

Selection criteria parameters for improving seed yield in hulled barley (*Hordeum vulgare* L.) under north-western Himalayan conditions

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Abstract

Knowledge of variability is crucial for predicting how much variation operates in genetic material for formulating an effective breeding plan. The experimental material, consisted of 28 F₁s developed by crossing 8 commercial varieties, germplasm, or local lines as per diallel mating design (excluding reciprocals) and further laid out in randomized block design along with parents with three replications during *rabi* 2019-20 to study genetic variability parameters, correlation and path analysis. Sufficient genetic variability was observed for all the characters studied. Estimates of variability indicated high values of phenotypic coefficient of variation and genotypic coefficient of variation for biological yield per plant and seed yield per plant. High heritability values coupled with high genetic advance were found for 1000 grain weight indicating prevalence of additive gene action, which provides good scope for further improvement by selection. Correlation studies revealed that seed yield per plant had significant and positive association with biological yield, spike length, number of tillers per plant, number of grains per spike, 1000 grain weight, plant height, days to maturity and harvest index. Path analysis indicated that traits such as biological yield per plant, harvest index, 1000 grain weight, number of grains per spike and peduncle length directly or indirectly influenced seed yield and may be selected for further improvement in seed yield of barley. Among all these traits, biological yield per plant and harvest index were found useful selection parameters and can be considered as potential indices for improvement of seed yield in future breeding programmes in barley.

Key words: Variability, correlation, path analysis, indices, biological yield and harvest index

1. Introduction

Barley (*Hordeum vulgare* L.) is a traditional crop of the Himalayan regions cultivated under rainfed conditions. Around 7000 BC, barley is assumed to have evolved from its wild progenitor, *Hordeum spontaneum* (C. Koch) Thell, in the Fertile Crescent region of the Near East

(Gadissa *et al.*, 2021). It is a true diploid (2n=14) species which belongs to the genus *Hordeum* of family *Poaceae* and tribe *Triticeae* (Kumar *et al.*, 2021). It is the fourth most important cereal crop after wheat, rice and sludge in the world with a share of 7 per cent of the global



cereal product (Giraldo *et al.*, 2019). Barley can grow in a wide range of surroundings than any other cereal, including axes of latitude, longitude and high altitude (Kishore *et al.*, 2016). Barley is substantially used as beast feed, mortal food, artificial raw accoutrements for malting and brewing, and as an important component in colourful healthy food fashions (Shaveta *et al.*, 2019). Recent exploration regarding salutary composition in food barley has renewed the interest attesting the health benefits of barley in daily diets (Brockman *et al.*, 2013; Sullivan *et al.*, 2013). Due to its ample environmental and morphological rigidity, colourful types of barley (downtime, spring, two-rowed, six-rowed, awned, awnless, hooded, covered, naked, malting, feed and food types) are grown throughout the world (Kumar *et al.*, 2018). The most essential pre-requisite for planning and prosecution of a resourceful parentage programme is the vacuity of desirable inheritable variability for important characters in the genotypes (Sunil *et al.*, 2017). Genetic variability is a basic requirement for crop improvement as this provides wider scope for selection (Kumar *et al.*, 2013). Studying the inheritable variability among the barley genotypes is pivotal for developing high yielding kinds (Kumar and Shekhawat *et al.*, 2013). Correlation coefficients provide a symmetrical measurement of the degree of association between two variables or characters, help us in understanding the nature and magnitude of association among yield and yield components. Path coefficient measures the influence of one variable upon another and allows the partitioning of correlation coefficient into direct

and indirect effects (Hailu *et al.*, 2016). Therefore, keeping in mind the usefulness of barley as a feed and forage crop, current research aims to determine the genetic parameters that influence barley yield and related traits.

2. Material and Methods

2.1 Experimental material and site

Material for the investigation comprised of 28 F₁ hybrids developed using eight barley genotypes (Table 1) which were crossed as per diallel mating design in all possible cross combinations, excluding reciprocals during *rabi* 2018-19 by hand emasculation and pollination under field conditions. These 28 F₁s and along with their parents were further evaluated in a Randomized Block Design (RBD) with three replications during *rabi* 2019-20 at the experimental farm of the Hill Agricultural Research and Extension Centre (HAREC), Bajaura, Kullu (HP), India. Each entry was raised in two rows of 2m length with row-to-row spacing of 23 cm and plant-to-plant spacing of 10 cm apart, respectively following recommended agronomic cultural practices under rainfed conditions.

