

Original Research Article

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## Genetic Diversity Studies in Kodo Millet (*Paspalum scrobiculatum* L.) Germplasm Accessions Based on Biometrical and Nutritional Quality Traits

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### ABSTRACT

#### Keywords

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D<sup>2</sup> analysis.

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In the present study, an attempt was made to assess the genetic divergence among the 103 kodo millet germplasm accessions using Mahalanobis D<sup>2</sup> statistic collected from Millet Breeding Station, Coimbatore. The observations were recorded on yield components and nutritional quality traits. The 103 germplasm lines were grouped into 11 different clusters based on D<sup>2</sup> analysis. Cluster I had a maximum of 63 genotypes, followed by clusters II and III with 14 each, cluster X with four genotypes and cluster VIII with two genotypes. Remaining clusters IV, V, VI, VII, IX and XI were mono-genotypic indicating wide divergence from other clusters. The highest intra cluster distance was observed in cluster X indicating differences in genotypes within cluster. The highest inter-cluster distance was observed between clusters III and X followed by clusters IV and VII suggesting the use of genotypes from these clusters to serve as potential parents for hybridization. The characters days to 50 per cent flowering contributed maximum towards divergence followed by Fe content, Zn content and grain yield per plant.

### Introduction

Kodo millet is a tropical small millet crop, which is indigenous to India (de Wet *et al.*, 1983) and grown for its grain and fodder. It is widely distributed in damp habitats across the tropics and subtropics of the world. In India, kodo millet occupies an area of 152.5 thousand hectares with the production and productivity of 41.2 thousand tones and 312 kg/ha, respectively (Padulosi *et al.*, 2009) and 3570 hectares of area and 6187 tonnes of production in Tamil Nadu (Season and Crop Report 2013-14). Among the small millets, productivity per unit area is highest in kodo millet (Ahamed and Yadava, 1996). It matures in three to four months with yields

varying from 250 to 1000 kg/ha (Hulse *et al.*, 1980) and a potential yield of 2000kg/ha (Harinarayana, 1989). The seeds have an excellent storage life and can be stored for several years (Hegde and Gowda, 1989). The quest for increasing yield is though, a primary concern for an increasing world population which has achieved self-sufficiency in food production quantitatively, but not in quality. Hence, priority of breeders may be to breed for quality with higher amount of micronutrients especially iron (Fe) and zinc (Zn) which is most frequent deficient minerals in cereal based human diets and globally estimated that five million people are

deficient in both the elements. Health consciousness among the consumers in recent years has shifted interest to traditional millet crops like kodo millet. The Kodo millet contains 9.8g Protein, 3.6g Fat, 3.3g Ash, 5.2g Crude fibre, 66.6g Carbohydrate, 353 kcal energy, 35 mg Calcium, 1.7 mg Iron, 0.15 mg Thiamin, 0.09 mg Riboflavin and 2.0 mg Niacin (Hulse *et al.*, 1980).

Being drought tolerant, the nutritional value of the protein has been found to be slightly better than that of foxtail millet but comparable to that of other small millets and has high levels of micronutrients, dietary fiber content and low glycemic index (GI) with potential health prospective (Chandel *et al.*, 2014; Dwivedi *et al.*, 2012; Saleh *et al.*, 2013), anti-oxidants (Chandrasekara and Shahidi 2010) and anti-diabetes principles (Hegde *et al.*, 2005). Till recently, only few genetic studies have been carried out for micronutrients especially for grain Fe and Zn.

Thus, improvement in nutritive quality of grains along with the sustained yield may prove useful for alleviating malnutrition. Aforesaid facts suggest that, kodo millet has all the potential and the success of any plant breeding programme largely depends on the existence of diversity among the genotypes (Allard, 1960). The study was conducted to determine genetic diversity for yields and its components among genotypes is important for planning the future crossing programme using Mahalanobis  $D^2$  statistics and different clustering procedures, based on yield and its component characters and assessing the relative contribution of different components to total divergence (Rao, 1952).

## Materials and Methods

The experimental materials consisted of 103 kodo millet genotypes and were grown in a randomized block design with three

replications at the Millet Breeding Station, Tamil Nadu Agricultural University (TNAU), Coimbatore during *khariif* 2015- 2016. Standard agronomic practices and plant protection measures were taken as per schedule. Observations regarding 13 morphological traits *viz.*, days to first flowering, days to 50 per cent flowering, plant height, number of basal tillers, number of productive tillers, flag leaf length, flag leaf width, peduncle length, inflorescence length, length of longest raceme, thumb length, thousand grain weight and grain yield per plant were recorded in three randomly selected plants in each replication and for nutritional quality traits (Zn and Fe content), the whole grain samples were finely ground and the samples were then oven dried at 60°C for 48 hours before analysis. Fe and Zn content was determined by diacid mixture (sulphuric acid: perchloric acid) method (Piper, 1966) and measured by using Atomic Absorption Spectrophotometer (AAS). Iron and zinc content estimated at Department of Soil Science and Agricultural Chemistry, TNAU. The genetic diversity between the genotypes was worked out using Mahalanobis  $D^2$  (1936) statistics and grouping of genotypes into clusters was done using Tocher's method (Rao, 1952).

