

Genetic Variability and Direct Selection Criterion for Seed Yield in Segregating Generations of Barley (*Hordeum vulgare* L.)

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Abstract

The aim of this study was to determine nature and extent of variability parameters and their utilization in barley breeding programme. A total of 45 F₁s along with their parents and F₂ populations were evaluated in a randomized block design with 3 replications during *Rabi* (winter season) 2014. The various traits measured were days to 50% flowering, days to maturity, plant height, flag leaf area, upper leaf area, tillers-plant, spikes-plant, spike length, grains-spike, spike weight, grain weight-spike, spike harvest index, 1000 grain weight, biological yield-plant, grain yield-plant (g), harvest index, grain size, husk content and protein content. Results showed that significant variation was observed for all the traits studied in the entire gene pool. The degree of genotypic and phenotypic coefficient of variation was high for tillers-plant, spike-plant, grain yield-plant, flag leaf area, harvest index, 1000 grain weight, grain weight-spike, upper leaf area and husk content. High heritability coupled with high genetic advance was recorded for tillers-plant, spikes-plant, grain yield-plant, flag leaf area, harvest index, grain weight-spike, upper leaf area, husk content, grain size and plant height suggesting that these traits are highly heritable and governed by additive gene action. Moderate heritability coupled with high genetic advance was observed for 1000 grain weight, biological yield-plant, spike length, protein content, grains-spike and spike weight; however, days to 50% flowering and days to maturity had moderate heritability coupled with low genetic advance suggesting preponderance on non-additive gene action in the inheritance of these traits. It could be concluded that the traits of tillers-plant, spikes-plant, grain yield-plant, flag leaf area, harvest index, grain weight-spike, upper leaf area, husk content, grain size and plant height were identified as most decisive factor intended towards developing high yielding barley cultivars.

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Keywords

Barley, Genetic Variability, Heritability, Genetic Advance

1. Introduction

Barley (*Hordeum vulgare* L.), is a major cereal grain commonly used in malting and brewing industries. The cultivated barley is a self-pollinating, diploid species $2n = 2x = 14$ [1] and one of the first domesticated crops [2]. Barley is a renowned crop extensively grown under varying agro-climatic regions for food, feed and forage. It has superior nutritional qualities due to presence of beta-glucan (anti-cholesterol substance), acetylcholine carbohydrate substance which nourishes our nervous system and recovers memory loss, easy digestibility due to low gluten content and high lysine, thiamin and riboflavin render cooling effect in the body [3] [4]. Barley is a relatively drought tolerant crop and more tolerant of soil salinity than wheat. About 25% of the barley is used for malting, for which it is the best-suited grain. It is a key ingredient in beer and whisky production. Malting barley is usually lower protein which shows more uniform germination, needs shorter steeping, and has less protein in the extract that can make beer cloudy [5].

The plant breeders now have recognized the importance of utilizing genetic variability and diversity in breeding programmes to meet the continuously expanding needs of hybrid and varietal improvement. Although the assemblage, evolution and preservation of the entire germplasm are essential to more rewarding breeding efforts, a selection of most potential lines on biometrical analysis and on genetic-diversity is very essential for the success of breeding programmes and also for increasing the agricultural productivity.

Seed yield is very complex character whose manifestation results from multiplicative interactions of several quantitative traits and environmental factors [6]. The systematic breeding programme involves the steps like creating genetic variability practicing selection and utilization of selected genotypes to evolve promising varieties. Genetic improvement of crop is largely depending on the magnitude of genetic variability and the extent to which desirable traits are heritable. Considerably high magnitude of variability and high degree of transmission of the various yields and its associated traits have been repeatedly emphasized in barley germplasm [4] [7]-[21]. It is necessary to find out the relative magnitude of additive and non-additive genetic variances, heritability and genetic gain with regard to the characters of concern to the breeder. A major factor limiting the rate of progress in plant breeding has low heritability of quantitative traits such as yield. The most important function of the heritability in the genetic study is the predictive role to indicate the reliability of the phenotypic values as a guide to breeding value. Keeping in view, the present study has been undertaken to estimate genetic variability parameters which will play an important role in exploiting future research projections of barley improvement programme.

2. Materials and Methods

2.1. Plant Material and Experimental Detail

A total of 45 F_1 s were synthesized in half diallel mating system involving ten barley genotypes (Table 1) and sufficient numbers of hand pollinated seeds were produced during winter season of 2012. Further, all the F_1 s were grown to raise F_2 seeds. The experimental material comprised with 45 F_1 s along with their F_2 populations and parents were evaluated in a randomized block design with 3 replications at Instructional farm of JNKVV, Rewa, India during winter season of 2014. The F_1 s was grown in single row, parents in two rows and F_2 populations in five rows of 3 m long bed with spacing of 25 cm between the rows. An approximate distance of 10 cm was maintained between plant to plant by hand thinning. The recommended agronomic practices were done timely to raise good crop stand.

