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Mycorrhizal species selectivity of sweet sorghum genotypes and their effect on nutrients uptake

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ABSTRACT

This study aimed to find the effects of several mycorrhiza species on agronomic characteristics and nutrient uptake of various sweet sorghum genotypes under the semi-arid Mediterranean soil conditions. Four sweet sorghum genotypes were inoculated with three mycorrhiza species under greenhouse conditions. The plants were evaluated for growth parameters such as shoot height, root length, root morphology (root surface, root diameter and volume), shoot and root dry weight, uptake of macro and micro mineral nutrients, root colonisation and mycorrhizal dependency. Mycorrhizal species significantly improved growth and productivity of sorghum genotypes. Inoculation of Funneliformis mosseae, Claroideoglomus claroideum and Claroideoglomus etunicatum resulted in the highest shoot and total dry matter biomass production in Ashana, Hereahri and Yellow genotypes, respectively. Mycorrhiza inoculated white genotype had higher root colonisation and root development, and shoot P, K, Ca and Mg contents. Yellow genotypes produced significantly higher shoot and total dry weight and also were highly mycorrhiza dependent among the four genotypes. Compared to the control treatment mycorrhizal inoculation increased shoot Zn concentration but had non-consistent effects on shoot Cu, Fe and Mn contents. Conclusively, our findings confirmed that sweet sorghum genotypes responded selectively to arbuscular mycorrhizal fungi (AMF) colonisation for their growth parameters and nutrients uptake.

Introduction

ssChallenges of the current era such as the climate changes, water scarcity, rapid world population growth, food safety and insurgency along with socioeconomic factors are great threat to the global food security (Watts-Williams et al., 2022). Considering the current scenario of the increase in world population, more food is needed to feed the world under diminishing resources, and it is argued that these needs cannot be met sufficiently and problem of hunger and starvation may exist especially in developing and underdeveloped countries (Ortas, 2019). It is argued that people living in arid and semi-arid regions will be affected at the highest levels (Saleh et al., 2013). The livestock production is an integral component of global food security, and the forage and feed crop production is required to be expanded in terms of area and yield per unit area. It is reported that there will be no significant change in the demand for livestock products in developed countries in the future (Hocquette and Gigli, 2005). To increase the livestock and dairy products, they must be fed with sufficient and high-quality roughage feed which is vital in the feeding of ruminant animals. In this context, agricultural products grown in arid and semi-arid conditions have become more significant. Cereals such as maize, sorghum and wheat that are produced in tropical and semi-arid regions have different varieties and small grains under the taxonomy groups, which are believed to increase their economic importance in the future.

Sorghum (Sorghum bicolor L.) is often known as millet or broom grass in many parts of the world. Sorghum has a widespread cultivation area in Africa and is used for the production of ethanol. Sorghum is a drought-tolerant plant, grown for humans and livestock food and known as a food security plant. Sorghum is considered rich nutritious crop needed by human and animals for their growth, survival, maintenance and reproduction (Watts-Williams et al., 2022). Sorghum is consumed in the 5th class after the rice, wheat, corn and barley in the class of grains cultivated and produced. It has become the main food source of millions of people in the West African Region, which contains inefficient soils. At the same time, since it is a good C4 plant, it does a high level of photosynthesis and has high production capability. Sweet sorghum is one of the

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KEYWORDS

Sweet sorghum genotypes; mycorrhiza species; mycorrhizal dependency; mineral nutrients; root morphology



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sugar-rich plants and has high biomass production containing both soluble (glucose and sucrose) and insoluble (cellulose and hemicellulose) carbohydrates (Dar et al., 2018).

Sweet sorghum cultivars have high biomass and carbohydrate and are recommended to be grown on marginal lands. The use of mycorrhizae as biofertiliser can reduce demand for chemical fertiliser and diminish chemical pollution. Soil beneficial microorganisms such as arbuscular mycorrhizal fungi (AMF) are known to stimulate sorghum growth and enhance plant productivity (Ortas et al., 1996). According to Sisaphaithong et al. (2012), sorghum growth is strongly stimulated by mycorrhizae. Plant productivity and ecosystem stability are mainly supplied with AMF as a key component of ecosystems (Powell and Rillig, 2018). Arbuscular mycorrhizal fungi are known for their ability to absorb water and mineral nutrients and increase plant growth under fertile soil conditions. However, in many infertile soils, efficient nutrient acquisition depends on rhizosphere mechanisms such as mycorrhizal inoculation. Arbuscular mycorrhizal fungi inoculation enhances the adaptation of higher plants to a series of environmental stresses such as drought, heat, salinity and heavy metal contamination (Garg and Chandel, 2011). It has been demonstrated that mycorrhizal inoculation increased microbial populations in sorghum rhizosphere (Kumar and Fulekar, 2019), and this could improve the rhizosphere microbial dynamic to increase soil quality (Ortaş, 2017).

