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DIVERSITY ANALYSIS AMONG GENOTYPES OF BARLEY (*HORDEUM VULGARE* L) BASED ON MORPHOLOGICAL PARAMETERS

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ABSTRACT
The present investigation was carried out with the aim to estimate extent of genetic diversity among genotypes of barley based on morphological characterization. The experimental materials consisted of 25 Barley genotypes including two checks. Analysis of variance revealed significant differences among all the genotypes for all the traits under study namely plant height, number of tillers per plant, flag leaf length, peduncle length, spike length with awn, number of grains per spike, ear length and test weight. The divergence studies through Mahalanobis D^2 statistics grouped the 25 genotypes into six clusters. The maximum numbers of genotypes (7) were grouped in cluster IV and VI and the lowest (1) in cluster II and III. Members of cluster III and VI (487.49) were found to be genetically most diverse on the basis of their inter cluster difference as opposite to clusters IV and V (69.24) which are closely related. Plant height contributed maximum (35.33%) towards genetic divergence followed by ear length (17.33%). These characters were considered to be most important for the genetic diversity. Lowest contribution was made by number of tillers per plant (4.286%) followed by spike length with awn (1.33%), peduncle length (1.67%).

KEYWORDS: *Hordeum vulgare L* , D^2 Analysis, Genetic diversity, Cluster analysis.

INTRODUCTION

As one of the first crop plants to be domesticated, barley (*Hordeum vulgare* L.) remains one of the most important crops today (Rao 1952). Ranking fourth in world acreage, barley is used for human consumption, as a fodder crop and as a raw material for brewing beer and whisky (Brown 1992). It belongs to the genus Hordeum, which comprises over 32 species, including diploid and polyploid, perennial and annual types, which are spread throughout the world. Genetic improvement is the only component to stabilize the crop improvement. Evaluation of genetic diversity is important to know the source of genes of a particular trait within the available germplasm (Tomooka 1991). Farmer preference and breeder selection create a narrow germplasm base (Duvick 2005). Some elite germplasms are often used as parents for the next cycle of breeding (Graner *et al.*, 1995). As a result, it leads to greater genetic uniformity and germplasm disappearance. To assure the safety of crop production, it is necessary to extend genetic background in crop breeding. It is well known that genetic diversity is the basis of biological diversity, and thus, it plays a key role in future breeding progress (Yao *et al.*, 2007). Intensive efforts should be done to access the genetic divergence of various genotypes so that they can be exploited for the development of high yielding varieties. The estimate of genetic divergence provides insight for the possible improvement of the characters under study. The objectives of the present study were, to access the diversity among twenty five genotypes of barley based on quantitative data so that it can help distinguishing between genotypes and which could be further used in appropriate breeding program for the genetic improvement of barley.

MATERIALS & METHODS

The present investigation was conducted at Barley Breeding Block, Institue of agricultural sciences, Banaras Hindu University,Varanasi.Twenty five genotypes of barley along with two checks was planted in randomized block design with two replications in the rabi season of year 2013 and 2014. Each experimental plot consisted of four rows each of five meters and normal agricultural practice was followed and the details about the genotypes are presented in the Table.1.Nine quantitative characters observations were recorded either on plot basis or on a sample of five plants per plot.

TABLE 1. Details of the genotypes under study

S.No.	Name of Genotypes
1.	DL 70
2.	DL 100
3.	DL 456
4.	DWR UB 52
5.	DWR UB 64
6.	BH 543
7.	BH 546
8.	BH 668
9.	K 409
10.	PL 708
11.	HUB 172
12.	HUBL 09 17
13.	HUBL 99 30
14.	ATHOULPA

15.	AMBER
16.	BEECHER
17.	VMORALES
18.	RATNA
19.	HIMANI
20.	RIHANI

Statistical analysis

Estimation of Genetic Divergence: The estimation of genetic divergence was done with the help of Mahalonobis' "D^2" statistic (generalized distance) as suggested by Rao (1952). Its calculation involved the following steps. **a**. A set of uncorrelated linear combinations (Y,s) was obtained by Pivotal condensation of the common dispersion matrix formed by a set of correlated variables (X,s). The common dispersion matrix was obtained with the help of error mean squares and sum of products. **b**. Using the relationship between Y,s & X,s the mean values of different genotypes for different characters were transformed into mean value of a set of uncorrelated linear combinations. **c**. The D^2 value between 'i^{th}' & 'j^{th}' genotypes for k^{th} character was calculated as: $D^2_{ij} = \sum^{k}_{t=1} (Y_{it} - Y_{jt})^2$

Group Constellation:

All the genotypes were grouped into clusters on the basis of D^2 values, as suggested by Tocher. In the said method, two genotypes belonging to the same cluster should at least, on the average, show a smaller D^2 value than those belonging to two different clusters.

