

## **Genetic Architecture for Yield and Quality Component Traits Over Two Environments in Barley (*Hordeum vulgare* L.)**

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### **Abstract**

Triple test-cross analysis involving three testers K-560, Narendra Jau-3 and their hybrid K-560 x Narendra Jau-3, were cross to 15 strains/varieties of barley to estimate the epistatic, additive and dominance components of genetic variance. Modified triple test-cross was done for eleven metric traits in two [normal fertile soil ( $E_1$ ) and saline sodic soil ( $E_2$ )] environments. Epistasis was evident for all the characters under study in both environments except plant height in  $E_2$ , protein content in  $E_1$  and lysine content in both conditions. The *i* type epistasis was significant for seed yield per plant in  $E_1$  only, while *j* and *l* type epistasis were significant for most of the traits. Additive (D) component was important in all cases in both conditions except number of effective tillers per plant in  $E_1$  and lysine content in  $E_1$  &  $E_2$  where as non fixable dominance (H) component were significant for all the characters in both conditions except number of effective tillers per plant in  $E_1$ , length of main spike in  $E_2$  and lysine content in both environments. The most of the traits showed partial dominance and directional element, F was non- significant for all the traits, suggesting ambidirectional nature of dominance.

**Key words:** barley, modified triple test-cross, genetic variation, protein content, seed yield

### **Introduction**

To enable present barley varieties acceptable in the international market, there is need to develop better quality genotypes suitable for making product with consumer acceptability. Thus there is an urgent need to improve grain quality as well as develop better quality genotypes for suitable processing industry. The consumer acceptability of genotype is affected by chemical constituent of the grains. It is therefore, desirable to access basic physiochemical characteristics of the grains so that these can be combined with high yield. The information about nature and magnitude of genetic components of variance for yield and quality characters is essential for planning an efficient breeding programme in any crop. The modified triple test-cross analysis of (Ketata *et al.*, 1976) provide efficient detection and estimation of epistatic variance along with unbiased estimates of additive and dominance component of genetic variance in determining the inheritance of eleven traits in barley using modified triple test-cross (TTC) analysis.

### **Materials and Methods**

Two barley pure lines, viz. testers K-560, Narendra Jau-3 and their hybrid (K-560 x Narendra Jau-3) were cross to 15 lines (Kedar, RD-2552, Narendra Jau-1, Narendra Jau-2, Narendra Jau-4, RD-2035, BL-2, BH-512, Ratna, Jagrati, DL-88, Azad, K-603, NDB-1173 and RD-2624) of barley to develop a set of 45 crosses. The experimental materials consisting of 3 testers, 15 lines,

30 single crosses and 15 three-way crosses were evaluated in randomized block design with three replications during *rabi* 2004-05 in two viz. normal fertile soil ( $E_1$ ) and saline sodic ( $E_2$ ) condition at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, U.P. India. Each entry was shown in a 3 m long single row plant with 10 cm spacing within and 25 cm between rows. Observations were recorded on five randomly selected competitive plants for eleven quantitative traits (Table 1). The pelshenke value, protein content and lysine content were estimated by the method of (Pelshenke, 1933; Lowery's, 1951; and Felker *et al.*; 1978) respectively. Character means were used for modified triple test-cross analysis (Ketata *et al.*, 1976).

## Results and Discussion

The triple test-cross (TTC) analysis revealed that significant epistasis was present for all the characters in both environments except plant height in  $E_2$ , protein content in  $E_1$  and lysine content in both conditions (Table 1). The partitioning of epistasis into *i* and *j* and *l* types showed that additive x additive (*i*) interaction was significant for seed yield per plant in normal fertile soil condition only. The *j* and *l* type epistasis was significant for all the characters in both the environments except days to maturity and protein content in  $E_1$  while lysine content in both environments. Existence of significant epistasis in inheritance of seed yield and some other yield components in barley was reported by others also (Gorshkova and Gorodov, 1981). Greater importance of *j* and *l* type epistasis than *i* component was reported earlier by (Singh, *et al.*, 1984; Tripathi and Singh, 1983; Verma and Yunus, 1986.). On the contrary, (Nanda, *et al.*, 1982) reported *i* type epistasis to be more important than *j* and *l* type epistasis, and (Singh, 1980) reported equal importance of these two sub components. The estimates of the components of genetic variance, additive (D), dominance (H) and F components and the degree of dominance ( $H/D^{0.5}$ ) are given in Table 2. The additive (D) component was important in all cases in both conditions except number of effective tillers per plant in  $E_1$  and lysine content in  $E_1$  &  $E_2$  where as non fixable dominance (H) component was significant for all the characters in both condition except number of effective tillers per plant in  $E_1$ , length of main spike in  $E_2$  and lysine content in both environments. The estimates of D were higher than H for most of the traits, which suggested partial dominance. The directional element of dominance, F was non-significant for all the characters in both environments indicated presence of ambidirectional dominance, and alleles with increasing and decreasing effects appear to be dominant and recessive to the same extent. The significant of additive component for seed yield and quality component traits, except number of effective tillers per plant and lysine content indicates that substantial improvement in yield status can still be achieved by following conventional breeding procedure in barley. The significant contribution of additive x additive type epistasis for seed yield suggested that this component should not be ignored while predicting the recombinants extractable from segregating generations. Further results provided evidence of *j* and *l* type epistasis for most of the traits studied. However, in autogamous crops like barley, where commercial exploitation of hybrid has started, this type of epistasis is of more use.

