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Research Article

Genetic diversity studies in kodo millet (*Paspalum scrobiculatum* L.)

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Abstract

The present investigation was undertaken to assess genetic diversity in seventy genotypes of kodo millet. The analysis of variance revealed the presence of significant variation among the genotypes for all 13 characters. Higher genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as per cent mean were recorded for thumb raceme length, number of productive tillers per plant, length of panicle, raceme length and grain yield per plant, indicating that simple selection could be practised for improving these traits. Seventy genotypes were grouped into seven different clusters on the basis of magnitude of D^2 values by Mahalanobis D^2 analysis. Cluster I had 51 genotypes followed by cluster II with 14 genotypes, while clusters III, IV, V, VI and VII were mono genotypic. The inter-cluster distance was high between clusters II and III and therefore it is suggested to use these genotypes as parents for hybridization to evolve potential segregants.

Key words: Diversity, Kodo millet, GCV, PCV, Heritability.

INTRODUCTION

Millets are a group of highly variable small-seeded grasses, widely grown around the world as grains for food and fodder. They are highly tolerant to extreme weather conditions and the nutrient contents are similar or higher than other major cereals. Kodo millet is one of the most important small millets grown in large areas of developing world especially in Africa and Asia. Kodo millet, *Paspalum scrobiculatum* L. is a self pollinated crop belonging to the *Poaceae* family, is a tetraploid ($2n=4x=40$) good source of minerals. Knowledge of genetic variability in respect of yield in any species is a very valuable estimation in plant breeding programme, since it helps in selection of ideal parents and or traits for selective hybridization. People have come across the importance of kodo millet and hence its demand is increasing. To fulfill the demand of kodo millet in future, extensive research is needed (Nirubana *et al.*, 2017). Therefore, the present study is conducted to analyse the genetic variability and diversity among 70 genotypes of Kodo millet.

MATERIALS AND METHODS

The present investigation was carried out at Educational and Research Farm, Department of Agricultural Botany, College of Agriculture, Dapoli, Dist. Ratnagiri, Maharashtra during *kharif*, 2020-21. The material comprised of 70 genotypes of Kodo millet collected from ICAR-Indian Institute of Millets Research, Rajendranagar, Hyderabad (**Table 1**). The experiment was conducted in Randomized Block Design with two replications. The seed was dibbled at a 30 cm distance between row to row and 20 cm distance plant to plant. Each plot had a 2.0 m \times 0.9 m area, with three rows per genotype. Each row had 10 plants thus constituting 60 plants in two replications. A standard package of practices was carried out to maintain a good crop stand. The observations were recorded on five plants selected randomly from each genotype for thirteen quantitative characters and two qualitative characters *i.e.* culm branching and panicle appearance (Bowen, 2009). The average values were used for further analysis.

Table 1. Kodo millet genotypes used in the present study

S. No.	Genotypes	S. No.	Genotypes
1	IPS 4	2	IPS 5
3	IPS 13	4	IPS 68
5	IPS 69	6	IPS 91
7	IPS 105	8	IPS 147
9	IPS 155	10	IPS 158
11	IPS 159	12	IPS 172
13	IPS 178	14	IPS 207
15	IPS 236	16	IPS 240
17	IPS 245	18	IPS 254
19	IPS 287	20	IPS 319
21	IPS 329	22	IPS 344
23	IPS 358	24	IPS 368
25	IPS 383	26	IPS 388
27	IPS 415	28	IPS 429
29	IPS 593	30	IPS 606
31	IPS 614	32	IPS 622
33	IPS 627	34	IPS 628
35	IPS 645	36	IPS 648
37	IPS 653	38	IPS 654
39	IPS 669	40	IPS 670
41	IPS 694	42	IPS 699
43	IPS 706	44	IPS 709
45	IPS 730	46	IPS 741
47	IPS 744	48	IPS 764
49	IPS 777	50	IPS 782
51	IPS 785	52	IPS 793
53	IPS 795	54	IPS 803
55	IPS 814	56	IPS 828
57	IPS 862	58	IPS 870
59	IPS 883	60	IPS 891
61	IPS 908	62	IPS 919
63	EDS 38	64	ERP 49
65	ERP 51	66	ERP 55
67	ERP 62	68	ERP 77
69	ERP 96	70	ER 96

