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DETECTION OF ADDITIVE, DOMINANCE AND EPISTATIC VARIATION USING SINGLE TESTER ANALYSIS IN BREADWHEAT

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ABSTRACT

Single-tester analysis of material generated from five breadwheat varieties, sown on two dates, was performed for five metric traits. With the availability of F_{2i} generation, five additional tests of epistasis were constructed, including three tests detecting additive × additive (*I*), additive × dominance (*J*), and dominance × dominance (*L*), kinds of epistasis individually in the single tester analysis. The epistatic variation was an important part of genetic variation for all traits. The significant epistasis was of *I* type for ear length, *I* and *L* type for ear number, *J* and *L* type for days to flowering, and only *L* type for height at flowering and total plant height. The epistasis × sowings, additive × sowings, and dominance × sowings interactions were all nonsignificant. The additive and dominance components were equally important for days to flowering and height at flowering, while the additive component was predominant for plant height and ear number. For ear length, only the additive component was significant. Because of presence of large additive component along with fixable nonallelic interactions simple breeding procedures like single seed descent method could be used for obtaining superior recombinant pure breeding lines.

Key words: Single-tester analysis, wheat, genetic components.

A general method, requiring only a single inbred tester, for the detection of epistasis, additive and dominance components of genetic variation, in a population of pure breeding lines, has been described by Chahal and Jinks [1]. The analysis overcomes the difficulties that can arise when the inbred testers share some common loci [2], but it retains most of the advantages of triple test-cross design of Kearsey and Jinks [3] later simplified by Jinks [4] and Jinks and Virk [5]. The design requires raising of 5 n progeny families consisting n of each P_i pure breeding lines, P_c (an arbitrarily chosen tester line); F_{1i} ($=P_c \times P_i$) families, B_{1i} ($=F_{1i} \times P_i$) and B_{ci} ($=F_{1i} \times P_c$) simultaneously in the same experiment. In addition, n F_{2i} families can also be produced, without extra time and labour in order to perform additional tests of epistasis. In the present paper we make use of 6 n progeny families for detection of epistasis and estimation of additive and dominance components of genetic variation in wheat.

MATERIALS AND METHODS

One pure breeding tester, Girija (P_c), was crossed with five breadwheat varieties, namely Kalyan Sona, Barani 70, C 591, Kharchia and WG 357, to generate five F_{1i}. The F_{1i} were selfed to produce F_{2i} and also back-crossed to P_i varieties and P_c generate B_{1i} and B_{ci} generations, respectively. The experimental material, tester to therefore, consisted of five sets of P_i, P_c, F_{1i}, F_{2i}, B_{1i} and B_{ci} generations. The material was grown in a single plant completely randomized experiment of 1050 plants with 210 individual assigned to each of the five crosses. The number of plants per generation was: $P_i = P_c = F_{1i} = 20$; $F_{2i} = 70$; $B_{1i} = B_{ci} = 40$. The experiment was conducted during 1979-80 at the Punjab Agricultural University, Ludhiana, under two dates of sowing i.e. 23 November, 1979 and 10 December, 1979. Data were recorded on individual plants for days to flowering, height at flowering, final plant height (cm), ear length (cm), and number of ears per plant.

Two tests of epistasis based on the variance of $(2\bar{B}_{1i} - \bar{F}_{1i} - \bar{P}_i)$ and $(2\bar{B}_{ci} - \bar{F}_{1i} - \bar{P}_c)$ were proposed by Chahal and Jinks [1]. With the availability of F_{2i} generation, additional tests of epistasis could be constructed. The variance of $(4\bar{F}_{2i} - 2\bar{F}_{1i} - \bar{P}_i - \bar{P}_c)$ and $(2\bar{B}_{1i} + 2\bar{B}_{ci} - 2\bar{F}_{1i} - \bar{P}_i - \bar{P}_c)$ will detect the presence of additive × additive (i) and dominance × dominance (l) type of epistasis as variance component, i.e. I $(= \sum_{i=1}^{k} i^2)$ and L $(= \sum_{i=1}^{k} l^2)$ together. The former is derived from the C scaling test of Mather and Jinks [6] and the latter is a combination of A and B scaling test given by Chahal and Jinks [1]. Another test that detects only I kind of epistasis is based on the variance of $(2\bar{B}_{1i} + 2\bar{B}_{ci} - 4\bar{F}_{2i})$ as described by Virk and Virk [7]. Additional tests of epistasis could be computed from the perfect fit solution of six generation means given by Mather and Jinks [6]. The variance of $(2\bar{B}_{ci} - 2\bar{B}_{1i} - \bar{P}_c + \bar{P}_i)$ and $(\bar{P}_i + \bar{P}_c + 2\bar{F}_{1i} + 4\bar{F}_{2i} - 4\bar{B}_{1i} - 4\bar{B}_{ci})$ derived in this way will detect J $(= \sum_{i=1}^{k} j^2$, the additive × dominance component) and L kind of epistasis, respectively. The two standard tests of epistasis [1] were simultaneously performed along with the additional five tests described here.

