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Mycorrhizal colonization and diversity and corn genotype yield in soils of the Cerrado region, Brazil

Colonização e diversidade micorrízica e produtividade de genótipos de milho, em solo de Cerrado

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Abstract

The degree of interaction between arbuscular mycorrhizal fungi (AMF) and host plants appears to depend on plant genotype, which differentially promotes symbiosis and leads to different degree of mycotrophism. The aim of the present study was to assess root colonization, spore density, and diversity of AMF, as well as yield of corn (*Zea mays*) genotypes in soil from the Cerrado region of Brazil. Number of spores (NS), mycorrhizal colonization (COL), plant and ear height, dry weight (DW), and grain yield (GY) were assessed in inbred lines and their hybrids. Randomized blocks were used for the experimental design, with 30 treatments (genotypes) and three repetitions. The experiment was conducted on the farm of the UNESP-São Paulo State University, Campus of Ilha Solteira, and the plots were composed of two 2-m-long rows, with 0.85 m between rows, and 0.20 m between plants. Qualitative and quantitative changes were observed in fungal compositions, as well as preferential associations between symbiotic partners. Analysis of AMF diversity revealed the presence of 12 species, with *Scutellospora calospora* and *Entrophospora colombiana* being the most abundant in all treatments. The species *Acaulospora longula*, *Glomus etunicatum*, *Glomus macrocarpum,* and *Gigaspora margarita* exhibited preferential associations with certain genotypes. COL and GY differed among inbred lines and single-cross hybrids and the significant correlations between COL and the DW and GY showed positive interactions between the plants and AMF. There was no correlation between heterosis for GY and heterosis for colonization. These single-cross hybrids HS83 × E3 and D3 × F5 exhibited high GY, evidencing a productivity potential for the low technological condition used.

Key words: *Zea mays*, arbuscular mycorrhizal fungi, single-cross hybrids, inbred lines, species richness

Resumo

O grau de interação entre o fungo micorrízico arbuscular (FMA) e a planta hospedeira parece depender do genótipo da planta, o qual estimula diferentemente a simbiose, acarretando um menor ou maior grau de micotrofismo. Este trabalho objetivou verificar a colonização radicular, densidade de esporos e diversidade de FMA e produtividade de genótipos de milho, no cerrado. Foram avaliados o número de esporos, colonização micorrízica (COL), altura da planta e da inserção de espiga, massa de matéria seca (MS) e produtividade de grãos (PROD) em linhagens endogâmicas e híbridos. O delineamento

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experimental foi em blocos casualizados, com 30 tratamentos (genótipos) e três repetições. O experimento foi implantado na Fazenda de Pesquisa, Ensino e Extensão da UNESP-Univ Estadual Paulista, Campus de Ilha Solteira, sendo as parcelas constituídas de duas linhas de 2 m de comprimento, espaçadas de 0,85 m entre linhas e 0,20 m entre plantas. Observou-se a ocorreram mudanças qualitativas e quantitativas na composição fúngica, com associações preferenciais entre os genótipos. Para diversidade de FMA foram constatadas 12 espécies, sendo *Scutellospora calospora* e *Entrophospora colombiana* as espécies de maior ocorrência para todos os tratamentos. As espécies *Acaulospora longula*, *Glomus etunicatum*, *Glomus macrocarpum* e *Glomus margarita* exibiram associações preferenciais entre os genótipos. A COL e a PROD diferiram entre linhagens e entre híbridos e as correlações significativas entre COL e a MS e PROD evidenciam interações positiva entre planta e FMA. A heterose para PROD não mostrou correlação com a heterose da colonização. Os híbridos HS83 x E3 e D3 x F5 exibiram alta PROD, evidenciando um potencial produtivo para as condições tecnológicas utilizadas.

Palavras-chave: *Zea mays*, fungos micorrízicos arbusculares, híbridos, linhagens, riqueza de espécies

Introduction

Brazil is the third largest producer of corn grain in the world. Corn is cultivated on approximately 12.91 million hectares in each season, behind only the USA and China (INSTITUTO FNP, 2010). In addition to occupying a significant cultivation area in Brazil and generating employment in the primary sector, corn is important for its direct use in human and animal diets, as well as in the industrial production of a variety of everyday products (SCHUCH, 2013). For these reasons, it is currently one of the most studied and improved species.

