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Agronomic Variability in Selected *Triticum turgidum* × *T. tauschii* Synthetic Hexaploid Wheats

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With one figure and 2 tables

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Abstract

Two trials were conducted at the Mexican National Institute of Agricultural Research Experiment Station at Yaqui Valley, Sonora, Mexico to investigate the nature and extent of agronomic variation in 50 synthetic hexaploid (SH) wheats ($2n = 6x = 42$, AABBDD) derived from *Triticum turgidum* ($2n = 4x = 28$, AABB) × *T. tauschii* ($2n = 2x = 14$, DD) crosses for subsequent use in wheat improvement. Plant height, spike length, days to flowering, physiological maturity, grain yield, above-ground biomass at maturity, harvest index, yield components and test weight were determined.

Significant agronomic variation was observed among the germplasm evaluated. Outstanding SH genotypes were identified with higher grain yield, above-ground biomass at maturity, 1000-grain weight, and spikes m^{-2} than the bread wheat (*Triticum aestivum* L.) check cultivar Seri 82. Genotypic correlations of grain yield with other character traits show that grain m^2 was the most important determinant of grain yield ($r = 0.993$). Data on agronomic traits subjected to complete linkage cluster analysis resulted in classifying the genotypes into two distinct phenotypic groups excluding Seri 82. Groups generally corresponded to durum progenitors of the SH with significant group differences for all characters. This demonstrates use of practical numerical analysis procedures to describe agronomic variation in representative SH genotypes. Clustering by quantitative traits may be valuable for identification of genotypes with divergent sources for breeding and agronomic purposes.

Key words: *Triticum turgidum*, *T. tauschii*, synthetic hexaploid (SH), agronomic variation, yield components, cluster analysis.

Introduction

Genetic diversity and variability in germplasm are necessary elements in wheat improvement. While many kinds of genetic variability may not be immediately useable because of space and resource limitations, it is desirable to maintain this diversity to safeguard against environmental stresses, pests and pathogens that may arise in the future. Consequently, one of our current objectives is to avoid the narrowing of variability in both pathological and agronomic characters during the

course of attempting to breed for high yield (RAJARAM et al. 1985).

Triticum tauschii (coss.) Schmal. (syn. *Aegilops squarrosa* L., $2n = 2x = 14$, DD) commonly known as goatgrass, with its diverse range of accessions and distribution provides a unique opportunity for exploiting novel genetic variability for wheat (*Triticum aestivum* L.) improvement associated with biotic and abiotic factors (GILL et al. 1985, GILL et al. 1986, KERBER and DYCK 1978, LIMIN and FOWLER 1981, PASQUINI 1980). Wheat germplasm has been developed with resistance to leaf rust,



Puccinia recondita f sp *tritici* and stem rust, *Puccinia graminis* f sp *tritici* (DYCK and KERBER 1970, GILL and RAUPP 1987, KERBER and DYCK 1969, RAUPP et al. 1983, SHARMA and GILL 1983, VILLAREAL et al. 1992), Hessian fly, *Mayetiola destructor* (GILL and RAUPP 1987, HATCHETT et al. 1981, MARTIN et al. 1982), greenbug, *Schizaphis graminum* (GILL and RAUPP 1987, HARVEY et al. 1980, JOPPA and WILLIAMS 1982, JOPPA et al. 1980, MARTIN et al. 1982) and Karnal bunt, *Tilletia indica* (VILLAREAL et al. 1994a) derived from *T. tauschii* accessions.

Though the general emphasis on utilization of the synthetic hexaploid (SH) wheats derived from *Triticum turgidum* × *T. tauschii* has been on resistance/tolerance to biotic and abiotic stresses, VILLAREAL et al. (1994b) have also studied parameters like pigmentation, pubescence and other taxonomic traits on some synthetic hexaploids. With regard to expression of *T. tauschii*'s genes on yield and other agronomic characteristics of SH wheats limited documentation exists to date. The present study was undertaken to evaluate the agronomic variation of some elite SH germplasm developed by CIMMYT's Wide Crosses Program, assess their yield potential and propose candidates for breeding.

Materials and Methods

Fifty SH wheats ($2n = 6x = 42$; AABBDD) derived from 13 crosses involving four high yielding *T. turgidum* cultivars and 11 *T. tauschii* accessions were included. The durum wheat and *T. tauschii* backgrounds of the test materials are indicated in Table 1. Seri 82, a widely grown high yielding cultivar in northwest Mexico was the *T. aestivum* check.

The 50 selected SH wheats and Seri 82 were grown in field trials at the Mexican Institute of Forestry, Agriculture, and Livestock, Campo Agrícola Experimental Valle del Yaqui (CAEVY) research station, Sonora, Mexico (27°20'N, 105°55'W elevation 39 m above sea level) during the 1989–90 and 1991–92 wheat production cycles. Each trial was grown as a randomized complete block design with two replicates. Three row plots, each 2.0 m long and 15 cm apart were hand sown at a seed rate of one seed per 10 cm in late November and reached maturity during May.