## Results and Discussion

Analysis of variance showed significant differences among the genotypes for all the characters studied. Based on  $D^2$  value, 103 genotypes were grouped into 11 clusters (Table 1) (Fig. 1). The distribution pattern of the genotypes into clusters indicated that cluster I was the largest, containing 63 genotypes followed by cluster II and III with 14 genotypes, cluster X with four genotypes and cluster VIII with two genotypes. Six clusters IV, V, VI, VII, IX and XI were solitary containing one genotype each. Solitary clusters revealed the presence of

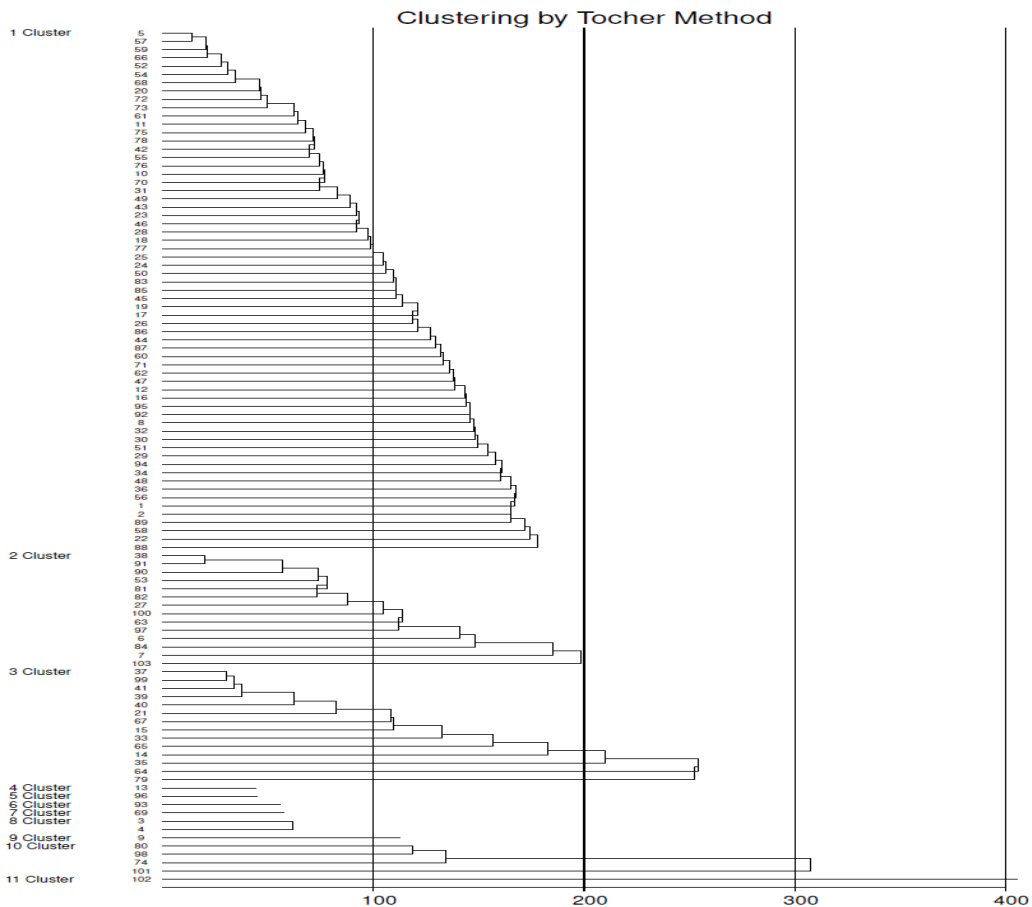
wide genetic divergence for various characters among these genotypes.

Padmaja (1998) in little millet and Ulaganathan and Nirmalakumari (2015) in finger millet also observed solitary clusters in their study. The presence of solitary clusters indicated extreme phenotypic performance in positive or negative directions for one or the other characters.

