



Contents lists available at ScienceDirect

Journal of the Saudi Society of Agricultural Sciences

journal homepage: www.sciencedirect.com

Cultivable soil fungi community response to agricultural management and tillage system on temperate soil

M.V. Moreno ^{a,*}, C. Casas ^{b,c}, F. Biganzoli ^d, L. Manso ^e, L.B. Silvestro ^{a,*}, E. Moreira ^{a,f}, S.A. Stenglein ^a^a Laboratorio de Biología Funcional y Biotecnología (BIOLAB-INBIOTEC-CONICET-CICBA), Facultad de Agronomía de Azul, Universidad Nacional del Centro de la, Provincia de Buenos Aires, Argentina^b Universidad de Buenos Aires, Facultad de Agronomía, Departamento de Recursos Naturales y Ambiente, Cátedra de Edafología, Buenos Aires, Argentina^c IFEVA, Universidad de Buenos Aires, CONICET, Facultad de Agronomía, Buenos Aires, Argentina^d Departamento de Métodos Cuantitativos y Sistemas de Información, Facultad de Agronomía, Universidad de Buenos Aires, Argentina^e Estación Experimental Barrow-INTA, Tres Arroyos, Provincia de Buenos Aires, Argentina^f Instituto Antártico Argentino, San Martín, Prov. de Buenos Aires, Argentina

ARTICLE INFO

Article history:

Received 2 October 2020

Revised 4 December 2020

Accepted 22 January 2021

Available online 6 February 2021

Keywords:

Fungi

Diversity

Tillage systems

Intense agriculture

Pastures

ABSTRACT

In agricultural soils, fungi constitute most of the total microbial biomass in the environment contributing with more than 50% of the soil biomass. The fungi should be considered as a link in the production not only by their attributes but also for their potential pathogenicity on crops chains. We aim to determine in what extent the combination of management styles and tillage systems control specific cultivable soil fungal community structure in temperate fertile Petrocalcic Argiudoll soil in a field experiment. We measured soil fungal richness, abundance and diversity along a one-year experiment (2009–2010). The plots were subjected to different tillage systems (conventional vs. zero) combined with different agricultural management histories (pasture/agriculture rotation vs. intensive agriculture). The measures were performed every three months along a year in three replicated plots. Rotation with pastures and zero tillage stimulated the saprophytic soil fungi community in detriment of pathogens. The clearest dissimilarity was given by the seasons. The results obtained from assay suggested that the seasons effect was strongest that the management or tillage on the soil fungal community.

© 2021 The Authors. Production and hosting by Elsevier B.V. on behalf of King Saud University. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

1. Introduction

One of the major causes of soil biodiversity loss and degradation is agricultural intensification (Foley et al. 2011; Ring et al. 2010). Consequently, one of the biggest challenges today is to satisfy the growing demand for goods, food and energy without degrading the environment (MEA, 2005). Changes in soil microbial community structure and its activity have direct consequences on the ecosystem functions since these communities are responsible for

fundamental processes such as nutrient cycling and carbon sequestration (Lehmann and Rillig 2015; Stockmann et al. 2013). In this context, it is necessary to develop alternative management of resources that meet the needs of both, food and energy production along with environmental (soil) conservation (Steffan-Dewenter et al. 2007).

Crop production has generated large impact in soil quality, the tillage management and crop rotation, it is one of the main responsible for soil degradation (Kladivko, 2001). Conventional tillage has been used as a management system which helps in weed and pest control and the zero tillage implies critical changes at ground level, such as stubble cover and no soil disturbance. These processes in the long term required of nitrogen and other nutrients availability, as well as carbon dioxide release. In the long term, this system led to critical reduction in crop yields mainly due to low values of nutrients availability in soil and it can affect the integrity of soil especially, that of soils of low stability (Forján and Manso, 2012).

The combination of pasture and crop cycles has been suggested as a suitable alternative to mitigate these soil degrading effects (Forján and Manso 2012). For instance, inclusion of pastures in

* Corresponding authors at: Laboratorio de Biología Funcional y Biotecnología (BIOLAB), Facultad de Agronomía de Azul, Universidad Nacional del Centro de la Provincia de Buenos Aires, República de Italia N° 780, Azul CP 7300, Prov. Buenos Aires, Argentina.

E-mail address: vmoreno@faa.unicen.edu.ar (M.V. Moreno).

Peer review under responsibility of King Saud University.



Production and hosting by Elsevier

field rotation increased soil organic matter, microbial and soil fauna biomass (Plaza Bonilla et al., 2016; Silvestro et al. 2017; 2018). As a clear outcome, this management systems generate different suit of soil conditions which impact on soil functioning and the ecosystem services it provides.

In agricultural soil, fungi are a major component of microbial biomass and their physiological activity is a critical role in crop production and soil functioning (Kalbitz et al. 2000). Apart from being responsible for complex organic molecules degradation which contributes to nutrients biochemical cycling (Klein and Paschke, 2004), soil fungi can be pathogenic or beneficial for plant and control insect pests. In addition, extra-radical hyphae contribute to stable aggregates formations (Miller and Jastrow, 2000) and soil fertility. At the same time, fungal activity may be controlled by agricultural management as well as crop rotation as both critically modify soil physical and chemical conditions. In this sense, the design of sustainable cropping system should consider the impact of management practices on soil fungal community.

Intensive crop production reduced soil fungal species richness which in turn, may trigger negative effects on nutrients availability for crops (Dominguez et al. 2009; Van Der Wal et al. 2006). Instead, including pastures in crop rotation increased soil organic carbon and therefore it might developed more beneficial microhabitats and this can be detected in the diversity of the fungal community. In turn, this less intensive management improved physical and chemical properties (Studdert et al., 1997) which improve soil fertility and crop potential productivity (Forján and Manso, 2012).

While several previous works have focused on tillage system or agriculture management effects on fungi community structure and its activity (Madejón et al., 2009; Silvestro et al., 2018), so far little information is available about the combined effects of the above two factors, especially based on a long-term agricultural scheme. We hypothesized that agricultural management and tillage system drive soil fungal abundance and community structure in short time. We predict that both, intensive management and conventional tillage interact reducing soil fungal abundance and change the community structure independently of time assay. The main objective was to evaluate the short-term response of the soil fungal community to different tillage in soils with different management history.

2. Materials and methods

2.1. Experimental design

The experiment was conducted under natural environmental conditions of light and temperature at Barrow Experimental Station of the National Institute of Agricultural Technology (38° 19' 25" S, 60° 14' 33" W, Tres Arroyos, Buenos Aires, Argentina) (Appendix A). The soil corresponded to a Petrocalcic Argiudoll, Series Tres Arroyos, 50 cm depth, clay loam texture (Soil Survey Staff, 2014) and slightly acid pH (6.4; 1:2.5 soil:water) (USDA, 2006). In this area, mean annual temperature is 14.9 °C (minimum and maximum temperatures reach 7.4 °C and 20.4 °C, respectively) and mean annual precipitation is 750 mm (Fig. 1).

We combined agricultural management and tillage system (two levels each) in a randomized strip-plot design to generate four different treatments in three blocks (Khuel 2001). Treatments were applied in 450 m² plots (15 × 30 m). The land-use history or agricultural management (M) as the row factor (two levels) and the tillage system (TS) as the column factor (two levels) (Gómez and Gómez, 1984). The agricultural management (row factor) were IM: intensive management response to a long and intensive agricultural management (12 years) without pastures. RM: Rotation

management: included each 4 years agricultural cycles with pasture *Medicago sativa* L. and *Dactylis glomerata* L. (alfalfa/orchard-grass). The column factor was the tillage systems (T) included conventional tillage (CT) which comprised mouldboard ploughing, disking (20 cm) and burying of crop residues (Agricultural Experimental Machinery Crucianelli[®] were used) and, zero tillage (ZT, No-till farming or direct drilling) which comprised cultivation without disturbing, the coverage with stubble or crop residues and the chemical weed control during fallow. The sequence of crops includes a two years cycle with sunflower (*Helianthus annuus* L.) in summer, wheat (*Triticum aestivum* L.) in winter and maize (*Zea mays* L.) following summer in both managements. The soil properties and the practice recommended in this area for cereal crops as application of herbicides, pesticides and simultaneous application of inorganic fertilizers were detailed in Tables 1a and 1b.

Data were collected every three months during a year, related to contrasting crop phenology: summer (postharvest of wheat; December 2009 and 2010), autumn (postharvest of summer crops; April 2010) and winter (tillering of wheat according Zadoks et al. (1974) stages; August 2010). Topsoil samples were randomly collected through 25 perforations in each plot by using a hydraulic borer and sealed in plastic freezer bags (0–15 cm depth, roughly 2 kg).

We calculated the cumulative precipitation during the previous month to each sampling date as a covariate to account for seasonal environmental variation. We used daily data provided by the Agrometeorological Station located at the same Barrow Experimental Station (<http://siga2.inta.gov.ar/en/datoshistoricos/>).

