Bulgarian Journal of Agricultural Science, 31 (No 1) 2025, 75–84

Tillage or no-tillage: impact on the root fungal community of cereals and legumes grown on several stations in the semi-arid region of Eastern Algeria

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Abstract

Madi-Djedid, N., Metahri, M. S. & Saadoun, N. (2025). Tillage or no-tillage: impact on the root fungal community of cereals and legumes grown on several stations in the semi-arid region of Eastern Algeria. *Bulg. J. Agric. Sci., 31*(1), 75–84

Plants harbor in their root systems non-pathogenic fungi called endophytes. They are able to confer to the host plants a better resistance to biotic and abiotic stresses. Understanding their responses to no-tillage practices could be a promising strategy for optimizing the profitability and sustainability of farming systems. In this context, the objective of the present work is to determine the composition of the root fungal community of cereal-legume agrosystems in semi-arid Algerian zones. The experimental set up consists in comparing the influence of no-tillage and conventional tillage on the nature of the root fungal community according to the nature of the plant and the site. The main results obtained show that tillage has little effect on root fungal communities. In contrast, the interaction of tillage effects with the nature of the plant and site significantly influences the composition of these communities. Although the nature of the plant is a factor in the variation of this community, The major effect would be mainly related to the station. This result suggests that the identified strains belong to a disturbance-resistant core soil microbiome that is transmitted to the roots, driven by soil environmental conditions and additional host effects. Finally, it appears that the combination of the effects of no-till with the crop and the site affects the nature of the endophytic fungi whose functional traits remain to be identified.

Keywords: root; fungi; direct seeding; microbiota; cereal; legume

Introduction

The growth and productivity of cereals and fodder legumes in the semi-arid high plains are limited by a number of abiotic constraints, of a hydric nature due to low rainfall (Chennafi et al., 2006) and of a technical nature, linked to conventional production practices based essentially on tillage (Lopez-Bellido, 1992; Saber & Mrabet, 2002). This type of practice is often blamed for soil degradation. Because of their exposure to erosion, which is responsible for their loss of fertility, and therefore the sustainability of their production capacity (Singh et al., 2012). The tillage causes organic matter to be buried deep down, and the depleted surface horizon is made up of loose, unstable aggregates whose dispersion reduces soil permeability (Hernanz et al., 2002). To avoid this type of practice, adopting conservation agriculture techniques would be an alternative technical model to conventional production systems (Giller et al., 2015). No-tillage is one of the main components of conservation agriculture (Aibar, 2006; García et al., 2014).

This practice limits soil degradation following the increase in organic matter content in the surface horizon (Duiker & Lal, 1999; Yang & Wander 1999; Fernández-Ugalde et al., 2009; Razafimbelo et al., 2018). It improves water retention and stimulates biological activity by preventing the soil from turning over, maintaining the surface layers of mulch and the root system of previous crops (Tebrügge & Düring, 1999). Improving biological activity generates a diverse and active soil biotic community, responsible for soil fertility (Legrand et al., 2018). Endophytic fungi, often identified in the rhizosphere, make up a large part of this biotope, known for their role in reinforcing the growth and defence of their hosts in the face of stress factors (Selosse et al., 2004; Dudeja et al., 2012; Kia et al., 2019). Some studies show that the composition and diversity of this rhizospheric fungal community vary significantly depending on the type of vegetation (Hartman et al., 2018) and according to soil preparation techniques, which play an important role in the formation of microbial communities associated with plant roots (Bünemann et al., 2006; Bulgarelli et al., 2012; Bonito et al., 2014; Higo et al., 2020).

However, there is little information on the plant fungal microbiota compared to the microbial microbiota (Michl et al., 2023) and more specifically on the direct impact of tillage techniques on endophytic fungi whose hyphal networks are likely to be sensitive to disturbances caused by conventional tillage practices. In this sense, we assume that the composition of the fungal root community of cereals and legumes would be significantly specific to each crop and significantly affected by tillage techniques, in terms of diversity, richness and composition. More specifically, we assume that certain taxa will be favored by the absence of tillage, while others will be more predominant under conventional tillage.

The objectives of the present work are therefore to identify the endophytic fungi of the roots of cereals and legumes grown in several stations in the semi-arid region. analyse the richness and generic diversity of each community according to the comparative effect between conventional tillage and no-till, assess the importance of the effect of these tillage techniques in relation to that of the nature of the crop (cereal, legume), the site and their interactions.

Materials and Methods

Description of study sites

Field trials were carried out during the 2017-2018 agricultural period, at four experimental stations, located in a semi-arid bioclimatic zone in the wilayas of Sétif and Bordj Bou Arreridj (Wilaya: administrative entity equivalent to a département) (Figure 1). These stations are run by the Institut

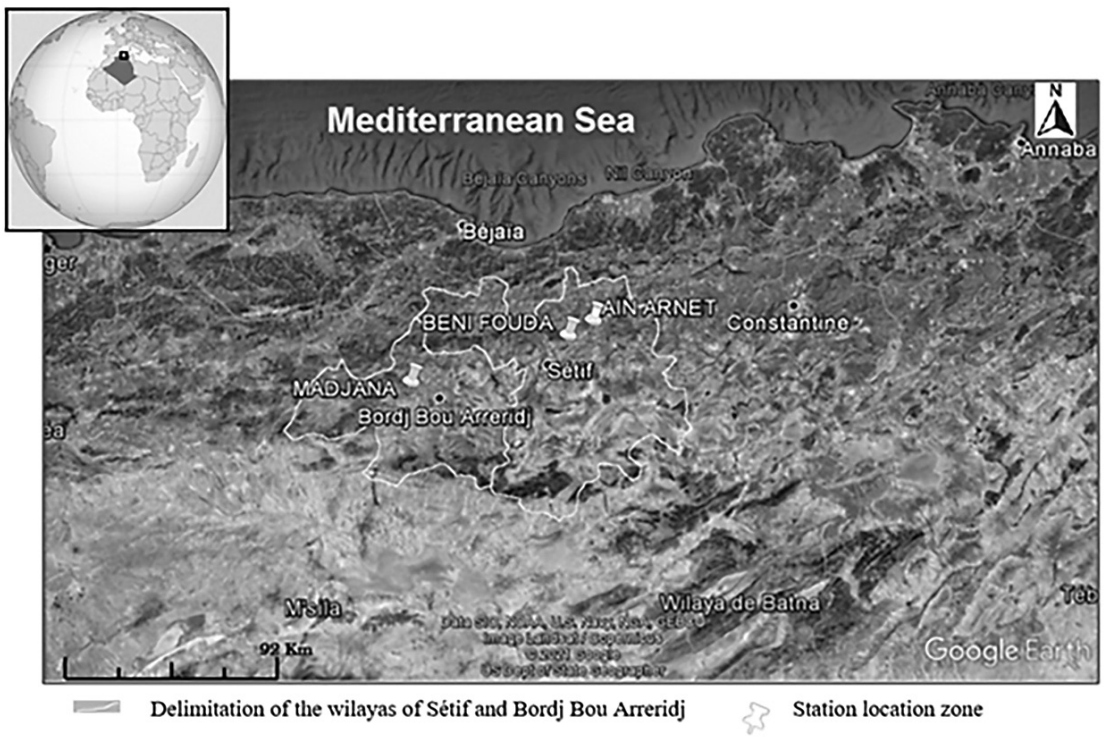

Fig. 1. Location of the study area (Ain Arnet, Beni Fouda, Madjana, Algeria) (Google Earth)