Intra and Intercluster Distances

To measure intracluster D^2 values, the following formula was used: Intracluster $D^2 = \sum D_i^2 / n$, $n = P(P-1)/2$ Where, $\sum D_i^2$ = is the sum of D^2 values between all possible combinations (n) of the populations (P) included in a cluster. n = all possible combinations among the populations in a cluster. P = number of populations included in a cluster. The square root of intercuster D^2 values ($d = \sqrt{D^2}$) was used to represent intra-cluster distance of a cluster.

Contribution of different character towards Divergence:

The relative contribution of different characters to the total D^2 between each pair of genotypes was given a score of 1 to P (P being the number of characters) based on the magnitude of D^2 values due to each character. A rank of 1 represents the highest contribution and P the lowest of character 'X'. Contribution of each character was calculated using the following formula:

Percent contribution of a character = $\frac{N(X)}{n(n-1)/2} \times 100$

Where, N(X) = Number of genotypic combinations which were ranked first for the character 'X', out of the total genotypic combinations of n(n-1)/2 and n = Number of genotypes.

RESULTS & DISCUSSION

Analysis of variance

Pooled analysis of variances over two consecutive season was carried out for all the 9 yield contributing characters under randomised block design and the results are presented in the Table.2.

TABLE 2. Analysis of variance for various characters in barley

		MEAN SQUARES								
Source of variation	d.f.	Plant height	Number of Tillers/plant	Flag leaf Length	Flag leaf Width	Peduncle Length	Spike Length With Awn	Number of grains/spike	Ear Length	Test weight
Replications	2	1.39	0.71	3.53	0.018	1.57	0.58	74.51	0.26	0.09
Treatments	24	414.93*	5.02*	11.4*	0.216	28.90*	8.17*	1026.86*	2.12*	154.44*
Error	48	7.13	0.95	2.31	0.013	3.08	0.98	59.05	0.102	4.61
SE (Mean)		1.51	0.55	0.86	0.06	0.99	0.56	4.34	0.18	1.21
CD at 5%		4.38	1.60	2.49	0.18	2.88	1.62	12.61	0.52	3.52

It provides that there were significant differences among genotypes for all the characters except for flag leaf width. The variances (mean square) for Plant height (414.93), Flag leaf length (11.40), Peduncle length (28.90), Spike length with awn (8.17), Number of grains per spike (1026.86) and Test weight (154.44) were found to be highly significant. This indicates sufficient genetic variability among the genotypes undertaken for study. Coefficient of variability was in the range of 2.56 to 12.09, which indicates the consistency of the experimental conditions. Although the results evidenced the existence of genetic variability in the genotype tested, this variability should be further increased by divergent crosses to raise the probability of finding superior recombinants. Parental diversity is considered desirable to exploit heterosis in any breeding program (Das *et al.,* 2013) and avoid future problems with inbreeding depression (Ferreira *et al.,* 2005), which improves the chances to select superior genotypes in the segregating populations derived from these divergent crosses.

Genetic divergence analysis based on morphological traits

The genetic divergence present among the genotypes was estimated by Mahalanobis D^2 statistic as described by Rao (1952). Based on D^2 values, the constellation of genotypes into clusters was done following Tocher's method (Rao 1952). All the twenty five genotypes of barley could be grouped into six clusters. The clustering pattern of these genotypes is given in Table.3. The cluster I comprised of five genotypes while the cluster II and cluster III consisted of one genotype each. Cluster IV and VI consisted of 7 genotypes whereas cluster V has four genotypes. There was nearly equal distribution of genotypes among four clusters, while the other groups comprised only 1 genotype. From this we infered that there was fairly appropriate level of divergence among the genotypes under study but the genotypes of cluster IV and

VI has maximum genotypes which indicate low level of divergence.This may have been due, to the narrow genetic basis of these genotypes or sharing the same pedigree. The selection in barley improvement programs is directed to traits of agronomic interest and, since it is a self pollinated crop selection is mainly practised in early segregating generation from a cross of two divergent parents so these genotypes can be recommended to generate large amount of variation in segeregating generation upon which the breeders can exlploit it according to their needs. These findings were confirmatory with the findings of Rahal-Bouziane *et al.,* 2015 and Amabile *et al.,*2015. Chourasia *et al.,* 2016 also reported that good segregants can be generated from divergent crosses.

