RESEARCH ARTICLE

VARIABILITY AND DIVERGENCE STUDIES IN KODO MILLET (*PASPALUM SCROBICULATUM* L.)

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Abstract: Fifteen kodo millet genotypes were grouped into six clusters using Tocher's method. Among the clusters, cluster I and II had four genotypes each, three genotypes in cluster III, two genotypes in cluster IV, cluster V and VI were solitary each containing single genotype. Maximum intra cluster distance was recorded for cluster III (187.36) followed by cluster II (151.48) and cluster IV (147.29), which suggested that genotypes in cluster III were relatively more diverse among themselves. Genotypes falling in V and VI exhibited higher inter cluster distances (2066.95), followed by cluster V and III (1553.74) and cluster VI and II (1536.57) indicating that genetic makeup of genotypes falling in these clusters may be entirely different from one another. Intermating of the genotypes in cluster III (TNAU 86, TNPSU 301 and PPK 1) with genotypes in cluster IV (GAK 3 and RPS 694), cluster V (KMNDL 1) and cluster VI (BK 14-48) would produce superior genotypes for the respective traits.

Keywords: Kodo millet, Divergence, Variability

INTRODUCTION

Kodo millet (*Paspalum scrobiculatum* L.) is grown as a minor food crop in India with the exception of Deccan plateau in India where it is grown as a major food source (Hariprasanna, 2017). It is a self pollinating tetraploid crop (2n = 4x = 40) belonging to family Poaceae and subfamily Panicoideae. It is a traditional long duration hardy and drought resistant millet crop grown for its fodder and grain. In india it is cultivated in about 2.44 lakh ha producing about 0.73 lakh t of grains with a productivity of about 312 kg/ha. The area under kodo millet cultivation is witnessing a declining trend in the post green revolution period due to predominance of major cereals such as rice and wheat. But this crop still contributes to regional food security in dry and marginal lands, where major cereal crops fail to yield. The seed can be stored for several years, as it possesses excellent storage life. In recent years thrust to grow millets is given due to their nutritional superiority as compared to major cereals (Abhinav *et al.,* 2016). More concentrated research efforts are required to evolve improved cultivars as productivity levels are very low in this crop (312 kg/ha). Wider range of genetic variability helps in selecting desired genotypes for breeding programme. In addition to the genetic variability, knowledge on heritability and genetic advance in the available material helps the breeder to employ suitable breeding strategy. Genetic variability together with heritability estimates would give a better idea on the amount of genetic gain expected out of selection (Burton, 1952 and Swarup and Chaugle, 1962). Progress in crop improvement mainly depends on the degree of divergence for the desired traits existing in the germplasm collection. Information on the nature and degree of genetic divergence would help the plant breeders for selecting right parents for breeding programmes (Vivekanandan and Subramanian, 1990). Hence the present study was conducted to estimate the genetic parameters and divergence for yield and yield attributing traits in kodo millet genotypes which may provide suitable selection indices for crop improvement.

MATERIALS AND METHODS

The experimental material consisted of fifteen kodo millet genotypes, grown in a randomized block design with two replications at Agricultural Research Station, Perumallapalle during Rabi, 2019-20. The crop was raised in four rows of 3 m length with a spacing of 22.5 x 10 cm. All the recommended package of practices were followed to raise healthy and good crop. Observations were recorded for plant height (cm), days to 50 % flowering, days to maturity, number of productive tillers per plant, inflorescence length (cm), raceme number, fodder yield per plant (g) and grain yield per plant (g). The estimates of GCV and PCV were worked out according to the method suggested by (Burton, 1952). Heritability in broad sense was calculated as per the formula given by (Lush, 1940). Range of heritability was categorized as suggested by (Robinson *et al.*, 1949). Genetic advance was estimated according to the method suggested by (Johnson *et al*., 1955). Genetic divergence between the genotypes was estimated by multivariate analysis using Mahalanobis D^2. (1936) statistics and grouping of genotypes into different clusters was done using Tocher's method given by Rao (1952).

