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Effect of genome combinations on stability of yield and yield components in wheats and triticales

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Summary. The data on number of grains/spike, 100 grain weight and grain yield/plant in eighteen genotypes of four genome combinations (*AABB*- 4 genotypes, *AABBDD*- 6 genotypes, *AABBRR*- 5 genotypes and *AABBDDRR*- 3 genotypes) were recorded for eight environments created by combining two dates of sowing, two fertilizer regimes and two spacings. Two stability parameters-regression coefficient (b) and deviation from regression ($S_d{}^2$) were computed. Joint regression analyses revealed that the genotypes differed significantly for these characters. A significant variation due to environments was also found. A comparative study of performance of genotypes belonging to four genome combinations revealed that the genes for stability are not uniformly distributed in these genome combinations. Stability may largely depend on gene combination rather than on genome combination.

Key words: Stability – Genome combinations – Wheat – Triticale

Introduction

Stable genotypes can be screened in any crop by growing a number of them in a variety of environments. Often, stability parameters for individual traits are estimated in different cultivars of the same crop. Since stability is genetically controlled, stability genes are expected to occur in all genomes involved in the constitution of different polyploids of Triticeae. Genetic systems in different genomes responsible for stability of a trait may, however, differ. Therefore, it may be interesting to study the manner in which different genome combinations may interact and influence stability levels for an individual trait in different cultivated species from the tribe Triticeae. It is also possible that in a polyploid some genomes confer higher stability than others. If the role of individual genomes and their interaction resulting in stability can be determined, the synthesis of cereals may be optimized for productivity and stability.

The present investigation was undertaken to study the role played by different genome combinations in phenotypic stability expressed by a polyploid.

Materials and methods

Eighteen genotypes belonging to four genome combinations (*AABB*-4, *AABBDD*-6, *AABBRR*-5 and *AABBDDRR*-3) were chosen for the experiment conducted at Meerut University farm. Eight micro-environments were created by using combinations of two spacings, two fertilizer regimes and two sowing dates (Table 1). The experiment was laid out in randomised block design consisting of three replications in each environment. Three rows of each genotype were raised in each environment and each replication. Five representative plants were chosen from the middle row of each genotype and grains/spike, 100 grain weight and grain yield/plant were recorded. The data so obtained was used for computation of the stability parameters as described by Eberhart and Russell (1966). For joint regression analyses, the Perkins and Jinks (1968) model was used. The G×E component was partitioned into linear (heterogeneity between regression) and non-linear (residual) mean squares which were then tested against error mean squares. In cases, where both linear and non-linear components were found to be significant, the mean squares due to linear component were tested against mean squares due to non-linear component.

Results

1 Joint regression analyses

The joint regression analyses (Table 2) revealed that the genotypes differed significantly for all characters. The mean squares for environment were found to be highly significant, indicating the presence of significant variation due to environments. The G×E mean squares were highly significant for all three characters. Therefore, the interactions of genotypes with environment were significant for all traits under study. The mean squares for linear and non-linear components of G×E interaction were significant for grains/spike and 100 grain weight. Therefore, the G×E interaction was shared by both predictable and unpredictable components in these two characters. However, in the case of yield/ plant, the non-linear component was not significant and therefore, in this case, the G×E interaction was predictable. For grains/spike and 100 grain weight, mean squares for linear component were significant when tested against the corresponding mean squares due to non- linear component. This indicated that, despite a significant non-linear component of G×E interaction, the linear component was predominant in these characters.

