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Evaluation of Genetic Diversity in Sodic Soil-grown Barnyard Millet (*Echinochloa frumentacea* (Roxb.) Link) Germplasm

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Aims: Barnyard millet (*Echinochloa frumentacea*) is a significant tiny millet crop characterized by because of its high nutritional value, exceptional ability to withstand extremes of climate, and short duration. Globally, the area under salt affected soil is expanding. Therefore, genetic diversity analysis was conducted to identify genetically diverse genotypes for yield improvement under sodic condition.
Study Design: Randomised block design.
Place and Duration of Study: An experiment was carried under sodic soil condition at Anbil Dharmalingam Agricultural College and Research Institute, Trichy, Tamil Nadu.
Methodology: Ninety two genotypes of barnyard millet, including two commercial check varieties, MDU1 and CO (KV) 2. Plant height (cm), inflorescence length (cm), inflorescence width (cm), lower

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raceme length (cm), flag leaf length (cm), flag leaf width (cm), number of leaves on main tiller, number of productive tillers per plant, and grain yield per plant (g) were the nine quantitative traits that were recorded. GENRES software version 3.11 was used for analysing the data.

Results: For all of the analysed attributes, the genotypes showed significant differences based on the analysis of variance. Ninety two genotypes were divided into nine groups according to nine quantitative features using Mahalanobis D2-Statistics. Cluster II was the one with the greatest number with 25 genotypes, followed by cluster V with 22 genotypes, Cluster VI with 17 genotypes, Cluster IV with 11 genotypes, Cluster I with 8 genotypes, Cluster VIII with 4 genotypes, Cluster III and VII with only 2 genotypes per cluster, and Cluster IX with just 1 genotype. Cluster IV was second in terms of intra-cluster distance, after Cluster VIII. The largest inter-cluster distance was observed between clusters I (TNAUF01000021 - EF 37, TNAUF01000022 - EF 38, TNAUF01000022 - EF 39, etc.) and IX (MDU1).

Conclusion: Choosing these genotypes as parents from genetically diverse clusters for breeding programmes might produce heterotic hybrids that produce enough genetic diversity in barnyard millet genotypes under sodic soil conditions.

Keywords: Barnyard millet; D^2-statistics; inter-cluster distance; grain yield; sodic soil.

1. INTRODUCTION

Small millets have a great chance of surviving in the stressful environment. Small millets are traditional grains in India because they can be cultivated in arid, dry climates with acidic soil among other challenging agricultural circumstances. As opposed to the previous 50 years, India's use of coarse grains restricts the growth of small millet. Finger millet, kodo millet, proso millet, foxtail millet, little millet and barnyard millet are all small millet crops that are important for sustainable agriculture. Millets exhibited a special ability to adapt to biotic and abiotic stress situations. These crops are suited for farming in dry and semi-arid regions of the world as they can sustain their grow with minimum water [1,2].

Barnyard millet is one of the most important small millet crop grown under marginal environments and benefited for subsistence farming community. It is an early maturing annual summer crop highly recommended for famine areas [3]. The grain has high nutrient potential especially iron content which is most wanted for anaemic patient. Recent times, this crop gains more attention by many countries due to its multi potential as healthy food of human beings and as well as fodder for livestock [4]. It contains carbohydrate in fewer amounts than cereals makes suitable for diabetic patients. It is most suitable crop where the rice crop cultivation is not possible. It is less susceptible to biotic and abiotic stresses [5].

Soil sodicity is a major stress factor that adversely influences water infiltration and air exchangeability in the soil which limits crop growth due to the swelling of clay saturated with sodium ions (Pessarakli and Szabolcs, 1999). These soils are characterised by high pH (>8.5) and Exchangeable Sodium Percentage (ESP > 15 %), low EC (< 4.0 dS/m) and imbalanced nutrition with ion toxicity which shows poor physical and chemical contribution for crop growth [6].

Very limited information is available in literature on barnyard millet performance under sodic soil condition [7]. Genetic diversity is pre-requisite for any crop improvement programme. Therefore an attempt was made to investigate the nature and magnitude of genetic divergence existing in barnyard millet genotypes under sodic soil condition.