2.2 Field Study and Data Evaluation

Observations were recorded in each entry for days to 50% flowering (D50%F), days to maturity (DTM) on plot basis and individual plants sampled in each replication for plant height (PH), number of effective tillers per plant (NOT), number of grains per spike (GPS), spike length (SL), peduncle length (PL), thousand grain weight (1000-GW), biological yield per plant (BY), grain yield per plant (GY) and harvest index (HI).

Table 1: List of hulled barley genotypes along with their pedigree and source

S No.	Genotype	Pedigree	2R/6R	Source
1.	HBL 316 (Gopi)	Mutant of HBL 98	6R	CSKHPKV, Palampur
2.	HBL 713 (Him Palam Jau 1)	HBL 276 × HBL 364	6R	CSKHPKV, Palampur
3.	HBL 804 (Him Palam Jau 2)	DWRUB 74 × HBL 316	6R	CSKHPKV, Palampur
4.	BHS 380 (Pusa Losar)	VIOLETA/MJA/7/ABNB/6/BA/ GAL/FZA-B/5/DG/DCB/PTBAR/3/ RAB/BA*3/4/TRYIGAL	6R	IARI, Regional station Tutikandi, Shimla
5.	BHS 400 (Pusa Sheetal)	34th IBON-9009	6R	IARI, Regional station, Tutikandi, Shimla
6.	VLB 118 (VL Jau 1)	14 th EMBSN-9313	6R	VPKAS, Almora
7.	Local Ropa	Local collection	6R	Village Ropa, Kullu, HP
8.	Losar	Local collection	6R	Village Losar, Lahaul & Spiti, HP



2.3 Statistical analysis

The mean data for each trait observed were analyzed using analysis of variance as per Panse and Sukhatme (1984). Estimates of variability *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2 bs) in broad sense and expected genetic advance (GA) expressed as % of mean resulting from the selection of 5% superior individuals was calculated as per Burton and De Vane (1953) Johnson *et al.*, (1955). The phenotypic and genotypic coefficients of correlation were computed as per Al-Jibouri *et al.*, (1958) and path coefficients of yield and other characters with seed yield following Dewey and Lu (1959).

3. Results and Discussion

3.1 Mean performance and Analysis of variance

The analysis of variance revealed highly significant differences amongst all the entries for all the characters under study (Table 2). Hence, variation in several traits under study revealed the measure of free variability present within the population of different genotypes, which would reflect the unforeseen impact of potential variability on yield. Therefore, these results corroborated with the earlier findings and showed fitting relevance of all the traits under study.

Table 2: Analysis of variance for seed yield and its component traits in barley

S No.	Characters	Replication	Genotypes	Error
	df	2	35	70
1.	D50%F	3.00	32.56*	1.86
2.	DTM	6.03	36.39*	1.94
3.	PH (cm)	32.54	151.93*	25.08
4.	NOT	0.95	2.57*	0.90
5.	GPS	2.94	275.27*	28.91
6.	SL (cm)	0.45	3.36*	0.41
7.	PL (cm)	1.96	27.12*	3.69
8.	1000-GW (g)	31.34	153.11*	6.58
9.	BY (g)	5.50	105.85*	20.68
10.	SY (g)	2.12	29.02*	6.10
11.	HI (%)	26.91	150.0*	34.95

Note: Days to 50% flowering (D50%F), Days to maturity (DTM), Plant height (PH), Number of effective tillers per plant (NOT), number of grains per spike (GPS), spike length (SL), peduncle length (PL), thousand grain weight (1000-GW), biological yield per plant (BY), grain yield per plant (GY) and harvest index (HI).

