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Screening of wild emmer wheat accessions (*Triticum turgidum* subsp. *dicoccoides*) for mycorrhizal dependency

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Abstract: Mycorrhizal dependency was studied in 23 wild emmer (*Triticum turgidum* subsp. *dicoccoides*) accessions originating from ecologically and geographically different locations in the Fertile Crescent covering Israel, Turkey, Lebanon, Jordan, and Syria. Wild emmer accessions were grown with mycorrhizae (*Glomus mosseae*) and non-mycorrhizae under greenhouse conditions, and harvested according to the Zadoks scale at growth stage 33. Root, shoot and total dry weight, growth response, root infection, and mycorrhizal dependency were calculated. It was determined that mycorrhizal inoculation increased 4.1-, 3.9-, and 3.9-fold for root, shoot, and total dry weight, respectively, compared to the control. It was found that wild emmer wheat exhibited a wide range of mycorrhizal dependency (56.8%-90.5%) and growth response (144.0%-990.4%), except root colonisation (70.0%-75.0%). Based on these observations, the hypothesis whether or not wild wheat chromosomes have a gene(s) for mycorrhizal response was tested. The experiment was done on the Langdon-*T. dicoccoides* substitution lines, each having an individual chromosome from "wild emmer wheat", *T. dicoccoides*, substituted into the tetraploid wheat cultivar "Langdon" background. Among the Langdon-*T. dicoccoides* substitution lines, mycorrhizal dependency and growth response varied from 70.9% to 87.0% and from 261.1% to 690.0%, respectively, whereas most of the substitution lines were significantly lower than Langdon for these traits. Disomic substitution lines for B genome chromosomes of *dicoccoides* showed a significant reduction in mycorrhizal dependency and growth response when compared with disomic substitution lines for A genome chromosomes of *dicoccoides*. These results revealed that B genome chromosomes had a more detrimental effect on mycorrhizal dependency than did A genome chromosomes. The results of this study showed that wild emmer wheat may be used as a source of mycorrhizal dependency in wheat breeding.

Key words: Growth response, mycorrhizal dependency, arbuscular mycorrhizae, wild wheat

Yabani gernik (*Triticum turgidum* subsp. *dicoccoides*) buğdayın mikorizaya bağımlılığının test edilmesi

Özet: İsrail, Türkiye, Lübnan, Ürdün ve Suriye'yi içerisine alan Verimli Hilal Bölgesi'nin farklı ekolojik ve coğrafik bölgelerinden toplanan 23 yabani gernik (*Triticum turgidum* subsp. *dicoccoides*) hattında mikorizaya bağımlılık çalışılmıştır. Yabani gernik genotipleri mikorizalı (*Glomus mosseae*) ve mikorizasız olarak sera koşullarında yetiştirilmiş ve Zadoks bitki büyüme skalası 33. evreye göre hasat edilmiştir. Kök, sap ve toplam kuru madde ağırlığı, büyüme tepkisi,

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kök infeksiyonu ve mikorizaya bağımlılık hesaplanmıştır. Yapılan bu ölçümlerde, kontrolle kıyaslandığında, mikoriza inokulasyonunun kök, sap ve toplam kuru madde ağırlığını sırasıyla, 4.1, 3.9 ve 3.9 kat arttırdığı saptanmıştır. Yabani gernik, mikorizaya bağımlılık (% 56.8-90.5) ve büyüme tepkisi (% 144.0-990.4) bakımından yüksek varyasyon göstermesine rağmen, kök kolonileşmesi (% 70.0-75.0) düşük bulunmuştur. Bu gözleme dayanarak, yabani gernik buğdayının mikorizaya bağımlılığı kontrol eden gen veya genleri taşıyıp taşımadığı araştırılmıştır. Deneme, her bir yabani gernik buğdayı (*T. dicoccoides*) kromozomunun tetraploid buğday genotipi Langdon'a aktarılmasıyla elde edilen yedeklenmiş hatlarda sürdürülmüştür. Bu denemede, Langdon-*T. dicoccoides* yedekli hatları arasında, mikorizaya bağımlılık ve büyüme tepkisinin sırasıyla % 70.9-87.0 ve % 261.1-690.0 arasında değişim gösterdiği, yedekli hatların çoğunluğunun bu özellikler bakımından Langdon çeşidinden önemli düzeyde daha düşük bulunduğu saptanmıştır. Yabani Gernik'in B genomu kromozumunun disomik yedekli hatları, A genomu kromozumunun disomik yedekli hatları ile karşılaştırıldığında, mikorizaya bağımlılık ve büyüme tepkisinde önemli düzeyde azalmalar gösterdiği belirlenmiştir. Bu sonuçlar, yabani gerniğin sahip olduğu B genomu kromozomlarının mikorizaya bağımlılık açısından, A genomu kromozomunlarından daha fazla zararlı etkiye sahip olduğunu göstermektedir Bu çalışmanın sonuçları, yabani gernik buğdayın, buğday ıslahında mikorizaya bağımlılık için bir gen kaynağı olarak kullanılabileceğini göstermiştir.