2.2. Traits Measurement

The morphological data recorded on 10 randomly competitive plants from the middle row *viz.*, days to 50% flowering, days to maturity, plant height (cm), flag leaf area (cm²), upper leaf area (cm²), tillers^{-plant}, spikes^{-plant}, spike length (cm), grains^{-spike}, spike weight (g), grain weight^{-spike} (g), spike harvest index, 1000 grain weight (g),

Table 1. List of genotypes, parentage and their origin.

S. No.	Variety	Parentage	Source/origin
1	K508	K394/K141	C.S.A.U. & T., KANPUR, U.P., India
2	JB 203	JB58XRD2552	J.N.K.V.V., REWA, M.P., India
3	RD2811	RD2579/JB26/RD2552	SKRAU, Durgapura, Rajasthan, India
4	RD2869	RD2670/RD2508/RD2715	C.S.A.U. & T., KANPUR, U.P., India
5	HUB113	KARAN280/C138	B.H.U., VARANASI, U.P., India
6	JB1	LAKHANXPL552	J.N.K.V.V., REWA, M.P., India
7	RD2035	RD103/PL101	C.S.A.U. & T., KANPUR, U.P., India
8	KB1201	K560/K475	C.S.A.U. & T., KANPUR, U.P., India
9	LAKHAN	K12/IB226	C.S.A.U. & T., KANPUR, U.P., India
10	JYOTI	K12/C251	C.S.A.U. & T., KANPUR, U.P., India

biological yield^{-plant} (g), grain yield^{-plant} (g), harvest index, grain size (mm²), husk content (%) and protein content (%).

2.3. Statistical Analysis

Data scored over morphological traits were subjected to statistical analyses for understanding the transmissibility of characters. The mean values were used to obtain analysis of variance as per methodology advocated by [22]. PCV and GCV were calculated by the formula given by [23], heritability in broad sense (h^2) by [24] and genetic advance were calculated by using the procedure given by [25].

3. Results and Discussion

3.1. Analysis of Variance (ANOVA)

The analysis of variance (**Table 2**) revealed highly significant difference for all the characters under study among the genotypes, indicating that the parents included in this investigation exhibit sufficient variability for the entire characters study. In the material under study maximum range of variability (**Table 3**) was observed for plant height (60.6 to 124.1 cm), flag leaf area (12.1 to 47.1 cm²), upper leaf area (24.5 to 79.5 cm²), grains^{-spike} (36.6 to 73.3), 1000 grain weight (22.7 to 81.3 g), biological yield^{-plant} (47.08 to 104.8 g), harvest index (3.9% to 63.6%), grain size (8.1 to 65.7 mm²), spike harvest index (51.1% to 95.3%) and days to 50% flowering (66.8 to 83.3 days). The characters showing high range of variation have more scope for improvement. All the characters under study exhibited high variability as evident from the ranges of mean values. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes. These findings are in consonance with the findings of earlier workers [4] [7]-[21].

3.2. Genotypic and Phenotypic Coefficients of Variation

Determination of genetic variability and partitioning it into heritable and non-heritable components using the genetic parameters *viz.*, phenotypic and genotypic coefficients of variation, heritability and genetic advance is necessary to have an insight into genetic nature of yield and its components on which selection can be effectively carried out. Character like seed yield is complex in inheritance and is improved through its component traits. High yield can be achieved by selection of those yield contributing characters that have high heritability coupled with high genetic advance. Consequently, the components of variance and heritable components with genetic parameters are important to plan a suitable breeding strategy.

The estimates of phenotypic variability cannot differentiate between the effects of genotype and environment. Hence, the study of genetic variability is effective in partitioning out the real genetic differences. The estimates of GCV and PCV are of greater use in determining the variability present in the material. Generally, the magnitude

Table 2. Analysis of variance (ANOVA) for various traits in barley.

