NEW INSIGHTS INTO MEDITERRANEAN PEATLANDS: LONG-TERM EFFECT OF CONVENTIONAL CONTINUOUS MAIZE ON SOIL QUALITY ASSESSED BY PHYSICO-CHEMICAL PARAMETERS, ARBUSCULAR MYCORRHIZAL FUNGAL DIVERSITY AND *IN-SITU* CO_2 FLUXES

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Abstract

Wetlands are species-rich habitats performing valuable ecosystem services such as flood protection, water quality enhancement and carbon sequestration, therefore their protection is a priority. These habitats cover about 6% of the global surface area and about 60% are represented by peatlands. In Europe, peatlands cover about 20% of the land area and, although most are located in the Baltic Sea basin, some narrow sites are situated also in the Mediterranean area. So far, despite several studies have been performed on the soil quality changes of peatlands, due to land use or management change, using physico-chemical parameters, up until now there is still a lack of information regarding the effects on the biological and biochemical parameters with specific regards to Mediterranean peatlands. In the present study, we evaluated the long-term effect of a conventional continuous maize (ConvMaize) on the soil quality of a drained Mediterranean peatland. This effect was compared to an ex-arable cropping land being uncultivated for 15 years (Aband). The main soil physico-chemical parameters, arbuscular mycorrhizal (AM) fungal molecular richness, composition and structure and *in situ* soil respiration partitioning were assessed. In contrast with expectations, the main soil physico-chemical parameters of the ConvMaize did not significantly differ respect to the Aband. As regard AM fungal community diversity, 11 different AM fungal molecular operational taxonomic units affiliated to *Funneliformis mosseae,* 5 different *Glomus* spp., *Rhizophagus manihotis, Rhizophagus irregularis, Sclerocystis sinuosa, Scutellospora dipurpurescens* and an uncultured Glomeromycota, were retrieved. Multivariate analysis showed that the ConvMaize significantly affected soil AM fungal communities and highlighted the presence of preferential and ubiquitous AM fungi. The cumulated values of soil CO_2 flux components were modeled using the selected Lloyd and Taylor equation. In the ConvMaize total and autotrophic respiration

cumulated CO_2 fluxes were significantly higher than in the Aband (9% and 63%, respectively). By contrast, the heterotrophic respiration component showed an opposite behavior (- 21%). In addition, the ConvMaize reduced the soil resilience to the air temperature changes in terms of soil CO_2 flux response. These findings enhance our knowledge on the biological and biochemical changes due to land use change of peatlands and can be used to protect and preserve the Mediterranean peatlands and to identify sustainable solutions for their management.

Keywords: peatland, sustainability, land use change, arbuscular mycorrhizal fungi (AMF), AM fungal diversity, soil CO_2 flux, soil respiration partitioning, heterotrophic respiration

1. Introduction

Wetlands are species-rich habitats performing valuables ecosystem services such as flood protection, water quality enhancement and carbon (C) sequestration and their protection is officially a priority for 168 nations that have ratified the Ramsar Convention (Verhoeven and Setter, 2010). These habitats cover about 6% of the global surface area and about 60% are represented by peatlands, which play an important role in global C cycle as a long-term sink (Clymo, 1984). In Europe peatlands cover about 20% of the land area and, although most are located in the Baltic Sea basin, some narrow sites are situated also in the Mediterranean area (Montanarella et al., 2006). Theneglectful management of these fundamental ecosystems, including theirdrainage for agricultural purposes, can lead to problems such as soil organic matter (SOM) oxidation with severe carbon dioxide (CO_2) emissions, subsidence, nutrient losses to water bodies, biodiversity losses and decrease of soil quality (Foley et al., 2005; Tiemeyer et al., 2007; Verhoeven and Setter, 2010).

As defined by Doran and Parkin (1994) soil quality is "the ability of soils to interact with the ecosystems in order to maintain the biological productivity, the environmental quality and to promote animal and vegetal health". Soil quality may be affected by environmental unfriendly land use and agricultural management practices because these may cause alterations of the soil physico-chemical, biochemical and biological properties (Lal, 1998; Schjønning et al., 2004) determining, in turn, a reduction of cropping productivity and sustainability and of the ecosystems services provided by the soil (Lal, 1998). As soil quality cannot be measured directly, indicators are assessed and evaluated for their suitability (Schloter et al., 2003). Adequate soil quality indicators should be sensitive, robust, accurate, precise, simple to be measured, work equally well in all environments, user-friendly and cost-effective (Doran andParkin, 1994; Karlen et

al., 1997). Within the most suitable and suggested set of soil physico-chemical, biochemical and biological indicators, the soil organic carbon (SOC) is one of the main chemical indicators influencing aggregation, nutrient availability, C storage and biodiversity (Baldock and Skjemstad, 2000).

As regards biochemical parameters, microbial biomass and soil respiration are the two main indicators and are used for their rapidity of reaction to environmental changes and reproducibility (Bloem et al., 2006). However, the *ex situ* measurements have limitations since they are assessed in defined laboratory conditions and cannot distinguish below-ground sources of soil respiration (Rs) and their individual responses to key environmental factors (Bloem et al., 2006). Rs is in fact a complex flux, resulting from the metabolic activity of plant roots (autotrophic respiration: Ra) and soil microorganisms such as bacteria, non-mycorrhizal and mycorrhizal fungi, actinomycetes and mesofauna (heterotrophic respiration, Rh) (Kuzyakov, 2006). Therefore, *in situ* measurements of CO_2 fluxes, using root exclusion, shading and clipping, tree girdling or isotopic techniques, have been largely used because of their capacity to distinguish soil respiration components (Hanson et al., 2000; Luo and Zhou, 2006; Heinemeyer et al., 2007). Moreover, the selection of an appropriate model for soil respiration is important for an accurate CO_2 flux gap filling (Richardson et al., 2006). Numerous empirical models have been devised and validated which are mostly simple functions of few independent variables and several parameters (Luo and Zhou, 2006). So far, in simple models the Rs has been scaled with air and soil temperature and showed exponential relationships.

Within biological indicators, arbuscular mycorrhizal (AM) fungal diversity has been shown to be a good and suitable biological indicator of the state and functioning of ecosystems. Arbuscular mycorrhizal fungi (AMF, phylum: Glomeromycota, Schüßler et

al. 2001) are one of the main components of the soil microbiota in most natural and agricultural ecosystems. They form mutualistic symbioses with the roots of most land plants andthey play fundamental rolessince they increase plant growth, enhance nutrient uptake, in exchange of photosynthetically fixed C (Bago et al. 2000), improve soil structure and protect against biotic and abiotic stressors (Smith and Read, 2008). However, several studies have shown that AM fungal diversity and their benefits are affected by land use change and agricultural system intensification (Moora et al., 2007; Oehl et al., 2010; Verbruggen and Kiers, 2010; Pellegrino et al., 2011; Davison et al., 2012). In fact, the intensification of land use, tillage and application of fertilizers and biocides together with cropping sequence choices (i.e., rotations with non-mycorrhizal hosts) have been shown to negatively modify AM fungal community composition and structure and soil aggregation (Helgason et al., 1998, 2007; Jansa et al., 2002; Oehl et al., 2010; Rillig et al., 2003; Rillig and Mummey, 2006; Borriello et al., 2012).

So far, despite several studies have been performed onthe soil quality changes of peatlands, due to land use or management change, using the main physico-chemical parameters (Tiemeyer et al., 2007; Pulleman et al., 2010), up until now there is still a lack of information regarding the effects on the biological and biochemical parameters. These studies are indeed lacking in Mediterranean peatlands and need to be included in conservation and preservation programs, as strongly suggested by the Convention for Biological Diversity (Sutherland et al., 2009).

In the present study, starting from the lack of information on the influence of land use change on soil organic matter degradation, CO_2 flux and AM fungal diversity in Mediterranean peatlands, we evaluated the long-term effect of a conventional continuous maize in comparison to an ex-arable cropping land, being uncultivated for 15 years, on the soil quality of a drained peatland in the Massaciuccoli Lake basin

130 (Tuscany, Italy). The continuous maize was chosen since it is the most widespread
131 cropping system in the lake basin (about 30% of the total UAA; Silvestri et al. 2012).
132 The main soil physico-chemical parameters, AM fungal molecular richness,
133 composition and structure and *in situ* soil respiration partitioning (Ra and Rh) were
134 utilized for this evaluation. In addition, a model selection for soil respiration was
135 performed in order to calculate the cumulative respiration fluxes.
136

137 **2. Materials and Methods**

138 *2.1. Field site*

139 The experimental site was situated in the southern part of the Massaciuccoli Lake
140 basin (43°49'N - 10°19'E) within the Regional Park of Migliarino-San Rossore-
141 Massaciuccoli (Pisa, Italy). Since 1930, most of the basin has been drained by a
142 complex network of artificial canals and ditches and pumping stations, forcing water
143 from reclaimed areas into the lake, causing a severe subsidence ranging from 3 to 4 cm
144 yr^{-1}, determined by the compaction and the peat oxidation (Pistocchi et al., 2012). The
145 soil was classified as *Histosol* according to the USDA system (Soil Survey Staff, 1975)
146 and as *Rheic Histosol* according to the FAO system (IUSS, 2006). The soil is classified
147 as a peat-topped soil (peatland) according to Montanarella et al. (2006) and as a sandy
148 clay loam (50.0% sand, 24.8% silt and 20.6% clay) with a mean values of SOM equal to
149 29.2% [minimum 20.1% - maximum 55.4% (Pistocchi et al., 2012)] (Walkley-Black),
150 pH of 4.9 and the following total nutrient concentrations: 12.9 g kg^{-1} N (Kjeldahl),
151 2896.4 mg kg^{-1} P and 75.2 mg kg^{-1} available P (Olsen). During the year the water table
152 depth is maintained at a quite stable level, ranging from 0.40 to 0.60 m by the pumping
153 stations (Rossetto R., personal communication). Climate at the experimental station is
154 Mediterranean (Csa) according to the Köppen Geiger climate classification map.

Summers are dry and hot, rainfall is mainly concentrated in autumn and spring (mean annual rainfall ca. 900 mm year^{-1}) and mean monthly air temperature ranges from 7°C in February to 30 °C in August (mean of 14.5 °C year^{-1}). Average monthly maximum, mean and minimum temperatures and rainfalls were recorded at the weather station of Metato (Pisa, Italy; 43°77'N - 10°38'E) in the period 1989-2012 (Fig. S1).

2.2. Experiment 1: evaluation of the impact of land use on soil physico-chemical parameters and AMF

This experiment aimed at evaluating the long-term effect of a conventional continuous maize system in comparison with land abandonment on physico-chemical soil parameters, root traits, such as the root biomass and the AM fungal colonization, and AM fungal diversity, composition and structure.

2.2.1. Experimental set-up

The experiment was a completely randomized design with land use as treatment and three replicates (n = 3; replicate plots of 7000 m^2). Land use types were:
(1) a conventional continuous maize (*Zea mays* L.) (ConvMaize). Each year at late spring plots were deeply ploughed (30-35 cm) and harrowed as main and secondary tillage, respectively. Maize was sown at the beginning of June at a rate of 75,000 seeds ha^{-1} with 75 x 17 cm row spacing and harvested on late September. Fertilization was applied at sowing and at mechanical weeding with rates of 32 kg ha^{-1} N, 96 kg ha^{-1} P, 96 kg ha^{-1} K and 138 kg ha^{-1} N, respectively. Chemical and mechanical post-emergence weed controls were applied. Average maize yield of the last 15 years was 6.4 tha^{-1};

(2) an ex-arable cropping land, being uncultivated for 15 years (Aband). Plots were left to develop under the natural succession vegetation. A floristic survey carried out in summer 2011 showed that the most common species were *Abutilon theophrasti* L., *Amaranthus retroflexus* L., *Arctiumlappa* L., *Artemisia* sp., *Atriplex* sp., *Bidens* sp., *Biphora* sp., *Calystegia* sp., *Datura stramonium* L., *Echinochloa crus-galli* L., *Galium* sp., *Humulus lupulus* L., *Linaria* sp., *Phragmites australis* L, *Typha latifolia* L., *Lythrum salicaria* L.,*Phytolacca americana* L., *Rumex crispus* L., *Silene alba* L. and *Xanthium* sp.. No fertilizers or other agricultural practices were applied, except for an annual vegetation cutting. Details of soil texture of the two land uses (ConvMaize and Aband) are given in Table 1.

2.2.2. Sampling

In July 2011 one combined soil sample, resulting from pooling three soil cores, was collected from each replicate plot (30 cm depth) in order to control physico-chemical and AM fungal spatial variability. Sampling was carried out only once in July since mid-summer is the best choice according to the fact that sampling must not be close to soil treatments and the variability of physico-chemical parameters slightly change during the year (Pellegrino et al., 2011). These facts, along with the fact that AMF among differently managed systems consistently maintain the same patterns of variability although showing seasonal changes (Vandenkoornhuyse et al., 2002; Oehl et al., 2010; Pellegrino et al., 2011; Di Bene et al., 2013), were taken into strong account for choosing as a single sampling time July.

Soil samples used for the physico-chemical parameter determinations were oven dried at 60 °C and sieved at 2 mm, while for genomic DNA extraction were stored at 4 °C after sieving. As regard to the root traits determinations, three turfs were extracted (20

206 cm depth) from each replicate plot and then combined. In laboratory, from each
207 combined sample, roots were collected, washed and dried at 60 °C for root dry weight
208 (DW) measurement, whereas for AM fungal root colonization assessment and genomic
209 DNA extraction, root subsamples were taken and stored at 4 °C.
210
211 *2.2.3. Soil physico-chemical analyses*
212
213 Soil samples were analyzed for: pH; electrical conductivity, EC; exchangeable
214 potassium, K_{exch}; total nitrogen, N_{tot}; ammonium, NH_4^+; nitrates, NO_3^-; soil organic
215 matter, SOM; total phosphorus, P_{tot}; available phosphorus, $P_{avail}$and organic phosphorus,
216 P_{org}. Soil pH and EC were measured in deionized water (1:2.5 and 1:2, w/v,
217 respectively) (McLean, 1982). K_{exch} was determined afterthe atomic absorption
218 (Thomas, 1982). P_{tot} and P_{avail} were determined by colorimetry using perchloric acid
219 digestion and a solution of sodium bicarbonate, respectively (Olsen and Sommers,
220 1982). P_{org} was evaluated using the Metha extraction (Hence and Anderson, 1962). N_{tot}
221 was determined by the macro Kjeldahl digestion procedure (Bremner and Mulvaney,
222 1982), while NO_3^- and NH_4^+ by the Keeney and Nelson method (1982). SOM was
223 measured using the modified Walkley-Black wet combustion method (Nelson and
224 Sommers, 1982). Soil C/N ratio was calculated dividing SOC ((SOM / 1.7) x 10) by
225 total N.
226
227 *2.2.4. Root determination and AM fungal root colonization*
228
229 From the combined turfs of each replicate plot, soil subsamples (mean soil DW ca.
230 400 g) were used to determine root DW. Roots were manually collected with forceps
231 and washed by wet-sieving and decanting down to a mesh size of 250 μm. After

