Environmental stability and heritability estimates for grain yield and test weight in triticale

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Abstract. Hexaploid triticale has many advantages over both parental species for both grain and forage production in certain environments. Additional information on environmental stability and heritability would be desirable to develop appropriate selection strategies in the production of superior widely-adapted cultivars. The grain yield of 22 diverse genotypes grown at four ecologically-distinct geographical locations [Quincy, FL, USA (approximate geographical coordinates (AGC) = 30°N 84°W, approximate elevation (AE) = 58 m), Plains, GA, USA (AGC = 32°N 84°W, AE = 76 m), Bozeman, MT USA (AGC = 45°N 111°W, AE = 1458 m), and Aberdeen, ID, USA (AGC = 42°N 112°W, AE = 1360 m)] was measured in two years with winter and spring planting dates only at Bozeman and Aberdeen. Test weight (grain weight in a given volume) was determined for two years at Bozeman and Aberdeen at both planting dates and one year at Quincy. Stability analyses indicated that significant (P < 0.01) variation in means, regression coefficients, and deviation mean squares of the genotypes were present for both characters. Realized heritability (h^2) estimates were as follows: grain yield ranged from –0.02 to 0.80 with a mean of 0.57; test weight ranged from 0.63 to 1.05 with a mean of 0.93. The results indicated that substantial genetic variation is present and selection for widely-adapted cultivars would be effective for both characters especially test weight.

Key words: Hexaploid triticale, ×*Triticosecale* Wittmack, genotypic variation, genotype × environment interaction, genetic selection, selection response.

Introduction

Hexaploid triticale (×*Tritiosecale* Wittmack) is a synthetic species. Studies have indicated that the grain production of newer and improved triticale cultivars both as a monocrop and in small grain mixtures was acceptable in a wide range of environments (Pfeiffer 1996; Juskiw et al. 2000 a,b). The forage production and silage yield and quality of hexaploid triticales both as a monocrop and in small grain mixtures were reported to be favorable in comparison with other small grains (Sun et al. 1996; Juskiw et al. 2000 a,b; Rao et al. 2000). These studies indicate that triticale has great potential to fit into current small grain areas and to contribute to the improvement of the grain and forage production in diverse geographical environments.

Increased acceptance and production of triticale depend on obtaining information on the extent of genetic diversity available and the response of triticale genotypes to a wide range of environmental conditions.

The purpose of this study was to determine the environmental stability of a number of diverse spring triticale genotypes to a broad range of environments including geographical locations, planting dates and years. The agronomically-important

characters, grain yield and test weight, were measured. Heritability estimates were also determined for each character to evaluate selection effectiveness.

Materials and methods

Twenty two diverse spring triticale genotypes (Table 1) were grown in randomized complete blocks with three replications at four geographical locations [Quincy, FL, USA (approximate geographical coordinates (AGC) = 30°N 84°W, approximate elevation (AE) = 58 m), Plains, GA, USA (AGC = 32°N 84°W, AE = 76 m), Bozeman, MT USA (AGC = 45°N 111°W, AE = 1458 m), and Aberdeen, ID, USA (AGC = 42°N 112°W, AE = 1360 m)] in the 1997–1998 and 1998–1999 seasons, with winter and spring planting dates at Bozeman and Aberdeen (Table 2). Grain yield was measured in all 12 environments (1QW8–12AW9, Table 2). Test weight (grain weight in a given volume after a standardized filling

Table 1. Information on the genotypes tested

Genotype	Name, line, and/or pedigree (origin)
G1	'Florida 201' (Florida USA)
G2	'Sunland' (Florida/Georgia USA)
G3	FLK89T168-W1 (Florida USA)
G4	FL90025-U2-G9-G10 (Florida USA)
G5	90T60-13-B3-G3 (Montana USA)
G6	86.46-D1-V1-W2 (Georgia USA)
G7	86T27-E13-G8 (Georgia USA)
G8	'Arcia' (North Carolina USA)
G9	Rhino 1R.1D (California USA)
G10	PFT213 (Brazil)
G11	PFT317 (Brazil)
G12	IAPAR23 (Brazil)
G13	233ITSN51-G6-G7, CIMMYT (Mexico)
G14	25ITSN166, CIMMYT (Mexico)
G15	26ITSN13, CIMMYT (Mexico)
G16	26ITSN153, CIMMYT (Mexico)
G17	26ITYN10, CIMMYT (Mexico)
G18	26ITYN26, CIMMYT (Mexico)
G19	26ITYN27, CIMMYT (Mexico)
G20	26ITYN45, CIMMYT (Mexico)
G21	26ITYN46, CIMMYT (Mexico)
G22	26ITYN49, CIMMYT (Mexico)