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RESULTS AND DISCUSSION

Analysis of variance showed higher significant differences among the genotypes for all the characters indicating the existence of sufficient amount of diversity among genotypes. The variability estimates for yield and yield contributing traits were given in Table 1. Phenotypic coefficient of variability is slightly higher than genotypic coefficient of variability indicating the influence of environment on the expression of genotypes. High GCV and PCV were observed for grain yield followed by number of productive tillers per plant indicating large variability for these traits among the genotypes. GCV and PCV were low for days to maturity indicating less variability for this trait in the genotypes. High heritability was observed for all the traits except for raceme number. Similar results were reported earlier by Sreeja (2014). High heritability along with high genetic advance as percent mean was recorded for grain yield and number of productive tillers per plant which indicates the predominance of additive genes, for which simple selection is effective.

Fifteen genotypes were grouped into six clusters using Tochers method (Table 2). The distribution pattern of genotypes into clusters indicated that the cluster I and II had four genotypes each, three genotypes in cluster III, two genotypes in cluster IV, cluster V and VI were solitary each containing single genotype. The presence of solitary clusters indicated extreme phenotypic performance in positive or negative directions for one or the other characters, which can be exploited for future breeding programme. Nirubana *et al.,* (2017) also reported solitary clusters in kodo millet. The intra and inter cluster distance analysis indicated (Table 3) that maximum intra cluster distance was recorded for cluster III (187.36) followed by cluster II (151.48) and cluster IV (147.29) which suggested that genotypes in cluster III were relatively more diverse among themselves. These results were in agreement with the findings of Abhinav *et al.,* (2016) and Nirubana *et al.,* (2017).

Genotypes falling in clusters V and VI exhibited higher inter cluster distances (2066.95), followed by cluster V and III (1553.74) and cluster VI and II (1536.57), indicating that genetic make up of genotypes falling in these clusters may be entirely different from one another, which may be utilized for crop improvement programme for developing high yielding kodo millet varieties. These results were in confirmation with the findings of Nirubana *et al.,* (2017). The knowledge on traits influencing divergence is an important aspect to a breeder. The percent contribution towards genetic divergence by yield and yield component traits is presented in Table 4. Maximum contribution towards genetic divergence was displayed by grain yield per plant (48.57) followed by inflorescence length (27.62) and fodder yield per plant (20.95). Similar results were reported for grain yield per plant by Nirubana *et al.,* 2017 and Suryanarayana and Sekhar, 2018 in little millet.

Cluster mean values for eight traits are presented in Table 5. The perusal of results revealed that highest mean values were observed for plant height (82 cm) and grain yield per plant (7.4 g/plant) in cluster V, number of tillers per plant (11.4) in cluster IV, inflorescence length (126 cm) in cluster III and fodder yield per plant (16.55 g/plant) in cluster VI. Minimum and maximum cluster mean values were distributed in relatively distant clusters. Thereby recombination breeding programme between genotypes of different clusters could be done to combine desirable characters of different accessions.

CONCLUSION

Higher variability, heritability and genetic advance was observed for number of productive tillers per plant and grain yield per plant. Higher inter cluster distance were found between cluster V and VI and clusters V and III. Cluster means were higher for plant height in cluster V, number of tillers per plant in cluster IV, inflorescence length in cluster III, fodder yield per plant in cluster VI and grain yield per plant in cluster V. Hence intermating of the genotypes in cluster III (TNAU 86, TNPSU 301 and PPK 1) with genotypes in cluster IV (GAK 3 and RPS 694), cluster V (KMNDL 1) and cluster VI (BK 14-48) would produce superior genotypes for the respective traits.

Table 1. Genetic variability parameters for grain yield and its component traits in Kodo millet

S. No.	Character	Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance as percentage of mean
		Genotypic	Phenotypic		
1.	Day to 50 % flowering	5.45	5.55	96.60	11.04
2.	Days to maturity	4.02	4.09	96.70	8.15
3.	Plant height (cm)	9.94	10.21	94.79	19.93
4.	Number of productive tillers per plant	23.47	24.97	88.39	45.46

5.	Inflorescence length (mm)	18.00	18.10	98.89	36.86
6.	Raceme number	9.88	14.52	46.26	13.84
7.	Fodder yield per plant (g)	17.32	17.68	96.04	34.97
8.	Grain yield per plant (g)	43.37	43.78	98.12	88.50

Table 2. Grouping of genotypes into clusters in Kodo millet

Cluster No.	No. of genotypes	Genotypes
I	4	TNPSU - 262, RPS - 520, BK - 36, GKM - 458
II	4	RK-390-25, TNPSU - 176, RBK - 155, GPUK - 3
III	3	TNAU - 86, TNPSU - 301, PPK 1
IV	2	GAK - 3, RPS - 694
V	1	KMNDL - 1
VI	1	BK - 14 - 48

