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Research Article

Characterization and clustering of kodo millet (*Paspalum scrobiculatum* L.) genotypes based on qualitative characters

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Abstract

Kodo millet accessions 103 numbers were evaluated and characterized for 21 qualitative characters. The traits *viz.*, leaf character, leaf blade pigmentation, panicle exertion, spikelet arrangement on rachis, panicle appearance, spike curvature, degree of culm branching, degree of lodging, shattering and grain colour showed higher variation and thus exhibits scope for selection of traits useful for breeding programmes. The traits growth habit, leaf sheath pigmentation, sheath base pigmentation, leaf juncture pigmentation, internode pigmentation, flag leaf at the second primary axis node, nerves on glumes, spike branching, spikelet density, senescence and grain shape showed no variations. Cluster analysis was carried out which grouped the 103 accessions into 13 clusters. Cluster III was the largest cluster with 39 accessions followed by cluster VII with 21, cluster IV with 13, cluster I with nine, cluster X with six, cluster IX with four, cluster V with three, cluster II and VIII with two accessions each and clusters VI, XI, XII and XIII with one accession each. The genotypes within the same cluster considered to have the similar phenotypic characters. And the genotypes between the clusters are more diverse ones. Therefore, the genotypes of most diverse cluster may be used as parents in hybridization programmes to develop high yielding varieties.

Key words
Characterization, Cluster analysis, Kodo millet, Qualitative traits

Introduction

Kodo millet (*Paspalum scrobiculatum* L.), is cultivated as an annual crop. It has been cultivated for 3000 years in India, where it is considered as a minor cereal crop except in the Deccan where it is a cereal of utmost importance. The seeds are used as human food grains are ground into meal and used for puddings (Quattrocchi, 2006). In Africa, it is harvested as a wild cereal (FAO/ICRISAT, 1996) and is mainly considered as a famine food. Kodo millet is well suited to dry conditions and can be grown in a variety of poor soil types from gravelly to clay (de Wet *et al.*, 1983b; M'Ribu and Hilu, 1996). It has superior nutritional properties including high 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) and low-GI carbohydrate diets help in the prevention of obesity, diabetes, and cardiovascular disease (Brand-Miller *et al.*, 2009). The basic information on the existence of variability is essential for any successful plant breeding programme. Selection of superior varieties would be effective only when variability exists in the material chosen for improvement. The objectives of this study were to evaluate and characterize the kodo millet genotypes based on qualitative traits and to identify the promising kodo millet genotypes for future breeding programs.

Materials and Methods

One hundred and three accessions of kodo millet obtained from the Department of Millets, Centre for Plant Breeding and Genetics, TNAU, Coimbatore were used for the study Table 1. The experiment was laid out during *Kharif* 2015 in a Randomized Block Design (RBD) with three replications. The evaluation and characterization was done for 21 characters *viz.*, Growth habit, leaf character, leaf sheath pigmentation, sheath base pigmentation, leaf juncture pigmentation, internode pigmentation, leaf blade pigmentation, panicle exertion, flag leaf at the second primary axis node, spikelet arrangement on rachis, nerves on glumes, panicle appearance, spike branching, spike curvature, spikelet density, degree of culm branching, degree of lodging, shattering, senescence, grain colour and grain shape based on the descriptors of *Paspalum scrobiculatum* developed by IBPGR, 1983. And the data were subjected to multivariate hierarchial cluster analysis.

Similarity matrix was prepared with similarity coefficient using Simqual option of similarity menu. Similarity matrix was converted into dendrogram by Sequential Agglomerative Hierarchial Non-overlapping (SAHN) clustering technique utilizing the Unweighted Pair Group Method with Arithmetic Averages UPGMA method with FIND option using the computer software NTSYSpc version 2.02i (Rohlf, 1998).

Results and Discussion

Qualitative characters exhibits stable and discrete inheritance and are generally used as plant descriptors to identify the genotypes, which are less influenced by environmental fluctuations. Twenty one qualitative characters were used for characterization of the germplasm lines. The results of qualitative traits are given in Table 2 and Figure 1. Among the characters studied greater frequency was observed for leaf character, leaf blade pigmentation, panicle exertion, spikelet arrangement on rachis, panicle appearance, spike curvature, degree of culm branching, degree of lodging, shattering and grain colour and thus exhibits scope for selection of traits useful for identifying the genotypes. The lines did not exhibit variations for the traits such as growth habit, leaf sheath pigmentation, sheath base pigmentation, leaf juncture pigmentation, internode pigmentation, flag leaf at the second primary axis node, nerves on glumes, spikelet density, spike branching, senescence and grain shape indicating that these traits will not be much use for distinguishing these genotypes.

