Original Research Article

Evaluation of genetic diversity in sodic soil-grown barnyard millet (Echinochloa frumentacea (Roxb.) Link) germplasm

Abstract

Aims: Barnyard millet (*Echinochloa frumentacea*) is a significant tiny millet crop because of its high nutritional value, exceptional ability to withstand extremes of climate, and short duration. One of the main abiotic stresses that lowers the yield of the barnyard millet crop is sodicity. In order to determine the kind and extent of genetic divergence

Study design: Randomised block design.

Place and Duration of Study: An experiment was carried under sodic soil condtion at Anbil Dharmalingam Agricultural College and Research Institute, Trichy, Tamil Nadu.

Methodology: Ninty 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 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 was used for analysing the data.

Resuts: 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, genotypes, diversity, grain yield, sodic soil

1. INTRODUCTION

Small millets had immense potentials for surviving under the stress condition. Small millets are traditional grains of India as they can be grown under stressed agricultural conditions such as less

water, drought and soil alkaline in addition to many factors. In India, consumption of coarse grains limits small millet cultivation compare to last 50 years. Small millet crops are finger millet, kodo millet, proso millet, foxtail millet, little millet and barnyard millet and play a key role in sustainable agriculture. Millets had unique adapting capacity at both biotic and abiotic stress condition. It needs less water for cultivation that makes these crops suitable for arid and semi-arid farming in the world.

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 (De Wet *et al.,* 1983). 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 (Lim *et al*., 2021). 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 (Renganathan *et al.,* 2020).

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 (Waskom *et al.,* 2007).

Very limited information is available in literature on barnyard millet performance under sodic soil condition (Dhanalakshmi *et al.,* 2019). Genetic diversity is pre-request 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 condtion at Anbil Dharmalingam Agricultural College and Research Institute, Trichy, Tamil Nadu. The experimental material involved 90 germplasm lines of barnyard millet which is derived from Ramiah Gene Bank, Department of Plant Genetic Resource, Tamil Nadu Agricultural University, Coimbatore and two commercial check varieties *viz..,* MDU1 and CO(KV) 2. The experiment was laid out in randomized block design with two replications and the recommended crop management practices were followed. 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). For each data recording, five plants of each accession selected randomly and the mean value derived. The data collected were subjected to analysis of variance (ANOVA) as suggested by Panse and Sukhatme (1967). The replicated data were used to estimate the Genetic divergence and intra and inter cluster distances by following D^2 analysis (Mahalanobis, 1936). Grouping of all the barnyard millet genotypes

into different clusters was carried out as per the procedure proposed by Radhakrishna Rao (1952). GENRES software was used for analysing the data.

3. RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed that the genotypes differed significantly for all characters under investigation. 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 8 genotypes, Cluster VIII had 4 genotypes, cluster III and VII included only 2 genotypes per cluster and the cluster IX ware the smallest and solitary ones. Cluster VIII recorded the highest intra-cluster distance followed by cluster IV. The genotypes grouped within the same cluster showed narrow genetic divergence and would be almost genetically similar, and the genotypes in different clusters exhibited a wider range of genetic variability. Under sodic soil condition, Intra (Diagonal) and inter cluster distance of the nine barnyard millet genotypes clusters are presented in Table 2. The intra cluster distance ranged from 1.83 (cluster III) to 5.91 (cluster VIII). Hence, the genotypes in cluster III (TNAUF01000076 - EF 123 and TNAUF01000085 - EF 136) was more similar. The genotypes in cluster VIII (TNAUF01000134 - TNAU 52, TNAUF01000136 - TNAU 57, TNAUF01000137 - TNAU 92 and TNAUF01000140 - TNAU 95) was more dissimilar among them 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 could gives good amount of beneficial segregants. Many researchers reported a similar divergence result (Anuradha *et al*., 2014; Nirosha *et al.,* 2016; Arya *et al*., 2018 and Dhanalakshmi *et al.,* 2019). The major contributing characters to 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). Therefore, this character was major determinant of genetic diversity and could be used for identify the diverse genotypes for breeding programme under sodic soil condition. The present findings were in agreement with the results of Dhanalakshmi *et al*. (2019) for grain yield per plant in sodic soil condition. In the same way, Anuradha *et al*. (2014) and Arya *et al*. (2018) reported genetic diversity in barnyard millet.

4. CONCLUSION

The highest contribution to genetic divergence was shown by the characteristics grain yield per plant (38.89%) and number of productive tillers per plant (17.56%); hence, this factor was an important indicator of genetic variety. Therefore, 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

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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 distance 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**

Figure 1: Contribution of nine quantitative characters towards genetic divergence