

## Study of Genetic parameters for yield and yield contributing trait of elite genotypes of barley (*Hordeum vulgare* L.)

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### Abstract

Selected 105 genotypes of barley (*Hordeum vulgare* L.) were evaluated in randomized block design with three replications, sown under three different environments to study character association for eleven yield and its component characters. Analysis of variance for genotypes reveals highly significant differences for most of the characters investigated. High GCV and PCV were observed for peduncle length (27.23, 34.43), grain yield per plant (21.23, 32.23) and effective tillers per plant (19.27, 29.35). Heritability in broad sense ranged from 29.00 (Spike length without awn) to 76.00 (Days to Maturity). High heritability coupled with high genetic advance as percent of mean was observed for plant height and grains per ear. There was positive significant correlation of seed yield per plant with grains per ear ( $r_p = 0.47$ ), effective tillers per plant ( $r_p = 0.36$ ), 1000 grain weight ( $r_p = 0.25$ ) and Plant Height ( $r_p = 0.19$ ) hence by exercising selection for these characters, it may be possible to isolate superior, high yielding genotypes

**Key words:** Barley, yield, genetic variability, correlation and stress

### Introduction

Barley (*Hordeum vulgare* L.) was the first domesticated vegetable crop (Borém, 2009). It is world's fourth important cereal crop after wheat, maize and rice (Langridge and Barr, 2003; Martin et al., 2006). The annual world harvest of barley in the late century was approximately 140 million tonnes from about 55 million ha. Average productivity in India is 19.3 q/ha as compared to 24.7 q/ha of world's average. Growers can obtain a harvest in areas with low precipitations, mainly because this crop has advantages in aspects such as salt tolerance, drought tolerance, frost tolerance and the early period of development. Barely is an autogamous plant and one of the oldest members of family Poaceae, its use in human's and animal's food, barely has attracted big attentions (Manli, 1985).

Barley is the most widely grown crop over broader environmental ranges than any other cereals and has persisted as a major cereal crop through many centuries. It is an important winter cereal crop grown in the northern plains of India comprising the states of Uttar Pradesh, Bihar, Haryana, Rajasthan, Punjab, Madhya Pradesh, Himachal Pradesh and Uttarakhand

that makes about 80% of total acreage of India. Although it is not popular in Southern States of India, even it is grown on very small areas of Maharashtra, Northern Karnataka and Nilgiri and Plane Hills of Tamil Nadu which shows its wider adaptability across the country. The state of Jammu & Kashmir, Gujarat, and Bihar are grown barley as a rainfed crop in poor marginal soils due to its low input demand and lower cost of cultivation.

There is a need for the development of new barley cultivars that tolerate abiotic and biotic stresses for the improvement of crop productivity (Ellis et al. 2000). This will require good understanding of the available genetic variation in both wild and cultivated barley. The rate of progress, however, will depend on the occurrence of desirable genetic variation and the availability of precise methods of identification, selection and transfer of superior genes (Ellis et al. 2000). Therefore it is required that precise and comprehensive information of the genetic parameters controlling the components of yield is collected and used for making decisions on the selection of an appropriate breeding method (Aghamiri et al., 2012). Therefore, in view of these fact 105 variety evaluated in this study, with an objective of the screening genetic variability present in the genotypes for yield and its contributing characters.

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## Materials and methods

The present investigation was carried out in Randomized Block Design with three replications. The experimental materials consisted of 105 genotypes of barley, obtained from the All India Co-ordinate Barley Improvement Project. These selected 105 genotypes were sown under three different environmental conditions [Uttar Pradesh (*Rabi* 2012-13), Uttar Pradesh (*Rabi* 2013-14) and Madhya Pradesh (*Rabi* 2013-14)] at Agriculture Research Farm, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi and at Farmers field (Village-Chhitipur, District-Shivpuri 38 Km from Jhansi in Madhya Pradesh).

All the 105 genotypes (Table 1) were sown on 2<sup>nd</sup> December 2012 at Agriculture Farm, BHU. Each entry were grown in three replications comprising two row of 1.5 m length with row to row spacing of 30 cm and plant to plant spacing of 10 cm. While as a same way all genotypes were sown on 3<sup>rd</sup> December 2013 at both locations i.e. BHU farm and farmer's farm. The recommended cultural practices were carried out to raise good crop. The pre and post-harvest observations were recorded on five plants, selected at random from two rows of each genotype in each replication for eleven characters. Mean of the data from the sampled plants of each plot in respect of different characters were used for various statistical analysis. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the method suggested by Burton (1952). Heritability in broad sense [ $h^2_{(b)}$ ] was calculated according to the formulae given by Lush (1940). From the heritability estimates, the genetic advance was estimated by the formula given by Johnson *et al.* (1955). Correlation coefficients were calculated for all the character combinations at genotypic and phenotypic levels as per the formula given by Miller *et al.* (1958).