The intra and inter-cluster distance analysis indicated that the maximum intra-cluster distance was observed for cluster X (17.08) followed by cluster III (13.61), cluster II (12.15), cluster I (11.69) and cluster VIII (7.85) (Table 2). This suggested that the genotypes in cluster X were relatively more

diverse among themselves. Similar findings were reported by Shinde *et al.*, (2013) in finger millet. Genotypes falling between cluster III and X exhibited maximum inter-cluster distances (33.02), showing high degree of genetic diversity indicating that genetic makeup of genotypes falling in this cluster may be entirely different from one another and thus may be utilized for future breeding programme for getting high yielding genotypes. These results of genetic diversity study were in agreement with the finding of Wolie *et al.*, (2013) and Dinesh *et al.*, (2010) in finger millet. Therefore the genotypes of most diverse cluster may be used as parents in hybridization programmes to develop high yielding varieties.

**Fig.1** Dendrogram based on  $D^2$  values for fifteen characters in kodo millet



**Table.1** Distribution of 103 genotypes into 11 clusters based on fifteen characters

Clusters	Number of genotypes	Accession number
I	63	Aamo 101, TNAU 108, TNAU 120, TNAU 130, TNAU 111, TNAU 104, TNAU 137, IPS 102, TNAU 146, TNAU 148, TNAU 123, RK 82, TNAU 150, TNAU 153, Sel 16, TNAU 105, TNAU 151, RK 51, TNAU 141, Sel 12, TNAU 98, TNAU 90, IPS 122, TNAU 93, Sel 1, ICK 1042, TNAU 152, IPS 125, IPS 123, TNAU 99, TNAU 165, TNAU 172, TNAU 92, ICK 7114, ICK 86, RBK 73, TNAU 174, TNAU 91, TNAU 177, TNAU 121, TNAU 145, TNAU 124, TNAU 96, RK 84, DPS 368, TNAU 195, TNAU 190, Aamo 271, Sel 14, Sel 11, TNAU 100, Sel 7, TNAU 194, Sel 17, TNAU 97, Sel 19, TNAU 107, Aamo 68, Aamo 83, TNAU 180, TNAU 109, IPS 118, TNAU 179
II	14	Sel 21, TNAU 188, TNAU 187, TNAU 102, TNAU 162, TNAU 164, RBK 155, Sel 16, TNAU 127, TNAU 201, Aamo 126, TNAU 171, Aamo 258, TNAU 86
III	14	Sel 20, GPUK 3, TNAU 85, TNAU 82, TNAU 84, IPS 113, TNAU 133, DPS 95, Sel 15, TNAU 129, RK 162, Sel 18, TNAU 128, TNAU 154
IV	1	RK 111
V	1	TNAU 197
VI	1	TNAU 191
VII	1	TNAU 140
VIII	2	Aamo 89, Aamo 90
IX	1	RK 50
X	4	TNAU 155, TNAU 236, TNAU 149, CO 3
XI	1	APK 1

**Table.2** Intra (diagonal) and inter cluster average distances among eleven clusters for 15 characters in kodo millet

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
<b>I</b>	<b>11.69</b>	16.11	15.35	14.56	14.49	15.39	13.75	15.65	23.06	25.80	29.35
<b>II</b>		<b>12.15</b>	22.90	16.71	17.47	16.88	19.73	15.88	16.53	19.31	25.80
<b>III</b>			<b>13.61</b>	19.95	20.01	22.26	17.55	19.00	30.37	33.02	32.79
<b>IV</b>				<b>0.00</b>	8.45	11.20	12.48	22.53	17.64	21.16	27.50
<b>V</b>					<b>0.00</b>	7.47	9.66	22.15	19.20	22.65	30.68
<b>VI</b>						<b>0.00</b>	11.72	21.75	18.90	20.52	32.59
<b>VII</b>							<b>0.00</b>	22.66	23.18	26.62	31.72
<b>VIII</b>								<b>7.85</b>	26.59	27.50	29.26
<b>IX</b>									<b>0.00</b>	14.40	26.59
<b>X</b>										<b>17.08</b>	29.15
<b>XI</b>											<b>0.00</b>