Table 1. List of environments created for stability analysis

	Sowing dates			
	November 10th 1982 Spacing		November 29th 1982 Spacing	
Fertilized				
[a]N = 120 kg/ha (60 + 60) K = 60 kg/ha P = 60 kg/ha	15×30 sq cm	15×15 sq cm	15×30 sq cm	15×15 sq cm
Unfertilized				
N = 0 K = 0 P = 0	15×30 sq cm	15×15 sq cm	15×30 sq cm	15×15 sq cm

[a] These values were obtained by using urea = 46% N, MOP = 40% K and double superphosphate = 32% P

2 Stability parameters

i) Number of grains/spike. Individual regression analysis revealed that the thirteen genotypes had significant regression mean squares, however the 'b' values did not deviate significantly from unity (Table 3). This means that for this character, 13 genotypes had an average sensitivity to environment. Five genotypes including 'Kalyan Sona', 'Coorong', 'Rosner', 'UC-130' and ('CS'×'King II')^2 showed significant remainder mean squares. In the case of ('CS'×'King II')^2 the regression mean square was not significant, meaning thereby that for this character, the performance of this genotype is influenced entirely in an unpredictable manner. In the other four cases, the regression mean squares were significant against the remainder. Therefore, any predictions made for performance of these genotypes in any environment will have some but limited reliability. 'DD-21', 'Jairaj', 'MPO-224', 'Sonalika', 'WG-377', 'HD-2009', 'VL-421', 'C-306' and 'TL-419' were found to be stable for this trait. Taking into account the mean values, 'TL-419', 'WG-377' and 'Jairaj', in that order, had high mean performances, average sensitivities and were stable. On the other hand, 'C-306' and 'Sonalika' were low performers.

ii) 100 grain weight. Only four genotypes, namely 'DD-21', 'Jairaj', 'Raj-1702' and 'UC-130', had significant regression mean squares. 'DD-21' had a regression coefficient which deviated significantly from unity. Therefore, barring 'DD-21', which had an above average sensitivity, the other three genotypes had average responsiveness to environment. In the other fourteen genotypes, regression mean squares were not significant. 'UC-130' was the only genotype having a high mean performance, a unit regression coefficient and non-significant remainder mean squares. Hence, for this trait, only one genotype, 'UC-130', was found stable.

Table 2. Joint regression analyses for three characters of eighteen wheat and triticale genotypes grown over eight environments

Source of variation	df	Mean squares		
		Grains/spike	100 grain weight	Grain yield/plant
Genotypes	17	$1,411.149^{**,\times\times}$	$2.702^{**,\times\times}$	$88.127^{**,\times\times}$
Environments	7	$773.256^{**,\times\times}$	$0.545^{**,\times\times}$	$894.844^{**,\times\times}$
G×E	119	$29.861^{\times\times}$	$0.138^{\times\times}$	$11.095^{\times\times}$
Linear	17	$58.582^{\times\times,++}$	$2.702^{\times\times,++}$	$35.883^{\times\times}$
Remainder	102	$25.081^{\times\times}$	$0.545^{\times\times}$	6.965
Pooled error	272	12.702	0.066	6.990

*,** Significant at 5% and 1% levels of probability, respectively, when tested against G×E mean squares

$^{\times,\times\times}$ Significant at 5% and 1% levels of probability, respectively when tested against error mean squares

$^{+,++}$ Significant at 5% and 1% levels of probability, respectively, when tested against significant remainder mean squares

Table 3. Estimates of stability parameters, regression coefficient (b), deviation from regression (S_d^2) and mean $\bar{X}$)