The trials received high levels of agronomic inputs and management. Prior to seeding, fertilizer was applied at the rate of 150 kg N ha⁻¹ in ammonium sulfate and 40 kg P ha⁻¹ in tri-superphosphate. The trials were surface irrigated just after planting. Irriga-

tion was continued as required until the latest maturing SH wheat reached physiological maturity. A preventive chemical program for the control of weeds, diseases, and insects was practiced. None of these factors affected yield in either trial.

Data were collected for seven agronomic characters: days to flowering and physiological maturity, plant height, spike length, grain yield, above-ground biomass at maturity and 1000-grain weight. Physiological maturity was recorded when 95% of the spikes in the plot had completely lost green color. Thousand grain weights were determined from two dried samples of 250 grains for each plot then multiplied by two.

Five characters were derived from the above measurement: (i) grainfilling period: the days from flowering to maturity; (ii) harvest index: calculated by dividing grain yield by above-ground biomass; (iii) number of spikes m⁻²; (iv) number of grains m⁻²; and (v) number of grains per spike.

All variables measured on each genotype were subjected to analysis of variance procedures using the PROC GLM of Statistical Analysis Systems (SAS Institute 1985). Because of the genotype selection procedure, genotype effects were assumed to be fixed. The genotypic correlation coefficient was calculated using the mean value of each variable for each genotype in all replications in the two trials as described by VARGHESE (1976).

The cluster analysis of 50 SH genotypes and the bread wheat cultivar check Seri 82 was performed using an agglomerative hierarchical clustering method with a dissimilarity (distance) matrix and the complete linkage strategy. The phenotypic means of the traits over replicates and years were standardized to a mean of 0 and a standard deviation of one since traits were measured on different scales. The PROC CLUSTER option COMPLETE (SAS Institute, 1985) was used. The cutting point was based on the usefulness of the subgroups resulting from it and set to a maximum distance between clusters of one. In general we were conservative and did not use very large subgroups from the dendrogram in order that genotypes within subgroups were homogeneous and phenotypically non-diverse.

Results and Discussion

This study was designed as a first attempt to evaluate the agronomic variation of some SH lines we have developed and to serve as a model for more extensive tests, either currently underway or in planning stages. It was also hypothesized that outstanding SH genotypes could be identified for utilization in the improvement of *T. aestivum*. Materials involved in this study represent the best advanced SH lines with cytogenetic stability, high fertility and resistance

to Karnal bunt (*Tilletia indica*) available (VILLAREAL et al. 1994a, b).

Plant height, flowering days, days to physiological maturity, grainfill period, grain yield, above-ground biomass at maturity, harvest index, yield components, spike length and 1000-grain weight data of 50 SH genotypes and the bread wheat cultivar check Seri 82 combined over two years of replicated yield tests at CAEVY, Mexico are summarized in Table 1. For each agronomic trait is also shown the standard error of the different values in comparing the traits between the test entries, as well as their respective coefficients of variation. Table 2 shows genotypic correlation coefficients for all variables measured for all the SH test entries. In addition, clustering of SH genotypes based on similarity of quantitative characters is presented (Fig. 1).

Grain yield

There was no significant genotype \times year interaction for grain yield, but differences were found among the genotypes (Table 1). The overall mean grain yield of the SH lines was 3540 kg ha⁻¹ as compared to Seri 82 (7214 kg ha⁻¹). Entry 39, a Duergand/*T. tauschii* (214) derived line yielded the highest (8028 kg ha⁻¹) while a entry 22 derivative from Chen/*T. tauschii* (205) gave the lowest yield (889 kg ha⁻¹). Entry 39 yielded 11.3 % higher than Seri 82 (8028 vs. 7214 kg ha⁻¹, $P < 0.05$). This however, does not imply a direct commercialization of this material since its other characteristics still need to be improved and stabilized through breeding, e.g. tight threshability, susceptibility to lodging, etc. Entry 11 from the cross Altar 84/*T. tauschii* (192) yielded 6921 kg ha⁻¹ comparable to the bread wheat check cultivar Seri 82. The 12 best yielding SH lines (entries 39, 42, 40 and 41) were from crosses involving Duergand/*T. tauschii* (214), Duergand/*T. tauschii* 221 (entries 43 and 45), Altar/*T. tauschii* 192 (entry 11), Altar/*T. tauschii* 198 (entry 12), Altar/*T. tauschii* 223 (entry 10), and Chen/*T. tauschii* 224 (entries 28, 35 and 36). Different yield responses were presumably due to gametic contribution and variability of the SH's progenitors. The experiments had a 8.4 % coefficient of variation.