Soil nutrient concentration especially phosphorus (P) availability control growth and development of many plants (Johnson and Graham, 2013). Kamaei et al. (2019) showed that the highest rate of sorghum physiological growth indexes of root such as root area index and net assimilation rate was obtained after inoculation with mycorrhiza along with nitrogen (N) fertiliser treatment. McGowan et al. (2019) found that the increases in soil organic carbon (SOC) were significantly correlated with greater root biomass and abundance of AMF. It is observed that some phosphorus-efficient cultivars have a capacity to increase P availability for root uptake than the other cultivars by converting non-available P forms into available ones (Rengel and Marschner, 2005; Subramanian et al., 2009). Sorghum plant is highly mycorrhizae dependent and its inoculation with mycorrhizal can promote plant growth (Ortas, 1996; Ortaş and Harris, 1996). After mycorrhizal inoculation, the direct competition of pathogens for uptake of nutrients decreases which improves plant nutrition to increase photosynthesis and carbohydrates production. Moreover, the mycorrhizal inoculation can help sorghum plant in efficient water uptake (Symanczik et al., 2020).

Arbuscular mycorrhizal fungi can enhance the growth, survival and nutrient uptake of sorghum by mitigating various biotic and abiotic stresses under droughts conditions (Badi et al., 2019). As a consequence of the increasing climate change effects, new plant species and genotypes would be needed that have greater yield potential and adaptability to ensure food and feed security. Under semi-arid climate conditions, it is expected that the increase in temperature will lead to water scarcity. Under those conditions, C4 plants such as sorghum genotypes will be suitable for food security and sustainable agricultural strategy. In this context, it is important to choose plant species or genotypes that require less fertiliser and water and show strong association with on mycorrhizae. It is expected that with mycorrhizal inoculation, some sorghum genotypes will get better benefit for nutrient uptake and growth under the Mediterranean climatic condition. The hypothesis is genotypes interact with different mycorrhiza species to increase sorghum growth under P and Zn deficiency soil conditions

The purpose of this study is to search the effects of several mycorrhizal species on the growth and mycorrhizal dependence of several sorghum genotypes under P and Zn deficiency soil conditions.

Material and Methods

Soil

Sultanönü soil was used as a growth material for the study. The soil was collected from GKTAEM Gateway Research Institute Area, Eskişehir-Turkey ('39°45' 43" N, and '30°29' 59 E"). Soil physical and chemical properties are given in Table 1.

Table	1.	Physical,	chemical	and	biological	properties	of
Sultanö	önü	soil.					

Properties	Unit	
Clay	%	50.6
Loam		30.6
Sand		18.8
CaCO3		16
Organic matter		0.75
Salt (soluble)		0.08
B (1)	mg B kg ⁻¹ soil	1.35
pH	(H ₂ O)	8.07
CEC	Cmolc kg ⁻¹	37
P_2O_5 (2)	kg/ha	13.03
Zn (3)	$(mg^{-1} kg)$	0.08
Fe(3)		1.37
Mn(3)		2.27
Cu(3)		0.69

(1) CaCO₂/Mannitol; (2) 0.5 N NaHCO₃ extractable; (3) DTPA extractable.

Plant and Mycorrhizae Species

Four different sorghum genotypes (Ashana, Hereahri, White and Yellow) and three different mycorrhizal species (*Funnelifomis mosseae (BEG 12), Claroideoglomus claroideum (BEG 31)* and *Claroideoglomus etunicatum* (*BEG 247)*) along with control were used in the study. Mycorrhizae spores were provided by BEG collection and multiplied under the clover host plant.

Experimental Design, Treatments and Growth Conditions

The experiment was established under greenhouses conditions following a complete randomised design (CRD) with three replicates for each treatment. Before sowing, sorghum seeds were surface sterilised by immersion for 2 min in 2% of sodium hypochlorite solution and rinsed three times in distilled water; 2 mm sieved soil was sterilised by autoclaved for 2 h. Five seeds of different sorghum genotypes were planted in 3 L pots; and filter paper was placed in the middle of the pots, in order to keep mycorrhizae spores. After the sowing of the seeds water was given to the soil for germination. One week after germination thinning was performed per pot. After three weeks from sowing 100 mg N kg⁻¹ soil was used as urea fertiliser to each pot. During the experiment, the plants were checked at regular intervals, and displacement was made according to the angle of sunlight. The inside of greenhouse temperature was at 26°C during the day and 20 during the evening. The relative humidity was at 70%.

