

# Triple Test Cross Analysis in F<sub>2</sub> Populations of Four Barley Crosses

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Summary. The triple test cross analysis of Jinks and Perkins (1970) was used to study different components of genetic variation in four barley  $F_2$  populations, C 164  $\times$  IB 226, C 164  $\times$  Jyoti, IB 226  $\times$  P 113 and DL 3  $\times$  P 113, for final plant height, spike length, 100-kernel weight, grain yield per plant and harvest index. The overall epistasis (i type) was, in general, a minor component but the j & 1 type epistasis was an important element for all five characters in cross 3 (IB 226  $\times$  P 113). Both the additive (D) and dominance (H) components were highly significant for all the five characters in all four crosses. The dominance was directional in all cases except for 100-grain weight in crosses 1 (C 164  $\times$  IB 226), 2 (C 164  $\times$  Jyoti) and 4 (DL 3  $\times$  P 113).

**Key words:** Genetic architecture — Gene action — Triple test cross — Barley

# Introduction

The success of any plant breeding programme depends, to a great extent, on the knowledge of the genetic architecture of population(s) being handled by the breeder. Therefore, the breeder needs a method which can provide reliable information about the nature and magnitude of gene action present in his material.

Among the existing genetical procedures used to detect and estimate different components of continuous variation, the triple test cross method is the most efficient. It also has the widest applicability as it can be used to investigate both segregating and non-segregating plant populations arising from different generations (F<sub>2</sub>, backcross and homozygous lines) (Kearsey and Jinks 1968; Jinks, Perkins and Breese 1969; Jinks and Perkins 1970; Perkins and Jinks 1970, 1971; Singh and Singh 1976, 1978; Jinks and Virk 1977; Chahal and Jinks 1978).

#### Material and Methods

# Experimental Design

Forty plants were randomly chosen from each of the four barley  $F_2$  populations, C 164 × IB 226, C 164 × Jyoti, IB 226 × P 113 and DL 3 × P 113. All these plants were backcrossed to their respective  $P_1$  (the larger parent),  $P_2$  (the smaller parent) and  $F_1$  ( $P_1$  ×  $P_2$ ) to obtain  $L_{1i}$ ,  $L_{2i}$  and  $L_{3i}$  families, respectively. Ten plants from each of the 480 families (120 from each original cross) thus produced were grown in completely randomized blocks with three replications, in November, 1977. The plants were scored for final plant height, spike length, 100-kernel weight, kernel yield per plant and harvest index.

## Statistical Analysis

The whole analysis was carried out according to Jinks and Perkins (1970). The sums of squares due to overall epistasis (i type) and j & 1 type epistasis were obtained for each character for 1 d.f. and 39 d.f., respectively. Similarly, sums of squares due to sums  $(\overline{L}_{1i} +$  $\overline{L}_{2i} + \overline{L}_{3i}$ , to detect and estimate additive component) and differences  $(\overline{L}_{1i} - \overline{L}_{2i})$ , to detect and estimate dominance component) were separately computed for 39 d.f. All items of the analysis were tested against a within families error (1/3 VL<sub>1</sub> + 1/3 VL<sub>2</sub> + 1/3 VL<sub>3</sub>, where VL<sub>1</sub> = average replicate variance of L<sub>1</sub> families, etc.) calculated for 3240 d.f. except where variance of L3 families differed significantly from that of L<sub>1</sub> and L<sub>2</sub> families. In the latter case, epistasis, sums and differences items were tested against 1/6  $VL_1 + 1/6 VL_2 + 4/6 VL_3$ ,  $1/3 (VL_1 + VL_2 + VL_3)$  and  $1/2 (VL_1 + VL_2 + VL_3)$ + VL<sub>2</sub>) within families errors, respectively. In case the replicate error (in the case of epistasis) or replicate interactions (in the case of sums and differences) were significant, they were used to test the significance of main items. All items of the analysis were based on the means of ten plants scored from each progeny family except the item within families error and, therefore, the latter was divided by 10 to make it comparable to other items of the analysis.

The estimates of additive and dominance components were obtained as  $\sigma^2$  s (sums) = 1/8 D and  $\sigma^2$  d (differences) = 1/8 H.

The parameter F was computed as the covariance of sums and differences, so that  $\sigma$  sums / differences =  $-\frac{1}{4}$  F. To test the significance of F, this covariance was converted into correlation (r sums/differences) and the significance of this correlation was tested for (n-3) d.f.

Table 1.	Mean squares due to epistasis and their significance levels in	1 four barley crosses, 1 (C 164 X
IB 226),	(C 164 × Jyoti), 3 (IB 226 × P 113) and 4 (DL 3 × P 113), fe	or five characters

Item		d.f.	Plant height	Spike length	100-kernel weight	Yield per plant	Harvest index
i type	1	1	26.28	6.42	2.78	49.80 <sup>a</sup>	8.05
epistasis	2	1	41.56	2.90	1.93	17.63	21.44
	3	1	109.66 <sup>b</sup>	8.20	0.95	12.12	28.12
	4	1	32.85	5.55	3.16	192.26 <sup>c</sup>	12.32
j & 1 type	1	39	14.05	2.80	0.72	20.50 <sup>b</sup>	17.25
epistasis	2	39	40.48 <sup>c</sup>	1.75	1.03	10.33	14.47
	3	39	18.11 <sup>b</sup>	4.60 <sup>a</sup>	10.88 <sup>c</sup>	31.75 <sup>c</sup>	32.84 <sup>b</sup>
	4	39	8.68	3.15	9.81 <sup>c</sup>	33.09 <sup>c</sup>	47.18 <sup>c</sup>

P = 0.05 - 0.01

## Results

The mean squares due to i type and j & 1 type epistasis for five characters in the four barley crosses are presented in Table 1. Whereas i type epistasis was non-significant in all four crosses for all the five characters, except for final plant height in cross 3 and yield per plant in crosses 1 and 4, the j & 1 type epistasis was significant for yield per plant in cross 1, final plant height in cross 2, all the five characters in cross 3 and 100-kernel weight, yield per plant and harvest index in cross 4.

