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Studies on Genetic Diversity in Finger Millet [*Eleusine coracana* (L.) Gaertn.] Genotypes

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Abstract

The present investigation was undertaken to assess the genetic divergence of twenty-one finger millet (*Eleusine coracana* L.) genotypes using D^2 analysis for seventeen characters, during *kharif,* 2021. Analysis of variance revealed significant variations with respect to all the seventeen characters *viz*., days to 50 per cent flowering, days to maturity, plant height, number of productive tillers per plant, ear head length, ear head width, number of fingers per ear head, peduncle length, finger length, flag leaf blade length, flag leaf blade width, flag leaf sheath length, test weight, straw yield, ear head weight, harvest index and grain yield per plant under study. Following Tocher's technique, the 21 genotypes were divided into seven clusters. Cluster II was the largest one with nine genotypes. The maximum intra cluster distance was exerted in cluster V. Inter cluster distance was maximum between the clusters V and VII. The cluster VII and VI showed high cluster mean values for seed yield per plant. Among the characters, grain yield per plant followed by ear head weight contributed more towards the genetic divergence. In Mahalanobis D^2 analysis, three divergent genotypes such as Ravallicvalli, Karunsuruttai and Paiyur-1 were identified as the most diverse genotypes in the population. Hence, these genotypes could be used in future breeding programmes to incorporate desirable features, such as high yield and high quality, to recipient finger millet genotypes, resulting in the creation of promising cultivars.

Keywords : Genetic divergence, Finger millet, Tocher's technique, Mahalanobis D^2

Finger millet is a self pollinated tetraploid and has morphological similarity to both *Eleusine indica* (L.) *Gaertn*. (2n = 18) and *Eleusine africana* (2n =36). The cytological evidences indicate that *Eleusine indica* has contributed one of the genomes (AA) to the cultivated *Eleusine coracana* (AA BB). The genome size of finger millet is 1,593 Mb and is a self-pollinated crop (Goron and Raizada, 2015). The generic name of *Eleusine* is derived from Greek Goddess of cereals 'Eleusine'. The term coracana is derived from kurukkan, the Singhali name of the grain. The word Ragi is derived from Sanskrit word 'Rajika' means red. The common name finger millet is derived from the finger like branching of the panicle. Finger millet is grown for food mainly in Africa and Southern Asia, India (the states of Uttar Pradesh, Bihar, Tamil Nadu, Karnataka and Andhra Pradesh) and Nepal. The long history of cultivation in the Indian subcontinent under diverse agro ecological conditions and the associated natural and human selection has resulted in large diversity of the crop. India is often considered as secondary centre of diversity for finger millet. Finger millet covers an area of 0.99 million hectares in India, with a production of 1.74 million tonnes and productivity of 1761 kg ha^{-1} during 2020-21. In Tamil Nadu, finger millet is

cultivated in an area of 0.78 lakh hectares, with a production of 2.56 lakh tonnes and productivity of 1966 kg ha^{-1} during 2020-2021(Directorate of Economics and Statistics, 2021).

Finger millet is commonly called 'Nutritious millet' as the grains are nutritionally superior to many cereals such as wheat, rice and maize. Finger millet is highly nutritious, non-glutinous and easy to digest. It is very useful to persons suffering from diabetes. It is the cheapest and preferred food crop of economically suppressed but physically hard working people. It contains protein, high amounts of fiber, B-complex vitamins including niacin, thiamin and riboflavin, the essential amino acid methionine, lecithin and some vitamin E. It is particularly high in the minerals calcium, iron, magnesium, phosphorous and potassium. The seeds are also rich in phytochemicals, including phytic acid, believed to lower cholesterol and phytate, which is associated with reduced cancer. It is an excellent source of dietary calcium and fiber for people suffering from calcium deficiencies. Finger millet can alleviate the wide spread micronutrient malnutrition in the developing countries.

In order to achieve the goal of increased production by increasing the yield potential of genotypes, knowledge of genetic divergence is essential for a plant breeder. The D^2 analysis developed by (Mahalanobis, 1936) for assessing the relative divergence of genotypes under study and also provides rational basis for selection of parents for hybridization programme is used. The identification of elite parents is imperative for the success of hybridization programme resulting in the identification of large number of superior segregants. Accordingly, the present investigation is a step towards elucidating genetic diversity among collected finger millet genotypes cultivated in Tamil Nadu.

