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Studies on path coefficient analysis and genetic divergence in feed barley (*Hordeum vulgare* L.)

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Abstract
An experiment was carried out at Crop Research Farm, Nawabganj, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur during *Rabi* 2016-17. Experimental material comprised of fifty genotypes of barley. Studies on variability, heritability and genetic advance showed that biological yield per plant, grain weight per spike, number of productive tillers and grain yield per plant are having considerable importance to the breeders for selection. Correlation studies showed that positive and significant correlations were observed between biological yield/plant and plant height, number of tillers/plant and days to maturity, grains/spike and number of tillers plant plant, main spike length and plant height, harvest index between number of tillers per plant and number of spike per plant. Path coefficient analysis suggested that biological yield per plant is showing positive and significant overall effects on grain yield per plant. So emphasis could be given on these characters during selection for varietal improvement programme. After D^2 analysis fifty genotypes were grouped into eight clusters. Cluster I had highest genotypes (11). The genotypes falling in Cluster I had the maximum divergence. The maximum and minimum divergence was found between cluster I and VIII, Cluster V and II, cluster III and cluster VI and cluster IV and cluster VII respectively. Cluster I and V are exhibiting high mean for most of the characters. For varietal improvement, the hybridization among genotypes falling in clusters III and IV should be done as they are the most divergent clusters.

Keywords: path coefficient analysis, genetic divergence, *Hordeum vulgare* L

Introduction
Barley (*Hordeum vulgare* L. 2n=14, sub family: poaceae) is frequently described as cosmopolitan crop grown over wide range of environments such as rainfed, irrigated, saline/alkaline soil, marginal lands, drought prone areas, diara lands, hill regions etc.Its input requirements is low while its adaptability is better under harsh environments in comparison to other cereals. Barley is mainly used as feed for animals and as malt for industrial uses. Barley is also used for green forage and is either directly fed to the animal or used for silage. It has immense potential as quality cereal especially for nutrition and medicinal point of view. Barley as sattu, dalia and chapatti is a staple food for every traditional family in Uttar Pradesh and now the population of barley is increasing day by day as functional food beneficial for human health.

Barley is one of the founder crops of old world agriculture and one of the first domesticated cereals. Barley rank fourth in world cereal crop production and used in order of importance; animal feed, brewing malt and human food. It became as a successful crop, because of its short life cycle and morphological, physiological, and genetic characteristics.

Wild barley (*H. vulgare spp. spontaneum*) is its most probable progenitor. It might have been introduced to India soon after the advent of the Aryans. Its Sanskrit name 'Yava' is mentioned in 'Veda' and use of barley in religious ceremonies has been described, which shows that barley was grown in India since ancient time and our ancestors were aware with the importance of crop. The important ways of barley use in India are as a grain food, feed to livestock and poultry. Its flour is used in preparing 'Chapaties'. Grains are roasted and grinded to use as 'sattu'. Grain can also be roughly grinded in 'pearl' barley which is used in preparation of soup. In European countries it is used as a breakfast food. Due to very low gluten, it is easily digestible as compared to wheat. Beer is also a most important product produced from barley, and it is probably the first drink developed by Neolithic human. Now Barley is key ingredient for beer and wine (whisky) industry.

Barley contains eight essential amino acids. According to recent study, eating whole grain barley can regulate blood sugar (i.e. reduce blood glucose respond to meal) up to 10 hour after consumption. As compared to wheat, Barley foods are beneficial in various ways and it also known as an diuretics, emollient used in case of pancreas and other digestive problems.

Most barley ingredients are whole grain, low fat and high in fiber, which make them ideal choices for individuals following the recommendations of the dietary guidelines for Americans. Barley foods have many health-enchaining attributes in addition to providing sound nutrition. The beta glucan or soluble fiber content of barley products provides low deposition of cholesterol property similar to oats. It is one of the important cereals of the world cultivated over an area of 575.00 lakh ha. The major barley growing countries are Russia, China, Canada, USA, Spain, France, Australia, UK, and India.

According to second estimate, in India barley is cultivated on area about 6.71 lakh ha with a total production of 147.04 lakh tons (2016-17). Barley is an important *Rabi* cereal in northern plains of India, comprising the states of Utter Pradesh, Haryana, Rajasthan, Punjab, Madhya Pradesh and Uttrakhand. The states of Bihar, J. & K. and Gujarat also grow barley at limited scale. Its low input demand and lower cost of cultivation is an important factor for its preference by farmers in these areas. The farmers in northern plains also cultivate barley in the marginal soils with limited resources and rain fed condition. Mostly the state of Haryana, Punjab, Rajasthan and Western U.P. grow barley under irrigated condition, which is subsequently being utilized by the malting and brewing industries located nearby because of its better grain development.