Majority of the germplasm lines have erect growth habit, droopy leaf character, devoid of leaf sheath pigmentation and leaf juncture pigmentation, greater frequency of sheath base pigmentation and internode pigmentation, lower frequency of leaf blade pigmentation, complete panicle exertion, well developed flag leaf at the second primary axis node, regular spikelet arrangement on rachis, broad nerves on glumes, open panicle appearance, spike branching, straight spike curvature, dense spikelet density, high degree of culm branching, extensive degree of lodging, shattering, brown grain colour, actively growing senescence and oval grain shape. Similar results were reported by Vetriventhan (2011) for growth habit and Reddy *et* al. (2006) for grain colour in foxtail millet. Joshi *et al.* (2014) reported majority of the kodo millet land races have erect growth habit, regular rows on spikelets, complete ear exertion and all the land races showed sheath base pigmentation and flag leaf at the second primary axis node akin to the observations made in the present study.

All the 103 germplasm accessions were subjected to cluster analysis based on similarity matrix and the genotypes were grouped into 13 clusters at the coefficients of 0.88. Clustering pattern based on quantitative characters was entirely different from the qualitative characters. Similar findings were reported by Nirubana *et al.* (2017) in kodo millet; and Salini *et al.* (2010) in proso millet List of clusters with constituent accessions were given in Table 3 and Figure 2. Cluster III was the largest cluster with 39 accessions from different origin followed by cluster VII with 21, cluster IV with 13, cluster I with nine, cluster X with six, cluster IX with four, cluster V with three, cluster II and VIII with two genotypes each and clusters VI, XI, XII and XIII with one genotype each. The genotypes such as Sel 21, TNAU 93, TNAU 201 and TNAU 102 formed solitary clusters which revealed the presence of wide diversity for various characters among these accessions. Similar results of solitary clusters were reported by Dangnachew Lule *et al.* (2012) in finger millet and Sao *et al.*, (2016) in kodo millet. The random pattern of distribution of different accessions into various clusters from different eco-geographic regions revealed that there was no association between genetic diversity and geographic diversity. The nature of selection forces operating under one eco-geographical region seemed to be similar to that of other regions since the accessions from different geographical regions were grouped together into same clusters Sao et al., (2016). The genotypes between the clusters are more diverse ones. Therefore, the genotypes of most diverse cluster may be used as parents in hybridization programmes to develop high yielding varieties.

This study reveals sufficient genetic diversity available in the kodo millet germplasm for following traits *viz.*, leaf character, leaf blade pigmentation, panicle exertion, spikelet arrangement on rachis, panicle appearance, spike curvature, degree of culm branching, degree of lodging, shattering and grain colour showed higher variations and these traits may be useful for identifying the genotypes as well as introgression of novel traits in breeding programmes. The cluster analysis showed that the genotypes such as Sel 21, TNAU 93, TNAU 201 and TNAU 102 formed solitary clusters which revealed the presence of wide diversity for various characters among these accessions and this can be exploited for future breeding programs.

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Table 1. List of kodo millet germplasm accessions