Anahtar sözcükler: Büyüme tepkisi, mikorizaya bağımlılık, arbusküler mikoriza, yabani buğday

Introduction

Mycorrhizal symbiosis is common in approximately 90% of plant families (Smith and Read 1997). Mycorrhizal fungi have been shown to benefit plants in a number of ways, including enhanced nutrient uptake, increased drought tolerance, improved tolerance to soil-borne pathogens, and resistance to other environmental stresses such as heavy metal toxicity (Kapulnik and Kushnir 1991). Especially in nutrient limiting soils, mycorrhizae are important for growth and reproduction of plants (Ortaş 2003).

The dependency of a plant species on mycorrhizae has been defined as "the degree to which a plant is dependent on the mycorrhizal condition to produce its maximum growth or yield, at a given level of soil fertility" (Gerdemann 1975; Ortaş 2003). Previous studies have shown that within a plant family such dependency might differ between cultivars (Mengel et al. 1978; Sawers et al. 2008). Furthermore, a significant interaction has been demonstrated between cultivars within a species and mycorrhizal colonisation (Mercy et al. 1990; Sing and Adholeya, 2004; Sawers et al. 2008).

Wheat is a major food crop all over the world, and considerable scientific effort has been expended on achieving improvement and sustainability in yield. The main aim of wheat breeding is to improve agronomic characteristics such as yield, fertiliser use efficiency, and increasing tolerance to biotic and abiotic stresses. However, in previous decades wheat breeders have typically not considered any interactions between plants and soil microflora. However, recently plant breeders have focused on the relationship between plant nutrition and genotype differences (Behl et al. 2003). Generally, plants are naturally fed by soil microflora, and one of the important components of soil micro-organisms is mycorrhizae. Therefore, management of mycorrhizal symbiosis could be helpful for utilising the potential of wheat to improve yield under low input agriculture. Various previous researchers (Azcon and Ocampo 1981; Young et al. 1985; Vierheilig and Ocampa 1991; Al-Karaki et al. 2004; Daei et al. 2009) found variation in plant dependency and degree of vesicular-arbuscular-mycorrhiza (VAM) infection in response to *Glomus mosseae* inoculation in different wheat (*T. aestivum*) cultivars.

The wild emmer tetraploid wheat, *Triticum turgidum* subsp. *dicoccoides* (hereafter referred to as *T. dicoccoides*), is the progenitor of tetraploid and hexaploid cultivated wheats. Wild emmer wheat has adapted to a wide range of habitats to meet the local macro- and micro-environmental conditions at the morphological, developmental, allozyme (Nevo 1986), and seed storage protein level (Feldman and Sears 1981; Levy and Feldman 1987). These studies showed that wild wheat harbours rich genetic resources for wheat improvement. However, the ecology of wild wheat is well understood, but the potential of mycorrhizal fungi to improve yield in wild emmer (*T. dicoccoides*) has not been extensively examined.

Interspecific substitution lines, in which one chromosome from wild relatives of wheat replaces one chromosome of wheat, are useful tools for studying the effect of different chromosomes on the plant characters of wheat. The chromosome substitution lines permit the examination of each individual chromosome and its influence on plant characteristics (Joppa 1993). For instance, Hetrick et al. (1995) used inter-varietal substitution lines to identify specific chromosomes that confer mycorrhizal responsiveness in hexaploid wheat. They reported that chromosomes 1A, 5B, 6B, 7B, and 7D of 'Cheyenne' had positive effects on mycorrhizal responsiveness in a "Chinese Spring" background.

