

D² ANALYSIS IN EARLY MATURITY HULL-LESS BARLEY (*Hordeum vulgare* L.)

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ABSTRACT

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Genetic diversity was assessed in 73 genotypes of barley (*Hordeum vulgare* L.) by using D² analysis. The genotypes were grouped into six clusters. Cluster I comprised 21 genotypes which was followed by cluster II and cluster V. Cluster with small statistical distances considered less diverse than those with large distances. The intra cluster value was maximum in cluster V and minimum in cluster I. Cluster IV showed the highest mean values for 1000 grain weight and grain yield per plant while cluster III revealed the lowest mean value for days to maturity. The characters responsible for genetic divergence were days to maturity, grain per spike and 1000 grain weight.

Key words: Genetic diversity, early maturity and barley

INTRODUCTION

Barley is a fourth most important cereal crop, cultivated successfully in a wide range of climate. This crop has potentials for growing under drought and saline condition. It requires less input like, fertilizer, irrigation, and insecticides. In the world, barley is increasingly being used as cattle feed. The entire barley kernel is used as feed after grinding. By product of the brewing process and malt sprout are also used in the USA as a live stock feed. Barley cultivation in Bangladesh is decreasing due to lack of high yielding and hull-less varieties. However, barley cultivation can be popularize among growers, if the crop could be made suitable for cultivation in the areas where it grows well and rice, wheat, maize cannot be grown profitable for the stress environment.

Germplasm may be considered as one of the important natural resources. The primary goals of germplasm enhancement are high yielding, good quality, resistance to biotic and abiotic stress and wider adaptation. Genetic improvement is the only component to stabilize the crop and crop improvement. Evaluation of genetic diversity is important to know the source of genes of a particular trait within the available germplasm (Tomooka, 1991). Most of the existing cultivars are of late maturity and hulled type. Knowledge of genetic diversity among population usually helps a breeder in choosing desirable parents for breeding program as selection of parents on the basis of divergence analysis. Therefore, the present investigation was undertaken to estimate the extent of genetic diversity in exotic early maturity hull-less barley genotypes available in Bangladesh.

MATERIALS AND METHOD

This trial consisted with seventy three early maturity barley (*Hordeum vulgare* L.) genotypes collected from ICARDA, Aleppo, Syria. This experiment was conducted at Bangladesh Agricultural Research Institute, Gazipur during the rabi season of 2005-2006. Seeds of each entry were sown in a single row of 2.5 m long with 25 cm spacing. Fertilizers N, P₂O₅, K₂O were applied at the rate of 100, 60, 40 kg/ha, respectively. Intercultural operations were done as and when necessary. Data were recorded from ten randomly selected plants from each plot for seven-quantitative characters viz., days to maturity, plant height (cm), number of tiller per plant, spike length (cm), number of grain per spike, 1000 grain weight (g) and yield per plant. These data were used to statistical analysis. Genetic diversity was studied following Mahalanobis's (1936) generalized distance (D²) extended by Rao (1952). Statistical analysis was done by using GENSTAT program.

RESULTS AND DISCUSSION

Seventy three genotypes were grouped into six different clusters by using clustering technique. The genotype distributions are presented in Table 1. The number of genotype in each cluster varied. The maximum number of genotypes were included in Cluster I (21 genotypes), which was followed by cluster II and cluster V. The cluster IV contained five genotypes.

The intra and inter cluster values among the six clusters are presented in Table 2. The intra cluster distance ranged from 0.17 to 2.36. The maximum inter cluster distance (7.33) was observed between II and III while the lowest between III and VI. The table revealed that the inter cluster distance was larger than the intra cluster distance which suggested wider diversity among the genotypes of different groups. Cluster with small statistical distances considered less diverse than those with larger distances.

The genetic differences between the clusters were reflected in the cluster means. A comparison of cluster means for the various characters is presented in Table 3. The cluster IV had the highest mean values for 1000 grain

weight and yield per plant. The lowest mean values for days to maturity and highest mean value for spike length and grain per spike was observed in Cluster III, indicating the early maturity genotypes are in this group.

Table 1. Distribution of 73 barley genotypes in different clusters

Cluster No.	No of Genotypes	Distribution of Genotypes
I	21	G1, G5, G7, G8 , G14, G15, G16, G19 G21,G22, G27, G31, G33, G45, G63, G64, G66, G67, G69, G70 and G73
II	16	G11,G12, G17, G18, G28, G29, G32, G43, G44, G46, G56, G57, G58, G59, G60 and G65
III	9	G13, G23, G26, G34, G35, G36, G37, G41,G42
IV	5	G6, G9, G24, G25 and G49
V	15	G2, G4, G10, G38, G39, G40, G47, G48 G50, G51, G52, G53,G54, G55 and G61
VI	7	G3, G20, G29, G30, G46, G71 and G72

Singh and Singh *et al.* (1980) stated that the genetic diversity may not be straightway related to geographical diversity and the similar trend was observed in barley. Updhyaya and Murty (1970) stated that genetic drift and natural selection in different environments can cause high diversity among the recess than geographic locations. Endang *et al.* (1971) stated that type of clustering pattern could be utilized for cross combination to generate the highest possible variability for various important characters.

Table 2. Average Inter-Intra (bold) clusters values among three clusters of 73 genotypes of barley

Cluster	I	II	III	IV	V	VI
I	0.43	2.87	5.07	4.03	6.75	4.97
II		1.18	7.33	3.37	4.05	2.69
III			1.06	5.89	3.77	1.83
IV				0.17	5.59	2.17
V					2.36	3.31
VI						0.97

Table3. Mean values of 3 clusters for seven characters of barley

Character	DM	PH	TP	SL	GSP	1000GW	YP
I	98	62.50	5	4	43	48	5.20
II	101	81.10	4	5	39	33	3.50
III	93	72.20	6	9	50	46	4.80
IV	100	76.00	7	7	47	50	6.00
V	96	87.70	8	4	35	35	3.02
VI	103	69.45	3	6	54	39	4.10

DH=Days to heading, PH=Plant height, TP=Tiller per plant, SL= Spike length, GSP=Grain per spike, 1000GW= Grain weight, YP= Yield per plant

Table 4. Relative contribution of the seven characters to the total divergence of hull-less barley

Character	Vector I	Vector II
Days to maturity	0.0531	0.1026
Plant height	-0.0357	0.0289
Tiller per plant	-0.0859	-0.0521
Spike length	0.0124	-0.1295
Grain per spike	0.1347	0.2330
1000 grain weight	0.0885	-0.0461
Yield per plant	-0.0342	0.1027

The mean values of the different cluster indicating the utility of divergence analysis in identifying useful parents for hybridization. In selection of the parent for hybridization, genetic divergence of both genotypes should be taken into account.

Contributions of characters towards divergence are presented in Table 4. The canonical variate analysis revealed that the values for both vectors (vector I and vector II) days to maturity, grain per spike and 1000-grain weight were found positive. Such results indicated that these three traits contributed maximum towards diversity of genotypes. Ram and Singh (1989) found spike length, grain per spike and grain weight, while Nessa *et al.* (1998) observed tiller number, spike length and plant height are the main characters contributing yield in barley. It may be concluded that the greater divergence in the genotypes due to these characters in the respective clusters would offer a good scope for the improvement of barley through rational selection.

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