2.2. Soil fungal community

To characterize active fungal mycelium in soil community, individual soil samples (100 g) were washed according to Parkinson and Williams (1961) modified by Cabello and Arambarri (2002). Each soil sample (100 g) was washed with sterile water through a sieve series (located in a vertical position: one above 2000 μ (mesh N°10), 1000 μ (mesh N° 18), another below 500 μ aperture (mesh N° 35) and finally a 250 μ sieve (mesh N° 60)) the soil particles retained in the last (0.25 mm) were washed (20 times for 2 min) and transferred to a sterile filter paper in a Petri dish and dried for one day. Fifty particles were taken from each soil sample previously retained in a 0.25 mm mesh sieve (in total 2400 soil particles). Particles were placed into Petri dishes (50 particles per plate) containing potato dextrose agar (PDA, Lab. Britania SA) amended with 250 mg chloramphenicol L⁻¹ to suppress bacterial growth. Plates were incubated during five days in a controlled chamber at 25 ± 2 °C under 12-h light/dark conditions. The isolates obtained were subcultures in new Petri dishes containing the necessary media for identification according the specific manuals (Barnett and Hunter, 1998; Barron, 1968; Cannon and Kirk, 2007; Charmichael et al., 1980; Domsch et al. 1980; Ellis, 1971, 1976; Kirk, 2001; Kubicek and Harman, 2002; Leslie and Summerell, 2006; Nelson et al. 1983; Samson and Vann Reenen-Hoekstra, 1988; Simmons, 2007; Watanabe, 2002), and the current names were confirmed in Index Fungorum <http://www.indexfungorum.org/Names/Names.asp>.

Data obtained was then useful to characterize fungal community according to the species richness (S) (as the raw number of taxa of each soil sample) and to the relative abundance Ra (number of isolates of each genus/ total number of isolates obtained) × 100, according to Marasas et al. (1988). The condition of saprotroph and pathogen was based on the existing literature for each identified species.

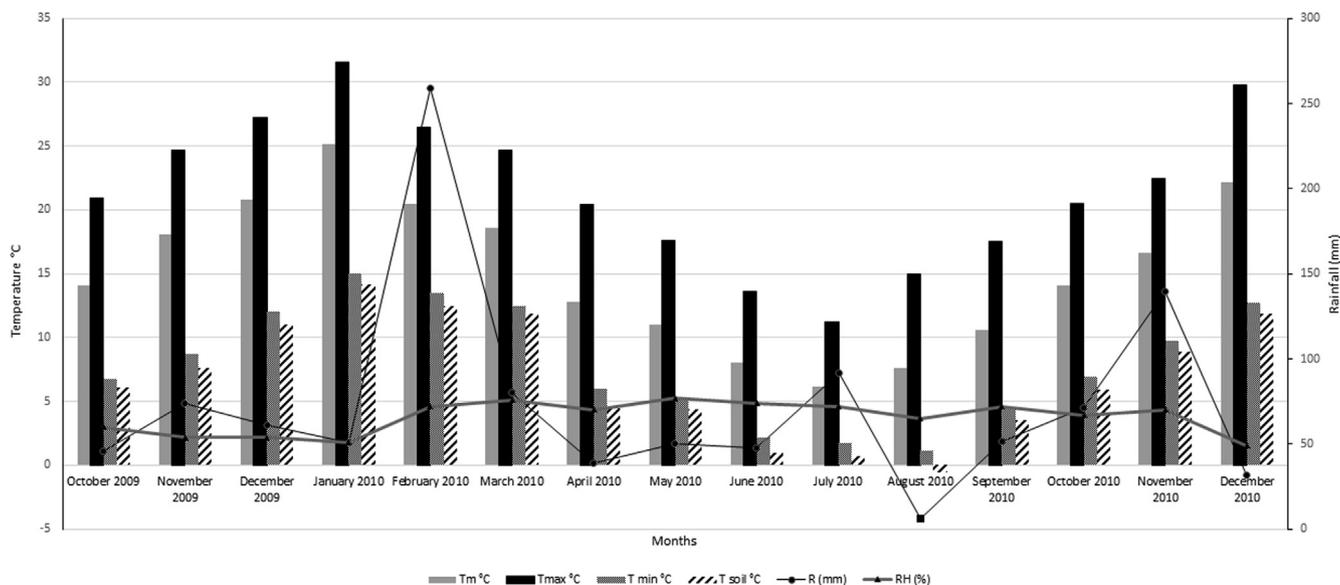


Fig. 1. Agroclimatic description of assay. Agrometeorological Station located at the same Barrow Experimental Station (<http://siga2.inta.gov.ar/en/datoshistoricos/>), during the sampling period. Tm (°C): temperature average; Tmax (°C): temperature maximum; Tmin (°C): temperature minimum; T soil (°C): temperature in the first 5 cm of soil; R (mm): rainfall; RH (%) relative humidity.

Table 1a

Soil characteristics at Barrow Experimental Station (38° 19' 25" S; 60° 14' 33" W), National Institute of Agricultural Technology, Tres Arroyos, Buenos Aires province, Argentina, during the sampling period.

	BD (Mg cm ⁻³)		PR (Mpa)		MWDC (cm)		NO ⁻³ (ppm)	P (ppm)	pH	SOC (g. kg ⁻¹)			
	depth	depth	depth	depth	depth	depth	depth	depth	depth	Sampling time			
	0–8 cm	0–5 cm	5–10 cm	10–15 cm	0–10 cm	0–20 cm	0–20 cm	0–20 cm	0–20 cm	Dec 2009	Apr 2010	Aug 2010	Dec 2010
RM-CT	1,22	0,39	0,69	1,17	2,6	32.1	14.3	6.6	23,53	20,13	19,3	29,77	
RM-ZT	1,28	0,54	1,21	1,63	2,44	38.3	30.8	6.7	20,17	20,4	19,8	26,03	
IM-CT	1,23	0,47	0,75	1,17	2,9	27.6	16.9	6.6	24,9	18,13	19,43	29,9	
IM-ZT	1,3	0,63	1,31	1,74	2,5	64.5	28.3	6.7	25,37	24,17	22,57	29,6	

RM-CT: Rotation management under CT: conventional tillage; RM-ZT: Rotation management under ZT: tillage; IM-CT: Intensive management under CT: conventional tillage; IM- ZT: Intensive management under ZT: zero tillage..

BD: bulk density (Mg cm⁻³) (Manso et al., 2012).

PR: Penetration Resistance (Mpa) (Manso et al., 2012).

CDMP: mean weigh diameter change (cm) (Roldán et al., 2014).

NO₃: Marban (1989).

P: Bray and Kurtz N°1(1945).

pH: Potentiometric method (1:2,5; soil: water) (USDA-NRCS 2004).

SOC: soil organic carbon (g. kg⁻¹) (Walkley and Black, 1934).

Sampling time: Dec 2009: December 2009; Apr 2010: April 2010; Aug 2010: August 2010; Dec 2010: December 2010.

2.3. Statistical analysis

A Bray–Curtis coefficient similarity matrix was obtained from the full-standardized data set of the fungal relative abundances [Square root transformation]. Subsequently, a non-metric multidimensional scaling (nMDS) was applied to the similarity matrix to order the samples in a two-dimensional plane according to their relevant similarity. A one-way statistical analysis (ANOSIM routine, test R) was performed on soil samples data to test for significant differences in the fungal relative abundance among season, rotational management (M) and tillage system (T). Finally, a Similarity Percentage analysis (SIMPER) was carried out in order to determine the contribution of each fungal specie to the similarity and differences between the soil samples.

After we estimated the richness and abundance pathogen, the saprophyte ratio was calculated. Comparisons were performed using linear mixed models. The values of soil fungal richness and fungal relative abundances were compared using the lme function [nlme package (Pinheiro et al., 2013; Pinheiro and Bates, 2000)]

with normal distribution of error and, considering rotational management (M), tillage system (T), precipitation corresponding to the previous month (P), soil carbon content (SOC) and, M × T, M × P and T × P interactions as fixed factors. We used mixed effects linear models which allow nesting plots within blocks and time correlated measures. Thus, each blocks and plots were random factors of the models. When necessary, variance functions were evaluated including weights: varFunc = varIdent (form=~1|factor) for Agricultural management or Tillage systems as well, varFunc = varExp(form=~1|factor) or varFunc = varPower(form=~1|factor) for precipitation and soil carbon. Variance function was applied for a single or a combination of two factors depending on each model fit. Auto-correlation between repeated measures was evaluated by the ACF function for the ordered normalized residuals with error probability of 0.05. When necessary the Correlation Structure: AR(1) (Formula: ~time |block/plot) was included (Zuur et al. 2009). Alternative models were compared with AICtab function from bbmle package (Bolker and Team, 2014). Fitted models were checked by plotting standardized residuals against fitted values and the model

Table 1b
Detail application of herbicides, pesticides and inorganic fertilizers during the sampling period.

Year	Crop	Fertilization	Herbicide/pesticide			
			December 2009	April 2010	August 2010	December 2010
2009/10	Wheat	Diammonium phosphate (DAP) (100 kg ha ⁻¹) Urea (140 kg ha ⁻¹) Dicamba (0.1L ha ⁻¹) Metsulfurón-methyl (6.7 g ha ⁻¹) Urea (65 kg ha ⁻¹)				ZT Glyphosate (2L ha ⁻¹)
ZT and CT	58.4% (1L ha ⁻¹)					
2010/11	Sunflower		ZT Glyphosate (2L ha ⁻¹)	ZT Glyphosate (2L ha ⁻¹)	ZT Glyphosate (2L ha ⁻¹)	ZT :Glyphosate (2L ha ⁻¹) ZT and CT Pre-emergent herbicides: flurochloridone (1,5L ha ⁻¹) acetochlor (1,5L ha ⁻¹)

CT: conventional tillage, ZT: zero tillage

factors (nlme package; Pinheiro and Bates 2009). Normal distribution was checked by the qqnorm(errors) and qqline(errors) functions. Inferential analyses were done through Anova function in package car (Fox and Weisberg, 2011) considering a probability error threshold of 0.01 (i.e.: p-value). We reduced error probability value to compensate restrictions imposed by the experimental design in strip-plot. All the analyses were performed with R environment; version 2.10.1.