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Table 1. ANOVA (mean square) of triple test-cross to test epistasis for eleven characters in barley under normal fertile soil (E<sub>1</sub>) and saline sodic soil condition (E<sub>2</sub>)

Sources of variation	Environments	d.f.	Days to maturity	Plant height (cm)	No. of effective tillers /plant	Length of main spike (cm)	Grains per spike	Seed yield/plant (g)	1000 seed weight (g)	Pelshenke value (minutes)	Protein content (%)	Lysine content (%)	Husk content (%)
'i' Type epistasis	E <sub>1</sub>	1	7.20	3.99	0.17	10.86	428.76	22.36*	9.16	2121.80	0.61	0.75	5.83
	E <sub>2</sub>		369.80	220.81	8.28	3.64	366.35	300.13	0.793	1355.77	2.11	1.49	1.12
'j+I' type pistasis	E <sub>1</sub>	14	37.53	34.78*	8.13**	1.64**	206.09**	81.08**	25.28**	315.23**	4.40	0.56	205.13**
	E <sub>2</sub>		74.66**	43.17* *	11.57**	1.21**	307.31**	169.98**	23.90*	330.28**	7.46**	0.97	131.66**
Total epistasis	E <sub>1</sub>	15	35.51*	32.73* *	7.60**	2.25**	220.93**	77.16**	24.20**	435.66**	4.15	0.57	191.84**
	E <sub>2</sub>		94.33**	55.01	11.35**	1.37**	311.24**	178.65**	22.36*	398.64**	7.10**	0.90	122.96**
'i' type epistasis x blocks	E <sub>1</sub>	2	1.80	1.00	4.34**	2.71**	107.19**	5.59	2.29**	530.45**	0.15	0.19	1.46
	E <sub>2</sub>		92.45**	55.20*	2.07**	0.91**	91.59*	75.03**	0.198	338.94**	0.527	3.73	0.28
'j+I' type epistasis x blocks	E <sub>1</sub>	28	15.64	7.92	0.14	0.43	24.12	3.34	0.18	32.68	9.62	1.28	2.03
	E <sub>2</sub>		2.53	14.17	0.32	0.15	23.78	0.723	12.15	11.18	0.71	1.80	0.31
Total epistasis x blocks	E <sub>1</sub>	30	14.72	7.46	0.14	0.55	29.66	3.49	0.32	36.86	10.00	2.42	1.99
	E <sub>2</sub>		8.53	16.91	0.43	0.20	28.30	5.68	11.36	33.03	0.69	2.68	0.49

\*, \*\* Significant at 5% and 1% probability levels, respectively.

Table 2. Estimates of additive (D) and dominance (H) components of variance, parameter F, and degree of dominance (H/D)<sup>0.5</sup> in barley under normal fertile soil (E<sub>1</sub>) and saline sodic soil (E<sub>2</sub>) condition

Sources of variation	Environments	Days to maturity	Plant height (cm)	Number of effective tillers / plant	Length of main spike (cm)	Grains per spike	Seed yield/ plant (g)	1000 seed weight (g)	Pelshenke value (minutes)	Protein content (%)	Lysine content (%)	Husk content (%)
D	E <sub>1</sub>	25.51**	429.12**	4.67	4.70**	520.15**	67.72**	17.21**	250.46**	16.77**	1.63	125.83**
	E <sub>2</sub>	40.72**	150.58**	2.64**	2.60**	239.90**	50.43**	22.74**	190.35**	14.75**	1.90	78.26**
H	E <sub>1</sub>	20.09**	20.06**	3.11	1.46**	167.30**	33.78**	12.57**	374.09**	4.89**	0.86	77.24**
	E <sub>2</sub>	37.45**	45.28**	4.41**	0.76	224.90**	69.57**	10.56**	237.02**	8.30**	0.65	57.05**
(H/D) <sup>0.5</sup>	E <sub>1</sub>	0.60	0.22	0.82	0.56	0.57	0.71	0.85	1.22	0.54	0.74	0.83
	E <sub>2</sub>	0.96	0.55	1.29	0.54	0.81	1.17	0.68	1.12	0.75	0.58	0.85
F	E <sub>1</sub>	0.28	0.18	0.31	0.03	0.02	0.04	0.26	-0.08	-0.06	-0.25	0.20
	E <sub>2</sub>	0.10	-0.02	0.15	0.12	0.11	-0.10	0.20	-0.27	0.01	-0.05	0.19

\*, \*\* Significant at 5% and 1% probability levels, respectively.