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Genetic Divergence Analysis among M_4 Mutant Lines of Finger Millet (*Eleusine coracana* L. Gaertn.)

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ABSTRACT: Induced genetic divergence was estimated in thirty one M_4 mutant lines of finger millet *var.* GPU 28 and twenty seven M_4 mutant lines of finger millet *var.* KMR 204, developed by gamma rays using multivariate analysis using Mahalanobis' (1936). Mutant lines of GPU 28 were grouped into seven clusters and of KMR 204 grouped into six clusters. Cluster I and IV of mutant lines of GPU 28 and cluster II and IV of mutant lines of KMR 204 were found to be more divergent than others indicates high amount of diversity between these clusters. Significant difference was observed among cluster means for most of the traits. Mutant lines from these clusters can be used to develop high yielding cultivars. Maximum percentage of contribution to the genetic divergence was displayed by 1000- seed weight (58.40) in mutated population of KMR 204 and days to 50 % flowering (47.10) in mutated population of GPU 28. Present study of D^2 analysis suggested that mutant lines belonging to the diverse clusters could be used in hybridization programme to enhance the productivity of finger millet.

Keywords: Induced genetic divergence, finger millet, Gamma rays, D^2 analysis, Mutant lines.

INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn.) Sub-species *coracana* belongs to family Poaceae/Graminae and generally known as ragi, nachani and nagli. It is a tetraploid (2n = 36) with morphological resemblance to both *E. indica* (L.) Gaertn. having chromosome number 2n = 18 and *E. Africana* O. Byrne with chromosome number 2n = 36. It was domesticated from Ethiopia to Uganda about 5000 years ago. In India, it was introduced around 3000 years ago. Finger millet is a widely grown traditional and highly nutritious grain cereal crop (Sawardekar, 2016). It is cultivated in the semi-arid areas of Eastern and Southern Africa and South Asia, where it is a staple food for millions of poor people. It is also acknowledged for its health advantageous effects, like antidiabetic, anti-diarrheal, anti tumerogenic, anti-inflammatory, atherosclerogenic, antiulcer, antimicrobial and antioxidant properties. An enormous number of small farmers cultivate finger millet with limited water resources and in numerous nations this crop is frequently known as "poor people's crop". It is cultivated in the semi-arid areas of Eastern and Southern Africa and South Asia, where it is a staple food for millions of poor people.

The long history of cultivation in Indian subcontinent under diverse agro ecological conditions and the associated natural and human selection has resulted in large diversity in the crop. India is often considered as secondary centre of origin for finger millet. In India, ragi is cultivated in an area of 1138.2 thousand-hectare with the production of 1821.9 mt and productivity of 1601 kg/ha majorly in Karnataka, Andhra Pradesh, Tamil Nadu, Maharashtra, Uttarakhand and Odisha (Anonymous, 2018). In India, area of finger millet stands sixth after wheat, rice, maize, sorghum and bajra (Chandra *et al.*, 2016). As we know, population is still expanding while no significant increase in arable lands is foreseen. There is need to enhance the productivity of finger millet to feed the large population. Heterosis breeding is one of the important ways to achieve high productivity. The hybrids between to two divergent groups normally show high amount of heterosis than the hybrids between two genetically similar groups (Dwivedi *et al.*, 1998; Melchinger, 1999). D^2 analysis was generally used by many researchers in order to find more divergent lines that can be used to make hybrids. Muduli and Misra (2008) have done genetic divergence analysis in micro-mutant lines in finger millet and found divergent mutant lines. Similarly, Patel *et al.* (2019); Suryanarayana *et al.* (2019); Keerthana and Chitra (2020) also conducted D^2analysis in finger millet and got divergent genotypes. In the present study, D^2 analysis was used to identify divergent mutant line from M_4 mutant lines of GPU 28 and KMR 204.

MATERIALS AND METHODS

The present study on induced mutations in finger millet was carried out at K block, GKVK, University of Agricultural Sciences; Bangalore represents Eastern Dry Agro Climatic Zone (Zone V) of Karnataka which

is located at 12.9716°N latitude and 77.5946°E longitude and an altitude of 920 m above MSL. Material used for the present study comprised of M_4 seeds selected for productivity per se traits form M_3 generation derived from the gamma irradiation of finger millet varieties GPU 28 and KMR 204. These 58 selected mutants (31 M_4 mutants of GPU 28 and 27 M_4 mutants of KMR 204) were evaluated in Randomized complete block design with three replications with two checks (GPU 28 and KMR 204). Observation on days to 50 per cent flowering and days to panicle maturity were recorded on plot basis. Plant height (cm), productive tillers plant^{-1}, fingers ear^{-1}, finger length (cm), ear weight plant^{-1} (g), seed yield plant^{-1} (g) and 1000 - seed weight (g) were recorded on five randomly selected plants for each line in every replication. Estimation of genetic divergence was done by multivariate analysis using Mahalanobis' (1936). D^2 statistic calculated as described by Rao (1952). Contribution of each trait to the divergence, intra and inter cluster distance and cluster means were estimated in the present study.