Biomass and harvest index

Differences were observed among test materials

in both above-ground biomass and harvest index at maturity (Table 1). There was no evidence of genotype \times year interaction for biomass and harvest index. Mean biomass yield ranged from 6.4 t ha⁻¹ (entry 38; Chen/*T. tauschii* 224) to 19.7 t ha⁻¹ (entry 39; Duergand/*T. tauschii* 214). Entries 39 and 41 had biomass yields (19.7 and 19.2 t ha⁻¹) significantly greater than Seri 82 (16.5 t ha⁻¹) at 0.05 level of probability. Entries 42 (18.2 t ha⁻¹), 43 (17.8 t ha⁻¹), 12 (17.5 t ha⁻¹), 45 (16.9 t ha⁻¹), 11 (16.6 t ha⁻¹), 36 (15.2 t ha⁻¹), 46 (14.7 t ha⁻¹), 48 (14.1 t ha⁻¹) and 21 (13.9 t ha⁻¹) possessed comparable biomass yields to Seri 82 ($P > 0.05$). Since biomass contributes to grain yield, SH materials with high biomass deserve emphasis in the *T. aestivum* hybridization program so as to assure a continued improvement in grain yield (EKMAN 1981). The overall mean biomass yield of all the SH lines was 11.8 t ha⁻¹. The coefficient of variation was 10.9 %.

The mean harvest index of SH over two years trials ranged from 9.9 % (entry 22) to 46.6 % (entry 34). Seventy-four percent of the SH lines had low harvest indices as compared to Seri 82 ($P < 0.05$). Three genotypes (entries 34, 28 and 29), all derived from Chen/*T. tauschii* (224) reached the mean harvest index of 42.4 % of Seri 82. However, no significant difference was observed at 0.05 level of probability. The overall mean harvest index of the SH lines was 29.5 %.

Yield components

Over the two replicated trials, SH lines averaged 324 spikes m⁻² while Seri 82 had 356 spikes m⁻². Thirteen SH had more spikes m⁻² than Seri 82 ($P < 0.05$), Table 1. The most number of spikes m⁻² were recorded on entry 39 (574 spikes m⁻²), a line derived from Duergand/*T. tauschii* (214). None of the SH genotypes tested in both years reached the mean 17 120 grains m⁻² of Seri 82. The overall mean grains m⁻² of the SH lines was 6229. The range was 1725 (entry 22) to 13 119 grains m⁻² (entry 39). Similarly, on grains per spike, Seri 82 with 49.5 grains was the highest among all genotypes tested ($P < 0.01$). The SH genotypes averaged 18.8 grains per spike with a range of 6.5 (entry 22) to 26.9 grains per spike (entry 45).

Thousand grain weight was significantly heavier in all the SH genotypes (56.5 g) than the bread wheat cultivar check Seri 82 (41.3 g) at

Table 1. Agronomic traits of 50 synthetic hexaploids derived from crosses involving four *Triticum turgidum* cultivars and 11 *T. tauschii* accessions and the bread wheat cultivar Seri 82 combined over two years of field tests at CAEVEY, Mexico