The analysis of variance was computed as suggested by Panse and Sukhatme, (1985). The phenotypic and genotypic coefficients of variation (PCV, GCV) were computed as per Burton and DeVane (1953). Heritability in a broad sense (H^2) was estimated by formulae suggested by Lush (1949) and the genetic advance was calculated in percent by the formula suggested by Johnson *et al.* (1955). Genetic diversity was estimated by Mahalanobis (1936) D^2 statistic technique as described by Rao (1952). The statistical package used for analysis was GENALEX. Protein and calcium content was estimated as per the standard procedure and expressed as per cent.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the genotypes for all the 13 quantitative characters indicating the presence of considerable genetic variation in the experimental material (Table 2). Based on qualitative characters, the 70 genotypes were classified into three distinct classes. Two genotypes showed high culm branching, 14 genotypes showed medium culm branching and 54 genotypes had low culm branching. While, 41 genotypes had open type panicles, 18 had semi-compact type panicles and 11 had compact type panicles (Table 3).

Table 2. Analysis of variance for different characters studied in Kodo millet genotypes

S. No. Characters	Mean sum of squares		
	Replication (1)	Treatment (69)	Error (69)
1. Days to 1 st flowering	0.03	40.31*	4.54
2. Days to maturity	5.80	40.22*	8.53
3. Number of productive tillers per plant	0.01	4.94*	0.20
4. Plant height	0.15	190.19*	6.35
5. Length of panicle	0.00	4.76*	0.12
6. Raceme length	0.01	1.66*	0.14
7. Raceme number	0.03	0.08*	0.02
8. Thumb raceme length	0.01	2.02*	0.10
9. Protein content	0.01	1.00*	0.20
10. Calcium content	0.00	0.05*	0.00
11. Grain yield per plant	0.04	4.35*	0.52
12. Straw yield per plant	0.00	6.27*	1.10
13. Harvest index	1.24	19.86*	3.10

*Significant at 5% level. Figures in parenthesis denotes degrees of freedom

A maximum range of variation was observed in plant height (35.10 to 73.40 cm) followed by days to first flowering (61 to 79 days) and days to maturity (85 to 104 days) (**Table 4**). Sao *et al.* (2017) reported similar results for plant height.

The phenotypic coefficient of variability was greater than the corresponding genotypic coefficient of variability. The genotypic coefficient of variation helps in assessing the genetic reliability of the different characters and enables to compare the magnitude of variation. The genotypes were highly variable for characters thumb raceme length (37.5%), the number of productive tillers per plant (27.7%), length of panicle (23.37%), grain yield per plant (23.10%), straw yield per plant (21.48%) and raceme length (21.40%) as indicated by the estimates of PCV (>20%). (**Table 4**). These results are in agreement with Brunda *et al.* (2014) for grain yield per plant, Nirubana *et al.* (2017) for the number of productive tillers per plant and Sao *et al.* (2017) for the length of panicle.

Among the traits, the highest value of GCV was registered for thumb raceme length (35.61%), number of productive tillers per plant (26.58%), length of panicle (22.79%) and grain yield per plant (20.47%) suggesting that these characters are under the influence of genetic control (**Table 4**). These results are in accordance with Keerthana *et al.* (2019).

