

# **Research Note** Genetic variability in barley (*Hordeum vulgare* L.)

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#### Abstract

Twenty two barley genotypes were evaluated for green fodder yield, grain yield and related morphological characters. Genotypes significantly differed for all the 14 characters indicating sufficient variability in the experimental material. The characters plant height, spike length, peduncle length, number of tillers per meter row length, test weight, green fodder yield and grain yield showed high GCV and PCV. High estimates of heritability along with high genetic advance (% of mean) were observed for plant height, spike length, peduncle length, number of tillers per meter row length, test weight, green fodder yield and grain yield. Therefore, selection will be effective for these characters.

Key words: Barley, genetic variability, heritability, genetic advance

Barley [Hordeum vulgare L.] is the world's fourth most important cereal crop after wheat, maize and rice. Barley belongs to the family Poaceae. Barley is a self-pollinated crop. Due to its self-pollinating nature, pure line varieties are cultivated. It is an excellent source of high quality carbohydrate (74%), particularly starch. Barley flour is easily digestible and is used for *chapati* making either alone or mixed with gram or wheat flour. The major use of barley grains is in the production of malt, which is used in breweries to make beer, industrial alcohol, whisky, malt syrups, malted milk and vinegar. The spent malt after brewing is used as a feed. It is believed to have cooling effect on human system. In several regions, it is preferred over wheat and other cereals particularly during summer. The straw provides an important source of roughage for animals, particularly in dry areas. Straw is also used to prepare paper, card board and as base material in mushroom production.

Barley is one of the most widely distributed rabi cereals cultivated throughout the temperate and tropical regions of the world. The major barley producing countries of the world are Canada, U.S.A., Germany, France, Spain, Turkey, U.K., Denmark, Russia, Central Asian State (CAS) and Australia. By virtue of its nature, lower cost of cultivation, superior nutritional qualities, barley is favoured in neglected agricultural areas, particularly in problematic soils like rainfed, dry alkaline land, saline and flood prone marginal/costal areas. In India, barley is grown on more than 7.23 lakh hectares, with the production of more than 17.70 lakh tonnes and a productivity of 24.40 q/ha (Anonymous, 2005). The major barley growing states are U.P., Rajasthan, M.P., Bihar, Punjab, H.P., Haryana, Jammu & Kashmir and Gujarat. Rajasthan ranks second after Uttar Pradesh, both in area and production in India. In Rajasthan, it is an important *rabi* cereal next to wheat in acreage and production. It is grown over an area of about 2.02 lakh hectares with the annual production of about 4.58 lakh tonnes and average yield of 22.70 q /ha (Agyat *et al.*, 2009).

A thorough understanding of genetic variability and other related parameters like heritability and genetic advance *etc*. for yield and yield attributing characters is necessary. The variability in plant population is the first requirement for improvement in any crop. The amount of variability in the germplasm of any crop sets the limits of progress that can be achieved through selection. Therefore, the present study was done to get information for the variation for grain yield, green fodder yield and related characters in barley for 22 improved genotypes.

The investigation was carried out during rabi season 2009-10 at Agricultural Research Station (SKRAU), Bikaner. The experimental farm is situated between 27<sup>0</sup> 11' N latitude and 71<sup>0</sup> 54' E longitude at an altitude of 228.5 meters above sea level. The experimental material consisted of 22 genotypes of barley. Genotypes were obtained from AICRP on Forage crops, Agricultural Research Station (SKRAU), Bikaner, which were differing in growth and morphological characters. The experiment was laid out in randomized block design with 3 replications. Each plot consisted of six rows of 5 meter length and the spacing between rows was 23 cm. Normal and uniform cultural operations were followed during the crop to raise a good crop. The sample size consisted of five plants, selected randomly from each plot. The



observations on different characters were recorded on the basis of five selected plants and mean was obtained. Days to 50 per cent flowering, number of tillers per meter row length, days to maturity, test weight, green fodder yield and grain yield were based on whole plot basis. Green fodder yield was recorded by cutting the crop after 55 days of sowing. After that, the crop was allowed to grow and grain yield was obtained.

Analysis of variance was done by subjecting the data to the statistical method as described by Panse and Sukhatme (1978). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as per formula suggested by Burton (1952) and Johnson *et al.* (1955). Heritability was estimated by the formula as suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956). The expected genetic advance at 5% selection intensity was calculated by formula as given by Lush (1940) and Johnson *et al.* (1955).

