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Multi-environment genetic divergence analysis in barnyard millet germplasm (*Echinochloa frumentacea* L.) for grain yield with its contributing traits and nutritional contents

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Abstract

The current experiment was aimed to quantify the nature of genetic divergence present in 50 barnyard millet accessions having five released check varieties namely, VL 29, VL 172, VL 207, TNAU 101 and K-1. Genotypes were grouped into total nine different clusters with regard of 12 biometrical traits by using Mahalanobis D2 analysis. Cluster II found the biggest cluster involving 17 different genotypes of barnyard millet collected from different source, followed by cluster number V which involved twelve genotypes of distinct origin. Cluster number VI and VII contained six different barnyard genotypes each in respective cluster. Cluster IV had the four different barnyard millet genotypes whereas cluster I included only two genotypes of barnyard millet. This pointed out wider diversity in terms of genetic parameters between the genotypes. Maximum intra-cluster distance was observed in cluster IV (D=2.96) followed by cluster VI (D =2.91), cluster VII (D=2.69), cluster V (D=2.57), cluster II (D=2.4) and cluster I (D=0.28). Hence, selection of accessions as parental material from these genetically diversified clusters for improvement programmes could result in heterotic hybrids and could outcome desirable amount of genetic variability in barnyard millet.

Keywords: Barnyard millet, cluster analysis, diversity, variability

Introduction

Barnyard a millet crop (*Echinochloa frumentacea* (Roxb.) Link) ($2n=4x=36$) further commonly known as Jhangora, Shyama, Sanwa, Madira is majorly a self-pollinated plant. The family poaceae has genus *Echinochloa* which combines two different domesticated species, namely *E. utilis* and *Echinochloa frumentacea*, generally they are named as Japanese and Indian barnyard millet respectively. This crop is among the most prime small millet crops cultivated under marginal environments and essential for subsistence farming community.

Barnyard millet is largely cultivated in China, Japan, India and Korea for dietary purpose along with animal feed (Upadhyaya *et al.*, 2014) ^[14]. Moisture stress tolerance ability (Dwivedi *et al.*, 2012) ^[4] minimum period for completion of growth with essential medicinal uses (Saleh *et al.*, 2013) ^[12] makes this millet ideal for nutritional sensitive agriculture in limiting condition. In Indian agriculture, states such as Uttarakhand, Madhya Pradesh, Tamil Nadu, Andhra Pradesh, Karnataka, Bihar Maharashtra have cultivation of barnyard millet.

Assessment and utilization of genetic divergence in any germplasm can ease grouping and recognition of genetically wide genotypes. Accurate knowledge regarding the magnitude of diversity in genetic parameters and nature an assist researcher in selecting the genetically wider lines for particular involvement in hybridization programme. In the present investigation, the genetic divergence was estimated in the fifty-three genotypes, including checks, were analysed means of both quantitative and qualitative traits.

Materials and Methods

The current investigation was conducted in the kharif of 2019 on the field of Sorghum Research Unit, Dr. PDKV, Akola (E1), NBPGR, RS, Akola (E2), Regional Research Station, Amravati (E3) and Agriculture Research Station, Buldana (E4).

The experimental material is for the present trial included 50 barnyard millet germplasm collection comprising of five release lines (VL 29, VL 172, VL 207, TNAU 101 and K-1), National Bureau of Plant Genetic Resources, Regional station, Akola was the allotting agency for the seed material. Randomized block design (RBD) was applied to conduct the trial with three replications. Sowing was done with a paired row of three-meter length having spacing of 30 x 10 cm.

The genotypes were evaluated on the basis of agromorphological data which was taken on 12 different qualitative traits viz., days to fifty percent flowering, days to maturity, total number of tillers per plant, total number of productive tillers per plant, plant height (cm), panicle length (cm), panicle width (cm), 1000 grain weight (g), grain yield per yield (g), straw yield per plant (g), grain Fe content (mg/100 g) and Grain Zn content (mg/100 g). for recording qualitative data five random plants were selected from each replication and their mean was worked out. Traits such as days to 50 percent flowering and days to maturity were recorded on a plot basis.

Different characters were evaluated on account of collected biometrical data and further driven to analysis of variance (ANOVA) as given by Panse and Sukhatme (1967) [10]. Genetic divergence as well as intra and inter cluster distances were worked out from the data taken from replicated trails replicated by analysing it into to 'D²' analysis (Mahalanobis, 1936) [7]. Procedure given by Radhakrishna Rao (1952) [11] was utilized for the grouping of barnyard millet germplasm into different diverse clusters.

