Indian J. Plant Genet. Resour. 32(2): 236-238 (2019)
DOI 10.5958/0976-1926.2019.00030.5

SHORT COMMUNICATION

Assessment of Genetic Variability and Diversity for Quantitative Characters in Naked Barley (*Hordeum vulgare* (L.) var. nudum Hk. f.)

Jogendra Singh*[1], Dinesh Kumar[1], Vishnu Kumar[1], Anil Khippal[1], Ajay Verma[1], RPS Verma[2], AS Kharub[1] and GP Singh[1]
[1]*ICAR-Indian Institute of Wheat and Barley Research, Karnal–132001, Haryana, India*
[2]*ICARDA, Morocco*

(Received: 29 November 2017; Revised: 11 February 2019; Accepted: 13 February 2019)

Forty genotypes of hulless barley were studied to understand the extent of genetic variability and diversity based on 7 quantitative characters. A wide range of variation was observed for seed yield per plot followed by plant height, tillers per meter and 1000-grain weight. High heritability coupled with high genetic advance as percent of mean was registered for seed yield per plot and tillers per meter in genotypes indicating the predominance of additive gene action for these traits. Based on D^2 statistics, 40 genotypes were grouped into 7 clusters in which cluster IV consisted of only single genotype (Geetanjali) while other six clusters involved multi-genotypes. The maximum inter-cluster distance was observed between cluster IV and VII (120.82) followed by cluster IV and V (107.43). Geetanjali of cluster IV exhibited highest seed yield per plot and tillers per meter along with early days to 50% heading. The genotypes involved in cluster IV and VII may be utilized in hybridization programme for improving the characters like early maturity, tillers/meter, short plant height and seed yield/plot.

Key Words: Diversity, Hulless barley, Quantitative characters, Variability

Hulless barley (*Hordeum vulgare* (L.) var. nudum Hk. f.) an important cereal crop is widely distributed all over the world, although it is highly preferred in East Asian countries such as China, Korea and Japan and chiefly high in Tibet and Northern parts of Nepal, India and Pakistan. In India, it is mainly grown in the high altitude areas of Himalaya and is utilized as food crop in the tribal areas of hills and plains. Hulless barley is utilized not only as grain crop, bio-fuel and livestock feed but also used as raw material for malt products such as beer. In recent years, importance of hulless barley is increasing as human food due to presence of water soluble plant fibers essential in human diets to reduce the serum cholesterol (Shimizu *et al*. 2008). In this perspective, hulless barley may be helpful in reducing the sugars of diabetic patients and also to lower the serum cholesterol of heart patients (Pins and Kaur, 2006). Thus, hulless barley is a potential crop and its genetic improvement is needed for high yield, wide adaptation, good quality and resistance to biotic and abiotic stresses.

Assessment of genetic variability and diversity is important to detect the source of genes for a particular character within the available germplasm. Hence, knowledge of nature and magnitude of genetic variability present in the germplasm and extent of heritability of economic characters is of greater help in identifying the parents with novelty and diversity for planning a suitable breeding strategy. Therefore, the present study was undertaken to understand the nature and magnitude of genetic variability and diversity in hulless barley genotypes collected from different geographic origins.

The present study was carried out on 40 hulless barley genotypes from mid-term storage facility at ICAR-IIWBR, Karnal. The experiment was conducted in a randomized block design with three replications; each plot had three rows of 2.5 meters long and 30 cm apart, under timely sown irrigated conditions at Seed and Research Unit, IIWBR, Hisar during 2014-15. The recommended package of practices was followed for raising the good crop stand. The data were recorded on 5 randomly selected plants for 7 quantitative characters viz., days to 50% heading, days to maturity, plant height (cm), tillers/meter, spike length (cm), 1000-grain weight (g) and seed yield/plot (g). The mean values of replicated data were subjected for analysis of variance as per standard statistical procedure. The genotypic

---

**Author for Correspondence: Email- jogendrasail@yahoo.co.in* and phenotypic variance, genotypic and phenotypic coefficients of variation and heritability were estimated as per the standard formulae (Singh and Chaudhary, 1985). Genetic advance was estimated by the method suggested by Johnson *et al*. (1955).The genetic diversity was analyzed by the non-hierarchical Euclidean cluster analysis for seed yield and its components using statistical software available at computer centre, IIWBR, Karnal, for clustering of genotypes into different groups and also to indicate the extent of diversity available in set of genotypes studied. Ward's minimum variance clustering method was used to classify genotypes in discrete clusters (Sneath and Sokal, 1973).