Plant Harvest and Analysis

Sorghum genotypes were grown under a greenhouse and plants were harvested at the end of 71 days from sowing. At harvest, plant height was measured. Root and above root fresh and dry weight were determined. Sorghum plants roots were washed and cleaned and scanned with an optical scanner reader. Total root length, root diameter and surface area have been determined by WinRHIZO Root Analysis System. Roots were cleaned and prepared for colonisation (Koske and Gemma, 1989) and were determined by using the gridline intersect method under a dissecting microscope at 40× magnification (Giovannetti and Mosse, 1980).

Dependency on Mycorrhiza (MD) was determined according to Ortas (2012b) using following formula:

 $MD(\%) = [(+M(SDW)) - (-M(SDW)/(+M(SDW))] \times 100.$

At harvest, shoot and root were dried at 70°C for 48 h and weighed for dry weight (DW) determination. Dried

shoot tissue was grinded, homogenised and digested with nitric and perchloric acid. The content of soil microelements (Cu, Fe, Mn and Zn) was extracted by diethylenetriaminepentaacetic acid (DTPA) and calcium, magnesium and potassium in the soil extracted NH₄-Ac method and nutrient concentrations were determined by the ICP-OES. Soil P contents were determined by the Olsen method and measured calorimetrically by spectrophotometer (Murphy and Riley, 1962).

Statistical Analysis

Data were analyzed by analysis of variance (ANOVA) using the Statistical Analysis System (SAS 9.1.3) package program. The least-square means differences between applications were determined by the Tukey multiple comparison method.

The principal component analyses (PCA) biplots were constructed based on genotypes and mycorrhiza species selection for efficient genotypes and mycorrhizae. Data were analyzed by Excel-State computer program.

Results

In the conducted research, it was determined that sorghum genotypes reacted differently to selected mycorrhiza species inoculation in terms of growth and development (Figure 1). Without considering the mycorrhizal inoculation, the highest plant length was measured in Hereahri, and the shortest length in Yellow genotypes was measured. Hereahri genotype seems to be early flowered than the other genotype. Without considering mycorrhizal inoculation Hereahri genotype. Without considering mycorrhizal inoculation Hereahri genotype has delayed flowering compared to other genotypes. The highest (*Cl. etunicatum* inoculated; 106.7 cm) and the lowest (control 55.0 cm) plant height were measured at the Ashana genotype (Table 2).

Yellow genotype have the highest mean of total dry weight (TDW) than that of Ashana genotype which produced the lowest TDW in terms of dry weight production. Increase in shoot dry weight (SDW), Yellow genotypes produced the SDW. Hereahri genotype has the lowest while the Ashana genotype has the highest mean of root dry weight (RDW). It is observed that Fu. mosseae mycorrhiza species inoculated to the Ashana and Yellow genotype have high shoot and total dry weight with Cl. etunicatum species. Cl. claroideum inoculation produced the highest shoot and total DW than the other mycorrhiza species in the Hereahri genotype. At the same time, Hereahri genotype has the highest plant height, however, noted less root and total dry weight compared to the other three genotypes. Among the genotypes, Hereahri had the lowest root/

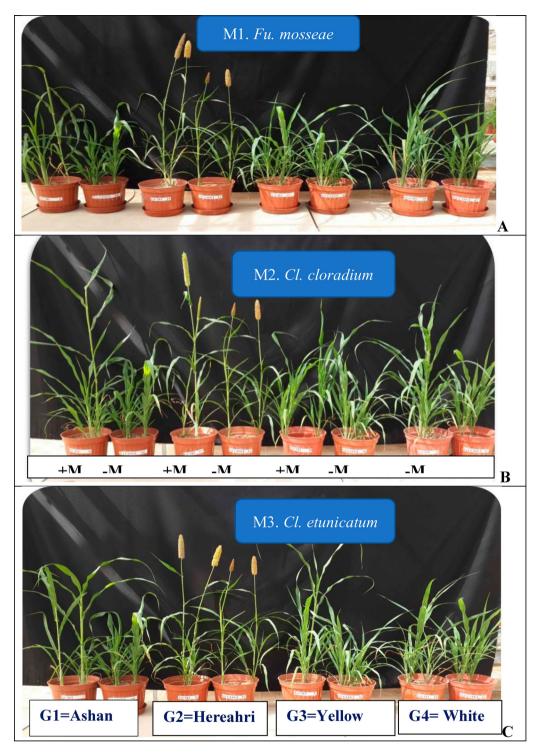


Figure 1. Effect of mycorrhiza species inoculation on different sorghum genotypes development. A: Fu. Mosseae, B: Cl. claroideum, C: Cl. etunicatum inoculated treatments.

