

Genetic variability and association study in some hulled and hulless genotypes of barley (*Hordeum vulgare* L.) in north western Himalayan region

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Abstract

The experimental material comprising of 31 genotypes along with four checks of barley were evaluated in Randomized Block Design with three replications over two years during *Rabi*, 2016-17 and *Rabi*, 2017-18. Sufficient genetic variability was observed for all the characters in pooled over environments. High PCV and GCV (>20%) values alongwith high heritability coupled with high genetic advance was recorded for number of grains per spike, biological yield per plant and seed yield per plant which indicated the predominance of additive gene action. Association study showed significant and positive correlation of biological yield per plant, number of grains per spike and number of tillers per plant with seed yield per plant. Path coefficient analysis also exhibited high positive direct and indirect contributions of these traits towards seed yield per plant indicating further selection based on these traits for effective improvement in barley.

Keywords: Barley, variability, correlation, path analysis

1. Introduction

Barley belongs to genus *Hordeum* of Poaceae family and tribe *Triticeae* along with wheat and rye. Barley is the fourth most important cereal crop after wheat, rice and maize in the world with a share of 7 per cent of the global cereal production. Barley can grow in a wide range of environments than any other cereal, including extremes of latitude, longitude and high altitude (Kishore *et al.*, 2016). In India, barley is cultivated on about 677 thousand ha area with production of 1788 thousand tonnes and productivity of 2641 kg/ha (Anonymous, 2018). Barley has considerable economic importance both in agriculture and industry in many countries. 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). In comparison to other cereal crops, barley has a better fodder value including grain and straw. In most of the developed countries, barley straw is used for animal bedding, whereas it is used as animal feed in the developing countries. Even under variable climate within the growing season, barley gives comparably better yield than wheat and other small grain cereals. Being one of the most widely adapted crops, the barley germplasm pool has the potential to contain

enough genetic diversity to breed for adaptation to different environmental conditions. Barley crop yield is directly or indirectly influenced by certain morphological and genetic factors. Identification of genetically superior parents is an important pre-requisite for developing promising strains for effective transfer of targeted genes controlling both quantitative and qualitative traits in the resultant progenies. The present study is an attempt to determine genetic parameters contributing to yield and related traits in barley.

2. Material and methods

The experimental material comprised of 16 hulled and 15 hulless barley genotypes alongwith three hulled barley checks namely HBL 113, BHS 400 and VLB 118 and one hulless barley check, BHS 352. All the genotypes were raised in Randomized Block Design (RBD) with three replications at experimental farm of Hill Agricultural Research and Extension Centre, Bajaura, Kullu, HP during *Rabi* seasons of 2016-2017 and 2017-2018 under rainfed conditions. Each genotype was accommodated in 4 rows of 2 metre length with row to row distance

of 23cm. Data were recorded on ten randomly selected plants for seed yield and yield contributing traits. The data were analysed as per the standard statistical procedures for parameters of genetic variability, correlation and path coefficient in pooled over the environments. The parameters of variability (PCV, GCV, heritability and genetic advance) were calculated following Burton and De Vane (1953) and Johnson *et al.* (1955a). Correlations

at phenotypic, genotypic and environmental levels among all the characters were obtained according to Johnson *et al.* (1955b). The path coefficient analysis was done following Dewey and Lu (1959).

3. Results and discussion

Analysis in pooled over environments (Table 1) showed highly significant values as indicated by presence of

Table 1. Variance and parameters of variability for seed yield and related traits in barley

