{29,32}. The homo and hetero-agglomeration of CNTs in soil might 307 explain this effect ⁴⁸. Indeed, when the ionic strength of the medium and/or the CNT concentration 308 309 increase, CNT tend to agglomerate and become less mobile and less prone to interactions with other 310 environmental components ⁶³. Despite the decrease in bacteria concentration over time at 0.1 mg.kg⁻ 311 ¹ of CNTs, no effect on decomposition potential was noticeable suggesting that decomposition was 312 maybe compensated by others decomposers.

Interestingly, in our exposure conditions the difference detected at the organisms and community levels (bacteria population and chlorophyll pigments) did not lead to any significant difference in gas exchange (CO_2 and CH_4) at the microcosm level, suggesting some compensation mechanisms at this scale.

317

318 4.2. Impacts of CNTs on N cycle

The quantification of genes involved in the nitrogen cycle showed an increase in *amoA*-AOA gene copies up to 144% in soils exposed to 10 mg.kg⁻¹ of CNT compared to the control. A similar trend was

321 noticeable on amoA-AOB gene copies, suggesting a dose-dependent induction of the nitrifier bacterial communities. In the literature, a study demonstrated a similar increase in amoA-AOA and 322 *amoA*-AOB gene abundances after 120 days of 0.5 mg.L⁻¹ and 5 mg.L⁻¹ exposure to GO in constructed 323 wetlands, while the increase was only significant for amoA-AOA gene abundance after exposure to 324 0.5 mg.L⁻¹ after 30 days ³⁶. In contrast, in another study after 180 days of wastewater exposure, the 325 326 addition of carbon-based nanomaterials (single-walled CNTs, multi-walled CNTs and fullerene, 10 and 1000 µg.L⁻¹) led to the decline of the relative abundance of *Nitrosomonas* which was the dominant 327 AOB and is mainly responsible for the oxidation of ammonia to nitrate ³⁸. Different parameters such 328 329 as exposure media, the physico-chemical characteristics of nanomaterials or different initial microbial communities could explain the discrepancies among studies ⁶⁴. These contrasted results 330 highlight the need for more mechanistic studies considering the influence of these confounding 331 332 factors for a better environmental risk assessment. However, there was no impacts of CNT exposure 333 on denitrifier communities (nosZ and nirK).

Additionally, this increase in nitrifier abundance could also be an indirect effect related to the increase of organic matter decomposition leading to an enhanced release of NH_4^+ which is the nitrifier substrate.

337 These different results suggest that the population of nitrifiers could be favored under exposure to 338 carbon nanomaterials compared to denitrifiers (nosZ and nirK genes unchanged abundance). This 339 nitrification potential increase could lead to enhanced nitrate release and could thus result in higher 340 plant uptake and therefore higher growth along the life cycle, in the eutrophication of water bodies 341 as well as in biodiversity loss. If over the time course of this experiment, no significant impact was 342 detected on plant fresh biomass, it would be interesting to assess this parameter after a full plant 343 life-cycle exposure. This highlights also the interest of working with microcosm to be able to 344 investigate cascading effects of a contaminant on an organism assemblage. In the literature, Mondal

et al. ¹⁸ evidenced similar results on *Brassica juncea* with an increase in DW/FW ratio after exposure
 to CNTs and oxidized CNTs at 2.3 and 23 μg.L⁻¹, respectively.

347

348 4.3. Impacts of CNTs on H₂O cycle

Concerning maize, the dry matter was on average 17.4% higher for plants exposed to 10 mg.kg⁻¹ of 349 350 CNT compared to control plants while the fresh weights were similar, suggesting a decrease in water 351 content. This dry matter increase has already been demonstrated to be a common response to other types of stress ^{65,66}. It can be also correlated with a decrease in some secondary metabolites in maize 352 353 exposed to CNTs confirming the fact that plants are suffering stress conditions. Decrease in 354 secondary metabolites such as phenolic compounds and tannins could impair plant defense capabilities as they are implied in many stress defense mechanisms such as high light, low 355 temperatures, pathogen infection, herbivores, nutrient deficiency and exposure to metals ^{67,68}. 356

Alternatively, this decreased water content in maize may also be associated with CNT water adsorption capabilities, decreasing water bioavailability for maize ^{69,70}. However, the dry mater content results obtained in this study do not follow the general trend observed in the literature which described an increase in water content with CNT exposure ^{71,72}. However, as demonstrated by Line *et al.* crop species have very contrasted response to the exposure to CNTs, which can partly be explained by different plant characteristics (morphology and/or physiology) ⁷³.