shoot ratios, and *Cl. etunicatum* with the White genotypes produced the highest shoot and total dry matter. Yellow genotypes produced the higher shoot and total dry weight more than the other genotypes. It is observed that *Cl. claroideum* mycorrhiza species inoculated to the Yellow genotypes produced more root and total DW compared to other genotypes. Statistically, all mycorrhiza species significantly affected the development of different sorghum genotypes plants. And there are differences between mycorrhizae inoculated and non-inoculated plants (Table 2). Anova per single genotype and mycorrhizae spores showed significant (P < .0001) differences for plant length and drw weight (DW) parameters. Combined interaction also showed

Genotypes Ashana	Mycorrhiza species	Plant	length	Shoot d	ry weight	Root dr	y weight	Total dry weight		
)	(cm)		g/pot		g/pot		g/pot		
	Fu. mosseae	96.67	±11.55	10.66	±1.60	9.60	±1.25	20.26	±2.80	
	Cl. claroideum	102.00	±11.27	9.18	±1.60	4.90	±0.95	14.08	±2.30	
	Cl. etunicatum	106.67	±5.77	10.13	±1.40	4.93	±0.38	15.07	±1.76	
	Control	55.00	±5.00	7.43	±0.60	4.47	±1.40	11.90	±1.71	
	Mean	90.08	±8.40	9.35	±1.30	5.98	±1.00	15.33	±2.14	
Hereahri	Fu. mosseae	97.67	±7.51	10.30	±3.32	3.70	±0.95	14.00	±2.80	
	Cl. claroideum	94.00	±3.61	15.89	±5.21	3.10	±0.10	18.99	±5.11	
	Cl. etunicatum	97.33	±2.52	10.75	±0.75	3.53	±1.18	14.28	±1.43	
	Control	95.00	±5.00	7.33	±0.76	3.01	±0.69	10.34	±0.85	
	Mean	96.00	±4.66	11.07	±2.51	3.34	±0.73	14.40	±2.55	
White	Fu. mosseae	66.67	±5.77	10.50	±2.50	5.40	±0.44	15.90	±2.86	
	Cl. claroideum	72.67	±6.81	10.24	±1.02	5.07	±0.64	15.30	±1.53	
	Cl. etunicatum	91.67	±7.64	13.00	±2.23	5.02	±0.52	18.02	±2.17	
	Control	59.67	±4.51	9.80	±0.70	4.60	±0.95	14.60	±1.05	
	Mean	72.67	±6.18	10.88	±1.61	5.02	±0.64	15.96	±1.90	
Yellow	Fu. mosseae	75.00	±5.00	18.16	±0.34	5.00	±1.08	23.16	±0.76	
	Cl. claroideum	79.00	±4.58	18.12	±0.78	5.23	±0.15	23.35	±0.69	
	Cl. etunicatum	59.00	±3.61	11.77	±1.03	4.84	±1.04	16.60	±0.98	

±2.65

±3.96

<.0001

<.0001

<.0001

6.83

13.72

<.0001

< .0001

0.0002

±1.53

±0.92

0.0004

<.0001

0.0001

4.50

4.89

±0.56

±0.71

11.33

18.61

+1.72

±1.03

Columns with different letters are significantly different ($P \le .05$). According to Tukey's test.

56.00

67.25

P value

<.0001

<.0001

<.0001

highly significant (P < .001) differences for genotype (G), mycorrhiza species (M) and their interaction effects for all measured traits.

Control

Mean

Df

3

3

9

Analysis of variance

Genotype (G)

G*M

Mycorrhizae (M)

Mycorrhiza species inoculated and non-inoculated genotypes root diameter, length, surface area and volume parameters were determined. Generally, without considering mycorrhizal inoculation the latest root parameters were measured in the Hereahri genotype, and the highest was measured in the White genotype. Statistically, genotypes were significantly different and mycorrhiza inoculation was not significant except root volume parameter (Table 3). There is significant interaction among the genotypes × mycorrhizal inoculation on root diameter and root length. Genotypes are also significantly different for plant growth and macronutrient concentrations.

Root colonisation with AMF varied significantly between the sorghum genotypes (Table 3). Compared to the control treatment without root colonisation, the White genotype has the highest (39%) whereas the Ashana genotypes have comparatively least (31%) root colonisation. All genotypes inoculated with Cl. etunicatum produced higher colonisation than the other mycorrhiza species. White and Yellow sorghum genotypes showed higher mycorrhizal colonisation.

