



Research Article

ASSESSMENT OF NATURE AND MAGNITUDE OF GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE FOR YIELD COMPONENT TRAITS OF BARLEY

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Abstract: The present investigation was carried out to assess the nature and magnitude of genetic variability, heritability and genetic advance for yield component traits of barley comprised of 6 lines and 3 testers. During 2015-16, all parents were evaluated at Genetics & Plant Breeding Research Farm of Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad. The six improved and diverse genotypes of barley (RD-2768, NDB-1618, RD-2909, RD-2899, NDB-1057 and HUB-240) and three testers (NDB-1173, NDB-3 and NDB-943). Observations were recorded for days to ear emergence, days to maturity, number of productive tillers per plant, ear length (cm), grains per spike, biological yield per plant (g), harvest index (%), 1000-grain weight and grain yield per plant (g). Analysis of variance that mean sum of squares had significant differences among evaluated traits. The moderate estimate of phenotypic and genotypic coefficient of variability was found for productive tillers/plant. High value of heritability in narrow sense (>30 %) were recorded for grains/spike, days to maturity, biological yield/plant, grain yield/plant (g) and harvest index while remaining traits showed moderate estimate. High heritability with high genetic advance in percent of means was recorded for grains/spike and grain yield/plant (g). High heritability coupled with low genetic advance in percent of mean was recorded for days to maturity, ear length(cm), biological yield/plant(g) and harvest index(%), while, low heritability coupled with low genetic advance in percent of mean was recorded for days to ear emergence and low heritability coupled with high genetic advance in percent of mean was recorded for productive tillers/plant and 1000-grain weight(g).

Keywords: Genetic variability, Heritability, Genetic advance

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Introduction

Barley (*Hordeum vulgare* L., 2n=14) belongs to the family Poaceae, tribe Triticeae and genus *Hordeum*. Since pre green revolution, barley a crop of winter season is grown ecofriendly Worldwide for food, feed and forage under various agro climatic situations. Due to its alternate use in brewing industry barley is considered as an important crop of present era which ranks fourth after wheat, rice and maize in the world, both in terms of quantity produced and in area of cultivation [1]. Of course, barley is considered as crop of rainfed and problematic soil conditions i.e. saline alkaline, drought and diara, marginal/coastal area of river. Barley flourishes well under less resource of irrigation and fertilizers. Thus, this crop has great elasticity of adaptation under various stress situations. Barley is an important crop in Ethiopian cereal production and in food security. Barley has superior nutritional quality like presence of beta-glucan (anticholesterol substance), acetylcholine substance (energize our nervous system and recover memory loss), low gluten, soluble and digestible fibers, lysine, thiamine and riboflavin vitamin B5 and also has antioxidant which improves our immune system. Barley reduces the risk for certain cancers, diabetes and heart disease. Barley grain contains 3 to 7% β -glucan, an important dietary fiber that has significant blood cholesterol lowering effects. During 2015-16 India had about 6.55 lakh ha area with production of 16.18 lakh metric tonnes and productivity of 24.70 q/ha. In U.P., barley occupied an area of 1.46 lakh ha with a total production of 3.58 lakh metric ton with productivity of 24.50 q/ha. Uttar Pradesh alone contributes more than one third of India's total production of barley [2]. Desirable improvement could be possible by creation and exploitation of genetic variability with the help of characterization of genetic variance. In the light of early reports, it seems that further improvement in yield potential of barley can be brought firstly, by suitably