SI. No	Accessions	Source/Origin
1	Aamo 68	Rewa, Madhya Pradesh
2	Aamo 83	Rewa, Madhya Pradesh
3	Aamo 89	Rewa, Madhya Pradesh
4	Aamo 90	Rewa, Madhya Pradesh
5	Aamo 101	Rewa, Madhya Pradesh
6	Aamo 126	Rewa, Madhya Pradesh
7	Aamo 258	Rewa, Madhya Pradesh
8	Aamo 271	Rewa, Madhya Pradesh
9	RK 50	Rewa, Madhya Pradesh
10	RK 51	Rewa, Madhya Pradesh
11	RK 82	Rewa, Madhya Pradesh
12	RK 84	Rewa, Madhya Pradesh
13	RK 111	Rewa, Madhya Pradesh
14	RK 162	Rewa, Madhya Pradesh
15	DPS 95	Dindori, Madhya Pradesh
16	DPS 368	Dindori, Madhya Pradesh
17	ICK 86	India
18	ICK 1042	India
19	ICK 7114	India
20	IPS 102	ICRISAT, Hyderabad
21	IPS 113	ICRISAT, Hyderabad
22	IPS 118	ICRISAT, Hyderabad
23	IPS 122	ICRISAT, Hyderabad
24	IPS 123	ICRISAT, Hyderabad
25	IPS 125	ICRISAT, Hyderabad
26	RBK 73	Selection from germplasm JNKVV, Jabalpur
27	RBK 155	Selection from germplasm no. GPLM 251, JNKVV, Jabalpur
28	Sel 1	TNAU, Tamil Nadu
29	Sel 7	TNAU, Tamil Nadu
30	Sel 11	TNAU, Tamil Nadu
31	Sel 12	TNAU, Tamil Nadu
32	Sel 14	TNAU, Tamil Nadu
33	Sel 15	TNAU, Tamil Nadu
34	Sel 17	TNAU, Tamil Nadu
35	Sel 18	TNAU, Tamil Nadu
36	Sel 19	TNAU, Tamil Nadu
37	Sel 20	TNAU, Tamil Nadu
38	Sel 21	TNAU, Tamil Nadu
39	TNAU 82	TNAU, Tamil Nadu
40	TNAU 84	TNAU, Tamil Nadu
41	TNAU 85	TNAU, Tamil Nadu
42	Sel 16	TNAU, Tamil Nadu
43	TNAU 90	Selection from IPS 117
44	TNAU 91	Selection from IPS 118
45	TNAU 92	Selection from IPS 122
46	TNAU 93	Selection from IPS 123
47	TNAU 96	Selection from IPS 131
48	TNAU 97	Selection from IPS 147
49	TNAU 98	Selection from IPS 160
50	TNAU 99	Selection from IPS 181
51	TNAU 100	Selection from IPS 194
52	TNAU 111	Selection from mutant TNAU 51-700-1-13-1
53	TNAU 102	Selection from IPS 122
54	TNAU 104	Selection from mutant TNAU 51-500-5-1-1
55	TNAU 105	Selection from mutant TNAU 51-600-3-1-1
56	TNAU 107	Selection from mutant TNAU 51-600-6-6-2

57	TNAU 108	Selection from mutant TNAU 51-700-1-3-2
58	TNAU 109	Selection from mutant TNAU 51-700-1-4-1
59	TNAU 120	Selection from mutant TNAU 51-600-2-4-2
60	TNAU 121	Selection from mutant TNAU 51-600-5-2-1
61	TNAU 123	Selection from mutant TNAU 51-600-6-2-1
62	TNAU 124	Selection from mutant TNAU 51-600-6-2-2
63	TNAU 127	Selection from mutant TNAU 51-700-1-3-2
64	TNAU 128	Selection from mutant TNAU 51-700-2-3-2
65	TNAU 129	Selection from mutant CO 3 -500-3-15-1
66	TNAU 130	Selection from mutant CO 3 -700-6-1-1
67	TNAU 133	Selection from mutant CO 3 – 700-6-1-2
68	TNAU 137	Selection from mutant CO 3 -500-10-5-1
69	TNAU 140	Selection from mutant CO 3 – 600-1-3-1
70	TNAU 141	Selection from mutant CO 3 – 700-2-14-1
71	TNAU 145	Selection from mutant CO 3 -700-9-16-1
72	TNAU 146	Selection from mutant TNAU 51-600-4-5-1
73	TNAU 148	Selection from mutant TNAU 51-600-6-1-2
74	TNAU 149	Selection from mutant TNAU 51- 600-6-7-1
75	TNAU 150	Selection from mutant TNAU 51- 600-6-11-1
76	TNAU 151	Selection from mutant TNAU 51-600-6-11-2
77	TNAU 152	Selection from mutant TNAU 51-700-2-2-1
78	TNAU 153	Selection from mutant CO 3-600-7-5-3
79	TNAU 154	CO 3-700-8-3-1
80	TNAU 155	Selection from Athipatti, Dharmapuri
81	TNAU 162	Selection from BK 5
82	TNAU 164	Selection from RK 15
83	TNAU 165	Selection from RK 58
84	TNAU 171	Selection from RK 5
85	TNAU 172	Selection from RK 137
86	TNAU 174	Selection from DPS 135
87	TNAU 177	Selection from Aamo 600
88	TNAU 179	Selection from Aamo 602
89	TNAU 180	Selection from Aamo 603
90	TNAU 187	Selection from Aamo 617
91	TNAU 188	Selection from Aamo 618
92	TNAU 190	Selection from Aamo 620
93	TNAU 191	Selection from Aamo 621
94	TNAU 194	Selection from Aamo 625
95	TNAU 195	Selection from Aamo 626
96	TNAU 197	Selection from Aamo 628
97	TNAU 201	Selection from Peruvaragu
98	TNAU 236	IC 426679 (from NBPGR, Hyderabad)
99	GPUK 3	Selection from germplasm GPLM 826, UAS, Bangalore
100	Sel 6	TNAU, Tamil Nadu
101	CO 3	A variety released by TNAU, through pure line selection (Gengia selection)
102	APK 1	Selection from Arupukotti
103	TNAU 86	Selection from IPS 85