232 removing organic debris, all live and dead root fragments were oven-dried and weighed
233 to determine root DW. Root DW per gram of soil was calculated by dividing root DW
234 for soil DW.
235 AM fungal root colonization was assessed under a stereomicroscope (Olympus SZX
236 9, Olympus Optics, Tokyo, Japan), after clearing and staining with lactic acid instead of
237 phenol (Phillips and Hayman, 1970), following the gridline intersect method
238 (McGonigle et al., 1990).
239
240 *2.2.5. AM fungal diversity: extraction of genomic DNA, PCR amplification, cloning and*
241 *sequencing*
242
243 Soil DNA was extracted from 0.5 g of soil using the PowerSoil®MoBio kit (Mo Bio
244 Laboratories Inc., NY, USA) (n = 6), while root DNA from 100-mg fresh root samples
245 using the DNeasy® Plant Mini Kit (n = 6) (Qiagen, Germantown, MD, USA). DNA was
246 stored at -20 °C until PCR amplification. PCR amplification was performed using the
247 primers pair NS31 and AM1 targeting the small subunit ribosomal RNA (SSU rRNA)
248 region (Simon et al., 1992; Helgason et al., 1998). The NS31/AM1 SSU region,
249 although the availability of long and highly discriminate regions (Krüger et al., 2009;
250 Pellegrino et al., 2012), was targeted because most data of Glomeromycota diversity are
251 obtained using it, providing a larger comparative DNA sequence data-set than other
252 obtained using other genomic regions. PCR was performed using the temperature
253 profile described by Helgason et al. (1998). PCR amplicons were generated from 10 ng
254 μL^{-1} genomic DNA in volumes of 20 µL with 0.5 U of GoTaq® Hot Start Polymerase
255 (Promega Corporation, Madison, WA, USA), 0.2 µM of each primer (NS31/AM1), 0.2
256 mM of each dNTP, 1.25 mM of $MgCl_2$ and 1x reaction buffer, using the S1000 Thermal
257 Cycler™ (BIORAD, USA). Before ligation, quantity and quality of the PCR amplicons

were checked by a spectrophotometer (NanoDrop®ND-1000, Germany). The PCR amplicons were then ligated into the pGem®-T Easy vector (Promega Corporation, Madison, WA, USA) and used to transform XL10-Gold® Ultracompetent*Escherichia coli* cells (Stratagene®, La Jolla, CA, USA). At least 25 recombinant clones per amplicon library (n = 12) were screened for the c. 550-bp-long NS31/AM1 fragment (Helgason et al., 1998) on agarose gels. A total of 270 PCR products obtained from clones (a mean of 23 per library) were sequenced using the NS31/AM1 primers in an ABI Prism® 3730XL automated sequencer (Applied Biosystem, Foster City, CA, USA) at the High-Throughput Genomics Unit (Seattle, WA, USA).

2.3. Experiment 2: evaluation of the impact of land use on soil CO_2 fluxes

This experiment aimed at evaluating the long-term effect of a conventional maize system in comparison with land abandonment on total soil respiration flux and autotrophic and heterotrophic CO_2 flux components.

2.3.1. Experimental set-up and sampling

The experimental design was as described above for experiment 1. Six experimental blocks (one for each replicate plot) were established within the area for soil respiration monitoring (Fig. S2a,b). Six blocks were considered an adequate number due to the soil texture homogeneity. In each plot the block was composed by two 20-cm diameter open-ended PVC collars (Plumb Centre, Pisa, IT; Toscana Tubi Srl, Livorno, IT): a surface collars (7.0-cm deep collar inserted 1 cm into the soil) pressed firmly onto the shallow surface layer without cutting any roots (Fig. S2a); a 25-cm deep collar tapered on the bottom inserted 20 cm into the soil (Fig. S2b). Plants inside the collars were removed, leaving the root systems intact, while litter was maintained. The surface and

284 the deep collars provided a measure of total soil respiration (Rs) and heterotrophic
285 respiration (Rh, soil microorganisms and mesofauna), respectively (Heinemeyer et al.,
286 2007). These measures were utilized to calculate the contribution of the root component
287 defined as autotrophic respiration (Ra = Rs- Rh). Soil CO_2 flux was measured *in situ*
288 using the manual dynamic chamber method, with a portable infrared gas analyzer
289 (IRGA) (Licor LI-820) connected to a steel accumulation chamber having a headspace
290 volume of 6186 cm^3 (chamber B, West Systems Srl, Pontedera, Italy). To guarantee a
291 tight seal with the collars, the chamber has a rubber ring that fits into the collar lip. The
292 CO_2 flux was checked for linearity over a period of 2-3 min and then recorded by a
293 portable device connected by a wireless Bluetooth connection. An internal fan allowed
294 the homogeneity of the air mixture inside the chamber during the measurement. Soil
295 moisture and temperature were recorded at each measurement next to each collar by a
296 probe (Decagon Devises ECH_2O-TE/EC-TM) inserted into a soil depth of 5 cm.
297 In 2012 a monitoring campaign was undertaken between 14 May and 13 August with
298 a measurement frequency of one or two times per week (a total of 21 measurements).
299 The sampling period was chosen taking into consideration that in order to evaluate the
300 impact of a land use change on soil biochemical parameters it is necessary to sample far
301 from soil treatments (Picci and Nannipieri, 2002). This fact, along with the fact that for
302 measuring such parameters it is recommended to sample far from extreme events (i.e.,
303 high rainfall), supported our choice (Conant et al., 2000; Picci e Nannipieri, 2002).Daily
304 mean temperatures and rainfalls during the sampling period (from May to August 2012)
305 were recorded. Measurements were made between 8 a.m. and 12 a.m., because it is
306 showed that mid-day values of CO_2 flux is representative of daily average (Davidson et
307 al., 1998; Luo and Zhou, 2006). Sampling started ten days after collars insertion.
308

309 *2.3.4. Modeling soil respiration*

310 The cumulated total and heterotrophic soil respiration (from 14 May to 13
311 August2012) were calculated using the exponential relationship between soil CO_2 flux
312 and air temperature (van't Hoff, 18848, Arrhenius 1898). The Van't Hoff empirical
313 exponential equation (Q10) (van't Hoff, 1884), a simplified version of the Rothamsted
314 Carbon Model (RothC; with temperature as independent variable (Coleman and
315 Jenkinson, 1999) and the Lloyd and Taylor (LT) (Lloyd and Taylor, 1994) models were
316 used in order to assess the sensitivity of soil respiration to air temperature. The three
317 models were fitted on measured soil CO_2 fluxes of total and heterotrophic respiration
318 for both land uses and correlated with air temperature.

319 The performance of the three models of CO_2 flux response to air temperature was
320 evaluated using different model selection criteria: the Akaike Information Criterion
321 (AIC); the Root Mean Squared Error (RMSE) and the Adjusted R-square value
322 (Rsd.ad). The best statistical fit was chosen to calculate the cumulate flux.

323

324 *2.4. Data and sequence analysis*

325 An updated AM fungal dataset of 59 NS31/AM1 public sequences (ca. 550 bp) was
326 created, including the majority of the AM fungal species listed in the phylotaxonomic
327 classification of Schüßler and Walker (2010) and Krüger et al. (2012) (this alignment
328 has been made accessible in an open-access database
329 https://sites.google.com/site/restomedpeatland/microbiology). The AM fungal dataset
330 was utilized for the further alignment of the newly generated sequences using Bioedit
331 (Hall, 1999), after having previously checked the quality of their electropherograms by
332 Vector NTI Advance 10 (Invitrogen, USA) and their affiliation to the Glomeromycota
333 phylum by Basic Local Alignment Search Tool (BLAST) search (Altschul et al., 1997).

Indeed, a total of 160 newly generated partial SSU Glomeromycota sequences was aligned with the sequences of the dataset and trimmed to the same length (ca. 490 bp). Such an alignment, optimized to a total of 195 sequences (34 from the dataset, 160 newly generated and the *Corallochytrium limacisporum* sequence L42528 as outgroup), was finally manually refined. Phylogenetic trees were inferred by the neighbor-joining (NJ) analysis using MEGA version 5.1 (Tamura et al., 2011; http://www.megasoftware.net) and the Kimura 2-parameter model (Kimura 1980). Branch support values correspond to 1000 boostrap replicates. The phylograms were drawn by MEGA 5.1 and edited by Adobe Illustrator CS6.

The phylogram was utilized to assign the newly generated AM fungal sequences to molecular operational taxonomic units (MOTUs) on the basis of a bootstrap value of 75. AM fungal MOTU richness and Shannon index (*H*') were calculated using Primer v6 (Clarke and Gorley, 2006; http://www.primer-e.com). The adequacy of the AM fungal community sampling was verified using individual-based rarefaction curves (Gotelli& Colwell, 2001) with clones/sequences considered as units of replication, and was calculated in EstimateS version 8.2 (Colwell et al., 1997; http://viceroy.eeb.uconn.edu/EstimateS) using the Coleman rarefaction curves (Coleman, 1981).

All newly generated sequences were submitted to the EMBL nucleotide sequence database (http://www.ebi.ac.uk/embl/) and are available under the accession numbers HG425705 - HG425864.

Soil physico-chemical parameters, root DW, AM fungal root colonization, soil and root AM fungal relative abundances of MOTUs, AM fungal MOTU richness, *H*' and cumulated soil CO_2 fluxes were analyzed by the independent sample *t*-test with the land

359 use as factor. In addition, to detect differences among the sampling dates within each
360 land use, soil CO_2 fluxes were analyzed by the one-way analysis of variance (ANOVA)
361 with sampling date as factor. All data were log- or arcsin-transformed when necessary
362 to fulfill the assumption for the *t*-test and the ANOVAs. Post-hoc Tukey's-b significant
363 difference tests were used for the comparisons among sampling dates. When the
364 assumptions for the parametric analysis were not fulfilled (soil CO_2 fluxes and the
365 coefficients of variation of the three components of soil CO_2 fluxes), even after the
366 appropriate transformation, data were analyzed using the Mann-Whitney nonparametric
367 test or the Kruskal-Wallis H non-parametric test, followed by the Mann-Whitney test.
368 All these analyses were performed in SPSS version 21.0 (SPSS Inc., Chicago, IL,
369 USA).
370 Constrained ordination analyses (Redundancy analysis, RDA) (van den Wollenberg,
371 1977) were used to investigate the influence of the different land use types (used as
372 explanatory variables) on the physico-chemical, root and CO_2 parameters and on the
373 AM fungal relative abundances of MOTUs (used as response variables). We utilized the
374 RDA linear method (Lepš and Šmilauer, 2003) since the response variables were in
375 different measurement units and the length of the gradient of the detrended
376 correspondence analysis was lower than four. All data were log-transformed, centered
377 and standardized by the response variables. Monte Carlo permutation tests were
378 performed using 499 random permutations (unrestricted permutation) in order to
379 determine the statistical significance of the relations between the land use types and the
380 response variables. RDA analyses were done by Canoco for Windows v. 4.5 (terBraak
381 and Šmilauer, 2002). The biplots were drawn by CanoDraw for Windows.
382
383 **3. Results**

3.1. Experiment 1: evaluation of the impact of land use on soil physico-chemical parameters, roots and AMF

3.1.1. Soil physico-chemical parameters, root dry weight and AM fungal root colonization

Unexpectedly, 15 years of continuous maize (ConvMaize) did not significantly modified soil quality, as measured by its main physico-chemical parameters, in comparison with the land abandonment (Aband) except for the soil NH_4^+ concentration that was around three-fold higher in the ConvMaize than in the Aband (Table 2). However, it is noteworthy to highlight a decline trend of the vital component of a healthy soil. Actually, the ConvMaize land use reduced soil organic matter (SOM) by 9% in comparison with the Aband, as well as for other chemical parameters, such as the P_{tot} and P_{avail} that were reduced by 8% and 5%, respectively.

As regard to roots, dry weight values (DW) were not significantly different between land uses, whereas AM fungal root colonization percentages were significantly lower (-30%) in the ConvMaize than in the Aband Table 3.

3.1.2. AM fungal diversity

The PCR primer pair NS31/AM1, which targets the 3' end of the SSU rRNA gene (≈ 550 bp), was used to amplify and screen the clone libraries obtained from the 12 crude DNA extracts of field root and soil samples. A total of 366 clones were screened and 270 showed the expected AM fungal band length. In detail, 138 positive clones were obtained from the ConvMaize (65 and 73 from root (R) and soil samples (S), respectively) and 132 from the Aband (63 e 69 from R and S, respectively). After

408 sequencing and BLAST checking, about 40% of the sequences were excluded due to
409 sequencing errors or PCR primer unspecificity.
410 The obtained sequences were grouped into 11 different AM fungal molecular
411 operational taxonomic units (MOTUs) (a total of eight and seven in the ConvMaize and
412 the Aband and six and eight in roots and soil, respectively) which were phylogenetically
413 affiliated to *Funneliformis mosseae* (Fun1_AMASS), 5 different *Glomus* spp. (from
414 Glo1_AMASS to Glo5_AMASS), *Rhizophagus manihotis* (Rhizo1_AMASS),
415 *Rhizophagus irregularis* (Rhizo2_AMASS), *Sclerocystis sinuosa* (Sclero1_AMASS),
416 *Scutellospora dipurpurescens* (Scut1_AMASS) and an uncultured Glomeromycota
417 (Uncult1_AMASS) (Fig. 1; Fig. S3). Three out of 11 MOTUs, although three
418 doubletons (Glo5_AMASS, Rhizo1_AMASS and Scut1_AMASS), were considered for
419 further analyses.
420 The rarefaction curves showing the relation between the number of sampled
421 sequences and the number of observed AM fungal MOTUs retrieved from roots and soil
422 of the ConvMaize and the Aband land uses (Fig. S4) demonstrated that the sampling
423 effort was sufficient as the accumulation curves reached the asymptote.
424 As shown in the pie charts of Fig. 1, four AM fungal MOTU were exclusively
425 retrieved in the soil of the ConvMaize (Glo2_AMASS, Glo5_AMASS,
426 Rhizo1_AMASS and Sclero1_AMASS), while three were only found in the Aband:
427 Fun1_AMASS in the soil and the others (Scut1_AMASS and Uncult1_AMASS) within
428 the roots. By contrast, Rhizo2_AMASS, affiliated to *R. irregularis*, showed a
429 ubiquitous behavior. In fact, it was retrieved in both land uses and matrixes. Along with
430 Rhizo2_AMASS, Glo1_AMASS and Glo4_AMASS occurred into the soil of both land
431 uses and within the roots of only the Aband, while Glo3_AMASS was present in both
432 land uses but just into the roots.