The results related to water use obtained at the plant organism scale were confirmed at the ecosystem scale with a decrease in H_2O flux in light condition in the microcosms exposed to CNTs. It might be related with a decreased stomatal opening in water-stressed CNT-exposed maize. Indeed, several studies demonstrated a dose-dependent decrease in stomatal conductance with the concentration of CNTs in *Orthosiphon stamineus*²³ and *Zea mays*²².

368

369 **4.4. Impacts of CNTs on agrosystem multifunctionality**

370 As stated by Holden et al in 2012 while writing about ecological nanotoxicology, "standard toxicity 371 testing anchored in single-organism, dose-response characterizations does not adequately represent real-world exposure and receptor scenarios and their complexities" ⁷⁴. A proper risk assessment 372 373 should thus derive from ecology: ie. the study of organisms' interactions with each other and their 374 environments and account for ecological interactions across scales from within organisms to whole 375 ecosystems. Indeed, impact at the organism scale could propagate to the population with 376 consequences on community and in turn on ecosystem functions. Even though this paradigm has 377 been stated more than 10 years ago, there are only few nano-ecotoxicological studies that use this 378 approach; probably because the upscaling is not so straightforward as it has been demonstrated also for other types of contaminants ⁷⁵. In our study, to account for different scale processes, we used 379 380 two types of markers: the biomarkers directed towards organism functioning and the so-called 381 ecomarkers (in particular gas exchange) who reflect the ecosystem functioning.

382 Also in the 2010's in the field of ecology, an interesting way to approach this question has emerged 383 with the development of multifunctionality indices that permits to gather in a same index different metrics related to the different components of a considered ecosystem ⁴³. Here, it allows to conclude 384 385 that the addition of CNT could lead to contrasted consequences on agrosystem multifunctionality 386 according to CNT concentration with a decreased multifunctionality at low concentration (0.1 mg.kg⁻ 387 ¹). At the highest concentration though, the index remained similar to the control conditions but this 388 might be related to the fact that opposite effects were averaged, thus hiding individual effect 389 contribution. Additionally, it is also interesting to mention that an increased multifunctionality would 390 not necessarily indicate a benefit for the agrosystem. For instance, an increase in total phenolic compounds suggests that the plant is undergoing stress ⁶⁷. Therefore, such an increase could not be 391 considered as an "improvement" for agrosystem functioning. More particularly, the SEM model 392 393 showed that increasing multifunctionality in response to CNT was mostly driven by increasing nitrate

reductase and CO_2 respiration. suggesting that CNT addition could promote the release of greenhouse gases (CO_2 , CH_4 and N_2O) from the system through direct effects on the microbiome.

396

397 5. Conclusion

In conclusion, despite some articles of the literature suggesting that CNTs could be used as fertilizer 398 399 to increase crop production, our results obtained using an integrative approach in microcosms 400 demonstrated an impairment of some of the major biogeochemical cycles with consequences both at 401 the organism and at the ecosystem level. It is also worth mentioning that unlike more "traditional" 402 contaminants, CNT toxicity was not dose-dependent: the highest impact on the ecosystem multifunctionality was observed at the lowest exposure concentration (0.1 mg.kg⁻¹, which is 403 404 environmentally relevant in agrosystems according to modeling studies available so far) rather than at the highest one (10 mg.kg⁻¹, simulating a worst-case scenario). 405