*Significant at $P \leq 0.05$

3.2 Variability estimates

The estimates of variability for all the traits under study are presented in Table 3. It was observed that the phenotypic coefficient of variability (PCV) was higher than genotypic coefficient of variability (GCV) for all the traits studied indicating that the apparent variation is not only contributed by the entries but also influenced by the environment. Hence, precautions must be taken while exercising selection of traits on the basis of phenotype due to the unpredictable environmental variation (Sharma *et al.*, 2022). Phenotypic coefficient of variability (PCV)

values were found to be high ($>30\%$) for BY (40.39%) and SY (39.15%) while moderate PCV estimates (10-30%) were observed for NOT, GPS, SL, PL, 1000-GW and HI. In comparison, high ($>30\%$) genotypic coefficient of variability (GCV) was observed for only trait i.e. BY (30.72%) whereas moderate GCV estimates (10-30%) were observed for NOT, GPS, SL, PL, 1000-GW, SY and HI. Similar results were observed in earlier studies (Al-Tabbal and Al-Fraihat, 2012; Sethi *et al.*, 1972; Jalata *et al.*, 2011; Kumar and Shekhawat, 2013; Kumar *et al.*, 2013; Kumar *et al.*, 2018; Dinsa *et al.*, 2018; Shiferaw *et al.*, 2020).



Table 3: Genetic parameters of variability for seed yield and related traits in barley

S No.	Characters	Mean \pm SE (m)	Range	PCV (%)	GCV (%)	h ² bs (%)	GA (% of Mean)
1.	D50%F	132.06 \pm 1.39	126.33-137.67	2.63	2.42	84.63	4.59
2.	DTM	173.94 \pm 0.80	165.00-179.33	2.11	1.95	85.54	3.71
3.	PH (cm)	86.49 \pm 2.89	73.93-99.80	9.49	7.52	62.76	12.27
4.	NOT	5.31 \pm 0.55	3-8	22.74	14.01	37.98	17.79
5.	GPS	68.78 \pm 3.10	50-94	15.35	13.20	73.96	23.38
6.	SL (cm)	8.14 \pm 0.37	5.1-10.2	14.56	12.30	71.30	21.39
7.	PL (cm)	27.15 \pm 1.10	20.5-32.33	12.49	10.30	67.94	17.48
8.	1000-GW (g)	39.47 \pm 1.48	21-50	18.89	17.73	88.13	34.30
9.	BY (g)	17.34 \pm 2.63	5.7-32.30	40.39	30.72	57.85	48.14
10.	SY (g)	9.47 \pm 1.43	2.27-16.70	39.15	29.19	55.58	44.83
11.	HI (%)	55.11 \pm 3.41	39.00-66.53	15.54	11.24	52.32	16.74

Note: Days to 50% flowering (D50%F), Days to maturity (DTM), Plant height (PH), Number of effective tillers per plant (NOT), number of grains per spike (GPS), spike length (SL), peduncle length (PL), thousand grain weight (1000-GW), biological yield per plant (BY), grain yield per plant (GY) and harvest index (HI).

Heritability is a measure of the extent of phenotypic variation caused by additive gene action. A perusal of the data (Table 3) revealed that the estimates of heritability in the broad sense for all the 11 characters under study ranged from 37.98 to 88.13 per cent. High heritability estimates (>60%) were observed for D50%F, DTM, PH, GPS, SL, PL and 1000-GW whereas rest of the characters showed moderate heritability estimates. Genetic advance as per cent of mean varied from 3.71 to 48.14 per cent. High genetic advance as percent of mean (>30%) were observed for 1000-GW, BY and SY while moderate genetic advance estimates (10-30%) were observed for PH, NOT, GPS, SL, PL and HI. High heritability coupled with high genetic advance estimates was observed for 1000-GW, whereas high heritability coupled with moderate genetic advance estimates were observed for PH, GPS, SL and PL. Moderate heritability coupled with high genetic advance estimates were found for BY and SY, whereas moderate heritability coupled with moderate genetic advance were recorded for NOT and HI. The results are in line with the findings of Eshghi *et al.*, (2010), Singh (2011), Jalal and Ahemad (2012), Dyulgerova *et al.*, (2014), Singh *et al.*, (2015), Jafar *et al.*, (2016) and Shrimali *et al.*, (2017). Therefore, these estimates suggests election of such traits under selection criteria particularly showing additive gene action which can be further brought under with simple phenotypic selection programmes.

