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A COMPARISON OF TRIPLE TEST CROSS AND MODEL FITTING ANALYSES IN TWO SPRING WHEAT CROSSES

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ABSTRACT

One hundred and twenty triple test cross families and a set of six basic generations arising from two breadwheat crosses (9 D x HD 2009, C 591 x WL 711) were grown in three blocks of randomized block design to detect additive, dominance and epistatic components of genetic variation for grain yield and tillers/plant, grains/spike, grain weight, harvest index, spikelets/spike, and spike length. The results obtained by triple test cross and model fitting analysis were in agreement with each other. Additive and additive x additive type of gene actions are more predominant in this material.

Key words: Triple test cross, model fitting analysis, breadwheat.

For the estimation of genetic parameters, a number of experimental designs are available. Among these, the triple test cross method described by Kearsey and Jinks [1] is the most efficient to detect and estimate different components of genetic variation. It provides not only precise estimates of epistasis but also gives unbiased estimates of additive (D) and dominance (H) components in the absence of epistasis. Model fitting analysis based on a set of six basic generations also provides precise estimates for the remaining parameters. In this study, the results obtained by model fitting analysis (first degree statistics) were compared with the triple test cross (second degree statistics).

MATERIALS AND METHODS

Two sets of experiments were laid out during 1982-83. In the first set, 20 plants were randomly selected from each of the Two F_2 populations (9D x HD 2009 and C 591 x WL 711) and were backcrossed to their respective P_1, P_2 and F_1 to obtain L_{1i}, L_{2i} and L_{3i} families, respectively. The experimental material consisted of 120 families (60 in each cross). In the second set of experiment, six basic generations, i.e. P_1, P_2, F_1, F_2, BC_1 and BC_2 were raised for both the crosses. In each replication five rows were assigned to each nonsegregating generation (P_1, P_2 and F_1) while F_2s and backcrosses were grown in 30 and 20 rows, respectively. In the triple test cross, a single row was sown from each family. Both the sets were grown in randomized block design with three replications keeping plant-to- plant and row-to-row distance 10 and 30 cm, respectively. Data were recorded on five plants in each row for yield/plant, tillers/plant, grains/spike, 1000-grain weight, harvest index, spikelets/spike, and spike length.

The triple test cross analysis was carried out according to Jinks and Perkins [2], using orthogonal set of comparisons. Model fitting analysis was done by the weighted least square technique [3].

RESULTS AND DISCUSSION

In triple test cross, significant epistasis was observed for yield/plant, grains/spike, grain weight, and harvest index in the cross 9 D x HD 2009. Epistasis was also detected in the cross C 591 x WL 711 for yield/plant, grains/spike, grain weight, and spikelets/spike. The partitioning of epistasis into i, j and l types revealed that in the cross 9 D x HD 2009, i type epistasis was present for yield/plant, grains/spike, grain weight, and harvest index. The j and l type epistasis was significant for grain weight only. In the cross C 591 x WL 711, i type epistasis was observed for yield/plant, grains/spike, grain weight, and spikelets/spike, whereas the j and l type epistasis were present for yield/plant and spikelets/spike (Table 1). This indicated the predominance of i type epistasis in both the crosses. The epistatic effects varied from character to character in the same cross and from

Table 1. Analysis of variance to test the epistasis from triple test cross analysis for seven characters in two wheat crosses

Source	d.f.	Mean squares						
		yield per plant	tillers per plant	grains per spike	1000-grain weight	harvest index	spikelets per spike	spike length
				9 D x HD 2009				
i type epistasis	1	4.21*	2.17	18.1*	0.26*	0.013**	5.14	18.7
j & l epistasis	19	1.35	1.63	5.1	0.07*	0.003	2.12	10.3
i x replicates	2	0.73	2.09	6.1	0.05	0.003	1.18	14.1
j & l x replicates	38	0.81	1.21	4.2	0.02	0.001	2.08	6.2
Within family error	720	0.95	1.45	4.5	0.03	0.002	2.95	8.14
				C 591 x WL 711				
i type epistasis	1	27.11*	0.61	49.9*	0.38	0.009	54.47*	32.6
j & l epistasis	19	5.42*	0.43	18.4	0.09	0.005	11.95*	20.9
i x replicates	2	5.38	0.57	22.1	0.14	0.007	7.08	12.2
j & l x replicates	38	3.09	0.24	11.2	0.07	0.003	5.29*	15.1
Within family error	720	3.18	0.32	12.4	0.08	0.004	4.16	17.7

*,**Significant at P = 0.05 and P = 0.01, respectively.

cross to cross for the same character with the exception of yield/plant, grains/spike, and grain weight, where epistatic gene effects were present in both the crosses.