In the present study, a high estimate of heritability in a broad sense was observed for the characters viz., length of panicle (95%), plant height (93%), number of productive tillers per plant (92%), thumb raceme length (90%),

raceme length (84%), calcium content (81%), days to first flowering (80%), grain yield per plant (78%), harvest index (73%), straw yield per plant (70%), protein content (66%) and days to maturity (65%), indicating that these characters may serve as effective selection parameters during the breeding programme for the improvement of kodo millet (**Table 4**). Sao *et al.* (2017) observed similar results.

The estimate of genetic advance as per cent of mean ranged from 6.95 (days to maturity) to 69.66 per cent (thumb raceme length). Thumb raceme length (69.66%), the number of productive tillers per plant (52.55%), length of panicle (45.8%), grain yield per plant (37.36%), raceme length (37.04%), plant height (36.73) and straw yield per plant (31.01%), showed higher GAM, indicated that top priority should be given for these characters while formulating selection strategies (**Table 4**). High GAM was recorded for number of productive tillers per plant by Keerthana *et al.* (2019), for plant height by Nirubana *et al.* (2017) and for days to maturity by Savankumar *et al.* (2018). High heritability coupled with high genetic advance was noticed in plant height (93%, 19.1), length of panicle (95%, 3.06), the number of productive tillers per plant (92%, 3.04), thumb raceme length (90%, 1.92) and days to first flowering (80%, 7.78) (**Table 4**). It revealed the presence of lesser environmental influence and prevalence of additive gene action in their expression. Similar results were recorded by Sao *et al.* (2017).

The seventy genotypes were grouped into seven clusters, which indicated a wide range of variation among

Table 3. Culm branching and panicle appearance in Kodo millet

S.No.	Genotype	Culm Branching	Panicle appearance	S.No.	Genotype	Culm Branching	Panicle appearance
1	IPS-4	Medium	Open	36	IPS-648	Low	Open
2	IPS-5	Medium	Open	37	IPS-653	Low	Open
3	IPS-13	Medium	Semi-compact	38	IPS-654	Low	Open
4	IPS-68	Low	Compact	39	IPS-669	Low	Semi-compact
5	IPS-69	Low	Compact	40	IPS-670	Low	Open
6	IPS-91	Low	Open	41	IPS-694	Low	Semi-compact
7	IPS-105	Low	Open	42	IPS-699	Low	Semi-compact
8	IPS-147	Low	Open	43	IPS-706	Low	Open
9	IPS-155	Low	Open	44	IPS-709	Low	Open
10	IPS-158	Low	Semi-compact	45	IPS-730	Low	Compact
11	IPS-159	Low	Open	46	IPS-741	Low	Open
12	IPS-172	Low	Semi-compact	47	IPS-744	High	Semi-compact
13	IPS-178	Low	Semi-compact	48	IPS-764	Low	Open
14	IPS-207	Low	Open	49	IPS-777	Low	Compact
15	IPS-236	Low	Semi-compact	50	IPS-782	Low	Open
16	IPS-240	Medium	Open	51	IPS-785	Low	Compact
17	IPS-245	Low	Open	52	IPS-793	Medium	Open
18	IPS-254	Low	Compact	53	IPS-795	Low	Compact
19	IPS-287	Medium	Open	54	IPS-803	Low	Open
20	IPS-319	Low	Semi-compact	55	IPS-814	Medium	Open
21	IPS-329	Low	Compact	56	IPS-828	Low	Open
22	IPS-344	Low	Compact	57	IPS-862	Low	Open
23	IPS-358	Low	Compact	58	IPS-870	Low	Compact
24	IPS-368	Low	Open	59	IPS-883	Low	Open
25	IPS-383	Low	Open	60	IPS-891	Low	Open
26	IPS-388	Low	Open	61	IPS-908	Low	Semi-compact
27	IPS-415	Low	Open	62	IPS-919	Low	Open
28	IPS-429	Low	Open	63	EDS-38	Low	Open
29	IPS-593	Low	Semi-compact	64	ERP-49	Medium	Semi-compact
30	IPS-606	Medium	Semi-compact	65	ERP-51	Medium	Semi-compact
31	IPS-614	Low	Semi-compact	66	ERP-55	Medium	Open
32	IPS-622	Low	Open	67	ERP-62	Medium	Open
33	IPS-627	Low	Open	68	ERP-77	Medium	Semi-compact
34	IPS-628	Low	Open	69	ERP-96	High	Open
35	IPS-645	Low	Semi-compact	70	ER-96	Medium	Open