Material and Methods

The present experiment was carried out at the Plant breeding farm, Faculty of Agriculture, during *kharif*, 2021. The material for present investigation comprised of twenty one finger millet genotypes including 10 traditional varieties and 11 released varieties (6 from Tamil Nadu and 5 from Karnataka) Table 1. The experiment was laid out in randomized block design with three replications. Seeds were sown in raised nursery bed and 20 days old seedlings were transplanted in three meter rows with spacing of 30 cm between rows and 10 cm between two hills in a row, maintaining one healthy and vigorous seedlings per hill. Data was recorded for 17 traits *viz*., plant pheonological (days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, peduncle length, finger length), physiological (flag leaf blade length, flag leaf blade width, flag leaf sheath length, harvest index) and ear head character (ear head length, ear head width, number of fingers per ear head, test weight, straw yield, ear head weight and grain yield per plant). Recommended cultural practices and required plant protection measures were judiciously followed. The data was analysed with the technique of D^2 statistics (Mahalanobis, 1936). The software package INDOSTAT version 8.5 was used to analyse the statistical data.

Results and Discussion

Analysis of Variance (ANOVA)

Analysis of variance is an important tool to determine the variability present among the genotypes. The analysis (ANOVA) revealed the presence of considerable variability among 21 genotypes for all the seventeen quantitative traits, indicating that the genotypes selected for the present study were genetically divergent. Hence, further analysis was appropriate.

Group Constellation by Tocher Method

On the basis of D^2 values, twenty one genotypes were clustered into seven clusters based on Tocher's method (Rao, 1952). This revealed the presence of a wide range of genetic diversity among the genotypes. These genotypes could well be exploited in cross breeding programmes where crosses among the divergent parents likely to yield desirable combinants. There fore, crossing programme may be initiated between the genotypes belonging

TABLE 1
List of genotypes selected for the present study

Genotype Code	Name of the Genotype	Source
G1	Pitchukatti	Anchety Local, Krishnagiri
G2	Kembu Ragi	Anchety Local, Krishnagiri
G3	Co (Ra)-13	TNAU, Coimbatore
G4	Saravathi	Anchety Local, Krishnagiri
G5	Co (Ra)-15	TNAU, Coimbatore
G6	GPU-67	Regional Research Station, Paiyur
G7	ML-365	KVK, Paparapatti
G8	Saratha	KVK, Paparapatti
G9	Co (Ra) 14	TNAU, Coimbatore
G10	Valathar Ragi	Anchety Local, Krishnagiri
G11	Indaf,Local	Anchety Local, Krishnagiri
G12	Ravallicvalli	Anchety Local, Krishnagiri
G13	GPU-28	Regional Research Station, Paiyur
G14	Bonda Ragi	Dharmapuri, Local
G15	GPU-66	Regional Research Station Paiyur
G16	Vellarium	Dharmapuri, Local
G17	Vensuruttai	Paiyur Local Landrace
G18	Paiyur-1	Regional Research Station, Paiyur
G19	Paiyur-2	Regional Research Station, Paiyur
G20	Karunsurutai	Paiyur Local Landrace
G21	Trichy-1	ADAC& RI, Trichy

to different clusters. With the help of Tocher's method seven clusters were formed from twenty-one genotypes of finger millet (Table 2 and Fig. 1). Among the seven clusters, cluster II the largest one was comprised of nine genotypes of diverse origin. It was followed by clusters I and IV which had three genotypes each and clusters III and V which comprised of two genotypes each; clusters VI, VII were monogenotypic in nature and was represented by a single genotype. The results are in corroboration with the findings obtained by Shivangi Negi *et al*., 2017 and Rani Jadav *et al*., 2014.

TABLE 2
Clustering pattern of 21 finger millet genotypes based on D^2 analysis.