433 The MOTU richness and Shannon biodiversity index (*H'*) were calculated to evaluate
434 the long-term sustainability of the two different land uses on AM fungal community
435 diversity, considering in this way, not only the number, but also the relative proportions
436 of taxa (Table 4). Unexpectedly, we observed a significantly higher AM fungal richness
437 and diversity into the soil of the ConvMaize than in the Aband. Interestingly, in the
438 continuous maize, the soil showed higher values of both indexes respect to the roots.
439 Along with this, considering the relative proportions of the AM fungal MOTU (Fig. 2
440 and Table S1), Glo2_AMASS and Sclero1_AMASS were significantly more abundant
441 into the soil of the ConvMaize than in the Aband, while Fun1_AMASS and
442 Glo1_AMASS were significantly less abundant. In fact, Glo2_AMASS and
443 Sclero1_AMASS, which were exclusively found in the ConvMaize soil, showed
444 relative abundances of 16.9% and 40.9%, respectively, whereas Fun1_AMASS,
445 exclusively found in the Aband soil, showed a relative abundance of 21.0%. Along with
446 Fun1_AMASS, Glo1_AMASS was three-fold more present in the Aband than in the
447 ConvMaize.
448 As regard to root, although a differential trend was found and both diversity indexes
449 were three-fold higher in the Aband than in the ConvMaize, 15 years of land use change
450 did not significantly affect AM fungal community richness and evenness (Table 4).
451 The t- or Mann-Whitney tests utilized to highlight the AM fungal relative abundance
452 difference between matrixes within each land use, showed that, for the ConvMaize,
453 Glo1_AMASS, Glo2_AMASS, Glo4_AMASS and Sclero1_AMASS were significantly
454 more abundant in the soil than in the roots, whereas an opposite trend was observed for
455 Rhizo2_AMASS (Table S1). Similarly, Rhizo2_AMASS was more present into the
456 roots than in the soil also in the Aband land use, while Fun1_AMASS and
457 Glo1_AMASS showed an opposite behavior.

458 RDAs, in line with the univariate tests, showed that land use change significantly
459 affected AM fungal composition and structure in the soil and that the different matrixes
460 have different AM fungal assemblages in both land uses. In detail, RDA showed that in
461 the soil land use explained 83.5% (I and II axes) of the whole variance (Fig. 3a), and
462 that its effect on the AM fungal communities was significant ($P = 0.002$), while in the
463 roots no differences were recorded ($P = 0.410$) (data not shown). With regard to soil
464 AM fungal assemblages, the arrows representing Glo2_AMASS, Sclero1_AMASS,
465 Glo5_AMASS and Rhizo1_AMASS point to the ConvMaize, while those representing
466 Glo1_AMASS and Fun1_AMASS point to the Aband, showing their preferential
467 presence in the corresponding land use (Fig. 3a). Moreover, Glo4_AMASS and
468 Rhizo2_AMASS did not show preferential behaviors. As regard to the ConvMaize and
469 the Aband, RDAs showed that the different matrixes explained 89.7% and 89.2% (I and
470 II axes) of the whole variance, respectively (Fig. 3b,c), and that their effect on the AM
471 fungal communities was significant ($P = 0.002$). As shown by the arrows, in the
472 ConvMaizeGlo2_AMASS, Sclero1_AMASS, Glo1_AMASS, Glo4_AMASS,
473 Glo5_AMASS and Rhizo1_AMASS are soil preferential, while Glo3_AMASS and
474 Rhizo2_AMASS are root preferential (Fig. 3b). Along with this, also in the Aband, the
475 arrows showed that Rhizo2_AMASS and Glo3_AMASS are preferential of the roots
476 and that Glo1_AMASS of the soil (Fig. 3c). Interestingly, such an RDA biplot
477 highlighted that Scut1_AMASS/Uncult1_AMASS and Fun1_AMASS, exclusively
478 present in the Aband, were preferential of the roots and of the soil, respectively.
479
480 *3.2. Experiment 2: evaluation of the impact of land use on soil CO_2 fluxes*
481
482 *3.2.1. Soil CO_2 flux measurements*

Both air and soil temperature and soil moisture strongly varied during the monitoring period (Fig. 4a,b). From May to August, the mean air and soil temperature ranged from 12.0 to 26.6 °C and from 16.1 to 30.2 °C, respectively; soil moisture (% v:v) decreased in both land uses from 30.8 to 15.8% and from 27.5 to 2.2% for the ConvMaize and the Aband, respectively (Fig. 4b). Soil temperatures of the ConvMaize and the Aband showed significant relationships ($P < 0.001$) with air temperature, as shown by the Pearson correlation (r = 84% and 90%, respectively) (data not shown). Total soil respiration (Rs), heterotrophic respiration (Rh) and autotrophic respiration (Ra) steadily increased following the trend of air and soil temperature (Fig. 4c,d,e). Rs ranged from 9.74 to 63.35 g CO_2 m^{-2} day^{-1} and from 19.97 to 54.95 g CO_2 m^{-2} day^{-1} in the ConvMaize and the Aband, respectively, while Rh from 6.79 to 29.12 g CO_2 m^{-2} day^{-1} and from 17.34 to 35.43 g CO_2 m^{-2} day^{-1} in the ConvMaize and the Aband, respectively. The ConvMaize showed significantly lower Rs and Rh values in the first period of the monitoring (from the middle to the end of May) than the Aband, whereas, later, we observed an opposite trend of the Rs. The Ra ranged from 2.33 to 38.55 g CO_2 m^{-2} day^{-1} and from 2.63 to 27.82 g CO_2 m^{-2} day^{-1} in the ConvMaize and the Aband, respectively. Actually, Rs and also Ra in the ConvMaize were significantly higher than in the Aband in the second part of both June and July (Fig. 4c,e). By contrast, Rh values were significantly higher in the Aband than in the ConvMaize in almost all July (Fig. 4d).

3.2.2. Model selection of soil CO_2 flux response to air temperature

To calculate the cumulated values of the two measured components (Rs and Rh) of the soil CO_2 respiration we made a selection of the best model among the most used ones: Q10, LT and simplified RothC. These models were compared on the basis of three selection criteria, such as AIC, RSME and Rsq.ad (Table 5). In detail, the LT model

showed the best goodness of fit for Rs and Rh in the ConvMaize and the Aband. Actually, the LT model minimized the AIC and the RSME values, while the simplified RothC model maximized the Rsq.ad values (Table 5). Therefore, the LT model was selected for modeling the soil CO_2 flux response to air temperature.

The plots of the relationships between the measured Rs and Rh and air temperature obtained utilizing the LT model are shown in Fig. S5. Clear relationships between Rs and Rh fluxes and air temperature were observed both in the ConvMaize and the Aband. Actually, in the ConvMaize strong and significant relationships were revealed (Rs Rsq.ad = 0.7; Rh Rsq.ad = 0.8; $P < 0.001$) (Table 5; Fig. S5a,c), while in the Aband significant relationships from moderate to weak were observed (Rs Rsq.ad = 0.5; Rh Rsq.ad = 0.3; $P < 0.001$) (Table 5; Fig. S5b,d, respectively).

3.2.3. Impact of land use change on the resilience of CO_2 fluxes and on cumulated soil CO_2 fluxes

The coefficients of variation of the Rs and Rh components were significantly higher in the ConvMaize than in the Aband, showing its lower resilience to air temperature changes in terms of soil CO_2 flux response (Table 6).

The curves of the Rs, Rh and Ra cumulated CO_2 fluxes are shown in Fig. 5. In the ConvMaize Rs and Ra cumulated CO_2 fluxes (4360 g m^{-2} $period^{-1}$ and 2316 g m^{-2} $period^{-1}$, respectively) were significantly higher than in the Aband (3999 g m^{-2} $period^{-1}$ and 1419 g m^{-2} $period^{-1}$, respectively) (Fig. 5). In detail, Rs and Ra cumulated soil CO_2 flux increases, calculated as ((ConvMaize – Aband)/Aband)) × 100, were 9 and 63%, respectively. By contrast, the Rh component showed an opposite behavior, showing significantly lower values in the ConvMaize than in the Aband (- 21%). Interestingly, in

532 the ConvMaize, the Rh and Ra soil CO_2 flux partitionings were 47% and 53%,
533 respectively, whereas in the Aband 65% and 35%, respectively.
534
535 *3.3. Main patterns of soil physico-chemical parameters, CO_2 fluxes and AM fungal*
536 *diversity as affected by land use*
537 RDA showed that land use explained 69.5% (I and II axes) of the whole variance and
538 that its effect on soil quality parameters was significant ($P = 0.002$), as shown by the
539 biplot arrows representing the ConvMaize and the Aband (Fig. 3d). The biplot clearly
540 suggested that NH_4^+, Ra, MOTU richness and H' of soil and Rs, showing higher values
541 in the ConvMaize respect to the Aband, and Rh and AM fungal colonization, showing
542 lower values in the ConvMaize respect to the Aband, where the most discriminant
543 variables between the two land uses.
544
545 **4. Discussion**
546 In this work we assessed for the first time the long-term effect of the land use change,
547 from a conventional continuous maize to uncultivated conditions, on the soil quality of
548 a drained Mediterranean peatland, belonging to the Massaciuccoli wetland area.
549 Multivariate analyses showed that 15 years of conventional continuous maize
550 (ConvMaize): (i) did not affect the main soil physico-chemical parameters, except for
551 the NH_4^+ that was higher in the ConvMaize than in the ex-arable cropping land
552 (Aband); (ii) decreased the AM fungal root colonization and the root AM fungal
553 taxonomic diversity, whereas increased the MOTU richness and the Shannon diversity
554 indexof the soil; (iii) enhanced soil and root respiration together with a decrease of the
555 microbial and mesofauna respiration component; (iv) reduced soil resilience to air
556 temperature changes in terms of soil CO_2 flux response.

557

558 *4.1. Evaluation of the impact of land use on soil physico-chemical parameters, roots*
559 *and AMF (Experiment 1)*

560

561 *4.1.1. Soil physico-chemical parameters*

562 The application of alternative farming, based on conservative tillage, fertilization
563 adjusted to soil nutrient traits and crop nutrient needs, agroecological friendly weed and
564 pesticide management, have been largely shown to lead to sustainability of
565 agroecosystems (Altieri, 1995; Matson et al., 1997; Tilman et al., 2002; Schjønning et
566 al., 2004). Such sustainability is determined not only by the positive effects on the
567 economic aspects, including crop productivity, but also on the environmental quality,
568 including air, water and soil quality. So far, land use change and intensification of
569 cropping systems has been largely studied using long-term experiments mainly focusing
570 on the effects of tillage and fertilization (Pulleman et al., 2000; Liebig et al., 2004;
571 Nassi o Di Nasso et al., 2011; Pellegrino et al., 2011). Our work confirmed previous
572 results showing no changes of the physico-chemical aspects of soil quality due to
573 conventional farming respect to uncultivated conditions (Liebig et al., 2004; Pellegrino
574 et al., 2011; Bell et al., 2012), even in an peculiar environment such as a Mediterranean
575 peat soil, characterized by a very high content of SOM and total N and P. By contrast,
576 some authors revealed negative trends of the main soil physico-chemical parameters due
577 to the intensification of land use (Pulleman et al., 2000; Celik, 2005; Gajić, 2013) and
578 cropping system (Shrestha et al., 2006; Birkhofer et al., 2008). These inconsistencies
579 might be attributed to depth and time factors. Actually, changes of the main chemical
580 parameters, especially of the SOM, after land use conversions are commonly detected in
581 the first 7.5 cm and may need more than 15 years in order to be discriminate (Liebig et

582 al., 2004; Shrestha et al., 2006; Gajić, 2013). The unique observed difference on NH_4^+
583 might be well explained by its high temporal variability (Kieft et al., 1998; Violante,
584 2000) and sampling closeness to N fertilization.
585
586 *4.1.2. Root dry weight and AM fungal root colonization*

587 Root dry weight was utilized to estimate the differences in the size of the root system
588 of maize and natural succession vegetation occurring in the conventional continuous
589 maize system (ConvMaize) and in the ex-arable cropping land (Aband), respectively.
590 Our data were in the range of those obtained at 0-30 cm depth of wheat, giant reed and
591 miscanthus (0.07-0.2, 0.4-1.6 and 2.9-4.3 mg g^{-1}, respectively; unpublished data) and
592 for maize and uncultivated natural weed fallow (0.04-1.8 mg g^{-1}) (Anderson, 1988;
593 Jonsson et al. 1988; Kothari et al., 1990; Mekonnen et al. 1997).
594 Maize has a root apparatus, composed by embryonic primary and seminal roots and
595 postembryonic shoot-borne and lateral roots, showing in the field strong AM fungal
596 root colonization (Gavito and Varela, 1993; Hochholdinger et al., 2004). Here, although
597 the well known highly mycotrophic status of the maize, its AM fungal root colonization
598 was lower than that in the roots of the natural succession vegetation, occurring in the
599 ex-arable cropping land. Actually, the difference between the ConvMaize and the
600 Aband AM fungal root colonization rates can not been explained by plant species
601 composition, as the 18 plant species occurring in the Aband belonged to 16 different
602 families (Amaranthaceae, Apiaceae, Asteraceae, Cannabaceae, Caryophillaceae,
603 Chenopodiaceae, Convolvulaceae, Lythraceae, Malvaceae, Phytolaccaceae, Poaceae,
604 Polygonaceae, Rubiaceae, Scrophulariaceae, Solanaceae, Typhaceae) mostly showing a
605 non-mycorrhizal status (Harley and Harley, 1987). Therefore, tillage, fertilization and
606 mechanical and chemical weeding, carried out in the ConvMaize, can well explain such

607 a difference because they have been largely shown to reduce mycorrhizal infection
608 potential of soil by “pluoghing up” the mycelium network (Helgason et al., 1998, 2007;
609 Jansa et al., 2002;Borriello et al., 2012; Verbruggen et al., 2012).
610

611 *4.1.3.AM fungal diversity*

612 Although in the past the importance of AMF in wetlands has not been taken into
613 account (Keddy et al., 2000), our study on AM fungal diversity of a Mediterranean
614 drained peatland was boosted by the increasing awareness of the their occurrence and
615 functionality in these key ecosystems (Miller, 2000; Cornwell et al., 2001; Wolfe et al.,
616 2007).
617 Different molecular markers belonging to the rRNA gene, such as the SSU, the
618 internal transcribed spacers (ITS1, 5.8S and ITS2) and the large subunit rRNA gene
619 (LSU), have been utilized to identify the glomeromycotan species and investigate their
620 phylogenetical diversity (Helgason et al., 1998; van Tuinen et al, 1998; Redecker et al.,
621 2003; Gollotte et al., 2004; Lee et al., 2008). Although the relatively lower variability
622 and species resolution power of the AM fungal NS31/AM1 SSU sequences and the
623 exclusion of basal lineages of Glomeromycota, such as Archeosporaceae and
624 Paraglomeraceae, this region is still utilized because it provides a larger comparative
625 sequence dataset than those available for the other single or combined genomic regions
626 (Opik et al., 2010; Stockinger et al., 2010; Borriello et al., 2012; Krüger et al., 2012;
627 Pellegrino et al., 2012). Therefore, since we aimed to study the AM fungal diversity in a
628 Mediterranean peatland for the first time, we selected the NS31/AM1 region. Here, in
629 addition to the root matrix that gives a picture of the symbiotically active community,
630 we carried out the direct extraction of the “environmental” DNA from the usually less

