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Genetic divergence studies in finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes

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Abstract

Thirty genotypes of finger millet (*Eleusine coracana* L.) were grouped into twelve distinct classes based on their genetic diversity using D^2 statistics. Six genotypes were grouped in cluster I followed by four genotypes in cluster XI and two genotypes each in the remaining clusters. The maximum intra cluster distance was recorded in cluster I (274.31) and minimum in cluster II (5.28). The maximum inter cluster distance was noticed between cluster VII and XI (1567.25) and minimum between cluster II and IX (15.83). Based on the inter cluster distance, cluster II, VII and XI are genetically more divergent and suggested to make crosses between the genotypes of these clusters to get transgressive segregants. The maximum percentage of contribution towards genetic divergence was displayed by grain yield q/ha (41.15) followed by number of productive tillers per plant (29.65) and main ear length (9.88). High mean values for number of productive tillers per plant and grain yield q/ha were seen in cluster VIII, where as low mean values for days to 50% flowering and days to maturity were noticed in cluster XI. Hence utilization of outstanding genotypes from these clusters will be useful for developing high yielding varieties.

Keywords: Genetic divergence, D^2-analysis in finger millet

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) is one of the important food crop and largely grown in southern states of India. In India, it is cultivated in 1.02 M ha, with a production of 1.39 Mt and a productivity of 1363 kg/ha, whereas in the state of Andhra Pradesh it occupies an area of 35,000 ha with a production of 44,000 t and productivity of 1277 kg/ha (Anonymous, 2019) [1]. The success of breeding programme depends upon the choice of suitable parents of diverse origin for obtaining large frequency of transgressive segregants. The D^2 statistics is one of the powerful tools to assess the relative contribution of different characters to the total diversity and thus helps in selection of genetically divergent parents in hybridization programme. Thus, this experiment was aimed at identifying genetically divergent finger millet genotypes with desirable traits for its utilization in hybridization programme to develop pureline varieties.

Material and Methods

The field experiment was conducted at Regional Agricultural Research Station, Chintapalle during *Kharif*, 2010. The experimental material consisting of 30 genotypes were sown in Randomized Block Design (RBD) with three replications. Each genotype was sown in 10 rows of 3 m length with a spacing of 22.5 cm between rows and 10 cm within a row. All the recommended package of practices were followed to raise a healthy crop. The observations were recorded on five randomly selected competitive plants in each replication for plant height (cm), number of productive tillers per plant, main ear length (cm), number of fingers per ear and observations for days to 50% flowering, days to maturity and grain yield q/ ha were recorded on per plot basis.

Genetic divergence was estimated by multivariate analysis using Mahalanobis' (1936) [3] D^2 statistic as described by Rao (1952) [6]. Intra and inter cluster distance, cluster means and contribution of each trait to the divergence were estimated as suggested by Singh and Chaudhary (1985) [8].

Results and Discussion

Mahalanobis' (1936) [3] D^2 statistics is an important tool to a plant breeder to classify the genotypes into different clusters based on genetic divergence between them. The genotypes were grouped into twelve clusters based on D^2 values indicating the presence of large amount of diversity among the genotypes (Table 1). Six genotypes were grouped in cluster I followed

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by four genotypes in cluster XI and two genotypes each in the remaining ten clusters.

The maximum intra cluster distance was recorded in cluster I (274.31) followed by cluster XI (234.10), cluster XII (141.15), cluster X (41.05), cluster IX (32.10), cluster VIII (28.75), cluster VII (13.06), cluster VI (12.63), cluster V (9.89), cluster IV (9.67), cluster III (5.63) and cluster II (5.28). The intra cluster distance in cluster I was highest (274.31) indicating the presence of wide genetic diversity among the genotypes present within this cluster (Table 2).

The inter cluster distances varied from 15.83 to 1567.25. The maximum inter cluster distance was noticed between cluster VII and XI (1567.25) followed by cluster XI and XII (1334.71) and cluster VIII and XI (1242.58). The lowest inter cluster distance was noticed between cluster II and IX (15.83) followed by cluster II and VI (18.14) indicating the close relationship and similarities for most of the traits of the genotypes in these clusters. Based on the inter cluster distance, cluster II, VII and XI are genetically more divergent and suggested to make crosses between the genotypes of these clusters after confirming their general combining ability for

evolving transgressive segregants for yield and yield components. Similar results in finger millet were reported by Devaliya *et al.*, (2017), Mahanthesha *et al.*, (2017), Suryanarayana *et al.*, (2014), Rani *et al.*, (2014) and Shinde *et al.*, (2013) [2, 4, 9, 5, 7].

The per cent contribution towards genetic divergence by seven contributing characters were presented in Table 3. The maximum percentage of contribution towards genetic divergence was displayed by grain yield q/ha (41.15) followed by number of productive tillers per plant (29.65), main ear length (9.88), days to 50% flowering (6.44), days to maturity (6.21), number of fingers per ear (5.75) and plant height (0.92) respectively.