The study on genetic variability revealed that a wide range of variation was observed for seed yield/plot followed by plant height, tillers/meter and 1000-grain weight indicating a wide scope for improving these characters through selection. These findings are in agreement with the results of Zeng (2015). In general, magnitude of phenotypic coefficient of variation (PCV) was greater than genotypic coefficient of variation (GCV) for all the characters, indicating the significant role of environmental interaction for the expression of all the characters studied. Seed yield/plot exhibited high difference between PCV and GCV in comparison to other characters indicating more environmental influence on this character. The range of PCV was registered from 2.92 to 35.44 whereas GCV ranged from 2.05 to 30.82. The high degree of phenotypic and genotypic coefficients of variation was observed for seed yield/plot and tillers/meter. Present findings are in confirmation with Eshghi *et al*. (2012).

Heritability and genetic advance are important genetic parameters in selection programme. In the present study, broad sense heritability (h^2) estimates ranged from 49.40% for days to maturity to 75.7 % for seed yield/plot (Table 1). The high values of heritability were recorded for seed yield/plot. Similar findings were observed by Derbew *et al*. (2013**)**. However, moderate heritability was observed for characters like tillers/meter, days to 50% heading, spike length, 1000-grain weight and plant height. These results are in agreement with Shtaya *et al.* (2015). High heritability coupled with high genetic advance as percent of mean was registered for seed yield/plot and tillers/meter in genotypes indicating the predominance of additive gene action for these traits, hence direct selection may be highly effective in barley improvement. Similar findings were reported by Yadav *et al.* (2015).

Forty genotypes of hulless barley comprising indigenous and exotic germplasm lines were grouped into 7 clusters in which cluster IV consisted of only single genotype while other six clusters involved multi-genotypes. Maximum number of genotypes (10) were observed in cluster VI followed by cluster V (8). However, Clusters II, I, VII and III encompass (7), (6), (5) and (3) genotypes, respectively. The composition of genotypes in each cluster is depicted in Figure 1. Geetanjali (Indigenous) was more divergent from other genotypes as it represents a separate cluster.

The inter-cluster distances were greater than intra-cluster, indicating wide genetic diversity among the genotypes of different clusters than those of same cluster. The maximum inter-cluster distance was revealed between cluster IV and VII (120.82) followed by cluster IV and V (107.43). On the other hand, minimum distance was noticed between cluster I and II (27.90), suggesting close relationship between these clusters would not play a critical role in improvement of barley. The greater distance between clusters showed wider genetic diversity among genotypes. The highly diverse genotype would create a broad spectrum of variability in the subsequent generations which enables further selection and improvement. The maximum intra cluster

Table 1. Analysis of variance and estimates of genetic parameters for seven characters in 40 hulless barley genotypes

Traits	Mean square (Genotype)	Mean ± S.E	Range of variation	Coefficient of variation		Heritability (in broad sense %)	Genetic advance (% of mean)
				GCV	PCV		
Days to 50% heading	22.95**	94.06 ± 1.42	86.50-99.50	3.27	3.91	70.10	5.64
Days to maturity	21.26**	129.25 ± 1.89	121.00-134.00	2.05	2.92	49.40	2.97
Plant height (cm)	323.73**	79.83 ± 7.17	50.28-97.55	13.16	18.29	51.70	19.50
Tillers/meter	308.89**	65.03 ± 4.8	41.00-86.50	17.60	20.51	73.70	31.12
Spike length (cm)	1.13**	7.33 ± 0.34	5.70-9.33	9.15	11.23	66.30	15.34
1000-grain weight (g)	38.64**	40.29 ± 2.37	29.06-50.14	9.19	12.39	55.00	14.05
Grain yield/plot (g)	27652.39**	353.99 ± 43.75	129.00-606.00	30.82	35.44	75.70	55.25