Results and Discussion

The genetic divergence estimates provide knowledge about germplasm diversity and association among genotypes with respect to genetic parameters that will benefit researchers in choosing prime germplasm in terms of trait breeding and improvement programme (Vivekananda and Subramanian, 1993; Govindaraj *et al.*, 2015; Manimekalai *et al.*, 2018) [15, 5, 8]. Diverse parental lines are of prime importance which will predict the genetic wideness in order to get the required combiners in the subsequent generations (Jaiswal *et al.*, 2010) [6].

Pooled analysis of variance for biometrical characters of the studied germplasm displayed that all the studied characters in terms of their mean sum of squares due to genotypes found superiorly significant which indicated significant variations among the genotypes or all the environments. Based on D² statistics, the 50 barnyard millet germplasm was grouped into nine different clusters (Table 1). From the

nine clusters, Cluster II found the biggest cluster involving seventeen different genotypes of barnyard millet collected from different source, followed by cluster number V which involved twelve genotypes of distinct origin. Cluster number VI and VII contained six different barnyard genotypes each in respective cluster. Cluster IV had the four different barnyard millet genotypes whereas cluster I included only two genotypes of barnyard millet. This pointed out wider diversity in terms of genetic parameters between the genotypes.

Table No.2 depicts the contribution in terms of percent of individual trait for the total divergence. Out of the total examine characters highest contribution towards genetic divergence was recorded by traits like, Grain Iron Content plant (30.06%) followed by Grain Zinc Content (22.78%), Straw yield per plant (13.49), Plant Height (7.8%), Days to 50% flowering (7.43%) and Grain yield per plant (7.02). Identical result was recorded in this crop by Arya *et al.*, (2018) [2] and Anuradha *et al.*, (2014) [1]. De *et al.*, (1988) [3] asserted that characters donating highest for the D² statistics should be allotted prime important in terms of choosing the clusters that will be utilized as motive of selection of lines for crossing programme. Hence, traits concentrate in the paper should form the base in choosing of parents for crossing programme. Remaining characters did contribute minimum, for the total genetic diversity which displayed that the lines have distinguished features for most of the characters studied.

In pooled analysis, the distances from same cluster (D values) varied from 0 to 2.96. maximum intra-cluster distance was observed in cluster IV (D=2.96) followed by cluster VI (D =2.91), cluster VII (D=2.69), cluster V (D=2.57), cluster II (D=2.4) and cluster I (D=0.28). The cluster in which a solitary genotype was grouped; the intra-cluster distance was found zero (D=0) and the cluster was III, VIII, IX having accessions IC-415234, IC-340185 and IC-340228 respectively. The highest inter-cluster distance values were observed between cluster VII and cluster IX (D=32.46) which was above cluster I and cluster IX (D=30.08), cluster VI and cluster IX (D=28.49). Inter-crossing between lines or genotypes from the diverse clusters namely, Ist and XIth cluster can be outcome in broad range of required recombination's. similar pattern of findings is in accordance with the outcomes given by Nirosha *et al.*, (2016) [9]. But in order to exploit heterosis, choosing of genotypes reflecting average diversity will be appropriate (Shahidullah *et al.*, 2009) [13].

Table 1: Cluste variation of 50 genotypes of Barnyard millet based on genetic divergence.

Sr. No.	Clusters	Number of Genotypes	Details of genotypes
1	I	2	IC-97031, IC-97034
2	II	17	IC-415230, IC-415242, IC-597287, IC-597323, IC-415310, IC- 413180, IC-415256, IC-415292, IC-340103, IC-597315, IC597347, IC-597324IC-415288, IC340187, IC-24848, IC-338960, IC-547333
3	III	1	IC-415234
4	IV	4	TNAU 101, K-1, IC-413181, IC-340155
5	V	12	IC-415248, IC-415304, IC-340124, IC-597339, IC-415249, IC415250, IC-52701, IC-415246, IC-597348, IC-340224, IC-326752, IC-338896
6	VI	6	IC-340240, IC-597322, IC-340242, IC-415313, IC-597339, IC-340241
7	VII	6	VL 29, VL172, VL207, IC-597308, IC-298404, IC-331109
8	VIII	1	IC-340185
9	IX	1	IC-340228

Table 2: Character wise contribution towards genetic divergence for pooled locations of 50 genotypes of Barnyard millet

Sr. No.	Character	Percent contribution	Times Ranked First
1	Days to 50% flowering	7.43%	91
2	Days to Maturity	0.33%	4
3	Total Number of Tillers per plant	0.08%	1
4	Total Number of Productive tillers per Plant	2.08%	44
5	Plant Height (cm)	7.8%	97
6	Panicle length (cm)	5.33%	64
7	Panicle Width (cm)	3.02%	37
8	1000 Grain Weight (g)	1.31%	16
9	Grain yield per plant (g)	7.02%	86
10	Straw yield per plant (g)	13.49%	132
11	Grain Iron Content (mg/100 g)	30.06%	376
12	Grain Zinc Content (mg/100 g)	22.78%	279