Shoot tissue P, K, Ca, Mg, Cu, Mn, Fe and Zn concentrations were determined. Results are presented in Table 4. All nutrient concentration is in the range of critical levels. Genotypes and mycorrhiza species have significant effects on phosphorus concentration. The White genotype had the highest and the Ashana genotypes had the lowest mineral nutrient concentrations. Mycorrhiza species and genotypes statistically significantly affected P concentration. Cl. etunicatum inoculated genotypes have the highest P concentration (%) (Table 4). Mycorrhiza species also significantly affected K, Ca and Mg mineral nutrient concentration among the genotypes. Usually, mycorrhizal species Fu. mosseae translocated a high concentration of Ca and Mg, when treated with the genotypes. Although other mycorrhiza species inoculation has not significant effects. Zn concentration was found maximum in all genotypes treated with mycorrhiza species compared to control. Similarly, micronutrients concentration was also varied with mycorrhiza inoculation with genotypes, and Cu, Fe and Mn concentrations were less than control plants. All data's pear correlation results show that Cu, Mn and Fe concentrations have a negative correlation with mycorrhizal colonisation.

The sweet sorghum genotypes growth and mycorrhizae dependency (MD) was significantly differed. Regarding MD, maximum value was noted in Yellow (62%) genotype and Fu. mosseae, the least was determined in White (55.91%) genotype and Cl. claroideum treatments. Yellow genotypes have the highest mean of MD (56%), White have the lowest mean of MD (12%). Hereahri genotype MD is 38% and Ashana genotype MD is 25%. Mycorrhiza species dependency effects also were analysed and Cl. etunicatum, Fu. mosseae and Cl. claroideum species have mean of 31%, 32% and 35% MD, respectively (Figure 2).

Genotypes	Mycorrhiza species	Root dia	ameter	Root length		Root surface		Root volume		Root colonisation	
		mm		cm		cm ²		cm ³		%	
Ashana	Fu. mosseae	0.27	±0.01	40901	±17867	3472	±1479	26.82	±4.46	35	±1
	Cl. claroideum	0.27	±0.01	48398	±6216	4164	±631	28.55	±5.17	41	±1
	Cl. etunicatum	0.27	±0.03	61030	±9306	5209	±1342	40.35	±4.98	47	±3
	Control	0.25	±0.03	73372	±9789	5634	±113	34.77	±3.66	0	±0
	Mean	0.27	±0.02	55925	±10795	4620	±891	32.62	±4.57	31	±1
Hereahri	Fu. mosseae	0.23	±0.01	33192	±3624	2342	±203	14.91	±3.35	38	±6
	Cl. claroideum	0.23	±0.04	36724	±8721	2709	±1096	16.19	±9.20	50	±0
	Cl. etunicatum	0.23	±0.02	49885	±18790	3628	±1613	21.07	±10.83	44	±3
	Control	0.23	±0.01	32014	±5772	2316	±418	13.37	±2.62	0	±0
	Mean	0.23	±0.02	37954	±9227	2749	±833	16.38	±6.50	33	±2
White	Fu. mosseae	0.26	±0.03	51581	±28368	4009	±1683	25.14	±7.65	46	±4
	Cl. claroideum	0.24	±0.01	73112	±17280	5482	±1169	32.75	±6.23	49	±б
	Cl. etunicatum	0.27	±0.04	61297	±27170	4936	±1331	32.26	±3.91	60	±9
	Control	0.29	±0.03	63063	±20341	5670	±1285	40.90	±5.86	0	±0
	Mean	0.26	±0.03	62263	±23290	5024	±1367	32.76	±5.91	39	±5
Yellow	Fu. mosseae	0.22	±0.01	81565	±6335	5524	±99	29.86	±1.38	46	±9
	Cl. claroideum	0.26	±0.04	60892	±11912	4878	±352	31.47	±1.93	43	±9
	Cl. etunicatum	0.28	±0.02	50568	±8997	4376	±479	30.25	±1.24	58	±18
	Control	0.29	±0.01	47822	±1836	4381	±277	31.97	±2.82	0	±0
	Mean	0.26	±0.02	60212	±7270	4790	±302	30.89	±1.84	37	±9
Analysis of variance	df	P value									
Genotype (G)	3	.0036	.0013	<.0001	<.0001	.0166					
Mycorrhizae (M)	3	.1820	.9294	.3232	.0162	<.0001					
G*M	9	.0515	.0228	.1235	.1033	.1655					

Table 3. Different mycorrhizae species effects on sweet sorghum genotypes root diameter, length, surface, volume and mycorrhizal colonisation.