In the present work, 23 wild emmer (*T. dicoccoides*) accessions originating from ecologically and geographically diverse locations in the Fertile Crescent were evaluated and screened for their mycorrhizal dependency under greenhouse conditions. In addition, Langdon-*T. dicoccoides* disomic substitution lines, each having an individual chromosome from wild emmer substituted into the tetraploid wheat cultivar 'Langdon' background, was used in order to identify whether or not specific chromosomes confer mycorrhizal dependency in wild emmer wheat.

Materials and methods

The soil used in the experiment was collected from the campus of Çukurova University, Adana, Turkey. The soil type was clay texture with low fertility (Table 1). The soil was sieved (2 mm), and then it was sterilised with steam at 121 °C for 2 h (Ortaş et al. 1999). Before potting, all pots were washed with 0.1% HCl and deionised water and filled with 2.75 kg of soil.

Twenty-three wild emmer wheat (*T. dicoccoides*) accessions, the durum wheat cv. Langdon, and 12 Langdon-*T. dicoccoides* substitution lines were used as plant material in this experiment (Table 2). *T. dicoccoides* and Langdon-*T. dicoccoides* substitution lines were kindly donated by Dr. M. Feldman, Weizmann Institute of Science, Israel, and Dr. L. Joppa, North Dakota State University, respectively.

Glomus mosseae (Nicol. and Gerd.) was used (Azcon and Ocampo 1981; Hetrick et al. 1992, 1993, 1995) as a mycorrhizae species. The experimental layout was set up with 216 pots with and without inoculation. On 28 February 2004, 10 to 15 seeds were sown in each pot. A suspension of 1000 spore pot^{-1} was inoculated 3 cm below seeds. After emergence (2-3-leaf stage), the pots (2.5 kg, 14 × 18 cm) were thinned to 4 seedlings, and were arranged in a randomised every 6-7 days. Plants were irrigated every day. After emergence, 5 mg kg^{-1} Zn soil was added once to the soil in the form of $ZnSO_4$, and 50 mg kg^{-1} N soil as Ca $(NO_3)_2$ was added weekly.

Experimental design, maintenance, and statistical analysis

Two independent experiments were carried out as a completely randomised design with three replications under greenhouse conditions at the Department of Soil Science, Faculty of Agriculture, University of Çukurova, Adana, Turkey, in 2004. In experiment 1, all wild emmer accessions were screened. In experiment 2, all substitution lines (2n = 28) and the durum cv. Langdon (2n = 28) were screened. All plants were harvested according to the Zadoks scale (Zadoks et al. 1974) at growth stage 33. After harvest, samples of shoot and root from the greenhouse were transported to the laboratory, washed with 0.1% HCl followed by 2 washes with deionised water, and dried at 65 °C for 48 h. After drying, shoot, root, and total dry weight were

Table 1. Some of the physical and chemical properties of soil used in this experiment*

OM	N	Salt	K_2O	P_2O_5	Cu	Mn	Fe	Zn	pH
	(%)		(kg ha^{-1})		(mg kg^{-1})				
0.513	0.025	0.17	1060.17	10.33	0.67	2.18	2.59	0.21	7.57

*: The Rhisophere Laboratory of Çukurova University, 2003; OM: Organic matter

Table 2. List of *T. dicoccoides* accessions used in this study

Name of accession	Origin	Locality
A Line	Israel	-
17902	Israel	Rosh-Pinnar East Galilee
PI 470988	Israel	Rosh Pinna
PI 538719	Israel	10 km N west of Majdal Shams near sea level
PI 503314	Israel	City limits of Safad on road to Rosh Pinna
PI 466926	Israel	Kazrin
PI 428013	Israel	Rosh Pinna, near Galilee
PI 538680	Israel	Korazin, 1 km East of Junction to Almagor below sea level
PI 428097	Israel	1 km east of junction of Almagor
PI 428086	Turkey	20.2 km from Siverek to Karacadağ
PI 538659	Turkey	52.5 km west of Diyarbakır in the Karacadağ
PI 554582	Turkey	Karacadağ road and highway/Diyarbakır
PI 554583	Turkey	3 km SE of Karacadağ road and Diyarbakır highway
IG 116184	Turkey	Gaziantep, between Ürünlü and Söğütlü villages
PI 554580	Turkey	Karacadağ road and Diyarbakır highway
PI 428063	Turkey	51 km west of Diyarbakır in the Karacadağ
PI 554581	Turkey	25 km SW of Diyarbakır
IG 46386	Jordan	Amman, 7 km west of Naur on Dead Sea highway
IG 45676	Jordan	Irbid, 16 km south-west of Irbid near Zubia
IG 46504	Syria	Damascus Province, May Saloun, 4 km before Tukeya
PI 487253	Syria	Der a Province
IG 110815	Lebanon	Biqaa AlGharbi, Karaoun, 1 km the road to the lake
PI 428132	Lebanon	Aiha-Kfarkouk, above "Sahlet"

