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YIELD OF SYNTHETIC-DERIVED BREAD WHEAT UNDER VARYING MOISTURE REGIMES

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Abstract

Synthetic-derived bread wheat populations are used as sources of resistance genes for biotic and abiotic stresses. This study used direct field evaluation of synthetic-derived wheat lines to assess grain yield and its associated traits under varying moisture regimes during 2005-06 and 2006-07 at Tel Hadya and Breda, International Center for Agricultural Research in Dry Areas (ICARDA), Syria. Forty synthetic-derived wheat lines and 8 check cultivars were tested in 5 experiments using alpha-lattice design with 3 replicates. Analyses of variance revealed significant ($p \leq 0.01$) differences for grain yield and its associated traits except for biomass. Interactions due to genotype and environment were significant for all traits except for 1000-kernel weight. Phenotypic correlation coefficients of grain yield with grains spike^{-1}, plant height and harvest index were $r = 0.80^{**}$, $r = 0.73^{**}$ and $r = 0.68^{**}$, respectively. Cluster analyses of genotypes and environments clarified the effects of yield components and phenology on grain yield. Based on the shift multiplicative model (SHMM) analyses for 48 genotypes and 5 environments, grains spike^{-1} and harvest index were the major contributing components towards grain yield. Frequency and distribution of precipitation during the crop cycle differentiated yield potential across years. However, performance of synthetic-derived lines at various moisture levels was not significantly affected within each year at Tel Hadya and thus can act as good sources for drought-prone environments. We identified some lines bearing *T. tauschii* germplasm with yields equal and superior in some of the yield components to that of the high-yielding cultivars used as checks, thus providing useful material to wheat breeders.

Introduction

The mandate of the bread wheat breeding program at the International Center for Agricultural Research in Dry Areas (ICARDA) is to develop broad-based and high yielding bread wheat germplasm for the developing countries to enhance wheat production worldwide. Resistance to diseases, insect pressures and erratic environmental stresses are major constraints, responsible for low wheat production. Wild relatives of wheat are useful sources of disease resistance for bread wheat improvement. The production of synthetic-derived lines through interspecific hybridization of the original donors of wheat genome is one of the strategies employed at CIMMYT for capturing the desirable characteristics of the *A. tauchii* (Trethowan, 2004). Synthetic hexaploid wheat, which resulted by crossing durum wheat with *A. tauschii* Coss., has been used as a bridge for capturing resistance genes from the wild relatives into present day cultivated wheat. Synthetic hexaploids have been reported to carry resistance to different diseases such as leaf rust (Kerber, 1987); karnal bunt (Villareal *et al.*, 1996); stripe rust (Ma *et al.*, 1995); tan spot (Siedler *et al.*, 1994), and spot blotch (Mujeeb-Kazi *et al.*, 1996; Mujeeb-Kazi & Delgado, 1998). Synthetic hexaploids performed well under cold temperature and salinity stresses (Gorham, 1990; Limin & Fowler, 1993). Comparative performance of *T. tauchii* genotypes and hexaploid wheat under different moisture levels revealed relatively high levels of tolerance to moisture deficit in certain *T. tauchii* lines compared to other drought-tolerant hexaploid wheat (Reddy *et al.*, 1996). Introgression of alleles from wild ancestors into domesticated species for resistance against biotic and abiotic stresses is not very common as it does not result immediately in highly productive cultivars. Synthetic-derived lines had higher grain yield than recurrent parents (Del Blanco *et al.*, 2001; Ogbonnaya *et al.*, 2007), suggesting that it may result in the transgressive segregation. Some quantitative traits of economic importance were improved through transfer of alleles from synthetic hexaploids into wheat (Del Blanco *et al.*, 2001; Van Ginkel & Ogbonnaya, 2007).

Although, synthetic hexaploids have been a source of mono- and oligo-genic traits, limited data supports their use for as a source of quantitative traits for quantitative trait improvement. The specific objectives of this research were to determine i) the potential of synthetic-derived hexaploid wheat as a source of germplasm for grain yield and yield-associated traits, and ii) investigate the relationship among grain yield and yield-associated parameters in synthetic-derived lines.