2. MATERIALS AND METHODS

An experiment was carried out to estimate the genetic divergence of barnyard millet under sodic soil condition at Anbil Dharmalingam Agricultural College and Research Institute, Trichy, Tamil Nadu. The experimental material comprised 90 germplasm lines of barnyard millet which were collected from different agroclimatic zones of Deccan plateau specifically Tamil Nadu and two commercial check varieties *viz..,* MDU1 and CO(KV) 2. These germplasms are currently conserved at Ramaiah Gene Bank, Department of Plant Genetic Resources, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The experiment was laid out in randomized block design with two replications and the recommended crop management practices were followed. Each genotype was raised in a four meter row adopting a row to row spacing of 25 cm and plant to plant spacing of 10 cm. The data were recorded on nine quantitative traits *viz.,* plant height (cm), inflorescence length (cm), inflorescence width (cm), lower raceme length (cm), flag leaf length (cm), flag leaf width (cm), number of leaves on main tiller, number of productive tillers per plant, and grain yield per plant (g) by following the descriptors of Barnyard millet (IPGRI, 1983). The data was recorded on five randomly selected plants from each accession. The data was subjected to ANOVA (analysis of variance) analysis to partition the variance components as suggested by Panse and Sukhatme [8]. The replicated data were used to estimate the genetic divergence in terms of per cent contribution of each trait towards divergence, intra- and inter- cluster distances by following D^2 analysis [9]. Grouping of all the barnyard millet genotypes into different clusters was carried out as per the procedure proposed by Rao [10]. GENRES software version 3.11 was used for analysing the data [11].

3. RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed significant differences between the genotypes for all the characters under study. For breeding programme, information about diversity and genetic relationships of germplasm is very essential for selecting elite genotypes. The Mahalanobis D^2 analysis grouped 92 genotypes into nine clusters based on Tocher's cut off value (Table 1). Among the nine clusters, cluster II was the largest, consisting of 25 genotypes followed by cluster V with 22 genotypes, cluster VI had 17 genotypes, cluster IV with 11 genotypes, cluster I with eight genotypes, cluster VIII had four genotypes, cluster III and VII included only two genotypes in each cluster. The cluster IX turned out to be singleton. Cluster VIII recorded the highest intra-cluster distance followed by cluster IV. The genotypes grouped within the same cluster showed narrow genetic divergence while between clusters wide genetic divergence was observed. The intra- (diagonal) and inter-cluster distances of the nine clusters are presented in Table 2.

The intra-cluster distance ranged from 1.83 (cluster III) to 5.91 (cluster VIII) indicating the genotypes in cluster III (TNAUF01000076 - EF 123 and TNAUF01000085 - EF 136) shared more common features within the cluster while the genotypes in cluster VIII (TNAUF01000134 - TNAU 52, TNAUF01000136 - TNAU 57, TNAUF01000137 - TNAU 92 and TNAUF01000140 - TNAU 95) shared comparatively fewer common features within the cluster. This was followed by cluster IV (5.58) and cluster V (5.14). Maximum inter-cluster distance was recorded between clusters I and IX (10.22) followed by clusters V and IX (8.94). Hybridisation between genotypes of the divergent clusters *viz*., clusters I and cluster IX might expand the variability available for the traits and give good amount of beneficial segregants. This study is an addition to the genetic diversity studies conducted in barnyard millet by Anuradha et al. [12], Arya et al. [13] and Dhanalakshmi et al*.* [7].

