

Estimation of genetic parameters and character association in barley (*Hordeum vulgare* L.)

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Abstract

Fifteen lines with four testers were crossed in a line \times tester ($L \times T$) mating design to estimate the variability, heritability and genetic advance for yield and its component traits in barley (*Hordeum vulgare* L.). The mean squares due to replications were positive and significant for days to 50 per cent flowering, days to maturity, biological yield plant⁻¹ and amylose content while, mean square due to treatments were positive and highly significant for all the characters. High PCV and GCV were recorded for grain main spike⁻¹ and number of grains ear⁻¹. High heritability coupled with high genetic advance was noted for biological yield plant⁻¹ amylose content and number of tillers plant⁻¹. High heritability along with moderate genetic advance was recorded for plant height, harvest index and 1000 grain weight. These characters were mainly under the influence of additive gene action and thus, there is ample scope for the improvement of traits through simple selection.

Keywords: Barley, genetic variability, heritability, genetic advance

Barley (*Hordeum vulgare* L. $2n = 14$, sub family Poaceae) is an important cereal crop which ranks fourth after wheat, rice and maize. It is a high energy, nutritionally and environmentally safe crop. It has potential to produce satisfactory yield under problematic soils, qualitatively and quantitatively. Keeping these objectives in mind, this study was carried out to improve grain yield. Genetic variability is a basic requirement for crop improvement as this provides wider scope for selection. It bears special significance due to its great elasticity of adaptation under various stresses and has lot of potential both for domestic and industrial uses. The major uses of barley grains however, are in the production of malt, which is used to make beer, beverage alcohol, whisky, malt syrups, malted milk and vinegar. The spent malt after brewing is used as feed. The line \times tester analysis method introduced by Kempthorne (1957) is one of the powerful tools available to estimate the combining ability analyses help in identification of desirable parents and crosses for their further exploitation in the breeding programme. Thus, effectiveness of selection is depends upon the nature, extent and magnitude of genetic variability presets in material and the extent to which it is heritable. Partition of observed variability into heritable and non heritable components is very much essential to get a true indication of genetic coefficient of variation and is a useful measure of the magnitude of genetic variance present in the population. Hence, in the present investigation, an attempt was needed to assess the indicatives of variability i.e. Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), Heritability in broad sense (h^2_{bs}) and genetic advance as percent of mean (GA).

Genetic advance refers to the improvement in the mean genotype value of the selected plants over base population. An attempt was made to study these aspects in the present investigation.

Experimental details: Fifteen homozygous and genetically diverse varieties and four testers were chosen to attempt sixty crosses. All parents and F_1 s populations were planted in individual rows spaced 25 cm apart keeping seed to seed distance at kept 10 cm apart at Genetics and Plant Breeding Research farm, N.D. University of Agriculture and Technology Kumarganj, Faizabad (U.P.) India. The standard package and practices was followed to raise a good crop. Observations were recorded on randomly selected plants from each entry in for fifteen quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), number of effective tillers per plant, number of grains per main spike, peduncle length (cm), ear length (cm), number of grains per ear, biological yield per plant (g), harvest index (%), 1000-grain weight (g), grain hardness (pressure), grain protein content (%), amylose content (%), and grain yield per plant (g) were recorded. The variance (GCA and PCV) following Burton and Devane (1953), heritability in broad sense (h^2_{bs}) by Hanson (1963) and genetic advance (GA) was estimated by Johnson (1955).

Variability: The analysis of variances revealed significant differences among the genotypes for all the characters studied indicating presence of sufficient genetic variability among the genotypes. The mean square due to replication were positive and significant for days to 50 per cent flowering, days to maturity, biological yield per plant and amylose content while, mean square due to treatment were positive and highly significant for all the characters and

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Table 1. Estimates of variation, heritability and genetic advance in barley

