

Genetics of Some Quantitative Traits in Six-Rowed Barley (*Hordeum vulgare* L.) over Three Environments

Yogendra Sharma^{1*}, P Joshi¹ and SN Sharma²

¹Department of Plant Breeding and Genetics, Rajasthan Agricultural University, SKN College of Agriculture, Jobner, Jaipur-303 329 (Rajasthan)

* Present Address: NBPGR Regional Station, Phagli, Shimla-171 004 (Himachal Pradesh)

²Agricultural Research Station, Durgapura, Jaipur-302 018 (Rajasthan)

Genetic component of variances were estimated for ten characters in a 10 x 10 diallel fashion over three environments. The findings revealed that both additive (D) and non-additive (H1 & H2) components of variation were important for all the characters. However, the relative magnitude of dominance component was higher than additive component i.e. prevalence of non-additive gene effects and over dominance suggested that on or the other form of biparental and/or recurrent selection procedures and diallel selective mating might give fruitful results for improving the grain yield in six rowed barley.

Key Works: Component Analysis, Genetic Component, Six-Rowed Barley

Research done on improvement of barley (*Hordeum vulgare* L.) in the recent past has revealed that grain yield is determined by component traits, is a highly complex and variable character and the genes for yield *per se* do not exist (Grafius, 1959). The present investigation was carried out to determine the genotype x environment interactions and suitable breeding methods for the genetic improvement in six-rowed barley and would provide clearer picture of relative importance of additive and dominance component in the control of characters.

Materials and Methods

Ten genetically diverse six-rowed barley (*Hordeum vulgare* L.) genotypes, viz., RD-2035, RD-2052, RD-2503, RD-2508, RD-2552, RD-2585, RD-387 (Raj Kiran), BL-2, ISBYT-4 and ISBYT-17 were crossed in all possible combinations excluding reciprocals. The 45 F_1 s, their F_2 s and 10 parents were grown in a randomized block design with three replications under early (E_1), normal (E_2) and late (E_3) sowing at Agricultural Research Farm, Asalpur, Jobner. Each plot consisted of 2 m long double rows for non-segregating materials i.e. parents and F_1 s and four rows for segregating materials i.e. F_2 s. Row to row and plant to plant distance was kept at 30 cm, respectively under all the three environments. Recommended cultural practices were followed for raising the crop. Ten competitive plants from each parents and F_1 s and 30 plants in F_2 s were randomly selected for recording observations for grain yield and its 10 component characters (Table 1) under each environment separately. Pooled analysis of variance over the

environments was done according to Panse and Sukhatame (1967). The variance component analysis was done as suggested by Hayman (1954).

Results and Discussion

The pooled analysis of variance over the environments for the experimental design (Table 1) showed highly significant differences among genotypes for all the traits indicating that the material used had enough genetic diversity. Significant differences among environments (sowing dates) also indicated the differential influence of environment on the character expression. The genotypes x environment interaction were also found significant for all the traits, indicating existence of non-linear response of genotypes to the varying environments.

Significant deviation of 'b' from zero and the non-significant departure of regression coefficient from unity in respect of flag leaf area, spike length, grains/spike, 1000-grain weight and grain yield/plant indicated that the aforesaid diallel assumptions were valid for these traits (Table 2). However, rest of the traits showed partial failure of the assumptions but estimates of the population parameters for that traits were still possible (Hayman, 1954) through certainly the estimates for such a trait are less reliable than they would have been, if all assumptions had been fulfilled. With the fulfillment of most of the assumptions of the diallel analysis fully or partially in the present study, the conclusions drawn are expected to be valid and should from a guideline for improvement in the genetic material studied.

Table 1. Pooled analysis of variance over environments for yield and its components in barley

Source of variation	d.f.	Days to heading	Plant height	Tillers/plant	Flag leaf area	Spike length	Spikelets/spike	Grains/spike	1000-grain weight	Harvest index	Grain yield
Environment (E)	2	2879.49**	1625.72**	2.86**	3.43**	0.81*	256.92**	215.73**	972.53**	104.70**	205.21**
Genotypes (G)	99	136.21**	561.55**	4.90**	2.26**	2.09**	139.47**	140.07**	53.26**	15.88**	86.28**
G × E	198	17.56**	15.86**	0.17**	0.42**	0.34**	20.42**	21.85**	4.40**	1.79**	4.26**
Error	596	6.28	6.61	0.09	0.17	0.29	8.30	5.87	1.68	1.40	1.05

*, ** Significant at 5 and 1% level, respectively.