Genotypes	Characters								
	Grains/spike			100 grain weight			Grain yield/plant		
	$\bar{X}$	b	S_d^2	$\bar{X}$	b	S_d^2	$\bar{X}$	b	S_d^2
4x Wheats									
'DD-21'	49.017	0.949**	−1.142	4.862	$3.179^{\times,**}$	0.022	11.186	0.923**	−4.874
'Jairaj'	54.200	1.468**	−6.574	4.354	2.453**	0.243**	13.235	1.222**	5.059
'MPO-224'	50.292	1.466**	1.292	3.983	1.017	0.013	16.573	$1.463^{\times,**}$	−0.790
'Raj-1702'	45.808	0.407	0.854	4.829	1.930*	0.111*	11.950	0.952**	−5.713
6x Wheats									
'Sonalika'	43.383	1.032**	8.829	5.004	0.948	0.091*	15.247	1.305**	1.686
'WG-377'	58.531	1.165**	1.824	3.917	0.558	0.084*	17.966	$1.289^{++,**}$	10.467*
'HD-2009'	53.869	1.077**	12.693	3.917	0.683	0.043	16.107	1.040**	2.568
'VL-421'	52.392	0.768*	−0.303	3.892	0.803	0.043	13.659	0.981**	−3.488
'Kalyan Sona'	69.542	$1.395^{+,**}$	45.405**	3.958	−0.038	0.059	16.654	1.139	−2.022
'C-306'	41.892	1.391**	−0.236	3.904	−0.813	0.024	14.188	1.170**	−2.022
6x Triticales									
'Welsh'	57.117	0.471	−9.707	4.117	0.925	0.125*	12.849	0.842**	−0.472
'Coorong'	36.583	$0.967^{+,**}$	22.558*	3.979	1.111	0.029	14.096	1.028**	−3.534
'Rosner'	78.117	$1.680^{++,**}$	32.097**	3.875	0.964	−0.033	12.738	1.021*	−1.367
'UC-130'	57.817	$1.457^{+,**}$	57.550**	4.608	1.195*	0.052	14.421	0.028**	7.839
'TL-419'	62.425	1.107**	−2.845	4.687	1.516	0.042	16.794	$1.362^{\times,**}$	−5.689
8x Triticales									
'8A-94'	23.142	0.534	6.432	2.833	0.586	0.023	5.052	0.230	−4.061
'TCLUM-octo'	37.150	0.056	7.207	4.883	0.986	0.078*	10.020	0.455*	−3.155
('CS'×'King II')^2	23.550	0.680	21.803*	3.242	0.005	0.002	7.704	0.547*	−0.580

*,** Significant at 5% and 1% levels of P, respectively, when tested against error mean squares
$^{+,++}$ Significant at 5% and 1% levels of P, respectively when tested against remainder mean squares
$^{\times,\times\times}$ 'b' deviates significantly from unity at 5% and 1% levels of P, respectively

iii) Grain yield/plant. Except for '8A-94', all other genotypes had significant regression mean squares. Two genotypes, namely 'MPO-224' and 'TL-419', had regression coefficients significantly deviating from unity. Therefore, other than these two, all 15 genotypes had average sensitivities. 'WG-377' was the only genotype having significant remainder mean squares and here too, the regression mean squares was predominant. Hence, 'DD-21', 'Jairaj', 'Raj-1702', 'Sonalika', 'HD-2009', 'VL-421', 'Kalyan Sona', 'C-306', 'Welsh', 'Coorong', 'Rosner', 'UC-130', 'TCLUM-octo' and ('CS'×'King II')^2 were found to be stable for this character. However, ('CS'×'King II')^2 and 'TCLUM-octo' had very low means. Any predictions in case of 'WG-377' would have limited reliability. The performances of 'MPO-224' and 'TL-419' will be greatly affected by changes in environment. No amount of improved cultural practices are likely to improve the yield in the case of '8A-94', which is a low performer. The yield of 6× triticale 'TL-419' was close to that of 6× wheat 'Kalyan Sona'. It was second only to that of 6× wheat 'WG-377' and its performance may be further improved by adequate improvement in cultural practices.

Six genotypes, 'WG-377', 'TL-419', 'Kalyan Sona', 'MPO-224', 'HD-2009' and 'Sonalika', in that order, had high means and need to be recognized. While 'TL-419', 'WG-377', 'MPO-224', 'HD-2009' and 'Sonalika' were stable for numbers of grains/spike, none of these high performers were stable for 100 grain weight. 'Kalyan Sona' was not stable either for number of grains/spike or 100 grain weight. Therefore, level of stability for grain yield/plant was predominantly affected by unstability of 100 grain weight in the case of 'WG-377', 'TL-419' and 'MPO-224'.