Figures in the results section show the averages of the replicates ± standard error.

3. Results

A total of 1880 fungal isolates were obtained. The 84% of the isolates were assigned to species level including to Phylum Ascomycota (75%), Mucoromycota (10%) and Basidiomycota (1%) (K. Fungi). The remaining 16% were assigned to the groups Oomycota (7%) (K. Chromista) and Mycelia sterilia (7%) (Appendix B).

The nMDS applied to the fungal composition (abundance) of soil samples revealed a clear separation between seasons (Fig. 2a, 2D stress: 0.25). The pairwise comparisons show that exist significant different among all season (ANOSIM test: Global R = 0.451, p = 0.001, p < 0.001 for all comparison).

The SIMPER analyses show that the percentages of dissimilarity among the seasons were from 72.07% to 83.71%. The greatest dissimilarity was observed between December 2009 and December 2010 and the less between April 2010 and August 2010 (Table 2). In general, to explain the 50% of dissimilarity for all seasons was necessary to have with 17/18 species.

The species that most contributed to dissimilarity were Trichoderma hamatum, Fusarium oxysporum, Rhizopus stolonifer and oomycota group in all samples. In summer 2009 the most frequent species were Trichoderma hamatum and Fusarium oxysporum. Whereas, the oomycota group were less abundant than in the rest of the sampling seasons considered. In April the group Oomycota was the most frequent. In august and december 2010 the most frequent was F. oxysporum. The most percentage of differences between the two summers (December 2009/10) was contributed by T. hamatum (Table 2).

The results of the nMDS analysis of the soil samples considering the Rotational Management (M), and tillage system (T) did not show a clear trend (Fig. 2b; 2c). ANOSIM post hoc test confirmed that were not statistically significant difference between treatments for both management (Rotational management: RM-IM Global R 0.023, p 0.18; Tillage management: CT-ZT Global R 0.037, p 0.11).

The soil fungal richness depended on precipitation range and management (Fig. 3a; Table 3). These effects on fungal richness did not influence on the pathogens: saprotroph ratio (Fig. 3b; Table 3) indicating that management, tillage and precipitation influence similarly on pathogens and saprotroph group. In average, the ratio between pathogens and saprotroph was 0.26 indicating that saprotroph richness was almost four folds greater than pathogens richness. The pathogen: saprotroph abundance ratio indicated that the relative abundance of the saprotroph was lower in average in the middle of the precipitation range (Fig. 3c; Table 3). Changes in the relative abundance of both groups were driven by the relative abundance of pathogenic fungi which also varied with precipitation while the relative abundance of saprotrophs was independent on the analysed variables (Appendix C). In both richness and relative abundance, saprotrophic fungi were higher than pathogenic ones as indicated ratios below one and we did not find evidences of tillage system or management effects.

The relative abundance of saprotrophic group depended on the interaction between richness, tillage and management (p < 0.001;

Fig. 4, Appendix B). This interaction implied that relative abundance of saprotrophic group was almost constant along richness gradient in RM-ZT and IM-CT. However, the relative abundance of saprotrophic group was lower in RM-CT and IM-ZT (Fig. 4).

4. Discussion

Fungi of soil have significant role on dynamics and structure of soil. In long-term experiments when the tillage systems and crop rotations don't vary, the richness and diversity of the soil fungi community are lower than in those where the rotation of crops

is applied. Can be detect changes in soil fungi community in short times in this type of assay?. The production systems of the mixed wheat region of southern Buenos Aires have modified their productive strategies according to the technological advances that have occurred in the last 25 years. In general, the mixed systems in rotation with pastures were displaced by sequences of permanent agriculture with a strong presence of summer crops (soybean, sunflower, corn, sorghum), interacting with traditional fine-grain cereals. Although direct sowing has spread to the region in recent years, many agricultural establishments maintain the use of tillage in their production schemes. However, during the last seven years

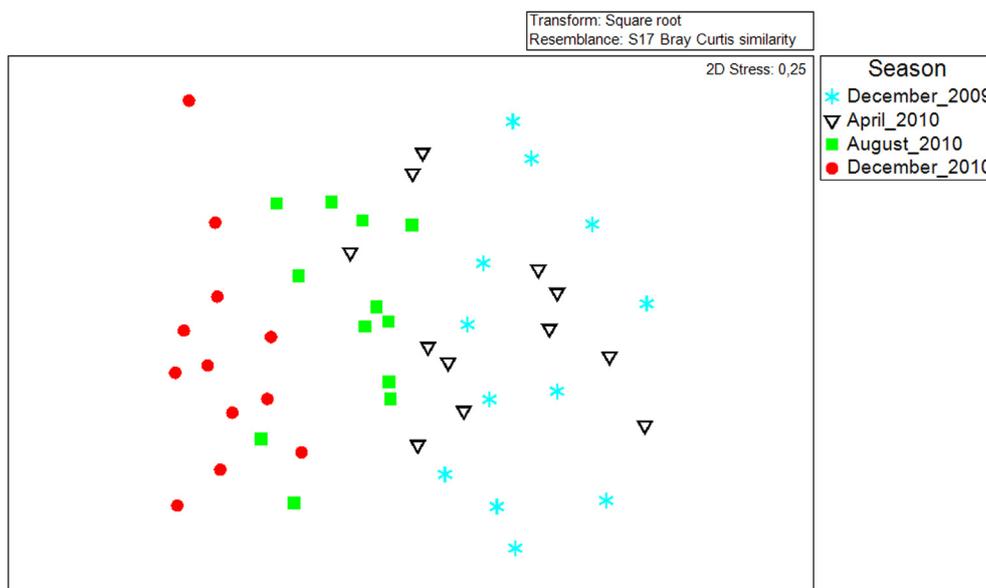


Fig. 2. A non-metric multidimensional scaling (nMDS) to detect the similarity matrix to order the samples in a two-dimensional plane according to Bray–Curtis coefficient similarity. The nMDS applied to the fungal composition (abundance) of soil samples. 2a) Seasons of sampling December 2009, April 2010, August 2010 and December 2010. 2b) Agricultural management (M) Red circles and circles represent sites under rotation including agriculture and pastures management (RM) and intensive agriculture and pastures management (IM) respectively. 2c) Tillage system (T) Red circles and circles represent sites under conventional tillage (CT) and zero tillage (ZT), respectively.

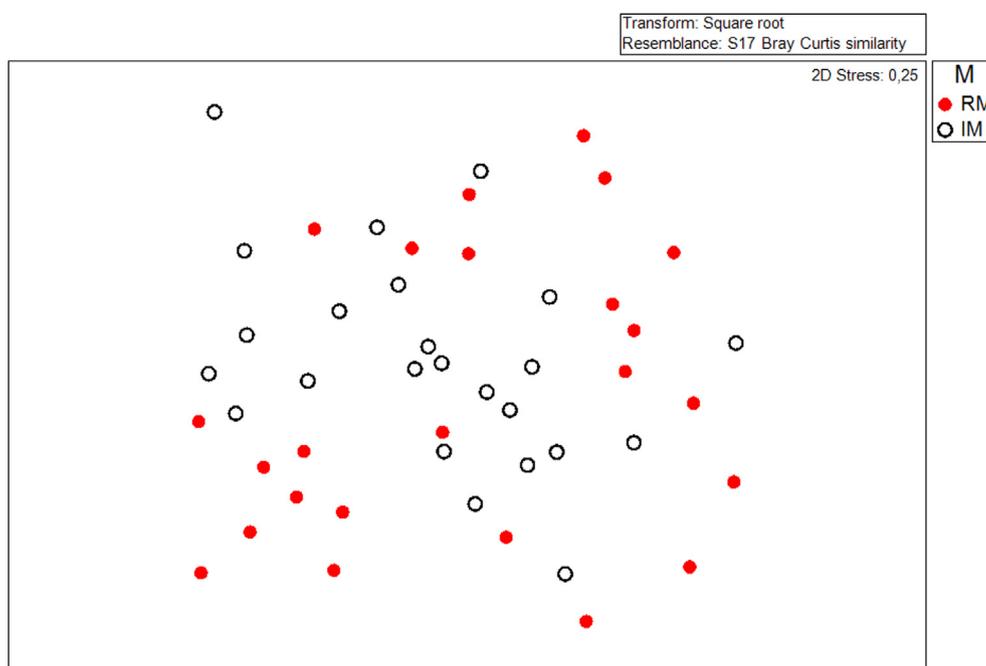


Fig. 2 (continued)