Technique des Grandes Cultures (I.T.G.C.) in Sétif, Algeria. They are in their sixth year of comparing no-tillage with conventional tillage, on cereal and legume crops grown on two adjacent plots. The stations concerned are: (Ain arnet – Sétif) cultivated by *Triticum durum* Desf/*Pisum sativum* L; (Beni fouda – Sétif); cultivated by *Triticum durum* Desf/ *Lens culinaris*; (Madjana 1- Bourdj Bou Arreridj) cultivated by *Triticum durum* Desf/ *Lens culinaris*;(Madjana 2- Bourdj Bou Arreridj) cultivated by *Triticum durum* Desf/*Vicia sativa* L.

Experimental design

The variation factors studied were site, tillage and crop. On each of the sites studied, the experiment involved two types of tillage (no-tillage, conventional tillage) in association with two types of crops (cereals and legumes). The experimental set-up is a split-plot over an area of 1.3 ha, with 2 types of tillage on the large plots and the type of crop in the small plots. To characterize the endophytic fungi (isolation, culture, identification), 3 samples were taken for each treatment. Ploughing is carried out using a ploughshare and a covercrop. No-tillage is carried out using a Semeato seed drill.

Sampling method

Root sampling was carried out in March, during the vegetative growth period of cereals and legumes. To do this, a quadrat of dimension (25 cm × 25 cm × 10 cm) was used, thrown at random three times in each of the small plots, and the root systems within each of these quadrats were sampled.

Isolation and cultivation of endophytic fungi

After drying the root biomass and separating it from the rhizospheric soil and the rhizoplane, we selected twenty fragments, about 1 cm long and 0.5 mm in diameter, at a depth of 10 cm of the root systems, taken from each of the quadras. These fragments are sterilised using the protocol of Schulz et al. (1993), to eliminate the epiphytes that remain in the rhizosphere. To do this, all the root fragments were washed under running water to remove any remains of rhizoplan, then treated with ethanol (95%) for 2 min and bleach (99.99%) for 3 min respectively. This sterilisation is completed by a second treatment with 95% ethanol for 30 seconds. Switching from one treatment to another is done after rinsing with sterilised distilled water. The root fragments are then inoculated on PDA with chloramphenicol, at a rate of four fragments per Petri dish. Finally, after four weeks' incubation at room temperature, the colonies obtained were sampled and identified.

Identification des isolats fongiques endophytes

The identification of the different fungal genera is based on the observation of microscopic characteristics, while taking into account the morpho-cultural characteristics on PDA, these include the general appearance of the colony surface, its texture and pigmentation (Suryanarayanan et al., 2003). Microscopic identification was performed by observation with an optical microscope (Bently, Labscope, LW Scientific 200), taking into account the morphological characteristics of hyphae: partitioning, coloration, and reproductive forms; fruiting bodies, spore shapes and colors (Kim et al., 2011). This was also in reference to the generic identification key of Morelet & Kiffer (1997) and Barnett & Hunter (1998).

Variables measured during the study period

The percentage of colonization was calculated using the formula of Pimentel et al. (2006):

$$(\%) = \left(\frac{Nc}{Nt}\right) \times 100,$$

where: *Nc* – number of segments colonized by endophytes;

Nt – total number of segments.

Based on the frequency of occurrence of fungi, the Shannon-Wiener and Simpson biodiversity indices were estimated for fungal populations (Magurran, 1988) as follows;

$$H' = \sum_{i=1}^{s} p_i lnp_i ,$$

where: *H′* – Shannon-Wiener biodiversity index;

I – a fungal genus of the study environment.

P_i – Proportion of a genus *i* compared to the total number of genera (S), which is calculated as follows:

$$P_i = \frac{ni}{N},$$

where: *ni* – number of individuals for genus *I*;

N – total number of individuals (all genera).

The Simpson biodiversity index (D) has been estimated for fungal populations (Sagar & Sharma, 2012) as follows:

$$D = 1 - \sum_{i=1}^{s} p_i^2,$$

where: D – Simpson's biodiversity Index;

I – a fungal genus of study environment.

Pi: Proportion of a genus *i* compared with the total number of genera (S), calculated as follows:

$$P_i = \frac{ni}{N},$$

where: *ni* – number of individuals for genus *I;*

N – total number of individuals (all genera).

Statistical analysis was carried out using R software (R Core Team, 2018). Means were compared using analysis of variance (ANOVA), while the means of the treatments were compared using the Student-Newman-Keuls multiple comparisons of means test, $p < 0.05$ values were considered significant; $p < 0.01$ highly significant and $p < 0.001$ highly significant.

Results

Root fungal phylum composition

After identifying the endophytic fungal community present on 960 root fragments, percentages were calculated to illustrate the phyla identified on these roots from cereal and legume seedlings grown on four stations with a comparative effect between no-tillage and conventional sowing. On the basis of these results, the fungal community shows a predominance of the genus *Ascomycota* contributing to (~86.05% ± 13.94%; Figure 2) on all the roots and a presence of the genus *Zygomicota* on very few of them with a variation of 0 ± 11.41% (Figure 2). The remainder are unidentified strains (UNS), which appear on most of the roots studied, with a variation of 0% ± 27.89% (Figure 2).