Clusters	Number of genotypes	Name of Genotypes
I	3	Pitchukatti, ML- 365, Vellarium
II	9	Kemburagi, Co (Ra)-13, Co (Ra)-15, Saravathi, Co (Ra) - 14, GPU-67, Saratha, Velathar Ragi, Bonda Ragi
III	2	Paiyur-2, Trichy-1
IV	3	Indaf, GPU-28, GPU-66
V	2	Ravallicvalli, Karunsuruttai
VI	1	Vensurutaai
VII	1	Paiyur-1

In this context, two important points could be considered,

i) Choice of the unique cluster from which geno types are to be selected as parents in breeding programme and

ii) Choice of distinct cultivar from selected groups

Intra-Cluster and Inter-Cluster Distances among the Finger Millet Germplasm

The greater the distance between two clusters, the broader is the genetic difference among the parents. Parents combining high yield with extensive genetic divergence are likely to yield elite segregates with in a short period. The basic idea behind formation of clusters is to get the intra and inter-cluster distances. The intra and inter cluster values are means derived from D^2 values of cluster elements. Crossing between the genotypes placed in clusters with large inter cluster distance will be more likely to give desirable results (Wolie and Belete 2013 and Suryanarayana *et al*., 2014). The intra and inter cluster distance among the seven clusters where computed and furnished in Table 3 and Fig. 2. Intra-cluster distance (D^2) ranged from 0.00 to 280.01.

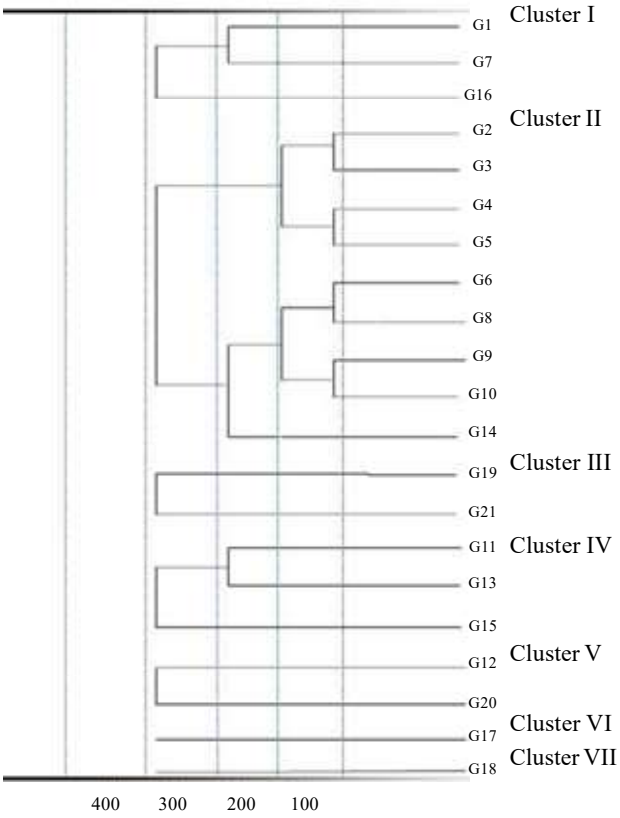

Fig. 1 : Dendrogram for grouping of finger millet genotypes by Tocher's method

At intra-cluster level, cluster V recorded the highest intra- cluster distance (280.01), followed by cluster IV (189.06), indicating that wide genetic divergence was existing among the genotypes within the clusters. The intra-cluster distance within cluster VI and VII was zero (0) as these clusters were composed of only single genotypes.

In the perusal of D^2 statistics, inter-cluster D^2 values ranged from 130.27 to 852.36. The inter-cluster D^2 value was highest between clusters V and VII

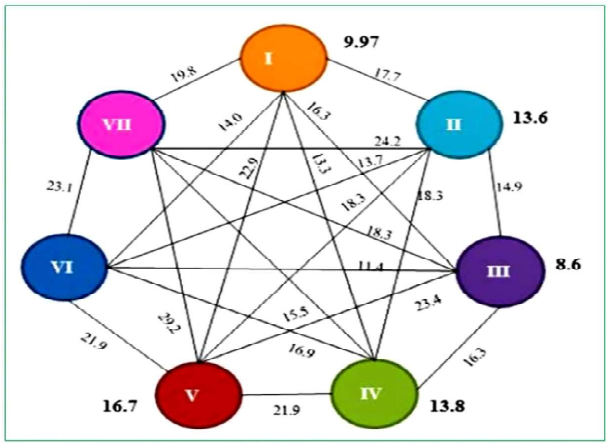

Fig. 2 : Average inter and intra cluster D values

TABLE 3

Average inter (D^2) and intra (D) cluster distance among seven clusters in finger millet genotypes