631 investigated soil to avoid the host effect selection (Borriello et al., 2012; Davison et al.,
632 2012).
633 Root and soil MOTU richness and Shannon index fell into similar range of previous
634 works (Helgason et al., 1998; Daniell et al., 2001; Husband et al., 2002;
635 Vandenkoornuyse et al., 2002; Hijri et al., 2006; Borriello et al., 2012), but were largely
636 lower than those reported by others (Bever et al., 1996; Abbott and Robson, 1997; Jansa
637 et., 2002; Wolfe et al., 2007; Mummey and Rillig, 2008; Oehl et al., 2010). These
638 inconsistencies might be due to the pedo-climatic dissimilarities, but also to the
639 differences between the methodology of detection. However, focusing on maize
640 molecular diversity, our data were similar to those reported by several works studying
641 the effect of tillage and fertilization on the diversity not only in roots, but also in soil
642 under monocropping systems (Daniell et al., 2001; Hijri et al., 2006; Borriello et al.,
643 2012). Here, root MOTU richness and Shannon index suggested that AM fungal
644 diversity associated with the maize "monoculture" is not depleted by the intensification
645 of cultivation as it had been previously described by field and microcosm studies
646 (Daniell et al., 2001; Johnson et al., 2004; Hijri et al., 2006). As the diversity of a soil
647 reflects its accumulated sporulation history and not the current symbionts of the crop,
648 the ConvMaize, although being a continuous cropping system, showed a higher
649 diversity respect to the Aband because of the mycorrhizal weed composition (Poaceae,
650 Solanaceae and Phytolaccaceae). Therefore, these weeds may have supported the AM
651 fungal root development and the resulting spore composition in the soil of the
652 ConvMaize.
653 The Glomeraceae and the Acaulosporaceae were commonly and largely retrieved in
654 agricultural soil, while the Gigasporaceae were more frequently observed in woodland
655 or uncultivated sites (Helgason et al., 1998; Daniell et al., 2001; Jansa et al., 2002;

Gollotte et al., 2004; Hijri et al., 2006; Pellegrino et al., 2011). As regard to the wetland areas, the Glomeraceae were the most abundant together with few members of the Acaulosporaceae and the Diversisporaceae (Wirsel et al., 2004; Wolfe et al., 2007). Our data on AM fungal composition and structure were consistent with the previous observations. Actually, the Glomeraceae was the unique family retrieved in the soil, while within the roots a member of the Gigasporaceae was also detected. Within the Glomeraceae, the dominance of the Rhizo2_AMASS within the roots of the maize suggests that it possess an ability to survive in agricultural conditions due to its ability to colonize the roots from mycelium fragments rather than from spores dispersal or intact mycelium (Biermann and Linderman, 1983) and to readily form anastomoses that reestablish the hyphal interconnection after its tillage destruction (De La Providencia et al., 2005). The presence of a MOTU phylogenetically affiliated to the *S.dipurpurescens* only within the roots of the natural succession vegetation occurring in the Aband can be well explained by the soil tillage disruption of the extraradical hyphae that are essential for the propagation of the Gigasporaceae (Jasper et al., 1993). Despite several authors highlighted the dominance of *F. mosseae* in arable land, grassland and also wetlands, unexpectedly we retrieved *F. mosseae* only into the soil of the Aband also without being the most representative. Interestingly, in the soil of the ConvMaize a MOTU phylogenetically affiliated to *S. sinuosa* was largely found.

4.2. Evaluation of the impact of land use on soil CO_2 fluxes (Experiment 2)

4.2.1. Soil CO_2 flux measurements and cumulated values

The differentiation of the soil CO_2 flux into its components, autotrophic and heterotrophic, has been recently shown to be an important method for evaluating and

681 interpreting soil CO_2 sources (Baggs, 2006; Kuzyakov, 2006). Here, the soil CO_2
682 sources were successfully monitored during the maize growing season using the root
683 exclusion method. In addition, in order to fill respiration gaps and to assess the total
684 respiration over the monitored period, the air temperature was used as the
685 environmental variable for CO_2 modelling. In fact, although some authors have modeled
686 soil respiration by using several environmental parameters such as soil and air
687 temperature, soil water content and water table depth (Almagro et al., 2009; Correia et
688 al., 2012; Rowson et al., 2013), most authors found a highly significant relationship
689 between soil or air temperature and soil respiration (Luo and Zhou, 2006; Richardson et
690 al., 2006; Subke et al., 2006). In this regard, we selected, on the basis of three different
691 criteria, the LT model respect to the Q10 and the simplified RothC, in agreement also
692 with the suggestions of Davidson et al. (2006) and Luo and Zhou (2006).
693 Here, the cumulated values of the total soil respiration (Rs), extrapolated by using the
694 LT model, were utilized to obtain the means of the daily Rs values. The calculated daily
695 Rs fluxes of the ConvMaize and the Aband (47.39 and 43.47 g CO_2 m^{-2} day^{-1},
696 respectively) are higher than those reported by several authors (from 0.77 to 26.6 g CO_2
697 m^{-2} day^{-1}) for fens and peatlands in boreal and temperate areas (Moore, 1986; Silvola et
698 al., 1996; Kasimir-Klemedtsson et al., 1997;Smith et al., 2007; Danivčič et al., 2010;
699 Berglund et al., 2011; Heinemeyer et al., 2011; Carter et al., 2012; Schrier-Uijl et al.,
700 2012; Wunderlich et al., 2012). These inconsistencies might be explained by the fact
701 that we monitored an unexplored habitat such as a Mediterranean peatland, which is
702 characterized, respect to the boreal and temperate peatlands, by high mineralization rate
703 and warmer temperatures in the spring-summer period. In addition to such factors, the
704 not limiting soil water content assessed in our peatland could have determined larger
705 fluxes respect to those commonly registered in the Mediterranean areas (from 3.19 to

706 25.09 g CO_2 m^{-2} day^{-1}) (Wang et al., 2000; Tedeschi et al., 2006; Almagro et al., 2009;
707 Mancinelli et al., 2010; Carter et al., 2012; Correia et al., 2012; Lai et al., 2012).
708 As suggested by Subke et al. (2006) we compared our results on soil CO_2 partitioning
709 using the Rh/Rs ratio instead of the Ra/Rh ratio because the Rh flux was directly
710 recorded, whereas the Ra was calculated by difference. The Rh/Rs ratio ranged from
711 0.47 to0.65 in the ConvMaize and the Aband, respectively. These ratios were similar to
712 those reported in Mediterranean croplands, where the mean ratio was around 0.50
713 (Wang et al., 2000; Subke et al., 2006; Lai et al., 2012). By contrast, our ratios were
714 lower than those reported for boreal and temperate peatlands, ranging from 0.72 to 0.97
715 (Silvola et al., 1996; Wunderlich et al., 2012). Consistently with Subke et al. (2006) in
716 the Aband, the Rh cumulated values were higher than the Ra values (+81%) and similar
717 to the pristine peatlands, whereas in the ConvMaize we detected an opposite trend (-
718 12%) similar to the croplands.
719
720 *4.2.2. Resilience of the CO_2 fluxes*
721 In agreement with our data, comparing the fluctuation of the CO_2 flux in the Aband
722 respect to the ConvMaize, Jackson et al. (2003) reported a lower resilience in the tilled
723 cropping systems than in the no-tilled ones. This behavior might be explained by the
724 higher porosity, the initial lower bulk density and the lower pore connectivity of the
725 long-term tilled soils compared to the no-till ones that result in slightly warmer
726 temperatures and in a consequent larger microbial metabolic activity (Silgran and
727 Shepherd, 1999). Furthermore, Laliberté et al. (2010) linked the reduction of the
728 resilience following a land-use intensification gradient to plant diversity and
729 functionality. Along with this, our monocropping maize system showed lower plant
730 diversity in comparison with the ex-arable cropping land.

Conclusions

Our study indicates that 15 years of conventional agriculture in a Mediterranean peatland alter soil quality mainly by decreasing root AM fungal taxonomic diversity, enhancing total soil CO_2 respiration and reducing resilience of the total and heterotrophic soil CO_2 fluxes. Although we did not attempt to measure the relationship between AM fungal diversity and composition and host functionality, we can argue that the conventional continuous maize might determine a loss of functionality and reliability linked to AMF in such a vulnerable ecosystem. In addition, the drainage and cultivation of these peatsoils clearly transform them in a large source of CO_2 due to the higher degradation rate of the SOM determined by an enhanced microbial activity. Actually, drainage and soil tillage modify the soil physico-chemical properties increasing aeration and porosity, resulting in an oxidizing environment and warmer temperatures that are factors boosting the microbial activity. This is a first direct confirmation that the biochemical oxidation of degraded peats is a major process determining the observed subsidence rate (3 to 4 cm yr^{-1}). These main findings can be used to protect and preserve the Mediterranean peatlands and to identify sustainable solutions for their management.

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759

760 **References**

761 Abbott, L.K., Robson, A.D., 1977. The distribution and abundance of vesicular-
762 arbuscular endophytes in some Western Australian soil. Australian Journal of Botany
763 25, 515-522.
764 Almagro, M., López, J., Querejeta, J.I., Martínez-Mena, M., 2009. Temperature
765 dependence of soil CO_2 efflux is strongly modulated by seasonal patterns of moisture
766 availability in a Mediterranean ecosystem. Soil Biology and Biochemistry 41, 594-
767 605.
768 Altieri, M.A., 1999. The ecological role of biodiversity in agroecosystems. Agriculture,
769 Ecosystems and Environment 74, 19-31.
770 Altschul, S.F., Madden T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W., Lipman,
771 D.J., 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database
772 search programs. Nucleic Acids Research 25, 3389-3402.
773 Anderson, E.L., 1988. Tillage and N fertilization effects on maize root growth and root:
774 shoot ratio. Plant and Soil 108, 245-251.
775 Arrhenius, S., 1898. The effect of constant influences upon physiological relationships.
776 Scandinavian Archives of Physiology 8, 367-415.
777 Baggs, E.M., 2006. Partitioning the components of soil respiration: a research
778 challenge. Plant and Soil 284, 1-5.
779 Bago, B., Pfeffer, P.E., Shachar-hill, Y., 2000. Carbon Metabolism and Transport in
780 Arbuscular Mycorrhizas. Plant Physiology 124, 949-958.

781 Baldock, J.A., Skjemstad, J.O., 2000. Role of the soil matrix and minerals in protecting
782 natural organic materials against biological attack. Organic Geochemistry 31, 697-
783 710.
784 Bell, L.W., Sparling, B., Tenuta, M., Entz, M.H., 2012.Soil profile carbon and nutrient
785 stocks under long-term conventional and organic crop and alfalfa-crop rotations and
786 re-established grassland. Agriculture, Ecosystems and Environment 158, 156-163.
787 Berglund, Ö., Berglund, K., 2011. Influence of water table level and soil properties on
788 emissions of greenhouse gases from cultivated peat soil. Soil Biology and
789 Biochemistry 43, 923-931.
790 Bever, J.D., Morton, J.B., Antonovics, J., Schultz, P.A., 1996. Host-dependent
791 sporulation and species diversity of arbuscular mycorrhizal fungi in a mown grassland.
792 Journal of Ecology 84, 71-82.
793 Biermann, B., Linderman, R.G., 1983. Mycorrhizal roots, intraradical vesicles and
794 extraradical vesicles as inoculum. New Phytologist 95, 97-105.
795 Birkhofer, K., Bezemer, T.M., Bloem, J., Bonkowski, M., Christensen, S., Dubois, D.,
796 Ekelund, F., Fließbach, A., Gunst, L., Hedlund, K., Mäder, P., Mikola, J., Robin, C.,
797 Setälä, H., Tatin-Froux, F., Van der Putten, W.H., Scheu, S., 2008. Long-term organic
798 farming fosters below and aboveground biota: implications for soil quality, biological
799 control and productivity. Soil Biology and Biochemistry 40, 2297-2308.
800 Bloem, J., Hopkins, D.W., Benedetti, A., 2006. Microbiological methods for assessing
801 soil quality, CABI Publishing, Cambridge, MA, USA.
802 Borriello, R., Lumini, E., Girlanda, M., Bonfante, P., Bianciotto, V., 2012. Effects of
803 different management practices on arbuscular mycorrhizal fungal diversity in maize
804 fields by a molecular approach. Biology and Fertility of Soils 48, 911-922.

Bremner, J.M., Mulvaney C.S., 1982. Nitrogen - total. In: Page, A.L., Miller, R.H., Keeney, D.R. (Eds.), Methods of Soil Analysis, Part 2, Chemical and Microbiological Properties, Agronomy Monograph (second ed.), vol. 9, American Society of Agronomy, Madison, WI, pp. 595-624.

Carter, M.S., Larsen, K.S., Emmett, B., Estiarte, M., Field, C., Leith, I.D., Lund, M., Meijide, A., Mills, R.T.E., Niinemets, Ü., Peñuelas, J., Portillo-Estrada, M., Schmidt, I.K., Selsted, M.B., Sheppard, L.J., Sowerby, A., Tietema, A., Beier, C., 2012. Synthesizing greenhouse gas fluxes across nine European peatlands and shrublands - responses to climatic and environmental changes. Biogeosciences 9, 3739-3755.

Celik, I., 2005. Land-use effects on organic matter and physical properties of soil in a southern Mediterranean highland of Turkey. Soil and Tillage Research 83, 270-277.

Coleman, B.D., 1981. On random placement and species-area relations. Mathematical Biosciences 54, 191-215.

Coleman, B.D., Mares, M.A., Willig, M.R., Hsieh, Y.H., 1982. Randomness, area, and species richness. Ecology 63, 1121-1133.

Coleman, K., Jenkinson, D. S., 1999. ROTHC-26.3. A model for the turnover of carbon in soils, Herts, Rothamsted Research, Harpenden, Hertfordshire, UK.

Colwell R.K., 1997. EstimateS: statistical estimation of species richness and shared species from samples. Version 5. http://viceroy.eeb.uconn.edu/EstimateS

Conant, R.T., Klopatek, J.M., Klopatek, C.C., 2000. Environmental factors controlling soil respiration in three semiarid ecosystems. Soil Science Society of America Journal 64, 383-390.

Cornwell, W.K., Bedford, B.L., Chapin, C.T., 2001. Occurrence of arbuscular mycorrhizal fungi in a phosphorus-poor wetland and mycorrhizal response to phosphorus fertilization. American Journal of Botany 88, 1824-1829.

Correia, A.C., Minunno, F., Caldeira, M.C., Banza, J., Mateus, J., Carneiro, M., Wingate, L., Shvaleva, A., Ramos, A., Jongen, M., Bugalho, M.N., Nogueira, C., Lecomte, X., Pereira, J.S., 2012. Soil water availability strongly modulates soil CO_2 efflux in different Mediterranean ecosystems: Model calibration using the Bayesian approach. Agriculture, Ecosystems and Environment 161, 88-100.

Clarke, K.R., Gorley, R.N., 2006. PRIMER v6: User Manual/Tutorial. PRIMER-E Ltd., Plymouth.

Clymo, R.S., 1984. The limits to peat bog growth. Philosophical Transactions of the Royal Society of London B 303, 605-654.

Danevčič, T., Mandic-Mulec, I., Stres, B., Stopar, D., Hacin, J., 2010.Emissions of CO_2, CH_4 and N_2O from Southern European peatlands. Soil Biology and Biochemistry 42, 1437-1446.

Daniell, T.J., Husband, R., Fitter, A.H., Young, J.P.W., 2001. Molecular diversity of arbuscular mycorrhizal fungi colonising arable crops. FEMS Microbiology Ecology 36, 203-209.

Davidson, E.A., Janssens, I.A., Luo, Y., 2006. On the variability of respiration in terrestrial ecosystems: moving beyond Q10. Global Change Biology 12, 154-164.

Davidson, E.A., Belk, E., Boone, R.D., 1998. Soil water content and temperature as independent or confounded factors controlling soil respiration in a temperate mixed hardwood forest. Global Change Biology 4, 217-227.

Davison, J., Öpik, M., Zobel, M., Vasar, M., Metsis, M., Moora, M., 2012. Communities of arbuscular mycorrhizal fungi detected in forest soil are spatially heterogeneous but do not vary throughout the growing season. PloS One 7, e41938.