The relative abundance of the phyla making up these root fungal communities differs significantly according to the type of tillage used (*Ascomycota*: $p > 0.05$; *Zygomycota*: $p > 0.05$; UNS: $p < 0.05$) and according to the comparative effect between cereals and legumes (*Ascomycota*: $p < 0.001$; *Zygomycota*: $p > 0.05$; UNS: $p < 0.05$). Significant variations were also obtained between the different stations (*Ascomycota*: $p > 0.05$; *Zygomycota*: $p > 0.05$; UNS: $p < 0.05$), because the fungi identified on the roots from the Ain arnet station are characterized by belonging entirely to the *Ascomycota* phylum. Unlike those identified on the roots from the Beni fouda station characterized by fungi belonging to the *Ascomycota* phylum and unidentified strains (UNS), in addition to *Zygomycota* for the two Madjana 1 and Madjana 2 stations. Overall, the structure of this fungal community is essentially down to the crops, because the *Ascomycota* phylum, which is very abundant, has only been affected by the latter. As for the interaction effects of these factors, significant effects were obtained in the case of the interaction of tillage techniques with the station (*Ascomycota*: $p > 0.05$; *Zygomycota*: $p > 0.05$; SNI: $p < 0.05$) and in the case of crop interaction with stations (*Ascomycota*: $p < 0.05$; *Zygomycota*: $p > 0.05$; SNI: $p > 0.05$).

Variation in generic fungal richness and diversity between tillage techniques, crops and sites

Tillage techniques had no significant impact on the richness and diversity of fungal genera obtained on the differ-

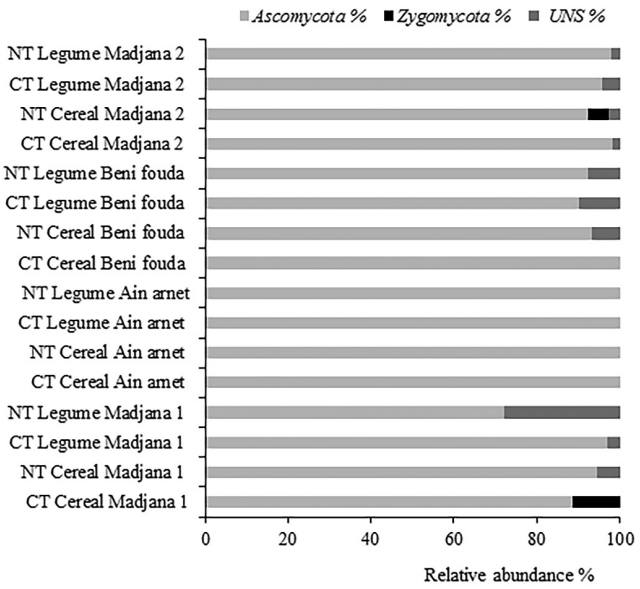

Fig. 2. Phylum composition of fungal communities (%) in the roots of cereals and legumes grown under no-tillage and conventional tillage, at different stations (UNS: unidentified strains; NT: no-tillage; CT: conventional tillage)

Table 1. Variation in the richness and diversity of generic fungi as a function of tillage, crop and station factors

Factors	Factors groups	Generic Richness	Simpson's index (D)	Shannon's index (S')
Tillage	CT	1.97 ± 0.10 ns	0.41 ± 0.03 ns	0.53 ± 0.04 ns
	NT	1.77 ± 0.09 ns	0.38 ± 0.03 ns	0.45 ± 0.04 ns
Crops	Cereal	2.10 ± 0.09 a	0.36 ± 0.02 ns	0.57 ± 0.04 a
	Legume	1.65 ± 0.10 b	0.43 ± 0.03 ns	0.41 ± 0.04 b
Station	Ain arnet	1.35 ± 0.12 a	0.35 ± 0.05 ns	0.28 ± 0.05 a
	Beni fouda	1.72 ± 0.12 ab	0.37 ± 0.04 ns	0.44 ± 0.05 ab
	Madjana 1	2.25 ± 0.14 c	0.43 ± 0.04 ns	0.59 ± 0.06 b
	Madjana 2	2.18 ± 0.13 bc	0.43 ± 0.03 ns	0.63 ± 0.06 b

All values are means ± SEM, SEM: standard errors of the mean, means followed by different letters in the same column are significantly different ($p \leq 0.05$), ns: not significant, CT: Conventional tillage, NT: no-tillage

Table 2. Variation in the richness and diversity of generic fungi as a function of the interaction of tillage, crop and site factors

Factors	Factors groups	Generic Richness	Simpson's index (D)	Shannon's index (S')
T*C	CT Cereal	2.28 ± 0.13 ns	0.39 ± 0.03 ns	0.65 ± 0.06 ns
	CT Legume	1.67 ± 0.15 ns	0.41 ± 0.05 ns	0.41 ± 0.06 ns
	NT Cereal	1.92 ± 0.13 ns	0.33 ± 0.04 ns	0.49 ± 0.06 ns
	NT Legume	1.01 ± 0.12 ns	0.44 ± 0.04 ns	0.41 ± 0.05 ns
T*S	CT Ain arnet	1.40 ± 0.21 a	0.38 ± 0.07 ns	0.30 ± 0.08 ns
	CT Beni fouda	1.67 ± 0.18 ab	0.37 ± 0.06 ns	0.42 ± 0.08 ns
	CT Madjana 1	2.23 ± 0.19 bc	0.38 ± 0.05 ns	0.59 ± 0.08 ns
	CT Madjana 2	2.60 ± 0.18 c	0.49 ± 0.04 ns	0.80 ± 0.07 ns
	NT Ain arnet	1.30 ± 0.14 a	0.32 ± 0.06 ns	0.27 ± 0.06 ns
	NT Beni fouda	1.77 ± 0.17 ab	0.36 ± 0.05 ns	0.46 ± 0.07 ns
	NT Madjana 1	2.27 ± 0.22 bc	0.48 ± 0.05 ns	0.60 ± 0.09 ns
	NT Madjana 2	1.77 ± 0.16 ab	0.37 ± 0.05 ns	0.46 ± 0.07 ns
C*S	Cereal Ain arnet	1.80 ± 0.16 b	0.27 ± 0.05 a	0.43 ± 0.08 ab
	Cereal Beni fouda	1.83 ± 0.15 b	0.29 ± 0.05 ab	0.45 ± 0.08 ab
	Cereal Madjana 1	2.66 ± 1.22 c	0.53 ± 0.04 b	0.81 ± 0.08 c
	Cereal Madjana 2	2.10 ± 0.15 bc	0.37 ± 0.04 ab	0.60 ± 0.08 bc
	Legume Ain arnet	0.90 ± 0.15 a	0.44 ± 0.08 ab	0.15 ± 0.06 a
	Legume Beni fouda	1.60 ± 1.19 ab	0.45 ± 0.06 ab	0.43 ± 0.07 ab
	Legume Madjana 1	1.83 ± 0.17 b	0.33 ± 0.05 ab	0.38 ± 0.07 ab
	Legume Madjana 2	2.26 ± 1.22 bc	0.48 ± 0.05 ab	0.68 ± 0.08 bc
T*C*S	CT Cereal Ain arnet	2.13 ± 0.29 bce	0.34 ± 0.08 ns	0.56 ± 0.13 bce
	CT Cereal Beni fouda	2.13 ± 0.25 bce	0.37 ± 0.07 ns	0.60 ± 0.12 bce
	CT Cereal Madjana 1	2.60 ± 0.29 ce	0.47 ± 0.06 ns	0.78 ± 0.11 ce
	CT Cereal Madjana 2	2.26 ± 0.21 bce	0.42 ± 0.06 ns	0.68 ± 0.10 bce
	NT Cereal Ain arnet	1.46 ± 0.13 ac	0.20 ± 0.06 ns	0.29 ± 0.08 ac
	NT Cereal Beni fouda	1.53 ± 0.16 ac	0.21 ± 0.06 ns	0.31 ± 0.09 ac
	NT Cereal Madjana 1	2.73 ± 0.33 de	0.58 ± 0.06 ns	0.84 ± 0.12 de
	NT Cereal Madjana 2	1.93 ± 0.23 bce	0.32 ± 0.06 ns	0.50 ± 0.11 ace
	CT Legume Ain arnet	0.66 ± 0.16 a	0.43 ± 0.12 ns	0.04 ± 0.04 a
	CT Legume Beni fouda	1.20 ± 0.20 ab	0.38 ± 0.09 ns	0.25 ± 0.08 ab
	CT Legume Madjana 1	1.86 ± 0.24 bce	0.30 ± 0.07 ns	0.42 ± 0.10 acd
	CT Legume Madjana 2	2.93 ± 0.28 e	0.55 ± 0.05 ns	0.93 ± 0.10 e
	NT Legume Ain arnet	1.13 ± 0.24 ab	0.44 ± 0.10 ns	0.25 ± 0.09 ad
	NT Legume Beni fouda	2.00 ± 0.29 bce	0.52 ± 0.07 ns	0.60 ± 0.11bce
	NT Legume Madjana 1	1.80 ± 0.24 ace	0.37 ± 0.08 ns	0.35 ± 0.10 acd
	NT Legume Madjana 2	1.60 ± 0.23 acd	0.42 ± 0.08 ns	0.42 ± 0.09 ace