Table 2. Designation and planting date information for the 12 environments tested

Environment designation[1]	Planting date
1QW8	10 Dec. 1997
2QW9	30 Nov. 1998
3PW8	12 Nov. 1977
4PW9	11 Nov. 1998
5BS8	28 Apr. 1998
6BS9	16 Apr. 1999
7BW8	15 Oct. 1997
8BW9	6 Oct. 1998
9AS8	7 May 1998
10AS9	16 Apr. 1999
11AW8	26 Sept. 1997
12AW9	30 Sept. 1998

[1]Designation code: first number = environment number (1 –12); first letter indicates geographical location (Q = Quincy, FL USA; P = Plains, GA USA; B = Bozeman, MT USA; A = Aberdeen, ID USA), respectively; second letter = planting date (W = winter, S = spring); and last number = season (8 = 1997-98, 9 = 1998–1999).

and leveling procedure) was recorded in nine environments, including Bozeman (5BS8–8BW9), Aberdeen (9AS8–12AW9) and one Quincy (1QW8) environment (Table 2). Individual Quincy plots were 6 rows, 3.34 m in length with 23 cm between rows, with the harvested area = 5.16 m^2. Individual Plains plots were 7 rows, 3.05 m in length with 18 cm between rows with the harvested area = 3.84 m^2. Individual Bozeman plots were 4 rows, 2.43 m in length with 36 cm between rows with the harvested area = 2.62 m^2. Individual Aberdeen plots were 4 rows, 2.43 m in length with 36 cm between rows with the harvested area = 2.62 m^2.

Environmental stability estimates were determined using the linear regression model procedure based on an environmental index (Finlay and Wilkinson 1963; Eberhart and Russell 1966). In this procedure, the response of a genotype to a number of environments is compared to the other genotypes in the study using three values: 1. Genotype mean over all environments; 2. Regression coefficient *(b* value) representing the response of the genotype to each environment with a *b* value of 1.00 indicating an average response to changing environmental conditions; and 3. Deviation mean square (DMS) which is the deviation from the linear regression line over all environments.

Heritability estimates (h^2) were determined using the truncated selection method in which the re-

sulting h^2 value is realized heritability and is determined from the generalized equation $h^2 = R/S$ where R = response to selection and S = selection differential (Pfahler 1971; Doolittle 1987). The following formula was applied:

$$h^2 = R / S \text{ or } [(\bar{x}_{S1} - \bar{x}_{P1})\, \sigma_o] / [(\bar{x}_{SO} - \bar{x}_{PO})\, \sigma_1],$$

where $\bar{x}_{S1}$ = mean of selected genotypes in one environment or 1; $\bar{x}_{P1}$ = mean of 22 genotypes in that environment; σ_o = standard deviation of the 22 genotype mean over all environments; $\bar{x}_{SO}$ = mean of selected genotypes over all environments; $\bar{x}_{PO}$ = mean of 22 genotypes over all environments; and σ_1 = standard deviation of the 22 genotypes in the one environment in which selection was conducted. The heritability estimates were determined by relating selection in each environment to the response over all environments. The comparison of each environment to the means over all environments indicates the potential to select high-yielding genotypes in an individual environment which would be adapted over diverse environments. To test the effect of locations, the genotype means over all environments were tested with the genotype means at each location. Three selection levels [higher 3 (14%), higher 6 (27%), higher 9 (41%) out of the 22 genotypes] were tested.

Minimum differences for significance in the tables were obtained by means of the revised Duncans ranges using for P only the maximum number of means to be compared (Harter 1960).