Columns with different letters are significantly different ($P \le .05$). According to Tukey's test.

In order to determine the genotype and mycorrhiza relationship, all data were analysed for principal component analysis (PCA). PCA analysis successfully identified genotypes and mycorrhiza species effects on plant measured parameters separately (Figures 3 and 4). Also all measured data's multiple correlations and genotypes and mycorrhiza species effectiveness were determined. To facilitate a less congested graphical presentation of many treatments, the second figure is used to make clear visualisation of the mycorrhiza species groups. Genotypes and mycorrhiza species 16 treatments for PCA analysis were used to determine the association of genotypes based on 17 measured parameter values. Grouping of mycorrhiza species on the base of all measured parameters is shown in Figure 3. There is a significant difference between mycorrhiza species effect on measured parameters than control treatments. Fu. mosseae, Cl. claroideum and Cl. etunicatum mycorrhiza species were clustered separately than control on the base of all measured parameters. Cl. claroideum and Cl. etunicatum mycorrhizae species are significantly associated with measured parameters. Fu. mosseae species have a negative loading.

In F1 axes, Mn, Fe, Cu, K, Mg and root parameters had high positive loading. Plant growth parameters and root colonisation had negative loading. Mycorrhizal species inoculated to genotype Ashana and Hereahri were clustered separately and were different from each other; however, both genotypes were close to each other and they have less effects on measured parameters compared to White and Yellow genotypes. White and Yellow weighted data are appeared to be clustered in a different group and have higher effects on measured parameters. Hereahri genotype was associated with plant length, dry weight and mineral nutrients. Genotypes Yellow and White were specifically associated with shoot and root parameters, Cu, Mn and Fe concentrations. Also, root parameters were positively correlated with Cu, Mn and Fe concentrations.

Discussion

We investigated the effects of AMF species on sorghum genotype under greenhouse conditions in P and Zn limited soil. Variance analyses results showed that all AM species inoculated sorghum genotypes increased plant growth, root colonisation and nutrient concentration compared with controls. It seems that sweet sorghum genotypes are very selective with mycorrhizal inoculations. Data presented in Table 2 showed that the highest shoot, root and total dry weight were obtained for the Yellow sorghum genotype inoculated with Cl. claroideum and Fu. mosseae. The Ashana genotypes inoculated with Cl. etunicatum and Cl. claroideum resulted in highest plant length followed Fu. mosseae inoculation. Mehraban et al. (2009) and Abdelhameid (2020) showed significant differences between sorghum genotypes and their interactions with