measured. For determination of mycorrhizal infection, roots were dried on tissue paper and preserved in a mixture (50:13:5) of ethanol, glacial acetic acid, and formalin (Ortaş, 1994). A small proportion of preserved roots was stained by the method described by Koske and Gemma (1989), and examined for the presence and degree of mycorrhizal infection (root colonisation) according to the method of Givonnetti and Mossea (1980). Growth response (GR) and mycorrhizal dependency (MD) were calculated for each plant species using the following formula given by Hetrick et al. (1992, 1993, 1995):

$$GR\ (\%) = \frac{(\text{Total dry weight}_{\text{mycorrhizal}} - \text{Total dry weight}_{\text{non-mycorrhizal}})}{\text{Total dry weight}_{\text{non-mycorrhizal}}} \times 100,$$

$$MD\ (\%) = \frac{(\text{Total dry weight}_{\text{mycorrhizal}} - \text{Total dry weight}_{\text{non-mycorrhizal}})}{\text{Total dry weight}_{\text{mycorrhizal}}} \times 100$$

Arcsine transformation was performed to normalise the data for mycorrhizal dependency, growth response, and root colonisation. The analysis of variance was performed using the Mstat-C (1991) statistical package, and the means were compared using Duncan's multiple range test. The data from the wild emmer wheat accessions and the substitution lines were analysed separately.

Results

Based on the ANOVA analysis, mycorrhizae, wild emmer wheat accessions, and their interaction significantly influenced root dry weight, shoot dry weight, and total dry weight (Table 3). The significant mycorrhizae × genotype interaction for all studied traits resulted from the different abilities of wild wheat accession to respond to mycorrhizae as a consequence of genetic differences. There were also highly significant differences among wild emmer accessions for mycorrhizal dependency and growth response, but not for root colonisation (Table 4). Total dry weight, shoot dry weight, and root dry weight of the inoculated wild wheat plants varied from 0.362 to 1.301 g plant^{-1}, 0.242 to 1.023 g plant^{-1}, and from 0.120 to 0.393 g plant^{-1}, respectively (Table 5). The inoculated wild wheat accession Israel A line had maximum total dry weight (1.301 g plant^{-1}) and shoot weight (1.023 g plant^{-1}). On the other hand, the mycorrhizae-inoculated wild wheat accession

Table 3. Analyses of variance for root dry weight, shoot dry weight, and total dry weight in wild emmer wheat (*T. dicoccoides*) accessions

Source of variance	Degree of freedom	Mean square		
		Root dry weight (g plant^{-1})	Shoot dry weight (g plant^{-1})	Total dry weight (g plant^{-1})
Genotype (G)	22	0.009**	0.036**	0.076**
Treatment (T)	1	1.173**	3.542**	8.853**
GxT	22	0.008**	0.019**	0.044**
Error	92	0.001	0.006	0.008
CV (%)		18.5	26.6	20.8

CV: Coefficient of variation, **: Significant at $P < 0.01$

Table 4. Analyses of variance for mycorrhizal dependency, growth response, and root colonisation in wild emmer wheat (*T. dicoccoides*) accessions

Source of variance	Degree of freedom	Mean square		
		Mycorrhizal dependency (%)	Growth response (%)	Root colonisation (%)
Replication	2	43.999	9050.4	136.742
Genotype	22	202.606**	139125.9**	103.481^{ns}
Error	44	68.942	22129.9	107.377
CV (%)		11.3	30.8	10.7

CV: Coefficient of variation, **: Significant at $P < 0.01$, ^{ns}: non-significant

