

Original Research Article

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Genetic Diversity Studies in Finger Millet under Terminal Moisture Stress

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ABSTRACT

The present investigation is carried out to study the genetic divergence among 108 Ragi genotypes for fifteen different characters using Mahalanobis D² statistics. The 108 finger millet genotypes were grouped into 7 clusters and 8 clusters under moisture stress free (MSF) and terminal moisture stress (TMS) conditions respectively, irrespective of geographical diversity, indicating no parallelism between geographic and genetic diversity. Under terminal moisture stress (TMS) condition, highest number of genotypes were observed in cluster I (33) followed by cluster III (28), cluster II (21), cluster IV (17), cluster V (8), cluster VIII (2) and remaining clusters such as clusters VI, cluster VII were solitary clusters and the highest inter-cluster distance was observed between cluster III and cluster VIII indicating wider range of variability and the genotypes of respective clusters can be utilized for introgressing useful traits for the development of elite cultivars.

Keywords

Moisture stress free condition (MSF), Terminal moisture stress (TMS)

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Introduction

Finger millet (*Eleusine coracana* L.) is a crop of antiquity and known for their suitability to dry lands and tribal agriculture of sustainable nature. The resilience exhibited by this crop is helpful in their adjustment to different ecological situations making it an ideal crop for climate change and contingency

planning. Finger millet belongs to family *Poaceae*, subfamily *Chloridoideae* and genus *Eleusine*. It is native to East Africa and came to India around 2000 BC. It is widely grown in arid and semiarid areas of Africa and Asia. In India, it ranks sixth in production after wheat, rice, maize, sorghum and bajra. India is a major producer of Ragi in Asia with a cultivated area of 1.19 million hectares,

production of 1.98 million tonnes giving an average productivity of about 1661 kg per hectare. The major finger millet growing states are Karnataka, Maharashtra, Uttarakhand, Tamil Nadu, Simandra, Orissa and Jharkhand. It is mainly grown and consumed in Karnataka, Andhra Pradesh, Tamil Nadu, Odisha, Maharashtra, Uttarakhand and Goa. In Karnataka, it is popularly known as “Ragi” grown in an area of 0.598 million hectares with a production of 0.86 million tones. Finger millet is considered to be one of the most nutritious cereals which contains about 65–75% carbohydrates, 5–8% protein, 15–20% dietary fibers and 2.5–3.5% minerals, 1–2% ether extractives. Of all the cereals and millets, finger millet has the highest amount of calcium (344 mg) and potassium (408 mg) (Devi *et al.*, 2014). Finger millet can be termed as smart food being “good for you, the planet and the farmer” and are fast becoming a favourite globally. With its high nutrient profile and being versatile in nature it is also known to be a promising immunity booster amid COVID-19 pandemic.

With the climate change looming large, shifts in rainfall pattern and vagaries of monsoon the crop frequently confronts drought stress (DS) at flowering and grain filling stages of the crop cycle is referred to “Terminal drought”. Terminal drought stress is the consequence of the crop growing and maturing in a progressively depleting soil moisture profile (Ludlow and Muchow, 1990; Krishnamurthy *et al.*, 1999). Acute water shortage is a threat to crop cycle and when this condition often coincides under arid and semiarid climates it causes a severe threat to productivity by limiting the rate and duration of grain filling growth. The present study was undertaken during *Rabi 2019* at Agricultural Research Station, Hagari, Ballari, Karnataka to know genetic diversity and to identify superior genotypes for yield and its

component traits under Terminal Moisture Stress (TMS) among finger millet accessions.

Materials and Methods

The experimental material consisted of one hundred eight Ragi genotypes, along with three checks *viz.*: ML365, GPU67 and GPU28. Two experiments were under taken in the augmented design where the Finger millet genotypes were raised in Moisture Stress Free (MSF) & Terminal Moisture Stress (TMS) environmental conditions. Each genotype was grown in 2 m long single row plot. Observations were recorded for fifteen characters *viz.*, days to fifty per cent flowering, days to maturity, plant height (cm), productive tillers per plant, finger length (cm), fingers per ear head, 1000 seed weight (g), harvest index (%), root length (cm), root volume (cc), root biomass (g), proline ($\mu\text{mole g}^{-1}\text{fr.wt}$), RWC (%), SCMR and grain yield per plant (g) on five competitive plants selected at random for each genotypes. The mean values on these observations were subjected for statistical analysis and the genetic divergence was computed using Mahalanobis D^2 statistics. Based on genetic distance, all the genotypes were grouped into different clusters (Rao, 1952).