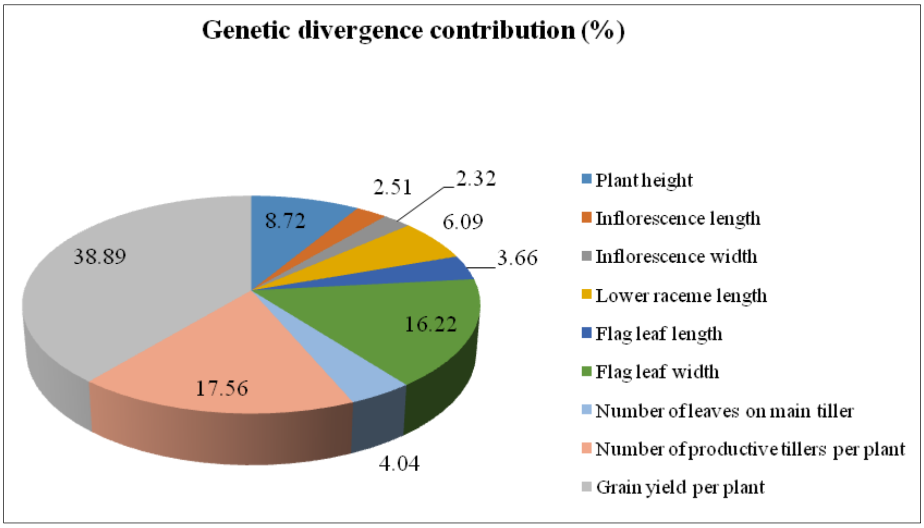

Fig. 1. Contribution of nine quantitative characters towards genetic divergence

Table 1. Distribution of 92 genotypes into nine clusters by D^2 analysis

Clusters	Number of genotypes	Name of the genotypes
I	8	TNAUF01000021 - EF 37, TNAUF01000022 - EF 38, TNAUF01000023 - EF 39, TNAUF01000025 - EF 40, TNAUF01000026 - EF 41, TNAUF01000028 - EF 43, TNAUF01000034 - EF 52, TNAUF01000046 - EF 71
II	25	TNAUF01000031 - EF 48, TNAUF01000032 - EF 49, TNAUF01000033 - EF 51, TNAUF01000035 - EF 53, TNAUF01000037 - EF 56, TNAUF01000038 - EF 57, TNAUF01000039 - EF 58, TNAUF01000042 - EF 62, TNAUF01000043 - EF 63, TNAUF01000044 - EF 64, TNAUF01000047 - EF 71/1, TNAUF01000048 - EF 76, TNAUF01000049 - EF 79, TNAUF01000051 - EF 81, TNAUF01000052 - EF 84, TNAUF01000053 - EF 85, TNAUF01000054 - EF 86, TNAUF01000055 - EF 87, TNAUF01000056 - EF 89, TNAUF01000057 - EF 90, TNAUF01000058 - EF 94, TNAUF01000059 - EF 95, TNAUF01000060 - EF 96, TNAUF01000111 - TNAU 25, TNAUF01000133 - TNAU 51.
III	2	TNAUF01000076 - EF 123, TNAUF01000085 - EF 136
IV	11	TNAUF01000061 - EF 97, TNAUF01000064 - EF 101, TNAUF01000065 - EF 102, TNAUF01000066 - EF 104, TNAUF01000067 - EF 105, TNAUF01000068 - EF 106, TNAUF01000069 - EF 109, TNAUF01000070 - EF 109, TNAUF01000071 - EF 115, TNAUF01000072 - EF 116, TNAUF01000138 - TNAU 93
V	22	TNAUF01000073 - EF 118, TNAUF01000074 - EF 119, TNAUF01000075 - EF 122, TNAUF01000077 - EF 124, TNAUF01000078 - EF 125, TNAUF01000080 - EF 127, TNAUF01000081 - EF 130, TNAUF01000083 - EF 133, TNAUF01000086 - EF 137, TNAUF01000087 - EF 138, TNAUF01000088 - EF 139, TNAUF01000089 - TNAU 78, TNAUF01000100 - TNAU 13, TNAUF01000101 - TNAU 14, TNAUF01000102 - TNAU 16, TNAUF01000103 - TNAU 17, TNAUF01000104 - TNAU 18, TNAUF01000105 - TNAU 19, TNAUF01000106 - TNAU 20, TNAUF01000107 - TNAU 21, TNAUF01000129 - TNAU 47, TNAUF01000119 - TNAU 34
VI	17	TNAUF01000108 - TNAU 22, TNAUF01000109 - TNAU 23, TNAUF01000110 - TNAU 24, TNAUF01000113 - TNAU 28, TNAUF01000114 - TNAU 29, TNAUF01000115 - TNAU 30, TNAUF01000128 - TNAU 44, TNAUF01000125 - TNAU 41, TNAUF01000117 - TNAU 32, TNAUF01000122 - TNAU 38, TNAUF01000120 - TNAU 35, TNAUF01000118 - TNAU 33, TNAUF01000126 - TNAU 42, TNAUF01000124 - TNAU 40, TNAUF01000130 - TNAU 48, TNAUF01000131 - TNAU 49, TNAUF01000132 - TNAU 50
VII	2	TNAUF01000135 - TNAU 52/1, CO (KV)2
VIII	4	TNAUF01000134 - TNAU 52, TNAUF01000136 - TNAU 57, TNAUF01000137 - TNAU 92, TNAUF01000140 - TNAU 95
IX	1	MDU1