The additive and dominance components of genetic variance were tested and estimated following Chahal and Jinks [1].

RESULTS AND DISCUSSION

For a population of unrelated pure breeding lines the biases caused by common loci shared by the two inbred testers of a triple test cross can be avoided when a single tester is used [1]. However, this demands raising of additional back cross generations. The single-tester analysis detects the presence of epistasis independent of the additive and dominance genetic variation. The additive and dominance components are also estimated orthogonally and with equal precision. Thus, the single-tester analysis retains the major advantages of triple test-cross design [3, 4].

Several tests of epistasis were applied simultaneously which are presented in Table 1. None of the tests detected significant interaction of epistasis with sowing dates. Also, none of the seven tests showed significant epistasis for all characters. The standard tests (i) and (ii) of Chahal and Jinks [1] detected epistasis for days

to flowering, height at flowering and total plant height, while test (i) was not significant for number of ears. Both (i) and (ii) tests did not show epistasis for ear length. Two tests, (iii) and (iv), corresponding to *C* scaling test of Mather and Jinks [6], and a combination of *A* and *B* scaling tests used by Chahal and Jinks [1], respectively, detect *I* + *L* kind of epistasis. Both these tests were significant for days to flowering, height at flowering and total plant height. Test (iii) was significant for number of ears, while both tests (iii) and (iv) were nonsignificant for ear length. Tests (v), (vi) and (vii), based on the statistical comparisons described by Mather and Jinks [6] for the analysis of generation means detect *I*, *J* and *L* types of epistasis, respectively. The *I* type epistasis was detected for ear length and ear number, *J*

Table 1. Analysis of variance for seven different comparisons that detect epistatic variation for five traits

Comparison	Item	d.f.	Days to flowering	Height at flowering	Plant height	Ear length	Ear number
$(2\bar{B}_{1i} - \bar{F}_{1i} - \bar{P}_i)$	Between sets	5	6.81**	14.57**	29.76**	0.03	0.11
	Sets × sowings	5	1.15	3.62	4.72	0.03	0.04
	Within sets	+	0.72	2.88	3.44	0.05	0.18
			(773)	(769)	(769)	(774)	(748)
$(2\bar{B}_{Ci} - \bar{F}_{1i} - \bar{P}_c)$	Between sets	5	6.03**	10.07**	43.95**	0.02	0.86**
	Sets × sowings	5	0.95	0.66	2.41	0.04	0.02
	Within sets	+	0.59	2.11	3.09	0.04	0.19
			(791)	(787)	(785)	(791)	(755)
$(4\bar{F}_{2i} - 2\bar{F}_{1i} - \bar{P}_i - \bar{P}_c)$	Between sets	5	3.36**	14.55**	37.78**	0.04	1.39**
	Sets × sowings	5	0.29	2.63	2.66	0.03	0.16
	Within sets	+	0.94	2.72	3.69	0.04	0.24
			(1343)	(1340)	(1341)	(1349)	(1316)
$(2\bar{B}_{1i}+2\bar{B}_{Ci}-2\bar{F}_{1i}-\bar{P}_i-\bar{P}_c)$	Between sets	5	6.18**	18.45**	41.67**	0.03	0.37
	Sets × sowings	5	0.90	1.24	3.66	0.03	0.04
	Within sets	+	0.57	2.20	2.86	0.04	0.17
			(1401)	(1394)	(1395)	(1403)	(1350)
$(2\bar{B}_{1i} + 2\bar{B}_{Ci} - 4\bar{F}_{2i})$	Between sets	5	1.19	3.80	2.24	0.08**	1.55**
	Sets × sowings	5	0.57	1.62	0.68	0.03	0.09
	Within sets	+	0.59	1.74	2.35	0.03	0.14
			(1706)	(1708)	(1708)	(1708)	(1688)
$(2\bar{B}_{Ci} - 2\bar{B}_{1i} - \bar{P}_c + \bar{P}_i)$	Between sets	5	1.61*	3.73	0.62	0.01	0.27
	Sets × sowings	5	0.40	3.40	0.58	0.03	0.07
	Within sets	+	0.59	2.25	2.94	0.04	0.16
			(1238)	(1232)	(1236)	(1241)	(1197)
$(\bar{P} + \bar{P}_c - 2\bar{F}_{1i} + 4\bar{F}_{2i} - 4\bar{B}_{1i}$	Between sets	5	3.02**	7.55**	8.91**	0.07	1.06**
	Sets × sowings	5	0.87	1.11	1.47	0.04	0.04
$- 4\bar{B}_{Ci})$	Within sets	+	0.68	2.23	2.97	0.04	0.17
			(2225)	(2221)	(2222)	(2230)	(2177)