The cluster mean values for seven characters were presented in Table 4. High mean values for number of productive tillers per plant and grain yield q/ha were seen in cluster VIII, plant height and main ear length in cluster X, number of fingers per ear in cluster XII, whereas low mean values for days to 50% flowering and days to maturity were noticed in cluster XI. Hence utilization of outstanding genotypes from these clusters will be useful for developing high yielding varieties.

Table 1: Distribution of 30 finger millet genotypes into twelve clusters based on D^2 analysis

Cluster No	No of genotypes in each cluster	Cluster members
Cluster 1	6	VR 959, VL 352, BBM 10, VL 353, TNAU 1063 and KB 105.
Cluster 2	2	PPR 2885 and GPU 45
Cluster 3	2	PR 202 and GPU 67
Cluster 4	2	DM 7 and DHRS 1-1
Cluster 5	2	BBM 11 and GPU 79
Cluster 6	2	GN 4 and OEB 532
Cluster 7	2	GPU 76 and BR 2
Cluster 8	2	GPU 75 and VR 948
Cluster 9	2	TNAU 1066 and DM 1
Cluster 10	2	BR 4 and GPU 78
Cluster 11	4	PRM 9002, KOPN 933, VL 351 and VL 149
Cluster 12	2	BR 7 and TNAU 1063

Table 2: Average intra and inter cluster D^2 values among twelve clusters in 30 genotypes of finger millet

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	274.31 (16.56)	149.66 (12.23)	198.05 (14.07)	142.54 (11.93)	188.90 (13.74)	173.96 (13.18)	411.52 (20.28)	280.44 (16.74)	146.11 (12.08)	397.20 (19.93)	672.74 (25.93)	336.78 (18.35)
II		5.28 (2.29)	113.55 (10.56)	23.22 (4.81)	124.08 (11.13)	18.14 (4.25)	287.21 (16.94)	225.33 (15.01)	15.83 (3.97)	291.98 (17.08)	609.35 (24.68)	230.37 (15.17)
III			5.63 (2.37)	95.66 (9.78)	26.85 (5.18)	130.51 (11.42)	96.30 (9.81)	56.04 (7.48)	83.16 (9.11)	97.20 (9.85)	981.33 (31.32)	82.04 (9.05)
IV				9.67 (3.10)	122.84 (11.08)	26.06 (5.10)	294.24 (17.15)	212.22 (14.56)	23.93 (4.89)	322.12 (17.94)	594.68 (24.38)	239.45 (15.47)
V					9.89 (3.14)	156.25 (12.50)	111.09 (10.54)	35.70 (5.97)	92.64 (9.62)	94.75 (9.73)	961.66 (31.01)	84.60 (9.19)
VI						12.63 (3.55)	291.70 (17.07)	240.69 (15.51)	33.23 (5.76)	323.02 (17.97)	653.11 (25.55)	246.25 (15.69)
VII							13.06 (3.61)	69.75 (8.35)	245.48 (15.66)	42.79 (6.54)	1567.25 (39.58)	63.13 (7.94)
VIII								28.75 (5.36)	180.67 (13.44)	76.82 (8.76)	1242.58 (35.25)	69.25 (8.32)
IX									32.10 (5.66)	254.43 (15.95)	654.29 (25.57)	191.67 (13.84)
X										41.05 (6.40)	1497.00 (38.69)	74.42 (8.62)
XI											234.10 (15.30)	1334.71 (36.53)
XII												141.15 (11.88)

Table 3: Contribution of characters towards genetic divergence in finger millet

Character	No of times ranked first	% Contribution towards divergence
Days to 50 % flowering	28	6.44
Days to maturity	27	6.21
Plant height (cm)	4	0.92
Number of productive tillers per plant	129	29.65
Main ear length (cm)	43	9.88
Number of fingers per ear	25	5.75
Grain yield (Q/ha)	179	41.15
Total	435	100

Table 4: Cluster mean values for seven characters in 30 genotypes of finger millet

Cluster No	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers per plant	Main ear length (cm)	Number of fingers per ear	Grain yield (Q/ha)
Cluster I	79.89	112.78	105.42	3.79	8.43	6.29	39.86
Cluster II	82.67	109.83	112.43	2.72	9.07	6.37	27.19
Cluster III	83.50	121.50	117.60	3.23	7.37	6.37	42.90
Cluster IV	82.33	110.00	105.97	2.67	7.73	6.63	40.12
Cluster V	82.67	121.83	122.13	4.20	9.12	6.57	49.84
Cluster VI	83.17	110.17	87.67	2.02	9.05	6.47	26.41
Cluster VII	91.00	127.50	122.80	3.17	9.37	6.80	48.36
Cluster VIII	86.00	126.33	104.20	4.57	9.17	7.00	51.92
Cluster IX	82.33	111.67	118.97	2.90	8.73	6.83	33.68
Cluster X	87.33	129.50	128.70	3.65	9.47	6.03	35.54
Cluster XI	62.50	93.25	105.27	2.67	7.61	6.19	27.78
Cluster XII	87.17	125.67	118.57	3.72	9.03	7.47	34.97

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