All values are means ± SEM, SEM: standard errors of the mean, means followed by different letters in the same column are significantly different ($p \leq 0.05$), ns: not significant, CT: Conventional tillage, NT: no-tillage, T: tillage, C: crops, S: station

ent roots ($p > 0.05$). However, significant variations were obtained between crops for generic richness ($p < 0.05$) and Shannon's diversity index ($p < 0.01$). And between the various stations; Generic richness: $p < 0.001$; Shannon index (S'): $p < 0.001$ (Table 1). It is important to note that tillage techniques have a highly significant effect on generic richness ($p < 0.01$) and the Shannon diversity index ($p < 0.01$) in the case of their simultaneous interaction with crops and stations (T*C*S), and generic richness ($p < 0.05$) in the case of their interaction with the station effect (T*S) (Table 2).

Variation in fungi genera

Tillage effect

The results show a dominance of the genus *Fusarium* on all the roots from no-tillage and conventional tillage (Figure 3). However, these results show a significantly higher pres-

ence of 3.39% for the genus Aspergillus and 4.41% for unidentified strains (UNS), on no-tillage roots compared with conventional roots. There was also a significant reduction of 8.97% in the *Alternaria* genus on no-tillage roots compared with those grown under conventional tillage.

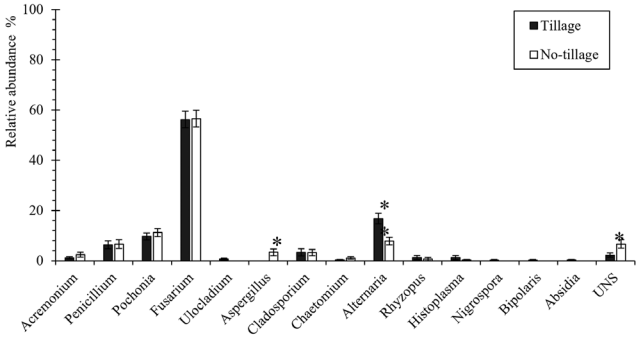

Fig. 3. Effect of tillage practices on the relative abundance of different fungal genera

Crop effect

The comparative effect between cereals and legumes showed significant differences in some fungal genera: *Fusarium, Aspergillus*, and unidentified strains (UNS) (Figure 4). More specifically, the *Fusarium* genera were found to decrease significantly on legume roots by 14.62%, unlike unidentified strains (UNS), which are significantly more abundant on legume roots by 5.22%. Fungi of the genus *Aspergillus* only appear significantly on legume roots, with an abundance of 3.65%.

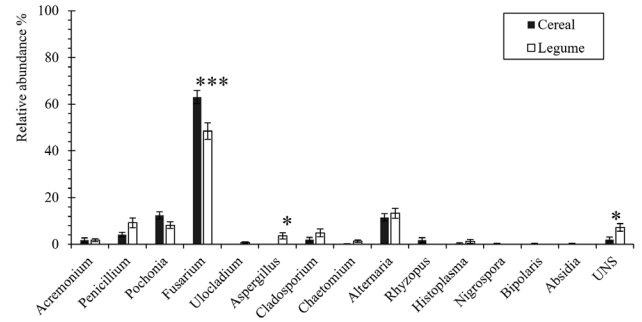

Fig. 4. Effect of crop type on the relative abundance of fungal genera

Station effect

The results of the comparative effect between the different stations (Figure 5) show a predominance of the genus *Fusarium* on all the stations studied, with a variation from 33.59% to 70.21%. Some fungi are also present in all the stations: *Penicillium* (from 2.72% to 10.79%), *Pochonia* (from 6.68% to 13.64%) and *Alternaria* (from 4.90% to 15.37%), although significant variation was only obtained for the *Alternaria* genus. The other fungal genera identified are less abundant and specific to some sites, such as the genus *Aspergillus*, which was identified exclusively at the Madjana 1 station, with a significant abundance of 6.43%.