*, ** Significant at 5% and 1% level of significant, respectively

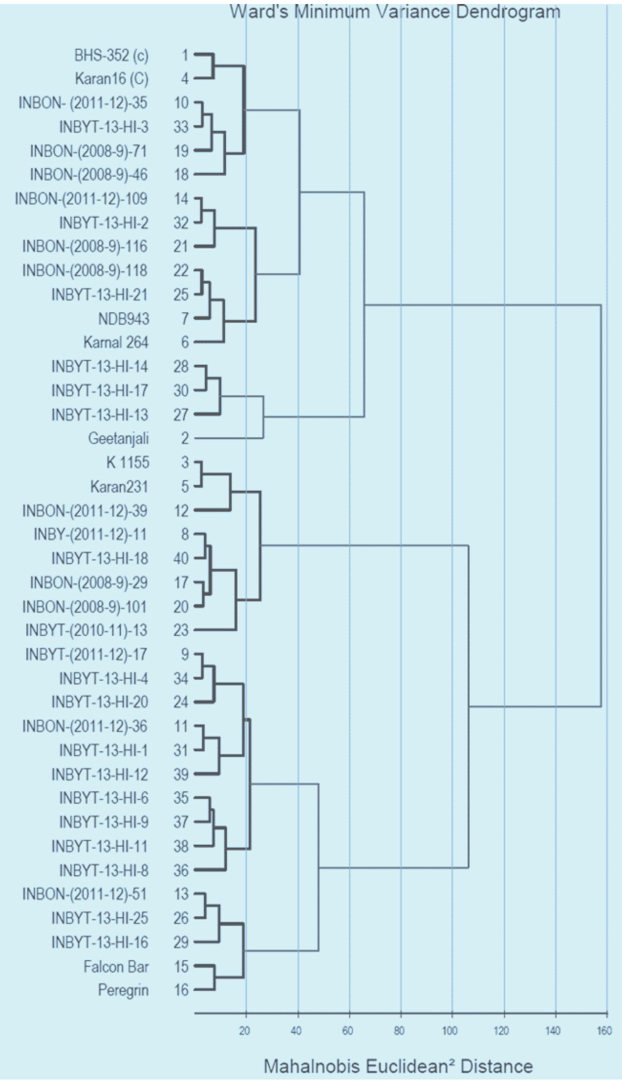

Fig. 1. Clustering of hulless barley genotypes (Wards' dendrogram)

distance was observed for cluster V (20.17) followed by cluster VII (19.86) and cluster VI (19.39). It is suggested that genotypes within the cluster with high degree of diversity would produce more desirable breeding material for attaining maximum genetic advance.

Cluster I revealed the highest mean values for spike length (8.08cm) with maximum 1000-grain weight (45.04g). However, cluster II exhibited the highest mean value (90.81cm) for plant height and better seed yield/plot (475.36g). Cluster IV consisted of highest mean values for tillers/meter (85) and seed yield/plot (563.00g) accompanied with early days to 50% heading (86). Cluster VII had short plant height (76.56cm). The use of genotypes from clusters IV and VII in hybridization for improving the yield and its contributing characters appears to be gainful. In addition, incorporation of diverse parents in hybridization is likely to produce heterotic hybrids and desirable transgressive segregants in further generations.

Cluster IV exhibited highest seed yield/plot and tillers/meter accompanied with early days to 50% heading whereas cluster VII had the genotypes exhibiting short plant height. The exotic genotypes involved in cluster VII such as INBON-(2011-12)-51, INBYT-(2013)-HI-25, INBYT-(2013)-HI-16, Falcon Bar and Peregrin and indigenous genotype (Geetanjali) in cluster IV may be used as a parent in hybridization programme for improving the characters like early maturity, plant height, tillers/meter and seed yield/plot.

References

Derbew S, E Urage and H Mohammed (2013) Land race collections from Southern Ethiopia. *International J. of Sci. and Res.* **2(12)**: 358-366.

Eshghi R, F Abrahimpour, J Ojaghi, S Salayeva, M Baraty and M Rahimi (2012) Evaluation of genetic variability in naked barley (*Hordeum vulgare* L.). *Intl J. Agri. Crop Sci.* **4(16)**: 1166-1179.

Johnson HW, HF Robinson and RE Comstock (1955) Estimation of genetic and environmental variability in soybean. *Agro. J.* **47**: 314-318.

Pins JJ and H Kaur (2006) A view of the effects of barley beta-glucan on cardiovascular and diabetic risk. *Cereal Food World*. **51**: 8-11.

Shtaya MJY, J Abdallah, H Al-Fares, H Abu-Qaoud, OA Baker, MV Korf and M Haddad (2015) Detecting genetic diversity among barley landraces grown in the West-bank, Palestine in 2010-11. *The J. of Animal and Plant Sci.* **25**(5): 1365-1370.

Shimizu C, M Kihara, S Aoe, A Araki, K Ito, K Hayashi, J Watari, Y Sakata and S Ikegami (2008) Effect of high β-glucan barley on serum cholesterol concentrations and visceral fat area in Japanese men-A randomized, double-blinded, placebo-controlled trial. *Plant Food Hum. Nuttr.* **63**: 21-25.

Singh RK and BD Choudhary (1985) Biometrical methods in quantitative genetic analysis, Kalyani Publishers, New Delhi.

Sneath PHA and RR Sokal (1973) Numerical Taxonomy, Freeman, San Francisco, CA, USA.

Yadav SK, AK Singh, P Pandey and S Singh (2015) Genetic variability and direct selection criterion for seed yield in segregating generations of barley (*Hordeum vulgare* L.). *American J. of Plant Sci.* **6**: 1543-1549.

Zeng XQ (2015) Genetic variability in agronomic traits of a germplasm collection of hulless barley. *Gen. and Mol. Res.* **14**(4): 18356-18369.