Table 2. Frequency distribution based on 21 qualitative characters in 103 kodo millet genotypes

Character	Phenotype	Score	Number of genotypes	Frequency percentage
Growth habit	Erect	3	103	100.00
	Decumbent	5	0	0.00
	Prostrate	7	0	0.00
Leaf character	Erect	3	20	19.40
	Droopy	5	83	80.60
Leaf Sheath pigmentation	Absent	1	103	100.00
	Present	9	0	0.00
Sheath base pigmentation	Absent	1	0	0.00
	Present	9	103	100.00
Leaf juncture pigmentation	Absent	1	103	100.00
	Present	9	0	0.00
Internode pigmentation	Absent	1	0	0.00
	Present	9	103	100.00
Leaf blade pigmentation	Absent	1	85	82.50
	Present	9	18	17.50
Panicle exertion	Complete	1	82	79.60
	Partial	9	21	20.40
Flag leaf at the second primary axis node	Absent	1	0	0.00
	Rudimentary	5	0	0.00
	Well developed	9	103	100.00
Spikelet arrangement on rachis	Regular	1	76	73.80
	Regular in upper half of inflorescence and regular in lower half	3	8	7.80
	Two to three irregular rows	5	17	16.50
	Two to four irregular rows	7	2	1.90
	Irregular	9	0	0.00
Nerves on glumes	Broad nerves (5 nerves)	3	102	99.00
	Closed nerved (7 nerves)	5	1	1.00
Panicle appearance	Open	3	93	90.30
	Semi compact	5	10	9.70
	Compact	7	0	0.00
Spike branching	Absent	1	0	0.00
	Present	9	103	100.00
Spike curvature	Straight	2	75	72.80
	Curved	4	28	27.20
Spikelet density	Sparse	3	0	0.00
	Intermediate	5	0	0.00
	Dense	7	103	100.00
Degree of culm branching	Low (upper 1-4 nodes rarely branched)	3	0	0.00
	Medium (upper 2-4 nodes produce inflorescence)	5	4	3.90
	High (most nodes produce inflorescence)	7	99	96.10
Degree of Lodging	Non lodging	0	40	38.80
	Slight	1	15	14.60
	Medium	5	7	6.80
	Extensive	9	41	39.80
Shattering	Absent	0	37	35.90
	Present	1	66	64.10
Grain colour	Dark grey	1	0	0.00
	Brown	2	76	73.80
	Light brown	3	27	26.20
	Grey	4	0	0.00
	Golden yellow	5	0	0.00
	Straw white / cream	6	0	0.00
Senescence	Dead	1	0	0.00
	Actively growing	9	103	100.00
Grain shape	Oval	2	103	100.00
	Elliptical	4	0	0.00

Table 3. Constituents of 13 clusters in kodo millet based on 21 qualitative characters

Clusters	Number of genotypes	Constituent accessions
I	9	Aamo 68, TNAU 96, TNAU 172, Aamo 83, RK 84, RK 51, TNAU 187, TNAU 90, Sel 6
II	2	DPS 368, TNAU 151
III	39	Aamo 89, DPS 95, Sel 1, TNAU 92, TNAU 97, TNAU 98, TNAU 197, TNAU 191, TNAU 190, TNAU 99, TNAU 179, TNAU 195, TNAU 171, TNAU 162, TNAU 107, TNAU 109, Aamo 101, ICK 1042, RK 82, ICK 86, TNAU 177, TNAU 133, Aamo 271, Sel 12, TNAU 145, IPS 102, TNAU 165, TNAU 194, TNAU 100, TNAU 111, RK 111, RBK 73, TNAU 105, TNAU 164, TNAU 154, RK 162, Sel 14, TNAU 174, TNAU 188
IV	13	RBK 155, TNAU 130, Sel 19, TNAU 124, TNAU 129, TNAU 236, TNAU 146, TNAU 153, TNAU 104, TNAU 108, TNAU 120, TNAU 180, TNAU 137
V	3	Aamo 90, Sel 17, TNAU 121
VI	1	TNAU 93
VII	21	Aamo 126, TNAU 127, Aamo 258, IPS 113, IPS 118, TNAU 84, TNAU 85, TNAU 148, TNAU 152, TNAU 150, IPS 125, TNAU 82, TNAU 123, GPUK 3, IPS 122, Sel 16, IPS 123, Sel 15, Sel 18, Sel 20, ICK 7114
VIII	2	Sel 7, TNAU 91
IX	4	Sel 11, TNAU 128, TNAU 141, TNAU 140
X	6	RK 50, CO 3, TNAU 86, APK 1, TNAU 149, TNAU 155
XI	1	Sel 21
XII	1	TNAU 201
XIII	1	TNAU 102