Entry No.	Cross	Entry Code	Plant height (cm)	Days to flowering	Days to		Grain yield (kg ha ⁻¹)	Above-ground biomass (t ha ⁻¹)	Harvest index (%)	Spikes m ⁻²	Grains m ⁻²	Grains per spike	1000-grain weight (gm)	Spike length (cm)
					Physio-logical maturity	Grainfill period (days)								
1	Altar 84/T. tauschii 219	1A219	99.5	104.0	138.2	34.2	3745.0	12.6	29.8	267.0	6515.0	24.4	57.6	12.0
2	Altar 84/T. tauschii 219	2A219	105.5	104.2	139.0	34.7	3093.0	10.3	29.9	232.0	5635.0	24.2	55.0	11.7
3	Altar 84/T. tauschii 219	3A219	101.5	102.7	134.7	32.0	3092.0	8.9	34.9	293.0	5476.0	18.9	56.4	12.7
4	Altar 84/T. tauschii 224	4A224	101.5	106.2	139.0	32.7	2926.0	9.6	30.4	222.0	4883.0	21.9	59.9	12.0
5	Altar 84/T. tauschii 224	5A224	98.5	104.0	138.2	34.2	2999.0	9.2	34.8	226.0	5002.0	22.1	59.9	11.7
6	Altar 84/T. tauschii 224	6A224	101.5	104.7	138.0	33.2	3707.0	9.4	39.5	262.0	6366.0	24.3	58.2	13.0
7	Altar 84/T. tauschii 224	7A224	89.5	107.5	140.7	33.2	2996.0	9.6	31.2	215.0	5085.0	23.6	58.9	13.0
8	Altar 84/T. tauschii 221	7A224	91.5	107.5	139.7	32.2	3372.0	11.8	28.6	226.0	5786.0	25.5	58.3	12.2
9	Altar 84/T. tauschii 223	9A223	100.7	107.5	139.7	32.2	4493.0	12.5	36.0	313.0	7963.0	25.5	56.4	12.0
10	Altar 84/T. tauschii 223	10A223	104.0	107.5	140.2	32.7	5300.0	13.7	38.5	413.0	9140.0	22.2	58.0	13.0
11	Altar 84/T. tauschii 192	11A192	101.2	107.5	139.7	32.2	6921.0	16.6	41.9	499.0	11548.0	23.1	59.9	12.0
12	Altar 84/T. tauschii 198	12A198	98.2	107.7	140.5	32.7	6547.0	17.5	37.5	502.0	10703.0	21.4	61.2	12.0
13	Altar 84/T. tauschii 198	13A198	104.5	108.0	138.7	30.7	3935.0	11.6	33.8	316.0	6463.0	20.5	60.9	11.7
14	Altar 84/T. tauschii 198	14A198	101.5	107.5	138.2	30.7	2460.0	7.3	33.7	228.0	4017.0	17.5	61.2	12.0
15	Altar 84/T. tauschii 211	15A211	99.5	108.0	141.0	33.0	3457.0	8.5	40.8	270.0	5805.0	21.5	59.6	12.0
16	Chen/T. tauschii 205	16C205	89.7	97.0	139.7	42.7	1739.0	10.9	16.0	251.0	3097.0	12.3	56.2	13.2
17	Chen/T. tauschii 205c	17C205	83.7	105.0	141.0	36.0	1286.0	6.9	18.6	240.0	2592.0	10.8	49.8	11.2
18	Chen/T. tauschii 205	18C205	84.2	101.0	141.5	40.5	1126.0	7.3	15.4	230.0	2026.0	8.8	55.6	12.2
19	Chen/T. tauschii 205	19C205	80.0	99.7	140.7	41.0	1294.0	7.8	16.7	222.0	2462.0	11.1	52.6	11.5
20	Chen/T. tauschii 205	20C205	81.2	102.0	138.7	36.7	1670.0	13.1	12.8	340.0	3051.0	8.9	54.7	13.0
21	Chen/T. tauschii 205	21C205	87.2	97.7	138.0	40.2	1869.0	13.9	13.4	420.0	3519.0	8.3	53.1	13.0
22	Chen/T. tauschii 205	22C205	87.5	101.7	138.2	36.5	889.0	8.9	9.9	263.0	1725.0	6.5	51.6	13.0
23	Chen/T. tauschii 205	23C205	89.7	101.7	139.5	37.7	1406.0	9.6	14.8	273.0	2853.0	10.4	49.3	13.2
24	Chen/T. tauschii 205	24C205	87.7	101.7	140.2	38.5	1660.0	11.2	14.9	295.0	3460.0	11.7	48.0	13.2
25	Chen/T. tauschii 205	25C205	90.5	98.7	140.2	41.5	1910.0	13.2	14.4	388.0	3746.0	9.6	51.0	13.0
26	Chen/T. tauschii 215	26C215	84.2	98.7	140.0	41.2	981.0	8.6	11.5	240.0	1800.0	7.5	54.5	12.0
27	Chen/T. tauschii 215	27C215	86.2	98.7	140.5	41.7	1688.0	13.8	12.3	366.0	3107.0	8.5	54.3	11.7