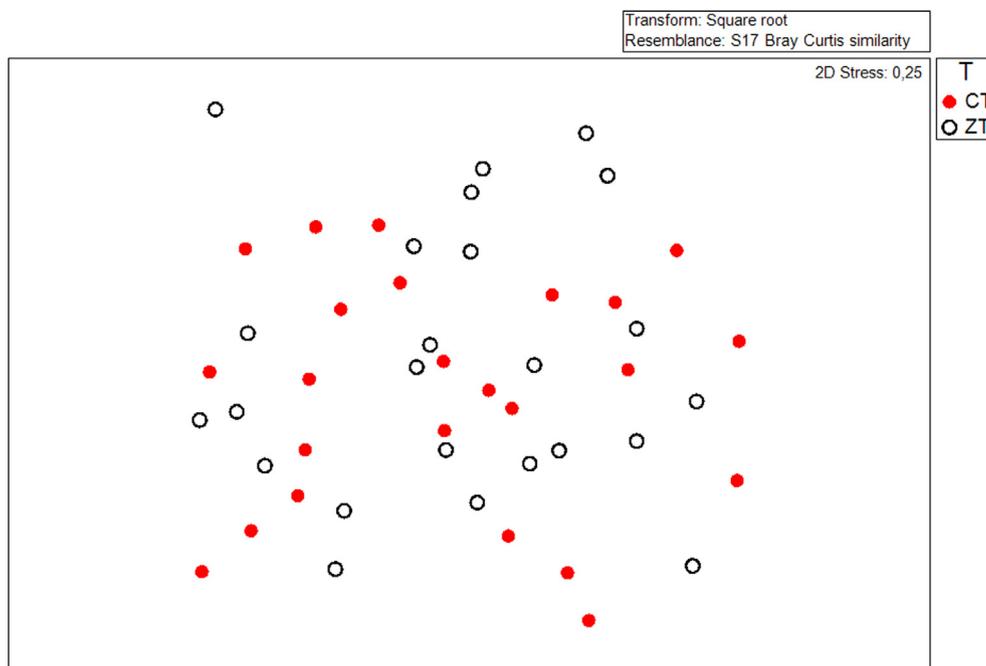


Fig. 2 (continued)

the incorporation of pastures in the rotation scheme showed that the soil enzyme activities increased and fungi community was favored (Silvestro et al., 2018). This situation is of great interest when analyzing the decomposition process of the different quantity and quality of waste that the crops contribute to the system (Forján and Manso, 2012). As well as the effect they will have on the soil fungal community, since it constitutes more than 50% of the biomass of cultivated soils (Heredia Abarca et al., 2004). We observed that the species richness was similar along the precipitation gradient under different options of managements and the soil organic carbon did not produce a statistical significant response in the fungal community. Therefore, the level of SOC in the soil in both situations would be similar due the long term of assay and in consequence the changes in soil fungi could not be detected through of parameters evaluated.

Although, the abundance of pathogen's group increased at low and high precipitation. Saprotrophic fungi abundance depended of interaction of richness, management and tillage. The effect of sampling time on fungal community has been described by Talley et al. (2002) who have suggested that the abundance and richness of fungi (in a habitat) are limited by the duration of unfavorable weather condition. Barbaruah et al. (2012) observed a positive correlation between the soil moisture and fungal species richness. Schneider et al. (2010) suggested that richness species was uniform in the year and that abundance was variable regardless of season. We observed a considerable presence of *Fusarium* sp. in lower levels of pp in soils under IM (CT and ZT). It is expected to obtain this result since those fungi that have survival strategies such as development of clamidospores are more successful under unfavorable conditions. The presence of saprotrophic fungi was diminished under IM at the same conditions. However, under RM the decrease was minor, this type of management would be providing better soil moisture conditions and prevent the loss of these species. Therefore, a management with pastures outside the type of tillage would be favouring the presence of saprotrophs with respect to pathogens despite presenting low pp levels. It is relevant that the pathogen more abundant was *Fusarium*. Once again it is

found that in long-term trials, no matter how much rotation exists with pastures and conservationist management, the pressure of *Fusarium* propagules increases.

Although the abundance of saprotrophs was relatively constant throughout the sampling year, it presented a negative slope towards the last sampling date in IMZT, however, for IMCT it presented its lowest abundance for low pp, which coincides with the increase in *Fusarium* recovering when the pp are higher and in this way the presence of saprotrophs is favoured, in this way a competitive relationship with the pathogens could be inferred.

The taxonomic composition of the soil fungi community showed difference. Saprotrophic fungi as *Trichoderma* sp. was one of the most abundant genera isolated and specially *T. hamatum* was one specie to most contributed to dissimilarity percentage differences. These results are in line with that reported by others authors (Hagn et al., 2003; Viaud et al., 2000; Silvestro et al. 2018). Kuprinsky et al. (2002) suggested that small changes in the environment could favor one species and inhibit another, and not necessarily these changes be reflected in an index of diversity. This was the case of *T. hamatum* on December 2009/10. Examples of this situation were *Acremonium fuscolum*, *Alternaria tenuissima*, *Apiospora montagnei*, *Botryotrichum piluliferum*, *Fusarium acuminatum*, *F. chlamydosporum*, *F. crookwelense*, *Idriella lunata*, *Nectria ventricosa*, *Penicillium funiculosum*, *Penicillium javanicum*, *P. thomii* and *Stachybotrys chartarum*. However, the studies on this association can help find out when, where or how many propagules of potential plant pathogens or biocontrol agents are available in the soil. In this way and with the results obtained, it is shown that with pasture rotation regardless of type of tillage and despite low pp, saprotrophs benefit from their abundance. At all sampling times the presence of saprotrophs was always greater than that of pathogens.

The seasonal sampling was the factor that most influenced the different parameters evaluated. The tillage systems did not cause significant effect of ecological parameters of soil fungi community as S. However, the taxonomic composition was modified and therefore the abundance of pathogens and saprotroph changed.

Table 2
SIMPER analysis for abundance composition of fungi of soil samples. Comparison between groups showing the average total dissimilarity (Av. Diss.) and the contribution of taxa to the dissimilarity (%). Results are given for pairwise comparisons between seasons (December_2009, April_2010, August_2010 and December_2010). Grey lines: pathogens, white lines: saprotrophs.