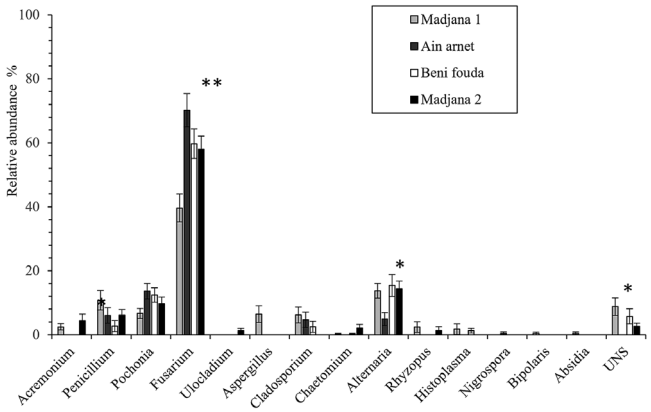

Figure 5. Effect of stations on the relative abundances obtained for each fungal genus

The comparative effect between tillage, crops and stations

Tillage techniques have a significant impact on certain fungi, in the case of their interactions with the other factors studied (Figure 6). In fact, tillage techniques have a significant impact on the genera; *Aspergillus* ($p < 0.05$), *Acremonium* ($p < 0.05$) et *Pochonia* ($p < 0.05$) in the case of their interactions with the nature of speculation T*C. They also have significant effects on the genera; *Aspergillus* ($p < 0.001$), *Penicillium* ($p < 0.05$), *Pochonia* ($p < 0.05$), *Fusarium* ($p < 0.01$) and *Ulocladium* ($p < 0.05$) in the case of their interactions with the station factor T*S. In addition, the simultaneous interaction of tillage techniques with these last two factors also produced significant effects on fungi of the genus *Ulocladium* ($p < 0.05$), *Aspergillus* ($p < 0.001$) et *Alternaria* ($p < 0.05$). As for the interaction between the effects of stations and crops S*C, the results indicate that *Aspergillus* ($p < 0.001$) et *Chaetomium* ($p < 0.005$) varied significantly between these two treatments (Figure 6).

Discussion

The results obtained show that tillage has no profound effect on root fungal communities, because the distribution pattern of the fungi making up these identified communities essentially comes back to the stations monitored by the crops. In this sense, our results go against the work of Hart-

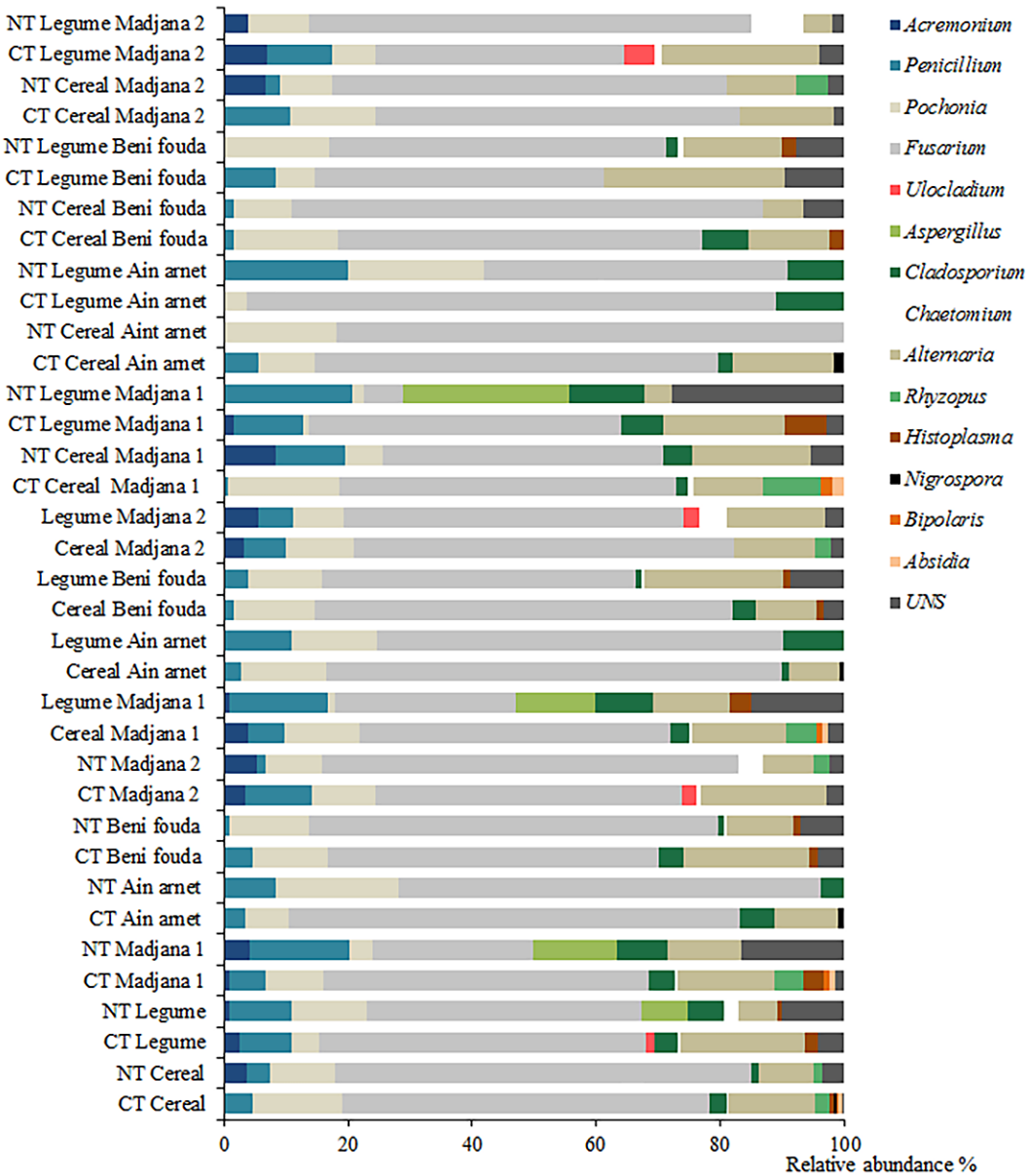

Fig. 6. Effect of the interaction of tillage techniques, crops and stations on fungal genera (CT: Conventional tillage; NT: no-tillage)

man et al. (2018) and Kia et al. (2019) who confirmed that tillage techniques induce profound disturbances on the root fungal community. Furthermore, very little work has been done on the direct impact of tillage on endophytic fungi at root level (Michl et al., 2023). Unlike the soil, where several studies have examined how this work affects its microbiome, considered to be the main vector for the transmission of endophytic fungi to roots. For example, Sharma-Poudyal et al. (2017) found that ploughing had an impact on fungal communities, but many of these fungi were not affected by no-tillage, presumed to be a generalist niche. Although we did not specifically study fungi at soil level, we consider that our results are consistent with this finding, since the composition of the soil microbial pool is a determining factor in the composition of root microbial communities (Haney et al., 2015).