Analysis of variance revealed highly significant differences among the genotypes for all the 14 characters (Table 1). High and significant variability for grain yield was reported by Ei-Hennawy (1997); for plant height and grain yield by Kishor et al. (2000); for plant height, spike length and test weight by Ortiz et al. (2001); for test weight by Wegrzyn and Bichonski (2001); for spike length and test weight by Kumar and Prasad (2002); for plant height, test weight and grain yield by Shafaeddin (2002); for spike length and yield by Shahinnia et al. (2005) and for plant height and ear length by Mishra et al. (2008). The magnitude of the phenotypic coefficient of variation higher than their corresponding genotypic coefficients of variation for all the characters, which indicated effect of environment on the character expression. The high GCV and PCV were observed for plant height, spike length, peduncle length, number of tillers per meter row length, test weight, green fodder yield and grain yield. Moderate GCV and PCV were observed for leaf length, leaf width, leaf area, number of spikelets per spike and number of grains per spike. Low GCV and PCV were observed for days to 50 per cent flowering and days to maturity.

High estimates of heritability were observed for plant height, spike length, number of spikelets per spike, peduncle length, number of tillers per meter row length, green fodder yield, grain yield and test weight. A wide range of expected genetic advance was observed for different characters. High estimates of expected genetic advance (% of mean) were observed for plant height, spike length, peduncle length, number of tillers per meter row length, test weight, grain yield and green fodder yield. High heritability along with high genetic advance (per cent of mean) was observed for plant height, spike length, peduncle length, number of tillers per meter row length, green fodder yield, grain yield and test weight. In this condition selection will be more effective. On the other hand, moderate heritability with low genetic advance (per cent of mean) was observed for days to 50% flowering and days to maturity. Hence selection may not be effective in these traits.

High heritability for various traits were reported by many authors as for test weight by Babu and Hanchinal (1998), for plant height by Kishor et al. (2000), for spike length by Kishor et al. (2000); for number of spikelets per spike by Prakesh and Verma (2006); for peduncle length by Prakash and Verma (2006); for number of tillers per meter row length by Babu and Hanchinal (1998) and for grain yield by Kumar and Prasad (2002). High genetic advance was also reported by many authors as for plant height by Kishor et al. (2000), for spike length by Kishor et al. (2000); for peduncle length by Prakash and Verma (2006); for number of tillers per meter row length by Babu and Hanchinal (1998); for test weight and grain yield by Babu and Hanchinal (1998).

Hence based on the foregoing discussion selection may be effective for the traits plant height, spike length, number of spikelets per spike, peduncle length, number of tillers per meter row length, test weight, green fodder yield and grain yield.

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## Table 1 Estimates of GCV, PCV, h<sup>2</sup>, GA and GA% of mean for 14 characters of barley

Character	Range	Mean	SE (diff.) ±	GCV	PCV	Heritability % (Broad sense)	GA (5%)	GA (%) of mean
Days to 50% flowering	80.00- 91.67	87.62	1.280	4.51	4.85	86.4	7.57	8.64
Leaf length (cm)	19.71- 25.62	21.93	0.916	5.26	7.34	51.4	1.70	7.75
Leaf width (cm)	1.07- 1.57	1.29	0.085	8.83	11.96	54.5	0.17	13.18
Leaf area (cm <sup>2</sup> )	18.90- 25.51	21.67	0.713	8.30	9.23	80.9	3.33	15.37
Plant height (cm)	50.63- 77.63	60.34	1.316	11.75	12.05	95.1	14.24	23.60
Days to maturity	122.00- 128.00	124.50	0.938	1.72	1.95	77.6	3.88	3.17
Spike length (cm)	6.60- 11.77	8.81	0.196	14.76	15.01	96.7	2.63	29.85
Number of spikelets/ spike	13.67- 17.67	15.94	0.283	6.58	6.93	90.1	2.05	12.86
Number of grains / spike	35.67- 44.67	40.17	0.649	5.31	5.67	87.8	4.12	10.26
Peduncle length (cm)	16.97- 28.33	22.32	0.763	14.32	14.92	92.1	6.32	28.31
Number of tillers/ meter row length	41.67- 86.00	55.79	1.326	18.71	18.93	97.6	21.24	38.07
Test weight (g)	27.80- 44.29	32.95	0.396	11.97	12.06	98.5	8.06	24.46
Green fodder yield (q/ha)	12.33- 27.83	18.33	0.584	22.37	22.71	97.0	8.32	45.39
Grain yield (q/ha)	6.62- 20.05	12.70	0.431	25.28	25.62	97.4	6.53	51.41