3.3 Correlation analysis

In order to improve complex trait such as SY, it is in the further interest of the breeder to know the nature

and magnitude of associations amongst the component traits contributing to SY. The SY or economic yield, in almost all the crops, is referred to as super character which results from the multiplicative interactions of several component characters that are termed as yield components. Thus, genetic architecture of grain yield in barley as well as in other crops is based on the balance or overall net effect produced by various yield components directly or indirectly by interacting with one another. Therefore, identification of important yield components and information about their association with yield and also with each other is very useful for developing efficient selection criteria for evolving high yielding varieties. Hence, estimates of correlation coefficients both at phenotypic and genotypic level becomes essential. In the present investigation, genotypic correlation coefficients were found 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 the environment (Fig 1). At phenotypic level, SY had significant positive association with DTM, PH, NOT, GPS, SL, 1000-GW, BY and HI whereas none of the traits under study showed significant negative associations with SY.

At genotypic level, DTM, NOT, GPS, SL, 1000-GW, BY and HI showed significant positive association with SY. D50%F was found to be significantly positively associated with DTM, PL and 1000-GW whereas negatively correlated with NOT and GPS. DTM showed significant positive correlation with



PH, NOT, 1000-GW and BY. PH and NOT were found to be significantly positively correlated with SL, PL, 1000-GW and BY while negatively associated with HI. GPS and SL has significant positive association with 1000-GW and BY. PL was positively correlated with 1000-GW and BY whereas negatively correlated with HI. 1000-GW showed positive association with BY. Hence, nature and magnitude of associations between these traits can be realized as important

selection traits for genetic improvement in barley breeding programmes. Earlier Shiferaw *et al.*, (2020) and Matin *et al.*, (2019) also reported that SY had significant and positive association with GPS, 1000-GW, BY and HI. Similar significant positive association with SY has also been reported earlier by Kumar and Prasad (2002), Yadav *et al.*, (2002), Soylu (2006), Verma and Verma (2011), Nasri *et al.*, (2013), Kumar *et al.*, (2018), and Vinesh *et al.*, (2018).

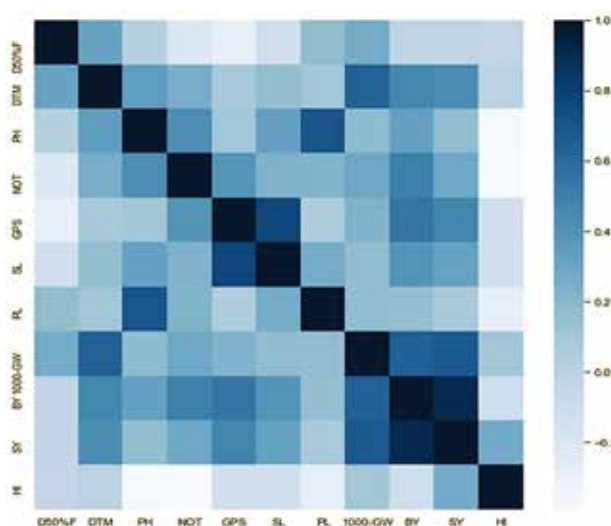


Fig 1: Correlation coefficient heat map among different traits in barley

3.4 Path analysis

To further understand the causal factors for these associations among all the traits under study, direct and indirect effects were computed using path analysis. At both genotypic and phenotypic levels, path analysis revealed that the traits *viz.*, BY followed by HI, 1000-GW, GPS and PL exerted positive direct effects on SY whereas the direct effects of other traits on seed yield/plant were negligible (Table 4). BY and 1000-GW had the maximum indirect contribution towards SY for enhancing the magnitude of association for the majority of the characters. The traits BY and 1000-GW proved to be of high significance, through which all the characters exerted positive indirect effects on SY. Therefore, NOT and PL *via* PH; SL and BY *via* GPS exhibited positive indirect effects on SY. However, negative indirect effects on SY *via* HI were also exerted by D50%F, PH, NOT, GPS, SL, PL and BY. Hence, it was evident from the analysis that the traits BY followed by HI, 1000-GW, GPS and PL directly or indirectly influenced SY and these may be selected for further improvement in SY of barley.

Conclusion

The success of any plant breeding programme depends on the nature and magnitude of correlation between traits as more positively and directly a trait is associated with SY. In this study, analysis of variance revealed significant differences among entries for all the traits suggesting prevalence of wide range of genetic variability. Variability studies indicated higher phenotypic coefficient of variability (PCV) than genotypic coefficient of variability (GCV) for all the traits studied indicating influence of environment. High values of PCV and GCV were observed for BY and SY. High heritability coupled with high genetic advance was observed for 1000-GW. Based on correlation and path analysis, SY showed significant and positive association with DTM, PH, NOT, GPS, SL, 1000-GW, BY and HI could be considered as promising indirect selection indices for yield improvement in barley. Among all these traits, BY and HI emerged to be most important selection indices. Therefore, these traits can be considered while exercising selection in barley for future breeding programme for genetic improvement in barley for seed yield.