This suggestion thus confirms the richness and notable generic fungal diversity obtained between the different stations. Since fungal contamination of plants and the performance resulting from their contamination can be affected by limiting factors in the soil (Milleret et al., 2009). More specifically, the minor effect of tillage techniques observed in this study is reflected in the absence of their direct effects on Shannon and Simpson fungal richness and diversity and by the reduced number of fungal genera directly affected by no-tillage, namely *Alternaria*, *Aspergillus* and UNS. Consequently, the resistance of the remaining fungal genera to no-tillage practices may lie with members of the central soil microbium (Shade et al., 2012), transmitted to the roots and which confers stability on the soil biological community as a response to disturbances (Rykiel & Edward, 1985). Similarly, the fungal community identified on all the roots is characterised by a dominant abundance of *Asocmycota*, considered to be the main players in the degradation of crop residues (Ma et al., 2013).

The type of tillage was not a determining factor in their relative abundance, unlike the comparative effect between cereals and legumes. since fungi of the genus *Fusarium* are the dominant genus of these *Ascomycota*, and their relative abundance decreases significantly on legume roots compared with cereal roots. It is interesting to note that these fungi are very prevalent at the four stations studied, they are considered to be bio-indicators of the ecological transition that is unfolding over time (Elmholt, 1996). This is because high levels of crop contamination have been reported, mainly in the case of no-tillage, due to the inoculum present mainly in crop residues (Miller et al., 1998; Baliukoniene et al., 2011). This finding suggests the need to apply no-tillage over the long term in order to have a similar effect on all the stations studied. The beneficial presence of these fungi lies in their role in improving the living conditions of crops grown in such an environment marked by severe climatic stress. In addition, their simultaneous presence with fungi of the Pochonia genus confers positive effects on host plants while competing with other fungal colonisers. In addition, their simultaneous presence with fungi of the *Pochonia* genus confers positive effects on host plants while competing with other fungal colonisers. As has already been demonstrated with regard to the incidence of barley disease caused by the pathogen *Gaeumannomyces graminis* var. *tritici* (Maciá-Vicente et al., 2009). With regard to the results obtained from the simultaneous effect of tillage techniques, stations and crops.

The significant presence of the genus *Aspergillus* on the roots of no-tillage legumes grown at Madjana 1, may be due to the presence of inoculum in crop residues and to changes in soil properties caused by these residues (Nesci et al., 2006; Zablotowicz et al., 2007; Essel et al., 2018). Moreover, the exclusive presence of *Aspergillus* in the Madjana 1 station, may be due to environmental conditions in the soil, linked to pH, electrical conductivity, nitrogen, carbon and saturation, which govern the transfer of these fungi from the soil to the plant (Hiba et al., 2015). As for the results relating to the significant and exclusive presence of the genus *Ulocladium* on the roots of conventionally sown legumes at Madjana 2, and a significant reduction in the *Alternaria* genus on the roots of no-tillage legumes and cereals. They may be due to environmental changes in the soil brought about by no-tillage techniques and the crop grown, since plants release substances, such as bioactive phytochemicals that have a direct effect on the fungi growing in their rhizospheres. In this sense, the significant reduction in the *Fusarium* genus obtained in legumes can be explained by the micro-organisms hosted in their nodules, which control the development of pathogens in a sustainable way (Bahroun et al., 2017). This has had a direct impact on the *Pochonia* genus.

For the abundance of UNS is significantly high in legumes, this can be explained by their ability to form numerous symbiotic associations with several fungi (Graham & Vance, 2003). Therefore, these results are in agreement with Harthman et al. (2018) who show that the root fungal community is directly related to vegetation type and according to Dudeja et al. (2012) and Gundel et al. (2012), it also depends on the fungal species, the host genotype and its stage of development. This shows the importance of including legumes in cereal crop rotations, because they are an essential lever for improving production by modifying root fungal diversity (Borrell et al., 2017). What's more, adding no-tillage to these cultivation techniques is a management strategy that can bring about changes in plant metabolism, which results in the production of secondary metabolites, which determine the passage of certain fungal genera from the soil to the plant (Żukiewicz-Sobczak et al., 2012).

Conclusion

Fungal communities identified on cereal and legume roots, from semi-arid zones are mainly composed of strains of the genus *Fusarium*, known for their role in improving the living conditions of crops, in the face of the region's biotic and abiotic constraints. The distribution pattern of the fungi that make up these communities depends essentially on the type of site and is followed by the type of crop. As for tillage techniques, a large proportion of these fungi were not affected by their direct effects, comparatively in the case of their interactions with the station and the crop. It is therefore assumed that these fungi belong to a central soil microbiome, resistant to disturbance, mainly transmitted to the roots, under the effect of the environ-

mental conditions of the soil and the additional effects of the host. Consequently, understanding the abundance patterns of tillage-sensitive fungi, is a strategy for managing endophytic fungi as part of intelligent agriculture.

References

Aibar, J. (2006). Weed control in no-till cereals. Main problems. *Options Méditerranéennes: Series A. Mediterranean Seminars, 69,* 19-26.

Bahroun, A., Jousset, A., Mhamdi, R., Mrabet, M. & Mhadhbi, H. (2017). Anti-fungal activity of bacterial endophytes associated with legumes against *Fusarium solani*: Assessment of fungi soil suppressiveness and plant protection induction. *Applied Soil Ecology*, *124*, 131-140. https://doi.org/10.1016/j.apsoil.2017.10.025.

Baliukoniene, V., Bakutis, B., Januskeviciene, G. & Miseikiene, R. (2011). Fungal contamination and *Fusarium* mycotoxins in cereals grown in different tillage systems. *Journal of Animal and Feed Sciences, 20*(4), 637-647. https://doi.org/10.22358/jafs/66222/2011.

Barnett, H. L. & Hunter, B. B. (1998). Illustrated Genera Of Imperfect Fungi. The American Phytopathological Society. US Department of Agriculture, Agricultural Research Service, Washington State University, Pullman. *APS Press.* USA. St. Paul, Minnesota USA, 218.

Bonito, G., Reynolds, H., Robeson, M. S., Nelson, J., Hodkinson, B. P., Tuskan, G., Schadt, C. W. & Vilgalys, R. S. (2014). Plant host and soil origin influence fungal and bacterial assemblages in the roots of woody plants. *Molecular Ecology*, *23*(13), 3356-3370. https://doi.org/10.1111/mec.12821.

Borrell, A. N., Shi, Y., Gan, Y., Bainard, L. D., Germida, J. J. & Hamel, C. (2017). Fungal diversity associated with pulses and its influence on the subsequent wheat crop in the Canadian prairies. *Plant and Soil*, *414*(1), 13-31.https://doi.org/10.1007/s11104-016-3075-y.