Besides, in view of recent economic liberalization and globalization resulting in the entry of multinational companies to cater the need of malted food, pharmaceuticals and beer industries in Indian market. D^2 analysis is the most important statistical tool to identify diverse genotypes for hybridization program me in order to exploit the heterosis and to isolate desirable sergeants', Multivariate analysis (Mahalnobis d^2 statistic) has been used in spring wheat (Bhatnagar *et al*. (2001) [2] for identifying genetically diverse parents for hybridization. Several breeders in different crops have used D^2 statistics, but Arunachalam (1981) [1] has suggested the technique and its limitations. Beale (1969) has advocated classificatory approaches, like principal component and clustering of genotype, to overcome the limitation of D.

Materials and Methods

The experimental material of the present study was comprised of 50 genotype of six rowed barley and were procured from Barley Breeder, Section of Rabi Cereals C.S. Azad University of Agriculture and Technology, Kanpur. These genotypes exhibited wide spectrum of variation for various agronomical and morphological characters. The experiment was planted in Randomized Block Design (RBD) with three replications on November 15, 2015. Each plot consisted of two rows of 3 m length with a spacing of 5 cm between plants and 30 cm between the rows. Observations were recorded on twelve characters viz. days to flowering, days to maturity, number of tillers/plant, plant height, main spike length, number of grains/spike, grains/spike, grain weight per spike, 1000 grain weight, biological yield/ plant, harvest index and grain yield/plant and number of spike per plant.

Heterosis expressed as per-cent increase or decrease of F_1 hybrid over the best commercial check (standard heterosis) were computed as per the method of Turner, (1953) and Hayes *et al.*, (1955).

$$\text{Heterosis over check (standard heterosis)} = \frac{\overline{F_1} - \overline{CC}}{\overline{CC}} \text{x } 100$$

Where: F_1= mean performance of F_1,CC = mean performance of the best commercial check. The differences in the magnitude of heterosis were tested by following procedure given by Panse and Sukhatme (1967)

$$\text{Critical difference for commercial check} = (2Me/r)^{1/2} \text{ x } t$$

Where: r = Number of replications, Me = Error mean sum of square from analysis of variance table, t = Table t value at error degrees of freedom corresponding to 5% or 1% level of significance.

Inbreeding depression is estimated when both F_1 and F_2 generations of the same cross are available. Inbreeding depression was measured as described by Miller and Marani (1963).

$$\text{Inbreeding depression} = \frac{\overline{F_1} - \overline{F_2}}{\overline{F_1}} \times 100$$

Where: F_1 and F_2 are the mean values of F_1 and F_2 progeny respectively of the same cross for a given character. Inbreeding depression may be high, medium, low and nil depending on cross.

Heritability values with regards to each to character were calculated as per the formula proposed by Burton and Devane (1953) [5].

$$h^2_a = \frac{Vg \text{ x } 100}{Vp}$$

Where,

h^2 = Heritability
Vg = Genotypic variance
Vp = Phenotypic variance

Genetic Advance

The genetics advance was calculated by the following formula suggested by Johanson *et al.* (1955a).

$$GA = H \text{ x } \sigma p \text{ x } K.$$

Results and Discussion

Present study revealed highly significant variation for all the traits indicated high variability among the genotype for different characters. Maximum variation was found for main spike length in respect of coefficient of variation and genotypic and phenotypic coefficient (14.44%, 13.11% and 18.65% respectively) indicated that simple selection for biological yield/plant may be advantageous as compared to other yield attributing traits. Other traits showing higher genotypic and phenotypic coefficient of variation were number of tillers/plant (11.79% and 18.65%), plant height (9.47% and 9.81%), number of spikes/plant (6.76% and 17.26%), biological yield/plant (5.22% and 8.23%), and grain yield/plant (3.56% and 7.57 indicating sufficient scope for improvement in these characters. In general, genotypic coefficient of variation is more important than phenotypic coefficient of variation because it is the consequence of genotype and responds to selection.

Raikwar and Vishwakarma (2003,) [14] Akanksa *et al*. (2012), Abdel *et al*. (2013) [18], Raikwar *et al*. (2014) [15] and Singh *et al* (2014)[1] also reported the same results in their studies for the characters plant height, main spike length, grain/plant, 1000 grain weight, grains/spike, and no. of tillers/plant.