Materials and Methods

Plant material, experimental design and growing conditions: Forty synthetic-derived bread wheat lines and 8 check cultivars (Table 1) were tested under different levels of moisture in alpha lattice design with 3 replicates during 2005-06 and 2006-07. Experiments 1 and 2 were grown on March 23, 2006 and February 02, 2006 at Tel Hadya under irrigated and rainfed conditions, respectively. Experiments 3 and 4 were grown on December 3 at Tel Hadya under irrigated and rainfed conditions, respectively. Experiment 5 was planted on November 14, 2006 at Breda under rainfed conditions. Hereafter 2005-06 will appear as year-1 and 2006-07 as year-2. Seedling rate was equal to 130 kg ha^{-1}. The soil type at Tel Hadya and Breda are low in organic matter, clays with a pH of 7.8 and 8.2 respectively. Upon severe dryness, it gets cracked. Plots consisted of 8 rows, 2.5 m long and 20 cm between rows. The plots were pre-plant fertilized with 45 kg ha^{-1} N and side dressed with another 45 kg ha^{-1} N. Other nutrients were determined to be sufficient for crop production based on soil test. Weedex, broad-leaf herbicide was applied to effectively control the weeds. Tel Hadya is 284 meter above sea level and between 36°01'N and 36°56'E whereas Breda is 300 meter above sea level and between 35°56'N and 37°10'E. The climate of these regions is semiarid with an average rain shower of 254 mm distributed mainly during winter season. Rainfall in spring is very erratic and usually no rain during summer months.

Collection of data: Days to heading were the number of days from planting to 50% spike emergence. Days to physiological maturity were the number of days from sowing to when 50% of the peduncles turned yellow. Plant height was average distance from the ground level to spike tips, excluding awns. Grain yield was obtained from each plot. Thousand kernel weight (TKW) was recorded by weighing 1000 kernels. Yield components were estimated as described by Sayre *et al.*, (1997) from a sub sample of 50 fertile tillers from each plot. Biomass production was calculated as above ground biomass. Grain filling days were the number of days from heading to physiological maturity. Field reaction of plants to yellow rust (YR), caused by *Puccinia striiformis* was converted into average coefficient of infection (ACI) as described by Stubbs *et al.*, (1986).

Table 1: Cultivars clusters, code, adjusted mean grain yield, agronomic characteristics, and disease reaction for 40 synthetic populations and check cultivars across 5 environments, 2005-06 and 2006-07