Clusters	I	II	III	IV	V	VI	VII
I	**99.56 (9.97)**	313.67 (17.71)	264.13 (16.25)	177.86 (13.33)	525.65 (22.92)	195.58 (13.98)	390.92 (19.77)
II		**183.77 (13.55)**	221.22 (14.87)	333.18 (18.25)	335.47 (18.31)	187.83 (13.70)	583.54 (24.15)
III			**73.41 (8.56)**	265.82 (16.30)	545.97 (23.36)	130.27 (11.41)	334.91 (18.30)
IV				**189.06 (13.75)**	481.01 (21.93)	284.41 (16.86)	240.88 (15.52)
V					**280.01 (16.73)**	481.08 (21.93)	852.36 (29.19)
VI						**0.00 (0.00)**	532.56 (23.07)
VII							**0.00 (0.00)**

Diagonal values (bold) – Intra cluster divergence, Off- Diagonal value (No bold) - Inter cluster divergence, D Values- value in parenthesis

TABLE 4

Cluster means for seventeen morphological traits in finger millet genotypes

Cluster	I	II	III	IV	V	VI	VII	Grand Mean
DT50%	74.78	69.95	71.22	71.7	66.44	69.78	72.67	70.8
DTM	110.11	104.04	102.89	107.59	99.33	103.67	105.67	104.92
PH	78.9	84.06	84.03	82.95	82.7	76.24	87.8	82.82
NPTPP	3.1	3.76	3.31	3.48	3.27	2.57	4.07	3.49
EHL	8.41	8.14	8.09	8.96	7.69	7.72	9.09	8.27
EHW	3.67	3.48	4.06	3.64	3.42	3.47	3.41	3.57
NFPEH	5.94	6.47	6.67	6.77	5.72	7.2	7.44	6.46
PL	22.82	21.8	22.99	23.7	22.92	20.14	24.08	22.47
FL	6.32	6.08	5.97	6.91	6.12	5.47	7.64	6.27
FLBL	26.53	26.3	24.74	26.37	27.47	26.26	24.75	26.23
FLBW	1.13	1	1.02	1.07	1.08	1.04	1.02	0.99
FLSL	11.65	12.04	11.47	12.44	11.87	11.31	12.7	11.97
TW	3.09	2.88	2.99	2.87	2.91	2.7	3.26	2.93
SY	30.06	28.64	27.07	36.47	39.23	22.81	43.78	31.43
EHWPP	22.29	24.56	25.42	26.37	23.24	21.6	34.25	24.77
HI	38.1	37.74	36.9	36.1	29.51	39.48	42.52	37.01
GYPP	11.12	10.49	10.08	13.07	10.13	9.04	18.11	11.17

DT 50 per cent - Days to 50 per cent flowering, DTM - Days to maturity, PH - Plant height (cm), NPTPP - Number of productive tillers per plant, EHL - Ear head length (cm), EHW - Ear head width (cm), NFPEH - Number of finger per ear head, PL - Peduncle length (cm), FL - Finger length (cm), FLBL - Flag leaf blade length (cm), FLBW - Flag leaf blade width (cm), FLSL - Flag leaf sheath length (cm), TW - Test weight (g), SY - Straw yield, EHWPP - Ear head weight per plant (g), HI - Harvest index, GYPP - Grain yield per plant (g)

(852.36), followed by clusters II and VII (583.54). The outstanding genotypes from different clusters may be utilized as parents for the future hybridization programme, as they could result in better yielding hybrids. Similar results were reported by Wanna Soe *et al*., 2022.

Cluster Means

The cluster mean values for seventeen quantitative traits were presented in Table 4. Mean values of traits varied in different clusters. The cluster mean for days to 50 per cent flowering was lowest in cluster V (66.44) while it was the highest in cluster I (74.78). For earliest maturity was recorded in cluster V (99.33) followed by cluster III (102.89). Taller plants were present in cluster VII (105.67) while shorter plant types were observed in cluster VI (76.24). For number of productive tillers per plant, cluster mean was highest in cluster VII (4.07) and lowest in cluster VI (2.57). Longer ear heads were grouped in cluster VII (9.09) while cluster V (7.69) had short ear heads. Ear head width was highest in cluster III (4.06) and lowest in cluster VII (3.41). Number of fingers per ear head was highest in cluster VII (7.44) while cluster V (5.72) had the least. Cluster mean for Peduncle length was highest in cluster VII (24.08) and lowest in cluster II (20.14). Cluster VII (7.64) had the longest fingers while cluster II (5.47) had the least. Flag leaf blade length was highest in cluster V (27.47) and lowest in cluster II (24.74). For flag leaf blade width the cluster mean was highest