Results

Grain yield

The variance analyses for grain yield are shown in Table 3 with highly significant F values found for both main effects [genotype (G), environment (E)] and their interactions [(G × E, G × E (linear)]. The genetic diversity among genotypes in their response to the environments is shown in the yield means (Table 4) among genotypes which ranged from 4709 kg ha^{-1} for G9 selected in California to 6133 kg ha^{-1} for G7 selected in Georgia. The environmental diversity is shown in the yield means (Table 5) among environments which ranged from 2341 kg ha^{-1} for 2QW9 to 8033 kg ha^{-1} for 12AW9. In general, the more northern locations (Aberdeen, Bozeman) had considerably higher yields than the southern locations (Quincy,

Table 3. Analysis of variance for grain yield and test weight with linear regression partitions of the G × E interaction

Source of variation	Grain yield		Test weight	
	df	MS[1]	df	MS
Genotype (G)	21	498**	21	9 659**
Environment (E)	11	24 550**	8	29 553**
G × E	231	111**	168	419**
G × E (linear regression)	21	219**	21	536**
Deviations from regression	210	101**	147	402**
Error	528	54	396	65

**F value significant at the 0.01 probability level
[1]Mean square = × 10^{-4}

Plains). F values indicated highly significant differences among genotypes in 10 out of the 12 environments.

A wide range of b values was found among the genotypes with highly significant differences between genotypes (Table 4). The positive correlation coefficient ($r = 0.778$**, df = 20) between mean yield and b value indicated that on the average, the highest yielding genotypes produced more at the most favorable environments and less at the less favorable environments. Most (15 out of 22 genotypes) of the DMS values were not significant indicating that the genotype responses to environmental conditions fitted linearity (Table 4).

A relatively broad range of heritability estimates was found among the comparisons but the differences within each comparison were relatively consistent regardless of the proportion of the genotypes tested (Table 6). When the individual environments were related to the overall environment mean (OM), the mean heritability estimates ranged from –0.02 at OM vs. 3PW8 to 0.73 at OM vs. 8BW9. However, when the values determined by regressing the overall means over all environments to the means of each of the four locations were examined, the values at the western locations (Bozeman, Aberdeen) were slightly higher and more consistent than those at Quincy and Plains.

Test weight

The variance analyses for test weight are shown in Table 3 with highly significant F values found for all main effects (genotype, environment) and their interactions. The genetic diversity among genotypes in their response to the environments are

Table 4. Means, regression coefficients (*b*) and deviation mean squares (DMS) for grain yield and test weight for each genotype

Genotype	Grain yield			Test weight		
	Mean	*b*	DMS	Mean	*b*	DMS
	kg ha^{-1}			kg hL^{-1}		
1	5681[1]	1.27[2]	95	68.3[1]	0.84[2]	119.5**
2	5293	1.00	124	72.9	0.95	18.7
3	4761	0.86	82*	75.0	1.02	25.9**
4	5401	1.08	70	70.8	0.74	14.3
5	5773	0.95	135	70.0	0.99	85.6**
6	4992	0.93	41	70.8	1.64	72.6**
7	6133	1.22	72	72.5	1.47	41.3**
8	5793	1.25	225**	70.1	1.02	110.4**
9	4709	0.78	46	74.6	0.83	72.2**
10	5497	0.99	129**	74.4	1.06	21.6**
11	5426	0.91	64	74.5	0.98	8.3
12	5598	0.97	118**	72.8	1.17	37.1**
13	5569	1.09	98	74.4	0.94	12.8*
14	5558	1.04	81**	73.5	1.04	5.9**
15	4820	0.82	93	73.6	0.63	22.1*
16	5626	0.99	96	69.9	1.02	43.8**
17	5813	1.15	129	71.9	1.11	61.4**
18	5233	0.92	41	74.6	0.83	11.0*
19	5113	0.88	77	73.0	1.01	31.2**
20	5694	1.00	96**	73.5	0.91	20.3*
21	5353	0.92	195*	73.3	0.94	49.4*
22	5795	0.99	30	74.1	0.77	13.1**