altering the genetic makeup of existing varieties through the process of recombination and secondly by employing the appropriate selection method for exploiting the different diverse populations [3,4]. Yield in barley crop, is a complex and the end product is the summation of a number of components, each of which is under polygenic control. All changes in yield must be accompanied by changes in one or more of the components [5]. The existing genetic variability in breeding population of barley available with the breeder is quite meager which is due to limited gene pools. This stresses for continuous efforts to increase and assess the nature and magnitude of genetic variability. A judicious choice of parents endowing substantial genetic diversity, frequently leads to the expression of beneficial effects of heterosis in hybrids and wide spectrum of genetic variability in the progeny. Success in selection programmes depends primarily upon the heritable portion of variability. The heritability estimates facilitate the evaluation of hereditary and environmental effects on phenotypic variation and thus help in selection. Genetic variability describes the occurrence of differences among individuals due to differences in their genetic composition and of the environment in which they are raised [6]. Genetic variability is a basic feature of crop improvement programme and effectiveness of selection depends upon its nature and magnitude in available genetic materials. The existence of genetic variability in the population and knowledge of nature of heritability and gene action provides ample opportunities for selection of genotypes with desired traits. The phenotypic and genotypic coefficients of variation can be used for assessing and comparing the nature and magnitude of variability existing for different traits in the breeding materials. The assessment of variability among the genotypes was done by computing selection parameters e.g. range, mean, and coefficient of variation at genotypic, phenotypic and environmental levels.

Analysis of variance was done by subjecting the data to the statistical method as described [7]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per formula suggested [8,9]. Heritability estimates together with genetic advance are generally regarded to be more useful in predicting the genetic gain through selection [9]. The genetic advance in percent of mean provides indication of expected selection response by taking into account the existing genetic variability and heritability of the character. Heritability was estimated by the formula as suggested by [9]. The expected genetic advance at 5% selection intensity was calculated by formula as given [9,10].

The most important function of the heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value [6,11]. Heritability in broad sense estimates the ratio of total genetic variance, including additive, dominance and epistatic variance to the phenotypic variance [6,12]. Heritability in narrow sense gives the precise idea of response to selection for the characters. Heritability in narrow sense represents the ratio of fixable additive genetic variance to total phenotypic variance. Estimates of heritability help in estimating expected progress through selection. The estimates of heritability in narrow sense (h²_{ns}) have been classified by [13] into three categories viz., high (> 30%), medium (10-30%) and low (<10%).

Material and Method

The study was conducted in Genetics and Plant Breeding Research Farm, Kumarganj, Faizabad with nine genotypes and one local check in 2015-16. Geographically, Narendra Nagar is situated between 26°47' N latitude, 82 ° 12' E longitude and at an altitude of 113 meters above the mean sea level. This area falls in sub-tropical climatic zone. Nearly 80 percent of total rainfall is received during monsoon season from July to September with few occasional showers in the winter. Row to row and plant to plant distance were kept 23cm. and 10cm, respectively. Intercultural operations were adopted to raise good normal crops. Statistical Analysis: The data collected for each quantitative trait were subjected to analysis of variance (ANOVA).

Analysis of variance for the design of experiment

The analysis of variance for the design of experiment was carried out according to the procedure outlined by Panse and Sukhatme (1967). The significance of difference among treatment means was tested by 'F' test. To test the hypothesis H₀: t₁ = t₂ = = t_v, the fixed effect model for the analysis of variance for Randomized Block Design is given below:

$$Y_{ij} = \mu + t_i + b_j + e_{ij}$$

Where,

Y_{ij} = Yield of ith entry in the jth replication

μ = General mean

t_i = Effect of the ith entry (i = 1, 2, -----, v.)

b_j = Effect of the jth replicate (j = 1, 2, -----, r.)

e_{ij} = Environmental effect

Estimation of coefficient of variability

The genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV) and environmental coefficient of variability (ECV) were computed following [14].

$$GCV = \frac{\text{Genotypic Standard Deviation}}{\text{Mean}} \times 100 \text{ or } \frac{\sigma_g}{\bar{x}} \times 100$$

$$PCV = \frac{\text{Phenotypic Standard Deviation}}{\text{Mean}} \times 100 \text{ or } \frac{\sigma_p}{\bar{x}} \times 100$$

$$ECV = \frac{\text{Environmental Standard Deviation}}{\text{Mean}} \times 100 \text{ or } \frac{\sigma_e}{\bar{x}} \times 100$$