Character	General mean±SE	Range		Coefficient of variation		Heritability in broad sense (%)	Genetic advance	Genetic advance in per cent of mean
		Parents	Crosses	Phenotypic	Genotypic			
Days to 50% flowering	88.46±0.81	83.17-94.17	82.53-98.40	3.85	2.92	69.80	6.46	7.30
Days to maturity	126.24±0.89	126.6-127.47	121.53-129.6	2.97	1.84	61.95	7.00	5.54
Plant height	84.34±2.29	73.67-97.20	71.73-94.33	9.24	7.58	82.03	13.54	16.05
Number of effective tillers/ plant	6.32±0.73	5.40-6.67	5.27-7.73	15.68	10.98	70.02	0.29	45.80
Number of grains main/ear	32.18±0.83	36.67-63.67	36.67-66.47	22.72	11.63	51.18	23.20	57.56
Peduncle length	8.65±0.75	5.80-9.50	7.47-10.23	15.77	10.24	64.93	1.38	15.95
Ear length	7.41±0.74	5.27-6.70	6.23-9.10	16.17	7.54	46.62	0.62	8.36
Number of grains/ main spike	47.64±0.81	36.67-66.40	36.40-66.40	23.36	12.26	52.48	22.90	48.06
Biological yield/plant	28.77±0.81	21.44-36.27	21.44-36.37	16.51	15.14	91.70	9.44	32.81
Harvest Index	39.21±0.81	35.62-4.47	33.62-45.61	9.72	8.39	86.31	7.45	19.00
1000 -grain weight	36.60±0.75	29.45-38.48	28.45-41.32	6.66	5.15	77.32	4.26	11.63
Grain hardness	12.88±0.80	11.27-15.33	11.27-15.47	11.02	6.86	62.25	1.46	11.33
Grain protein content	10.77±0.84	9.27-12.67	9.60-12.55	11.84	6.05	51.09	0.94	8.72
Amylose content	10.70±0.89	8.33-12.60	8.33-12.60	18.59	14.53	78.26	2.87	26.82
Grain yield/plant	14.52±0.82	10.46-15.49	11.76-20.44	11.76	7.66	65.13	1.67	11.50

high value was estimated for biological yield per plant (61.75) followed by plant height (57.59), harvest index (38.63) and days to 50 per cent flowering (35.74). Similar findings were reported by Dhananjay *et al.* (2012); Bharat *et al.* (2013). The estimates of phenotypic coefficient variation (PCV) were higher than genotypic coefficient variation (GCV) for all the traits studied in (Table1). However, relatively low magnitude of difference was observed between GCV and PCV indicating less environmental influence. The high PCV recorded for number of grain per main spike, number of grain per ear, amylose content, biological yield per plant, ear length, and number of effective tiller per plant, peduncle length, and grain protein content, grain yield per plant and grain hardness showed moderate PCV. High GCV was recorded for number of grain per main spike, number of grain per ear, amylose content, biological yield per plant, peduncle length and number of effective tiller per plant. Similar results were earlier reported by Sandeep *et al.* (2002) and Mishra *et al.* (2007).

Heritability: High heritability was recorded for biological yield per plant followed by harvest index, 1000 grain weight, amylose content and plant height. Moderate heritability was recorded for traits like days to 50 per cent flowering, days to maturity, number of effective tiller per plant, peduncle length, number of grain per ear, grain hardness, protein content and grain yield per plant, where all the remaining traits showed low heritability.

These finding were supported with the finding of Yadav *et al.* (2004) and Therrien *et al.* (2006). High genetic advance were recorded for number of grains per main spike, number of grain per ear, number of effective tiller per plant, biological yield per plant and amylose content, whereas the traits plant height, peduncle length, harvest index, 1000 grain weight, grain hardness and grain yield were recorded moderate genetic advance. The results confirm the finding of Chauhan *et al.* (1988). The estimates of heritability coupled with genetic advance are more useful selection parameter than heritability alone. High heritability coupled with high genetic advance was noted for biological yield per plant, amylose content and number of tillers per plant. High heritability along with moderate genetic advance was recorded for plant height, harvest index and 1000 grain weight. Similar results were also reported by Mishra *et al.* (2007).

The present investigation concluded that genetic variability is a logical start within any crop improvement programme. The results revealed presence of wide exploitable variability and heritability in the material examined with respect to various morphological traits indicating thereby, immense scope of genetic up gradation in barley. The high estimates of phenotypic and genotypic

coefficient of variability were found for number of grains per main spike and number of grains per ear in normal soil. High heritability (h^2b) coupled with high genetic advance in percent of mean were recorded for biological yield per plant, amylose content and number of tillers per plant in normal soil. These above traits can be used for further breeding programme and ample scope of selection in barley.

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