Cluster	Code	Populations/check cultivar	Heading	Maturity	GFD§	P. height	Spikes	Grains	TKW ¶	Yield	Biomass	HI‡	YR*
			days			cm	ha^{-1}	$spike^{-1}$	g	$kgha^{-1}$	$kgha^{-1}$	%	ACI#
A1	1	ALTAR 84/AEGILOPS SQUARROSA (TAUS)//OPATA	118	141	22	62	3087600	13	26	1244	5520	16	2
A1	25	QAFZAH-13	118	141	23	63	3219813	15	27	1286	5636	19	2
A1	8	REBWAH-7	118	142	23	64	3372764	16	28	1437	5709	21	2
A1	36	GIRWILL-9	118	142	24	64	3409341	16	29	1466	5980	24	3
A1	10	REBWAH-13	118	143	24	65	3434607	16	29	1468	6052	25	3
A1	11	REBWAH-17	118	143	24	65	3515844	16	29	1494	6322	26	3
A1	9	REBWAH-11	118	143	24	65	4270350	17	30	1576	6923	26	4
A1	26	QAFZAH-18	119	143	25	69	4300423	18	30	1580	7235	26	4
A1	5	CROC-1/AE.SQUARROSA (205)//2*BCN	119	143	25	70	4358200	18	30	1581	7462	27	6
A1	3	CROC-1/AE.SQUARROSA (224)//OPATA	120	143	25	70	4662317	19	31	1690	7850	28	7
A1	39	PASTOR/KAUZ/3/CROC-1/AE.SQUARROSA (224)//OPATA	120	144	26	72	7262700	21	32	1738	9865	30	17
A2-1	12	ATTILA-7	115	139	22	56	3132085	13	25	1616	5342	23	1
A2-1	18	CHAM-6	116	139	22	58	3167469	16	26	1644	5983	24	1
A2-1	41	CROC-1/AE.SQUARROSA (224)//OPATA/3/PASTOR	116	139	22	59	3208902	16	26	1692	6077	25	1
A2-1	48	HUBARA-5	117	140	22	61	3242355	16	28	1711	6092	26	2
A2-1	33	CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/KAUZ	117	140	22	63	3272858	16	28	1715	6128	26	2
A2-1	43	CROC-1/AE.SQUARROSA (224)//OPATA/3/PASTOR	117	140	22	63	3412184	17	28	1762	6146	27	2
A2-1	13	REBWAH-21	117	140	22	63	3488836	17	28	1764	6147	27	2
A2-1	30	GIRWILL-7	118	140	22	64	3516172	17	28	1768	6321	27	2
A2-1	31	QAFZAH-33	118	140	23	64	3553629	17	29	1786	6322	27	2
A2-1	34	CROC-1/AE.SQUARROSA (205)//KAUZ/3/SASIA	116	141	23	65	3599334	18	29	1795	6357	27	2
A2-1	28	QAFZAH-26	118	141	23	65	3654248	18	29	1796	6381	28	2
A2-1	35	CROC-1/AE.SQUARROSA (205)//KAUZ/3/SASIA	118	141	23	66	3657500	18	29	1802	6478	28	2
A2-1	44	CROC-1/AE.SQUARROSA (224)//OPATA/3/PASTOR	118	141	23	66	3697453	18	30	1803	6480	28	2
A2-1	21	CHEN/AEGILOPS SQUARROSA (TAUS)//FCT/3/STAR	118	142	23	66	3756703	18	30	1811	6515	29	2
A2-1	6	HUBARA-9	118	142	24	66	3794175	19	30	1831	6533	29	3
A2-1	29	QAFZAH-32	118	142	24	66	3795570	19	31	1876	6559	29	3
A2-1	32	QAFZAH-35	118	142	24	66	3821283	19	31	1884	6624	29	3
A2-1	7	REBWAH-3	118	142	24	67	3828848	19	31	1889	6696	29	4
A2-1	45	SKAUZ/BAV92/3/CROC-1/AE.SQUARROSA (224)//OPATA	118	142	24	67	3869458	19	31	1891	6788	29	4
A2-1	24	DEBEIRA	119	142	24	67	3956349	20	31	1902	6791	29	4
A2-1	2	DVERD-2/AE.SQUARROSA (214)//2*ESDA	119	142	24	68	3960398	20	31	1909	6829	30	4
A2-1	27	QAFZAH-23	119	142	24	69	4057095	20	31	1954	6854	30	5
A2-1	42	KATILA-13	119	142	24	69	4124475	20	32	2004	6876	31	6
A2-1	38	CROC-1/AE.SQUARROSA (205)//KAUZ/3/ATTILA	119	143	24	70	4317304	20	32	2030	6886	31	7
A2-1	40	MUNIA/CHTO/3/PFAU/BOW//VEE#9/4/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN	119	143	24	71	4324928	21	33	2052	7022	31	8
A2-1	47	TAM200/TUI/MILAN/KAUZ/3/CROC-1/AE.SQUARROSA (224)//OPATA	119	143	24	72	4565933	21	33	2054	7099	32	9
A2-1	37	CROC-1/AE.SQUARROSA (205)//KAUZ/3/ATTILA	119	143	25	72	4650027	21	33	2071	7102	33	9
A2-1	46	MILAN/KAUZ/3/URES/JUN//KAUZ/4/CROC-1/AE.SQUARROSA (224)//OPATA	119	143	25	73	5191463	21	33	2123	7140	34	12
A2-2	4	CROC-1/AE.SQUARROSA (205)//2*BCN	120	144	25	75	6327183	21	34	2241	8970	39	13
B	14	QIMMA-2	119	143	24	60	3143405	13	32	1135	6041	18	1
B	19	QIMMA-8	119	143	24	60	3251319	13	33	1178	6139	18	1
B	16	QIMMA-4	119	143	24	60	3449903	13	33	1182	6445	19	2
B	15	QIMMA-3	120	144	24	60	3804748	14	33	1200	7304	19	3
B	17	QIMMA-6	120	144	24	61	4067791	14	35	1223	7353	19	3
B	20	QIMMA-12	120	144	24	61	4128577	14	35	1302	7469	20	3
B	22	QAFZAH-8	120	144	24	61	4284193	15	35	1305	8155	20	4
B	23	QAFZAH-11	120	144	24	62	4345882	15	38	1333	8171	23	7
		LSD0.05	1	1	1	5	998064	3	5	336	-	4	-
		CV	1	1	6	10	38	25	21	28	-	22	-