Heritability

Heritability in narrow sense (h²_n) was calculated as suggested by [15].

$$\text{Heritability } h^2_n = \frac{2\sigma^2_g}{2\sigma^2_g + \sigma^2_s + \sigma^2_e} \times 100$$

Where,

σ²_g = Variance due to GCA

σ²_s = Variance due to SCA

σ²_e = Variance due to error

Heritability in broad sense (h²_b) was calculated according to the formula suggested by [16].

$$h^2_b = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

σ²_g = Genotypic variance

σ²_p = Phenotypic variance

Genetic advance

Genetic advance (Ga) was estimated by using the formula given by [9].

Genetic advance (Ga) = hb².K.σ_p

Genetic advance in percent of mean = $\frac{Ga}{\bar{x}} \times 100$

Where,

K = Selection differential at 5 percent selection intensity. (K = 2.06)

h²_b = Heritability coefficient (Broad sense)

σ_p = Phenotypic standard deviation

\bar{x} = Mean of the character

Result and Discussion

Data analysis showed favourable indication in context of nature and magnitude of genetic variability, heritability and genetic advance for yield component traits of barley. Genetic variation and heritability studies for yield and yield components in barley genotypes under normal and limited moisture conditions [17]. Whereas, Genotypic variance of characters varied widely from 0.02 for grain weight per spike to 49.18 for plant height. Genotypic coefficient of variation ranged from 4.99% for days to maturity to 32.24% for number of spikelets per spike. Broad sense heritability ranged from 12.14% for harvest index to 81.70% for number of spikelets per spike. The highest genetic advance as percent of mean was recorded for number of spikelets per spike (60.03%) and the least for harvest index (4.38%). Generally, the magnitude of genetic variability among the studied plant material showed great variations for desirable traits and thus confident enough to expect genetic progress if further breeding activities are carried out [18].

Genetic variability

The variability was estimated by selecting parameters viz; range, mean, and coefficient of variation at genotypic, phenotypic and environmental levels among the barley genotypes. Estimates of range, mean, phenotypic and genotypic coefficients of variations, broad sense heritability (H²), genetic advance (GA) and percent of the mean (GAM %) for the present study are indicating in [Table-1]. It was corroborated the similar findings on genetic variability, heritability and genetic advance for yield component traits of barley [12,19].

Table-1 Analysis of variance for Randomized Block Design for nine characters in barley

Characters	Source of variation		
	Replications	Treatments	Parents
d.f.	2	26	8
Days to ear emergence	0.32	4.71**	2.98
Days to maturity	2.53	4.03**	5.54**
Number of productive tillers/plants	0.77	3.19**	2.31**
Ear length (cm)	0.24	0.79**	1.08**
Grains/spike	12.32	47.15**	90.34**
Biological yield/plant (g)	0.81	6.70**	4.01*
Harvest index (%)	3.67	5.67**	5.37**
1000- grain weight (g)	0.53	24.87**	18.54**
Grain yield/plant (g)	0.15	1.09**	1.05**

Range and mean

Days to ear emergence ranged from 93 to 96 days, days to maturity ranged from 126-131, number of productive tillers/plant from 6 to 9, ear length ranged from 8 to 10cm, grains/spike was from 52 to 67, biological yield/plant ranged from 26 to 32, harvest index was from 30 to 34, 1000 grain weight ranged from 31 to 40 and grain yield/plant ranged from 9 to 10g.