Heritability and genetic advance

The effectiveness of selection for any character depend not only the amount of variability for the character present in the population but on the proportion of variation, which is transmitted from parents to offspring. The portion of heritable and fixable variation can be obtained through heritability and genetic advance estimates.

The heritability estimates along with genetic advance give more reliable information than the heritability estimate alone in predicting the ultimate effect of selection because heritability alone does not provide ample evidence regarding the genetic improvement, which could be possible through selection. If heritability is mainly due to non additive gene effect, the value of genetic gain would be low but if heritability is mainly due to additive gene effect then value of genetic gain would be high. Therefore, estimates of heritability and genetic advance were estimated for various traits and have been discussed as under.

As per the results observed by Hanson and Robinson (1957) high estimates of heritability were recorded for all the characters. This indicated possibility of obtaining substantial response to selection in these traits owing to their high transmissibility, even if, variability was in lower degree.

High estimates of heritability were recorded plant height, days to flowering, main spike length, grain weight/spike, biological yield/plant 1000 grain weight and no. of spike/plant. Moderate heritability was recorded for no. of spike/plant, grains/spike, grain yield/plant and harvest index.

Yadav *et al*. (2002), Sandeep *et al.* (2002) and Soylu (2002) also reported high heritability and genetic advance as per cent of mean for plant height, grains per spike, grain yield per plant and productive tillers per plant. Fox *et al.* (2011), Jalata *et al* (2011), Akanksha *et al* (2012) and Abdel-Ghani (2013) [18], found high heritability for all characters studied.

Path coefficient analysis

The analysis of path coefficient was undertaken with a view to understand the underlying causes of given effects and the relationship between a component character and dependent character as measured by genotypic and phenotypic correlation coefficient and was subdivided into direct effect of these characters. Path Coefficient Analysis was carried out by the method modified by Dewey and Lu (1959) [6] from the technique originally proposed by Wright (1921) [22]. Path coefficient were obtained by simultaneous equations which express basic relationship between correlation and path analysis.

Table 1: Mean sum of squares for the twelve quantitative characters in barley genotypes

Source of variance	d. f.	Days to flowering	Days to maturity	Number of tillers / plant	Plant height (cm)	Main Spike length (cm)	No. of spikes/ plant	Grains/spike	Grain weight/ spike (g)	Biological yield /plant	Grain yield/ plant (g)	Harvest index	1000 grain weight
Replication	2	0.18	0.88	1.40	2.13	1.25**	4.04**	0.72	0.0002	9.10**	0.45	8.10**	1.41
Treatment	49	21.67**	12.17**	3.64**	151.43**	3.35**	2.04**	8.77**	0.0018**	9.82**	1.34**	8.99**	2.35**
Error	98	2.22	3.41	1.21	3.55	0.53	1.34	3.97	0.0004	3.25	0.72	5.11	0.98

Significant at 5% level of significance.

** Significant at 1% level of significance

Table 2: Heritability and Genetic advance for twelve characters in barley

S. No.	Character	Heritability coefficient	Heritability	Genetic advance	Genetic advance percent over mean
	Days to flowering	0.745	74.50	4.52	5.20
	Days to maturity	0.461	46.10	2.39	1.74
	Number of tillers/plant	0.400	40.00	1.17	15.37
	Plant height (cm)	0.933	93.30	13.96	18.85
	Main spike length (cm)	0.639	63.90	1.59	21.58
	No. of spikes/plant	0.154	15.40	0.39	5.46
	Grains/spike	0.287	28.70	1.39	3.04
	Grain weight/spike (g)	0.531	53.10	0.03	2.20
	Biological yield/plant	0.403	40.30	1.93	6.83
	Grain yield/plant (g)	0.221	22.10	0.44	3.45
	Harvest index	0.201	20.10	1.05	2.34
	1000 grain weight	0.317	31.70	0.78	2.01

Table 3: Genotypic and Phenotypic coefficient of variation for twelve characters in barley