Cultivation areas in the Cerrado region currently include extensive crops of cereals, legumes, and oilseeds. In Brazil, corn is grown in regions that are under some type of environmental stress, such as the Cerrado region, where small- and medium-scale farmers are responsible for more than 70% of the production (IBGE, 2008).

Among the microorganisms widely spread in terrestrial ecosystems, arbuscular mycorrhizal fungi (AMF) constitute a key functional group of soil organisms due to their effects on soil properties (RILLIG, 2004; GIANINAZZI et al., 2010). These fungi belong to the Phylum Glomeromycota, Class Glomeromycetes (STÜRMER; SIQUEIRA, 2006), and form symbiotic associations with most land plants. These associations are characterized by the development of highly branched hyphae known as arbuscules in the plant root cortex (GUTJAHR; PARNISKE, 2013).This association is advantageous for AMF, which establish mutualistic symbiotic relationships with the roots of more than 80% of existing plant species (SMITH; READ, 2008). The abundant fungal mycelia that result from root colonization participate in soil structuring and allow the fungus to absorb a greater amount of mineral nutrients and water (RILLIG; MUMMEY, 2006), which are transferred to the plant host, increasing their photosynthetic activity, enzyme activity, and development.

Specific interactions between fungi and plant genotypes allow the association to be more advantageous, regardless of colonization level. Analysis of fungus-host compatibility and the overall behavior of the interacting species (POUYÚ-ROJAS et al., 2006) indicate differential selectivity in fungus-host relationships and the presence of combinations with a highly variable symbiotic efficiency for the host plants.

The identification of correlations between the fungal characteristics and agronomic properties of specific plants will enable genetic improvements, particularly in rustic genotypes, benefitting farmers using low-cost technology and supplies as in the present study. If corn cultivars respond differentially to root colonization by AMF (REIS et al., 2008), it is important for improvement on breeding programs to consider the distinct relationships between corn genotypes and mycorrhizal fungi. Therefore, this study aimed to assess root colination, diversity and spore density of AMF, as well as yield of corn (*Zea mays*) genotypes in soil from the Cerrado region, Brazil.

Material and Methods

The experiment was conducted on the farm for Research, Teaching and Extension of the Faculty of Engineering, UNESP-Campus of Ilha Solteira, in the municipality of Selvíria-MS (51°22′W, 20°22′S), at an altitude of 335 masl. Mean annual temperature is 23.5 °C, and mean annual rainfall is 1.370 mm. The soil was classified as a Hapludox (EMBRAPA, 1999).

The area was originally covered by cerrado *sensu stricto*; however, it has since been cultivated. During the 2 years preceding the experiment, the area had been under no tillage system, without fertilization, and under a crop-rotation system with corn and *Crotalaria juncea*. Sowing was performed in December using hand planters and included the application of 20 kg ha^{-1} of N (urea) to the furrow. This was the only fertilization procedure and was intended to simulate low-technology conditions.

Before the start of the experiment, four samples of soil were collected, at a depth of 0 m to 0.15 m, and each sample comprised 10 individual samples The number of autochthonous AMF spores in the area was determined using part of the samples. Chemical characterization was performed using the remaining material, as described by Raij et al. (2001). The following results were obtained: pH ($CaCl_2$), 4.5; P (mg dm^{-3}), 20; OM (g dm^{-3}), 21; K, Ca, Mg, H+Al, Al, BS and CEC, 1.4, 11, 9, 42, 3, 22.2, and 64.2 mmol$_c$ dm^{-3}, respectively, and V = 35 (%).