De La Providencia, I.E., De Souza, F.A., Fernández, F., Delmas, N.S., Declerck, S., 2005. Arbuscular mycorrhizal fungi reveal distinct patterns of anastomosis formation

855 and hyphal healing mechanisms between different phylogenic groups. New
856 Phytologist 165, 261-271.
857 Di Bene, C., Pellegrino, E., Debolini, M., Silvestri, N., Bonari, E., 2013. Short- and
858 long-term effects of olive mill wastewater land spreading on soil chemical and
859 biological properties. Soil Biology and Biochemistry 56, 21-30.
860 Doran, J.W., Parkin, T.B., 1994. Defining and assessing soil quality, p. 3-21. In: Doran,
861 J.W. et al. (Eds.), Defining soil quality for a sustainable environment. SSSA Spec.
862 Publ. No. 35, Soil Sci. Soc. Am., Inc. and Am. Soc. Agron., Inc., Madison, WI.
863 Felsenstein, J., 1985. Confidence limits on phylogenies: An approach using the
864 bootstrap. Evolution 39, 783-791.
865 Foley, J.A, Defries, R., Asner, G.P., Barford, C., Bonan, G., Carpenter, S.R., Chapin,
866 F.S., Coe, M.T., Daily, G.C., Gibbs, H.K., Helkowski, J.H., Holloway, T., Howard,
867 E.A., Kucharik, C.J., Monfreda, C., Patz, J.A., Prentice, I.C., Ramankutty, N., Snyder,
868 P.K., 2005. Global consequences of land use. Science 309, 570-574.
869 Gajić, B., 2013. Physical properties and organic matter of Fluvisols under forest,
870 grassland, and 100 years of conventional tillage. Geoderma 200-201, 114-119.
871 Gavito, M.E., Varela, L., 1993. Seasonal dynamics of mycorrhizal associations in maize
872 fields under low-input agriculture. Agriculture, Ecosystems and Environment 45, 275-
873 282.
874 Gollotte, A., Van Tuinen, D., Atkinson, D., 2004. Diversity of arbuscular mycorrhizal
875 fungi colonising roots of the grass species *Agrostis capillaris* and *Lolium perenne* in a
876 field experiment. Mycorrhiza 14, 111-117.
877 Gotelli, N.J., Colwell, R.K., 2001. Estimating species richness., Frontiers in measuring
878 biodiversity, Oxford University Press, New York.

879 Hall, T.A., 1999. BioEdit: a user-friendly biological sequence alignment editor and
880 analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41, 95-98.
881 Hanson, P.J., Edwards, N.T., Garten, C.T., Andrews, J.A., 2000. Separating root and
882 soil microbial contributions to soil respiration: a review of methods and observations.
883 Biogeochemistry 48, 115-146.
884 Harley, J.L., Harley, E.L., 1987. A check-list of mycorrhiza in the British flora. New
885 Phytologist 105, 1-102.
886 Heinemeyer, A., Hartley, I.P., Evans, S.P., Carreira De La Fuente, J.A., Ineson, P.,
887 2007. Forest soil CO_2 flux: uncovering the contribution and environmental responses
888 of ectomycorrhizas. Global Change Biology 13, 1786-1797.
889 Heinemeyer, A., Di Bene, C., Lloyd, A.R., Tortorella, D., Baxter, R., Huntley, B.,
890 Gelsomino, A., Ineson, P., 2011. Soil respiration: implications of the plant-soil
891 continuum and respiration chamber collar-insertion depth on measurement and
892 modelling of soil CO_2 efflux rates in three ecosystems. European Journal of Soil
893 Science 62, 82-94.
894 Helgason, T., Daniell, T.J., Husband, R., Fitter, A.H., Young, J.P., 1998. Ploughing up
895 the wood-wide web? Nature 394, 431.
896 Helgason, T., Merryweather, J.W., Young, J.P.W., Fitter, A.H., 2007. Specificity and
897 resilience in the arbuscular mycorrhizal fungi of a natural woodland community.
898 Journal of Ecology 95, 623-630.
899 Hence, R.J., Anderson, G., 1962. A comparative study of methods of estimating soil
900 organic phosphate. Journal of Soil Science 13, 225-230.
901 Hijri, I., Sýkorová, Z., Oehl, F., Ineichen, K., Mäder, P., Wiemken, A., Redecker, D.,
902 2006. Communities of arbuscular mycorrhizal fungi in arable soils are not necessarily
903 low in diversity. Molecular Ecology 15, 2277-2289.

Hochholdinger, F., Park, W.J., Sauer, M., Woll, K., 2004. From weeds to crops: genetic analysis of root development in cereals. Trends in Plant Sciences 9, 42-48.

Husband, R., Herre, E.A, Turner, S.L., Gallery, R., Young, J.P.W., 2002. Molecular diversity of arbuscular mycorrhizal fungi and patterns of host association over time and space in a tropical forest. Molecular Ecology 11, 2669-2278.

IUSS Working Group WRB, 2006.World reference base for soil resources. World. Soil Resources Reports No. 103. FAO, Rome.

Jackson, L.E., Calderon, F.J., Steenwerth, K.L., Scow, K.M., Rolston, D.E., 2003. Responses of soil microbial processes and community structure to tillage events and implications for soil quality. Geoderma 114, 305-317.

Jansa, J., Mozafar, A., Anken, T., Ruh, R., Sanders, I.R., Frossard, E., 2002. Diversity and structure of AMF communities as affected by tillage in a temperate soil. Mycorrhiza 12, 225-234.

Jasper, D.A., Abbott, L.K., Robson, A.D., 1993. The survival of infective hyphae of vesicular–arbuscular mycorrhizal fungi in dry soil and interaction with sporulation. New Phytologist 124, 473-479.

Johnson, D., Vandenkoornhuyse, P.J., Leake, J.R., Gilbert, L., Booth, R.E., Grime, J.P., Young, J.P.W., Read, D.J., 2004. Plant communities affect arbuscular mycorrhizal fungal diversity and community composition in grassland microcosms. New Phytologist 161, 503-515.

Jonsson K., Fidjeland L., Maghembe J.A., Hogberg P., 1988. The vertical distribution of fine roots of five tree species and maize in Morogoro, Tanzania. Agroforestry Systems 6, 63-69.

927 Karlen, D.L., Mausbach, M.J., Doran, J.W., Cline, R.G., Harris, R.F. ,Schuman, G.E.,
928 1997. Soil quality: a concept, definition and framework for evaluation. Soil Science
929 Society of America Journal 61, 4-10.
930 Kasimir-Klemedtsson, Å., Klemedtsson, L., Berglund, K., Martikainen, P., Silvola, J.,
931 Oenema, O., 1997. Greenhouse gas emissions from farmed organic soils: a review.
932 Soil Use and Management 13, 245-250.
933 Keddy P., 2000. Wetland ecology: principles and conservation, Cambridge University
934 Press, NewYork.
935 Keeney, D.R., Nelson, D.W., 1982. Nitrogen-inorganic forms. In: Page, A.L., Miller,
936 R.H., Keeney, D.R. (Eds.), Methods of Soil Analysis, Part 2, Chemical and
937 Microbiological Properties, Agronomy Monograph (second ed.), vol. 9, American
938 Society of Agronomy, Madison, WI, pp. 403-430.
939 Kieft, T.L., White, C.S., Loftin, S.R., Aguilar, R., John, A., Skaar, D.A., 1998.
940 Temporal dynamics in soil carbon and nitrogen resources at a grassland-shrubland
941 ecotone. Ecology 79, 671-683.
942 Kimura M., 1980. A simple method for estimating evolutionary rates of base
943 substitutions through comparative studies of nucleotide sequences. Journal of
944 Molecular Evolution 16, 111-120.
945 Kothari, S.K., Marschnerf, H., George, E., 1990. Effect of VA mycorrhizal fungi and
946 rhizosphere microorganisms on root and shoot morphology, growth and water
947 relations in maize. New Phytologist 116, 303-311.
948 Krüger, M., Krüger, C., Walker, C., Stockinger, H., Schüssler, A., 2012. Phylogenetic
949 reference data for systematics and phylotaxonomy of arbuscular mycorrhizal fungi
950 from phylum to species level. New Phytologist 193, 970-984.

951 Krüger, M., Stockinger, H., Krüger, C., Schüssler, A., 2009. DNA-based species level
952 detection of Glomeromycota: one PCR primer set for all arbuscular mycorrhizal fungi.
953 New Phytologist 183, 212-223.
954 Kuzyakov, Y., 2006. Sources of CO_2 efflux from soil and review of partitioning
955 methods. Soil Biology and Biochemistry 38, 425-448.
956 Lai, R., Seddaiu, G., Gennaro, L., Roggero, P.P., 2012. Effects of nitrogen fertilizer
957 sources and temperature on soil CO_2 efflux in Italian ryegrass crop under
958 Mediterranean conditions.Italian Journal of Agronomy 7, 196-201.
959 Lal, R., 1998. Soil quality and agricultural sustainability. Ann Arbor Press, Chelsea, MI.
960 Lee, J., Lee, S., Young, J.P.W., 2008. Improved PCR primers for the detection and
961 identification of arbuscular mycorrhizal fungi. FEMS Microbiology Ecology 65, 339-
962 349.
963 Laliberté, E., Wells, J. A, Declerck, F., Metcalfe, D.J., Catterall, C.P., Queiroz, C.,
964 Aubin, I., Bonser, S.P., Ding, Y., Fraterrigo, J.M., McNamara, S., Morgan, J.W.,
965 Merlos, D.S., Vesk, P.A., Mayfield, M.M., 2010. Land-use intensification reduces
966 functional redundancy and response diversity in plant communities. Ecology Letters
967 13, 76-86.
968 Lepš, J., Šmilauer, P., 2003. Multivariate Analysis of Ecological Data Using CANOCO,
969 Cambridge University Press, Cambridge.
970 Liebig, M., Tanaka, D., Wienhold, B., 2004. Tillage and cropping effects on soil quality
971 indicators in the northern Great Plains. Soil and Tillage Research 78, 131-141.
972 Loyd, J., Tayor, J.A., 1994. On the temperature dependence of soil respiration.
973 Functional Ecology 8, 315-323.
974 Luo, Y., Zhou, X., 2006. Soil respiration and the environment, Elsevier, London, UK.

975 Mancinelli, R., Campiglia, E., Di Tizio, A., Marinari, S., 2010. Soil carbon dioxide
976 emission and carbon content as affected by conventional and organic cropping systems
977 in Mediterranean environment. Applied Soil Ecology 46, 64-72.
978 Matson, P.A., Parton, W.J., Power, A.G., Swift, M.J., 1997. Agricultural intensification
979 and ecosystem properties. Science 277, 504-509.
980 McGonigle, T.P., Miller, M.H., Evans, D.G., Fairchild, G.L., Swan, J.A., 1990. A new
981 method which gives an objective measure of colonization of roots by vesicular-
982 arbuscular mycorrhizal fungi. New Phytologist 115, 495-501.
983 McLean, E.O., 1982. Chemical equilibrations with soil buffer systems as bases for
984 future soil testing programs. Communications in Soil Science and Plant Analysis 13,
985 411-433.
986 Mekonnen, K., Buresh, R.J., Jama, B., 1997. Root and inorganic nitrogen distributions
987 in sesbania fallow, natural fallow and maize fields. Plant and Soil 188, 319-327.
988 Miller, S.P., 2000. Arbuscular mycorrhizal colonization of semi-aquatic grasses along a
989 wide hydrologic gradient. New Phytologist 145, 145-155.
990 Montanarella, L., Jones, R.J.A., Hiederer, R., 2006. The distribution of peatland in
991 Europe. Mires and Peat 1, 1-10.
992 Moora, M., Daniell, T., Kalle, H., Liira, J., Püssa, K., Roosaluste, E., Öpik, M.,
993 Wheatley, R., Zobel, M., 2007. Spatial pattern and species richness of boreonemoral
994 forest understorey and its determinants - A comparison of differently managed forests.
995 Forest Ecology and Management 250, 64-70.
996 Moore, T.R., 1986. Carbon dioxide evolution from subarctic peatlands in eastern
997 Canada. Arctic and Alpine Research 18, 189-193.

998 Mummey, D.L., Rillig, M.C., 2008. Spatial characterization of arbuscular mycorrhizal
999 fungal molecular diversity at the submetre scale in a temperate grassland. FEMS
1000 Microbiology Ecology 64, 260-270.
1001 Nassi o Di Nasso, N., Bosco, S., Di Bene, C., Coli, A., Mazzoncini, M., Bonari, E.,
1002 2011. Energy efficiency in long-term Mediterranean cropping systems with different
1003 management intensities. Energy 36, 1924-1930.
1004 Nelson, D.W., Sommers, L.E., 1982.Total carbon, organic carbon and organic matter.
1005 In: Page, A.L. Miller, R.H., Keeney, D.R. (Eds.), Methods of Soil Analysis, Part 2,
1006 Chemical and Microbiological Properties, Agronomy Monograph (second ed.), vol. 9,
1007 American Society of Agronomy, Madison, WI, pp. 539–579.
1008 Oehl, F., Laczko, E., Bogenrieder, A., Stahr, K., Bösch, R., van der Heijden, M.,
1009 Sieverding, E., 2010. Soil type and land use intensity determine the composition of
1010 arbuscular mycorrhizal fungal communities. Soil Biology and Biochemistry 42, 724-
1011 738.
1012 Olsen S.R., Sommers L.E., 1982. Phosphorus. In: Page, A.L., Miller, R.H., Keeney,
1013 D.R. (Eds.), Methods of Soil Analysis, Part 2, Chemical and Microbiological
1014 Properties, Agronomy Monograph (second ed.), vol. 9, American Society of
1015 Agronomy, Madison, WI, pp. 403-430.
1016 Öpik, M., Vanatoa, A., Vanatoa, E., Moora, M., Davison, J., Kalwij, J.M., Reier, Ü.,
1017 Zobel, M., 2010.The online database MaarjAM reveals global and ecosystemic
1018 distribution patterns in arbuscular mycorrhizal fungi (Glomeromycota). New
1019 Phytologist 188, 223-241.
1020 Pellegrino, E., Di Bene, C., Tozzini, C., Bonari, E., 2011. Impact on soil quality of a 10-
1021 year-old short-rotation coppice poplar stand compared with intensive agricultural and

1022 uncultivated systems in a Mediterranean area. Agriculture, Ecosystems and
1023 Environment 140, 245-254.
1024 Pellegrino, E., Turrini, A., Gamper, H.A., Cafà, G., Bonari, E., Young, J.P.W.,
1025 Giovannetti, M., 2012. Establishment, persistence and effectiveness of arbuscular
1026 mycorrhizal fungal inoculants in the field revealed using molecular genetic tracing and
1027 measurement of yield components. New Phytologist 194, 810-822.
1028 Phillips, J.M., Hayman, D.S., 1970. Improved procedures for clearing roots and staining
1029 parasitic and vesicular-arbuscular mycorrhizal fungi for rapid assessment of infection.
1030 Transactions of the British Mycological Society 55, 158-161.
1031 Picci, G., Nannipieri, P., 2002. Metodi di analisi microbiologica del suolo, Franco
1032 Angeli, Roma, Italy.
1033 Pistocchi, C., Silvestri, N., Rossetto, R., Sabbatini, T., Guidi, M., Baneschi, I., Bonari,
1034 E., Trevisan, D., 2012. A simple model to assess nitrogen and phosphorus
1035 contamination in ungauged surface drainage networks: application to the
1036 Massaciuccoli Lake Catchment, Italy. Journal of Environmental Quality 41, 544-553.
1037 Pulleman, M.M., Bouma, J., Van Essen, E.A., Meijles, E.W., 2000. Soil organic matter
1038 content as a function of different land use history. Soil Science Society of America
1039 Journal 64, 689-693.
1040 Redecker, D., Hijri, I., Wiemken, A., 2003. Molecular identification of arbuscular
1041 mycorrhizal fungi in roots: Perspectives and problems. Folia Geobotanica 38, 113-
1042 124.
1043 Richardson, A.D., Braswell, B.H., Hollinger, D.Y., Burman, P., Davidson, E.A., Evans,
1044 R.S., Flanagan, L.B., Munger, J.W., Savage, K., Urbanski, S.P., Wofsy, S.C., 2006.
1045 Comparing simple respiration models for eddy flux and dynamic chamber data.
1046 Agricultural and Forest Meteorology 141, 219-234.