Table 2. Estimation of genetic component of variation for yield and yield component pooled over three environments

Source of components	Days to heading	Plant height	Tillers per plant	Flag leaf area	Spike length	Spikelets per spike	Grains per spike	1000-grain weight	Harvest index	Grain yield
D	5.57*	8.52*	0.11**	0.12**	0.08**	7.44*	7.25*	1.95**	0.38*	2.07*
H ₁	67.21**	151.94**	2.29**	2.56**	1.49**	98.59**	94.14**	29.08**	8.36**	47.41**
H ₂	44.22*	125.89**	1.60**	1.72**	1.08**	83.75**	78.36**	20.53**	6.43**	35.77**
F	12.04	10.99	0.37*	0.61*	0.33*	11.34*	10.83*	6.87*	1.51*	9.00*
E	1.82*	6.91**	0.05**	0.05**	0.04**	1.46	1.25	0.49*	0.22**	0.37
h ²	4.10*	5.33	0.18**	0.08*	0.00	0.23	4.17	0.90	0.08	1.17
(H ₁ /D) ^{1/2}	3.47	4.22	4.56	4.62	4.31	3.64	3.60	3.86	4.69	4.78
H ₂ /4H ₁	0.16	0.21	0.17	0.17	0.18	0.21	0.21	0.18	0.19	0.19
(4DH ₁) ^{1/2} + F/										
(4DH ₁) ^{1/2} - F	1.90	1.36	2.17	3.55	2.89	1.89	1.90	2.68	2.47	2.66
(b-0)/sb	1.54	1.04	0.97	2.56*	2.31*	2.76*	2.65*	3.73**	5.51**	2.60*
(1-b)/sb	1.51	4.36**	4.11**	1.23	0.32	6.37**	1.24	0.46	3.11*	0.51

*, ** Significant at 5 and 1% level, respectively.

The estimates of genetic components of variation (D, H₁, H₂, h² and F) and various ratios based on these components are presented in Table 2. The estimates of additive genetic variance (D) were significant for all the traits. The two measures of dominance H₁ (dominant effect) and H₂ (proportion of dominance due to positive and negative genes) were also highly significant for all the traits. However, the magnitude of H₁ component was higher than that of D for all the traits indicating the greater role of non-additive gene effects in the inheritance of these traits. These results are in agreement with Bhatnagar and Sharma (1995), El-Seidy (1997), Singh *et al.* (1999) and Bhatnagar *et al.*, (2001).

The estimates of 'F' value which indicated the relative frequency of dominant and recessive alleles in parents were found to be positive and highly significant for tillers/plant, flag leaf area, spike length, spikelets/spike, grains/spike, 1000-grain weight, harvest index and grain yield/plant indicating an excess of dominant alleles. Positive but non-significant 'F' in days to heading and plant height gave some indications of the excess of dominant alleles in the parental lines. The environmental component (E) was significant for days to heading, plant height, tillers/plant, flag leaf area, spike length, 1000-grain weight and harvest index. The overall dominance effect (h²) was significant for days to heading, tillers/plant and flag leaf area.

The average degree of dominance (H₁/D)^{1/2} indicated over dominance for all the characters. The proportion of dominant genes with positive or negative effects in parents (H₂/4H₁) was less than the expected value 0.25, for all the traits which indicated asymmetrical distribution of positive and negative dominant genes in the parents. The ratio (4DH₁)^{1/2} + F (4DH₁)^{1/2} - F indicates the proportion of total number of dominant and recessive genes among the parents was greater than unity indicating accumulation of dominant alleles.

The present study revealed that non-additive component of genetic variance was involved in governing the inheritance of yield and its components. In this situation biparental mating and/or diallel selective mating offers good prospects for increasing the frequency of genetic recombination and hastening the rate of genetic improvement in six-rowed barley.

References

- Bhatnagar VK and SN Sharma (1995) Diallel analysis for combining ability for grain yield and its component in barley. *Indian J. Genet.* 55: 3, 228-232.
- Bhatnagar VK, SN Sharma and EVD Sastry (2001) Genetics of quantitative characters in six rowed barley over environments. *Indian J. Genet.* 61, 4: 358-359.
- El-Seidy ESH (1997) Inheritance of earliness and yield in some barley crosses. *Ann. Agril. Sci. Moshtohor.* 35: 2, 715-730.
- Grafius JE (1959) Heterosis in barley. *Agron. J.* 51: 551-554.

Hayman BI (1954) The theory and analysis of diallel crosses. *Genetics*. **39**: 789-809.

Panse VG and PV Sukhatme (1967) *Statistical Methods for Agricultural Workers*. Ed 2: 145-156, ICAR, New Delhi.

Singh I, SL Dashora, SN Sharma, EVD Shastry and I Singh (1999) Inheritance of some quantitative characters in six-rowed barley. *Indian J. Genet.* **59**: 1, 99-101.