A reference to Table 2 shows that the components D and H were highly significant in all four crosses for all the five characters, except for 100-kernel weight in cross 4 for which the H component was borderline (P = 0.05). Whereas there was either complete dominance or overdominance in cross 2, except for harvest index where the additive component predominated over the dominance component, crosses 3 and 4 showed that the D component was more important than H for all five characters except the 100-kernel weight in cross 3 the H component was relatively more important than the D component. In cross 1, however, the D component was more important for final plant height, spike length and harvest index while, on the other hand, component H was more important for 100-kernel weight and yield per plant.

The parameter F was significant in all four crosses for all the characters studied except for 100-kernel weight in crosses 1, 2 and 4 where it was non-significant (Table 2).

# Discussion

The procedure followed in the present investigation detects epistasis regardless of allelic frequencies, mating system or gene correlation. The presence of epistasis de-

Table 2. Estimates of D, H and F and their significance levels in four barley crosses, 1 (C 164 × IB 226), 2 (C 164 × Jyoti), 3 (IB 226 × P 113) and 4 (DL 3 × P 113), for five characters

Com po- nent		Plant height	Spike length	100- kernel weight	Yield per plant	Harvest index
D	1	89.40 <sup>c</sup>	24.70 <sup>c</sup>	8.70°	69.45°	84.15 <sup>c</sup>
	2	70.69 <sup>c</sup>	18.20 <sup>c</sup>	11.62 <sup>c</sup>	108.52 <sup>c</sup>	80.65 <sup>c</sup>
	3	61.82 <sup>c</sup>	30.04 <sup>c</sup>	10.48 <sup>c</sup>	72.44 <sup>c</sup>	101.56 <sup>c</sup>
	4	128.50 <sup>c</sup>	42.65 <sup>c</sup>	15.22 <sup>c</sup>	51.83 <sup>c</sup>	136.13 <sup>c</sup>
Н	1	55.92 <sup>c</sup>	8.07 <sup>c</sup>	9.88 <sup>c</sup>	79.20 <sup>c</sup>	34.27 <sup>c</sup>
	2	70.26 <sup>c</sup>	19.17 <sup>c</sup>	14.04 <sup>c</sup>	106.18 <sup>c</sup>	29.17 <sup>c</sup>
	3	39.60 <sup>c</sup>	10.25°	18.11 <sup>c</sup>	13.75 <sup>b</sup>	31.40 <sup>c</sup>
	4	52.49 <sup>c</sup>	8.21 <sup>c</sup>	2.80 <sup>a</sup>	15.12 <sup>b</sup>	18.22 <sup>b</sup>
F	1	19.12 <sup>c</sup>	4.21 <sup>c</sup>	0.58	10.40 <sup>c</sup>	-10.68 <sup>c</sup>
	2	15.82 <sup>c</sup>	3.08 <sup>b</sup>	-1.08	14.50 <sup>c</sup>	-9.68 <sup>c</sup>
	3	10.78 <sup>c</sup>	6.31 <sup>c</sup>	3.76 <sup>c</sup>	7.02 <sup>c</sup>	7.95 <sup>c</sup>
	4	-15.45 <sup>c</sup>	2.71 <sup>a</sup>	-0.50	5.76 <sup>b</sup>	11.14 <sup>c</sup>

P = 0.05 - 0.01

tected for plant height (crosses 2 and 3), spike length (cross 3), 100-kernel weight (crosses 3 and 4), yield per plant (crosses 1, 3 and 4) and harvest index (crosses 3 and 4) in this study indicates that one would not have obtained a clear picture about the genetic systems controlling these characters had he used a procedure assuming no epistasis. Whereas the advantage of additive (i type) epistasis can be used in evolving homozygous cultivars by following standard hybridization and selection procedures, j & 1 type epistasis (which is an important element in the present study) is useful in the development of hybrids. In self-pollinated crops such as barley, however, where pro-

b P = 0.01 - 0.001

c P < 0.001

b P = 0.01 - 0.001

P < 0.001

duction of commercial hybrids is still in the distant future this second type of epistasis (j & l) is of little use.

The relative importance of additive and dominance gene effects varied from character to character in the same cross and from cross to cross for the same character with the exception of harvest index where additive gene effects showed predomination over the dominance gene effects in all four crosses. But since both additive and non-additive gene effects accounted for all the characters studied in all four crosses, conventional selection procedures will not help much in achieving improvement in these characters.

However, since the present experiment was conducted at one location for only one year, the estimates of additive and dominance components are confounded with environmental effect (location, year, etc.). The characters which showed an absence of epistasis may give evidence of epistasis under other environmental conditions. Similarly, the characters which showed presence of significant epistasis may not do so if tested in other environments. Therefore, more eloborate experiments conducted at different locations for more than one year will give a clearer picture about the genetic systems controlling these characters and help in developing more efficient breeding procedures.

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Received December 5, 1978 Accepted April 9, 1979 Communicated by A. Robertson

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