RESULTS AND DISCUSSION

A. Distribution of M_4 mutant lines into different clusters

Diversity analysis is very crucial for plant breeders for identification of divergent genotypes which will help further in exploitation of heterosis. Mahalanobis'(1936) D^2 analysis is one of the important tool to classify the genotypes into different clusters. In the present study, the M4 population of GPU 28 was classified into 7 clusters and m4 population of KMR 204 into six clusters (Table 1&2). This indicates the presence of the diversity among the mutant lines of both genotypes. In both the mutated population, cluster 1 showed maximum number of mutant lines. Cluster I of mutated population of GPU 28 has 8 lines and of KMR 204 has 12 mutant lines. Similar diversity analysis was done by Muduli and Misra (2008) in micro-mutants of finger millet and classified into different clusters.

Table 1: Distribution of thirty one M_4 mutant lines of finger millet var. GPU 28 into seven clusters based on D^2 values.

Cluster No.	No. of mutant lines	Names of mutant lines
I	8	G1, G12, G27, G28, G31, G14, G24, G17
II	6	G2, G16, G3, G8, G13, G9
III	5	G4, G20, G21, G6, G10
IV	3	G5, G11, G19
V	2	G7, G22
VI	2	G15, G18
VII	5	G23, G26, G29, G25, G30

Table 2: Distribution of twenty seven M_4 mutant lines of finger millet *var*. KMR 204 into seven clusters based on D^2 values.

Cluster No.	No. of mutant lines	Names of mutant lines
I	12	K23, K26, K14, K16, K15, K9, K12, K22, K21, K18, K19, K24
II	8	K13, K27, K25, K8, K11, K2, K3, K7
III	2	K17, K20
IV	2	K5, K6,
V	2	K1, K4
VI	1	K10

Inter- cluster and intra cluster D^2 value indicates the amount of diversity among and within the clusters. Maximum inter cluster distance (392.01) was observed between cluster I and cluster IV and lowest inter cluster distance (52.73) was between cluster III and cluster IV in mutated population of GPU 28 (Table 3). In case of mutated population of KMR 204, maximum inter cluster distance (710.60) was observed between cluster II and cluster IV and lowest inter cluster distance (140.52) was observed between cluster I and cluster III (Table 4). Maximum intra cluster distance (40.78) was observed in cluster V and lowest (16.50) in cluster VI in mutated population of GPU 28 (Table 3). Maximum intra cluster distance (84.08) was found in cluster V and cluster VI has intra cluster distance is zero because of only one genotype in the cluster in the mutated population of KMR 204 (Table 4). Inter cluster distance was found to be maximum between cluster I and IV in mutated population of GPU 28 and between II and IV in case of mutated population of KMR 204. This indicates high amount of diversity between these clusters. Diversity is very important factor in exploitation of heterosis. Hybrid between diverse genotypes belongs to different cluster would be more effective than hybrid between less diverse genotypes. So, mutant lines from these diverse clusters can be used in hybridization programme in order to get high yielding hybrids or to get vast variability among the segregants. Similar results in finger millet were reported by Devaliya *et al.* (2017); Suryanarayana *et al.* (2014); Mahanthesha *et al.* (2017); Keerthana and Chitra (2020).

Table 3: Average intra (bold) and inter cluster D^2 values among seven clusters in thirty one M_4 mutant lines of finger millet *var.* GPU 28.

Cluster No.	I	II	III	IV	V	VI	VII
I	**30.71**	244.48	247.43	392.01	142.80	61.40	111.55
II		**30.05**	72.11	97.25	55.56	145.85	246.01
III			**26.26**	52.73	90.92	187.29	145.96
IV				**25.99**	153.09	318.96	236.11
V					**40.78**	87.34	190.37
VI						**16.50**	168.57
VII							**18.40**

Table 4: Average intra (bold) and inter cluster D^2 values among seven clusters in thirty one M_4 mutant lines of finger millet *var.* KMR 204.