S.N.	Character	Replication	Genotypes	Error
		(df = 02)	(df = 54)	(df = 108)
1	Days to 50% flowering	0.5	35.65**	5.87
2	Days to maturity	8.22	47.42**	7.98
3	Plant height cm	15.26	635.48**	37.25
4	Flag leaf area (cm ²)	0.44	237.74**	12.74
5	Upper leaf area(cm ²)	43.79	531.49**	52.58
6	Tillers/ plant	0.1	236.44**	4.46
7	Spikes/plant	3.68	146.77**	5.56
8	Spike length (cm)	4.09	35.21**	3.61
9	Grains/spike	16.21	213.60**	33.01
10	Spike weight (g)	0.19	1.29**	0.38
11	Grain weight/ spike (g)	0.14	0.99**	0.07
12	Spike harvest index	91.07	371.28**	109.33
13	1000 grain weight (g)	13.02	413.51**	51.81
14	Biological yield/ plant (g)	167.64	502.43**	76.3
15	Grain yield/ plant (g)	27.09	422.32**	29.23
16	harvest index	49.95	428.96**	36.72
17	Grain size(mm ²)	15.18	70.21**	6.21
18	Husk content (%)	0.78	11.92**	0.53
19	Protein content (%)	0.28	6.76**	0.91

*, ** Significant at 5% and 1% probability levels, respectively, d.f. = degree of freedom.

Table 3. Genetic variability parameters for different characters in barley.

S.N.	Character	Mean	SE	Range		GCV	PCV	h ² (BS)	GA
				Lowest	Highest				
1	Days to 50% flowering	75.5	1.4	66.8	83.3	4.17	5.26	62.8	6.8
2	Days to maturity	110.3	1.6	101.7	118.3	3.29	4.17	62.3	5.3
3	Plant height cm	95.8	3.5	60.6	124.2	14.74	16.06	84.3	27.9
4	Flag leaf area (cm ²)	28.2	2.1	12.1	47.1	30.72	33.22	85.5	58.5
5	Upper leaf area (cm ²)	54.3	4.2	24.6	79.5	23.26	26.82	75.2	41.6
6	Tillers/ plant	18.7	1.2	5.5	40.7	47.13	48.47	94.6	94.4
7	Spikes/plant	16.8	1.4	7.7	33	40.94	43.29	89.4	79.8
8	Spike length (cm)	19.9	1.1	12	25	16.32	18.91	74.5	29
9	Grains/spike	51.9	3.3	36.7	73.3	14.94	18.59	64.6	24.7
10	Spike weight (g)	3.3	0.4	1.6	4.9	16.73	24.96	44.9	23.1
11	Grain weight/spike (g)	2.3	0.2	1	3.4	23.63	26.31	80.6	43.7
12	Spike harvest index	71.9	6	51.1	95.3	13	19.51	44.4	17.8
13	1000 grain weight (g)	45.6	4.2	22.7	61.3	24.08	28.79	69.9	41.5
14	Biological yield/plant (g)	66.7	5	47.8	104.8	17.87	22.15	65.1	29.7
15	Grain yield/plant (g)	30.5	3.1	9.9	63.6	37.53	41.5	81.8	69.9
16	harvest index	45.1	3.5	8.1	65.7	25.34	28.68	78.1	46.1
17	Grain size (mm ²)	26.6	1.4	17.6	36.1	17.38	19.75	77.5	31.5
18	Husk content (%)	9.3	0.4	6.4	14	20.88	22.3	87.7	40.3
19	Protein content (%)	8.5	0.6	66.8	83.3	16.52	20.01	68.1	28.1

*SE = Standard error, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, h² (BS) = Broad sense heritability, GA = Genetic advance.

of phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the characters (**Table 3**) indicating that the apparent variation was not only due to genotype but also due to the favorable influence of environment and selection for these traits sometimes may be misleading. This environmental effect could be due to heterogeneity in soil fertility status and other unpredictable factors.

High degree of genotypic and phenotypic coefficient of variation (>20%) were observed in case of tillers^{-plant} (47.13%, 48.47%) followed by spike^{-plant} (40.94%, 43.29%), grain yield^{-plant} (37.53%, 41.5%), flag leaf area (30.72%, 33.22%), harvest index (25.35%, 28.68%), 1000 grain weight (24.08%, 28.79%), grain weight^{-spike} (23.63%, 26.31%), upper leaf area (23.26%, 26.82%), husk content (20.88%, 22.3%) while; biological yield^{-plant} (17.87%, 22.15%), spike weight (16.73%, 24.96%) and protein content (16.52%, 20.01%) had moderate GCV with high PCV suggesting that sufficient variability was present in the gene pool thus ample scope for genetic improvement through selection with these traits.

The moderate estimates (>10% to <20%) were recorded for spike length (16.32%, 18.91%), grains^{-spike} (14.94%, 18.59%), plant height (14.74%, 16.06%) and spike harvest index (13.00%, 19.51%). However, the low estimates of GCV and PCV were observed for days to 50% flowering (4.17%, 5.26%) and days to maturity (3.29%, 4.17%). The character possessing high genotypic coefficient of variation value has better scope of improvement through selection. The influence of environment on each trade could be determined on the basis of difference between phenotypic coefficient of variation and genotypic coefficient of variation. These findings were in close agreement with the findings of earlier workers [4] [11]-[21].