*, **Significant at 5% and 1% levels, respectively. + Degrees of freedom for within sets are given in parentheses since the number of plants varied for different traits.

type for days to flowering, and *L* for days to flowering, height at flowering, total plant height, and number of ears. These results indicate that epistasis is an important part in the inheritance of all the five traits and hence the estimates of additive and dominance components would be biased to an unknown extent.

The tests of additive and dominance components presented in Table 2 show that both these components were significant for all the five traits, except for nonsignificant dominance variation for ear length. The interactions of both additive and dominance variation with sowing dates were nonsignificant. Only additive genetic variation was significant for ear length. For plant height and ear number, the additive genetic variation was predominant ($\sqrt{H/D} < 1.0$), while for days to flowering and height at flowering both additive and dominance components were equally important ($\sqrt{H/D} = 1.0$).

Table 2. Mean squares, estimates (in squared brackets) of additive genetic (D) and dominance (H) variance components and average degree of dominance for five characters in wheat

Comparison	d.f.	Days to flowering	Height at flowering	Plant height	Ear length	Ear number
$(\bar{B}_{Ci} - \bar{B}_{1i} - \bar{P}_c + \bar{P}_i)$, additive (D)	4	3.94** [27.68]	8.54** [53.20]	27.85** [202.97]	0.11* [0.55]	0.61** [3.62]
$(\bar{B}_{Ci} - \bar{B}_{1i} - \bar{P}_c + \bar{P}_i) \times$ sowings	4	0.37	3.33	0.34	0.04	0.17
$(\bar{B}_{Ci} + \bar{B}_{1i} - \bar{P}_c - \bar{P}_i)$, dominance (H)	4	5.28** [38.42]	9.23** [58.68]	7.16* [38.45]	0.05 [—]	0.37* [1.75]
$(\bar{B}_{Ci} + \bar{B}_{1i} - \bar{P}_c - \bar{P}_i) \times$ sowings	4	0.96	1.55	4.08	0.04	0.07
Within sets	+	0.48 (1238)	1.89 (1232)	2.48 (1236)	0.04 (1241)	0.15 (1197)
$(H/D)^{1/2}$, degree of dominance		1.18	1.05	0.43	—	0.70

*, ** Significant at 5% and 1% levels, respectively. + Degrees of freedom for within sets are given in parentheses since the number of plants varied for different traits. Dash indicates not estimated.

The presence of only additive component and additive × additive (*I*) type of epistasis suggests that all variation is fixable for ear length. The predominance of additive genetic variance and the significance of *I* type epistasis for number of ears points out that these variations can be fixed in recombinant lines. For plant height, additive genetic variance was predominant along with *L* type of nonfixable epistasis. For number of days to flowering and height at flowering, both the genetic components were as important as nonfixable epistasis. The presence of considerable additive variation with or without fixable epistasis for different traits indicates that simple procedures like single seed descent, bulk method of breeding, and their various modifications should be rewarding in obtaining superior recombinant pure breeding lines in wheat.

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