28	Chen/ <i>T. tauschii</i> 224	28C224	101.2	97.0	127.7	30.7	6206.0	13.4	46.2	469.0	10 307.0	22.0	60.2	13.2
29	Chen/ <i>T. tauschii</i> 224	29C224	90.5	98.0	127.7	29.7	2902.0	6.8	42.9	266.0	4727.0	17.8	61.4	13.2
30	Chen/ <i>T. tauschii</i> 224	30C224	93.7	101.5	138.2	36.7	4257.0	10.8	39.7	309.0	7075.0	22.9	60.2	12.7
31	Chen/ <i>T. tauschii</i> 224	31C224	88.0	103.5	139.2	35.7	4619.0	13.2	35.0	316.0	7145.0	22.6	64.7	12.7
32	Chen/ <i>T. tauschii</i> 224	32C224	91.7	103.5	138.5	35.0	3820.0	13.3	29.0	269.0	6530.0	24.3	58.5	13.2
33	Chen/ <i>T. tauschii</i> 224	33C224	94.7	97.2	124.5	27.2	1762.0	7.6	23.6	221.0	3080.0	13.9	57.2	13.2
34	Chen/ <i>T. tauschii</i> 224	34C224	90.7	97.7	124.5	30.7	3850.0	8.4	46.6	324.0	6276.0	19.4	61.4	12.0
35	Chen/ <i>T. tauschii</i> 224	35C224	91.7	96.7	127.5	30.7	5394.0	13.7	39.4	437.0	8583.0	19.7	62.9	12.0
36	Chen/ <i>T. tauschii</i> 224	36C224	91.2	99.5	133.5	34.0	5516.0	15.2	36.5	451.0	9174.0	20.3	60.1	13.7
37	Chen/ <i>T. tauschii</i> 224	37C224	94.7	98.0	126.7	28.7	2592.0	7.0	37.6	220.0	4193.0	19.0	61.9	12.0
38	Chen/ <i>T. tauschii</i> 224	38C224	98.7	107.5	138.7	31.2	1700.0	6.4	26.5	223.0	3517.0	15.7	48.3	12.0
39	Duergand/ <i>T. tauschii</i> 214	39D214	107.2	100.2	134.0	33.7	8028.0	19.7	40.7	574.0	13 119.0	22.9	61.2	11.2
40	Duergand/ <i>T. tauschii</i> 214	40D214	107.0	100.2	133.5	33.2	5814.0	13.8	42.2	466.0	9873.0	21.2	58.9	11.2
41	Duergand/ <i>T. tauschii</i> 214	41D214	100.5	100.0	136.0	36.0	5538.0	19.2	28.8	512.0	9980.0	19.4	55.5	12.0
42	Duergand/ <i>T. tauschii</i> 214	42D214	104.2	103.5	135.2	31.7	6207.0	18.2	34.1	432.0	10 760.0	24.9	57.8	11.2
43	Duergand/ <i>T. tauschii</i> 214	43D214	110.5	97.0	127.5	30.5	5033.0	17.8	28.8	379.0	8989.0	23.6	56.0	12.2
44	Duergand/ <i>T. tauschii</i> 221	44D221	104.7	97.7	123.2	25.5	3621.0	12.7	28.7	330.0	6410.0	19.4	56.5	11.5
45	Duergand/ <i>T. tauschii</i> 221	45D221	104.5	98.0	123.0	25.0	5516.0	16.9	33.0	399.0	10 718.0	26.9	51.4	12.2
46	Duergand/ <i>T. tauschii</i> 221	46D221	101.7	97.5	122.7	25.2	4433.0	14.7	30.2	324.0	7936.0	24.4	55.9	11.2
47	Laru/ <i>T. tauschii</i> 309	47L309	102.5	104.7	138.5	33.7	2315.0	7.9	30.0	272.0	4285.0	15.8	54.0	12.0
48	Laru/ <i>T. tauschii</i> 309	48L309	98.7	103.5	138.2	34.7	3879.0	14.1	27.8	417.0	7156.0	17.1	54.2	11.5
49	Laru/ <i>T. tauschii</i> 309	49L309	94.7	106.2	141.7	35.5	1364.0	8.8	15.5	213.0	2610.0	12.2	52.0	12.0
50	Laru/ <i>T. tauschii</i> 309	50L309	97.5	104.5	140.7	36.2	2413.0	10.9	18.9	341.0	4311.0	12.6	56.0	11.2
51	Seri 82 (Bread wheat check)	Seri 82	99.3	88.1	129.3	41.0	7214.0	16.5	42.4	356.0	17 120.0	49.5	41.3	10.4
	Standard error of the difference		0.9	0.8	1.4	1.3	298.0	1.3	3.2	19.0	538.0	0.9	0.6	0.3
	Coefficient of variation (%)		1.0	1.0	1.0	3.9	8.0	10.9	9.0	5.9	9.0	4.9	1.1	2.5

Table 2. Genotypic coefficients for 12 traits measured on 50 synthetic hexaploids derived from *Triticum turgidum* × *T. tauschii* crosses during the 1989–90 and 1991–92 wheat cycles at CAEYV, Mexico

	Plant height	Days to flowering	Days to physio-logical	Grain filling period	Grain yield	Above-ground biomass	Harvest index	Spikes m ⁻²	Grains m ⁻²	Grains per spike	1000-grain weight
Days to flowering	0.206*										
Days to phys. maturity	-0.320***	0.665***									
Grainfilling period	-0.613***	-0.007	0.736***								
Grain yield	0.627***	0.036	-0.339***	-0.485***							
Above-ground biomass	0.381***	-0.158	-0.174*	-0.086	0.764***						
Harvest index	0.606***	0.163*	-0.391***	-0.673***	0.780***	0.222**					
Spikes m ⁻²	0.336***	-0.217**	-0.215**	-0.094	0.771***	0.873***	0.344***				
Grains m ⁻²	0.656***	0.028	-0.353***	-0.497***	0.993***	0.789***	0.750***	0.782***			
Grains per spike	0.688***	0.269**	-0.317***	-0.665***	0.766***	0.379***	0.832***	0.223**	0.765***		
1000-grain weight	0.261**	0.041	-0.242**	-0.362***	0.581***	0.189*	0.731***	0.219**	0.496***	0.579***	
Spike length	-0.385***	-0.212**	0.025	0.224**	-0.192*	-0.175*	-0.089	-0.110	-0.203*	-0.179*	-0.053