§ GFD = Grain filling days, ¶ TKW = Thousand-kernel weight, ‡ HI = Harvest index, * YR = Yellow rust, and # ACI = Average coefficient of infection

Statistical analysis: Separate analyses of variance were carried out for all traits. The combined analysis of variance over 5 environments showed a significant genotype by environment interaction for all traits except 1000-kernel weight and biomass. Therefore, genotype main effects were tested against the genotype by environment interaction mean square, which was used to calculate Fisher's protected least significant difference (LSD) at the 5% probability level. Phenotypic correlation coefficients among all characters were computed from the mean values over 5 environments. The SAS (Anon., 1996) procedures and programs were used for these calculations.

Results and Discussion

Distribution and characteristics of high yielding lines: Genotypes exhibited significant ($p \leq 0.01$) differences for days to heading, days to maturity, plant height, grain-filling duration, spikes ha^{-1}, grains $spike^{-1}$, 1000-kernel weight, grain yield, harvest index, yellow rust reaction and non-significant ($p \geq 0.05$) for biomass, as reported by Inamullah *et al.*, (2006). Interactions due to genotype by environment were significant ($p \leq 0.01$) for all traits except 1000-kernal weight and biomass. Five synthetic-derived bread wheat lines codes No. 47, 43,4, 41 and 45 possessed grain yield equivalent to the best three bread wheat checks- 'HUBARA-5', 'CHAM-6' and 'ATTILA-7'. These accounted for 16% of the top mean grain yield (Table 1). Higher grain yield of synthetic-derived line 43 and 'HUBARA-5' can be attributed to their higher grains $spike^{-1}$ and harvest index. Synthetic-derived line 45 was among top 16 % high yielding lines that did not come up among 16% top performing lines for other traits indicating that high grain yield in this population could be the cumulative effect of all components rather than specific component.

Sixteen percent high yielding lines (synthetic-derived = 5 and check cultivars = 5) possessed higher grains $spike^{-1}$ but not necessarily higher performance for other components, signifying that major contribution towards higher grain yield was the result of higher grains $spike^{-1}$, as previously reported (Inamullah *et al.*, 2006 ; Del Blanco *et al.*, 2001., Garcia del Moral *et al.*, 2003). This is based on the fact that grain yield in wheat is frequently sink limited (Slafer & Andrade, 1991), and for this reason, the number of grains $spike^{-1}$ has been found as a promising trait for improving grain yield in wheat, especially under moisture stress environments (Nachit *et al.*, 1992; Simane *et al.*, 1993; Slafer & Andrade., 1991). Long-term increase in wheat grain production has been reported to be the result of more grains m^{-2} (Sayre *et al.*, 1997; Inamullah *et al.*, 2006). Fourteen synthetic-derived lines were statistically at par with five check cultivars for grains $spike^{-1}$.

Thirteen synthetic-derived lines had higher 1000-kernel weight than all check cultivars. The non-significant ($p \geq 0.05$) genotype by environment interaction for 1000-kernel weight implies that genotypes showed stability in 1000-kernel weight ranking across environments and the possible reason could be the high remobilization of stored pre-anthesis assimilates, confirming the earlier reports under different drought treatments (Garcia del Moral *et al.*, 2003). Seventeen synthetic-derived lines and four check cultivars exhibited similar spikes ha^{-1} but higher than other genotypes (Table 1). Eleven synthetic-derived lines and one check cultivar were taller than all other genotypes (Table 1). Eight synthetic-derived lines took more days to heading but similar to one of the check cultivars 'GIRWILL-9'. Thirteen synthetic-derived lines and 'GIRWILL-9' took more days to maturity (Table 1). Genotypes had non-significant differences for biomass production.

