

ASSESSMENT OF GENETIC VARIABILITY FOR METRIC TRAITS IN BARLEY UNDER DIFFERENT SOWING CONDITIONS

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SUMMARY

Fifty diverse genotypes of barley (*Hordeum vulgare* L.) were grown in the two environments with three replications during *Rabi* 2016-17 at Barley Research Area of Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar (India). The objective of investigation was to study the genetic variability for ten metric traits *i.e.* days to heading, days to maturity, plant height (cm), spike length (cm), number of tillers per meter row, number of grains per spike, 1000 grain weight (g), grain yield (kg/plot), biological yield (kg/plot) and harvest index (%). Genotypes significantly differed for all the traits under both the environments indicating enough variability in the experimental material. The mean performance of genotypes under timely sown for most all characters was higher than under late sown condition. The results under investigation also revealed wide range for all the traits under both the environments. Among all the traits under both the conditions, number of grains per spike had highest phenotypic and genotypic coefficient of variation followed by grain yield per plot. Moderate to high heritability in broad sense observed under timely sown for all the traits except of plant height, harvest index and number of tillers per meter which exhibited low heritability. However, under late sown conditions, all the traits showed moderate to high heritability except plant height. Highest genetic advance as per cent of mean was recorded for number of grains per spike followed by grain yield under both environments. Moderate to high heritability coupled with high genetic advance under timely sown was observed for number of grains per spike, grain yield, 1000-grain weight, biological yield and spike length likewise, for number of grains per spike, grain yield, number of tiller per meter, biological yield and 1000 grain weight under late sown indicating the importance of these traits in selection and crop improvement.

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

Globally the major utilization of barley is for feed and malting purposes, because of its nutritional value barley is also consumed as a staple food in North and Sub-Saharan Africa (SSA), Central Asia, and South-West Asia. In terms of total production, barley ranks fourth in the world among cereals after wheat, maize, and rice. In India, 1.73 million tonnes barley was produced during the crop season 2018-19 from an area of 0.66 million hectare with an average productivity of 26.17 q/ha. Haryana state achieved a production level of 57,990 tons on 18,100 hectares. The average crop productivity in barley is highest in Punjab (3800 kg/ha) followed by Haryana (3204 kg/ha), Rajasthan (2950 kg/ha) and Uttar Pradesh (2801 kg/ha) (Anonymous, 2019).

The most essential pre-requisite for planning and execution of a resourceful breeding programme is the availability of desirable genetic variability for

important characters in the genotypes (Sunil *et al.*, 2017). Possibility of achieving improvement in any crop species mainly depends on the magnitude of genetic variability. The phenotypic variability expressed by the genotypes in any species can be partitioned into genotypic and environmental components. The genotypic component being the heritable portion of the total variability, it's magnitude on yield and its component traits influence the selection strategies to be adopted by the plant breeders. The total variability present in the population is not only due to genotypes but it includes environment also. Only the heritable portion of total variance is transferred to the future generation which is known as heritability. Therefore study of heritability directly helps in selection of elite genotypes from homozygous lines and predicting the gain under selection. The present variability in a population can be characterized by genetic parameters

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such as coefficients of variation, heritability and genetic advance to serve as criteria for selection of desirable genotypes than existing ones. Assessment of magnitude of genetic variability within a crop is fundamental for its breeding programme and the conservation of genetic resources, which is particularly useful as a general guide in the choice of parents for developing hybrids. Therefore the present study was undertaken with the objective to investigate the presence of genetic variability for various metric traits in barley.

MATERIALS AND METHODS

The experiment was conducted at Barley Research Area of Department of Genetics & Plant Breeding, CCS Haryana Agricultural University, Hisar during *rabi* 2016-17 under irrigated conditions. The experimental location is situated at latitude of 29°10'N, longitude of 75°46'E and altitude of 215.2 m above sea level in subtropical region of North Western Plain Zone of India.

The experimental material was consisted of 50 barley genotypes (Table 1) comprising 33 six and 17 two rowed types. Each genotype was grown in randomized block design (RBD) with three replications under timely and late sown conditions having a plot size of 3.0 m × 0.69 m. Under timely sown condition, the experiment was planted on 15 November, 2016 and on 14 December, 2016 under late sown condition.

Observations were recorded for 10 metric traits *viz.*, days to heading, days to maturity, plant height (cm), spike length (cm), number of tillers per meter row, number of grains per spike, 1000 grain weight (g), biological yield (kg/plot), grain yield (kg/plot) and harvest index (%). Five randomly selected competitive plants were recorded in each replication for all the traits under study except of days to heading, days to maturity, biological yield and grain yield which were recorded on plot basis. Further, the value of harvest index was calculated as per the formula given by Donald and Humblin (1976).