*, **, *** Statistically significant at P = 0.05, 0.01 and 0.001, respectively

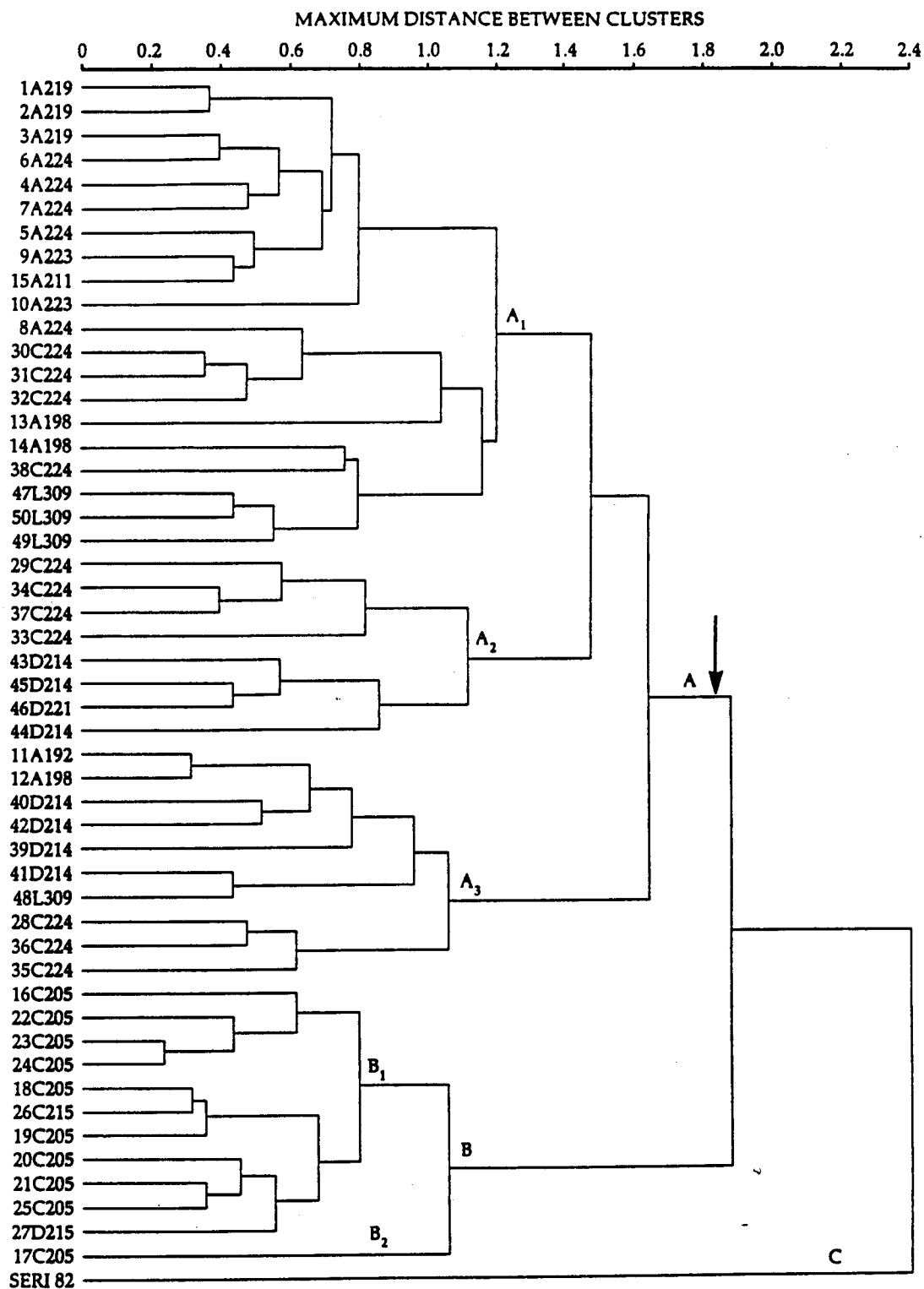


Fig. 1. Dendrogram depicting average distance between clusters of synthetic hexaploid wheats and the bread wheat cultivar Seri 82 as determined from complete linkage cluster analysis of quantitative data. Genotype abbreviations are defined in Table 1

0.01 level of probability. The SH line with the heaviest 1000-grain weight was entry 31 (64.7 g) followed by entries 35 and 37 with 62.9 and 61.9 g respectively. All these lines were derived from Chen/*T. tauschii* (224) cross. The lowest mean 1000-grain weight was in entry 24 (48.0 g), a Chen/*T. tauschii* (205) derivative. Desirable coefficients of variations were calculated for all the yield component characters.