## Result and discussion

In the present investigation, analysis of variances for genetic advance showed highly significant difference among the genotypes for all the eleven characters studied, including appreciable amount of variability between the genotypes. Considering the magnitude of phenotypic and genotypic coefficient of variation it was revealed that, peduncle length, grain yield per plant and effective tillers per plant showed wide range of variation and these finding are in agreement with those of Singh *et al.* (2008), Mishra *et al.* (2008), Jalata *et al.* (2011), Singh *et al.* (2014) and Ahmad *et al.* (2003). Lowest phenotypic and genotypic variation was observed for days to maturity, 75% heading and plant height. An

overall observation on phenotypic and genotypic coefficients of variation showed that the magnitude of difference between them were more for most of traits indicated that influence of environment is much in compare to genetic effect (Figure 1).

Heritability is the genetic component of variation transmitted from one generation to the next generation and is exploited in selection programme. Broad sense heritability estimate was highest for days to maturity followed by grains per ear, plant height and peduncle length. These finding was in accordance with Eshghi *et al.* (2011), Akanksha *et al.* (2012), Singh *et al.* (2014) and Ram Kishor *et al.* (2000). The high heritability in broad sense along with high genetic advance was observed for plant height and grains per ear which indicates the presence of greater contribution of additive genetic component in the inheritance of these attributes. Similar results were obtained by Singh *et al.* (2008), Akanksha *et al.* (2012) and Begum and Khatun (1997). (Table 2)

There was positive, significant correlation of seed yield per plant with grains per ear, effective tillers per plant, 1000 grain weight, Plant height, peduncle length and spike length without awn, hence by exercising selection for these characters, it may be possible to isolate superior, high yielding genotypes. While, it was negatively and significantly correlated with day's to 75% heading (Table 3) and these finding are in agreement with those of Rachana *et al.* (1978), Najeeb and Wani (2004), Ozturk *et al.* (2007) and Singh *et al.* (2008).

**Table 2: Mean, Range, Co-efficient of variation, Heritability (broad-sense) and Genetic advance as per cent of mean for 11 characters in barley over three different environments**

S. No.	Character	Mean	Range	Phenotypic co-efficient of variation	Genotypic co-efficient of variation	Heritability in broad sense (%)	Genetic advance as % of mean
1.	Days to 75% heading	77.02	61.00 – 88.33	5.99	4.80	64	7.90
2.	Days to Maturity	105.54	92.33 – 113.33	3.80	3.31	76	5.92
3.	Plant Height(cm)	103.02	79.60-122.45	10.70	8.61	65	14.28
4.	Effective Tillers/ Plant	6.56	3.54 – 11.97	29.35	19.27	43	26.05
5.	Peduncle length (cm)	9.69	5.09 – 15.03	34.43	27.23	63	44.36
6.	Spike length with awn(cm)	18.36	8.95 – 22.38	13.63	10.01	54	15.15
7.	Spike length without awn(cm)	7.86	5.13 – 11.03	19.63	10.56	29	11.70
8.	Flag leaf length(cm)	15.06	8.62 – 20.60	22.58	15.26	46	21.25
9.	Grains /ear	46.14	19.74 – 64.16	25.97	21.83	71	37.82
10.	1000 grain weight(g)	38.35	28.77 – 58.82	16.22	12.31	58	19.23
11.	Grain yield/plant(g)	9.4	5.04 – 16.04	32.23	21.23	43	28.82

Table 3: Estimates of phenotypic correlation coefficient between yield and its related characters of 105 genotypes of barley.

Character	Plant Height cm	Peduncle Length (cm)	Spike length With awn (cm)	Spike length Without awn (cm)	Flag leaf length (cm)	Effective tillers/ plant	Grain yield/ plant g	1000 grain weight (g)	Days to 75% Heading	Days to Maturity	Grains/ ear
Plant Height	1.00	0.46**	0.34**	0.24**	0.27**	0.02	0.19**	0.10**	0.16**	0.15**	0.15**
Peduncle Length		1.00	0.10**	0.12**	0.26**	-0.11**	0.15**	0.08*	-0.19**	0.02	0.22**
Spike length with awn			1.00	0.48**	0.24**	0.11**	0.06*	0.23**	0.01	-0.07*	-0.03
Spike length without awn				1.00	0.27**	0.05	0.10**	0.05	0.06	0.09**	0.12**
Flag leaf length cm					1.00	-0.09**	0.01	0.14**	-0.06	0.17**	0.15**
Effective tiller/plant						1.00	0.36**	0.13**	-0.09**	-0.09**	-0.14**
Grain yield/ plant							1.00	0.25**	-0.08*	0.06*	0.47**
1000 grain weight								1.00	-0.10**	0.01	-0.27**
Days to 75% Heading									1.00	0.27**	-0.05
Days to Maturity										1.00	0.10**

\* Significant at 5% level and \*\* significant at 1% level against pooled error

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