Cluster No.	I	II	III	IV	V	VI
I	**68.40**	257.61	140.52	377.70	497.12	462.73
II		**64.28**	256.44	710.60	507.53	181.83
III			**40.38**	172.92	193.13	293.21
IV				**65.14**	220.69	672.28
V					**84.08**	272.58
VI						0.00

B. Cluster means of different traits used under study

Results indicated the significant difference among cluster means for most of the trait used under study in both the mutated population (Table 5 & 6). In case of mutated population of GPU 28, lowest value (101.17) for days to panicle maturity was observed in cluster I, highest value (8.46) was found for fingers ear^{-1} in cluster III, highest value for productive tillers $plant^{-1}$ (5.14), highest value for finger length (8.74) and highest value for ear head weight (56.52), all were observed in cluster IV. Cluster VII had the highest mean value for seed yield $plant^{-1}$ (36.39) and for 1000-seed weight (3.43). In case of mutated population of KMR 204, Cluster I had the highest mean value for the seed yield $plant^{-1}$ (36.19), ear head weight $plant^{-1}$ (55.98), fingers ear^{-1} (8.23) and productive tillers $plant^{-1}$ (5.52). Cluster IV had the highest mean value for 1000-seed weight (3.43). Cluster V had the highest mean value for finger length (7.67). Mutant lines from these clusters can be used to develop high yielding cultivars.

Table 5: Mean of 9 traits in different clusters of thirty one M_4 mutant lines of finger millet *var.* GPU 28.

Cluster No.	DFF	DPM	PH	PT	FN	FL	TW	EW	Y
I	65.00	101.17	88.78	4.09	7.36	7.12	2.62	44.12	27.06
II	82.11	114.50	101.74	3.56	7.38	7.43	2.81	44.14	26.28
III	78.27	113.13	106.01	4.71	8.46	8.32	3.26	54.97	34.22
IV	83.33	117.00	96.79	5.14	8.34	8.74	3.32	56.52	35.85
V	79.00	112.00	101.85	4.42	7.88	7.49	2.42	48.90	29.35
VI	70.00	109.00	97.12	3.74	6.70	7.33	2.59	39.52	21.88
VII	64.60	101.87	86.04	4.99	8.15	8.54	3.43	56.49	36.39

Table 6: Mean of 9 traits in different clusters of thirty one M_4 mutant lines of finger millet *var.* KMR 204.

Cluster No.	DFF	DPM	PH	PT	FN	FL	TW	EW	Y
I	64.97	101.72	85.54	**5.52**	**8.23**	7.56	3.25	**55.98**	**36.19**
II	64.58	101.71	86.49	4.10	7.55	6.10	2.51	43.25	26.75
III	71.17	111.50	89.20	3.96	7.59	7.18	3.10	46.63	30.73
IV	79.00	114.00	109.48	4.84	7.88	7.03	**3.43**	50.16	29.53
V	82.00	113.67	105.08	4.58	7.32	**7.67**	2.72	48.33	27.51
VI	74.33	108.67	72.00	5.10	7.24	6.67	2.25	47.79	27.88

C. Trait contribution to the genetic divergence

Trait contribution to the genetic divergence for both the mutated population were presented in Fig. 1 and 2. Maximum percentage of contribution to the genetic divergence was displayed by 1000- seed weight (58.40) followed by days to 50 % flowering (25.64), finger length (9.12) and days to panicle maturity (3.99) in mutated population of KMR 204. In mutated population of GPU 28, maximum percentage of contribution to the genetic divergence was displayed by days to 50 % flowering (47.10) followed by 1000- seed weight (40.43), finger ear^{-1} (5.16) and plant height (3.01). Similar results were reported by Patel *et al.* (2019) in finger millet.

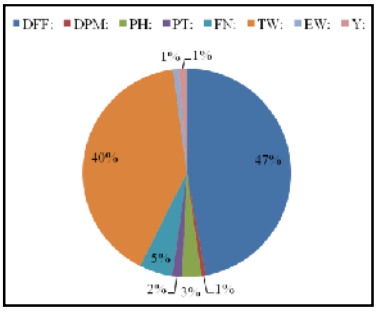

Fig. 1. Trait contribution to the genetic divergence in D^2 analysis of M_4 mutant lines of finger millet *var.* GPU 28.

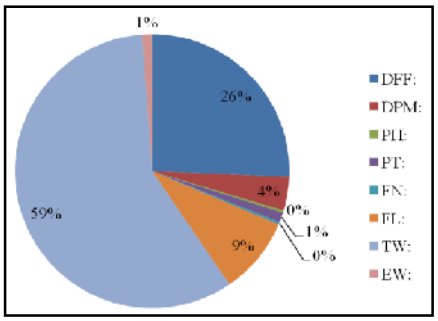

Fig. 2. Trait contribution to the genetic divergence in D^2 analysis of M_4 mutant lines of finger millet *var.* KMR 204.

CONCLUSION

Genetic divergence study using D^2 statistic showed the presence of substantial diversity among the mutant lines of both the varieties. D^2 analysis grouped the mutant lines of GPU 28 into 7 clusters and KMR 204 into 6 clusters. Cluster I and IV were found to be more divergent in cluster analysis of mutant line of GPU 28 and cluster II and IV were divergent among mutant lines of KMR 204. Mutant lines from these divergent clusters could be used in future hybridization programme to get desirable segregates.

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Conflict of Interest. None.

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