Spikes m^{-2} and 1000-grain weight were two important yield components of the SH wheats which can be used to improve the yield potential of bread wheats. Grain yield components are thought to be more under simple genetic control than grain yield itself and hence should be easier to select for these separately (SAMPSON 1971). Also component measurements are economically obtained than plot yields.

Plant height and spike length

The mean plant height of the SH lines was 95.9 cm as compared to 99.3 cm of Seri 82. Forty-eight percent of the test entries were shorter than Seri 82 by at least 3.5 cm ($P < 0.05$). Moreover, 38 % were taller than Seri 82 ranging from 2.2 cm to 12.2 cm. Plant height of the SH ranges from 80.0 (entry 19) to 110.5 cm (entry 43). All SH wheats tested had longer spikes than Seri 82 ($P < 0.05$). The longest spike recorded was 13.7 cm for entry 36, a Chen/*T. tauschii* (224) derivative, that was 31.7 % longer than Seri 82 (10.4 cm). The mean overall spike length of the test entries was 12.2 cm. The coefficients of variation were 1.0 % for plant height and 2.5 % for spike length.

Days to flowering, physiological maturity and grainfill duration

There was high variability in flowering date, grainfill duration and days to physiological maturity among the SH lines ($P < 0.01$). All test entries flowered later than the Seri 82. Entry 13, an Altar/*T. tauschii* (198) derivative flowered the latest (108 days) after emergence. On the other hand, entry 35 (Chen/*T. tauschii* 224 derived line) flowered the earliest (96.7 days). Sixty-four percent of the materials flowered after 100 days as compared to 88.1 days of Seri 82. The mean grainfilling period of the test entries was 34 days with entry 45 being the shortest (25 days) and entry 16 the longest (42.7 days). Eight SH lines (entries 16, 18, 19, 21,

24, 25, 26 and 27) had a comparable grainfilling period to Seri 82 ($P < 0.05$). Days to physiological maturity averaged over two years ranged from 122.7 days (entry 46) to 141.7 days (entry 49) with an overall mean of 135.9 days for all the SH. Five lines had comparable maturity to Seri 82 (considered of intermediate maturity in Sonora, Mexico). Five lines were earlier in maturity than Seri 82, while 40 SH lines were late.

Genotypic correlations

The genotypic correlations agreed closely with the phenotypic correlation ($r = 0.997$, $P < 0.001$). These were usually large, hence only those similarities due to genetic effects are discussed. A summary of the character correlations among the 50 SH is presented in Table 2. Fifty significant associations (29 positive and 21 negative) among the agronomic traits were identified. The highest predictor of mean grain yield was grains m^{-2} (0.993, $P < 0.001$). Strong association between grain yield and grain number has been demonstrated for bread wheat before in the Yaqui Valley (WADDINGTON et al. 1986). High positive correlations ($P < 0.001$) were obtained between grain yield and above-ground biomass yield at maturity (0.764), harvest index (0.780), spikes m^{-2} (0.771), grains per spike (0.766), 1000-grain weight (0.581) and plant height (0.627). Negative relationships however, were found between grain yield and days to physiological maturity (-0.339 , $P < 0.001$), grainfilling period (-0.485 , $P < 0.001$) and spike length (-0.192 , $P < 0.05$). The relationships between above-ground biomass yield at maturity and harvest index, five yield components and plant height showed a similar trend. Moreover, a negative association was found with days to physiological maturity (-0.174 , $P < 0.05$).

The correlations of harvest index with other character traits suggest that grains per spike was the most important determinant of harvest index, followed by grains m^{-2} , 1000-grain weight, grainfilling period (negative), plant height, days to physiological maturity (negative), spikes m^{-2} and least important, days to flowering (Table 2).

Among the yield components measured, significant coefficients were found for spikes m^{-2} , grains m^{-2} and grains per spike with 1000-grain weight (positive), plant height (positive)

and days to physiological maturity (negative). Strong associations were also found for spikes m^{-2} and grains m^{-2} (0.782, $P < 0.001$), grains per spike (0.223, $P < 0.01$), and days to flowering (-0.217 , $P < 0.01$). Number of grains m^{-2} showed positive relationships with grains per spike (0.765, $P < 0.001$) and plant height (0.656, $P < 0.001$) but expressed negative associations with spike length (-0.203 , $P < 0.05$) and grainfilling period (-0.497 , $P < 0.001$). The relationships between grains per spike, spike length (-0.179 , $P < 0.05$) and grainfilling period (-0.665 , $P < 0.001$) was also negative. Associations between 1000-grain weight and plant height were positive but negative for days to physiological maturity and grainfilling period. Spike length and grainfilling period was positively correlated (0.224, $P < 0.01$), but negatively correlated with plant height (-0.385 , $P < 0.001$) and days to flowering (-0.212 , $P < 0.01$).