Randomized blocks were used for the experimental design, with 30 treatments (genotypes) and three repetitions. The plots were composed of two 2-m-long rows, with 0.85 m between rows, and 0.20 m between plants. The 30 genotypes used were as follows: ten inbred endogamic lines (S_5) originated from the Flintisa (F1, F2, F3, F4, and F5) and Dentado (D1, D2, D3, D4, and D5) populations, three lines derived from the ESALQ - PB 1 (E1, E3, and E5) population, three single-cross hybrids of SEMEALI (Sementes Antoniali Ltd) (HS10, HS32, and HS83), five single-cross hybrids (D1 × F2, D2 × F4, D3 × F5, D4 × F3, and D5 × F1) and nine three-way cross hybrids (HS10 × E1, HS10 × E3, HS10 × E5, HS32 × E1, HS32 × E3, HS32 × E5, HS83 × E1, HS83 × E3, and HS83 × E5).

The Flintisa and Dentado populations were selected for low-technology conditions in an breeding program developed at UNESP, Campus of Ilha Solteira. Flintisa was obtained by recombination with the ESALQ - VF 1, SUWAN and CATETO COLÔMBIA populations, and underwent seven selection cycles before be used to produce the lines. Dentado population was obtained from the Germoplasm collection of the Embrapa-National Center for Research on Corn and Sorghum, Sete Lagoas, MG, and underwent six selection cycles before be used to produce the inbred endogamic lines The ESALQ - PB 1 population was obtained from seven short plant varieties at the Institute of Genetics of ESALQ/USP. The SEMEALI single-cross hybrids represent female parents used in the production of commercial hybrids.

Five plants were randomly selected from the grid 110 days after sowing. Plant height (PH), ear height (EH), and dry weight of the aerial portion (DW) were measured. Grain yield (GY) was calculated using the weight of grains produced in the grid area (grain moisture kept constant at 13%). EH and GY were measured and corrected to an ideal stand of 20 plants per plot by the covariance method, between GY and the stand.

Fifty-five days after sowing, when the plants developed tassels, a composite sample of 10 individual samples per block composed of soil and roots, was collected at a depth of 0 m to 0.15 m for microbiological analysis. The roots were washed in running water, cleared in a 10% KOH solution, acidified with 1% HCl, stained with 0.05% trypan blue, and stored in lactoglycerol (PHILLIPS; HAYMAN, 1970). Root colonization was assessed by light microscopy using 100 root segments per repetition. The spores of AMF were counted using a stereoscopic microscope (× 40 magnification) and 100 g of soil per sample, from which they were extracted via wet sieving and centrifugation in sucrose (50%).

Although AMF spore isolation for quantitative analysis followed the previously described method, but only the soil samples corresponding to the two single-cross hybrids that exhibited the highest grain yields and their parents were used. For the purpose of fungal identification, all spores were collected and transferred to permanent slides prepared using polyvinyl alcohol resin, lactic acid, and phenol (WALKER, 1979). The identification of AMF species was based on the manual by Schenck and Pérez (1990), and on the websites of the International Culture of Collection of Arbuscular Mycorrhizal Fungi (INVAM) (http://invam.caf.wvu.edu) (maintained by Dr. Joseph Morton), and the Department of Plant Pathology of the University of Agriculture, Szczecin, Poland (maintained by Dr. Janusz Blaszkowski) (http://www.agro.ar.szczecin.pl/~jblaszkowski/index.html). For statistical analysis, the square mean of treatments was used for the comparison among inbred lines, single-cross hybrids and for the contrast lines *versus* hybrids, using the F test. The means within each group were compared using the Tukey test, at a significance level of 5%, and Pearson's correlation was calculated among all the assessed characters. Heterosis was calculated relative to the mean of the parents [$h = 100(F_1-(P_1+P_2)/2)/(P_1+P_2)/2$] and relative to the superior parent [$hs = 100(F_1-P_s)/P_s$], with regard to grain yield and mycorrhizal colonization in the various crossbreeds. Heterosis relative to the superior parent (P_h) was calculated using the formula: $hs\ (\%) = 100\ (F_1 - P_h)\ /\ P_h$,, where F_1 is the mean of the hybrid, $(P_1+P_2)/\ 2$ is the mean of the hybrid's parents, and P_h is the mean of the best parental performance.

Results and Discussion

The initial chemical analysis revealed acidic soil conditions, characteristic of soils in the Cerrado region of Brazil. These soils exhibit a high phosphorus (P) adsorption capacity, leading to a low concentration of the soluble element in the soil and a reduced availability to plant roots (CLARK; ZETOS, 1996).