Table 3. Average Intra (diagonal) and Inter Cluster distances in Kodo millet

Cluster No.	I	II	III	IV	V	VI
I	**66.44**	271.13	711.88	356.73	247.76	1110.05
II	271.13	**151.48**	1149.27	537.99	333.54	1536.57
III	711.88	1149.27	**187.36**	957.71	1553.74	334.36
IV	356.73	537.99	957.71	**147.29**	472.85	977.57
V	247.76	333.54	1553.74	472.85	**0**	2066.95
VI	1110.05	1536.57	334.36	977.57	2066.95	**0**

Table 4. Contribution of each character to divergence in Kodo millet

Character	No. of times ranked 1st	% contribution
Day to 50 % flowering	1	0.95
Days to maturity	0	0
Plant height (cm)	1	0.95
Number of productive tillers per plant	1	0.95
Inflorescence length (mm)	29	27.62
Raceme number	0	0
Fodder yield per plant (g)	22	20.95
Grain yield per plant (g)	51	48.57

Table 5. Cluster means for grain yield and its component traits in Kodo millet

Cluster No.	Days to flowering	Days to maturity	Plant Height	No. of tillers per plant	Inflorescence length (mm)	Raceme number	Fodder yield per plant	Grain yield per plant
I	69.5	106	71.75	6.8	106.8	2.85	12.78	5.09
II	68.63	103.5	64.38	7.2	76.3	3.2	12.7	4.15
III	78.17	114.17	71.33	7.73	126.0	3.03	13.83	2.43
IV	70.75	107	73.75	11.4	103.5	3.1	19.4	7.08
V	70.5	105.5	82	7.9	96.0	3.7	15.35	7.4
VI	71.5	106.5	76	9	115.0	3.1	16.55	1.9

REFERENCES

Sao, S., Singh, P., Kumar, P. and Panigrahi, P. (2016). Genetic Divergence Studies in indian kodo millet (*Paspalum scrobiculatum* L.). National Journal of Life Science, 13(2): 129-132.

Burton, G.W. (1952). Quantitative inheritance in grasses. In: Proc. of the 6th International Grassland Congress, 1277-1283.

Hariprasanna, K. (2017). Kodo millet, *Paspalum scrobiculatum* L. In: Patil JV, editor. Millets and sorghum: biology and genetic improvement, 1st Edn. UK: John Wiley & Sons Ltd. 199–225.

Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimation of genetic variability and environmental variability in soybean. Agronomy Journal, 47: 314-318.

Lush, J.L. (1940). Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters.. In: Proc. of American Society of Animal Production, 33:293-301.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. Proceedings of National Institute of Science, India, 2: 49-55.

Nirubana, V., Ganesamurthy, K., Ravikesavan. R. and Chitdeshwari, T. (2017). Genetic Diversity Studies in Kodo Millet (*Paspalum scrobiculatum* L.) Germplasm Accessions Based on Biometrical and Nutritional Quality Traits. International Journal of Current Microbiology and Applied Sciences. 6(10): 832-839.

Rao, C. R. (1952). Advanced Statistical Methods in Bio-metrical Research. John Wiley and sons. New York, 236-272.

Robinson, H.F., Comstock, R.E. and Harvey, P.H. (1949). Estimates of heritability and the degree of dominance in corn (*Zea mays*). Agronomy Journal. 41: 353-359.

Sreeja, R. (2014). Characterization and selection of Kodo millet (*Paspalums corniculate* L.) genotypes with high culm strength to suit mechanical harvesting. Ph.D. Thesis, Tamil Nadu Agric. Univ., Coimbatore, India,

Suryanarayana, L. and Sekhar, D. (2018). Studies on genetic variability, character association and path analysis in little millet (*Panicum sumatrense* L.) Genotypes. The Pharma Innovation Journal, 7(7): 908-910.

Swarup, S. and Chaugle, B.S. (1962). Studies on genetic variability in Sorghum; phenotypic variation and heritable component in some quantitative characters contributing towards yield. Indian J Genet. Pl. Breed. 22:31-36.

Vivekanandan, P. and Subramanian, S. (1990). Genetic divergence in rainfed rice. *Oryza*, 30: 60-62.