Negative relationships between plant height, days to physiological maturity (-0.320) and grainfilling period (-0.613) were found to be significant at 0.001 level of probability. Plant height, however, had a positive correlation with days to flowering (0.206, $P < 0.05$). Finally, significant positive coefficients ($P < 0.001$) were found for days to flowering, physiological maturity (0.665) and between days to physiological maturity and grainfilling period (0.736).

Clustering of SH genotypes

Complete linkage cluster analysis demonstrated significant agronomic variation among the SH genotypes classified. The test materials fell into three major groups; A, B, and C (Fig. 1). The largest group was cluster A which included 78 % of the germplasm evaluated. All the SH with cultivars Altar 84, Duergand and Laru as their *T. turgidum* parents were classified within this group. The cluster A genotypes recorded the highest average 1000-grain weight (58.1 g) and the longest spike length (12.1 cm) as compared with the other genotype groups. Three distinct subgroups (A1 to A3) existed within the A cluster. Sixty-five percent of the A1 subgroup genotypes were from Altar 84-derived crosses. On the average A1 SH lines flowered 6 days later and were physiologically the latest to mature (137.5 days) as compared to other SH groups. The 8 SH lines in the A2 subgroup originated from crosses involving Chen and

Duergand and *T. tauschii* accessions 214, 221 and 224. The materials within this subgroup possessed early flowering and maturity. The A3 genotypes came from divergent crosses of the four durum cultivars in combination with accessions 192, 198, 214, 224 and 309 of *T. tauschii*. The SH genotypes in this subgroup have the highest mean yield (6005 $kg\ ha^{-1}$), aboveground biomass yield at maturity (16.1 $t\ ha^{-1}$), and grain no. m^{-2} (10 120).

Cluster B is composed of 12 SH lines and is further divided into two distinct subgroups (B1 and B2). All genotypes within this group were related to durum cultivar Chen and shared a long grainfilling duration (37.9 days), late physiological maturity (140.3 days) and short stature (84.9 cm). The *T. aestivum* cultivar Seri 82 emerged as a separate group (C) from the SH entries. It possessed short spikes (10.4 cm) and lighter 1000-grain weight (41.3 g) as compared to the SH. These are some of the traits that can be improved upon hybridization with SH wheats.

The clusters formed by qualitative characters (VILLAREAL et al. 1994b) are similar to the study in pattern, particularly in placing most similar durum parentage genotypes together. We also demonstrate that substantial agronomic variation exists in the SH genotypes studied. An improved understanding of this variation may be especially valuable in efforts to utilize this germplasm resource for genetic, breeding and agronomic studies. Finally, the limited but outstanding SH genotypes identified in the present study provides breeders with parental variation selection for bread wheat improvement.

Zusammenfassung

Agronomische Variabilität in ausgelesenen *Triticum turgidum* × *T. tauschii*-synthetischen hexaploiden Weizen

Es wurden zwei Versuche am Mexican National Institute of Agricultural Research Experiment Station, Yaqui Valley, Sonora, Mexiko, durchgeführt, um die Natur und den Grad agronomischer Variation von 50 synthetischen hexaploiden (SH) Weizen ($2n = 6x = 42$, AABBDD), die von *Triticum turgidum* ($2n = 4x = 28$, AABB) × *T. tauschii* ($2n = 4x = 14$, DD)-Kreuzungen entwickelt worden waren, für die Verwendung in einem Weizenverbesserungsprogramm zu verwenden. Pflan-

zenhöhe, Ährenlänge, Tage bis zur Blüte, physiologische Reife, Kornertrag, Über-Grund-Biomasse zur Reife, Ernteindex, Ertragskomponenten und Testgewicht wurden bestimmt. Es wurde eine signifikante agronomische Variation zwischen den verschiedenen Linien festgestellt. Überlegene SH-Genotypen wurden hinsichtlich eines höheren Kornertrages, Über-Grund-Biomasse zur Reife, Tausendkorngewicht und Ähren/m² im Vergleich zu Brotweizen (*Triticum aestivum* L.)-Vergleichskultivar Seri 82 beobachtet. Die genotypischen Korrelationen des Kornertrages mit anderen Eigenschaften zeigten, daß Korn/m² die am stärksten bestimmende Determinante des Kornertrages ($r = 0,993$) war. Daten agronomischer Eigenschaften, die einer kompletten linkage-cluster-Analyse unterworfen wurden, führten zur Klassifizierung von Genotypen in zwei distinkte phänotypische Gruppen unter Ausschluß von Seri 82. Die Gruppen korrespondierten grundsätzlich zum Durum-Elter der SH mit signifikanten Gruppendifferenzen für alle Eigenschaften. Dies zeigt die Verwendung einer praktischen numerischen Analyse, um agronomische Variation in repräsentativen SH-Genotypen zu beschreiben. Cluster-Analyse mit quantitativen Eigenschaften kann geeignet für die Identifikation von Genotypen mit unterschiedlichen Herkünften für die Züchtung und agronomische Verwendung sein.

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