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Genetic Analysis in Wheat

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ABSTRACT

The weighted least square estimates of gene effects for five characters of four wheat crosses indicated that additive-dominance model was adequate to explain variation in six basic generations for majority of characters. The significance of additive (*d*) and dominance (*h*) parameters however could be detected only in few cases. The *d* and dominance × dominance interaction (*l*) played significant role in genetic determination of tiller number of Raj 1972 × WH 283. For spike length of Kalayansona×Lok 1 *d*, *h* and *l* effects were significant. Grain yield per plant and kernels per spike of two hybrids registered significant epistatic effects alongwith *d* and *l* components. The cross VW 110 × WH 291 depicted significant role of dominance in the interaction of kernels per spike and kernel weight. The latter character was found to be influenced by significantly negative *d* and *l* effects. In view of significant contribution of interaction effects, the population improvement approach was suggested for generating transgressive segregants.

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INTRODUCTION

The primary objective of breeding wheat, an autogamous cereal, is to improve both, grain yield and quality. Grain yield is a complex trait being dependent on several component characters. The information on inheritance of these quantitative characters is useful in designing the appropriate breeding procedure and also predicting the performance of the material before the actual practice of selection. The generation mean analysis has been used earlier by several workers for genetical analysis of quantitative traits. However, most of these studies have exploited either three of six parameters model.This paper describes genetical analysis of five characters recorded in four wheat crosses based on the employment of best fitting three, four or five parameter models.

MATERIALS AND METHODS

The basic set of six generations viz., P_1, P_2, F_1, F_2, B_1 ($F_1 \times P_1$) and B_2 ($F_1 \times P_2$) derived from four wheat crosses namely, Raj 1972 × WH 283 (cross 1), Kalyansona × Lok 1 (cross 2) VW 110 × WH 291 (cross 3), UP 301 × Sonalika (cross 4) wer each raised in a seperate block of land during rab 1984-85 following individual plant randomizatio as described by Mather and Jinks (1977). Fo planting of experiments, the family size wa deliberately varied with the kind of generation. I was set at as low as 30 for the genetically uniform parents and F_1s. For segregating families, it was 10 for F_2's. and 70 for back crosses in each cross t compensate for the greater variation expected i these segregating families. The seeds were sown at distance of 100 cm in 2.25 metre long row plot wit inter row spacing of 30 cm. Recommended packag of practices were followed throughout the cro season. The observations were recorded on individual plant basis for five characters in each cross (Table 1). Cavalli's, (1952) joint scaling test was employed to detect the presence of epistasis as well as to obtain weighted least square estimates of additive (d) and dominance (h) gene effects. Whenever this simple additive dominance model failed to be adequate to explain the variation in generation means, the six parameters perfect fit solution advocated by Jinks and Jones (1958) was used to estimates main and interaction effects. The

veighted least square estimates of best fitting four r five parameter models were obtained after emoval of non-significant interaction parameters n six parameters model as described by Mather and inks (1971).

RESULTS AND DISCUSSION

The estimates of genetic parameters for different characters recorded in four crosses are presented in Table 1. Since the variation among six generation means was not significant for tiller number in cross 1 and spike length in crosses 1 and 4, their data were not subjected to generation mean analysis. The goodness of fit of the model concerned was tested through chi-square test. The non-significant x^2 values associated with different characters (Table 1) suggested that the models used were adequate and the parameters estimated were sufficient to explain the variation in generation means. The parameters m was found to be significant in all cases. For tiller number only in Raj 172 × WH 283, the additive (d) and dominance × dominance (l) interaction effects were significant. Singh *et al.* (1984 b) and Vaghani (1985) have also reported importance of additive and epistatic interaction for tiller number in wheat. The genetic of this character was not clear in crosses 3 and 4 where additive-dominance model was found to be adequate but both (d) and (h) effects were non significant. The additive (d), dominance (h) and dominance × dominance (l) effects played significant role in the genetic control of spike length of progenies of Kalyansona × Lok 1. Similar results were also reported by Singh *et al.* (1984 a) but Vaghani (1985) did not observe influence of epistatic interaction for spike length. The analysis of kernels per spike suggested that though simple model was satisfactory for crosses 2 and 3, only dominance effect was significant in cross 3. Except for (i) interaction all the effects were significant in cross 2 for this trait. This result corroborates the findings of Singh *et al.* (1984 a). The significant role of dominance and additive × additive effects was noted in cross 4.