The mean number of AMF spores per 100 g of soil in the area was 391 before the start of the experiment. After cultivation, the means of the lines and single-cross hybrids were 427 and 468 spores per 100 g of soil, respectively (Tables 1 and 2). Similar values were reported by Carrenho et al. (2002) in a corn crop (415.2 spores per 100 g of soil). There were no significant differences that could be attributed to the stability of the communities associated with each genotype. There were significant differences among the lines only with regard to COL, whereas both COL and GY exhibited significant differences among the single-cross hybrids. The interaction between lines and single-cross hybrids resulted in significant differences concerning all the attributes, with the exception of NS (Table 1).

Table 1. Mean values of ear height (CH), plant height (PH), production of dry matter (DW), number of spores (NS), colonization by autochthonous mycorrhizal fungi (COL), and grain yield (GY) in corn breding endogamic lines.

Lines	EH (m)	PH (m)	DW (kg ha^{-1})	NS (100 g solo^{-1})	COL$^{(1)}$ (%)	GY (kg ha^{-1})
F3	0,89	1,77	1.337	489	30,83a	3.259
F2	0,91	1,69	2.142	343	27,60ab	2.281
F4	0,78	1,54	1.832	484	21,70abc	2.009
E1	0,66	1,26	2.106	441	23,92abc	1.991
E5	0,86	1,66	1.790	483	20,50abc	1.961
E3	0,60	1,19	1.878	434	13,33bc	1.537
D3	0,94	1,69	2.280	466	15,67abc	1.494
D1	0,87	1,61	2.766	436	15,66abc	1.488
D5	0,75	1,65	1.619	403	22,83abc	1.182
F5	0,97	1,75	1.839	480	17,08abc	1.172
D2	0,87	1,39	1.976	384	23,25abc	1.107
D4	0,79	1,57	1.854	397	19,08abc	1.020
F1	0,81	1,49	2.607	308	12,16c	639
Médias	0,82	1,56	2.002	427	20,28	1.626
Valor F	1,52^{ns}	2,53^{ns}	1,28^{ns}	1,16^{ns}	3,28*	1,66^{ns}
CV (%)	12,90	9,11	16,98	3,11	7,18	20,86
Média geral	0,95	1,78	965,34	2,65	1,36	1.214,82

Means followed by the same letter in a given column did not differ, according to the Tukey test at a probability level of 5%. (1) For statistical analysis the original values were transformed into log (x + 1).

The comparison between the mean values of COL in the lines showed that lines F3 (30.83%) and F2 (27.66%) exhibited the highest values, and F1 (12.16%) and E3 (13.33%) the lowest values (Table 1). These results are similar to those obtained by Reis et al. (2008) for corn genotypes tested for P absorption efficacy, which varied between 31.97% and 46.91% when inoculated with *Glomus etunicatum*.

Although there were no significant differences among lines with regard to GY, the means varied between 3,259 kg ha^{-1} (F3 line) and 639 kg ha^{-1} (F1 line) (Table 2), and the general mean for the treatments was considered low (1,215 kg ha^{-1}). The high coefficient of variation was probably a consequence of the different values obtained between the inbred lines (Table 1).

There were differences in the mean COL and GY among the single-cross hybrids (Table 2). The highest and the lowest COL values were observed for the treatments HS83 × E5 (43.92%) and D1 × F2 (15.42%), respectively. The highest mean GY was obtained in the HS83 × E3 (7,108 kg ha^{-1}) and D3 × F5 single-cross hybrids (7,048 kg ha^{-1}), and the lowest in HS10 × E1 (3,089 kg ha^{-1}). The mean GY value was higher in the hybrids than in the lines (1,215 kg ha^{-1}). Tewari et al. (1993), in a study with millet genotypes inoculated with *Glomus caledonium*, reported that the plant genotype affected the rate of colonization by AMF and that mycorrhizal efficacy was highly significant to P absorption, suggesting that the host plant's demand can affect AMF performance.