Taxa	Group	Group	Contrib. %	Taxa	Group	Group	Contrib. %
Av. Diss. = 73.32%							
Oomycota	December_2009	April_2010	5.63	<i>Fusarium acuminatum</i>	0.00	0.32	1.01
<i>Trichoderma hamatum</i>	2.29	1.34	4.22	<i>Fusarium sporotrichiodes</i>	0.00	0.34	0.98
<i>Fusarium oxysporum</i>	1.01	0.93	3.81	<i>Eupenicillium javanicum</i>	0.00	0.33	0.96
<i>Rhizopus stolonifer</i>	0.91	0.97	3.66	<i>Alternaria tenuissima</i>	0.35	0.00	0.95
<i>Botryothichum piluliferum</i>	0.08	1.16	3.58	<i>Acremonium kiliense</i>	0.08	0.28	0.94
<i>Trichoderma koningii</i>	1.05	0.68	3.36	<i>Fusarium konzum</i>	0.20	0.17	0.87
<i>Trichoderma harzianum</i>	0.79	0.49	2.97	<i>Penicillium expansum</i>	0.25	0.08	0.85
<i>Fusarium solani</i>	0.47	0.80	2.80	<i>Trichocladium opacum</i>	0.28	0.00	0.84
<i>Penicillium citrinum</i>	0.84	0.74	2.76	<i>Penicillium rubrum</i>	0.28	0.00	0.84
<i>Trichoderma strigosum</i>	0.74	0.22	2.70	<i>Aspergillus niger</i>	0.08	0.25	0.83
<i>Micelia sterilia</i>	1.28	1.02	2.55	<i>Epicoccum nigrum</i>	0.00	0.28	0.77
<i>Fusarium sambucinum</i>	0.50	0.45	2.27	<i>Acremonium fuscolum</i>	0.25	0.00	0.76
<i>Humicola griseae</i>	0.25	0.60	1.99	<i>Penicillium funiculosum</i>	0.00	0.25	0.72
<i>Aspergillus fumigatus</i>	0.60	0.42	1.96	<i>Fusarium subglutinans</i>	0.2	0.08	0.72
<i>Trichoderma polysporum</i>	0.41	0.28	1.90	<i>Trichoderma aureoviridae</i>	0.00	0.23	0.71
<i>Emericella nivea</i>	0.17	0.45	1.82	<i>Fusarium chlamydosporum</i>	0.00	0.24	0.67
<i>Humicola fuscoastrae</i>	0.44	0.20	1.81	<i>Trichoderma longibrachiatum</i>	0.08	0.14	0.65
<i>Cylindrocarpon dydimum</i>	0.50	0.28	1.81	<i>Fusarium merismoides</i>	0.00	0.24	0.64
<i>Absidia glauca</i>	0.12	0.51	1.74	<i>Stachybotrys cylindrospora</i>	0.12	0.12	0.63
<i>Nectria ventricosa</i>	0.12	0.52	1.73	<i>Aspergillus flavus</i>	0.08	0.17	0.62
<i>Cladosporium cladosporioides</i>	0.30	0.26	1.63	<i>Gliocladium roseum</i>	0.23	0.00	0.62
<i>Trichoderma pseudokoningii</i>	0.19	0.33	1.48	<i>Idriella lunata</i>	0.23	0.00	0.62
<i>Gilmaniella humicola</i>	0.37	0.25	1.44	Av. Diss. = 72.07%			
<i>Penicillium restrictum</i>	0.43	0.00	1.44	April_2010	August_2010		
<i>Mortierella vinacea</i>	0.39	0.08	1.37	<i>Fusarium oxysporum</i>	0.93	2.00	5.68
<i>Apiospora montagnei</i>	0.08	0.39	1.28	<i>Rhizopus stolonifer</i>	0.97	1.77	4.51
<i>Fusarium graminearum</i>	0.20	0.25	1.22	<i>Trichoderma hamatum</i>	1.34	0.59	3.68
<i>Trichoderma viridae</i>	0.12	0.31	1.21	<i>Botryothichum piluliferum</i>	1.16	0.08	3.60
<i>Fusarium scirpi</i>	0.26	0.14	1.12	<i>Fusarium scirpi</i>	0.14	1.00	3.45
<i>Trichoderma piluliferum</i>	0.29	0.08	1.12	<i>Humicola griseae</i>	0.60	1.11	3.44
<i>Penicillium expansum</i>	0.25	0.17	1.08	<i>Calicium Pers.</i>	0.08	1.09	3.35
<i>Trichocladium opacum</i>	0.28	0.08	1.04	<i>Oomycota</i>	2.27	1.89	3.04
<i>Alternaria tenuissima</i>	0.35	0.00	1.04	<i>Fusarium solani</i>	0.80	0.27	2.61
<i>Acremonium kiliense</i>	0.08	0.28	1.02	<i>Micelia sterilia</i>	1.02	1.39	2.59
<i>Penicillium lilacinium</i>	0.25	0.08	0.96	<i>Penicillium citrinum</i>	0.74	0.46	2.47
<i>Aspergillus niger</i>	0.08	0.25	0.92	<i>Trichoderma koningii</i>	0.68	0.23	2.36
<i>Penicillium rubrum</i>	0.28	0.00	0.92	<i>Aspergillus fumigatus</i>	0.42	0.82	2.22
<i>Acremonium fuscolum</i>	0.25	0.00	0.84	<i>Levadura</i>	0.08	0.60	2.00
<i>Idriella lunata</i>	0.23	0.08	0.83	<i>Trichoderma polysporum</i>	0.28	0.43	1.91
<i>Trichoderma longibrachiatum</i>	0.08	0.20	0.79	<i>Absidia glauca</i>	0.51	0.37	1.89
<i>Cylindrocarpon magnusianum</i>	0.00	0.27	0.75	<i>Trichoderma harzianum</i>	0.49	0.33	1.89
<i>Levadura</i>	0.17	0.08	0.69	<i>Humicola fuscoastrae</i>	0.20	0.38	1.61
<i>Gliocladium roseum</i>	0.23	0.00	0.68	<i>Nectria ventricosa</i>	0.52	0.00	1.52
<i>Fusarium merismoides</i>	0.00	0.20	0.67	<i>Emericella nivea</i>	0.45	0.00	1.51
Av. Diss. = 76.47%				<i>Fusarium crookwelense</i>	0.08	0.43	1.45
				<i>Acremonium kiliense</i>	0.28	0.28	1.38
<i>Trichoderma hamatum</i>	2.29	0.59	5.24	<i>Fusarium sambucinum</i>	0.45	0.00	1.31
<i>Fusarium oxysporum</i>	1.01	2.00	4.94	<i>Aspergillus niger</i>	0.25	0.25	1.30
Oomycota	0.61	1.89	4.19	<i>Mortierella vinacea</i>	0.08	0.39	1.29
<i>Rhizopus stolonifer</i>	0.91	1.77	4.06	<i>Apiospora montagnei</i>	0.39	0.08	1.28
<i>Fusarium scirpi</i>	0.26	1.00	3.30	<i>Fusarium merismoides</i>	0.20	0.24	1.26
<i>Humicola griseae</i>	0.25	1.11	3.19	<i>Cylindrocarpon dydimum</i>	0.28	0.14	1.22
<i>Calicium Pers.</i>	0.00	1.09	3.14	<i>Trichoderma viridae</i>	0.31	0.08	1.13
<i>Trichoderma koningii</i>	1.05	0.23	3.03	<i>Fusarium acuminatum</i>	0.00	0.32	1.12
<i>Trichoderma harzianum</i>	0.79	0.33	2.54	<i>Fusarium sporotrichiodes</i>	0.00	0.34	1.09
<i>Penicillium citrinum</i>	0.84	0.46	2.44	<i>Eupenicillium javanicum</i>	0.00	0.33	1.06
<i>Micelia sterilia</i>	1.28	1.39	2.32	<i>Cladosporium cladosporioides</i>	0.26	0.08	1.03
<i>Trichoderma strigosum</i>	0.74	0.00	2.19	<i>Trichoderma pseudokoningii</i>	0.33	0.00	1.03
<i>Aspergillus fumigatus</i>	0.60	0.82	2.08	<i>Trichoderma piluliferum</i>	0.08	0.27	1.02
<i>Trichoderma polysporum</i>	0.41	0.43	2.02	<i>Penicillium lilacinium</i>	0.08	0.24	0.96
<i>Humicola fuscoastrae</i>	0.44	0.38	1.92	<i>Trichoderma longibrachiatum</i>	0.20	0.14	0.95
<i>Levadura</i>	0.17	0.6	1.80	<i>Penicillium funiculosum</i>	0.08	0.25	0.91
<i>Fusarium solani</i>	0.47	0.27	1.78	<i>Alternaria alternata</i>	0.12	0.20	0.88
<i>Cylindrocarpon dydimum</i>	0.5	0.14	1.62	<i>Epicoccum nigrum</i>	0.00	0.28	0.85
<i>Mortierella vinacea</i>	0.39	0.39	1.62	<i>Gilmaniella humicola</i>	0.25	0.00	0.85
<i>Penicillium restrictum</i>	0.43	0.12	1.48	<i>Trichoderma aureoviridae</i>	0.00	0.23	0.79
<i>Fusarium sambucinum</i>	0.50	0.00	1.47	<i>Cylindrocarpon magnusianum</i>	0.27	0.00	0.76
<i>Trichoderma piluliferum</i>	0.29	0.27	1.44	Av. Diss. = 83.71%			
<i>Fusarium crookwelense</i>	0.12	0.43	1.39	December_2009	December_2010		
<i>Absidia glauca</i>	0.12	0.37	1.26	<i>Trichoderma hamatum</i>	2.29	0.08	5.83
<i>Penicillium lilacinium</i>	0.25	0.24	1.17	<i>Fusarium oxysporum</i>	1.01	1.53	3.69
<i>Cladosporium cladosporioides</i>	0.30	0.08	1.04	<i>Fusarium hostae</i>	0.00	1.22	3.14
<i>Gilmaniella humicola</i>	0.37	0.00	1.03	<i>Rhizopus stolonifer</i>	0.91	0.78	2.98
				<i>Micelia sterilia</i>	1.28	1.78	2.88
				<i>Trichoderma koningii</i>	1.05	0.00	2.75