TABLE 3. Clustering patterns of 25 genotypes on the basis of D^2 values

Cluster No.	Genotypes included	No. of genotypes
I	DL 70,DWR UB 52,DL 100,DL 456 and BEECHER	5
II	HORMAL	1
III	DWR UB 64	1
IV	BH 668,HIMANI,VMORLES,RATNA,BH664,HUBL 99-30 and REHANI	7
V	ATHOULPA,PRESTIGE,YARDU,PL-708	4
VI	HUB 172,AMBER,BH-556,HUB 09-17,LAKHAN,BH-543 and K 709	7

TABLE 4. Average inter and intra-cluster (diagonal) D^2 values

Clusters	I	II	III	IV	V	VI
I	**61.587**	**113.589**	**265.205**	**117.575**	**164.645**	**195.239**
II		**0**	196.185	244.424	282.177	351.797
III			**0**	319.203	227.817	487.495
IV				47.296	69.24	87.393
V					39.574	149.084
VI						**60.626**

Intra and inter-cluster divergence

Intra-cluster average D^2 values ranged from 0.00 to 61.587. It was maximum in cluster VI (60.62) with seven genotypes followed by cluster I (61.58) having five genotypes, cluster IV (47.29) with seven genotypes, cluster V (39.57) with four genotypes. Cluster II and III has only one genotype each, thus intra-cluster distance in these clusters was zero. The inter-cluster average D^2-value was maximum between cluster III and VI (487.49), indicating high genetic diversity between these two clusters. Thus, exploitation of genotypes within these two clusters as parents for crossing could produce good segregants. This was followed by average D^2-value between cluster II and VI (351.79) and average D^2-value between cluster III and cluster IV (319.20). The minimum inter-cluster average D^2-value was found between cluster IV and V (69.24) followed by between cluster IV and VI (87.39). This might indicate the close relationship and likelihood between genotypic groups within these clusters. These results might be concluded that high D^2 value was due to genetic dissimilarity among genotypes and low D^2 value was due to genetic similarity among genotypes. It is concluded that hybridization of genotypes from two distant clusters is likely to yield desirable recombinants. Hybridization between genetically distant genotypes for exploiting hybrid vigour was frequently suggested in other crops species also. Therefore, two important considerations for future breeding are the selection of parents from genetically distant parents and selection of particular barley genotypes based on higher variability among the progenies.

Contribution of different characters towards genetic divergence

The clustering of the genotypes into different clusters and the measurement of genetic distance between them alone does not account for the analysis of diversity in the population. It is highly important to ascertain how much do each component character accounts for the total divergence. The relative contribution of different characters towards the expression of genetic divergence was calculated following standard method as suggested by Singh and Chaudhary (1977) and presented in Table.5.

TABLE 5. Contribution of different characters towards divergence in barley genotypes

S. No.	Character	Contribution percent
1	Plant height (cm)	35.33
2	Number of tillers/plant	0.33
3	Flag leaf length (cm)	3.00
4	Flag leaf width (cm)	9.33
5	Peduncle length (cm)	1.67
6	Spike length with awn (cm)	1.33
7	Number of grains/spike	13.67
8	Ear length	17.33
9	Test weight (gm)	9.206

The study on individual contribution of characters indicated that the maximum contribution towards divergence was given by plant height (35.33%) followed by test weight (18.00%), ear length (17.33%), number of grains per spike (13.67%), flag leaf width (9.33%) and flag leaf length (3.00%) . Ali *et al.* (2007) also reported that Plant height contributes the maximum towards divergence. This can also be inferred. it is useful to

include this character in divergence analysis. Ali *et al.,* (2007) and Shekhawat *et al.* (2001) narrated that Plant weight significantly adds to genetic diversity among barley genotypes. This came true in the present research as it contributes 35.33% to divergence.

Lowest contribution was made by number of tillers per plant (0.33%) followed by spike length with awn (1.33%) and peduncle length (1.67%). Alam *et al.* (2007) also reported that number of tillers per plant was the least contributor in genetic diversity

CONCLUSION

All the twenty five genotypes of barley were grouped into six clusters based on D^2 statistics. The characters studied may be considered important from the point of view of genetic diversity in general and in experimental material in specific. The clustering and genetic distance also gives an idea for developing the diverse genetic pool for successful breeding programme. Higher the D^2 value, more diverse the genotypes are and these identified genotypes can be used as parents for comprehensive hybridisation programme.

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