*,**F value for DMS values significant at the 0.05 and 0.01 probability level, respectively.
[1]Minimum differences among means at the 0.05 and 0.01 probability levels, respectively were; grain yield = 422 and 547; and test weight = 1.2 and 1.5
[2]Minimum differences among *b* values at the 0.05 and 0.01 probability levels, respectively were; grain yield = 0.25 and 0.33; and test weight = 0.41 and 0.53

shown in the test weight means (Table 4) among genotypes which ranged from 68.3 kg hL^{-1} for G1 selected in Florida to 75.0 kg hL^{-1} for G3 also selected in Florida. The environmental diversity was shown in the test weight means (Table 5) among the 9 environments ranged from 69.1 kg hL^{-1} for 9AS8 to 75.7 kg hL^{-1} for 12AW9. In general, there was no consistent pattern among locations in test weight variation.

A wide range of *b* values was found among the genotypes with highly significant differences between genotypes (Table 4). The correlation coefficient ($r = -0.186$ NS, df = 20) between mean test weight and *b* values indicated that no relationship between the test weight and the environment was present. Most (19 out of 22 genotypes) of the DMS values were significant indicating that the genotype response to the environments did not fit a linear regression model (Table 4).

The heritability estimates were relatively high and grouped within a narrow range with the differences within each comparison relatively consistent (Table 6). When the individual environments were related to the overall environment mean

(OM), the mean heritability estimates ranged from 0.63 at OM vs. 10AS9 to 1.05 at OM vs. 1QW8. When the estimates determined by regressing the overall means over all environments to the means of each of the 3 locations were examined, very small differences among locations were present.

Discussion

The accuracy and practical value of stability analyses depend on the extent of genetic diversity present among genotypes and the range of environments under which they are tested (Becker and Leon 1988). In this study, highly significant F values were found for both main effects [genotype (G), environment (E)] and their interactions [G × E, G × E (linear)] for grain yield and test weight indicating substantial genetic diversity among the genotypes and variation among environments suggesting genetic control of environmental stability. To reinforce this conclusion, highly significant differences among the genotypes in the measures

Table 5. Mean, range and significance among populations at each environment for grain yield and test weight

Character	Environment	Mean	Range (high-low)	F value
Grain yield (kg ha^{-1})	1QW1	2507	3023–1524	9.16**
	2QW2	2341	3011–1334	3.33**
	3PW1	3390	4119–2326	0.71
	4PW2	4945	6219–3850	5.77**
	5BS1	5953	7223–4717	15.66**
	6BS2	6474	7800–4841	12.48**
	7BW1	5150	6225–4133	4.51**
	8BW2	7685	9026–6149	10.55**
	9AS1	4836	5805–3480	3.72**
	10AS2	6645	8545–5299	11.15**
	11AW1	7245	9139–5974	1.31
	12AW2	8033	10021–6549	2.39**
Test weight (kg hL^{-1})	1QW1	73.3	76.9–64.3	79.20**
	5BS1	73.3	77.3–69.0	59.23**
	6BS2	73.4	76.0–69.4	54.99**
	7BW1	70.1	72.9–65.5	33.14**
	8BW2	73.0	75.6–69.1	51.76**
	9AS1	69.1	73.3–64.1	13.42**
	10AS2	71.2	73.8–65.8	78.75**
	11AW1	74.7	77.2–70.1	61.76**
	12AW2	75.7	77.7–71.8	4.92**

**F value among populations at each environment significant at the 0.01 probability level with df = 21, 42

of environmental stability (means, *b* values, DMS) were found.

Very few studies examining environmental stability are available in triticale especially for grain yield and test weight (Royo et al. 1995; Oettler 1996; Qualset et al. 1996; Furman et al. 1997). In general, the reports indicated considerable variation in a wide range of genotypes for various morphological characteristics and disease. In the study reported here, considerable genetic diversity within triticale for grain yield and test weight at diverse geographic areas was found indicating that selection for specific environments would be possible.