S. No.	Character	GCV	PCV	coefficient of variation
1.	Days to flowering	2.92	3.39	1.713
2.	Days to maturity	1.24	1.83	1.345
3.	Number of tillers/plant	11.79	18.65	14.447
4.	Plant height (cm)	9.47	9.81	2.543
5.	Main Spike length (cm)	13.11	16.40	9.859
6.	No. of spikes/plant	6.76	17.26	15.878
7.	Grains/spike	2.76	5.15	4.354
8.	Grain weight/spike (g)	1.47	2.01	1.382
9.	Biological yield/plant	5.22	8.23	6.367
10.	Grain yield/plant (g)	3.56	7.57	6.682
11.	Harvest index	2.53	5.64	5.046
12.	1000 grain weight	1.73	3.08	2.546

References

1. Arunachalam V. Grnrtic basis of plant breeding. In plant breeding theory and practices (ed.) V. L. Choptra, Oxford and IBH Publishing Co. Ltd., New Delhi, 1989.
2. Bhatnagar VK, Sharma SN, Shastry EVD. Genetics of quantitative characters in six-rowed barley over environments. Indian J Genet. 2001; 61:358-359.
3. Bergale S, Billore M, Holkar AS, Ruwali KN, Prasad SVS, Mridulla B. Genetic variability, diversity and association of quantitative traits with grain yield in bread barley (*Hordeum vulgare* L.). Madras Agricultural Journal. 2001; 88(7-9):457-461.
4. Fox G, Borgognone MG, Flinn P, Poulsen D. Genetic and environmental analysis of NIR feed quality predictions on genotypes of barley, 2011.
5. Burton GW. Quantitative inheritance in grasses. Proc.6thInt. Grassland Cong. 1952; 1:227-83.
6. Dewey OR, Lu KH. A correlation and path coefficient analysis of components of crested wheatgrass seed production J Agron. 1959; 57:515-18.
7. Dixit RK, Singh P. Path analysis and selection indices as an aid for the improvement of grain yield in Lentil (*Lens esculenta Moench*). Plant Sci. 1975; 7:84-86.
8. Hanson WD, Johnson HW. Method of calculating and evaluating a general selection index obtained by pooling information from two or more experiments., Genetics. 1957; 42:421-32.
9. Mahalanobis PC. A statistical study at Chinese Head measurement. J Asiatic Soc. Bengal. 1928; 25:301-77.
10. Murty BR, Arunchalam V. The nature of divergence in relation to breeding system in some crop plants. Indian J Genet. 1965; 26A:188-198.
11. Verhalan LM, Murray JC. A diallel analysis of several fibre property traits in upland cotton (*Gossypium hirsutum* L.). Crop Sci. 1969; 9:311-15.
12. Warner JN. A method for estimating heritability. Agron. J. 1952; 44:427-30.
13. Jalata Z, Ayana A, Zeleke H. Variability, heritability and genetic advance for some yield and yield related traits in Ethiopian Barley (*Hordeum vulgare* L.) landraces and crosses. International Journal of Plant Breeding and Genetics. 2011; 5(1):44-52.
14. Raikwar RSS, Viswakarma SR. Genetic diversity in barley. Farm science journal, 2003; 12(2):116-117.
15. Raikwar RS, Upadhyay AK, Tyagi PK. Heritability and genetic variability for yield components under two regimes of soil in barley (*Hordeum vulgare* L.). The Bioscan, 2014; 9(4):1613-1617.
16. Singh SK, Gupta PK, kumar jitendra, singh rajvir, singh Lokendra, Nigam PN. Variability and correlation studies for some quantitative traits in rainfed barley (*Hordeum vulgare* L.). Society for science development in agriculture and technology, progressive research 2014; 9(1):219-221.
17. Akanksha Sirohi A, Kumar S, Kant S, Pal K, Kumar A, Singh M. Genetic improvement through variability, heritability and genetic advance in barley crop (*Hordeum vulgare* L.). Environment and Ecology. 2012; 30(4):1343-1345.
18. Abdel-Ghani AH. Selection of high yielding lines from heterogeneous Jordanian barley landraces under well watered and drought stress conditions. Bulletin of Faculty of Agriculture, Cairo University. 2013; 64(1):13-29.
19. Yadav VK, Ram L, Kumar R, Singh SP. Genetics of yield component and some malting components in barley (*H. vulgare*). Proc. Agric., 2002; 2(1):14-18.
20. Sandeep Kumar S, Prasad LC, Kumar S. Variavility and correlation studies in barley*;* Research on crop. 2002; 432-436.
21. Soylu S. A study of combinig ability for grain yield and other agronomic charecters in barley. Agriculter Mediterranean. 2002; 132(1):9-14.
22. Wright S. Correlation and causation. J Agric. Res. 1921; 20:257-256.