Traits	Variance	Mean \pm SE(m)	Range	GCV (%)	PCV (%)	h ² bs	GA (%)
Days of flowering	80.53*	123.34 \pm 0.75	115.33-130.00	2.91	3.14	85.91	5.55
Number of tillers/plant	6.72*	5.55 \pm 0.26	4.00-7.33	17.48	20.31	74.08	30.99
Peduncle length (cm)	84.80*	27.83 \pm 0.92	17.33-38.33	12.87	13.97	84.81	24.41
Spike length (cm)	4.86*	8.00 \pm 0.34	6.33-10.33	9.92	12.47	63.32	16.26
Number of grains/spike	992.42*	41.67 \pm 1.32	23.33-64.00	30.71	31.27	96.41	62.11
Plant height (cm)	256.12*	86.24 \pm 2.54	74.67-101.33	6.95	8.57	65.61	11.59
Days of maturity	71.62*	168.48 \pm 0.79	162.33-176.67	1.97	2.13	85.11	3.74
Biological yield/plant (g)	243.20*	26.18 \pm 1.39	16.03-38.40	23.45	25.15	86.96	45.05
Harvest index (%)	121.00*	36.28 \pm 1.21	27.08-42.29	9.98	11.37	77.11	18.05
1000 seed weight (g)	249.50*	43.92 \pm 1.08	34.33-57.67	14.29	15.46	85.5	27.22
Protein content (%)	6.10*	8.77 \pm 0.15	6.43-10.50	11.43	11.78	94.13	22.85
Seed yield/plant (g)	28.13*	9.41 \pm 0.44	5.49-14.44	22.46	24.09	86.96	43.15

*Significant at $P \leq 0.05$; PCV and GCV represent phenotypic and genotypic coefficients of variation, respectively; h²bs: Heritability in broad sense; GA (%): Genetic advance (%) of mean

significant differences among the genotypes for all traits studied. Previous studies on evaluation of barley also indicated that significant variations existed for many of these traits (Singh *et al.*, 2008; Virvand Sultan, 2013; Derbew *et al.*, 2013). Interaction between genotypes and environments in pooled over environments showed significance for all the traits except for 1000-grain weight. Rodriguez *et al.* (2008) also reported significant genotype by environment interactions in barley landraces, recombinant inbred lines and varieties for all the measured traits. The knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is helpful in predicting the amount of variation present in the given genetic stock which in turn helps in formulating an efficient breeding programme. A wide range of variability was observed for all the characters studied (Table 1). The estimates of PCV were higher than corresponding GCV for all the characters studied which indicated that the apparent variation is not only due to genotypes but also due to the influence of environment. High PCV and GCV ($>20\%$) was recorded for number of grains per spike, biological yield per plant and seed yield per plant, whereas high PCV with moderate GCV was exhibited for number of tillers per plant. Similar results were observed in earlier studies (Al-Tabbal and Al-Fraihat, 2012; Sethi *et al.*, 1972;

Jalata *et al.*, 2011; Verma and Verma, 2011; Idris *et al.*, 2012; Kumar and Shekhawat, 2013; Kumar *et al.*, 2013). Moderate estimates (10-20%) of GCV were recorded for number of tillers per plant, 1000-grain weight and protein content, whereas the traits peduncle length, spike length, harvest index, 1000-grain weight and protein content showed moderate PCV values (Derbew *et al.* 2013). Heritability estimates provide information about the index of transmissibility of quantitative characters of economic importance and are essential for an effective crop breeding strategy having desired degree of expected genetic progress. In the present study, high heritability ($>80\%$) was observed for number of grains per spike followed by protein content, biological yield per plant, seed yield per plant, days to 50 per cent flowering, 1000-grain weight, days to maturity and peduncle length. The results are in line with the findings of Nanak *et al.* (2008), Verma and Verma (2011), Kumar *et al.* (2013), Singh *et al.* (2014) and Addisu and Shumet (2015). Moderate heritability (50-80%) was recorded for number of tillers per plant, spike length, plant height and harvest index. Low heritability indicates that a character is highly influenced by environmental factors and genetic improvement through selection will be difficult due to masking effects of the environment on the genotypic effects. For an effective selection programme,

knowledge of estimates of heritability alone is not sufficient and genetic advance if studied along with heritability is more useful. Genetic advance may or may not be in proportion to genetic variability and heritability estimates because both high heritability and high genetic variability are important to obtain higher genetic gain. The high expected genetic advance (>30%) expressed as percent of mean was observed for number of grains per spike followed by biological yield per plant, seed yield per plant and number of tillers per plant. High heritability estimates coupled with high genetic advance were observed for number of grains per spike, biological yield per plant and seed yield per plant. Traits having high heritability and high genetic advance are supposed to be under control of

additive genes; hence, these can be improved by selection based on phenotypic performance. High heritability with moderate genetic advance was observed for peduncle length, 1000-grain weight and protein content which suggested the involvement of non-additive gene action in their inheritance. In the present investigation, genotypic correlation coefficients, in general, were higher than their corresponding phenotypic correlation coefficients for most of the traits indicating that there was an inherent association among the various characters under study and the phenotypic expression of correlations was lessened under the influence of environment (Table 2). Biological yield per plant followed by number of grains per spike and number of tillers per plant exhibited significant and