a) Leaf character

Droopy

Erect

b) Pigmentation

Leaf blade pigmentation

Internode pigmentation

Sheath base pigmentation

c) Panicle exertion

Complete

Partial

d) Spikelet arrangement on rachis

Regular

Regular in upper half & irregular in lower half

2-3 irregular rows

2-4 irregular rows

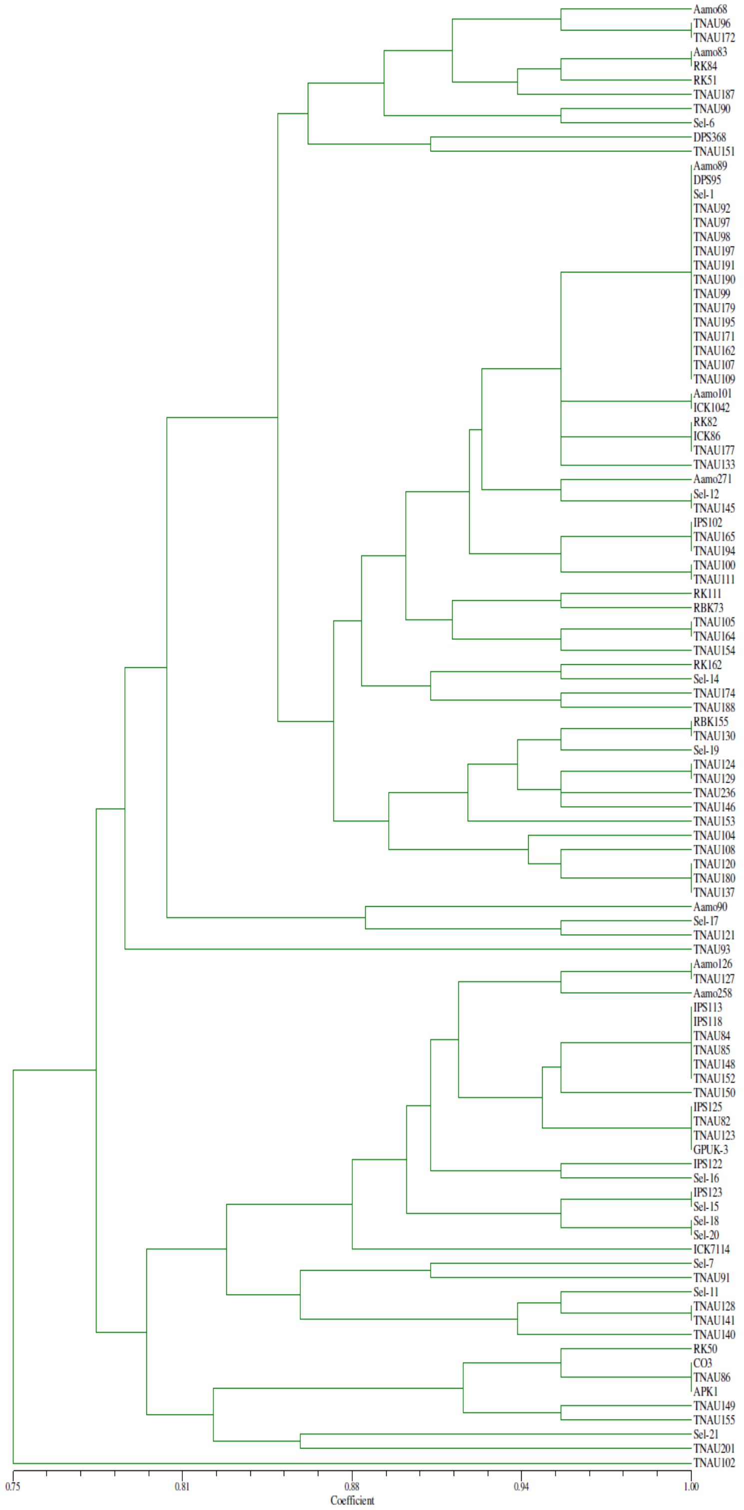
e) Degree of lodging

f) Grain colour

Brown

Light brown

Fig.1. Morphological differences among kodo millet genotypes



Each separate line indicates a cluster
Mean genetic dissimilarity – 0.8

Fig. 2. Clustering of 103 germplasm of kodo millet based on SM coefficient

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