Genotypes	Mycorrhiza species		2		K	(a	М	g	C	u		Fe		1n		Zn
	,				%	6							mg	y kg ^{−1}			
Ashana	Fu. mosseae	0.08	±0.01	1.89	±0.28	0.87	±0.09	0.84	±0.21	6.10	±0.87	57.20	±3.44	60.50	±9.78	16.60	±5.06
	Cl. claroideum	0.08	±0.01	1.55	±0.15	0.63	±0.11	0.72	±0.04	5.40	±1.01	43.90	±5.28	60.70	±12.49	12.37	±4.28
	Cl. etunicatum	0.11	±0.02	2.06	±0.32	0.67	±0.11	0.71	±0.02	5.63	±1.00	41.53	±10.13	63.97	±19.10	20.97	±1.69
	Control	0.08	±0.01	1.61	±0.22	0.55	±0.03	0.67	±0.12	10.60	±1.55	82.00	±10.20	106.15	±2.05	15.87	±4.27
	Mean	0.09	±0.01	1.78	±0.24	0.68	±0.08	0.73	±0.10	6.93	±1.11	56.16	±7.26	72.83	±10.86	16.45	±3.83
Hereahri	Fu. mosseae	0.10	±0.01	1.94	±0.08	0.75	±0.19	0.57	±0.05	7.23	±0.81	52.90	±5.86	60.80	±6.52	14.95	±0.95
	Cl. claroideum	0.11	±0.02	2.14	±0.34	0.68	±0.11	0.63	±0.15	7.17	±1.29	50.30	±6.94	61.80	±22.65	16.10	±4.44
	Cl. etunicatum	0.12	±0.01	2.45	±0.17	0.65	±0.16	0.76	±0.13	9.77	±2.73	66.57	±9.67	79.87	±9.45	12.30	±2.30
	Control	0.12	±0.01	2.13	±0.23	0.57	±0.04	0.64	±0.12	9.15	±0.75	77.53	±2.83	128.00	±48.44	11.60	±3.20
	Mean	0.11	±0.01	2.16	±0.20	0.66	±0.12	0.65	±0.11	8.33	±1.39	61.83	±6.33	82.62	±21.77	13.74	±2.72
White	Fu. mosseae	0.11	±0.01	2.65	±0.25	0.93	±0.11	0.89	±0.05	9.50	±1.22	64.20	±0.50	129.53	±12.63	16.13	±15.0
	Cl. claroideum	0.10	±0.01	2.29	±0.28	0.87	±0.19	0.87	±0.07	8.35	±0.05	69.35	±4.85	136.40	±5.30	15.65	±1.15
	Cl. etunicatum	0.11	±0.03	2.21	±0.26	0.77	±0.09	0.78	±0.19	8.10	±1.87	70.15	±17.77	82.93	±21.40	15.85	±2.55
	Control	0.10	±0.00	2.52	±0.02	0.58	±0.03	0.78	±0.10	12.40	±0.80	85.30	±2.60	213.50	±10.10	8.20	±0.40
	Mean	0.10	±0.01	2.42	±0.20	0.79	±0.10	0.83	±0.10	9.59	±0.99	72.25	±6.43	140.59	±12.36	13.96	±4.79
Yellow	Fu. mosseae	0.11	±0.04	2.26	±0.28	0.64	±0.11	0.81	±0.08	9.63	±2.05	69.33	±14.89	95.55	±2.15	16.63	±5.73
	Cl. claroideum	0.10	±0.01	1.86	±0.11	0.61	±0.10	0.78	±0.07	7.47	±1.03	62.90	±10.54	94.63	±4.74	9.83	±1.56
	Cl. etunicatum	0.11	±0.01	2.17	±0.16	0.59	±0.02	0.69	±0.06	6.70	±0.30	59.80	±7.80	93.25	±19.25	9.60	±1.00
	Control	0.06	±0.00	1.94	±0.08	0.53	±0.06	0.65	±0.01	12.27	±2.31	73.90	±1.48	167.50	±15.18	8.39	±0.68
	Mean	0.10	±0.02	2.06	±0.16	0.59	±0.07	0.73	±0.05	9.02	±1.42	66.48	±8.68	112.73	±10.33	11.11	±2.24
ANOVA	df	P value															
Genotype (G)	3	.0074	<.0001	.0032	.0016	.0004	.0005	<.0001	.0813								
Mycorrhi (M)	3	.0078	.0235	.2159	<.0001	<.0001	<.0001	<.0001	.0884								
G*M	9	.0754	.0315	.3131	.5430	.0298	.0242	.0087	.3443								

Table 4. Different mycorrhizae species effects on sweet sorghum genotypes shoot P, K, Ca, Mg, Fe, Zn, Cu and Mn concentration.

Columns with different letters are significantly different ($P \le .05$). According to Tukey's test.

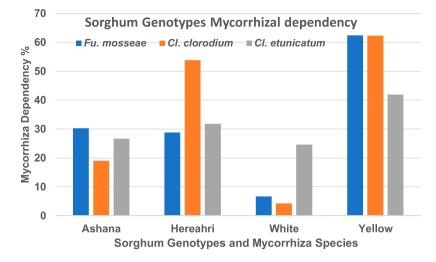


Figure 2. Percentage of sorghum genotypes dependent on mycorrhizae (%).

mycorrhizae for plant height, biomass and root colonisation. Mycorrhizal colonisation rate was significantly positively correlated with plant length, P concentrations, shoot length and total dry weight. The research findings showed that all genotypes performed higher root infection with *Cl. etunicatum*. Root parameters of sorghum genotypes differ statistically significantly and the data in Table 3 are consistent with findings by Liang et al. (2017).

In terms of sorghum plant growth, pronounced genetic variations were determined within genotypes. Previously, Leiser et al. (2016) reported there they detected a genetic difference for AMF root colonisation; however, the trait appears to be highly polygenic. Our findings divulged that the White genotype response to mycorrhizal dependency is low. White genotype had the highest root length and root surface area. Root

surface is directly related to nutrient uptake. White et al. (2013) indicated that under infertile soil conditions the development of crop genotypes with root traits increasing mineral nutrient acquisition should increase yields as well. The lower mycorrhizal growth response of the White genotype was combined based on shoot high Ca, K, Mg, Cu, Fe and Mn concentrations. Previously reported that genotypes are different from each other in terms of nutrient uptake (Clark 2002). Also, Clark and Reinhard (1991) reported that sorghum genotypes differed in most growth traits, especially dry matter yields, nutrient uptake and root lengths. But there was non-significant relationship between mycorrhizal species on root parameters. However, plant nutrient concentrations were not much different in general as shown previously high contents of plant-available soil P may have inhibited the symbiotic contribution