Table 3: Average inter and intra cluster distance $D = \sqrt{D^2}$ among 50 genotypes of Barnyard millet.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	0.28	11.62	8.41	7.66	21.31	15.13	4.68	14.39	30.08
II		2.4	4.13	5.47	6.04	5.96	8.74	3.86	14.05
III			0	6.39	13.89	8.29	3.89	4.15	22.16
IV				2.96	11.7	5.56	7.08	10.03	24.12
V					2.57	11.72	20.74	7.21	6.88
VI						2.91	10.66	11.92	28.49
VII							2.69	10.35	32.46
VIII								0	10.43
IX									0

Conclusion

Highest contribution towards total genetic diversity was recorded by grain Fe content per plant and plant height. A considerable amount of genetic divergence was registered in the evaluating germplasm on the basis of their categorization into different diverse clusters for various traits. Among the total formed clusters, VII and IX were the most diverse. On this basis, the genotypes IC-597308, IC-298404, IC-331109 (cluster VII), IC-97031 and IC-97034 (cluster I), IC-340241, IC-597339, IC-340242 and IC-597322 (cluster VI) and IC-340228 from cluster IX were consider as selected for hybridization. Inter mating among diverse clusters certainly would directs to larger opportunity for crossing over and revealing hidden variability by disrupting the unwanted linkages. The hybrids resulted from such diverse lines may furnish a larger scope for extracting transgressive segregants in advanced generations especially in barnyard millet. Therefore, such germplasm lines could be employed in a multiple crossing projects to exploit desirable transgressive segregants.

References

- Anuradha N, Patro TSSK, Bhanu UK, Madhuri J, Sowjanya A. Multivariate analysis in barnyard millet (*Echinochloa frumentacea* (Roxb.) Link). International Journal of food, Agriculture and Veterinary Science. 2014;4:194-199
- Arya R, Bhatt A, Kumar V. Study of Genetic Divergence in Barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) Germplasm. International Journal of Bio Resource and Stress Management. 2018;9:192-196.
- De RN, Seetharaman R, Sinha MK, Banerjee SP. Genetic divergence in rice. The Indian Journal of Genetics and Plant Breeding. 1988;48:189-194.
- Dwivedi S, Upadhyaya H, Senthilvel S, Hash C, Fukunaga K, Diao X, *et al.* Millets: Genetic and Genomic Resources. Plant Breeding Review. 2012;35:247-375.
- Govindaraj M, Vetriventhan M, Srinivasan M. Importance of genetic diversity assessment in crop plants and its recent advances: An overview of its analytical perspectives. Genetics research international; c2015. p. 431- 487
- Jaiswal JP, Mamta A, Anil K, Rawat RS. Assessing genetic diversity for yield and quality traits in indigenous bread wheat germplasm. Electronic Journal of Plant Breeding. 2010;1:370-378
- Mahalanobis PC. On the generalized distance in statistics. National Institute of Science of India; c1936.
- Manimekalai M, Dhasarathan M, Karthikeyan A, Murukarthick J, Renganathan VG, Thangaraj K, *et al.* Genetic diversity in the barnyard millet (*Echinochloa frumentacea*) germplasms revealed by morphological traits and simple sequence repeat markers. Current Plant Biology. 2018;14:71-78.
- Nirosha R, Thippeswamy S, Ravindrababu V, Reddy VR, Spandana B. Genetic diversity analysis of zinc, iron, grain protein content and yield components in rice. Electronic Journal of Plant Breeding. 2016;7:371-377.
- Panse VG, Sukhatme PV. Statistical methods for agricultural workers. Indian Council for Agricultural Research. New Delhi, India; c1967. p. 87-89.
- Rao RC. Advanced statistical methods in biometric research. A Division of Macmillan Publishing Co, Inc New York; Collier-Macmillan Publishers; London; c1952. p. 390.
- Saleh ASM, Zhang Q, Chen J, Shen Q. Millet Grains: nutritional quality, processing, and potential health benefits. Comprehensive Reviews in Food Science and Food Safety. 2013;12(3):281-295.
- Shahidullah SM, Hanafi MM, Ashrafuzzaman M, Ismail MR, Khair A. Genetic diversity in grain quality

- and nutrition of aromatic rices. *African Journal of Biotechnology*. 2009;8:1238-1246.
14. Upadhyaya H, Dwivedi S, Singh S. Forming core collections in barnyard, kodo and little millets using morpho-agronomic descriptors. *Crop Science*. 2014;54:1-10.
 15. Vivekanandan P, Subramanian S. Genetic divergence in rainfed rice. *Oryza*. 1993;30:60-60.