Discussion

An attempt will now be made to piece together the information presented earlier and bring out the effect of different genome combinations on stability, if any.

1 Tetraploid wheat (AABB)

Except for 'Raj-1702', each of the other three tetraploid wheat strains ('DD-21', 'MPO-224' and 'Jairaj') had a significant regression which did not deviate significantly from unity. These three were found to be stable for grains/spike. For 100 grain weight, none of the tetraploid wheats could be classified as stable. Although all

Table 4. Comparative study of stability of different genome combinations for three characters

Character \ Genome combination	*AABB*	*AABBDD*	*AABBRR*	*AABBDDRR*
No. of grains/spike	Stable	Stable	Unstable	Unstable
100 grain weight	Unstable	Unstable	Unstable	Unstabel
grain yield/plant	Stable	Stable	Stable	Stable

the tetraploid wheats had significant regression mean squares for grain yield/plant, the regression coefficient deviated significantly from unity only in 'MPO-224'. None was found to have significant deviation from regression. Therefore, 'DD-21', 'Jairaj' and 'Raj-1702' were stable for this trait.

Considering the *AABB* genome combination to be stable for traits where fifty per cent or more of the genotypes of this group were stable, it was found that tetraploid wheats were stable for number of grains/spike and grain yield/plant, but were unstable for 100-grain weight (Table 4).

2 *Hexaploid wheat (AABBDD)*

Out of the six hexaploid wheats entered, five, namely 'WG-377', 'Sonalika', 'HD-2009', 'VL-421' and 'C-306' were stable for number of grains/spike. None was stable for 100 grain weight, while 'Sonalika', 'HD-2009', 'VL-421', 'Kalyan Sona' and 'C-306' were stable for grain yield/plant.

Taking hexaploid wheats to be stable in general for characters for which more than fifty per cent of the genotypes of this group were stable, it was found that hexaploid wheats were stable for number of grains/spike and grain yield/plant. They were unstable for 100 grain weight (Table 4).

3 *Hexaploid triticale (AABBRR)*

Only one hexaploid triticale, 'TL-419', was stable for number of grains/spike. Similarly, for 100 grain weight, only 'UC-130' was stable. However, for grain yield/plant, 'Welsh', 'Coorong', 'Rosner' and 'UC-130' were stable. Therefore, the *AABBRR* genome combination was stable for grain yield/plant and unstable for number of grains/spike and 100 grain weight (Table 4).

4 *Octoploid triticale (AABBDDRR)*

None of the three octoploid triticales entered was stable for number of grains/spike and 100 grain weight. However, two of them, 'TCLUM-octo' and ('CS'×'King II')^2, were stable for grain yield/plant. Therefore, this genome combination was stable for grain yield/plant but unstable for grains/spike and 100 grain weight (Table 4).

A perusal of Table 4 indicates that stability for different traits may not be uniformly distributed in four genome combinations. This will be partly due to interactions between genes situated in different genomes and partly due to distribution of genes in different genomes. In two out of three traits considered here, however, the stability levels are the same in all four combinations. While all four genome combinations were stable for grain yield/plant, they were unstable for 100 grain weight. This nonspecificity of genomes for stability may be due to similar selection criteria followed in all four groups thus leading to selection of similar genes for these traits. For number of grains/spike, genome combinations *AABB* and *AABBDD* were stable while *AABBRR* and *AABBDDRR* were unstable. If we extend this generalization to the whole range of these genome combinations, it appears that the introduction of genome *RR* leads to unstability of this trait. We may like to add that this generalization is based on a very limited sample and, therefore, needs to be viewed with caution.

We may thus conclude that although for some traits genome specificities for stability may be present, stability largely depends on gene combination rather than on genome combination, and that the presence or absence of this gene combination would depend on the selection history of the genotypes irrespective of the genome combination.

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