1047 Rillig, M.C., Ramsey, P.W., Morris, S., Paul, E.A., 2003. Glomalin , an arbuscular-
1048 mycorrhizal fungal soil protein , responds to land-use change. Plant and Soil 253, 293-
1049 299.
1050 Rillig, M.C., Mummey, D.L., 2006. Mycorrhizas and soil structure. New Phytologist
1051 171, 41–53.
1052 Rowson, J.G., Worrall, F., Evans, M.G., Dixon, S.D., 2013. Predicting soil respiration
1053 from peatlands. The Science of the Total Environment 442, 397-404.
1054 Saitou, N., Nei, M., 1987. The neighbor-joining method: a new method for
1055 reconstructing phylogenetic trees. Molecular Biology and Evolution 4, 406-425.
1056 Schrier-Uijl, A.P., Kroon, P.S., Hensen, A., Leffelaar, P.A., Berendse, F., Veenendaal,
1057 E.M., 2010. Comparison of chamber and eddy covariance-based CO_2 and CH_4
1058 emission estimates in a heterogeneous grass ecosystem on peat. Agricultural and
1059 Forest Meteorology 150, 825-831.
1060 Schjonning, P., Elmholt, S., Christensen, B.T., 2004. Managing Soil Quality Challenges
1061 in Modern Agriculture, CABI publishing, Cambridge, MA.
1062 Schloter, M., Dilly, O., Munch, J., 2003. Indicators for evaluating soil quality.
1063 Agriculture, Ecosystems and Environment 98, 255-262.
1064 Schüβler, A., Schwarzott, D., Walker, C., 2001. A new fungal phylum, the
1065 Glomeromycota: phylogeny and evolution. Mycological Research 105, 1413-1421.
1066 Schußler, A., Walker, C., 2010. The Glomeromycota. A species list with new families
1067 and new genera. The Royal Botanic Garden Edinburgh, The Royal Botanic Garden
1068 Kew, Botanische Staatssammlung Munich, Oregon State University.
1069 Shrestha, R.K., Ladha, J.K., Gami, S.K., 2006. Total and organic soil carbon in
1070 cropping systems of Nepal. Nutrient Cycling in Agroecosystems 75, 257-269.

1071 Silvestri, N., Pistocchi, C., Sabbatini, T., Rossetto, R., Bonari, E., 2012. Diachronic
1072 analysis of farmers' strategies within a protected area of central Italy. Italian Journal of
1073 Agronomy, 7139-145.
1074 Silvola, J., Alm, J., Ahlholm, U., Nyhanen, H., Martikainen, P.J., 1996. The
1075 contribution of plant roots to CO_2 fluxes from organic soils. Biology and Fertility of
1076 Soils 23, 126-131.
1077 Simon, L., Lalonde, M., Bruns, T.D., 1992. Specific amplification of 18S fungal
1078 ribosomal genes from vesicular arbuscular endomycorrhizal fungi colonizing roots.
1079 Applied Environmental Microbiology 58, 291-295.
1080 Soil Survey Staff, 1975. Soil taxonomy: a basic system of soil classification for making
1081 and interpreting soil surveys. USDA-SCS Agric. Handb. 436. U.S. Gov. Print. Office,
1082 Washington, DC.
1083 Smith, P., Smith, J., Flynn, H., Killham, K., Rangel-Castro, I., Foereid, B., Aitkenhead,
1084 M., Chapman, S., Towers, W., Bell, J., Lumsdon, D., Milne, R., Thomson, A.,
1085 Simmons, I., Skiba, U., Reynolds, B., Evans, C., Frogbrook, Z., Bradley, I., Whitmore,
1086 A., Falloon, P., 2007. ECOSSE: Estimating Carbon in Organic Soils-Sequestration
1087 and Emissions: Final Report.
1088 Smith, S.E., Read, D.J., 2008. Mycorrhizal Symbiosis, 3rd ed, Academic Press,
1089 Amsterdam, NL.
1090 Stockinger, H., Krüger, M., Schüssler, A., 2010. DNA barcoding of arbuscular
1091 mycorrhizal fungi. New Phytologist 187, 461-474.
1092 Subke, J.A., Inglima, I., Francesca Cotrufo, M., 2006. Trends and methodological
1093 impacts in soil CO_2 efflux partitioning: A metaanalytical review. Global Change
1094 Biology 12, 921-943.

1095 Sutherland, W.J., Adams, W.M., Aronson, R.B., Aveling, R., Blackburn, T.M., Broad,
1096 S., Ceballos, G., Cote, I.M., Cowling, R.M., Da Fonseca, G.A.B., Dinerstein, E.,
1097 Ferraro, P.J.,Fleishman, E., Gascon, C., Hunter, M., Hutton, J., Kareiva, P., Kuria, A.,
1098 MacDonald, D.W., MacKinnon, K., Madgwick, F.J., Mascia, M.B., McNeely, J.,
1099 Milner-Gulland, E.J., Moon, S., Morley, C.G., Nelson, S., Osborn, D., Pai, M.,
1100 Parsons, E. C.M., Peck, L. S., Possingham, H., Prior, S.V., Pullin, A. S., Rands,
1101 M.R.W., Ranganathan, J., Redford, K.H., Rodriguez, J.P., Seymour, F., Sobel, J.,
1102 Sodhi, N.S., Stott, A., Vance-Borland, K., Watkinson, A.R., 2009. One Hundred
1103 questions of importance to the conservation of global biological diversity.
1104 Conservation Biology 23, 557-567.
1105 Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S. 2011. MEGA 5:
1106 Molecular evolutionary genetics analysis using maximum likelihood, evolutionary
1107 distance, and maximum parsimony methods. Molecular Biology and Evolution 28:
1108 2731-2739.
1109 Tedeschi, V., Rey, A., Manca, G., Valentini, R., Jarvis, P.G., Borghetti, M., 2006. Soil
1110 respiration in a Mediterranean oak forest at different developmental stages after
1111 coppicing. Global Change Biology 12, 110-121.
1112 ter Braak, C.J.F., Šmilauer, P., 2002. CANOCO Reference Manual and CanoDraw for
1113 Windows User's guide: Software for Canonical Community Ordination (version 4.5),
1114 Microcomputer Power, Ithaca, USA.
1115 Thomas, G.W., 1982. Exchangeable cations. In: Page, A.L., Miller, R.H., Keeney, D.R.
1116 (Eds.), Methods of Soil Analysis, Part 2, Chemical and Microbiological Properties,
1117 Agronomy Monograph (second ed.), vol. 9, American Society of Agronomy, Madison,
1118 WI (1982), pp. 159-165.

1119 Tiemeyer, B., Frings, J., Kahle, P., Kohne, S., Lennartz, B., 2007. A comprehensive
1120 study of nutrient losses, soil properties and groundwater concentrations in a degraded
1121 peatland used as an intensive meadow - Implications for re-wetting. Journal of
1122 Hydrology, 345 80-101.
1123 Tilman, D., Cassman, K.G., Matson, P.A., Naylor, R., Polasky, S., 2002. Agricultural
1124 sustainability and intensive production practices. Nature 418, 671-677.
1125 van Tuinen, D., Jacquot, E., Zhao, B., Gollotte, A., Gianinazzi-Pearson, V., 1998.
1126 Characterization of root colonization profiles by a microcosm community of
1127 arbuscular mycorrhizal fungi using 25s rDNA-targeted nested PCR. Molecular
1128 Ecology 7, 879-887.
1129 Vandenkoornhuyse, P., Husband, R., Daniell, T.J., Watson, I.J., Duck, J.M., Fitter, A.
1130 H., Young, J.P.W., 2002. Arbuscular mycorrhizal community composition associated
1131 with two plant species in a grassland ecosystem. Molecular Ecology 11, 1555-1564.
1132 van't Hoff, J. H., 1884. Etudes de dynamique chimique (Studies of chemical dynamics).
1133 Frederik Muller and Co., Amsterdam, NL.
1134 Verbruggen, E., Van Der Heijden, M.G.A., Weedon, J.T., Kowalchuk, G.A., Röling,
1135 W.F.M., 2012. Community assembly, species richness and nestedness of arbuscular
1136 mycorrhizal fungi in agricultural soils. Molecular Ecology 21, 2341-2353.
1137 Verhoeven, J.T.A., Setter, T.L., 2010. Agricultural use of wetlands: opportunities and
1138 limitations. Annals of Botany 105, 155-163.
1139 Violante, P., 2000. Metodi di analisi chimica del suolo. Franco Angeli, Milano, IT.
1140 Wang, Y., Amundson, R., Niu X.-F., 2000. Seasonal and altitudinal variation in
1141 decomposition of soil organic matter inferred from radiocarbon measurements of soil
1142 CO_2 flux. Global Biogeochemical Cycles 14, 199-211.

1143 Wirsel, S.G.R., 2004. Homogenous stands of a wetland grass harbour diverse consortia
1144 of arbuscular mycorrhizal fungi. FEMS microbiology ecology 48, 129-138.
1145 Wolfe, B.E., Mummey, D.L., Rillig, M.C., Klironomos, J.N., 2007. Small-scale spatial
1146 heterogeneity of arbuscular mycorrhizal fungal abundance and community
1147 composition in a wetland plant community. Mycorrhiza 17, 175-183.
1148 Wunderlich, S., Borken, W., 2012. Partitioning of soil CO_2 efflux in un-manipulated
1149 and experimentally flooded plots of a temperate fen. Biogeosciences 9, 3477-3489.
1150

1151 **Captions**

1152

1153 **Figure 1**. Neighbor-Joining (NJ) tree (Saitou and Nei, 1987) of arbuscular mycorrhizal fungal
1154 sequences derived from roots and soil (shown as triangle and circle, respectively) of a conventional
1155 continuous maize system (ConvMaize) and an ex-arable cropping land, being uncultivated for 15
1156 years (Aband) (red/filled and green/open symbols, respectively). In the ConvMaize roots were
1157 represented by maize, whereas in the Aband by native plant species. The analysis is based on partial
1158 nuclear small subunit ribosomal RNA gene sequences (SSU ≈ 550 bp; NS31/AM1 fragment), and
1159 the tree is rooted with a reference sequence of *Corallochytrium limacisporum* (L42528). Clades of
1160 sequences were affiliated to *Funneliformis mosseae* (8), *Rhizophagus manihotis* (4), *Rhizophagus*
1161 *irregularis* (5), *Sclerocystis sinuosa* (3), *Scutellospora dipurpurescens* (10) and to additional taxa,
1162 such as *Glomus* spp. (1, 2, 6, 7, 9), or uncultured Glomeromycota (11). Pies indicate the proportions
1163 of sequences into the two land uses (ConvMaize, red; Aband, green) and matrixes (roots, light
1164 color; soil, dark color). The tree is drawn to scale, with branch lengths in the same units as those of
1165 the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were
1166 computed using the Kimura 2-parameter method (Kimura, 1980) and are in the units of the number
1167 of base substitutions per site. Bootstrapping is based on 1000 replicates (Felsenstein, 1985). The
1168 analysis involved 195 nucleotide sequences. Evolutionary analyses were conducted in MEGA5
1169 (Tamura et al., 2011). Sequences obtained in the present study are shown by symbols and their
1170 accession numbers are shown in Fig. S2.

1171

1172 **Figure 2.** Arbuscular mycorrhizal fungal (AMF) community diversity showed as relative
1173 abundances of molecular operational taxonomic units (MOTUs) in the soil and within the roots of
1174 native plant species and maize of a conventional continuous maize system (ConvMaize) and an ex-
1175 arable cropping land, being uncultivated for 15 years (Aband), respectively. AMF diversity is
1176 represented by the following clades: *Funneliformis mosseae* (Fun1_AMASS); *Glomus* spp. (from

1177 Glo1_AMASS to Glo5_AMASS); *Rhizophagus manihotis* (Rhizo1_AMASS); *Rhizophagus*
1178 *irregularis* (Rhizo2_AMASS); *Sclerocystis sinuosa* (Sclero1_AMASS); *Scutellospora*
1179 *dipurpurescens* (Scut1_AMASS); uncultured Glomeromycota (Uncult1_AMASS). Numbers in
1180 brackets are referred to the clades shown in Fig. 1 and Table S1.
1181
1182 **Figure 3.** Redundancy Analysis (RDA) biplot based on the soil relative abundances of arbuscular
1183 mycorrhizal fungal (AMF) molecular operational taxonomic units (MOTUs) (*Funneliformis*
1184 *mosseae*, Fun1_AMASS; *Glomus* spp., from Glo1_AMASS to Glo5_AMASS; *Rhizophagus*
1185 *manihotis*, Rhizo1_AMASS; *Rhizophagus irregularis*, Rhizo2_AMASS; *Sclerocystis sinuosa*,
1186 Sclero1_AMASS; *Scutellospora dipurpurescens*, Scut1_AMASS; uncultured Glomeromycota,
1187 Uncult1_AMASS), used as response variable, and land uses [a conventional continuous maize
1188 system (ConvMaize) and an ex-arable cropping land, being uncultivated for 15 years (Aband)] (a).
1189 RDA plots of the AM fungal MOTUs, used as response variables, and matrixes (soil and roots),
1190 used as environmental variables in the ConvMaize (b) and the Aband (c). RDA biplot based on soil
1191 physico-chemical parameters (pH; electrical conductivity, EC; exchangeable potassium, K_{exch}; total
1192 nitrogen, N_{tot}; ammonium; nitrates; soil organic matter, SOM; carbon/nitrogen ratio, C/N; total
1193 phosphorus, P_{tot}; available phosphorus, P_{avail}; organic phosphorus, P_{org}); CO_2 fluxes (total soil
1194 respiration, Rs; heterotrophic respiration, Rh; autotrophic respiration, Ra); root measurements (total
1195 root dry weight, total root DW; AMF root colonization, AMF coloniz); AMF diversity (AMF
1196 MOTU richness of roots and soil, MOTUr and MOTUs, respectively; and Shannon index (*H'*) of
1197 roots and soil, *H*' roots and *H*' soil, respectively), used as response variables and the land uses,
1198 ConvMaize and Aband, used as environmental variables (d). The 1st and 2nd axes accounted for
1199 83.5%, 89.7%, 89.2% and 69.5% of the total variance explained by all canonical axes for a, b, c and
1200 d, respectively. The Monte Carlo permutational tests showed that AM fungal assemblages were
1201 statistically different between the soil of the ConvMaize and of the Aband and between soil and
1202 roots of both ConvMaize and Aband (P = 0.002) (a, b and c) and that such land use were also