Table 2. Estimates of correlation coefficients among seed yield and other related traits at phenotypic (P) and genotypic (G) levels

Traits		Days to flowering	Tillers/plant	Peduncle length (cm)	Spike Length (cm)	Grains/spike	Plant height (cm)	Days to maturity	Biological yield/plant (g)	Harvest Index (%)	1000-seed weight (g)	Protein content (%)
Tillers/plant	P	0.411**										
	G	0.481**										
Peduncle length (cm)	P	0.072	-0.117									
	G	0.044	-0.207*									
Spike length (cm)	P	0.163	0.189	0.034								
	G	0.244*	0.384**	0.079								
Grains/spike	P	-0.352**	-0.423**	-0.145	-0.187							
	G	-0.367**	-0.504**	-0.163	-0.257**							
Plant height (cm)	P	0.093	0.076	0.581**	0.416**	-0.244*						
	G	0.106	0.053	0.680**	0.629**	-0.307**						
Days to flowering	P	0.501**	0.366**	-0.204*	0.031	-0.319**	-0.09					
	G	0.636**	0.466**	-0.261**	0.078	-0.356**	-0.141					
Biological yield/plant (g)	P	0.233*	0.564**	-0.212*	0.074	0.247*	-0.012	0.282**				
	G	0.248*	0.557**	-0.271**	0.103	0.256**	-0.060	0.331**				
Harvest index (%)	P	-0.566**	-0.442**	0.051	-0.090	0.507**	-0.033	-0.481**	-0.339**			
	G	-0.662**	-0.577**	0.032	-0.088	0.579**	-0.077	-0.585**	-0.335**			
1000-seed wt. (g)	P	0.077	0.268**	0.243*	0.143	-0.672**	0.357**	0.190	0.060			
	G	0.090	0.356**	0.267**	0.233*	-0.720**	0.462**	0.241*	0.049			
Protein content (%)	P	0.311**	0.039	0.005	0.051	-0.056	0.108	0.281**	0.115	-0.238*	0.033	
	G	0.372**	0.055	0.005	0.075	-0.061	0.128	0.318**	0.144	-0.301**	0.042	
Seed yield/plant (g)	P	-0.033	0.360**	-0.177	0.044	0.525**	-0.025	0.057	0.880**	0.136	-0.080	-0.015
	G	-0.042	0.304**	-0.237*	0.076	0.552**	-0.084	0.069	0.890**	0.123	-0.127	-0.009

** Significant at $P \leq 0.05$

positive association with seed yield per plant at both genotypic and phenotypic levels, whereas peduncle length was negatively correlated with seed yield per plant. Based on correlation studies, it may be concluded that seed yield per plant was significant and positively correlated with biological yield per plant, number of grains per spike and number of tillers per plant and hence, selection through these traits would be effective. The results are in conformity with the findings of Kumar and Prasad (2002), Emine and Necmettin (2012) and Rika *et al.* (2013) and Bedasa *et al.* (2014). Though, the correlation coefficients are quite helpful in determining the components of a

complex trait like seed yield yet, an exact picture of the relative importance of the direct and indirect influences of each component trait is not provided by such studies as these estimates provide nature and magnitude but, not its cause. Path coefficient analysis under such circumstances plays an important role in partitioning the correlation coefficient into direct and indirect effects of a specific causal factor (Dewey and Lu, 1959). The study revealed that the direct effects obtained at genotypic level were markedly different from those at phenotypic level. These differences might be due to varying degree of influence of environment on various traits studied. Path coefficient

analysis (Table 3) revealed that biological yield per plant followed by harvest index, number of grains per spike, 1000-grain weight, spike length, peduncle length, number of tillers per plant, days to 50 per cent flowering and days to maturity exerted positive direct effects on seed yield per plant, whereas negative direct effects were shown by protein content and plant height on seed yield per plant. Biological yield per plant and number of tillers per plant

had maximum indirect contribution towards seed yield per plant for enhancing the magnitude of association for majority of the characters. Therefore, on the basis of present investigation it can be inferred that selection based on biological yield per plant, number of tillers per plant and number of grains/spike in the barley genotypes under study would be rewarding.

