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Short Communication

Genetic variability for yield and yield related traits in barley (*Hordeum vulgare* L.)

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Abstract

The study was carried out during *Rabi* season of 2019-20 at HAREC, Bajaura Farm, to evaluate genetic variability for yield and yield related traits in two hundred ten barley germplasm lines (144 exotic and 66 indigenous) and six standard check varieties [HBL 113 (Vimal), HBL 713 (Him Palam Jau 1), HBL 804 (Him Palam Jau 2), BHS 400 (Pusa Sheetal), BHS 352 (Himadri) and VLB 118 (VL Jau 118)] in Augmented Design. The analysis of variance indicated significant difference among entries (ignoring blocks), checks, varieties and checks v/s varieties for all quantitative characters except peduncle length in case of checks vs. varieties. The mean squares due to blocks were non-significant for most of the characters under study except for peduncle length (cm), plant height (cm) and days to 75% maturity. High values of PCV and GCV (>20%) were observed for grain yield/plant, number of effective tillers/plant, biological yield/plant and number of grains/spike in this set of experimental barley genotypes indicating high response to selection. High heritability coupled with high genetic advance as per cent of mean was observed for number of grains/spike, biological yield/plant and grain yield/plant, indicated their importance for grain yield improvement in barley.

Key words: Barley, PCV, GCV, heritability, genetic advance, selection

Barley (*Hordeum vulgare* L. emend Bowden.), 2n=14, is one of the first domesticated crops and ancient among cereals. Barley is currently the fourth most important cereal of India and the World, both in area and tonnage harvested, after rice, wheat and maize. It is considered as a principal food in regions where other major cereals cannot be grown. It is the main crop of higher elevation under rainfed conditions and of high hill dry temperate zone, generally grown on marginal lands and has several uses for the hilly people- food, feed, fodder and local beverages (Al-Tabbal and Al Fraihat 2012). In Himachal Pradesh, barley is cultivated on about 20 thousand ha area with a production of approximately 34 thousand tonnes having productivity of 17.69 q/ha (Anonymous, 2018-19). Owing to its vast morphological and environmental adaptability, various types of barley (winter, spring, two-rowed, six-rowed, awned, awnless, hooded, covered, naked, malting, feed and food types) are grown throughout the world. Around 55-60 per cent of barley is used for feed, 30-40 per cent for malt, 2-3 per cent for food and 5 per cent for seed (Ullrich 2010). The extent of genetic variability present in the germplasm for various traits is in fact revealed by the genotypic coefficient of variation but it does not provide full scope to assess the variation which is heritable. Heritable variation is very useful for permanent genetic improvement. To choose a suitable breeding programme, it is important to assess the heritable and non heritable components in the total variability observed. The heritable component can be worked out by studying the phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and predicted genetic advance. The most important role of 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. The genotypic coefficient of variation along with heritability estimates provide reliable estimates of the amount of genetic advance to be expected through phenotypic selection. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates.

The experiment was conducted to evaluate two hundred sixteen germplasm lines of barley including six checks under irrigated conditions in Augmented Design (Federer 1956) with ten blocks. Checks were repeated in each block along with 21 test entries. Thus, each block contained 21 test entries with six checks. Each genotype was sown in a 2 metre long single row plot having row to row distance of 23cm. The recommended package of practices was followed to raise a good crop. Phenotypic and Genotypic coefficient of variation (PCV and GCV) for different characters were estimated as suggested by Burton and Devane (1953). Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed as percentage (Falconer, 1981). Genetic advance and genetic advance as per cent of mean was worked out by adopting the formula given by Johnson *et al.* (1955).