The heritability estimates indicated that selection would be relatively effective for both characters in most environments and locations with relative consistency among the three selection levels tested. The values for grain yield were intermediate with considerable variation depending on the environment and location. The values for test weight were unexpectedly high and were not greatly influenced by environment and/or location. For yield, the heritability estimates obtained

by comparing the overall means to each of the 12 location-year-planting date combinations had an extremely broad range (–0.02 to 0.77) not closely associated with any location, year or planting date. However, the heritability estimates for grain yield obtained by comparing the overall means to each 4 locations indicated that in general, selection in the western locations (Bozeman, Aberdeen) would be substantially more effective than either of the southern locations (Quincy, Plains) in selecting for the overall mean over all environments. The heritability estimates for test weight were relatively high when the overall means were compared to each of the 9 location-year-planting date combinations or each of the three locations. One major disadvantage of triticale is meiotic instability resulting in shriveled kernels which, in-turn, leads to unacceptable low test weight (Gupta and Priyadarshan 1982; Schlegel 1996). The finding in this study that test weight has relatively high heritability indicates that this disadvantage can be reduced by appropriate selection procedures. Similar heritability values for both yield and test weight in triticale have been reported (Royo et al.

Table 6. Heritability (h^2) estimates for grain yield and test weight determined by the truncated selection method with the highest 3, 6 and 9 out of the 22 populations tested

Character	Section	Comparison	Number selected/22			Mean
			3/22	6/22	9/22	
Grain yield[1]	A	OM vs. 1QW8	0.83	0.78	0.69	0.77
		OM vs. 2QW9	0.40	0.42	0.55	0.46
		OM vs. 3PW8	−0.09	−0.09	0.13	−0.02
		OM vs. 4PW9	0.53	0.48	0.36	0.46
		OM vs. 5BS8	0.32	0.53	0.89	0.58
		OM vs. 6BS9	0.79	0.61	0.74	0.71
		OM vs. 7BW8	0.30	0.39	0.69	0.46
		OM vs. 8BW9	0.75	0.63	0.81	0.73
		OM vs. 9AS8	0.52	0.63	0.54	0.56
		OM vs. 10AS9	0.54	0.67	0.73	0.65
		OM vs. 11AW8	0.34	0.62	0.66	0.54
		OM vs. 12AW9	0.64	0.51	0.59	0.58
	B	OM vs. Q	0.47	0.42	0.62	0.50
		OM vs. P	0.88	0.36	0.42	0.55
		OM vs. B	0.83	0.74	0.83	0.80
		OM vs. A	0.73	0.77	0.75	0.75
Test weight[2]	A	OM vs. 1QW8	1.04	1.02	1.10	1.05
		OM vs. 5BS8	0.75	0.85	0.91	0.84
		OM vs. 6BS9	0.95	0.96	1.01	0.97
		OM vs. 7BW8	0.99	1.06	1.01	1.02
		OM vs. 8BW9	0.62	0.79	0.92	0.78
		OM vs. 9AS8	0.64	0.83	0.96	0.81
		OM vs. 10AS9	0.64	0.57	0.69	0.63
		OM vs. 11AW8	1.05	1.08	0.96	1.03
		OM vs. 12AW9	0.93	1.05	0.94	0.97
	B	OM vs. Q	1.04	1.02	1.10	1.05
		OM vs. B	0.93	0.97	0.96	0.95
		OM vs. A	1.03	1.08	1.03	1.05

[1]For grain yield, the estimates in section A were determined by selecting among the 22 population means in each of the 12 environments tested and determining the response over all 12 environments (OM) while the estimates in section B were determined by selecting among the 22 population means in each of the 4 locations (Q = Quincy, FL; P = Plains, GA; B = Bozeman, MT; A = Aberdeen, ID) tested and determining the response over all 12 environments (OM)

[2]For test weight, the estimates in section A were determined by selecting among the 22 population means in each of the 9 environments tested and determining the response over all 9 environments (OM) while the estimates in section B were determined by selecting among the 22 population means in each of the 3 locations (Q = Quincy, FL; B = Bozeman, MT; A = Aberdeen, ID) tested and determining the response over all 9 environments (OM)

1995; Oettler 1996; Qualset et al. 1996; Furman et al. 1997).

The results of this study indicated that considerable genetic diversity and environmental stability for yield and test weight are present in triticale and genetic improvement programs should be successful in developing cultivars with high yield and test weight adapted for a broad range of environments.

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