Tocher cut off value: 188

**Table.3** Cluster mean values for fifteen characters in kodo millet

<b>Cluster</b>	<b>DF</b>	<b>DFE</b>	<b>PH</b>	<b>NBT</b>	<b>PT</b>	<b>FLL</b>	<b>FLW</b>	<b>PL</b>	<b>IL</b>	<b>LLR</b>	<b>TL</b>	<b>TGW</b>	<b>Zn</b>	<b>Fe</b>	<b>GY</b>
<b>I</b>	57.23	60.24	58.20	16.65	6.16	13.74	0.68	5.34	12.45	6.06	5.67	3.59	3.76	15.55	15.14
<b>II</b>	64.55	67.79	70.51	18.34	7.56	13.90	0.73	5.78	13.78	6.85	7.29	3.91	4.54	10.96	18.28
<b>III</b>	52.02	54.83	44.03	18.26	6.08	12.23	0.68	4.63	11.55	5.56	4.91	3.57	1.95	15.74	11.88
<b>IV</b>	61.67	65.33	71.09	18.89	5.40	16.36	0.76	6.93	12.59	5.94	5.71	3.67	0.20	20.48	18.64
<b>V</b>	61.00	64.00	68.33	22.22	8.19	14.74	0.66	5.41	11.79	6.50	6.63	3.96	3.40	24.56	20.93
<b>VI</b>	62.67	66.33	71.10	18.00	6.00	14.56	0.57	6.58	12.51	5.76	6.50	3.46	5.66	24.27	14.33
<b>VII</b>	58.33	60.33	49.60	12.11	5.60	13.22	0.72	4.11	14.30	6.07	5.11	3.11	4.70	24.69	19.92
<b>VIII</b>	58.33	61.67	54.63	22.89	8.82	15.18	0.69	5.86	11.97	4.71	5.30	4.01	6.50	6.93	10.43
<b>IX</b>	70.67	75.33	79.90	14.67	9.00	11.69	0.71	6.94	19.26	8.32	11.62	4.73	1.21	15.56	22.89
<b>X</b>	74.00	78.25	78.75	17.94	6.66	12.22	0.75	6.74	14.51	7.58	8.62	4.11	3.12	15.67	13.64
<b>XI</b>	65.00	69.67	86.35	23.67	7.80	11.37	1.62	6.33	18.86	8.03	9.63	4.91	2.98	7.73	16.13

Abbreviations used: DF- Days to first flowering (days); DFE- Days to 50 per cent flowering (days); PH- Plant height (cm); NBT-Number of basal tillers (count); PT- Number of productive tillers (count); FLL- Flag leaf length (cm); FLW- Flag leaf width (cm); PL- Peduncle length (cm); IL- Inflorescence length (cm); LLR- Length of the longest raceme (cm); TL- Thumb length (cm); TGW- Thousand grain weight (g); Zn- Zinc content (mg/100g); Fe- Iron content (mg/100g); GY- Grain yield per plant (g).

**Table.4** Percentage contribution of fifteen characters to genetic divergence in 103 kodo millet genotypes

Character	Times Ranked 1st	Contribution %
Days to first flowering	17	0.32
Days to 50% flowering	1815	34.55
Plant height (cm)	110	2.09
Number of basal tillers	119	2.27
Number of productive tillers	39	0.74
Flag leaf length (cm)	34	0.65
Flag leaf width (cm)	123	2.34
Peduncle length (cm)	3	0.06
Inflorescence length (cm)	44	0.84
Length of the longest raceme (cm)	9	0.17
Thumb length (cm)	3	0.06
Thousand grain weight (g)	40	0.76
Zn content (mg/100g)	790	15.04
Fe content (mg/100g)	1694	32.25
Grain yield per plant (g)	413	7.86

A perusal of results of cluster means (Table 3) revealed that cluster IX exhibited highest mean value for the characters number of productive tillers (9.00), peduncle length (6.94 cm), inflorescence length (19.26 cm), length of the longest raceme (8.32 cm), thumb length (11.62 cm) and grain yield per plant (22.89 g). Cluster XI had highest mean value for plant height (86.35 cm), number of basal tillers (23.67), flag leaf width (1.62 cm) and thousand grain weight (4.91 g). Cluster VIII had highest mean value for flag leaf length (15.18 cm) and Zn content (6.50 mg/100g). Cluster VII had highest mean value for Fe content (24.69 mg/100g). The lowest mean value for days to first flowering (52.02), days to 50 per cent flowering (54.83) was shown by the cluster III. All the minimum and maximum cluster mean values were distributed in relatively distant clusters. However the cluster IX recorded highest mean value for most of the characters. Thereby recombination breeding between genotypes of different clusters could be done to combine the desirable characters of different accessions.

The selection and choice of parents mainly depends upon contribution of characters towards divergence (Table 4). The maximum contribution in the manifestation of genetic divergence was exhibited by Fe content followed by Zn content, days to 50 per cent flowering, grain yield per plant, flag leaf width, number of basal tillers and plant height suggesting scope for improvement in these characters. In other words, selection for these characters may be rewarding. Similar results were reported for Zn content and grain yield per plant in barnyard millet by Plawani Panda (2015). Shinde *et al.*, (2013) for Iron content in finger millet, Ulaganathan (2013) in finger millet for days to 50 per cent flowering, Sirisha (2008) in foxtail millet for number of tillers and Manimozhi Selvi (2014) for grain yield per plant in little millet. Contribution of the characters towards diversity indicated that flowering time, Fe and Zn content had more variability among the lines. Hence the nutritional quality and the duration of the kodo millet can be targeted utilizing the variability showed among the lines tested.

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