406

407 **Conflicts of interest**

408 There are no conflicts of interest to declare.

409

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Figure captions

587

Figure 1: A. Gene copy quantification for the universal gene 16S and for selected genes involved in N cycle: *nosZ*, *nirK*, *amoA*-AOB and *amoA*-AOA by qPCR (normalized by the initial number of gene copies) and litter decomposition (B), for the 3 CNT modalities ($0 = 0 \text{ mg.kg}^{-1}$, $0.1 = 0.1 \text{ mg.kg}^{-1}$, 10 = 10mg.kg⁻¹) after a 6-week exposure in soil. Same lowercase letters indicate treatments that do not differ significantly (p-value > 0.05) following an ANOVA or a Kruskal-Wallis test (n = 5).

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Figure 2: Plant morphological parameter assessment: dry weight/ fresh weight proportion (% of dry matter) (A), height (B), fresh weight (FW, C), and leaf area (D) of maize exposed for 6 weeks in soil contaminated with 3 CNT modalities ($0 = 0 \text{ mg.kg}^{-1}$, $0.1 = 0.1 \text{ mg.kg}^{-1}$, $10 = 10 \text{ mg.kg}^{-1}$). Same lowercase letters indicate treatments that do not differ significantly (p-value > 0.05) following an ANOVA (n = 5).

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Figure 3: Quantum yield (A), total chlorophyll (B), total phenolic compounds (C), tannin concentration (D) and principal component analysis (PCA, E) on the micro- and macro-nutrient content (Ca, Cu, Fe, Cu, Mg, Mn, Na, P, S, Zn) represented by individuals and correlation circle graphs for maize leaves exposed to the 3 CNT modalities ($0 = 0 \text{ mg.kg}^{-1}$, $0.1 = 0.1 \text{ mg.kg}^{-1}$, $10 = 10 \text{ mg.kg}^{-1}$) after a 6-week exposure in soil. Cos2 corresponds to the level of variable contributions (elements) to dimensions 1 and 2. Same lowercase letters indicate treatments that do not differ significantly (pvalue > 0.05) following an ANOVA (n = 5).

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Figure 4: GreenHouse Gas exchange. Net Ecosystem Exchange (NEE, A), Ecosystem respiration (RECO, B), H₂O emission measured in the light (C) or in the dark (D) and CH₄ emission measured in the light (E) or in the dark (F) for microcosms exposed to the 3 CNT modalities (0 = 0 mg.kg⁻¹, 0.1 = 0.1 mg.kg⁻¹, 611 $10 = 10 \text{ mg.kg}^{-1}$) after a 6-week exposure. Same lowercase letters indicate treatments that do not 612 differ significantly (p-value > 0.05) following an ANOVA or a Kruskal-Wallis (CH₄ in darkness) (n = 5).

613 Figure 5: A. Multifunctionality index of microcosms exposed to the 3 CNT modalities (0 = 0 mg.kg⁻¹, $0.1 = 0.1 \text{ mg.kg}^{-1}$, $10 = 10 \text{ mg.kg}^{-1}$) after a 6-week exposure. Same lowercase letters indicate 614 615 treatments that do not differ significantly (p-value > 0.05) following an ANOVA (n=5). B. Structural 616 Equation Modeling investigating the impact of carbon nanotube (CNT) addition on agrosystem 617 multifunctionality through different functions: N cycle (nitrification represented by amoA-AOA gene 618 expression and denitrificiation represented by nirK gene expression, in yellow), H₂O cycle (with H₂O 619 flux in the system, in blue), C cycle (including organic matter decomposition, ecosystem respiration – 620 RECO – and, CH₄ emission, in green) and crop resistance and nutrition (represented by tannin and 621 mineral concentrations in plants, in red). Dashed arrows indicate a non-significant path (p values > 622 0.05), plain arrows indicate a significant positive correlation (p values < 0.05). The numbers adjacent 623 to arrows are standardized path coefficients. Model fit was overall good with P = 0.436, AIC=184.0, RMSEA = 0.090, CFI = 0.988, SRMR=0.104. 624





628 Figure 2



630 Figure 3





636 Figure 5

