A study on Genetic Variability and Heritability in Barley (*Hordeum vulgare* L.)

Ankush Katiyar[1], Aarti Sharma[2*], Snehanshu Singh[3], Akaknsha Srivastava[1] and S. R. Vishwakarma[1]

[1]*Department of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad, UP, India*
[2]*Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, UP, India*
[3]*Indian Institute of Wheat and Barley Research, ICAR, Karnal, Haryana, India*

*Corresponding author

A B S T R A C T

In the present investigation, 21 F_1s were generated by crossing seven lines and three testers following Line x Tester mating design. Nine yield traits of barley were studied on 21 crosses to estimate heritability in narrow sense, genetic advance in per cent of mean, phenotypic and genotypic coefficient of variation. The estimates of heritability in narrow sense were observed to be high for only two traits *viz*., days to maturity (57.83%) and ear length (31.54%); while some traits showed moderate heritability *viz*., harvest index (22.80%) and grains/spike (19.49). High heritability in narrow sense (h^2n) coupled with high genetic advance in per cent of mean were recorded only for ear length while the remaining traits showed low genetic advance indicating non-additive gene action. The moderate estimates of phenotypic coefficient of variability were found in grain yield/plant, productive tillers/plant. Estimated of GCV were lower than PVC for all traits.

Introduction

Barley is a cereal crop which is cultivated in summer season in temperate regions and winter season in tropical regions. In India, Barley is cultivated in states of Rajasthan, Uttar Pradesh, Madhya Pradesh, Haryana, Punjab, Bihar, Himachal Pradesh, Uttarakhand and Jammu & Kashmir. Barley is the fourth largest cereal produced in world, after maize, wheat and rice. Barley is a resistant crop and can be grown in problematic soil *viz*., (saline, alkaline, drought and diara). Apart from its uses as human food and animal feed; barley has potential use as health tonic like, horlicks, maltova and barley syrups and in making malt and beer. These uses, makes barley an important crop and encourages more research in the crop.

The estimates of heritability can be used to assess whether the trait can be improved or not. It can predict gain from selection and can be used to choose which selection strategy

will be most effective in improvement of traits in breeding programs. Further, genetic advance under selection indicates advancement made from one generation to another. Therefore a study was undertaken to estimate the heritability and genetic advance in percent of mean in crosses of barley.

Materials and Methods

The present study was undertaken at Genetics and Plant Breeding Research farm of Narendra Deva University of Agriculture & Technology, Narendra Nagar, Kumarganj, Faizabad (U.P.) during *Rabi* 2013 and *Rabi* 2014 in barley crop.

In *Rabi* 2013, the selected barley genotypes were crossed following Line x Tester mating design; seven lines *viz*., EC-667526, EC-667509, EC-667498, EC-667458, EC-667377, EC-667365, EC-667454 were crossed with three tester *viz*., NDB-3, Azad, RD-2552.

The 21 F_1s along with their parents (10 genotypes) were sown in two replications in Randomized Block Design in *Rabi* 2014. Proper package of practice was followed to ensure a healthy crop stand.

Five plants were randomly selected and tagged from each line of the two replications to collect data on traits: days to fifty ear emergence, days to maturity, number of effective tillers per plant, number of grains per main ear, ear length, biological yield/plant, harvest index, 100-grain weight and yield per plant.

Statistical analysis

Phenotypic and genotypic coefficient of variation (PCV and GCV) was calculated by formula given by Burton (1952).

$$GCV = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$PCV = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

Heritability in narrow sense (h^2ns) was calculated as suggested by Kempthorne and Curnow (1961).

$$\text{Heritability} (h^2\text{ns}) = \frac{2\sigma^2 g}{2\sigma^2 g + \sigma^2 s + \sigma^2 e} \times 100$$

$\sigma^2 g$= Variance due to GCA; $\sigma^2 s$= Variance due to SCA; $\sigma^2 e$= Variance due to error

Genetic advance (Ga) was estimated by using the formula given by Johnson *et al.,* (1955).

Genetic advance (Ga) $= h_b^2 . K . \sigma_p$

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

Where, K = Selection differential at 5 per cent selection intensity; (K = 2.06)

$h^2 b$ = Heritability coefficient (Broad sense)

σ_p = Phenotypic standard deviation

Results and Discussion

Experimental findings

In this study, estimates of phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all the traits. The difference in magnitude between phenotypic and genotypic coefficient of variation is an indication of relatively low influence of environment on the phenotypic expression of the trait (Table 1).

Table.1

Trait	Coefficient of variation (%)		Heritability (%)	Genetic component		Degree of dominance (DD)	Genetic advance (GA)	Genetic advance in % of mean (GM%)
	Genotypic	Phenotypic	h2ns	Additive Variance (σA2)	Dominance Variance (σD2)			
Days to 50% ear Emergence	2.51	3.03	@23.13	-0.92	3.59	2.64	4.09	4.27
Days to maturity (75%)	2.07	2.43	57.83	4.23	1.92	0.62	4.61	3.65
Productive tillers/ plant	7.95	10.09	@12.27	-0.04	0.26	1.94	0.72	12.91
Ear length	9.26	10.17	31.54	0.83	1.50	1.02	3.19	17.36
Grains/ Spike	8.30	8.84	19.49	3.70	13.80	1.22	9.02	16.07
Biological yield/ plant	6.44	9.13	@41.79	-1.46	3.40	5.75	2.66	9.36
Grain Yield/ Plant	8.88	11.97	@12.81	-0.08	0.45	2.12	1.20	13.57
Harvest Index (%)	3.68	4.90	22.80	0.41	0.86	1.07	1.79	5.68
1000 Grain Weight	7.46	8.25	6.81	0.40	4.79	1.44	4.70	13.91

Estimates of phenotypic (PCV) and genotypic (GCV) coefficient of variation, heritability and genetic advance in per cent of mean among nine traits in barley

The traits which exhibited moderate estimates (10-20%) of PCV were observed in grain yield/plant, productive tillers/plant while remaining traits recorded low PCV. The high estimates of PCV and GCV were not recorded for any traits. Observations on higher PCV and GCV for these traits are in close agreement with the results of Kumar *et al.,* (2002), Mishra *et al.,* (2007) and Singh *et al.,* (2008) in barley.