The relationship between GY and COL observed in the present study has also been reported in wheat (HETRICK et al., 1996) and corn (KAEPPLER et al., 2000) cultivars, respectively. Both authors suggest that selection during genetic improvement affects plant-AMF symbiosis due to the generation of cultivars that are less responsive to the fungus. Therefore, the differential symbiotic performance resulting from the interactions between distinct autochthonous AMF populations and species of genetically improved plants should be taken into account when developing current agricultural practices.

Table 2. Mean values of ear height (CH), plant height (PH), production of dry matter (DW), number of spores (NS), colonization by autochthonous arbuscular mycorrhizal fungi (COL), and grain yield (GY) in single-cross hybrid corn genotypes.

Hybrids	CH (m)	PH (m)	DW (kg ha^{-1})	NS (100 g solo^{-1})	COL $^{(1)}$ (%)	GY (kg ha^{-1})
HS 83 x E3	1,11	1,96	3.674	456	24,30abc	7.108a
D3 x F5	1,11	2,13	3.817	378	17,33bc	7.048a
HS 10 x E3	1,17	2,08	3.365	453	26,90abc	6.107ab
HS 83 x E1	1,03	1,97	4.489	578	32,60abc	6.047ab
HS 32 x E1	0,96	1,88	3.155	365	35,75ab	5.819abc
HS 83 x E5	1,02	1,89	3.594	436	43,92a	5.480abc
HS 32 x E5	1,03	1,98	3.007	569	33,90abc	5.376abc
HS 32	1,04	1,88	3.512	537	19,60abc	5.315abc
HS 10 x E5	1,11	1,92	3.029	542	21,80abc	4.928abc
HS 32 x E3	1,11	1,95	3.627	456	32,40abc	4.915abc
HS 83	1,17	2,13	3.258	573	28,40abc	4.873abc
F3 x D4	1,12	1,93	3.181	396	25,20abc	4.538abc
HS 10	1,02	2,00	3.655	435	25,30abc	4.398abc
D2 x F4	0,99	1,97	3.371	434	39,00ab	4.150bc
F1 x D5	0,92	1,78	3.562	446	24,30abc	3.468bc
D1 x F2	0,92	1,86	3.448	409	15,42c	3.393bc
HS 10 x E1	1,01	1,89	3.404	499	19,10abc	3.089c
Médias	1,05	1,95	3.479	468	27,39	5.062
Valor de F	$0,81^{ns}$	$0,66^{ns}$	$1,05^{ns}$	$1,24^{ns}$	$3,49^{**}$	$4,94^{**}$
CV (%)	12,90	9,11	16,98	3,11	7,18	20,86
Média geral	0,95	1,78	965,34	2,65	1,36	1.214,82

Means followed by the same letter in a given column did not differ, according to the Tukey test at a probability level of 5%. $^{(1)}$ For statistical analysis the original values were transformed into log (x + 1).

With regard to yield rates, the best performing single-cross hybrids (HS83 × E3 (7,108 kg ha^{-1}) and D3 × F5 (7,048 kg ha^{-1})) did not differ; however, they differ from D4 × F4, F1 × D5, D1 × F2, and HS10 × E1, indicating a productivity potential under the low technological conditions used. Most single-cross hybrids exhibited positive heterosis for all characters. All hybrids showed heterosis relative to the higher parent, with the exception of the three-way cross hybrids HS10 × E1, HS32 × E3, and HS32 × E5. Heterosis was higher in single-cross hybrids, probably because the parentswere lines, whereas in the case of three-way cross hybrids one of the parents is a vigorous single-cross-cross hybrid (Table 3).

The lines and single-cross hybrids did not differ significantly with regard to PH, CH, DW, GY, and COL; however, significant and positive correlations showed that the higher plant growth rates resulted in higher CH and PH, and then in higher DW and GY (Table 4). COL correlated significantly and positively with all characters, with the exception of NS; however, some of the most productive genotypes exhibited low COL.

Table 3. Values of heterosis relative to the mean of the parents (h, %) and heterosis relative to the superior parent (hs, %) with regard to grain yield (GY) and colonization by autochthonous arbuscular mycorrhizal fungi (COL) in the corn hybrids.