The mean performance of individual genotypes was recorded and employed for statistical analysis. Analysis of variance to test the significance for each character was carried out as per methodology advocated by Fisher (1925) and described by Panse and Sukhatme (1967). Phenotypic Coefficient of Variability (PCV) and Genotypic Coefficient of Variability (GCV) were calculated by the formula given by Burton (1952), heritability in broad sense (h^2) was calculated by using the formula suggested by Hanson *et al.* (1956) and genetic advance that is the

expected genetic gain was calculated by using the procedure given by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The details of the genotypes used in the study are provided in Table 1 which indicates the appropriate representation of 2-row (17) and 6-row (33) types. The analysis of variances revealed significant differences among the genotypes for all the characters studied indicating presence of sufficient genetic variability among the genotypes under timely (Table 1) as well as late sown (Table 2) conditions. The estimates of genetic variability parameters for all the characters are presented in Table 4 & 5. It is apparent from the results that mean performance of genotypes for almost all characters under timely sown condition were higher than under late sown condition except for number of grains per spike, suggesting the cultivation of crop under normal sown condition. In general, the results under investigation revealed wide range for all the traits under both the environments.

The estimates of phenotypic coefficients of variation (PCV) were greater than genotypic coefficients of variation (GCV) for all the characters under study in both timely as well as under late sown conditions which reflect the influence of environment on the expression of traits. Similar findings were also cited by Jalata *et al.* (2011). Among all the traits under both the conditions, number of grains per spike had highest phenotypic and genotypic coefficient of variation followed by grain yield per plot. Phenotypic and genotypic coefficients of variation were recorded moderate to high for number of tillers per meter row, biological yield and harvest index under timely sown condition, whereas under late sown condition, 1000 grain weight, biological yield, harvest index and number of tillers per meter row showed moderate to high PCV and GCV indicating availability of sufficient genetic variability and thus exhibited scope for genetic improvement through selection. However, days to heading, maturity and plant height revealed least phenotypic and genotypic coefficients of variation. Similar results were also substantiated by Jalata *et al.* (2011), Singh *et al.* (2015a) and Yadav *et al.* (2015) for number of grains per spike and grain yield and Chand *et al.* (2008) for biological yield.

The estimates of heritability as depicted in Table 3 ranged from 44.13 per cent for plant height to 92.45 per cent for number of grains per spike under timely sown while under late sown from 56.75 per cent for plant height to 97.19 per cent for days to heading. For timely sown, moderate to high heritability

TABLE 1
Detail of barley genotypes used in the study

S. No.	Name of Genotypes	Row Type	S. No.	Name of Genotypes	Row Type
1.	IBYT-HI-19	6	26.	DWRB 101	2
2.	IBYT-HI-13	6	27.	MGL 105	6
3.	IBYT-HI-17	2	28.	MGL-117	6
4.	IBYT-HI-16	6	29.	IBON-HI-1 (2015-16)	6
5.	IBYT-HI-18	6	30.	IBON-HI-3 (2015-16)	2
6.	IBYT-HI-23	2	31.	IBON-HI-13 (2015-16)	6
7.	IBYT-HI-15	6	32.	IBON-HI-37 (2015-16)	6
8.	IBYT-HI-20	6	33.	IBON-HI-67 (2015-16)	6
9.	BH 959	6	34.	BH 902	6
10.	DWR 123	2	35.	2nd GSBSN-15-8	6
11.	DWR 137	6	36.	INBON-15-16	6
12.	MBGSN 145	2	37.	INBON-15-22	6
13.	RD 2904	2	38.	2nd GSBSN-15-35	2
14.	RD 2909	6	39.	AZAD	6
15.	UPB 1059	6	40.	DWRB 143	2
16.	HUB 242	6	41.	BH 13-20	2
17.	2nd GSBSN-28 (2015)	6	42.	BH 13-22	6
18.	2nd GSBYT-23 (2015)	6	43.	BH 13-26	2
19.	K 560	6	44.	BH 14-25	2
20.	JB 481	6	45.	BH 14-42	6
21.	2nd GSBSN-60 (2015)	6	46.	BH 15-17	2
22.	2nd GSBYT-02 (2015)	2	47.	BH 15-30	6
23.	MGL-58	6	48.	BH 946	6
24.	MGL-62	2	49.	BH 885	2
25.	MGL-64	6	50.	DWRUB 52	2