Table 4. Estimates of genetic parameters for various characters of Kodo millet genotypes

S. No.	Characters	Mean	Range		PCV (%)	GCV (%)	H ² bs (%)	GA	GAM (%)
			Min.	Max.					
1.	Days to 1 st flowering	69	61	79	6.85	6.11	80	7.78	11.25
2.	Days to maturity	95	85	104	5.19	4.18	65	6.61	6.95
3.	Number of productive tillers per plant	95	2.7	10.1	27.70	26.58	92	3.04	52.55
4.	Plant height (cm)	52	35.1	73.4	19.06	18.44	93	19.10	36.73
5.	Length of panicle (cm)	6.69	4.3	11.6	23.37	22.79	95	3.06	45.80
6.	Raceme length (cm)	4.44	2.8	6.9	21.40	19.61	84	1.65	37.04
7.	Raceme number	1.88	1.3	2.2	11.76	8.89	57	0.26	13.84
8.	Thumb raceme length (cm)	2.75	1.1	6	37.50	35.61	90	1.92	69.66
9.	Protein content (%)	7.75	6.48	8.75	10.00	8.14	66	1.06	13.65
10.	Calcium content (%)	3.15	2.9	3.55	5.17	4.67	81	0.27	8.68
11.	Grain yield per plant (g)	6.76	4.65	11.3	23.10	20.47	78	2.53	37.36
12.	Straw yield per plant (g)	8.94	5.9	14.05	21.48	17.98	70	2.77	31.01
13.	Harvest index (%)	43.01	35.17	48.44	7.88	6.73	73	5.09	11.84

Table 5. Grouping of Kodo millet genotypes into different clusters by Tocher method

Cluster	Number of genotypes	Name of the genotypes
I	51	IPS-415, IPS-670, IPS-709, IPS-622, IPS-785, IPS-368, IPS-628, IPS-158, IPS-795, IPS-814, IPS-358, IPS-645, IPS-344, IPS-730, IPS-648 IPS-68, IPS-782, IPS-155, IPS-803, IPS-69, IPS-614, IPS-245, IPS-777, IPS-919, IPS-828, IPS-429, IPS-669, IPS-862, IPS-908, IPS-764, IPS-627, IPS-699, IPS-793, IPS-207, IPS-105, IPS-883, IPS-159, IPS-653, IPS-172, IPS-319, IPS-741, IPS-654, IPS-13, IPS-147, IPS-254, IPS-240, IPS-329, IPS-388, IPS-178, IPS-706, IPS-383.
II	14	ERP-51, IPS-287, ERP-77, ER-96, IPS-593, ERP-55, ERP-62, EDS-38, ERP-96, IPS-891, IPS-5, ERP-49, IPS-4, IPS-744.
III	1	IPS-236
IV	1	IPS-606
V	1	IPS-91
VI	1	IPS-694
VII	1	IPS-870

the genotypes studied. Cluster I was the largest which consisted of 51 genotypes, followed by clusters II with 14 genotypes. The clusters III, IV, V, VI and VII were monogenotypic (Table 5, Fig. 1). More solitary clusters indicate that only a few individuals of the entire germplasm are diverse from each other.