Table 2. Intra- (diagonal) and inter-cluster distances of barnyard millet genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	**4.96**	5.10	5.30	6.04	5.62	5.39	8.31	6.58	10.22
II		**4.68**	4.65	5.39	5.38	5.25	7.84	6.78	8.91
III			**1.83**	5.17	4.33	4.29	8.02	6.59	8.35
IV				**5.58**	5.77	5.65	7.47	7.38	8.32
V					**5.14**	4.92	8.06	6.75	8.94
VI						**4.55**	6.97	5.91	8.17
VII							**4.59**	6.64	5.53
VIII								**5.91**	8.43
IX									**0.00**

The major contributing characters towards genetic divergence were grain yield per plant (38.89%) followed by number of productive tillers per plant (17.56%) and flag leaf width (16.22) (Fig. 1). These traits turned out to be the major determinant of genetic diversity and could be used for identifying the diverse genotypes for breeding programme under sodic soil condition. The results get along with the findings of Dhanalakshmi et al. [7] for grain yield per plant in Barnyard millet under sodic soil condition [14].

4. CONCLUSION

Barnyard millet has rarely sought the attention of the researchers and farmers everywhere despite its nutritional and agronomic merits. The present study under sodic field condition, identified grain yield per plant and number of productive tillers per plant as key traits playing predominant role in differentiating the genotypes. The number of productive tillers per plant being one of the component traits for yield improvement turns out to be an added advantage for simultaneous improvement of yield while attempting crosses between diverse parents of the former trait. To further expand the variability available for the traits, the genotypes from the identified diverse clusters can be employed in hybridization programme which forms the base for bridging the gap between the availability and utilization of germplasm. Still, the progress of barnyard millet breeding programme is extremely sluggish due to the lack of genomic resources which need to be attended in the future studies.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Singh RP, Qidwai S, Singh O, Reddy BR, Saharan S, Kataria SK, Kumar L. Millets for food and nutritional security in the context of climate resilient agriculture: A Review. International Journal of Plant and Soil Science. 2022;939-953.
2. Gowda NN, Siliveru K, Prasad PV, Bhatt Y, Netravati BP, Gurikar C. Modern processing of Indian millets: a perspective on changes in nutritional properties. Foods. 2022;11(4):499.
3. De Wet JMJ, Rao KP, Mengesha MH, Brink DE. Domestication of mawa millet (*Echinochloa colona*). Economic Botany.1983;37(3):283-291.
4. Lim EA, Lee KW, Choi BR, Park HS, Woo JH, Kim DI, Lee SH. A Study on Features of Forage Barnyard Millet and Related Research Trends. Journal of The Korean Society of Grassland and Forage Science. 2021;41(3):217-222.
5. Renganathan VG, Vanniarajan C, Karthikeyan A, Ramalingam J. Barnyard millet for food and nutritional security: current status and future research direction. Frontiers in Genetics. 2020;11:500.
6. Waskom RM, Bauder T, Davis JG, Andales AA. Diagnosing saline and sodic soil problems (Doctoral dissertation, Colorado State University. Libraries); 2007.

7. Dhanalakshmi R, Subramanian A, Thirmurugan T, Elangovan M, Kalaimagal T. Genetic diversity study in barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) germplasm under sodic soil condition. Plant Archives. 2019;19(2):2487-2494.
8. Panse VG, Sukhatme PV. Statistical methods for agricultural research workers. ICAR, New Delhi. 1964;381.
9. Mahalanobis PC. On the generalized distance in statistics. National Institute of Science of India; 1936.
10. Rao CR. Advanced Statistical Methods in Biometric Research. John Willey and Sons, New York. 1952;390.
11. GENRES. 1994. Data entry module for genres statistical software pascal intl software solution. Version 3.11.
12. Anuradha N, Patro TSSK, Udaya Bhanu K, 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.
13. Arya R, Bhatt A, Kumar V. Study of Genetic Divergence in Barnyard millet (*Echinochloa frumentacea* (Roxb.) Link) Germplasm. International Journal of BioResource and Stress Management. 2018;9:192-196.
14. Pessarakli M, Szabolcs I. Soil salinity and sodicity as particular plant/crop stress factors. In Handbook of Plant and Crop Stress, Fourth Edition. CRC press. 2019; 3-21.

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