Taxa	Group	Group	Contrib. %	Taxa	Group	Group	Contrib. %
<i>Fusarium solani</i>	0.47	1.03	2.66	<i>Emericella nivea</i>	0.45	0.00	1.30
<i>Penicillium thomii</i>	0.00	0.99	2.38	<i>Trichoderma harzianum</i>	0.49	0.00	1.28
<i>Calicium Pers.</i>	0.00	0.88	2.28	<i>Fusarium scirpi</i>	0.14	0.37	1.23
Oomycota	0.61	0.83	2.23	<i>Cladosporium cladosporioides</i>	0.26	0.25	1.21
<i>Penicillium funiculosum</i>	0.00	0.90	2.20	<i>Humicola fuscoatra</i>	0.20	0.33	1.15
<i>Penicillium citrinum</i>	0.84	0.00	2.18	<i>Fusarium sambucinum</i>	0.45	0.00	1.14
<i>Epicoccum nigrum</i>	0.00	0.87	2.17	<i>Apiospora montagnei</i>	0.39	0.08	1.10
<i>Trichoderma harzianum</i>	0.79	0.00	2.12	<i>Trichoderma polysporum</i>	0.28	0.12	1.01
<i>Aspergillus fumigatus</i>	0.60	1.28	2.08	<i>Trichoderma pseudokoningii</i>	0.33	0.00	0.89
Levadura	0.17	0.77	1.98	<i>Cylindrocarpon dydimun</i>	0.28	0.08	0.88
<i>Trichoderma strigosum</i>	0.74	0.00	1.95	<i>Trichoderma viridae</i>	0.31	0.00	0.79
<i>Humicola griseae</i>	0.25	0.82	1.93	<i>Penicillium lilacinium</i>	0.08	0.20	0.75
<i>Eupenicillium javanicum</i>	0.00	0.68	1.73	<i>Fusarium proliferatum</i>	0.00	0.25	0.75
<i>Stachybotrys chartarum</i>	0.17	0.63	1.63	<i>Gilmaniella humicola</i>	0.25	0.00	0.73
<i>Aspergillus niger</i>	0.08	0.60	1.54	<i>Fusarium chlamydosporum</i>	0.00	0.25	0.73
<i>Humicola fuscoatra</i>	0.44	0.33	1.53	<i>Aspergillus candidus</i>	0.00	0.25	0.70
<i>Fusarium scirpi</i>	0.26	0.37	1.43	<i>Fusarium acuminatum</i>	0.00	0.25	0.68
<i>Acremonium kiliense</i>	0.08	0.48	1.36	<i>Alternaria alternata</i>	0.12	0.17	0.66
<i>Trichoderma polysporum</i>	0.41	0.12	1.32	<i>Cylindrocarpon magnusianum</i>	0.27	0.00	0.65
<i>Fusarium sambucinum</i>	0.50	0.00	1.31	<i>Penicillium purpurascens</i>	0.00	0.20	0.62
<i>Cylindrocarpon dydimun</i>	0.50	0.08	1.30	<i>Trichoderma piluliferum</i>	0.08	0.17	0.61
<i>Cladosporium herbarum</i>	0.00	0.51	1.30	<i>Fusarium graminearum</i>	0.25	0.00	0.61
<i>Cladosporium cladosporioides</i>	0.30	0.25	1.23	<i>Aspergillus parasiticus</i>	0.00	0.25	0.61
<i>Penicillium restrictum</i>	0.43	0.00	1.16	<i>Fusarium merismoides</i>	0.20	0.00	0.58
<i>Trichoderma piluliferum</i>	0.29	0.17	1.08	Av. Diss. = 72.57%	August_2010	December_2010	
<i>Mortierella vinacea</i>	0.39	0.00	1.04	<i>Fusarium oxysporum</i>	2.00	1.53	5.17
<i>Penicillium lilacinium</i>	0.25	0.2	0.96	<i>Rhizopus stolonifer</i>	1.77	0.78	4.70
<i>Gilmaniella humicola</i>	0.37	0.00	0.91	Oomycota	1.89	0.83	3.84
<i>Fusarium proliferatum</i>	0.17	0.25	0.90	<i>Fusarium hostae</i>	0.08	1.22	3.45
<i>Aspergillus candidus</i>	0.17	0.25	0.88	<i>Fusarium scirpi</i>	1.00	0.37	3.38
<i>Alternaria tenuississima</i>	0.35	0.00	0.85	<i>Micelia sterilia</i>	1.39	1.78	3.16
<i>Trichocladium opacum</i>	0.28	0.00	0.75	<i>Humicola griseae</i>	1.11	0.82	3.10
<i>Penicillium rubrum</i>	0.28	0.00	0.74	<i>Calicium Pers.</i>	1.09	0.88	3.08
<i>Idriella lunata</i>	0.23	0.08	0.72	<i>Fusarium solani</i>	0.27	1.03	3.00
<i>Fusarium chlamydosporum</i>	0.00	0.25	0.68	<i>Penicillium thomii</i>	0.00	0.99	2.71
<i>Acremonium fuscolum</i>	0.25	0.00	0.68	<i>Penicillium funiculosum</i>	0.25	0.90	2.43
<i>Penicillium expansum</i>	0.25	0.00	0.66	Levadura	0.6	0.77	2.42
<i>Fusarium acuminatum</i>	0.00	0.25	0.64	<i>Epicoccum nigrum</i>	0.28	0.87	2.30
<i>Penicillium purpurascens</i>	0.00	0.20	0.58	<i>Eupenicillium javanicum</i>	0.33	0.68	1.96
<i>Nectria inventa</i>	0.08	0.17	0.57	<i>Aspergillus fumigatus</i>	0.82	1.28	1.93
<i>Aspergillus parasiticus</i>	0.00	0.25	0.57	<i>Stachybotrys chartarum</i>	0.00	0.63	1.85
<i>Gliocladium roseum</i>	0.23	0.00	0.55	<i>Trichoderma hamatum</i>	0.59	0.08	1.78
<i>Trichoderma pseudokoningii</i>	0.19	0.00	0.51	<i>Aspergillus niger</i>	0.25	0.60	1.77
<i>Nigrospora sphaerica</i>	0.12	0.08	0.51	<i>Acremonium kiliense</i>	0.28	0.48	1.77
<i>Fusarium subglutinans</i>	0.20	0.00	0.51	<i>Fusarium acuminatum</i>	0.32	0.25	1.61
<i>Fusarium graminearum</i>	0.20	0.00	0.5	<i>Humicola fuscoatra</i>	0.38	0.33	1.57
Av. Diss. = 81.28%	April_2010	December_2010		<i>Trichoderma polysporum</i>	0.43	0.12	1.51
Oomycota	2.27	0.83	4.36	<i>Cladosporium herbarum</i>	0.00	0.51	1.47
<i>Fusarium oxysporum</i>	0.93	1.53	3.98	<i>Penicillium citrinum</i>	0.46	0.00	1.38
<i>Trichoderma hamatum</i>	1.34	0.08	3.54	<i>Fusarium crookwelense</i>	0.43	0.08	1.32
<i>Rhizopus stolonifer</i>	0.97	0.78	3.46	<i>Fusarium chlamydosporum</i>	0.24	0.25	1.32
<i>Fusarium hostae</i>	0.00	1.22	3.36	<i>Trichoderma piluliferum</i>	0.27	0.17	1.14
<i>Micelia sterilia</i>	1.02	1.78	3.36	<i>Mortierella vinacea</i>	0.39	0.00	1.11
<i>Botryotrichum piluliferum</i>	1.16	0.00	3.21	<i>Absidia glauca</i>	0.37	0.00	1.11
<i>Fusarium solani</i>	0.8	1.03	2.96	<i>Penicillium lilacinium</i>	0.24	0.20	1.10
<i>Penicillium thomii</i>	0.00	0.99	2.53	<i>Fusarium sporotrichiodes</i>	0.34	0.00	0.99
<i>Calicium Pers.</i>	0.08	0.88	2.44	<i>Trichoderma harzianum</i>	0.33	0.00	0.98
<i>Aspergillus fumigatus</i>	0.42	1.28	2.44	<i>Alternaria alternata</i>	0.20	0.17	0.97
<i>Penicillium funiculosum</i>	0.08	0.90	2.32	<i>Aspergillus parasiticus</i>	0.17	0.25	0.92
<i>Epicoccum nigrum</i>	0.00	0.87	2.31	<i>Trichoderma aureoviridae</i>	0.23	0.08	0.89
Levadura	0.08	0.77	2.11	<i>Cladosporium cladosporioides</i>	0.08	0.25	0.85
<i>Humicola griseae</i>	0.60	0.82	1.97	<i>Fusarium proliferatum</i>	0.00	0.25	0.79
<i>Penicillium citrinum</i>	0.74	0.00	1.91	<i>Aspergillus candidus</i>	0.00	0.25	0.74
<i>Trichoderma koningii</i>	0.68	0.00	1.88	<i>Staphylotrichum coccosporum</i>	0.08	0.20	0.72
<i>Eupenicillium javanicum</i>	0.00	0.68	1.85	<i>Penicillium purpurascens</i>	0.00	0.20	0.66
<i>Aspergillus niger</i>	0.25	0.60	1.82	<i>Trichoderma koningii</i>	0.23	0.00	0.66
<i>Stachybotrys chartarum</i>	0.00	0.63	1.75	<i>Fusarium merismoides</i>	0.24	0.00	0.65
<i>Acremonium kiliense</i>	0.28	0.48	1.66	<i>Cylindrocarpon dydimun</i>	0.14	0.08	0.62
<i>Cladosporium herbarum</i>	0.17	0.51	1.47	<i>Acremonium furcatum</i>	0.20	0.00	0.59
<i>Absidia glauca</i>	0.51	0.00	1.40	<i>Penicillium brevicompactum</i>	0.19	-	0.52
<i>Nectria ventricosa</i>	0.52	0.00	1.32				