Table 5. Total, shoot, and root dry weight of wild emmer wheat (*T. dicoccoides*)

Accession Name	Total dry wt (g plant^{-1})		Shoot dry wt (g plant^{-1})		Root dry wt (g plant^{-1})	
	M	NM	M	NM	M	NM
PI 428086	1.044 b	0.099 jk	0.685 b	0.061 hij	0.360 ab	0.038 j
Israel A line	1.301 a	0.134 h-k	1.023 a	0.099 e-h	0.279 b-e	0.035 j
PI 538659	0.636 e-i	0.086 k	0.416 d-j	0.042 ij	0.219 c-f	0.044 ij
17902	0.739 c-g	0.118 ijk	0.544 b-f	0.083 ghi	0.195 efg	0.035 j
PI 554582	0.779 c-g	0.166 d-j	0.444 c-i	0.103 e-h	0.336 ab	0.062 efg
PI 554583	0.567 f-j	0.122 h-k	0.361 f-j	0.074 hij	0.206 d-g	0.048 g-j
PI 470988	0.749 c-g	0.174 c-i	0.465 c-h	0.113 d-h	0.284 bcd	0.061 e-h
IG 46386	0.953 bc	0.228 a-e	0.560 b-e	0.164 a-d	0.393 a	0.064 ef
PI 428063	0.502 hij	0.129 h-k	0.312 g-j	0.088 f-i	0.190 fg	0.041 j
PI 554580	0.842 b-e	0.214 a-f	0.564 b-e	0.132 c-g	0.278 b-e	0.083 bcd
IG 110815	0.496 hij	0.131 h-k	0.329 g-j	0.089 f-i	0.167 fg	0.042 j
PI 538719	0.927 bcd	0.253 ab	0.628 bc	0.166 abc	0.299 bc	0.087 a-d
IG 116184	0.559 g-j	0.142 f-k	0.358 f-j	0.093 f-i	0.202 d-g	0.049 f-j
IG 46504	0.689 d-h	0.181 b-i	0.402 d-j	0.109 e-h	0.287 bcd	0.072 d-e
PI 503314	0.934 bc	0.269 a	0.592 bcd	0.209 a	0.342 ab	0.059 e-i
PI 466926	0.559 g-j	0.161 e-j	0.335 g-j	0.113 d-h	0.224 c-f	0.048 f-j
IG 45676	0.797 c-f	0.237 a-d	0.497 b-g	0.175 abc	0.300 bc	0.063 efg
PI 428013	0.946 bc	0.277 a	0.620 bc	0.185 ab	0.326 ab	0.092 ab
PI 428097	0.439 ij	0.141 g-k	0.264 ij	0.096 fgh	0.175 fg	0.045 hij
PI 554581	0.362 j	0.120 h-k	0.242 j	0.030 j	0.120 g	0.090 abc
PI 538680	0.663 e-i	0.211 a-g	0.436 c-j	0.137 b-f	0.227 c-f	0.074 cde
PI 428132	0.485 hij	0.192 b-h	0.297 hij	0.130 c-g	0.188 fg	0.061 e-h
PI 487253	0.613 e-i	0.247 abc	0.396 e-j	0.148 b-e	0.217 c-f	0.099 a
Mean	0.721	0.175	0.468	0.115	0.253	0.061

M: Inoculated with VAM *Glomus mosseae*, NM: Non-inoculated with *Glomus mosseae*

PI554581 produced minimum total dry weight, shoot dry weight, and root dry weight. The wild wheat accessions produced significantly greater total dry weight, shoot dry weight, and root dry weight in the presence of mycorrhizal fungi when compared to non-mycorrhizal plants (Table 5). In wild wheat accessions, mycorrhizal dependency and growth response ranged from 56.8% to 90.5% and from 144.0% to 990.4%, respectively. The root colonisation in wild wheat accessions varied from 70% to 75% (data not shown). Mycorrhizal dependency and growth response were highest in PI 428086, followed by Israel A (Table 6). In this study, there was no relationship between accession origin and mycorrhizal dependency. For instance, although PI 428086 and PI 554581 were sampled from the same region (Karacadağ/Diyarbakır), they had different mycorrhizal dependency (Table 6).