1203 statistically different considering soil physico-chemical, CO_2 fluxes, root measurements and AMF
1204 diversity ($P = 0.002$) (d).
1205
1206 **Figure 4.** Daily maximum, mean and minimum temperatures (°C) and total rainfall (mm) over the
1207 monitoring campaign (a). Mean soil temperature (°C) (shown as circle) and moisture (%; v:v)
1208 (shown as square) of a conventional continuous maize system (filled symbols; ConvMaize) and an
1209 ex-arable cropping land, being uncultivated for 15 years (open symbols; Aband) (b). Soil
1210 temperature and moisture were measured outside the six blocks (see Fig. S1) used during the CO_2
1211 flux monitoring campaign. Three components of the soil CO_2 fluxes, total soil respiration (Rs;
1212 shown as triangle (c), heterotrophic respiration (Rh; shown as diamond) (d) were measured in the
1213 two different land uses ConvMaize *vs* Aband. The autotrophic respiration (Ra; shown as circle) was
1214 calculated as difference between Rs and Rh. The monitoring campaign ranges from the 14^{th} of May
1215 to the 13^{th} of August 2012 with one or two soil CO_2 flux measurements per week (n = 21). Values
1216 are means ± SE of three replicate plots for each treatment (land use). For each sampling date and
1217 soil CO_2 flux component, statistically significant differences between land uses are shown by
1218 different letters according to the *t*-test or the Mann-Whitney non-parametric test ($P < 0.05$). Open
1219 and filled symbols represent the Aband and the ConvMaize, respectively.
1220
1221 **Figure 5.** Cumulated of three components of the soil CO_2 fluxes: total soil respiration, R_s (shown as
1222 triangle); heterotrophic respiration, R_h (shown as diamond) and autotrophic respiration, R_a (shown
1223 as circle). The measurements (n=21) were recorded from May to August 2012 in a conventional
1224 continuous maize (ConvMaize; filled symbols) *vs* an ex-arable cropping land, being uncultivated
1225 for 15 years (Aband; open symbols). Values are means of three replicate plots for each treatment
1226 (management). Statistically significant differences between managements are shown by different
1227 letters according to the *t*-test ($P < 0.05$).
1228

Table 1

Texture (0-30 cm depth) of a conventional continuous maize system (ConvMaize) and of an ex-arable cropping land, being uncultivated for 15 years (Aband). Both sites are located in a Mediterranean peatland of the Regional Park of San Rossore-Migliarino-Massaciuccoli, Pisa, Italy.

Parameters	ConvMaize	Aband
clay (%)	23.4 ± 8.5[a]	26.5 ± 5.0
silt (%)	24.0 ± 1.8	26.0 ± 3.9
sand (%)	52.6 ± 10.0	47.4 ± 8.6

[a]Values are means ± SE of three plots for each treatment. Values are not statistically different according to the *t*-test.

Table 2

Soil physico-chemical parameters (0-30 cm depth) of a conventional continuous maize system (ConvMaize) and of an ex-arable cropping land, being uncultivated for 15 years (Aband).

Physico-chemical parameters	ConvMaize	Aband
pH[a]	4.6[b]	5.3
EC (mS cm^{-1})	1.8	0.9
K_{exch} (mg kg^{-1})	397.0	560.0
N_{tot} (g kg^{-1})	13.0	11.8
NO_3^- (mg kg^{-1})	42.3	59.0
NH_4^+ (mg kg^{-1})	148.0 b	56.3 a
SOM (%)	25.7	28.3
C/N	11.5	13.7
P_{tot} (mg kg^{-1})	2709.0	2846.7
P_{avail} (mg kg^{-1})	70.3	76.3
P_{org} (mg kg^{-1})	2153.3	2054.7

[a]EC: electrical conductivity; K_{exch}: exchangeable potassium; N_{tot}: total nitrogen; NO_3^-: nitrate; NH_4^+: ammonium SOM: soil organic matter; C/N: carbon/nitrogen ratio; P_{tot}: total phosphorus; P_{avail}: available phosphorus; P_{org}: organic phosphorus; [b]Values are means ± SE of three plots for each treatment. Values in the same row followed by different letters are statistically different between management according to the *t*-test ($P < 0.05$).

Table 3

Root dry weight and arbuscular mycorrhizal (AM) fungal root colonization of maize and of the natural succession vegetation[a] occurring in a conventional continuous maize system (ConvMaize) and in an ex-arable cropping land (Aband), respectively. The Aband was uncultivated for 15 years.

Parameters	ConvMaize	Aband
Root dry weight (mg g^{-1} soil)	0.55[b]	1.08
AM fungal root colonization (%)	22.2 a	33.2 b

[a]Natural succession vegetation was composed by Amarantaceae (*Amaranthus retroflexus* L.); Apiaceae (*Biphora* sp.); Asteraceae (*Arctium lappa* L., *Bidens* sp., *Xanthium* sp., *Artemisia* sp.); Cannabiaceeae (*Humulus lupulus* L.); Cariophillaceae (*Silene alba* L.); Chenopdiaceae *(Atriplex* sp.); Convolvulaceae (*Calistegia* sp.); Lythraceae (*Lythrum salicaria* L.); Malvaceae (*Abutilon theophrasti* L.,); Phytolaccaceae (*Phytolacca americana* L.); Poaceae (*Phragmites australis* L., *Echinochloa crus-galli* L.); Polygonaceae (*Rumex crispus* L.); Rubiaceae *(Galium* sp.); Scrophulariaceae (*Linaria* sp.); Solanaceae (*Datura stramonium* L.); Thyphaceae (*Thypha latifolia* L.); [b] Values are means of three plots for each treatment. Values in the same row followed by different letters are statistically different between managements according to the *t*-test ($P < 0.05$).

Table 4. Arbuscular mycorrhizal (AM) fungal molecular operational taxonomic unit (MOTU) richness and Shannon (*H'*) index within the maize roots and the soil of a conventional continuous maize system (ConvMaize) and within the native plant species roots and the soil of an ex-arable cropping land, being uncultivated for 15 years (Aband).

	Roots		Soil	
Parameter	ConvMaize	Aband	ConvMaize	Aband
MOTU richness	1.7[a] A	4.3	6.0 b B	3.3 a
Shannon index (*H'*)	0.4 A	1.1	1.5 b B	1.0 a

[a]Values in the same row followed by different small letters are statistically different between land uses, according to the *t*-test ($P < 0.05$).

Table 5

Comparison of three models of CO_2 flux response to air temperature using different model selection criteria: the Akaike Information Criterion (AIC), the Root Mean Squared Error (RMSE) and the Adjusted R-square value (Rsd.ad). The measurements (n = 21) were recorded from May to August 2012 in a conventional continuous maize system (ConvMaize) and in an ex-arable cropping land, being uncultivated for 15 years (Aband).

Criteria	Q10 [a]		LT		RothC	
Rs	ConvMaize	Aband	ConvMaize	Aband	ConvMaize	Aband
AIC	472.9 [b]	317.9	469.9	317.2	531.0	365.3
RSME	9.8	9.1	9.6	9.0	15.9	16.2
Rsq.ad	0.6	0.5	0.7	0.5	0.8	0.7
Rh						
AIC	331.7	296.6	326.4	296.6	384.8	334.5
RSME	3.2	7.1	3.1	7.1	5.0	11.3
Rsq.ad	0.8	0.3	0.8	0.3	0.8	0.7

[a] Q10: Van't Hoff's Q_{10} model; LT: Lloyd and Taylor model; RothC: simplified Rothamsted Carbon Model; [b] Fit model values.

Table 6

Coefficient of variation of the total soil respiration (Rs) and of the heterotrophic (Rh) and autotrophic respiration (Ra) of two land uses [a conventional continuous maize system (ConvMaize) *vs* an ex-arable cropping land, being uncultivated for 15 years (Aband)] over the monitoring campaign.

Parameter	Coefficient of variation	
	ConvMaize	Aband
CV_Rs (%)	32.0[a] b	23.3 a
CV_Rh (%)	28.9 b	19.1 a
CV_Ra (%)	36.7	39.3

[a]Values in the same row followed by different letters are statistically different between land uses according to the Mann-Whitney nonparametric test ($P < 0.05$).

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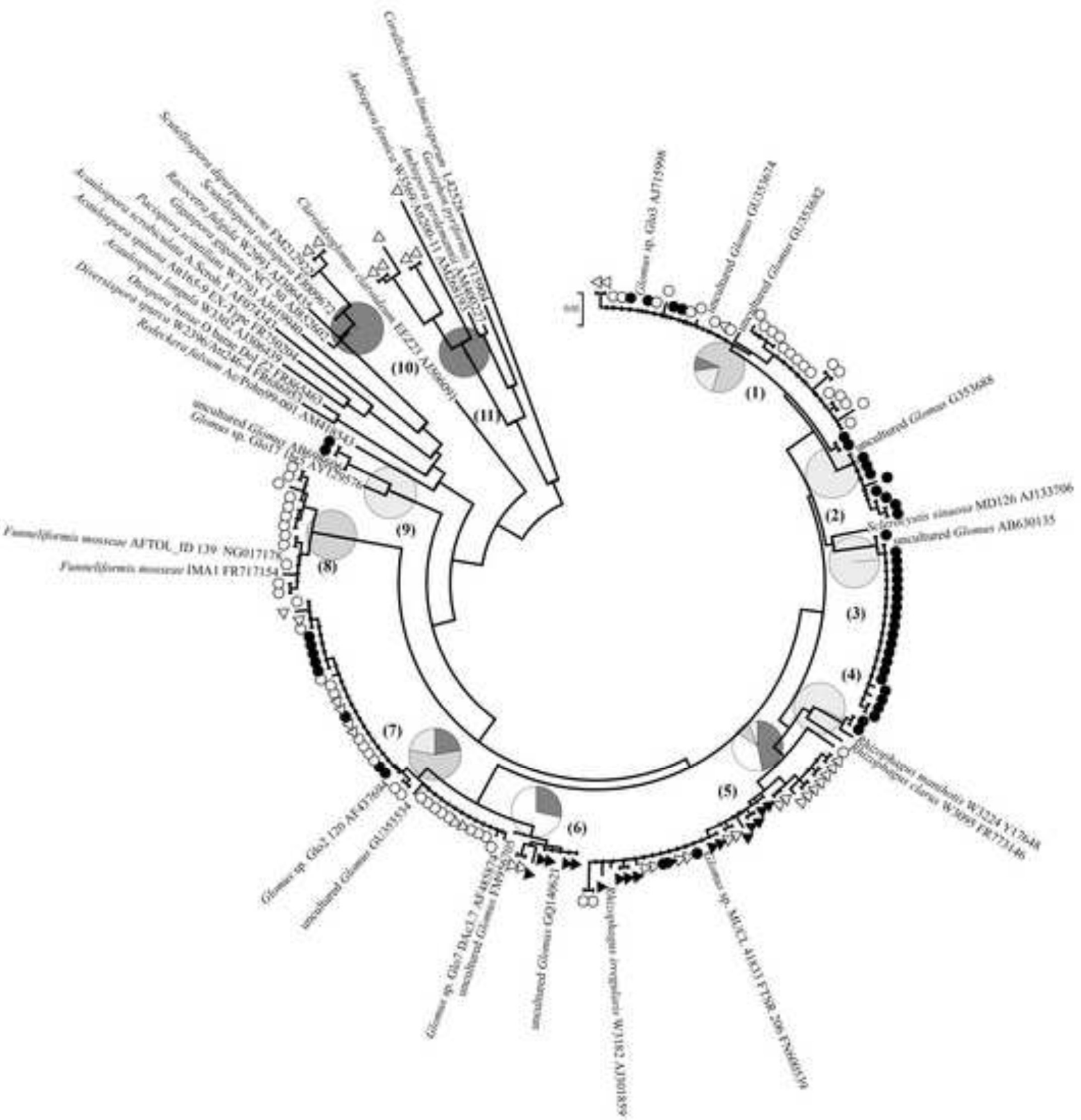

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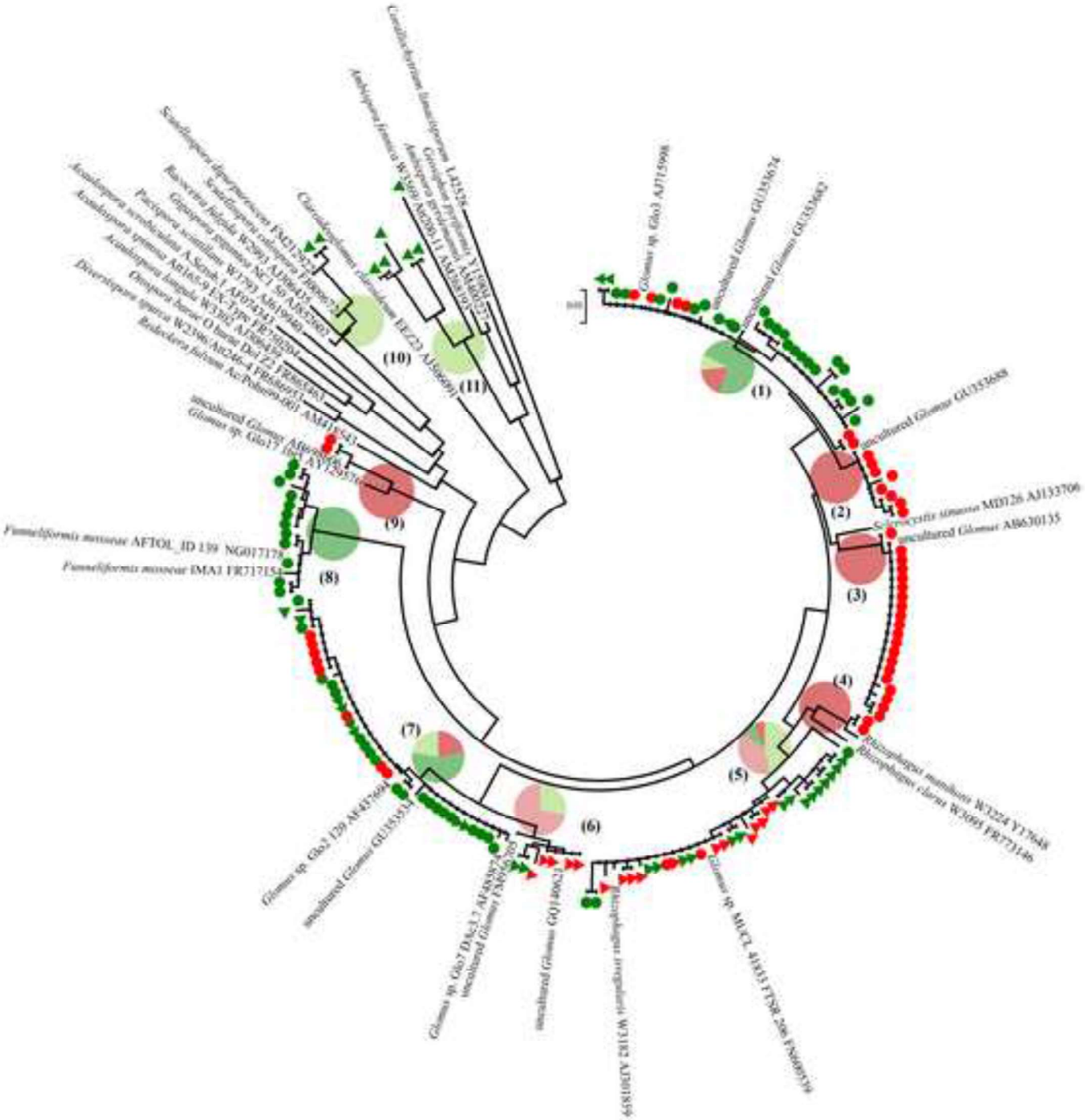