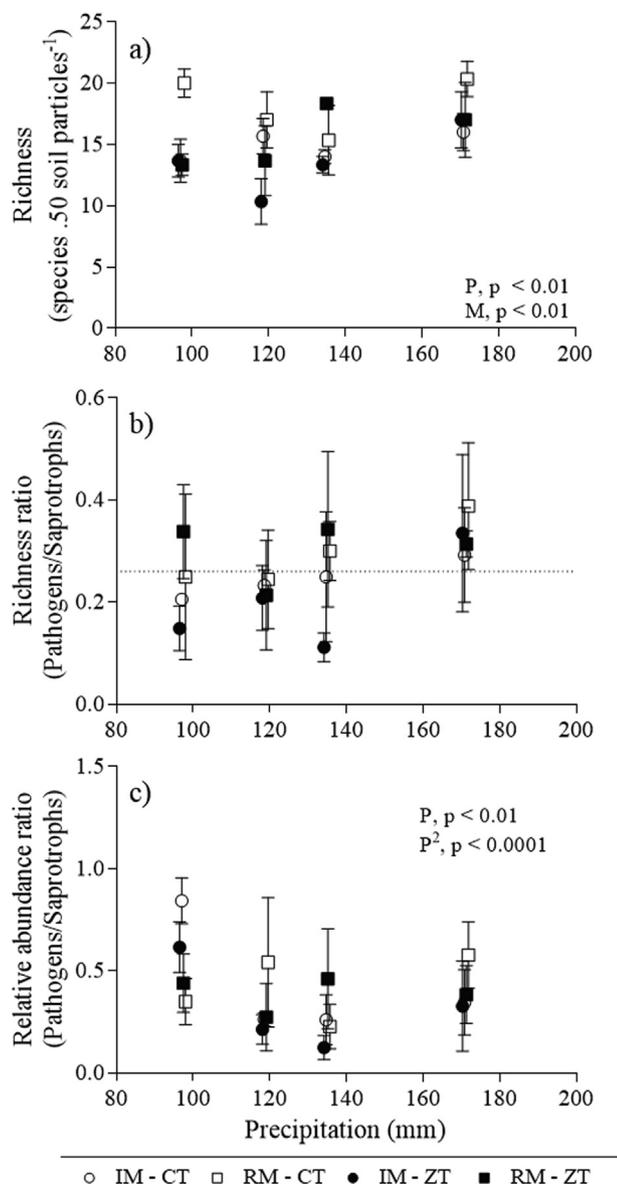


Fig. 3. Soil fungal richness and relative abundance: 3a) total fungal richness (genus 0.50 soil particles⁻¹); 3b) pathogens: saprotrophic richness ratio; and 3c) pathogens: saprotrophic relative abundance ratio in relation to previous two months precipitation. Open and dark symbols represent sites under zero (ZT) or conventional tillage (CT), respectively. Circles and squares represent sites under intensive agriculture management (IM) or rotation including agriculture and pastures management (RM), respectively. Symbols show the mean ± standard error. Vertical axis units and scales vary according to the variable which represent. Significant effects for Precipitation (P), Agricultural management (M), Tillage system (T) and Soil organic carbon (C) and their interactions are showed in the figure (p-value). In b) dotted line indicates the average value of all data. On each precipitation value, mean value points are jittered to avoid overlapping.

The saprotrophic species abundance was favored by the RM. Based on this result, we suggest that these parameters showed the strongest relationship with the seasonal sampling. Studies of the land use history are relevant due to the increased agriculturalization, i.e. the extension of the agricultural cycle on the same plot (Forján and Manso 2012). Even if crop production, tillage management and crop rotation have direct consequences on soil quality our results suggested that these factors have not significant implications in short times in the develop on soil fungal community along one year when the assay was installed a long term.

Table 3

Deviance analyses of the models for soil fungal total richness, richness and abundance pathogens: saprotrophic ratio. The columns show the term of the model, degrees of freedom (df), Chi squared (Chisq) and p-value (p). Column term present the factors soil organic carbon (SOC), precipitation (P), rotation management (M), tillage system (T), and the corresponding interactions. Bold number indicates statistically significant terms (p-values < 0.01).

	df	Richness		Pathogens:Saprotrophic			
		Chisq	p	Richness		Abundance	
				Chisq	p	Chisq	p
M × T	6	1.84	0.174	0.1	0.75	0.29	0.588
P × T	31	0.61	0.437	0.06	0.81	0.25	0.616
P × M	31	0.14	0.704	0.21	0.65	4.08	0.043
SOC (g.kg ⁻¹)	31	2.91	0.088	0.59	0.44	0.07	0.796
Precipitation (mm)	31	6.85	0.009	2.45	0.12	7.03	0.008
Precipitation ²	31	4.21	0.040	1.13	0.29	15.67	<0.0001
Management	6	7.40	0.007	2.13	0.14	0.17	0.678
Tillage	6	5.08	0.024	0.23	0.63	1.52	0.218

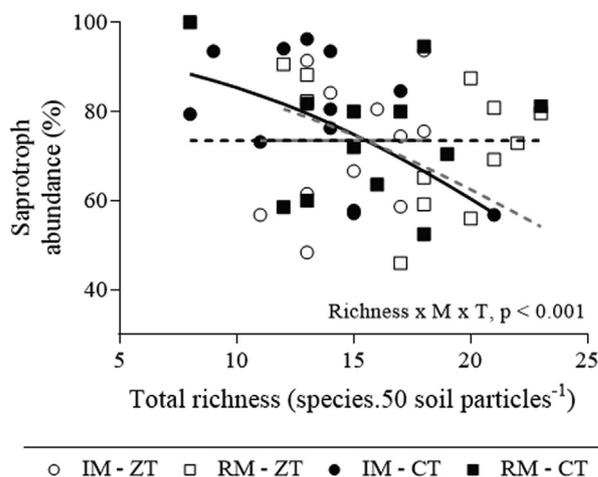


Fig. 4. Saprotoph relative genus abundance (%) in relation to total species richness (genus 0.50 soil particles⁻¹). Open and dark symbols represent sites under zero (ZT) or conventional tillage (CT), respectively. Circles and squares represent sites under intensive agriculture management (IM) or rotation including agriculture and pasture management (RM), respectively. Symbols show value for all measurements. Significant effects for Richness, Agricultural management (M), Tillage system (T) and their interactions are showed in the figure (p-value).

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgments

This manuscript is in memoriam of Dra. Arambarri. This work was supported by funding from the PIP 111220130100280 CO and FONCYT-SECYT PICT N° 2018-03171.

Appendix A. Supplementary material

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.jssas.2021.01.008>.