Hybrids	GY		COL	
	h	hs	h	hs
D3 x F5	429	372	5,85	1,46
F1 x D5	281	193	39,10	6,60
D2 x F4	166	106	73,37	67,80
HS 83 x E3	122	49	20,65	-13,50
F3 x D4	112	39	1,16	-18,12
HS 10 x E3	106	39	43,00	6,24
D1 x F2	80	49	-28,84	-44,30
HS 83 x E1	76	24	24,84	14,96
HS 83 x E5	60	12	64,58	54,55
HS 32 x E1	59	9	64,04	81,77
HS 10 x E5	55	12	-13,20	-13,82
HS 32 x E5	48	1	52,03	35,93
HS 32 x E3	43	-7	102,62	64,84
HS 10 x E1	-3	-30	-22,16	-24,34

Table 4. Diversity of autochthonous arbuscular mycorrhizal fungi (%) before sowing and of the genotypes with superior grain and their respective parents.

FMA species	Antes	D3	F5	D3 x F5	HS 83	E3	HS 83 x E3
Acaulospora longula	8,74	0,00	1,18	0,00	0,00	0,00	0,00
Acaulospora scrobiculata	4,85	4,00	3,55	10,71	0,00	7,37	2,14
Entrophospora colombiana	29,13	17,60	11,83	45,23	15,79	16,84	8,56
Glomus clarum	5,82	11,20	10,06	4,76	2,63	1,05	3,21
Glomus diaphanum	18,45	3,20	1,78	1,19	0,88	1,05	1,60
Glomus etunicatum	0,97	7,20	11,24	4,76	0,00	2,11	3,74
Glomus macrocarpum	0,97	11,20	4,14	0,00	1,75	0,00	5,88
Glomus margarita	2,91	0,00	1,78	0,00	0,00	2,11	3,21
Glomus sp.	9,71	0,80	0,00	3,57	0,00	0,00	0,00
Scutellospora calospora	5,82	34,40	51,48	23,81	68,42	60,00	58,29
Scutellospora gilmorei	1,94	0,80	1,18	1,19	0,88	1,05	2,14
Scutellospora pellucida	10,68	9,60	1,78	4,76	9,65	8,42	11,23
Total	100	100	100	100	100	100	100
Species richness	12	10	11	9	7	9	10

Costa et al. (2001) reported differential responses between Miró and Barbados *Malpighia emarginata* D.C. genotypes, inoculated with distinct AMF species, with the Barbados genotype and *Gigaspora margarita* combination exhibiting the highest plant growth. According to the authors, the efficiency of the AMF-*Malpighia emarginata* plant association was affected by the genotypes of both symbionts. This indicates that the degree of interaction between the fungus and the plant depends greatly on the plant's genotype and that a specific combination between plant and fungus are advantageous, regardless of colonization level (JANOS, 1996).

Before sowing, analysis of AMF species richness showed the presence of 12 species (Table 2). The most abundant was *Entrophospora colombiana* (29.1%), followed by *Glomus diaphanum* (18.45%), and *Scutellospora pellucida* (10.68%). Of these, the percentage of *Entrophospora colombiana* in the soil was higher in the presence of the D3 × F5 single-cross hybrid (45.23%) and was the second most frequent in all lines. The percentage of *Scutellospora calospora*, which was present in the soil before sowing (5.82%), increased the most, in the presence of every corn genotype tested, and was the most abundant species associated with the D3 (34.4%), F5 (51.48%), HS 83 (68.42%), and E3 (60%) lines, as well as with the HS 83 × E3 single-cross hybrid (58.29%). The percentages of the remaining fungal species (10) were increased poorly in the presence of all lines and hybrids included in the study (varying between 0% and 11.24%).

These results show the preference of fungal species for specific hosts, in this case, the genotypes. Preferential associations were also reported by Carrenho et al. (2002), who described 10 AMF species in a corn crop, with a predominance of *Acaulospora longula* (46.5%), *Glomus claroideum* (17.4%), and *Entrophospora colombiana* (15.4%). Oliveira et al. (2009) observed that different corn genotypes exhibit different P absorption capacity and that the plant's genotype has a greater impact on the mycorrhizal community than the level of P in the soil.