TABLE 2
Estimates of genetic variability in barley under timely sown condition

S. No.	Characters	Mean±S. E. (d)	Range	Coefficient of variation (%)		Heritability (bs) (%)	Genetic advance (% mean)
				PCV	GCV		
1.	Days to heading	84.20±1.16	77.0-98.0	5.60	5.34	90.92	10.48
2.	Days to maturity	125.30± 0.87	119.0-133.0	2.93	2.81	91.59	5.54
3.	Plant height (cm)	92.42±6.22	45.0-126.0	10.93	7.18	44.13	9.72
4.	Spike length (cm)	8.01±0.56	5.07-12.77	15.46	12.82	68.77	21.91
5.	No. of tillers/meter	112.14±10.33	72.0-172.0	17.58	13.48	58.83	21.31
6.	No. of grains/spike	49.66±3.99	20.0-82.0	35.80	34.42	92.45	68.19
7.	1000 grain weight (g)	40.15±1.41	25.40-58.20	15.26	14.63	92.00	28.92
8.	Biological yield/plot (g)	2098.33±180.35	1150.0-3150.0	18.06	14.66	65.92	24.53
9.	Grain yield/plot (g)	564.33±61.09	200.0-950.0	24.21	20.25	70.00	34.92
10.	Harvest index (%)	27.11±2.86	16.36-40.86	19.22	14.24	54.86	21.73

in broad sense estimated for all the traits except plant height, harvest index and number of tillers per meter which exhibited low heritability. All the traits under late sown except of plant height showed moderate to high heritability. High heritability for different characters under investigation indicated that these characters were less influenced by the environment. Singh *et al.* (2006) also reported similar findings for number of grains per spike, 1000 grain weight and grain yield. High heritability for days to heading and maturity in barley was also cited by Kumar *et al.* (2013).

Under both the environments, highest genetic advance as per cent of mean was recorded for number of grains per spike followed by grain yield, however, days to maturity and plant height exhibited lowest genetic advance. The estimates of heritability are more advantageous when expressed in terms of genetic advance. Moderate to high heritability coupled with high genetic advance under timely sown was observed for number of grains per spike, grain yield, 1000-grain weight, biological yield and spike length likewise, for number of grains per spike, grain yield, number of tillers per meter, biological yield and 1000 grain weight

TABLE 3
Estimates of genetic variability in barley under late sown condition

S. No.	Characters	Mean±S. E. (d)	Range	Coefficient of variation (%)		Heritability (bs) (%)	Genetic advance (% mean)
				PCV	GCV		
1.	Days to heading	81.54±0.88	70.0-97.0	7.89	7.78	97.19	15.80
2.	Days to maturity	114.90±0.79	110.0-123.0	2.36	2.20	87.08	4.23
3.	Plant height (cm)	87.81±5.66	60.0-124.0	12.21	9.04	56.75	14.04
4.	Spike length (cm)	8.01±0.49	5.33-12.00	13.75	11.46	69.50	19.69
5.	No. of tillers/meter	93.64±10.76	46.0-158.0	24.24	19.74	66.33	33.13
6.	No. of grains/spike	54.98±3.39	23.0-92.0	35.11	34.29	95.35	68.98
7.	1000 grain weight (g)	32.75±1.50	20.20-47.50	17.61	16.69	89.83	32.58
8.	Biological yield/plot (g)	1668.33±149.00	900.0-2700.0	21.58	18.60	74.32	33.04
9.	Grain yield/plot (g)	368.06±41.29	150.0-800.0	31.64	28.51	81.15	52.90
10.	Harvest index (%)	22.20±2.67	11.25-33.36	23.63	18.48	61.15	29.77

under late sown indicating the importance of these traits in selection and crop improvement. High genetic advance for number of grains per spike and grain yield had also been observed by Yadav *et al.* (2015); for biological yield and 1000 grain weight by Kumar *et al.* (2013). High heritability along with high genetic advance indicates that there are additive genetic effects and simple selection may be effective for improvement of these characters. However, it is always not necessary that a trait has high heritability to be associated with high genetic advance. High heritability coupled with high genetic advance as per cent of mean was also recorded by Mishra *et al.* (2008) for grains per spike and biological yield per plant which indicated the prevalence of additive gene action in the expression of this trait. Similar results for one or more characters have also been delineated by Jalata *et al.* (2011), Kumar *et al.* (2013), Singh *et al.* (2015b) and Yadav *et al.* (2015). Higher estimates of heritability along with high genetic advance provide good scope for further improvement in advance generation if these characters are subjected to mass progeny.

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