Table 2. Phenotypic correlation coefficients with significance level among different agraonomic data, 2005-06 and 2006-07

	Heading	Maturity	GFD§	P. height	Spikes	Grains	TKW ¶	Yield	Biomass	
	days			cm	ha^{-1}	$spike^{-1}$	g	$kgha^{-1}$	$kgha^{-1}$	
Heading (d)		0.99**	-0.60**	-0.40**	0.28**	-0.76**	-0.04	-0.68**	-0.23**	-0.4
Maturity (d)			-0.59**	-0.34**	0.28**	-0.76	-0.02	-0.68**	-0.23**	-0.4
GFD				0.35**	-0.25**	0.70**	0.31**	0.73**	0.30**	0.4
P. height (cm)					-0.18**	0.31**	0.30**	0.33**	0.15**	0.1
Spikes (ha^{-1})						-0.52**	-0.23**	-0.14**	0.52**	-0.4
Grains ($spike^{-1}$)							0.05	0.80**	0	0.7
TKW (g)								0.19**	0.01	0.1
Yield ($kgha^{-1}$)									0.29**	0.6
Biomass ($kgha^{-1}$)										-0.2
HI (%)										

** = Significant at 1%, § GFD = Grain filling days, ¶ TKW = Thousand-kernel weight, ‡ HI = Harvest index

Associations among traits: The phenotypic correlations of grain yield with grains spike^{-1}, plant height, harvest index, grain-filling duration, 1000-kernel weight and biomass were significantly ($p \leq 0.01$) positive but significantly negative with days to heading, days to maturity and spikes ha^{-1} (Table 2). Grains spike^{-1} ($r = 0.80$), plant height ($r = 0.73$) and harvest index ($r = 0.68$) were major contributing factors towards grain yield, based on high correlation coefficients with grain yield (Table 2). The positive phenotypic correlations of harvest index with plant height and grains spike^{-1}, and its significantly negative correlation with biomass indicate that the taller genotypes developed more grains spike^{-1}. Days to heading and spikes per hectare tended to be negatively associated with grain yield; therefore, longer cycle and profuse tiller genotypes had lower grain yield. (This makes sense, many of the synthetic hexaploids respond to chilling. This seems like some of the lines were partially facultative).The effect of inadequate moisture was more conspicuous in genotypes having more tillers: thus development of less number of kernel sites and forced heading were observed. The trend in phenotypic correlation analysis towards grain yield confirms the insight of cluster grouping. (Excessive biomass is often a detriment to drought stress because of its association to transpiration rates per seed unit. It often leads to precocious water use in a drought environment characterized by declining water availability.

The negative correlations of spikes ha^{-1} with grains spike^{-1} and grain yield indicate that the genotypes with profuse tillers could not develop all kernel sites into kernels and consequently these genotypes had less number of grains spike^{-1} and ultimately lower grain yield. Cropping season experienced lack of precipitation due to unexpected less frequent rain shower during the vegetative phase; thus the shortage of moisture had more aggravated effects on genotypes having more tillers. Days to heading and maturity were negatively correlated with plant height, grain-filling duration and grains spike^{-1}; the longer cycle had adverse effects on growth and development of plant height, grain-filling and grains spike^{-1}; these traits are source driven; therefore, erratic and uneven distribution of precipitation disturbed constant mobilization of substrate towards growth and grain development, hence there were less number of grains spike^{-1}. Post-anthesis high temperature and dry spell disturbed grain filling, leaving grains shriveled. To recover crop from extreme drought stress, a supplemental irrigation was applied before maturity which delayed maturity but could not help recovering grain filling.