Results and Discussion

One hundred eight genotypes of finger millet were grouped into 7 clusters and 8 clusters under moisture stress free (MSF) and terminal moisture stress (TMS) conditions respectively (Table 1) and (Table 2). Under moisture stress free (MSF) condition, cluster I (56) recorded highest number of genotypes followed by cluster II (28) and cluster IV (23) while cluster III, V, VI, and VII were solitary clusters. Under terminal moisture stress (TMS) condition, highest number of genotypes was observed in cluster I (33) followed by cluster III (28), cluster II (21),

cluster IV (17), cluster V (8), cluster VIII (2) and remaining clusters such as clusters VI, cluster VII were solitary clusters. Genotypes of different geographical areas fall in one group and also the genotypes of same geographical area were clubbed into different groups indicating there is no formed relationship between geographical diversity and genetic diversity (Surnarayana *et al.*, 2014; Devaliya *et al.*, 2017 and Patil *et al.*, 2018).

Intra and inter cluster D^2 values were worked out using D^2 values from divergence analysis for both moisture stress free (MSF) (Table 3) and terminal moisture stress (TMS) conditions (Table 4). Under moisture stress free (MSF), cluster IV (741.23) had maximum intra cluster distance followed by cluster I (577.91) and cluster II (510.14). This implies that these clusters have the genotypes with varied genetic architecture. Cluster III, cluster V, cluster VI and cluster VII showed zero intra cluster distance due to monogenotypic nature. High intra-cluster genetic distance in cluster IV was because of heterogeneous composition of that cluster. Likely under terminal moisture stress (TMS) condition, cluster V (1278.03) had maximum intra cluster distance followed by cluster IV (880.011), cluster III (780.91), cluster II (707.79), cluster VIII (608.14) and cluster I (536.98). While, cluster VI and cluster VII showed zero intra cluster distance due to monogenotypic nature under moisture stress.

Under moisture stress free (MSF) environment, maximum inter-cluster distance was observed between cluster IV and cluster VII (3763.54) followed by cluster III and cluster VI (3285.3), cluster II and IV (3130.41), cluster II and cluster V (2703.06), cluster IV and cluster VI (2408.84), cluster III and cluster VI (2231) and cluster II and cluster III (2043.47). The inter cluster between cluster II and cluster VI (1936.02),

cluster V and cluster VII (1826.24), cluster III and cluster V (1708.64), cluster I and cluster VII (1516.1), cluster I and cluster II (1465.51), cluster IV and cluster V (1358.64), cluster I and cluster IV (1260.48), cluster II and cluster VII (1148.24), cluster VI and cluster VII (1010.98) and cluster I and cluster VI (1010.14) were also high. The clusters with higher inter-cluster distances indicated that the genotypes included in those clusters had high genetic variation and hybridization between genotypes of these clusters may result heterotic hybrids because of convergence of diverse genes scattered in parents to progeny (Rawat *et al.*, 2018). The minimum estimate for inter-cluster distance were recorded between cluster V and cluster VI (617.16) followed by cluster I and cluster V (821.14), cluster III and cluster IV (873.57) and cluster I and cluster III (903.78).

Under terminal moisture stress (TMS) condition, maximum inter-cluster distance was observed between cluster III and cluster VIII (7828.66) followed by cluster V and cluster VIII (5718.33), cluster VII and VIII (5177.83), cluster VI and cluster VIII (4953.03), cluster I and cluster VIII (4306.52), cluster III and cluster IV (3480.8), cluster II and cluster VIII (2826.01), cluster IV and cluster V (2808.3), cluster IV and cluster VII (2781.26), cluster II and cluster III (2419.4), cluster IV and cluster VI (2373.62), cluster V and cluster VII (2210.03) and cluster III and cluster V (2162.11). The inter cluster between cluster IV and cluster VIII (1938.55), cluster V and cluster VI (1907.19), cluster I and cluster VII (1823.34), cluster II and cluster V (1706.39), cluster III and cluster VII (1644.16), cluster I and cluster III (1551.25), cluster I and cluster IV (1502.82), cluster I and cluster VI (1423.49), cluster II and cluster VII (1373.49), cluster III and cluster VI (1252.06) were also high. The minimum estimate for inter-cluster distance were recorded between cluster II and cluster