Bulgarelli, D., Rott, M., Schlaeppi, K., Ver Loren van Themaat, E., Ahmadinejad, N., Assenza, F., Rauf, P., Huettel, B., Reinhardt, R., Schmelzer, E., Peplies, J., Gloeckner, F. O., Amann, R., Eickhorst, T. & Schulze-Lefert, P. (2012). Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota. *Nature*, *488*(7409), 91-95.

Bünemann, E. K., Schwenke, G. D. & Van Zwieten, L. (2006). Impact of agricultural inputs on soil organisms. *Australian Journal of Soil Research*, *44*(4), 379-406. https://doi.org/10.1071/SR05125.

Chennafi, H., Aïdaoui, A., Bouzerzour, H. & Saci, A. (2006). Yield response of durum wheat (*Triticum durum* Desf.) cultivar Waha to deficit irrigation under semi-arid growth conditions. *Asian Journal of Plant Sciences*, *5*(5), 854-860. http://docsdrive.com/pdfs/ansinet/ajps/2006/854-860.pdf.

Dudeja, S. S., Giri, R., Saini, R., Suneja-Madan, P. & Kothe, E. (2012). Interaction of endophytic microbes with legumes. *Journal of Basic Microbiology*, *52*(3), 248-260. https://doi.org/10.1002/jobm.201100063.

Duiker, S. W. & Lal, R. (1999). Crop residue and tillage effects on carbon sequestration in a Luvisol in central Ohio. *Soil and Tillage Research*, *52*(1-2), 73-81. https://doi.org/10.1016/S0167-1987(99)00059-8.

Elmholt, S. (1996). Microbial activity, fungal abundance and distribution of *Penicillium* and *Fusarium* as bioindicators of a temporal development of organically cultivated soils. *Biological Agriculture and Horticulture 13*(2), 123–140. https://doi.org/10.1080/01448765.1996.9754772.

Essel, E., Li, L., Deng, C., Xie, J., Zhang, R., Luo, Z. & Cai, L. (2018). Evaluation of bacterial and fungal diversity in a long-term spring wheat–field pea rotation field under different tillage practices. *Canadian Journal of Soil Science, 98*(4), 619-637. https://doi.org/10.1139/cjss-2017-0155.

Fernández-Ugalde, O., Virto, I., Bescansa, P., Imaz, M. J., Enrique, A. & Karlen, D. L. (2009). No-tillage improvement of soil physical quality in calcareous, degradation-prone, semiarid soils. *Soil and Tillage Research*, *106*(1), 29-35. https://doi.org/10.1016/j.still.2009.09.012.

García, A. L., Royo-Esnal, A., Torra, J., Cantero-Martinez, C. & Recasens, J. (2014). Integrated management of *Bromus diandrus* in dryland cereal fields under no-till. *Weed Research Journal*, *54*(4), 408-417. https://doi.org/10.1111/wre.12088.

Giller, K. E., Andersson, J. A., Corbeels, M., Kirkegaard, J., Mortensen, D., Erenstein, O. & Vanlauwe, B. (2015). Beyond conservation agriculture. *Frontiers in Plant Science, 6*, 870. https://doi.org/10.3389/fpls.2015.00870.

Graham, P. H. & Vance, C. P. (2003). Legumes: Importance and Constraints to Greater Use. *Plant Physiology*, *131*(3), 872–877. https://doi.org/10.1104/pp.017004.

Gundel, P. E., Martínez-Ghersa, M. A., Omacini, M., Cuyeu, R., Pagano, E., Ríos, R. & Ghersa, C. M. (2012). Mutualism effectiveness and vertical transmission of symbiotic fungal endophytes in response to host genetic background. *Evolutionary Applications*, *5*(8), 838-849. https://doi.org/10.1111/j.1752-4571.2012.00261.x.

Haney, C. H., Samuel, B. S., Bush, J. & Ausubel, F. M. (2015). Associations with rhizosphere bacteria can confer an adaptive advantage to plants. *Nature Plants*, *1*(6), 1-9. https://doi.org/10.1038/nplants.2015.51.

Hartman, K., van der Heijden, M. G., Wittwer, R. A., Banerjee, S., Walser, J. C. & Schlaeppi, K. (2018). Cropping practices manipulate abundance patterns of root and soil microbiome members paving the way to smart farming. *Microbiome*, *6*(1), 1-14. https://doi.org/10.1186/s40168-017-0389-9.

Hernanz, J. L., López, R., Navarrete, L. & Sanchez-Giron, V. (2002). Long-term effects of tillage systems and rotations on soil structural stability and organic carbon stratification in semiarid central Spain. *Soil and Tillage Research*, *66*(2), 129-141. https://doi.org/10.1016/S0167-1987(02)00021-1.

Hiba, A., Laid, D. & Noreddine, K. C. (2015). The pattern of pathogen diversity and abundance in Lentil (*Lens culinaris*) fields in Constantine region, Algeria. *African Journal of Agricultural Research*, *10*(13), 1536-1542. https://doi.org/10.5897/AJAR2014.9310.

Higo, M., Tatewaki, Y., Iida, K., Yokota, K. & Isobe, K. (2020). Amplicon sequencing analysis of arbuscular mycorrhizal fungal communities colonizing maize roots in different cover cropping and tillage systems. *Scientific Reports, 10*(1), 6039.

Kia, S. H., Pallesch, S., Piepenbring, M. & Maciá-Vicente, J. G.

(2019). Root endophytic fungi show low levels of interspecific competition in planta. *Fungal Ecology*, *39*, 184-191.

Kim, J. Y., Yeo, S. H., Baek, S. Y. & Choi, H. S. (2011). Molecular and morphological identification of fungal species isolated from bealmijangmeju. *Journal of Microbiology and Biotechnology, 21*(12), 1270-1279. http://dx.doi.org/10.4014/jmb.1105.05013.

Legrand, F., Picot, A., Cobo-Díaz, J. F., Carof, M., Chen, W. & Le Floch, G. (2018). Effect of tillage and static abiotic soil properties on microbial diversity. *Applied Soil Ecology*, *132*, 135-145. https://doi.org/10.1016/j.apsoil.2018.08.016.

Lopez-Bellido, L. (1992). Mediterranean cropping systems. Ecosystems of the World, Field Crop Ecosystems. *Pearson, CJ (eds), Elsevier*, 311-356.

