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## Genetic diversity of finger millet (*Eleusine coracana* (L) Gaertn) germplasm under Sodic condition

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### Abstract

The experimental material comprised of 122 diverse genotypes of finger millet (*Eleusine coracana* (L) Gaertn). The data on eleven quantitative characters were recorded to assess the magnitude of genetic diversity through D<sup>2</sup> analysis. Based on genetic distance, finger millet genotypes were grouped into six clusters. Among the six clusters, cluster VI had the highest number of genotypes (52) and cluster II had the lowest number of 2 genotypes. The range of inter cluster distance was 39.545 (between cluster III and IV) to 27.234 (between cluster II and VI). The genotypes in cluster III and cluster IV exhibited high degree of genetic diversity due to maximum inter cluster distance between them and these genotypes may be utilized under hybridization programme for getting high yielding and desirable recombinants.

**Keywords:** Finger millet, genetic diversity, cluster, D<sup>2</sup> analysis

### 1. Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn) is the third most important millet grown in many states of India under diverse situations of soil, temperature and rainfall? Genetic improvement through conventional breeding approaches depends mainly on the availability of diverse germplasm and the amount of genetic variability present in the population. India is having rich germplasm of finger millet. However, only a very small fraction of the available germplasm has been used in the national breeding programme. Hence, the present study was conducted to assess the genetic diversity of 122 finger millet genotypes under sodic soil conditions.

### Materials and methods

The experiment was conducted during *Kharif* 2018 at Anbil Dharmalingam Agricultural College and Research Institute, Trichy under sodic conditions. The experimental material consisted of 120 finger millet genotypes along with two check varieties (TRY1 and Paiyur 2) which were raised in randomized block design with two replications. The observations such as plant height, number of tillers per plant, number of productive tillers per plant, flag leaf length, ear head length, number of fingers per ear head, finger length, 1000 grain weight, Na<sup>+</sup>/K<sup>+</sup> ratio, straw yield per plant and grain yield per plant were recorded and analysed statistically. The genetic divergence was estimated by multivariate analysis using Mahalanobis (1936) [2] D<sup>2</sup> statistics described by Rao (1952) [4]. On the basis of D<sup>2</sup> values 122 finger millet accessions were grouped into different clusters.

### Result and discussion

The 122 finger millet genotypes which were collected from different geographical areas were grouped into 6 clusters. The clustering composition and the grouping of genotypes into different clusters were depicted in Table 1. Among the six clusters, cluster VI had the highest number of genotypes (52) and cluster II had the lowest number of 2 genotypes.

The cluster means with respect to thirteen characters were displayed in Table 2. Among the clusters, the cluster V was suitable for early flowering, early maturity and number of fingers per earhead, whereas cluster IV for dwarf plant type. Hence, cluster V may be selected for developing early maturity types also cluster IV as a donor for dwarfness. The cluster II had the maximum mean value for six traits *viz.*, number of tillers per plant, number of productive tillers per plant, 1000 grain weight, Na<sup>+</sup>/K<sup>+</sup> ratio, straw yield per plant and grain yield per plant. The cluster III had the genotypes with the highest mean value for flag leaf length, earhead length and finger length. Hence, these clusters may be chosen for transferring the traits

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through hybridization programme. The selection of genotypes based on cluster mean for the better exploitation of genetic potential also reported by Wolie and Belete (2013) [5].

The average D<sup>2</sup> distances within and between clusters which were presented in Table 3 (Fig. 1). The intra cluster distance ranged from 34.821 (cluster V) to 6.748 (cluster II). The higher intra cluster distance was recorded by the cluster V (34.821) followed by cluster IV (33.417), cluster III (31.185), cluster VI (29.711) and cluster I (29.103) indicating that the genotypes present within a cluster were more diverse than other clusters. The least intra cluster distance was found in cluster II revealed that presence of more similarity between the genotypes present in this cluster. Similar germplasm grouping also was reported by Prabu *et al.*, 2008 [3].

