

## Genetics of Yield and its Components in Barley (*Hordeum vulgare* L.)

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**Abstract:** Estimation of gene effects based on analysis of generation means were obtained for grain yield per plant, and its three components namely number of ears per plant, number of grains per ear and 100-grain weight in three crosses of barley (*Hordeum vulgare* L.). The contribution of dominance gene effects (h) were found more important than additive gene effects (d) in the inheritance of these traits. Among the epistatic effects, all were found to be of considerable importance in all the characters.

**Key words:** Barley (*Hordeum vulgare* L.), gene effect.

Knowledge of gene effect for a character is essential while formulating systematic breeding program for its improvement. Generation mean analysis, a first degree statistics, is simple and useful technique for characterizing gene effects for a polygenic character. The greatest merit of generation mean analysis lies in the estimate of epistatic gene effects, viz., additive x additive (i), additive x dominance (j), and dominance x dominance x dominance (I). An attempt was made to examine the gene effects in barley.

### Material and Methods

The experiment comprised of 6 generations, i.e., P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, B<sub>1</sub> and B<sub>2</sub> of three crosses, viz., B-13-183 x B-27-15; B-24-60 x B-27-15 and B-25-136 x B-27-15. The parents involved in crosses are derived from genetically diverse sources. These 6 generations were grown in randomized block design with three replications at Agricultural Research Station (Rajasthan

Agricultural University), Banswara. Each plot of P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, B<sub>1</sub> and B<sub>2</sub> generations consisted of two rows, while F<sub>2</sub> consisted of four rows. The row length was 2 metre spaced 30 cm apart. Within rows plant to plant distance was 10 cm. Ten competitive plants from P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, B<sub>1</sub>, and B<sub>2</sub>, while 20 plants from F<sub>2</sub> generation were used for recording the data on number of ears per plant, 100-grain weight (g), number of grains per ear and grain yield per plant (g) (Table 1). Scaling test (Mather, 1949) as well joint scaling test (Cavalli, 1952) were applied to test adequacy of additive-dominance model and interaction components.

### Results and Discussion

Analysis of variance indicated significant differences among the progenies for all the characters. The scaling tests (Mather, 1949) indicated epistatic interactions in all the characters for all the crosses under study. The joint scaling test (Cavalli, 1952)

crosses B-13-183 x B-27-15 and B-25-136 x B-38-25.

For number of grains per ear, both the additive (d) and dominance (h) and all the epistatic interactions of 6-parameter model viz., (i), (j) and (l) were found significant in all the crosses which are in agreement to the findings of Abdulamonov and Nigmatullin (1984). Duplicate type of epistasis exhibited in all three crosses.

The dominance (h) and the interaction (j) was significant in all three crosses while parameter (d) and (i) was found significant in the crosses B-13-183 x B-13-183 x B-27-15 and B-25-136 x B-27-15 for grain yield per plant. The parameter (l) was significant in the crosses B-13-183 x B-27-15 and LB-24-60 x B-27-15. Chaudhary (1987) and Nigmatullin and Abdulamonov (1986) indicated the similar kind of findings. Complementary type of epistasis was exhibited by the cross B-13-183 x B-27-15 while cross B-13-183 x B-27-15 while cross B-24-26 showed duplicate type of epistasis.

According to reproductive mechanism involved, mass and pedigree selection methods have been employed in developing cultivars in barley. These breeding methods however, impose a serious restriction on the population so far the manipulation of its genetic expression and flexibility is concerned. Considering different gene effects over all the characters in present material, the magnitude of dominance (h) was much higher than additive (d) gene effects. This suggested that as the inheritance of quantitative characters become more complex,

the contribution of dominance (h) gene effects to their inheritance becomes greater. Further, all the type of digenic interactions additive x additive (i), additive x dominance (j) and dominance x dominance (l) played an important role for all the characters. Thus, the present study indicated that most of the traits were under the control of both additive and non additive genetic components, the latter being more important. Hence, maximum improvement may be expected through recurrent selection (Compton, 1968). Breeding procedures involving multiple crosses also hold promise, as they will utilize simultaneously both types of genetic components.

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