The analysis of mycorrhizal diversity among hybrids and their progeny showed the following predominance of species: *Entrophospora colombiana* followed by *Scutelospora calospora* in the D3 × F5 hybrid; *Scutellospora calospora* followed by *Entrophospora colombiana* in the parent lines D3 and F5; and *Scutellospora calospora* in the HS 83 × E3 hybrid and their parent lines. *Scutellospora calospora* was the most abundant species in association with all genotypes, with the exception of the D3 × F5 hybrid (Table 2).

With regard to species richness, 12 species were present before sowing. The number of species in association with the D3 × F5 hybrid was lower than that of species associated with their parent lines (D3 and F5): 9, 10, and 11 species, respectively. Moreover, the HS 83 × E3 hybrid and the parent lines (HS 83 and E3) were colonized by 10, 7, and 9 species, respectively (Table 2). Carrenho et al. (2001) observed the presence of 25 species in areas with successive corn crops. In the present study, the number of species differed from that reported by other authors; however, it was similar to those described by Trufem and Bononi (1985) and Siqueira et al. (1989), who found nine and ten species in soils from the Cerrado region, respectively.

The number of AMF species found in the rhizosphere of a particular plant varies significantly, both for the same culture as between different plants, as shown in the literature. It has been suggested that a greater fungal diversity in an area improves the performance of plant species with regard to absorption of soil nutrients and water, since although there is no host specificity, the effects of symbiosis differ according to the plant-fungus combination (SILVA et al., 2014; COSTA et al., 2001; POUYÚ-ROJAS et al., 2006).

Benedetti et al. (2005) observed that the genera *Acaulospora* and *Glomus* were the most abundant in corn crops and were dominant relative to the species of the genera *Scutellospora* and *Gigaspora*. Similar results were obtained in the present study. Even though *Glomus diaphanum* is commonly described as a species with low acidity tolerance (COLOZZI-FILHO; CARDOSO, 2000), it was the second most abundant in the soil before the start of the present study (18.45%), and its percentage in the soil was slightly affected by all genotypes (varying between 0.88% and 3.2%, whereas *Entrophospora colombiana* varied between 45.23% and 8.56%).

Plant improvement can generate genotypes with different nutritional requirements and different nutrient absorption capacity (TRINDADE et al., 2001). Moreover, populations in the autochthonous AMF community and their interactions with superior genotypes need to be better understood. Therefore, the identification of genotypes, particularly pure lines, that exhibit highly contrasting mycorrhizal colonization, will allow the production of F_1 and F_2 generations and backcrossing with better understood genetic traits.

AMF affects processes such as plant performance (nutrient absorption processes), the diversity and abundance of plant communities, and processes related to ecosystem stability (BERBARA et al., 2006). In this sense, to achieve agricultural production sustainability, plant improvement and selection programs should aim to obtain genotypes that are less dependent on external input, that absorb maximum nutrients with low solubility, or originate from organic matter recycling, and that are able to develop root symbiosis with AMF (REIS et al., 2008).

Some AMF species rapidly colonize the host and sporulate abundantly, whereas others require more time to sporulate or exhibit little sporulation and persist in the environment mainly in their active form (mycelium) and not as spores (GOMIDE et al., 2009). This may explain the results obtained in the present study.

Conclusions

There were qualitative and quantitative changes in fungal composition as well as preferential associations between fungi and plants.

The AMF diversity analysis showed the presence of 12 species, with *Scutellospora calospora* and *Entrophospora colombiana* the most abundant in all treatments. *Acaulospora longula*, *Glomus etunicatum*, *Glomus macrocarpum*, and *Gigaspora margarita* exhibited preferential associations among the genotypes.

COL and GY differed among lines and single-cross hybrids and significant correlations between COL and DW and GY showed positive plant-AMF interactions.

GY heterosis was not correlated with colonization heterosis. The HS83 × E3 and D3 × F5 single-cross hybrids exhibited high GY, which indicates a positive productive potential under the technological conditions used.

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