The range of inter cluster distance was 39.545 (between cluster III and IV) to 27.234 (between cluster II and VI). The genotypes in cluster III and cluster IV exhibited high degree of genetic diversity due to maximum inter cluster distance

between them and these genotypes may be utilized under hybridization programme for getting high yielding and desirable recombinants. Likely, the crosses may be attempted between genotypes in cluster III and V and cluster IV and V. The lowest inter cluster distance was observed between cluster II and V followed by cluster I and II and cluster I and VI showing that these clusters were comparatively less divergent and crosses between them cannot produce better recombinants. These results were in accordance with Wolie and Belete (2013) [5] and Kumar *et al.* (2010) [1].

### Conclusion

From the D<sup>2</sup> analysis, it could be concluded that only five genotypes (FIN2856, FIN2992, FIN3026, FIN3016 and FIN3928) were more diverse and may be selected as parents for hybridization to throw desirable genes from both the parents.

**Table 1:** Cluster classification of finger millet genotypes

Cluster	Number of genotypes	Finger millet genotypes				
		FIN 2882	FIN 3064	FIN 3037	FIN 2881	FIN 3047
I	49	FIN 3039	FIN 2850	FIN 3044	FIN 3048	FIN 3036
		FIN 3027	FIN 3056	FIN 3060	FIN 3017	FIN 2890
		FIN 3055	FIN 2887	FIN 3075	FIN 3046	FIN 2874
		FIN 2886	FIN 3019	FIN 2889	FIN 3063	FIN 3074
		FIN 3045	FIN 2885	FIN 3049	FIN 3057	FIN 3015
		FIN 3053	FIN 2851	FIN 3077	FIN 2876	FIN 3040
		FIN 3042	FIN 3061	FIN 3079	FIN 3066	FIN 3968
		FIN 3041	FIN 2875	FIN 3032	FIN 3014	FIN 3873
		FIN 3050	FIN 3029	FIN 3030	FIN 2849	
		II	2	FIN 3928	FIN 4202	
III	6	FIN 2992	FIN 3025	FIN 2861		FIN 2899
		FIN 2856	FIN 3062			
IV	5	FIN 3038	FIN 4183	FIN 3065	FIN 4109	FIN 3021
V	8	FIN 3016	FIN 3026	FIN 2867	FIN 2869	FIN 3022
		FIN 3028	FIN 2858	FIN 2854		
VI	52	FIN 4605	FIN 2848	FIN 4135	FIN 4198	FIN 4205
		FIN 2857	FIN 4268	FIN 3091	FIN 4035	FIN 3068
		FIN 2852	FIN 2859	FIN 3076	FIN 3154	FIN 4218
		FIN 2860	FIN 4219	FIN 3144	FIN 3966	FIN 3182
		FIN 2855	FIN 3033	FIN 2960	FIN 3174	FIN 4487
		FIN 2871	FIN 4119	FIN 3171	FIN 3078	FIN 4270
		FIN 2870	FIN 3034	FIN 3173	FIN 4288	TRY 1
		FIN 2873	FIN 4048	FIN 3155	FIN 4238	Paiyur 2
		FIN 2872	FIN 3104	FIN 3907	FIN 3089	
		FIN 2896	FIN 3965	FIN 3994	FIN 4401	
FIN 2864	FIN 3067	FIN 3088	FIN 4166			