Table 4: Estimates of direct and indirect effects of different traits on seed yield/plant at phenotypic (P) and genotypic (G) levels in barley

Characters	D50%F	DTM	PH	NOT	GPS	SL	PL	1000-GW	BY	HI	Correlation with SY
D50%F	P	0.0192	-0.0140	0.0003	0.0040	-0.0052	0.0001	0.0142	0.0318	-0.0200	0.0314
	G	-0.2033	0.0508	-0.0052	0.0977	-0.0534	0.0276	0.0542	-0.547	-0.0023	-0.0548
DTM	P	0.0060	-0.0446	0.0070	-0.0044	0.0020	0.0007	0.0311	0.3823	-0.0055	0.3743*
	G	-0.0645	0.1600	-0.0483	-0.1794	0.0127	-0.0331	0.1353	0.4822	0.0016	0.4883*
PH	P	0.0002	-0.0117	0.0268	-0.0107	0.0045	0.0063	0.0066	0.2688	-0.0968	0.1933*
	G	-0.0090	0.0658	-0.1175	-0.1968	0.0085	0.1183	0.0481	0.3473	-0.0474	0.1523
NOT	P	-0.0029	-0.0075	0.0109	-0.0265	0.0081	0.0016	0.0130	0.4384	-0.0784	0.3563*
	G	0.0463	0.0669	-0.0539	-0.4291	0.0727	0.0389	0.0914	0.05651	-0.0542	0.2988*
GPS	P	-0.0043	-0.0038	0.0051	-0.0090	0.0236	0.0008	0.0115	0.5035	-0.0202	0.5059*
	G	0.0660	0.0124	-0.0061	-0.1895	0.1645	0.0042	0.0534	0.5224	-0.0164	0.4516*
SL	P	-0.0013	-0.0073	0.0097	-0.0052	0.0180	0.0026	0.0098	0.3639	-0.0339	0.3544*
	G	0.0274	0.0259	-0.0374	-0.0948	0.1279	-0.0018	0.0405	0.3910	-0.0164	0.3053*
PL	P	0.0022	-0.0036	0.0183	-0.0045	0.0019	0.0092	0.0084	0.0913	-0.0950	0.0278
	G	-0.0416	0.0212	-0.0843	-0.1012	0.0042	0.1649	0.0400	0.1990	-0.0292	0.1165
1000-GW	P	0.0051	-0.0261	0.0033	-0.0065	0.0051	0.0015	0.0531	0.5294	0.0277	0.5924*
	G	-0.0532	0.1046	-0.0273	-0.1894	0.0425	0.0318	0.2070	0.6716	0.0123	0.7598*
BY	P	0.0006	-0.0182	0.0077	-0.0123	0.0127	0.0009	0.0299	0.9397	-0.0563	0.9040*
	G	0.0118	0.0818	-0.0433	-0.2571	0.0911	0.0348	0.1474	0.9433	-0.0082	0.9169*
HI	P	-0.0010	0.0006	-0.0068	0.0054	-0.0013	-0.0023	0.0039	-0.1385	0.3819	0.2422*
	G	0.0048	0.0027	0.0581	0.2429	-0.0289	-0.0503	0.0266	-0.0806	0.0958	0.3062*

Note: Days to 50% flowering (D50%F), Days to maturity (DTM), Plant height (PH), Number of effective tillers per plant (NOT), number of grains per spike (GPS), spike length (SL), peduncle length (PL), thousand grain weight (1000-GW), biological yield per plant (BY), grain yield per plant (GY) and harvest index (HI).

*Significant at P≤0.05



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Author's contribution: Conceptualization of research (CG and VR); Designing of the experiments (CG and VR); Contribution of experimental materials (VR); Execution of field experiments and data collection (CG, VR and AR); Analysis of data and interpretation (CG, AR and P); Preparation of the manuscript (CG and AR).

Declaration:

The authors declare no conflict of interest.

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