The high intra-cluster distance indicated the presence of a high degree of variability within the cluster and thus offers scope for improvement by various selection methods. The highest intra cluster distance was observed for cluster II (D=8.60) indicating the highest variability followed by cluster I (D=7.75). Cluster III, IV, V, VI and

VII showed no intra cluster distance being solitary (Table 6). The maximum inter cluster distance was observed between clusters II and III (D=19.46) (Table 6). The genotypes grouped in these genetically diverse clusters could be used in a hybridization programme for further crop improvement on Kodo millet. Genotypes included in cluster II had good mean values for days to first flowering, days to maturity (here we are considering maximum days), number of productive tillers per plant, plant height, length of panicle, raceme length, raceme number, thumb raceme length, protein content, grain yield per plant, straw yield per plant and harvest index. The cluster III comprised of one

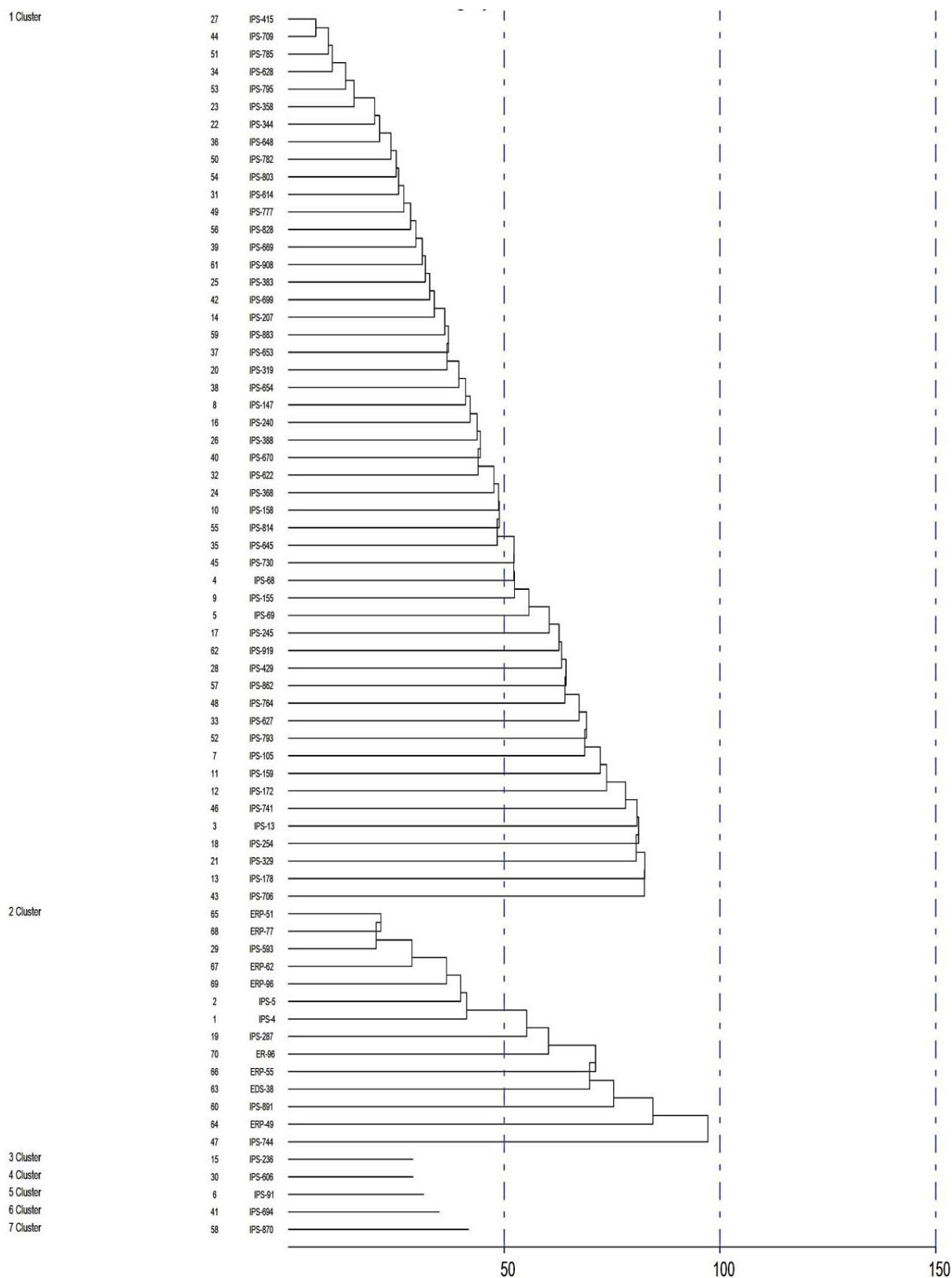


Fig. 1. Clustering by Tocher Method (Dendrogram)

Table 6. Average intra and inter cluster values in 7 clusters (D) = ($\sqrt{D^2}$) in Kodo millet genotypes

Cluster	I	II	III	IV	V	VI	VII
I	7.75	13.16	10.60	10.55	9.71	10.03	12.79
II		8.60	19.46	10.86	15.21	17.10	11.47
III			0.00	13.62	13.76	8.01	17.51
IV				0.00	16.23	12.38	11.57
V					0.00	14.09	15.05
VI						0.00	15.02
VII							0.00

Table 7. Cluster mean performance and contribution towards divergence of 13 characters in 70 genotypes of Kodo millet

Character	Clusters							Population mean	Per cent contribution
	I	II	III	IV	V	VI	VII		
Days to 1 st flowering	68.18	72.66	72.1	74.2	60.8	75.1	65.1	69.73	3.44
Days to maturity	94.35	98.36	97.6	100.7	84.8	101.2	89.1	95.16	1.10
Number of productive tillers per plant	5.41	7.42	4.4	9	2.7	4.9	4.2	5.43	5
Plant height (cm)	50.68	60.11	35.1	37.8	63.3	41.6	36.1	46.38	3