Table 3. Estimates of direct and indirect effects of different traits on seed yield at Phenotypic (P) and Genotypic (G) levels

Trait		Days to flowering	Tillers/plant	Peduncle length (cm)	Spike length (cm)	Grains/spike	Plant height (cm)	Days to maturity	Biological yield/plant (g)	Harvest index (%)	1000-grain weight (g)	Protein content (%)
Days to flowering	P	0.012	0.008	0.002	0.004	-0.035	-0.001	0.007	0.232	-0.256	0.003	-0.008
	G	0.030	0.029	0.002	0.006	-0.066	-0.003	0.007	0.235	-0.281	0.008	-0.010
Tillers/plant	P	0.005	0.019	-0.003	0.004	-0.042	-0.001	0.005	0.561	-0.200	0.012	-0.001
	G	0.015	0.060	-0.009	0.010	-0.091	-0.002	0.005	0.528	-0.245	0.034	-0.001
Peduncle length (cm)	P	0.001	-0.002	0.025	0.001	-0.014	-0.007	-0.003	-0.211	0.023	0.011	0.000
	G	0.001	-0.012	0.042	0.002	-0.029	-0.021	-0.003	-0.257	0.014	0.025	0.000
Spike length (cm)	P	0.002	0.004	0.001	0.022	-0.018	-0.005	0.000	0.074	-0.041	0.006	-0.001
	G	0.007	0.023	0.003	0.026	-0.046	-0.019	0.001	0.098	-0.038	0.022	-0.002
Grains/spike	P	-0.004	-0.008	-0.004	-0.004	0.098	0.003	-0.004	0.246	0.229	-0.029	0.001
	G	-0.011	-0.030	-0.007	-0.007	0.180	0.009	-0.004	0.242	0.246	-0.068	0.002
Plant height (cm)	P	0.001	0.001	0.014	0.009	-0.024	-0.012	-0.001	-0.011	-0.015	0.015	-0.003
	G	0.003	0.003	0.029	0.017	-0.055	-0.030	-0.002	-0.057	-0.033	0.044	-0.003
Days to maturity	P	0.006	0.007	-0.005	0.001	-0.031	0.001	0.014	0.281	-0.217	0.008	-0.007
	G	0.019	0.028	-0.011	0.002	-0.064	0.004	0.011	0.314	-0.249	0.023	-0.008
Biological yield/plant (g)	P	0.003	0.011	-0.005	0.002	0.024	0.000	0.004	0.995	-0.153	0.003	-0.003
	G	0.008	0.033	-0.011	0.003	0.046	0.002	0.004	0.947	-0.142	0.005	-0.004
Harvest index (%)	P	-0.007	-0.008	0.001	-0.002	0.050	0.000	-0.007	-0.338	0.452	-0.012	0.006
	G	-0.020	-0.035	0.001	-0.002	0.104	0.002	-0.007	-0.317	0.425	-0.037	0.008
1000-grain wt. (g)	P	0.001	0.005	0.006	0.003	-0.066	-0.004	0.003	0.060	-0.130	0.043	-0.001
	G	0.003	0.021	0.011	0.006	-0.130	-0.014	0.003	0.046	-0.167	0.094	-0.001
Protein content (%)	P	0.004	0.001	0.000	0.001	-0.006	-0.001	0.004	0.114	-0.108	0.001	-0.026
	G	0.011	0.003	0.000	0.002	-0.011	-0.004	0.004	0.136	-0.128	0.004	-0.026

*Significant at $P \leq 0.05$; Residual effect $P = 0.011$; $G = 0.005$; Bold diagonal values denote the direct effects.

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