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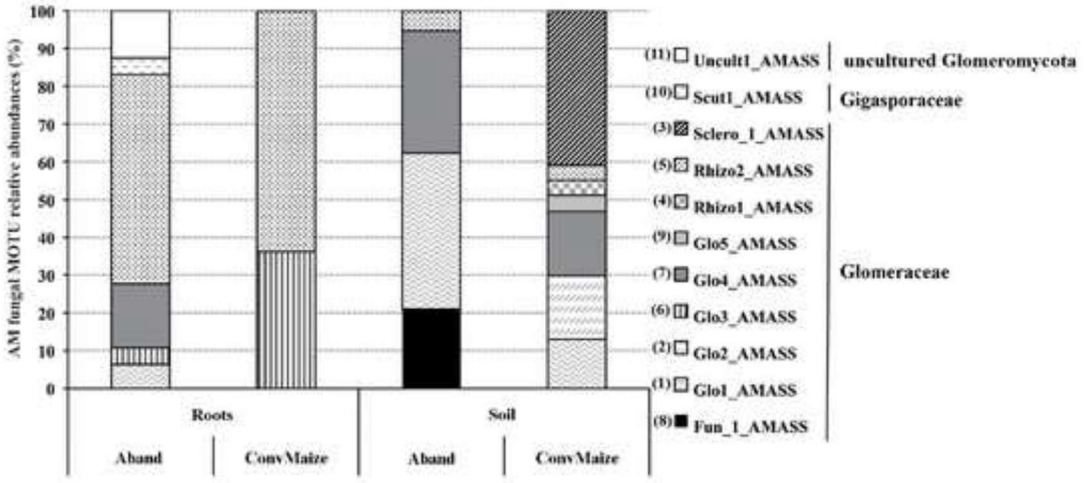

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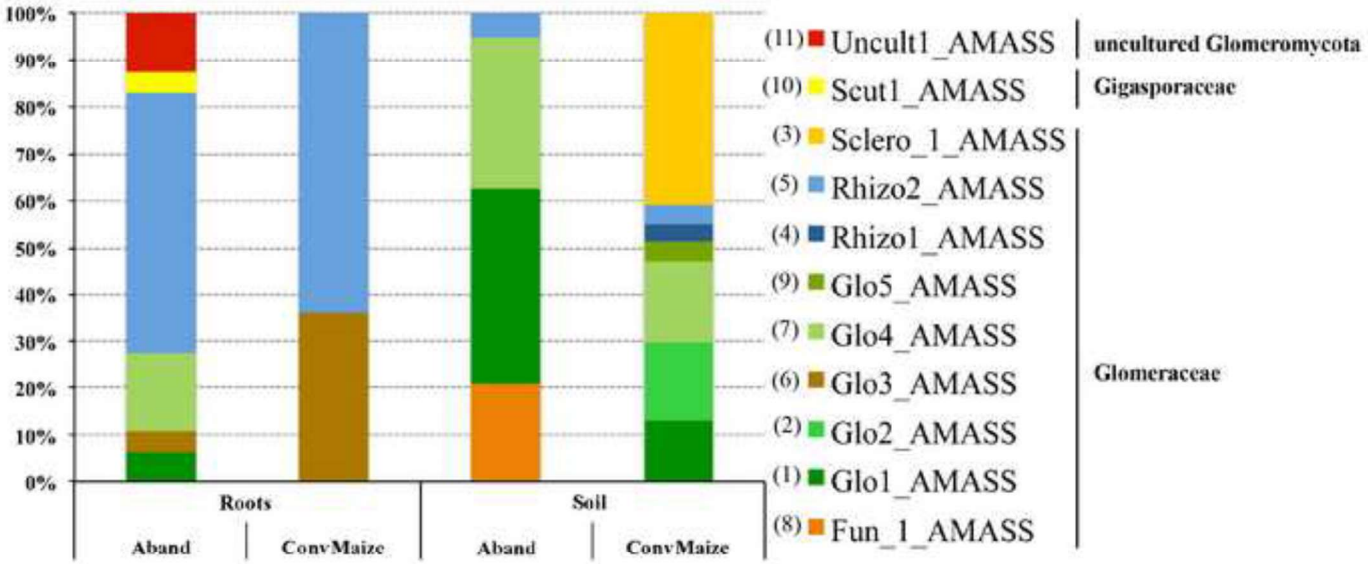

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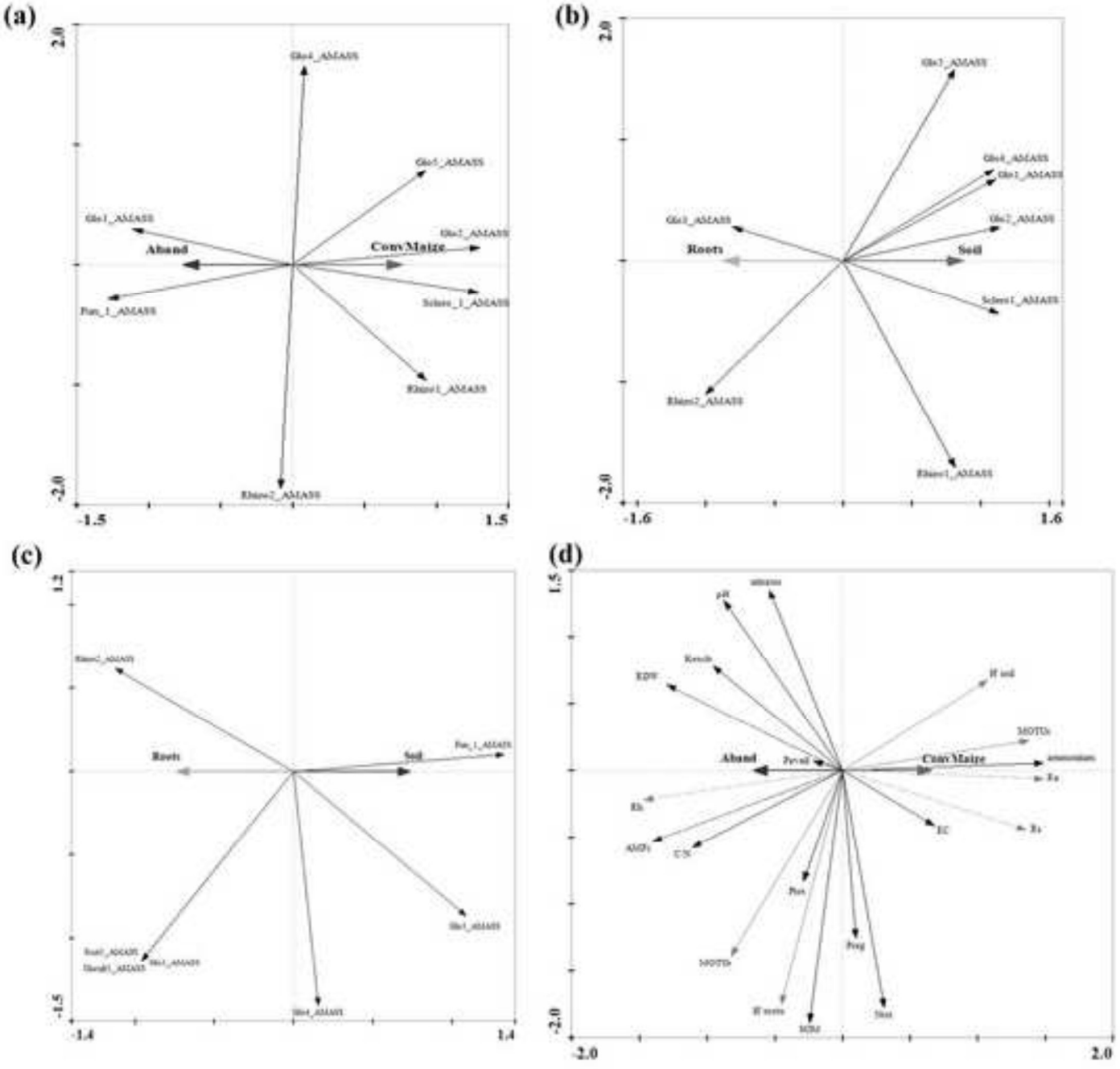

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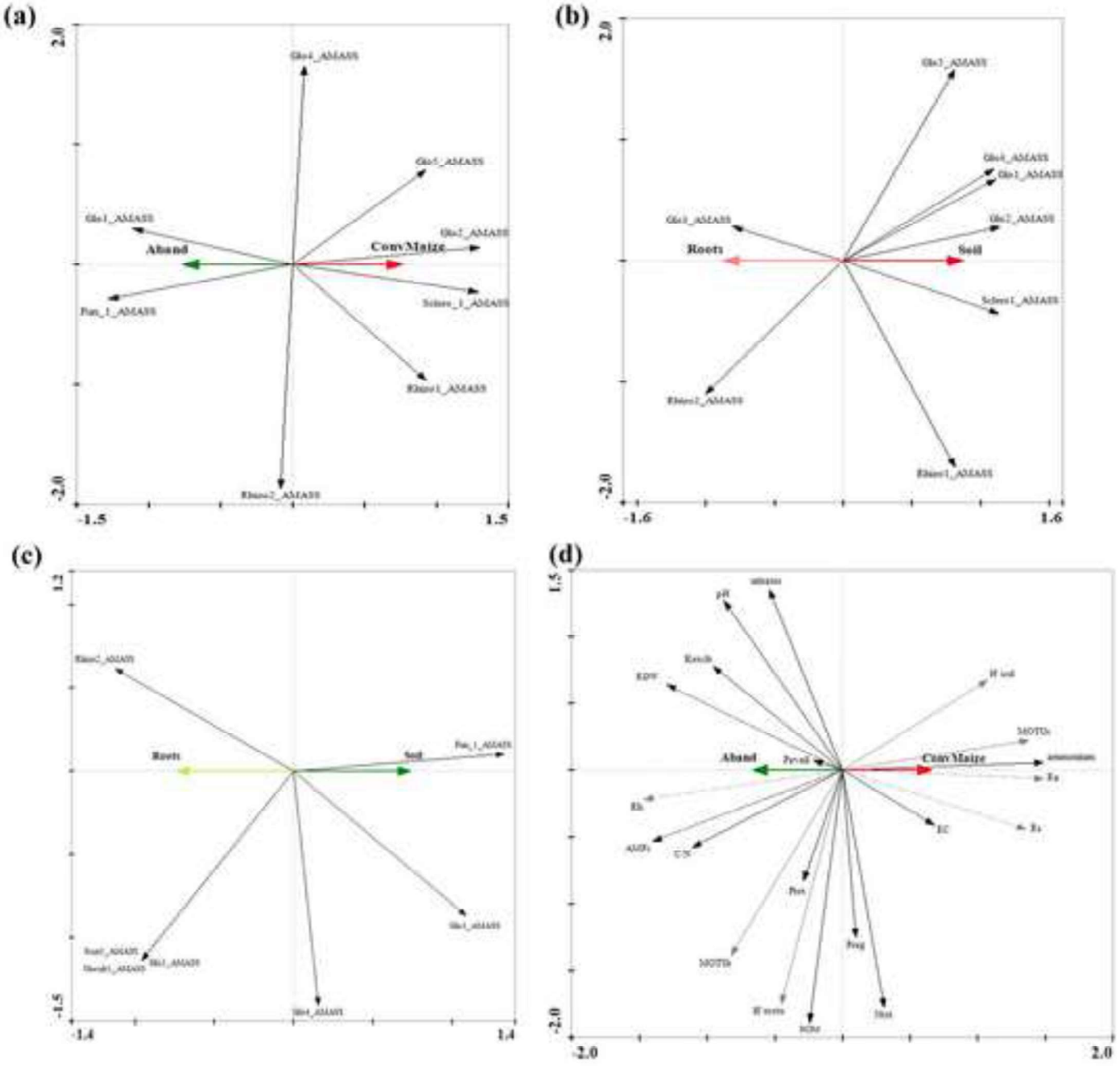

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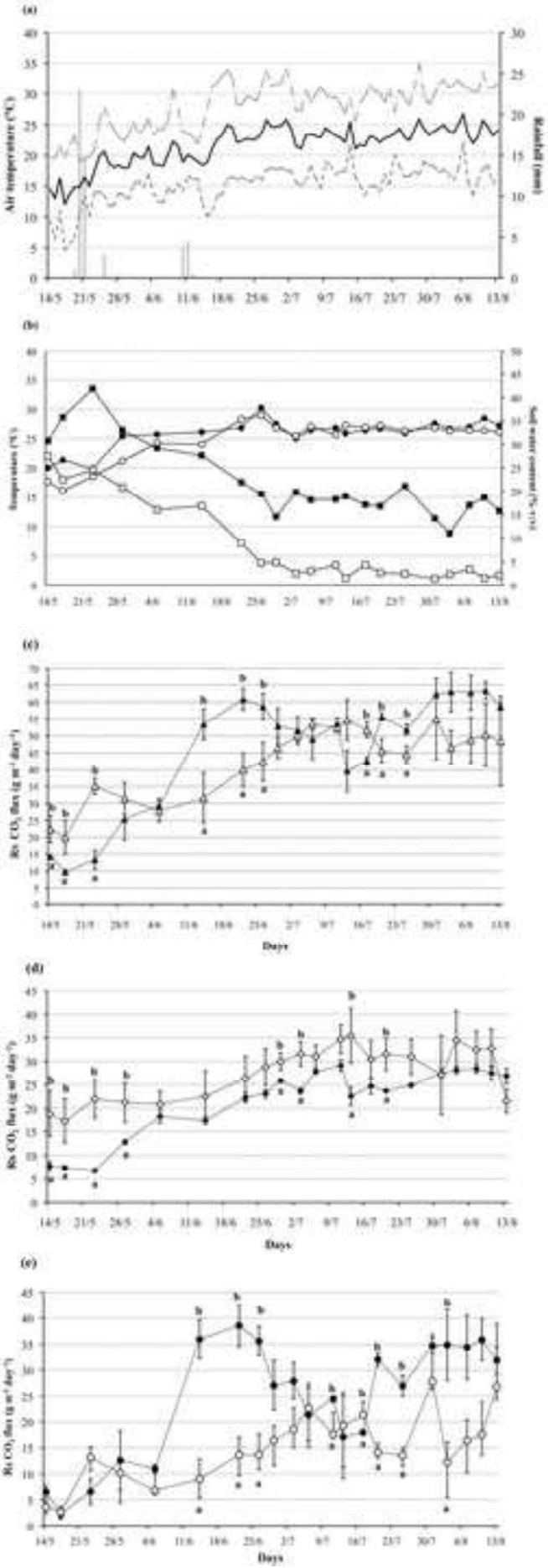

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