in cluster I (1.13) and the lowest in cluster II (1.00). Cluster mean for test weight was highest in cluster VII (3.26) and lowest in cluster VI (2.70). Cluster mean for straw yield was highest in cluster VII (43.78) and lowest in cluster VI (22.81). Heavy ear heads were present in cluster VII (34.25) while cluster VI (21.60) had lighter ear heads. The cluster mean for harvest index was highest in cluster VII (42.52) and the lowest in cluster V (29.51). Grain yield per plant was highest in cluster VII (18.11) and lowest in cluster VI (9.04). Similar results were reported by Nandini *et al*., 2018, Nagaraja *et al*., 2023. The desirable traits were highly dispersed among clusters. It is always desirable to identify genotypes with more than one favourable trait as in the case of cluster V which was superior for days to 50 per cent flowering and days to maturity and VII which was superior for number of productive tillers per plant, ear head weight, test weight and grain yield per plant. The crosses involving genotypes of clusters V and VII could produce recombinants that would be high yielding as well as early maturing progenies. The genotypes Karunsuruttai, Ravallicvalli and Paiyur-1 were found superior based on per se values, which belonged to clusters V and VII.

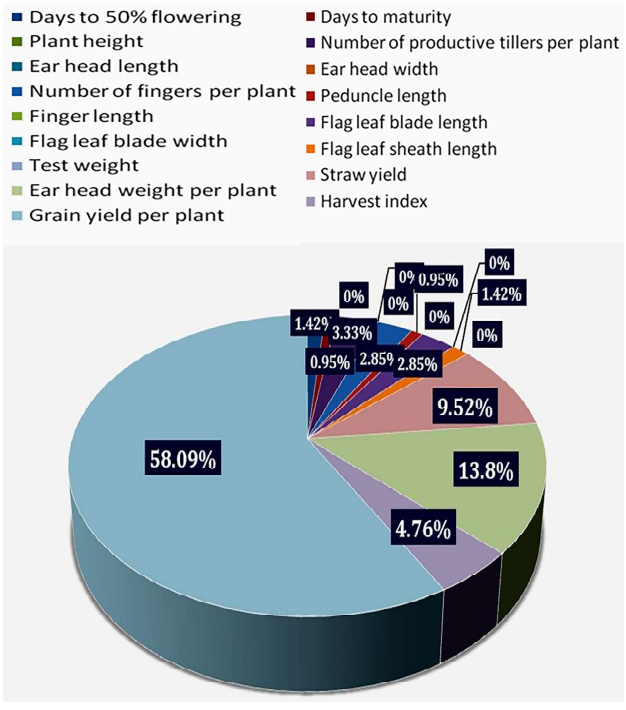

Fig. 3 : Diagrammatic representation of per cent contribution of each character towards genetic divergence in genotype

Contribution of Characters Towards Genetic Divergence

The relative contribution of each character towards D^2 depend upon the inter cluster distance in all combination (Fig. 2). The selection and choice of parents mainly depend upon contribution of characters in manifestation of genetic divergence which were exhibited by grain yield per plant (58.09 per cent) followed by ear head weight (13.80 per cent), straw yield (9.52 per cent) and harvest index (4.76 per cent). Similar results were reported by (Saundarya kumari and Satish kumar singh, 2015). The major trait contributing to the total divergence can be utilized as the criterion in selecting genetically diverse parents.

In the present investigation, based on the genetic diversity studies, the most divergent genotypes can be selected for further breeding programme. These genotypes selected from divergent clusters identified based on the phenotypic traits could be utilized in crop improvement programme to improve and to widen the genetic base of finger millet for the selection of superior lines in segregating generation. Genotypes with multiple superior traits could be utilized for simultaneous transfer of multiple traits/genes in breeding programme. The current study resulted in identification of three genotypes of finger millet namely Paiyur-1, Ravallicvalli and Karunsuruttai as the most divergent parents which could be used in future breeding programme.

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