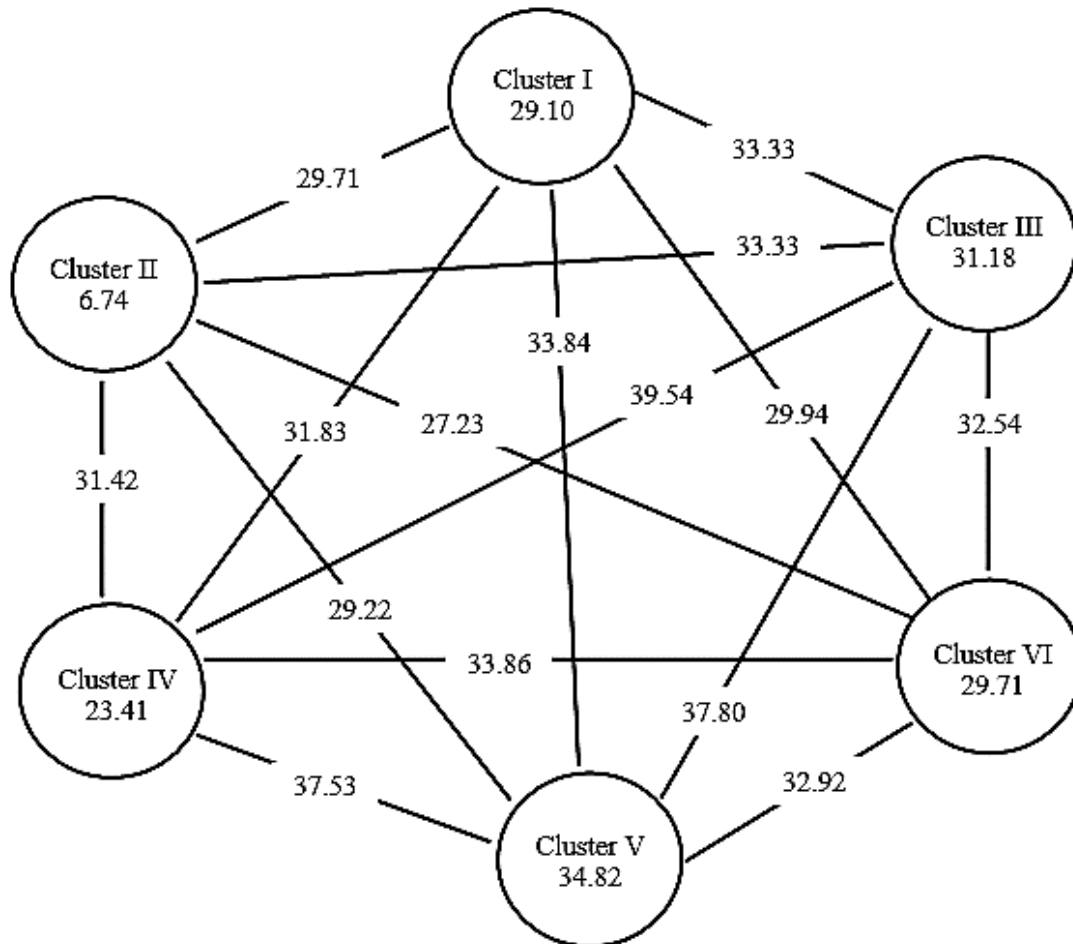
**Table 2:** Cluster mean values of thirteen quantitative characters

Cluster	DFE	DM	PH	NOT	NOPT	FLL	EL	NOF	FL	TW	Na <sup>+</sup> /K <sup>+</sup>	SY	GY
I	95.49	128.55	90.62	5.57	5.31	32.82	9.71	7.31	7.16	2.50	0.27	89.28	22.28
II	97.0	132.25	98.10	9.60	9.60	27.24	8.57	6.89	7.30	2.86	0.03	142.62	41.65
III	107.20	138.91	110.17	5.75	5.75	33.35	11.04	6.89	8.75	2.79	0.26	88.54	24.99
IV	94.50	133.30	75.71	7.06	5.64	27.77	8.87	6.82	6.59	2.68	0.26	97.78	22.15
V	92.31	125.43	96.15	7.11	6.79	31.39	9.28	9.58	6.90	2.38	0.19	110.34	33.40
VI	95.36	129.03	96.56	6.81	6.49	31.97	9.97	7.61	7.10	2.68	0.20	95.21	29.97

DFE- Days to 50% flowering, DM-Days to maturity, PH-Plant height, NOT-Number of tillers per plant, NOPT-Number of productive tillers per plant, FLL-Flag leaf length, EL-Ear head length, NOF-Number of fingers per ear head, FL-Finger length, TW-1000 grain weight, Na<sup>+</sup>/K<sup>+</sup> - Na<sup>+</sup>/K<sup>+</sup> ratio, SY-Straw yield per plant, GY-Grain yield per plant

**Table 3:** Intra (bold) and inter cluster distances of various clusters

Cluster	I	II	III	IV	V	VI
I	29.103	29.714	33.336	31.834	33.849	29.944
II		6.748	32.874	31.421	29.224	27.234
III			31.185	39.545	37.800	32.546
VI				33.417	37.537	33.869
V					34.821	32.928
VI						29.711

**Fig 1:** Intra and inter cluster distances of various clusters

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