Shifted multiplicative model clustering of cultivars: The dendrogram from clustering 40 synthetic-derived wheat lines and eight check cultivars with the shift multiplicative model (SHMM) clustering method is shown in Fig. 1. At the two group level 32 synthetic-derived lines and 8 check cultivars formed cluster A while six sister lines of synthetic-derived 'Qimma' population and two sister lines (codes. 8 and 11) of synthetic-derived 'Qafzah' population formed cluster B. Group A had higher grain yield, harvest index, plant height, grains spike^{-1}, spikes per hectare, YR ACI rating compared to group B. However, group A had lower biomass, 1000-kernel weight, days to heading and days to maturity. All the eight check cultivars were in the high yielding cluster at two group level. At two group level grains spike^{-1}, harvest index and plant height appeared to have more contribution towards higher grain yield. Surprisingly, the high yielding group did not have higher 1000-kernel weight rather they clustered with the lower mean grain yield had high 1000-kernel weight (Table 3), suggesting that genotypes having relatively bigger grains yielded lower than that of small grains genotypes. Similar results were found in durum wheat (Nachit *et al.*, 1992). The possible explanation for the higher 1000-kernel weight in the lower cluster group is that there was no source limitation to the relatively smaller sink because of less number of grains spike^{-1} while on the other hand spikes with more grains did not receive sufficient amount of source for development and thus suffered. At three group level, the genotypes in cluster B were remained together but the cluster A split into two groups A1 and A2 (Table 3). Group A1 comprised 10 lines and one check cultivar 'Girwill-9' while group A2 had 21 lines and seven check cultivars (Fig. 1). Group A2 expressed high grain yield compared to group A1. Thus, SHMM clustering of genotypes at the three group level could be attributed mainly to differences in grains spike^{-1} and harvest index. At four group level, only cluster A2 divided further into subgroups A2-1 and A2-2. Subgroup A2-2 maintained high grain yield at four group level (Table 3). Cluster analysis at four group level revealed that grains spike^{-1} was the only trait, responsible for higher grain yield.

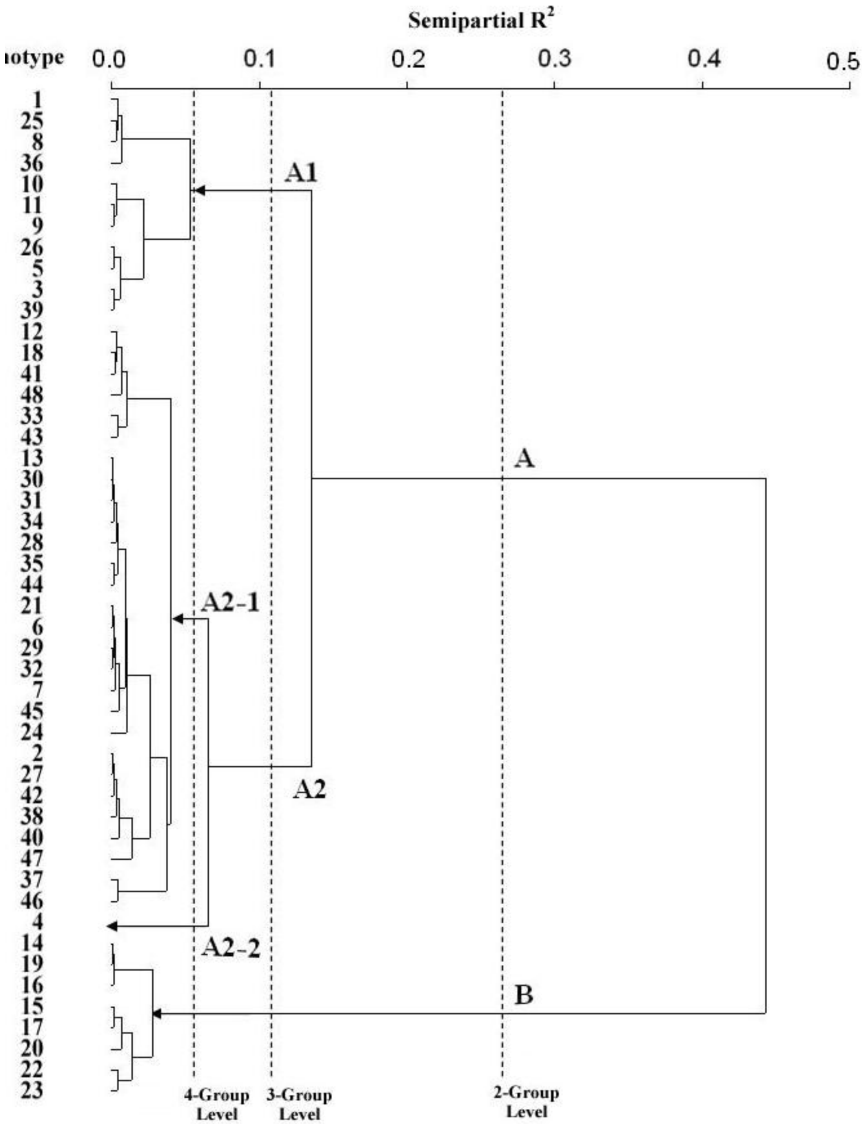

Fig. 1. Dendrogram resulting form shifted multiplicative model cluster method on 48 genotypes. Final groups of genotypes are marked with arrows.