The magnitude of the estimated (h) component for spike length and kernels per spike was higher than (d) component and the negative sign associated with it indicated that the genes possessed by low scoring parents for these characters were in general dominant over the genes possessed by higher scoring parents. Moreover, the influence of largely duplicated type of epistatis was noted for kernels per spike in cross 2 in view of opposite sign associated with (h) and (l) parameters. The x^2 test showed that simple additive-dominance model was satisfactory to describe variation in generation means for kernel weight per spike in first three hybrids whereas for forth hybrid, the model involving additional (i) parameter was adequate. Neither additive (d) nor dominance (h) effect was significant for first three crosses except (h) component in case of cross 3 for this trait. In cross 4 (h) and (i) genetic parameters were significant and negative. The additive and dominance components for grain yield per plant were not significantly different from zero in crosses 2 and 3 where adequacy of simple model was indicated by joint scaling test. Fitting of five parameter model showed that the grain yield per plant was governed by (d) and (j) effects in cross 1 and (h) and (l) effects in cross 4. The significance of interaction effects for grain yield in wheat in addition to main effects has also been reported by Singh *et al.* 1984 a and b, and Vaghani 1985. The opposite sign associated with later two parameters suggested that duplicated type of gene action was operative for this character in cross 4. This was also the case with the results reported by Ketata *et al.* (1976). As described by Mather & Jinks (1971) in a polygenic system where many pairs of interacting genes are at work, the sign of i's, j's or d's of individual pair of genes or the sign of their balance can not be safely infered from the sign of absolute value of (i), (j) or (d). Moreover, the dispersion of homozygous loci in the parents influences these three genetic parameters. The (h) and (l) remain free from such influence. Therefore, the sign associated with (h) and (l) parameters was considered reliable to describe the type of largly present epistasis in the present study.

As explained earlier, the goodness of fit for six parameter model of Jinks and Jones (1958) could not be tested in the present study because the number of parameters estimated were equal to number of generation means available which left no degress of freedom for x^2 test. Therefore, the non significant interaction parameters of a perfect fit solution were omitted and weighted least square estimates based on the remaining four or five parameters were obtained in such cases. It was observed that this exercise resulted into increased precision of the estimated parameters in addition to

TABLE 1

Estimate of gene effects for different characters of four crosses based on best fitting model.

Character	*Cross (a)*	*m*	*(d)*	*(h)*	*(i)*	*(j)*	*(l)*	*(x^2)*	*d.f.(+)*
Tiller number	1	9.50** ±0.70	2.41** ±0.62	-5.16 ±2.90	— —	— —	6.91* ±3.11	1.41	2
	3	5.48** ±0.66	-0.23 ±0.63	2.64 ±1.44	—	—	—	0.55	3
	4	7.43** ±0.70	0.84 ±0.66	0.62 ±1.36	—	—	—	5.76	3
Spike length	2	9.91** ±0.14	1.13** ±0.14	-3.44** ±0.71	—	—	3.82** ±0.84	0.59	2
	3	10.42** ±0.37	0.56 ±0.31	0.61 ±0.73	—	—	—	0.66	3
Kernels per spike	1	49.31** ±1.63	-0.63 ±1.51	1.06 ±3.11	—	—	—	3.86	3
	2	62.32** ±2.04	17.55** ±2.04	-25.58** ±8.11	—	-20.83** ±7.18	24.74** ±8.20	0.72	1
	3	56.40** ±3.79	0.57 ±3.40	17.01* ±7.08	—	—	—	2.57	3
	4	81.32** ±6.11	2.91 ±1.95	-38.29 ±9.50	-39.66** ±6.56	—	—	2.25	2
Kernel weight per spike	1	2.34** ±0.11	-0.01 ±0.01	0.31 ±0.20	—	—	—	2.87	3
	2	3.05** ±0.14	-0.01 ±0.13	-0.03 ±0.22	—	—	—	2.00	3

1	2	3	4	5	6	7	8	9	10
	3	2.44** ±0.19	-0.09 ±0.18	0.99** ±0.36	—	—	—	0.56	3
	4	3.16** ±0.34	-0.12 ±0.11	-0.93* ±0.45	-1.23** **0.37	—	—	0.14	2
Grain yield per plant	1	18.61** ±1.69	4.19* ±1.91	-6.66 ±8.11	—	12.10* ±6.08	14.36 ±7.74	0.72	1
	2	18.67** ±1.69	-0.70 ±1.49	-1.30 ±3.28	—	—	—	4.76	3
	3	11.70** ±1.89	0.01 ±1.69	6.66 ±3.98	—	—	—	2.27	3
	4	11.16** ±1.70	1.96 ±1.76	25.04** ±7.44	—	-4.01 ±7.24	-24.15** ±7.84	0.47	1

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

(a) Cross 1 = Raj 1972 × WH 283, 2 = Kalyansona × Lok 1, 3 = VW 100 × WH 291, 4 = UP 301 × Sonalika.
(+) d.f. = degree of freedom.

providing the test of goodness of fit of the model. There was a considerable change in magnitude of the estimates itself, reduction in standard error of the parameter and change in sign of some of the effects. The change in significance was found to be mainly due to the relative reduction of Cii (error component) term of the inverted matrix.

In the present study it was observed that in majority of cases the estimated parameters and (d) in particular, were smaller than respective standard error or non significantly different from zero. Whenever the (d) or (h) parameters were significant, the contribution of interaction effects was also significant. Under a situation of this type, it would be difficult for the breeder to get promising segregants better than parents through conventional breeding methods such as making simple crosses and their exploitation through straight pedigree method. In order to generate transgrassive segregants, breeding procedures involving multiple crosses, growing large sized populations in each generation and biparental matings in early generations may be resorted to. The use of population improvement concept (Frey, 1975) as an alternative to conventional method may also become amenable solution.

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