Table-2 Range, mean, variance, heritability, genotypic and phenotypic coefficient of variations and genetic advance as percent of mean for characters of barley genotypes

Characters	Range	Mean±S.E.mean	H ² (%)	GCV (%)	PCV (%)	GA	GAM
Days to ear emergence	93-96	94.25±0.72	29.3	1.08	1.72	1.7	1.81
Days to maturity	126-131	128±0.78	41.87	0.67	1.25	1.21	0.95
Number of productive tillers/plants	06-9	6.45±0.43	20.87	14.55	18.52	1.94	30.17
Ear length	08-10	8.41±0.25	36.63	5.31	7.43	0.84	10
Grains/spike	52-67	57.11±1.44	64.41	6.47	7.8	8.09	14.17
Biological yield/plant	26-32	28.81±0.78	36.77	4.41	6.46	2.29	7.96
Harvest index	30-34	31.09±0.79	36.32	3.62	5.69	1.89	6.08
1000-grain weight	31-40	34.55±0.78	17.92	8.02	8.92	6.58	19.05
Grain yield/plant	09-10	9.09±0.31	40.76	5.68	8.17	0.95	10.44

Coefficient of variation

Phenotypic and genotypic coefficient of variation varied between 1.25-18.52 and 0.67-14.55, respectively. The lowest PCV and GCV (1.25 and 0.67), respectively were obtained for days to maturity. Phenotypic coefficient of variation was slightly higher than the corresponding genotypic coefficient of variation for all the traits studied. The difference in magnitude between phenotypic and genotypic coefficient of variation is an indication of the relative influence of environment on the phenotypic expression of the character. Some authors corroborated with the results of present study [20-22]. While the moderate estimates (10-20%) of PCV and GCV were recorded for number of productive tillers per plant (18.52 and 14.55), respectively.

Heritability

In this study, narrow sense heritability (H²) estimate varied from 17.92% (1000 grain weight) to 64.41% (grains/spike). High estimates of heritability in narrow sense (>30%) were recorded for six characters viz. days to maturity (41.87%), ear length (36.63%), grains/spike (64.41%), biological yield/plant (36.77%), grain yield/plant (40.76%) and harvest index (36.32%). High heritability for various traits was reported by many authors as for ear length by [23] and for grain yield by [24]. While, [25] also reported higher heritability for spike length, grain yield and number of spikelets per spike. A moderate estimate of heritability in narrow sense (10 to 30%) was observed for days to ear emergence (29.30%), productive tillers/plant (20.87%) and 1000-grain weight (17.92%). Similar findings were observed by [26-28].

Genetic advance

The genetic advance in percent of mean was not found to be very high (>50%) for any character. Besides, high estimates of this parameter (>20 - 50%) was found for only one character viz. productive tillers/plant (30.17%) and moderate (>10-20%) genetic advance in percent of mean was observed for biological yield per plant, ear length, grains/spike, 1000-grain weight and grain yield/plant. The high heritability in narrow sense with high genetic advance in percent of mean was recorded for grains/spike followed by grain yield/plant while high heritability with low genetic advance in percent of mean for days to maturity followed by biological yield/plant and harvest index. Low heritability with high genetic advance in percent of mean was recorded for number of productive tillers/plant and 1000 grain weight while low heritability with low genetic advance in percent of mean for days to ear emergence. Some authors [22,26,29] also reported the same observations.

Conclusion

The moderate estimate of phenotypic and genotypic coefficient of variability was found for productive tillers/plant, indicating the existence of wide spectrum of variability for this trait and greater opportunities for desired gain through phenotypic selection. Grain yield per plant had strong and positive genotypic correlation with number of productive tillers/plant, grains/spike and 1000-grain weight. The high heritability in narrow sense with high genetic advance in percent of mean represent the additive gene action and high heritability with low genetic advance in percent of mean represent non additive gene action and moderate heritability with low genetic advance in percent of mean represent non additive gene action and low heritability with low genetic advance in percent of mean represent non additive gene action.

Application of research: This study indicated that there was genetic variability among the genotypes. The analysis of variance for treatments and parents (except for days to ear emergence) was highly significant for all traits indicating the sufficient variability in treatments and parents for all traits.

Research Category: Genetics and Plant Breeding

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Study area / Sample Collection: Narendra Deva University of Agriculture & Technology, Kumarganj, Faizabad, 224 229

Cultivar / Variety / Breed name: Barley (*Hordeum vulgare* L., 2n=14)

Conflict of Interest: None declared

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Ethical Committee Approval Number: Nil

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