Table 3. Mean of agronomic data with ranges in parenthesis and disease reaction of shifted multiplicative model grouping of 48 synthetic wheat genotypes and 5 environments at various group levles, 2005-06 and 2006-07 at Tel Hadya and Breda

Cluster Grouping of Genotypes

Groups	Heading	Maturity	GFD§	P. height	Spikes	Grains	TKW ¶	Yield	Biomass	HI‡	YR*
	days	days		cm	ha^{-1}	$spike^{-1}$	g	$kgha^{-1}$	$kgha^{-1}$	%	ACI#
					Two group level						
A	118	142	24	66	3945954	18	30	1768	6652	28	4
	(115-120)	(139-144)	(22-26)	(56-75)	(3087600-7262700)	(13-21)	(25-34)	(1244-2241)	(5342-9865)	(16-39)	(1-17)
B	120	144	24	61	3809477	14	34	1232	7135	19	3
	(119-120)	(143-144)	(24-24)	(60-62)	(3143405-4345882)	(13-15)	(32-38)	(1135-1333)	(6041-8171)	(18-23)	(1-7)
					Three group level						
A1	119	143	24	66	4081269	17	29	1506	6777	25	5
	(118-120)	(141-144)	(22-26)	(62-72)	(3087600-7262700)	(13-21)	(26-32)	(1244-1738)	(5520-9865)	(16-30)	(2-17)
A2	118	141	23	66	3894628	18	30	1868	6605	29	4
	(115-120)	(139-144)	(22-25)	(56-75)	(3132085-6327183)	(13-21)	(25-34)	(1616-2241)	(5342-8970)	(23-39)	(1-13)
B	120	144	24	61	3809477	14	34	1232	7135	19	3
	(119-120)	(143-144)	(24-24)	(60-62)	(3143405-4345882)	(13-15)	(32-38)	(1135-1333)	(6041-8171)	(18-23)	(1-7)
					Four group level						
A1	119	143	24	66	4081269	17	29	1506	6777	25	5
	(118-120)	(141-144)	(22-26)	(62-72)	(3087600-7262700)	(13-21)	(26-32)	(1244-1738)	(5520-9865)	(16-30)	(2-17)
A2-1	118	141	23	66	3905174	18	30	1862	6596	29	4
	(115-119)	(139-144)	(22-25)	(56-75)	(3132085-6327183)	(13-21)	(25-34)	(1616-2241)	(5342-8970)	(23-39)	(1-13)
A2-2**	120	143	23	63	3599334	20	29	2052	6854	29	4
B	120	144	24	61	3809477	14	34	1232	7135	19	3
	(119-120)	(143-144)	(24-24)	(60-62)	(3143405-4345882)	(13-15)	(32-38)	(1135-1333)	(6041-8171)	(18-23)	(1-7)

§ GFD = Grain filling days, ¶ TKW = Thousand-kernel weight, ‡ HI = Harvest index, * YR = Yellow rust, A2-2** = Range not given as it contains one element, and # ACI = Average coefficient of infection

Conclusion

Grain yield in this study appears to be most determined by grains spike^{-1} and harvest index. Selection for these traits may contribute to important increases in grain yield, particularly in drought-prone environments. Difference in grain yield was the result of acquiring more grains rather than heavier grains. More grains in turn increased harvest index. Therefore, the character of grains spike^{-1} was the sole contributing factor towards higher yield in this study. Seed containers in plants can be determined at an early stage of development and thus can act as best criterion for screening a large number of genotypes for drought conditions. Similar grain yield of the synthetic-derived lines in irrigated and rainfed conditions with in each year at Tel Hadya suggests that they can be considered best alternatives for moisture-stressed environments. This study further reveals that more rain showers during the month of March and prevalence of temperature above 0˚C during winter tended to have more favorable effects on grain yield. Cluster analyses of genotypes and environments were helpful in clarifying the effects of yield components and phenology on grain yield formation. We identified some lines bearing *T. tauschii* germplasm with yields equal and superior in some of the yield components to that of the high-yielding cultivars used as checks, thus providing useful material to wheat breeders.

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