The estimates of heritability in narrow sense (h^2_{ns}) have been classified by Robinson (1966) into three categories *viz.,* high (> 30%), medium (10-30%) and low (<10%). 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 genetic advance in per cent of mean provides indication of expected selection response by taking into account the existing genetic variability and heritability of the trait. High estimates of heritability in narrow sense were recorded for two traits *viz.* days to maturity (57.83%) and ear length (31.54%). EI-Hasany *et al.,* (1992), Mladenov (1993), Kumar *et al.,* (2002), Yadav *et al.,* (2004), and Therrien *et al.,* (2006) observed similar findings in their work.

Moderate estimates of heritability in narrow sense (10 to 20 %) were observed for harvest index (22.80%) and grains/spike (19.49%). For days to 50% ear emergence, productive tillers/plant, biological yield/plant and grain yield/plant the h^2_{ns} could not be estimated due to negative value of genetic variance for these traits. 1000-grain weight show low estimates of h^2ns which reflects poor index for improvement through selection. Observations on moderate estimates of heritability for traits in this study are in close agreement with the results of Yadav *et al.,* (2004) and Raikwar *et al.,* (2014).

In the present study, genetic advance in per cent of mean values were classified into low (less than 10%); moderate (10-20%); and high (more than 20%) following Johnson (1955a). High estimates of genetic advance in per cent of mean were not observed for any trait in present study. However, moderate (>10-20%) genetic advance in per cent of mean were observed for biological yield per plant ear length, grains/spike, 1000-grain weight, grain yield/plant and productive tillers/plant. Low heritability (<10%) were observed for biological yield/plant, harvest index, days to 50% ear emergence and days to maturity. The high heritability in narrow sense with high genetic advance in per cent of mean represent the additive gene action and high heritability with low genetic advance in per cent of mean represent non additive gene action and moderate heritability with low genetic advance in per cent of mean represent non additive gene action and low heritability with low genetic advance in per cent of mean represent non additive gene action.

These findings are in congruent with works of Kumar *et al.,* (2002) and for grains per ear by Chauhan *et al.,* (1988), Yadav *et al.,* (2002) and Mishra *et al.,* (2007).

In conclusion the results indicated considerable amount of non-additive gene action in the inheritance of traits. The low estimates of PCV resulted into low estimates of genetic advance in per cent of mean. The traits for which high heritability were recorded can be advanced to exploit genetic gain form it. Similarly, traits which recorded low heritability estimates can be improved imposing a lower selection pressure and advancing more high potential genotypes.

References

Burton, G.W. (1952). Quantitative inheritance in grasses. Proc. Intern Grassland Cong.

1: 277-283.

Chauhan, B.P.S. Tiwari, S.N. and Singh, V. (1988). Studies on variability and coheritability in barley. *Journal of Maharastra Ag. Univ*., 13(1): 50-53.

El-Hasary, A.A. Mahrous, M.A. and Abul-Nass, A.A. (1992). Genetical studies in barley (*Hordeum vulgare* L.) for earliness, some growth attributes and yield. *Egypt. J. Agro.,* 17 (1-2): 15-26.

Johnson, H.W., Robinson, H.F., Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybean. *Agron. J*. 47: 314-318.

Kempthorne, O. and Curnow.R. N. (1961). The partial diallel cross. Biometrics, 17:229-250.

Kumar, S., Prasad, L.C, and Kumar, S. (2002). Variability and correlation studies in barley *Res. Crops* 3(2):432-436.

Falconer, D.S. (1989). Introduction to quantitative genetics (3rd Ed.). Logman Scientific and Technical, Logman.

Mishra, C.N., Singh, S.K., Singh, P.C., Bhardwaj, D.N. and Singh, H.L. (2007). Genetic variability in barley. *Inter. J. Plt. Sci.,* 3(2): 220-221.

Mladenov, N. (1993). Grain yield and quality of some homozygous winter wheat lines selected from crossing between different parental genotypes. Review of Res., Faculty Agriculture Belagrade, 38 (2): 61-70.

Raikwar, R. S., Upadhyay A. K. and Tyagi, P. K. (2014). Heritability and genetic variability for yield components under two regimes of soil in barley (*Hordeum Vulgare* L.). *The Bioscan* 9(4): 1613-1617.

Robinson, H.F. (1966). Quantitative genetics in relation to breeding of the centennial of mendalism. *Indian J Genet*. 26: 171-187.

Singh, S.K., Sirohi, A., Kerkhi, S.A., Singh, D., Kumar, V., Singh, S.P. and Singh, R.P. (2008). Genetic variability and correlation coefficient for grain yield in barley. *Environment and Ecology,* 26 (4C): 2379-2381.

Therrien, M.C. (2006). Estimates of heritability of major malting quality traits in Conidian Barley. *Newsletter*, 36: 10-11

Yadav, V.K., Kendurkar, P.S. and Yadav, P. (2004). Analysis of heritability and genetic association in malting barley. *Plant Archives*, 4(1):129-132.

Zeng, Y. and Chen, L. (2001). Combining ability and heterosis in forage barley. *Indian J. Genet*., 61(9):71-73.