References

- Barbaruah, B., Chutia, M., Boruah, P., 2012. Soil hyphomycetes population dynamics in disturbed and undisturbed tropical soils of North-eastern India. *Af. J. of Microb. Res.* 6, 5344–5352. <https://doi.org/10.5897/AJMR12.191>.
- Barnett, H.L., Hunter, B., 1998. *Illustrated genera of Imperfect Fungi*. APS Press, The America Phytopathological Society st. Paul Minnesota., p. 218.
- Barron, G.L., 1968. *The Genera of Hyphomycetes from Soil*. Williams & Wilkins, Company.
- Bolker, B., Team, R.D.C., 2014. *bbmle: Tools for general maximum likelihood estimation*. R Packag. version 1.0.17.
- Cabello, M.N., Arambarri, A.M., 2002. Diversity in soil fungi from undisturbed and disturbed *Celtis tala* and *Scutia buxifolia* forests in the eastern Buenos Aires province (Argentina). *Microbiol. Res.* 157, 115–125 <http://www.urbanfischer.de/journals/microbiolres>.
- Cannon, P.F., Kirk, P.M., 2007. *Fungal families of the world*. CAB International, Wallingford, UK.
- Charmichael, J.W., Bryce Kendrick, W., Connors, I.L., Sigler, L., 1980. *Genera of Hyphomycetes*. The University of Alberta Press, Edmonton, Alberta, Canada, p. 386.
- Dominguez, G.F., Diviovalvi, G.A., Studdert, G.A., Monterubbianesi, M.G., 2009. Soil organic C and N fractions under continuous cropping with contrasting tillage systems on mollisols of the southeastern pampas. *Soil Tillage Res.* 102, 93–100. <https://doi.org/10.1016/j.still.2008.07.020>.
- Domsch, K.H., Gams, W., Anderson, T.H., 1980. *Compendium of soil Fungi*. Academic Press, London, p. 993.
- Ellis, M.B., 1971. *Dematiaceous Hyphomycetes*. Commonwealth Mycological Institute, Kew, Surrey, England, p. 608.
- Ellis, M.B., 1976. *More Dematiaceous Hyphomycetes*. Commonwealth Mycological Institute, Kew, Surrey, England, p. 507.
- Foley, J.A., Ramankutty, N., Brauman, K.A., Casidi, E.S., Gerber, J.S., Johnson, M., Mueller, N.D., O'Connell, C., Ray, D.K., West, P.C., Balzer, C., Bennett, E.M., Carpenter, S.R., Hill, J., Monfreda, C., Polasky, S., Rockström, J., Sheehan, J., Siebert, S., Tilman, D., Zaks, D.P.M., 2011. Solutions for a cultivated planet. *Nature* 478, 337–342. <https://doi.org/10.1038/nature10452>.
- Forján, H., Manso, L., 2012. La secuencia de cultivos. In: Forján, H., Manso, L. (Eds.), *Rotaciones y secuencias de cultivos en la región mixta cerealera del centro sur bonaerense*. INTA, Argentina, pp. 25–34.
- Fox, J., Weisberg, S., 2011. *An R Companion to Applied Regression*. SAGE Publications Inc, p. 472.
- Gómez, K.A., Gómez, A.A., 1984. *Statistical procedures for agricultural research*. John Wiley & Sons, New York.
- Hagn, A., Pritsch, K., Scholter, M., Munch, J.C., 2003. Fungal diversity in agricultural soil under different farming management systems, with special reference to biocontrol strains of *Trichoderma* spp. *Biol. Fertil. Soil.* 38, 236–244. <https://doi.org/10.1007/s00374-003-0651-0>.
- Heredia Abarca, G., Reyes Estebanez, M., Arias Mota, R.M., 2004. Adiciones al conocimiento de la diversidad de los hongos conidiales del bosque mesófilo de montaña del estado de Veracruz. *Acta Botánica Mexicana* 66, 1–22.
- Kalbitz, K., Solinger, S., Park, J.H., Michalzik, B., Matzner, E., 2000. Controls on the dynamics of dissolved organic matter in soils. A review. *Soil Sci.* 165, 277–304. <https://doi.org/10.1097/00010694200004000-00001>.
- Khuel, R.O., 2001. *Diseño de experimentos*. Thomson Learning International, Mexico, p. 680 pp.
- Kirk, P.M., 2001. *Dictionary of the fungi*. Waslingford, UK, CAB International, p. 655.
- Kladivko, E.J., 2001. Tillage systems and soil ecology. *Soil Tillage Res.* 61, 61–76. [https://doi.org/10.1016/S0167-1987\(01\)00179-9](https://doi.org/10.1016/S0167-1987(01)00179-9).
- Klein, D.A., Paschke, M.W., 2004. Filamentous fungi: the indeterminate lifestyle and microbial ecology. *Microbial Ecol.* 47, 224–235 <https://link.springer.com/article/10.1007/s00248-003-1037-4>.
- Kubicek, C.P., Harman, G.E. 2002. *Trichoderma and Gliocladium*. Basic Biology, taxonomy and Genetics. Vol 1. Taylor and Francis. London 300 pp.
- Lehmann, A., Rillig, M.C., 2015. Understanding mechanism of soil biota involvement in soil aggregation: A way forward with saprobic fungi? *Soil Biol. Biochem.* 88, 298–302. <https://doi.org/10.1016/j.soilbio.2015.06.006>.
- Leslie, J.F., Summerell, B.A., 2006. *The Fusarium Laboratory Manual*. Blackwell, Oxford, UK <https://doi.org/10.1002/9780470278376>.
- Madejón, E., Murillo, J.M., Moreno, F., López, M.V., Arrue, J.L., Alvaro-Fuentes, J., Cantero, C., 2009. Effect of long-term conservation tillage on soil biochemical properties in Mediterranean Spanish areas. *Soil Till. Res.* 105, 55–62. <https://doi.org/10.1016/j.still.2009.05.007>.
- Manso, M.L., Forjan, H.J., Studdert, G.A., San Martino, S., 2012. Efecto de sistemas de labranza contrastantes sobre algunas propiedades de un molisol de Tres Arroyos bajo distintos usos previos. *Rev. FCA- UN Cuyo* 44, 85–99.
- Millennium Ecosystem Assessment, 2005. *Ecosystems and human well-being*.
- Miller, R.M., Jastrow, J.D., 2000. Mycorrhizal fungi influence soil structure. In: Kapulnik, Y., Douds, D.D. (Eds.), *Arbuscular Mycorrhizas: Physiology and Function*. Kluwer Academe, mic Publishers, Dordrecht, The Netherlands, pp. 3–18.
- Nelson, P.E., Tousson, T.A., Marasas, W.F.O., 1983. *Fusarium species*. In: *An illustrated manual for identification*. The Pennsylvania State University Press, p. 190.
- Parkinson, D., Williams, S.T., 1961. A method for isolate fungi from soil microhabitats. *Plant and Soil* 13, 347–355.
- Pinheiro, J., Bates, D., 2000. *Mixed-Effects Models in S* an S-PLUS. Springer.
- Pinheiro, J., Bates, D., Deb Roy, S., Sarkar, D., 2013. the R Development Core Team. *nlme: Linear and Nonlinear Mixed Effects Models*. R package version 3, 1–108.
- Plaza Bonilla, D., Nolot, J.M., Passon, S., Raffailac, D., Justes, E., 2016. Grain legume-based rotations managed under conventional tillage need covers crops to mitigate soil matter losses. *Soil Tillage Res.* 156, 33–43. <https://doi.org/10.1016/j.still.2015.09.021>.
- Ring, I., Hansjürgens, B., Elmqvist, T., Wittmer, H., Sukhdev, P., 2010. Challenges in framing the economics of ecosystems and biodiversity: The TEEB initiative. *Curr. Opin. Sustain.* 2, 15–26. <https://doi.org/10.1016/j.cosust.2010.03.005>.
- Roldán, M.F., Videla, C., Studdert, G.A., San Martino, S., 2014. Distribución y estabilidad de agregados en Molisoles bajo labranzas constantes. *Ciencia del Suelo* 32, 247–257.
- Samson, R.A., Vann Reenen-Hoekstra, E.S., 1988. *Introduction to food borne pathogens*. Centralalbureau von Schimmelcultures, Netherlands.
- Schneider, T., Gerrits, B., Gassmann, R., Schmid, E., Gessner, M.O., Richter, A., Battin, T., Eberl, L., Riedel, K., 2010. Proteome analysis of fungal and bacterial involvement in leaf litter decomposition. *Proteomics* 10, 1819–1830. <https://doi.org/10.1002/pmic.200900691>.
- Silvestro, L.B., Biganzoli, F., Forjan, H., Albanesi, A., Arambarri, A.M., Manso, L., Moreno, M.V., 2017. Mollisols: biological characterization under zero tillage with different crops sequences. *Journal of Agricultural Sci. Technol.* 19, 245–257. ISSN: 1680-7073.
- Silvestro, L.B., Biganzoli, F., Stenglein, S.A., Forjan, H., Manso, L., Moreno, M.V., 2018. Mixed cropping regime promote the soil fungal community under zero tillage. *Anton van Leeuw. Int. J. G.* 111, 1055–1064. <https://doi.org/10.1007/s10482-017-1005-5>.
- Simmons, E.G., 2007. *Alternaria An identification manual*. CBS Fungal Biodiversity Centre Utrecht, Netherlands.
- Soil Survey Staff. 2014. *Keys to Soil Taxonomy*. United States Department of Agriculture, Natural Resources Conservation Service. 12th Edition, 372 pp
- Steffan-Dewenter, I., Kessler, M., Barkmann, J., Bos, M.M., Buchori, D., Erasmi, S., Faust, H., Gerold, G., Glenk, K., Gradstein, S.R., Guhardja, E., Hartevelde, M., Hertel, D., Höhn, P., Kappas, M., Köhler, S., Leuschner, C., Maertens, M., Marggraf, R., Migge-Kleian, S., Mogeia, J., Pitopang, R., Schaefer, M., Schwarze, S., Sporn, S.G., Steingrebe, A., Tjitrosoedirdjo, S.S., Tjitrosoemito, S., Twele, A., Weber, R., Woltmann, L., Zeller, M., Tschardtke, T., 2007. Trade-offs between income, biodiversity, and ecosystem functioning during tropical rainforest conversion and agroforestry intensification. *PNAS* 104, 4973–4978. <https://doi.org/10.1073/pnas.0608409104>.
- Stockmann, U., Adams, M.A., Crawford, J.W., Field, D.J., Henakaarchchi, N., Jenkins, M., Minasny, B., McBratney, A.B., de Courcelles, V., Singh, K., Wheeler, I., Abbott, L., Angers, D.A., Baldock, J., Bird, M., Brookes, P.C., Chenu, C., Jastrow, J.D., Lal, R., Lehmann, J., O'Donnell, A.G., Parton, W.J., Whitehead, D., Zimmermann, M., 2013. The knowns, known unknowns and unknowns of sequestration of soil organic carbon. *Agri. Ecosyst. Environ.* 164, 80–99. <https://doi.org/10.1016/j.agee.2012.10.001>.
- Studdert, G.A., Echeverría, H.E., Casanovas, E.M., 1997. Crop-pasture for sustaining the quality and productivity of a typical argudoll. *Soil Sci. Soc. Am. J.* 61, 1466–1472.
- Talley, S.M., Coley, P.D., Kursar, T.A., 2002. The effect of wheater on fungal abundance and richness among 25 communities in the intermountain west. *BMC Ecol.*
- USDA-NRCS. 2004. *Soil Survey Laboratory Methods Manual*. Soil Survey Investigations Report number 42. Version 4.0. USDA (United States Department of Agriculture)- NRCS (Natural Resources Conservation Service) – National Soil Survey Center.
- USDA, 2006. *Keys to soil taxonomy, 10th ed.* EEUU, p. 332.
- Van der Wal, A., Van Veen, J.A., Smant, W., Boschker, H.T.S., Bloem, J., Kardol, P., Van der Putten, W.H., De Boer, W., 2006. Fungal biomass development in a chronosequence of land abandonment. *Soil Biol. Biochem.* 38, 51–60. <https://doi.org/10.1016/j.soilbio.2005.04.017>.
- Viaud, M., Pasquier, A., Brygou, Y., 2000. Diversity of soil fungi studied by PCR-RFLP or ITS. *Mycol. Res.* 104, 1027–1052. <https://doi.org/10.1017/S0953756200002835>.
- Walkley, A., Black, I., 1934. An examination of the Degtjareff method for determining soil organic matter and a proposed modification of the chromic acid titration method. *Soil Sci.* 37, 29–38.
- Watanabe, T., 2002. *Pictorial atlas of soil and seed fungi: morphologies of cultured fungi and key to species*. T. Watanabe (ed.), Second Ed. CRC Press, Washington DC.
- Zadoks, J.C., Chang, T.T., Konzak, C.F., 1974. A decimal code for the growth stages of cereals. *Weed Res.* 14, 415–421.
- Zuur, A.F., Ieno, E.N., Walker, N.J., Saveliev, A.A., Smith, G.M., 2009. *Mixed Effects Models and Extensions in Ecology with R*. Springer.

Further reading

- Kuprinsky, J.M., Bailey, K.L., Mc Mullen, M.P., Gossen, B.D., Turkington, T.K., 2002. Managing plant disease risk in diversified cropping systems. *Agron. J.* 94, 198–209.

R-Core team. <http://www.R-project.org/>.