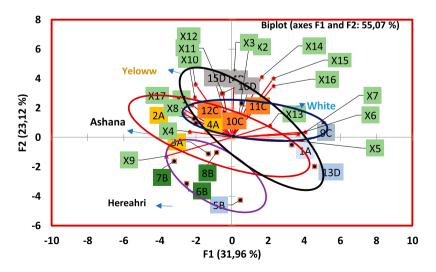


Figure 3. Biplot analysis for F1 (on x-axis) and F2 (y-axis) for all genotypes and mycorrhizae species interaction of 16 treatments based on all measured plant and nutrients analysed values.

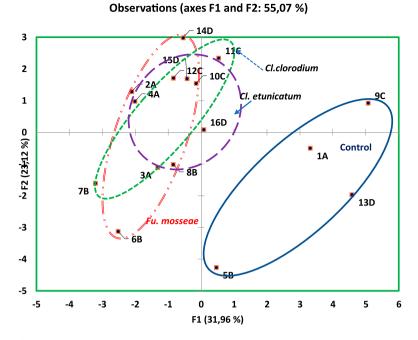


Figure 4. Biplot analysis for F1 (on *x*-axis) and F2 (*y*-axis) without considering the genotypes 16 treatments of mycorrhizae species interactions based on all measured parameters values. Codes 1A, 5B, 9C and 13D are no inoculated control treatments; codes 2A, 6B, 10C and 14D are *Fu. Mosseae* inoculated treatments; codes 3A, 7B, 11C, 15D are *Cl. claroideum* inoculated treatments; 4A, 8B, 12C, 16D codes are *Cl. etunicatum* inoculated treatments.

plants. Similarly, Cobb et al. (2016) showed that sorghum cultivars were significantly more responsive to mycorrhizal colonisation than commercial hybrids for mineral nutrient content.

The genetic diversity of wild sorghum genotypes that come from sweet sorghum needs to be searched for other beneficial rather than their shoot DM production and P acquisition efficiency. Similar work was done by Abdelhalim et al. (2019) and Abdelhalim et al. (2020) first time, they found that Sudanese sorghums genotypes and their growth responsiveness to AMF and P acquisition. In another work by Abdelhalim et al. (2019), it has been indicated that mycorrhiza response and phosphorus acquisition efficiency of sorghum genotypes differing in plant's roots produced. de Oliveira et al. (2021) also indicated that root exudates such as strigolactone composition in sorghum genotypes have effects on growth and P uptake. It probably showed less need for mycorrhiza because it absorbs better nutrients. Therefore, it is critical that nutrient use efficient sorghum genotypes be assessed with mycorrhiza species to found potential mycorrhizal partnership. Also, there is a significant difference in terms of MD within genotypes. White genotype has the lowest MD, Yellow genotype has the highest MD. Previously, Janos (2007) and Ortas (2012a) suggested that there is a great difference in species in terms of their dependence and responsiveness to mycorrhizas. Identification and introduction of genotypes that are highly addicted to mycorrhizae and produce more biomass are important in ecological and economic aspects.

PCA also showed that Yellow genotype inoculated to *Cl. claroideum* and *Cl. etunicatum* mycorrhiza species can be potentially be used to provide higher plant growth and nutrient uptake. Also, there is a significant correlation between nutrient uptake and root parameters. Mehraban et al. (2009) and Badi et al. (2019) showed that only a few Rhizoglomus species dominated without host plant genotype specificity in a semi-arid Sudanese cropland region.

Conclusion

Our study reported that the sweet sorghum genotypes were selectively associated with AMF inoculations for growth, root parameters and nutrient concentrations. The sorghum genotypes were significantly and highly responsive to AMF dependency. *Fu. mosseae* and *Cl. claroideum* inoculated Yellow sorghum genotype produced the highest total dry weight and MD. Early flowering Hereahri genotypes showed significantly higher plant height than the other genotypes. It is of great interest to search further for the best combination of genotype and mycorrhizal species under marginal soil conditions. Also, it is important to find the relationship between sweet sorghum genotypes' sugar content and mycorrhiza species preferences. Successful and high levels of root colonisation are an important step to further experiment to explore the best mycorrhizal colonisation with sorghum genotype growth and nutrient uptake in terms of the root exudate content of each sorghum genotype. Future work should be focused on sweet sorghum genotypes carbon sequestration, higher sugar content and mycorrhizae carbon demand related to soil quality and biofuel production as well.

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Disclosure of potential conflicts of interest

No potential conflict of interest was reported by the author(s).

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