Table 6. Mycorrhizal dependency and growth response of wild emmer wheat (*T. dicoccoides*) accessions

Accession name	Mycorrhizal dependency (%)	Growth response (%)
PI 428086	90.5 a	990.4 a
Israel A line	89.7 a	873.5 ab
PI 538659	85.1 ab	709.1 bc
17902	83.4 bc	529.1 cd
PI 554582	78.6 cd	370.1 de
PI 554583	78.4 cd	364.8 de
PI 470988	76.6 de	337.2 de
IG 46386	75.9 de	327.0 de
PI 428063	74.6 de	295.7 de
PI 554580	73.8 def	335.1 de
IG 110815	73.6 def	309.3 de
PI 538719	73.1 d-g	278.8 de
IG 116184	72.9 d-g	349.3 de
IG 46504	71.8 e-h	325.0 de
PI 503314	70.6 e-h	270.0 de
PI 466926	70.5 e-h	270.6 de
IG 45676	70.3 e-h	243.2 de
PI 428013	70.2 e-h	242.3 de
PI 428097	67.6 fgh	216.8 e
PI 554581	66.9 gh	203.4 e
PI 538680	65.7 hi	242.9 de
PI 428132	60.2 ij	152.0 e
PI 487253	56.8 i	144.0 e
Mean	73.8	364.3

To test whether wild wheat chromosomes have a gene(s) for mycorrhizal response, we used Langdon-*T. dicoccoides* disomic substitution lines, each having an individual chromosome from "wild emmer wheat", *T. dicoccoides* (demonstrated as responsive to mycorrhizae in this study, accession name: Israel A line, see Table 6) substituted into tetraploid wheat cultivar "Langdon" background. Based on the analyses of variance, mycorrhizae, Langdon-*T. dicocoides* substitution lines, and their interaction significantly influenced root dry weight, shoot dry weight, and total dry weight of Langdon-*T. dicocoides* substitution lines (Table 7). There were also highly significant differences among Langdon and Langdon-*T. dicoccoides* substitution lines for mycorrhizal dependency and growth response, but not for root colonisation (Table 8).

Total dry weight, shoot dry weight, and root dry weight of the inoculated Langdon and Langdon-*T. dicoccoides* substitution lines varied from 0.933 to 1.620 g plant^{-1}, 0.744 to 1.310 g plant^{-1}, and from 0.181 to 0.468 g plant^{-1}, respectively (Table 9). Among the Langdon-*T. dicoccoides* substitution lines, mycorrhizal dependency and growth response varied from 70.9% to 87.0% and from 261.1% to 690.0%, respectively (Table 10). In addition, root colonisation in all substitution lines was around 75.0% (data not shown). When mycorrhizal dependency was compared, it was found that mycorrhizal dependency in one of the disomic substitution lines (Langdon-Dic-2A) was higher than that in tetraploid wheat Langdon (Table 10). The disomic substitution lines for B genome chromosomes of *T. dicoccoides* lines in the "Langdon" background showed lower mycorrhizal dependency

Table 7. Analyses of variance for root dry weight, shoot dry weight, and total dry weight in *T. dicoccoides* chromosome substitution lines

Source of variance	Degree of freedom	Mean square		
		Root dry weight (g plant^{-1})	Shoot dry weight (g plant^{-1})	Total dry weight (g plant^{-1})
Genotype (G)	12	0.010**	0.047*	0.081**
Treatment (T)	1	1.118**	13.13**	22.22**
G × T	12	0.006*	0.047*	0.064*
Error	52	0.003	0.020	0.029
CV (%)		26.8	24.3	22.2

CV: Coefficient of variation, **, *: Significant at $P < 0.01$ and $P < 0.05$, respectively

Table 8. Analyses of variance for mycorrhizal dependency, growth response, and root colonisation in Langdon-*dicoccoides* chromosome substitution lines

Source of variance	Degree of freedom	Mean square		
		Mycorrhizal dependency (%)	Growth response (%)	Root colonisation (%)
Replication	2	115.545	74208.1	1.786
Genotype	12	77.845*	52293.7*	1.511^{ns}
Error	24	32.555	20796.9	1.786
CV (%)		7.21	32.9	1.3

CV: Coefficient of variation, *: Significant at $P < 0.05$, ^{ns}: non-significant

Table 9. Total, shoot, and root dry weight of Langdon-*dicoccoides* chromosome substitution lines