The analysis of variance indicated significant differences ($p<0.05$) among entries (ignoring blocks), checks, varieties and checks v/s varieties for all agro-morphological characters except for checks vs. varieties in case of peduncle length (Table1). The results of analysis of variance indicated that mean squares due to genotypes were highly significant for all the characters studied. Verma and Verma (2011) also found significant differences for grain yield, grain weight, days to heading, biological yield, days to maturity, harvest index, tillers per metre and grains per spike. Among various characters studied, biological yield per plant possessed the highest range (Table 2), followed by plant height (cm) and number of grains

Table 1. Analysis of variance of augmented design for eleven characters in barley genotypes

		Mean Squares										
Source of Variation	**d.f.**	**Days to 50% flowering**	**No. of tillers per plant**	**Peduncle length (cm)**	**Spike length (cm)**	**Number of grains per spike**	**Plant height (cm)**	**Days to 75% maturity**	**Biological yield per plant (g)**	**1000-grain weight (g)**	**Grain yield per plant (g)**	**Harvest index (%)**
Block (eliminating Check + Var.)	9	0.06	0.54	10.46	0.96	*25.48	*405.21	*46.20	2.97	2.92	1.26	1.78
Entries (ignoring Blocks)	215	45.29*	3.85*	16.42*	1.51*	175.98*	132.45*	38.42*	207.26*	18.35*	41.48*	7.45*
Checks	5	467.38*	54.66*	210.75*	2.78*	982.02*	462.93*	195.55*	6524.79*	198.63*	798.78*	153.16*
Varieties	209	30.36*	1.64*	11.83*	1.37*	128.80*	119.78*	33.21*	13.42*	13.33*	2.51*	3.97*
Checks vs. Varieties	1	1053.97*	211.04*	4.21	23.58*	6000.41*	1127.74*	340.80*	21019.46*	165.81*	4400.61*	7.85*
Error Variance		0.052	0.40	2.18	0.56	12.74	27.66	6.4	1.50	1.61	0.48	1.42

* Significant at 5 % probability level

Table 2. Mean, range, heritability, coefficient of variation and GA as % mean for 11 characters in barley germplasm

Characters	**Mean ± SE**	**Range**	**Coefficient of Variation (%)**		**Heritability broad sense H^2 bs (%)**	**Genetic Advance (% of mean)**
			PCV	**GCV**		
Days to 50% flowering	120.41± 0.38	103.8-136	4.58	4.57	99.82	9.42
No. of effective tillers per plant	4.48 ±0.09	1.91-11	28.58	24.83	75.48	44.52
Peduncle length(cm)	26.05±0.23	14.33-34.19	13.20	11.92	81.56	22.21
Spike length(cm)	5.88±0.07	3.38-9.94	19.91	15.59	58.75	24.13
No. of grains per Spike	35.89±0.81	15.25-62.62	31.61	30.01	90.10	58.77
Plant height (cm)	76.91±0.76	36.1-116.76	14.22	13.21	86.23	25.31
Days to 75% maturity	173.77±0.41	160.15-186.81	3.31	2.97	80.45	5.50
Biological yield per plant(g)	12.86±0.47	4.52-89.61	28.47	26.83	88.78	52.15
1000-Grain weight(g)	42.98±0.24	36.81-54.81	8.49	7.96	87.85	15.39
Grain yield per Plant(g)	5.05±0.18	1.89-32.30	31.39	28.23	80.86	52.37
Harvest index (%)	39.10±0.15	33.37-46.93	5.09	4.08	64.08	6.73