Analysis of variance for sums and differences indicated the significance of sums for all the seven characters in both crosses, except for grain weight in C 591 x WL 711 (Table 2). Significant differences were observed for tiller number, grains/spike, and spikelets/spike in the cross 9D x HD 2009, whereas in C 591 x WL 711, this parameter was significant for grains/spike, grain weight, spikelets/spike, and spike length. The significant components of genetic variances D and H are presented in Table 3. Both the triple test crosses exhibited higher magnitude of additive genetic variances than dominance variances, except for grains/spike in the cross 9 D x HD 2009 and for grain weight in C 591 x WL 711. The estimates of genetic components D and H were biased due to epistasis, except for characters tiller number, spike length and spikelets/spike in the cross 9 D x HD 2009 and tiller number, harvest index and spike length in C 591 x WL 711.

Our finding that the model fitting results were similar to the results obtained from triple test crosses is in agreement with the results of Tapsell and Thomas [4] in barley. In general,

Table 2. Analysis of variance to detect additive and dominance components for seven characters in two wheat crosses

Source	d.f.	Mean squares						
		yield per plant	tillers per plant	grains per spike	1000-grain weight	harvest index	spikelets per spike	spike length
				9 D x HD 2009				
Sums ($L_{1i} + L_{2i} + L_{3i}$)	19	2.95^{**}	0.65^{*}	16.37^{*}	0.17^{**}	0.015^{**}	0.38^{*}	0.47^{**}
Sums x replicates	38	0.72	0.28^{*}	7.95^{*}	0.06	0.005^{*}	0.09	0.12^{**}
Within family error	720	0.98	0.13	4.13	0.07	0.003	0.18	0.08
Differences ($L_{1i} - L_{2i}$)	19	0.71	0.34^{*}	7.91^{*}	0.19	0.008	0.37^{*}	0.17
Differences x replicates	38	0.52	0.14	2.217	0.09	0.004	0.20	0.08
Within family error	480	0.62	0.16	3.32	0.13	0.006	0.21	0.13
				C 591 x WL 711				
Sums ($L_{1i} + L_{2i} + L_{3i}$)	19	2.95^{**}	0.97^{*}	29.97^{**}	0.13	0.007^{*}	1.94^{**}	0.32^{**}
Sums x replicates	38	1.09	0.41	10.13^{**}	0.09	0.003	0.62^{**}	0.08
Within family error	720	1.17	0.48	7.96	0.11	0.004	0.32	0.13
Differences ($L_{1i} - L_{2i}$)	19	2.97	0.73	11.14^{*}	0.31^{*}	0.009	1.43^{*}	0.31^{*}
Differences x replicates	38	2.08	0.61	6.47	0.16	0.005	0.73	0.16
Within family error	480	2.13	0.66	6.63	0.17	0.007	0.84	0.18

*,**Significant at P = 0.05 and P = 0.01, respectively.

the model fitting results (Table 4) were similar to those obtained from triple test cross analysis. In model fitting, additive effects (d) were highly significant for all the characters studied in both the crosses. Additive x additive components were significant for yield/plant, grains/spike, harvest index, and spike length in the cross 9 D x HD 2009 and for yield/plant, grain weight, harvest index, spikelets/spike, and spike length in C 591 x WL 711.

Table 3. Estimates of D, H and degree of dominance in triple test cross progenies for seven characters in two wheat crosses

Cross	Component	Yield per plant	Tillers per plant	Grains per spike	1000-grain weight	Harvest index	Spikelets per spike	Spike length (cm)
9 D x HD 2009	D	1.98	0.33	7.48	0.10	0.009	0.26	0.31
	H	—	0.27	7.65	—	—	0.23	—
	$(H/D)^{1/2}$	—	0.89	1.01	—	—	0.93	—
C 591 x WL 711	D	1.65	0.49	17.64	—	0.004	1.17	0.21
	H	—	—	6.23	0.20	—	0.93	0.20
	$(H/D)^{1/2}$	—	—	0.59	—	—	0.89	0.97

It is clear from the results that additive and additive x additive gene actions are more important in this material. Such gene action is of interest, being of fixable nature. Early generation selection may be effective in this material.

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