Accession Name	Total dry wt (g plant^{-1})		Shoot dry wt (g plant^{-1})		Root dry wt (g plant^{-1})	
	M	NM	M	NM	M	NM
Langdon	0.987 c	0.150 e	0.746 c	0.111 e	0.241 cd	0.039 e
LDN-(Dic-1A)	1.615 a	0.292 a-d	1.310 a	0.181 a-e	0.305 bcd	0.112 ab
LDN-(Dic-2A)	1.620 a	0.209 b-e	1.152 ab	0.144 b-e	0.468 a	0.065 d
LDN-(Dic-3A)	1.244 abc	0.349 a	0.856 bc	0.233 a	0.388 ab	0.117 a
LDN-(Dic-4A)	1.322 abc	0.187 de	1.039 abc	0.137 cde	0.283 bcd	0.050 de
LDN-(Dic-5A)	1.426 ab	0.314 abc	1.103 ab	0.221 abc	0.323 bc	0.093 c
LDN-(Dic-6A)	1.439 ab	0.274 a-d	1.123 ab	0.206 a-d	0.316 bcd	0.069 d
LDN-(Dic-7A)	1.315 abc	0.207 b-e	1.039 abc	0.156 a-e	0.276 bcd	0.051 de
LDN-(Dic-1B)	1.245 abc	0.284 a-d	0.988 abc	0.217 a-d	0.258 bcd	0.068 d
LDN-(Dic-4B)	1.153 bc	0.258 ab	0.864 bc	0.190 a-e	0.289 bcd	0.068 d
LDN-(Dic-5B)	1.239 abc	0.326 a-d	0.896 bc	0.228 ab	0.342 abc	0.098 bc
LDN-(Dic-6B)	1.031 bc	0.288 cde	0.744 c	0.223 abc	0.287 bcd	0.065 d
LDN-(Dic-7B)	0.933 c	0.194 cde	0.752 c	0.132 de	0.181 d	0.062 d
Mean	1.274	0.256	0.970	0.183	0.304	0.073

M: Inoculated with VAM *Glomus mosseae*, NM: Non-inoculated with *Glomus mosseae*

Table 10. Mycorrhizal dependency and growth response of the durum wheat cv. Langdon and Langdon-*dicoccoides* chromosome substitution lines

Accession name	Mycorrhizal dependency (%)	Growth response (%)
LDN-(Dic-1A)	81.7 a-d	456.6 a-d
LDN-(Dic-2A)	87.0 a	690.0 a
LDN-(Dic-3A)	72.2 cd	261.1 d
LDN-(Dic-4A)	85.7 a	602.3 ab
LDN-(Dic-5A)	77.8 a-d	411.3 bcd
LDN-(Dic-6A)	80.5 a-d	447.7 a-d
LDN-(Dic-7A)	83.8 ab	553.2 abc
LDN-(Dic-1B)	77.3 a-d	387.8 bcd
LDN-(Dic-4B)	77.1 a-d	361.5 bcd
LDN-(Dic-5B)	73.3 bcd	279.6 cd
LDN-(Dic-6B)	70.9 d	289.8 cd
LDN-(Dic-7B)	78.6 a-d	394.6 bcd
Langdon	83.1 abc	550.2 abc
Overall mean	79.2	437.8
Average of the disomic substitution lines for A genome chromosome of *T. dicoccoide*s	81.2	484.3
Average of the disomic substitution lines for B genome chromosome of *T. dicoccoide*s	75.4	342.7

and growth response when compared with disomic substitution lines for A genome chromosomes of *T. dicoccoides* lines in the "Langdon" background (Table 10).

Discussion

The interaction between crop genotypes and mycorrhizae has been discussed in the literature. For instance, in natural field conditions, Mercy et al. (1990) found considerable variation in colonisation ranging from 0.0% to 28.6% in cowpea. In a greenhouse experiment, Azcon and Ocampo (1981) demonstrated that mycorrhizal dependency differed among 13 wheat cultivars. Wheat cultivar differences in response to mycorrhizae have also been observed by Young et al. (1985) and Vierheilig and Ocampo (1991). However, investigations with 27 wheat lines (Kapulnik and Kushnir 1991) and 10 barley lines (Jakobsen and Nielsen 1983) did not show significant variation in mycorrhizal colonisation. Hetrick et al. (1992, 1993) and Manske (1989) reported that modern wheat cultivars tend to be less responsive to mycorrhizal symbiosis, when compared to landraces. In previous studies, it was also found that diploid wheat showed strong responsiveness to mycorrhizal symbiosis, when compared to tetraploid and hexaploid wheat (Kapulnik and Kushnir 1991). Kapulnik and Kushnir (1991) and Hetrick et al. (1992, 1993) reported that tetraploid wheat showed low or no responsiveness to mycorrhizal symbiosis.