3.3. Heritability and Genetic Advance

These values alone are not helpful in determining the heritable portion of variation [26]. The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability [27]. In this context, the high estimates of heritability (>75%) was recorded by spike^{-plant} (94.5%) followed by spike length (89.4%), husk content (87.7%), flag leaf area (85.4%), plant height (84.26%), grain yield^{-plant} (81.7%), grain weight^{-spike} (80.6%), harvest index (78.1%), grain size (77.5%) and upper leaf area (75.2%). however spike length (74.5%), 1000 grain weight (69.9%), protein content (68.2%), biological yield^{-plant} (65.1%), grains^{-spike} (64.6%), days to 50% flowering (62.8%), days to maturity (62.3%), spike weight (44.9%) and spike harvest index (44.4%) had moderate estimates. The characters with exhibited high heritability, suggested that the selection will be more effective. According to [28] such characters governed predominantly by additive gene action and could be improved through individual plant selection; whereas, low heritability indicated that the characters were highly influenced by environmental effect and genetic improvement through selection will be difficult due to effect of genotypes.

The genetic advance shows the improvement that can be made in a particular character by applying certain amount of selection intensity. The genotypic coefficient of variation x selection differential estimates the maximum effectiveness of selection and heritability indicates how closely the goal can be achieved. However, by increasing the genetic diversity, the expected genetic advance can still be increased. The character exhibiting high heritability may not necessarily to always give high genetic advance [25]. The highest value of genetic advance was shown by tillers^{-plant} (94.4%), while days to maturity (5.30%) had lowest value for this parameter. The characters exhibiting high estimates of genetic advance (>20%) were spike^{-plant} (79.8%), grain yield-plant (69.9%), flag leaf area (58.5%), harvest index (46.1%), grain weight^{-spike} (43.7%), upper leaf area (41.6%), 1000 grain weight (41.5%), husk content (40.3%), grain size (31.5%), biological yield-plant (29.7%), spike length (29.0%), protein content (28.1%), plant height (27.9%), grains-spike (24.7%) and spike weight (23.1%). The moderate estimate observed for spike harvest index (17.8%) however, days to 50% flowering (6.8%) and days to maturity (5.3%) had low genetic advance.

It can be find out with greater degree of accuracy when heritability in conjunction with genetic advance is studied [29]. Thus a character possessing high heritability along with high genetic advance will be valuable in the selection programme. High heritability coupled with high genetic advance were recorded for tillers^{-plant}, spikes^{-plant}, grain yield^{-plant}, flag leaf area, harvest index, grain weight^{-spike}, upper leaf area, husk content, grain size and plant height; suggesting preponderance of additive gene action in the expression of these characters. Therefore, selection may be effective through these characters in segregating generations for genetic improvement of barley.

Moderate heritability coupled with high genetic advance was observed for 1000 grain weight, biological

yield^{-plant}, spike length, protein content, grains-spike and spike weight; while, spike harvest index had moderate estimates of both. However, days to 50% flowering and days to maturity had moderate heritability coupled with low genetic advance suggesting preponderance on non-additive gene action in the inheritance of these traits; hence in this case selection may not be effective. Most of the above results in respect to heritability and genetic advance are in agreement with earlier reports [4] [10]-[14] [16]-[20].

4. Conclusion

Barley is a renowned crop extensively grown under varying agro-climatic regions for food, feed and forage. Genetic improvement of any crop is largely depending on the magnitude of genetic variability and the extent to which desirable traits are heritable. In our study considerable variability was present in the entire gene pool. The degree of genotypic and phenotypic coefficient of variation was high for tillers^{-plant}, spike^{-plant}, grain yield^{-plant}, flag leaf area, harvest index, 1000 grain weight, grain weight^{-spike}, upper leaf area and husk content. High heritability coupled with high genetic advance was recorded for tillers^{-plant}, spikes^{-plant}, grain yield^{-plant}, flag leaf area, harvest index, grain weight^{-spike}, upper leaf area, husk content, grain size and plant height suggesting that these traits are highly heritable and governed by additive gene action. The traits of viz., tillers^{-plant}, spikes^{-plant}, grain yield^{-plant}, flag leaf area, harvest index, grain weight^{-spike}, upper leaf area, husk content, grain size and plant height were identified as most important direct selection criterion intended at developing high yielding barley genotypes.

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