per spike. This showed that these characters were responsible for wide variation in grain yield of various genotypes. Lodhi *et al*. (2015) also reported similar results for plant height. In order to choose a suitable breeding programme, it is important to assess the heritable and non heritable components in the total variability observed. High values of PCV and GCV (>20%) were observed for grain yield per plant (31.39, 28.23), number of effective tillers per plant (28.58, 24.83), biological yield per plant (28.47, 26.83) and number of grains per spike (31.61, 30.01), whereas moderate estimates (10-20%) of PCV and GCV were observed for peduncle length (13.20, 11.92), spike length (19.91, 15.59) and plant height (14.22, 13.21). Whereas low values (<10%) were observed for test weight (8.49, 7.96), days to maturity (3.31, 2.97), days to 50% flowering (4.58, 4.57) and harvest index (5.09, 4.08). Lodhi *et al*. (2015) also noticed high PCV and GCV for grain yield per plant, number of effective tillers per plant and peduncle length. Samah *et al*. (2018) also observed low GCV and PCV for days to heading and days to maturity. Matin *et al*. (2019) also reported high GCV for number of grains per spike, grain yield per plant, number of effective tillers per plant. The differences between PCV and GCV were relatively very small for all the characters studied except number of effective tillers per plant, spike length and grain yield per plant which showed least environmental influence. Greater difference between PCV and GCV indicated that these traits were more influenced by the growing environment and can be improved by providing optimum growing environment. A perusal of the data presented in Table 2 revealed that the estimates of heritability in broad sense for all the eleven characters studied ranged from 58.75 to 99.82%. High heritability estimates (Above 80%) were observed for days to flowering (99.82%), number of grains per spike (90.10%), biological yield per plant (88.78%), 1000-grain weight (87.85%), plant height (86.23%), peduncle length (81.56%), grain yield per plant (80.86%) and days to maturity (80.45%). Moderate estimates (30%-80%) were obtained for number of effective tillers per plant (75.48%), spike length (58.75%), harvest index (64.08%). The most important role of 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 programme.

The genotypic coefficient of variation along with heritability estimates provide reliable estimates of the amount of genetic advance to be expected through phenotypic selection. High heritability estimates for days to 50% flowering, biological yield per plant, grain yield per plant, number of grains per spike, days to maturity, peduncle length, spike length, plant height, test weight indicate a high scope of selection for these traits. Kumar *et al*. (2018) also reported high heritability for number of grains per spike, biological yield per plant and seed yield per plant. Matin *et al*. (2019) also observed high heritability for 1000-grain weight followed by yield per plant, grain per spike, days to heading and spike length. The characters which have high heritability estimates are of great importance as it permits selection at phenotypic level and there would be greater correspondence between phenotypic worth and breeding values. Adhikari *et al*. (2018) also observed high heritability estimates for days to flowering and days to maturity in rice, therefore suggesting that these traits were under high genetic control. Yadav *et al*. (2018) reported moderate estimates of heritability for harvest index. Moderate heritability estimates might be due to the variation of environment component involved for those traits and vice-versa.

As the conventional breeding approach is mainly based on the phenotypic performance of the genotypes so, estimates of high heritability would be helpful for breeding superior genotypes. However, Prasad *et al*. (1980) reported that heritability value along with genetic advance is a much better approach to select the desirable individuals rather than heritability value alone. Higher values (above 50%) of genetic advance as per cent of mean were observed for number of grains per spike (58.77), grain yield per plant (52.37), and biological yield per plant (52.15) which indicated that these characters can be improved better. Moderate (30%-50%) genetic advance as percentage of mean was found for number of effective tillers per plant (44.52). Low genetic advance as percentage of mean was found for plant height (25.31), spike length (24.13), peduncle length (22.21), test weight (15.39), days to 50% flowering (9.42), harvest index (6.73) and days to maturity (5.50). Malik *et al*. (2018) also reported high genetic advance as per cent of mean for characters like number of grains per spike, biological yield per plant and grain yield per plant and low value of genetic advance for characters such as days to flowering and days to maturity. The estimates of high heritability and high estimated per expected genetic advance show that the character in question has high workable variability and expects the character to be improved to higher scale. Thus, the heritability estimates will be reliable if accompanied by high genetic advance.

Conclusion

The analysis of variance revealed significant difference ($p<0.05$) among entries (ignoring blocks), checks, varieties and checks v/s varieties for all quantitative characters except for checks vs varieties in case of peduncle length. High to moderately high values of PCV and GCV were observed for grain yield/plant, number of effective tillers/plant, biological yield / plant and number of grains/spike in this set of experimental barley genotypes indicating high scope of selection.

Conflict of interest: The authors declare that there is no conflict of interest among the authors in this research paper.

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