Length of panicle (cm)	6.03	9.14	4.3	8	5.5	5.6	9.1	6.81	5
Raceme length (cm)	4.05	5.89	3.3	4.9	4.2	4.1	5.3	4.53	6
Raceme number	1.87	1.91	1.9	1.9	2.1	1.6	2	1.90	5
Thumb raceme length (cm)	2.37	4.22	1.4	2.9	1.8	1.8	4.5	2.71	12.01
Protein content (%)	7.79	7.69	7.18	8.4	7.35	6.48	7.88	7.54	2.53
Calcium content (%)	3.14	3.14	3	3.23	3	3.53	3.38	3.20	7.41
Grain yield per plant (g)	6.3	8.68	5.25	9.05	5.4	5.4	5.5	6.51	22.65
Straw yield per plant (g)	8.49	10.7	8.2	10.95	7.1	9.95	6.8	8.88	12.43
Harvest index (%)	42.64	44.92	39.12	45.25	43.16	35.17	44.7	42.14	14.43

genotype which had better mean value for the characters days to first flowering and days to maturity (**Table 7**). Among the 13 characters studied the character grain yield per plant (22.65%) contributed the highest for divergence followed by harvest index (14.43%), straw yield per plant (12.43%) and thumb raceme length (12.01%). However, the character number of productive tillers per plant (5%), length of panicle (5%), raceme number (5%), days to first flowering (3.44%) and plant height (3%) recorded the lowest contribution (**Table 7**). Thippeswamy *et al.* (2018) found similar results for plant height, Jyoti *et al.* (2020) for the number of productive tillers per plant.

From the present investigation, it is evident that a wide range of variability is present for different traits coupled with high heritability and high genetic advance as percentage of the mean for important yield traits like thumb raceme length, the number of productive tillers per plant, length of panicle and raceme length; hence selections based on these traits could improve productivity in kodo millet. While, clusters II and III were most diverse to each other,

hence genotypes present in these clusters are suggested to provide a broad-spectrum variability in the evolution of segregating generation.

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