Ma, A., Zhuang, X., Wu, J., Cui, M., Lv, D., Liu, C. & Zhuang, G. (2013). Ascomycota members dominate fungal communities during straw residue decomposition in arable soil. *PloS one*, *8*(6), e66146. https://doi.org/10.1371/journal.pone.0066146.

Maciá-Vicente, J. G., Rosso, L. C., Ciancio, A., Jansson, H. B. & Lopez-Llorca, L. V. (2009). Colonisation of barley roots by endophytic *Fusarium equiseti* and *Pochonia chlamydosporia*: effects on plant growth and disease. *Annals of Applied Biology*, *155*(3), 391-401. https://doi.org/10.1111/j.1744-7348.2009.00352.x.

Magurran, A. T. (1988). Ecological Diversity and Its Management. *Princeton University Press,* New Jersey, USA.

Michl, K., Berg, G. & Cernava, T. (2023). The microbiome of cereal plants: The current state of knowledge and the potential for future applications. *Environmental Microbiome, 18*(1), 28.

Miller, D. J., Culley, J., Fraser, K., Hubbard, S., Meloche, F., Ouellet, T., Lloyd Seaman, W., Seifert, K. A., Turkington, K. & Voldeng, H. (1998). Effect of tillage practice on *Fusarium* head blight of wheat. *Canadian Journal of Plant Pathology*, *20*(1), 95-103.

Milleret, R., Le Bayon, R. C. & Gobat, J. M. (2009). Root mycorrhiza and earthworm interactions: their effects on soil structuring processes, plant and soil nutrient concentration and plant biomass. *Plant and soil*, *316*(1), 1-12.

Morelet, M. & **Kiffer, E.** (1997). Deuteromycetes: Classification and generic identification keys. *Editions Qua,*1-306.

Nesci, A., Barros, G., Castillo, C. & Etcheverry, M. (2006). Soil fungal population in preharvest maize ecosystem in different tillage practices in Argentina. *Soil and Tillage Research, 91*(1-2), 143-149. https://doi.org/10.1016/j.still.2005.11.014.

Pimentel, I. C., Glienke-Blanco, C., Gabardo, J., Stuart, R. M. & Azevedo, J. L. (2006). Identification and colonization of endophytic fungi from soybean (*Glycine max* (L.) Merril) under different environmental conditions. *Brazilian Archives of Biology and Technology*, *49*, 705-711. https://doi.org/10.1590/S1516-89132006000600003.

R Core Team (2018). A Language and Environment for Statistical Computing. R Foundation for Statistical Computing. Vienna, Austria.

Razafimbelo, T. M., Andriamananjara, A., Rafolisy, T., Razakamanarivo, H., Masse, D., Blanchart, E., Falinirina, M. V., Bernard, L., Ravonjiarison, N. & Albrecht, A. (2018). Climate smart agriculture impact on soil organic carbon stocks in Madagascar. *Cahiers Agricultures*, *27*(3), 35001. https://doi.org/10.1051/cagri/2018017.

Rykiel, J. R. & Edward, J. (1985). Towards a definition of ecological disturbance. *Australian Journal of Ecology*, *10*(3), 361-365. https://doi:10.1111/j.1442-9993.1985.tb00897.x.

Saber, N. & Mrabet, R. (2002). Influence of tillage and crop rotations on the quality of a swelling clay soil in a semi-arid Moroccan environment. *Etude et gestion des sols, 9*(1), 43-53.

Sagar, R. & Sharma, G. P. (2012). Measurement of alpha diversity using Simpson index (1/Lamda): the jeopardy. *Environmental Skeptics and Critics*, *1*(1), 23.

Schulz, B., Wanke, U., Draeger, S. & Aust, H. J. (1993). Endophytes from herbaceous plants and shrubs: effectiveness of surface sterilization methods. *Mycological Research*, *97*(12), 1447-1450. https://doi.org/10.1016/S0953-7562(09)80215-3.

Selosse, M. A., Baudoin, E. & Vandenkoornhuyse, P. (2004). Symbiotic microorganisms, a key for ecological success and protection of plants. *Comptes Rendus Biologies, 327*(7), 639-648. https://doi.org/10.1016/j.crvi.2003.12.008.

Shade, A., Peter, H., Allison, S. D., Baho, D. L., Berga, M., Bürgmann, H., Huber, D. H., Langenheder, S., Lennon, J. T., Martiny, J. B. H., Matulich, K. L., Schmidt, T. S. & Handelsman, J. (2012). Fundamentals of Microbial community resistance and Resilience. *Frontiers in Microbiology*, *3*, 417. https://doi.org/10.3389/fmicb.2012.00417.

Sharma-Poudyal, D., Schlatter, D., Yin, C., Hulbert, S. & Paulitz, T. (2017). Long-term no-till: a major driver of fungal communities in dryland wheat cropping systems. *PLoS one*, *12*(9), e0184611. https://doi.org/10.1371/journal.pone.0184611.

Singh, P., Sharratt, B. & Schillinger, W. F. (2012). Wind erosion and PM10 emission affected by tillage systems in the world's driest rainfed wheat region. *Soil and Tillage Research, 124*, 219-225. https://pubag.nal.usda.gov/download/56864/pdf.

Suryanarayanan, T. S., Venkatesan, G. & Murali, T. S. (2003). Endophytic fungal communities in leaves of tropical forest trees: diversity and distribution patterns. *Current Science*, *85*(4), 489-493.

Tebrügge, F. & Düring, R. A. (1999). Reducing tillage intensity - a review of results from a long-term study in Germany. *Soil and Tillage Research*, *53*(1), 15-28. https://doi.org/10.1016/S0167-1987(99)00073-2.

Yang, X. M. & Wander, M. M. (1999). Tillage effects on soil organic carbon distribution and storage in a silt loam soil in Illinois. *Soil and Tillage Research*, *52*(1-2), 1-9. https://doi.org/10.1016/S0167-1987(99)00051-3.

Zablotowicz, R. M., Abbas, H. K. & Locke, M. A. (2007). Population ecology of *Aspergillus flavus* associated with Mississippi Delta soils. *Food Additives and Contaminants*, *24*(10), 1102-1108. https://doi.org/10.1080/02652030701546198.

Żukiewicz-Sobczak, W., Cholewa, G., Krasowska, E., Zwoliński, J., Sobczak, P., Zawiślak, K., Chmielewska-Badora, J., Piątek, J. & Wojtyła, A. (2012). Pathogenic fungi in the work environment of organic and conventional farmers. *Advances in Dermatology & Allergology*, *29*(4), 252-262, doi. org/10.5114/pdia.2012.30463.

Received: **September, 04, 2023**; *Approved*: **December, 14, 2023;** *Published:* **February, 2025**