A shortcoming of several studies reported above was the absence of data for wild emmer wheat. In this study, we therefore, investigated the impact of a mycorrhizal fungus on wild emmer wheat, *T. dicoccoides*. It was observed that the mycorrhizal

fungus (*G. mosseae*) successfully colonised in wild emmer wheat. We found very high variation for mycorrhizal dependency and growth response, but not for root colonisation. This result showed that although wild wheat accession did not have variation for root colonisation (70%-75%) the ability of symbiosis to improve total dry weight, shoot dry weight, and root dry weight varied significantly. It is clear from the present studies and from those by Kapulnik and Kushnir (1991) that there is no relationship between the degree to which a plant is colonised and the potential for the plant to benefit from colonisation. Previous research demonstrated that mycorrhizal fungi can significantly affect plant growth (Zhu and Smith 2001). Our results also suggest that the growth of wild wheat can be improved by mycorrhizal application (Table 8). To understand the interaction between mycorrhizae and wild emmer wheat and to identify the best mycorrhizae type for wild emmer wheat or alternatively identify the best wild emmer accession for *G. mosseae*, additional research is particularly needed for developing strategies for their use in wheat breeding programmes.

The heritability of mycorrhizal responsiveness in plants has been suggested by several previous studies that describe responsiveness among cultivars of various crops, such as *Arachis hypogaea* (Kesava Rao et al. 1990) and *T. aestivum* (Azcon and Ocampo 1981). For instance, Neal et al. (1973) reported that a single chromosome substitution line in the plant genotype may alter the composition of the microbial community. In our study, we found that wild emmer wheat accessions exhibited a wide range of mycorrhizal dependency and growth response, but not root colonisation. To determine whether specific chromosomes of wild emmer wheat replacement in a background of tetraploid wheat can affect the mycorrhizal dependency or growth response we used the Langdon-*T. dicoccoides* substitution lines. It was observed that among all substitution lines mycorrhizal dependency and growth response varied from 70.9% to 87.0% and from 261.1% to 690.0%, respectively. The disomic substitution lines for B genome chromosomes of *T. dicoccoides* showed significant reductions in mycorrhizal dependency and growth response when compared with disomic substitution lines for A genome chromosomes of *T. dicoccoides*. These results showed that B genome chromosome disomic substitution lines had a greater detrimental effect on mycorrhizal dependency than A genome disomic substitution lines. Similar results were also reported by Kapulnik and Kushnir (1991), who suggested that factors limiting mycorrhizal dependency in wheat are controlled by the A and B genomes, but are epistatic to the more consistently dependent D genome contributors. Hetrick et al. (1995) used inter-varietal substitution lines to identify specific chromosomes that confer mycorrhizal responsiveness in wheat. They reported that chromosomes 1A, 5B, 6B, 7B, and 7D of 'Cheyenne' had positive effects on mycorrhizal responsiveness in a "Chinese Spring" background. In our study, we did not observe any genes located on chromosomes of *T. dicoccoides* that affected mycorrhizal dependency or growth response in tetraploid wheat cultivar "Langdon" background. However, in this study, 2 substitution lines, namely Langdon-Dic-2B and Langdon-Dic-3B, were not used. Therefore, these lines might carry some gene(s) for mycorrhizal dependency or growth response. Further research is necessary to clarify this point.

It appears that wild emmer wheat may be used as a source of mycorrhizal dependency in wheat breeding because the use of mycorrhizae in cultivated crops increases the uptake of macro- and micro-elements (Sawers et al. 2008), making a decrease in the use of fertiliser possible. Improvement of new wheat varieties having high mycorrhizal dependency will open novel ways to increase the agronomic potential of wheat by highlighting beneficial associations between plants and fungus.

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