IV (1195.42), cluster I and cluster V (1162.53), cluster II and cluster VI (1137.28), cluster I and cluster II (1023.44) and cluster VI and cluster VII (227.75). The clusters with lowest inter- cluster distances indicated that genotypes present in these cluster pairs were genetically close to each other. The crosses between genotypes belonging to clusters separated by low inter cluster distance were likely to throw promising recombinants in the segregating generations. Wolie *et al.*, (2013) suggested that most diverse cluster may be used as parents in hybridization programme to develop high yielding varieties, while selection and choice of parents mainly depends upon contribution of characters towards divergence as stated by Dinesh *et al.*, (2010).

Cluster means for all fifteen characters under moisture stress free (MSF) and terminal moisture stress (TMS) conditions are depicted in Table 5 and Table 6 respectively. The

results indicated appreciable difference among clusters means for most of the characters.

Under moisture stress free (MSF), as far as cluster means are concerned, cluster II had the lowest mean values for days to fifty per cent flowering, days to maturity and 1000 seed weight. Cluster III had the highest mean values root length, root volume and root biomass, while it showed lowest mean values for characters finger length, harvest index, proline, RWC, SCMR and grain yield. Cluster IV had the highest mean value for plant height. Cluster V had the highest mean values for days to fifty per cent flowering, proline and RWC. Cluster VI had the highest mean values for days to maturity, productive tillers per plant, fingers per ear head and SCMR. Cluster VII had the highest mean values for finger length, harvest index and grain yield.

Table.1 Clustering pattern of finger millet genotypes under moisture stress free environment

Clusters	No. of genotypes	Genotypes
I	56	HR55,HR53,HR51,HR39,HR32,HR23,HR31,HR38,HR14,HR60,HR59 HR58,HR2,HR34,HR33,HR12,HR20,HR3,HR9,HR40,HR16,HR11,HR5 HR21,HR57,HR6,KMR652,PR1639,ML365,HR24,HR41,HR42,WN562 HR19,HR56,TNEC1297,TNEC1299,HR18,HR54,TNEC1302,HR30,HR37 KMR650,GPU28,HR35,HR28,HR22,HR61,HR50,GPU99,HR36,HR17 HR4,HR26,GPU98,WN591.
II	28	PPR1082,PR1506,VR1125,VL376,VR1112,VL400,VL399, BR14-2 PRSW43,GPU101,RAUF21,OEB608,KOPN1112, IIMR-R18-5725 PRS38,TNEC1311,DPLN2,KWFM47, PPR1091, PR202, IIMRFM8023, GPU100,IIMRFM8011, KMR704, KMR703,HR13,BR14-27,GSMC1
III	1	GPU 45
IV	23	HR27,HR49,HR46,HR1,VR1110,HR45,HR15,HR25, RAUF17, OEB604, HR48,GPU67,VL382,HR10,VR117, VL394, VR1125, HR29, PR202, HR44, HR7, HR43, HR19
V	1	HR 8
VI	1	HR 13
VII	1	HR 52

Table.2 Clustering pattern of finger millet genotypes under terminal moisture stress environment

Clusters	No. of genotypes	Genotypes
I	33	HR39,HR20,HR23,HR38,HR14,HR32,HR31,HR55,HR19, HR53, HR50,HR58,HR59,HR56,HR2,HR40,HR9,HR3,HR46HR42,HR51, HR12,HR34,HR37,HR35,HR60,ML365,RAUF17,HR6,HR61,HR41, HR30,HR22
II	21	HR33,HR57,HR36,HR11,VR117,GPU45,GPU98,HR43, HR16, KMR652,GPU99,KMR650,PR1639,GPU67,GPU28, GSMC1, WN591,HR24,VR1110,PR202,OEB604
III	28	PRSW43,RAUF21,OEB608,VL399,VL376,KOPN1112, GPU100, VL400,BR142,VR1125,VR1112,PR1506,PR202, KWFM47, GPU101,TNEC1297,TNEC1311,IIMR R18-5725, PPR1082, TNEC1299,IIMRFM8023,TNEC1302,KMR703,PRS38,IIMRFM8011, PPR1091,DPLN2,HR13
IV	17	HR25,HR26,VL382,HR10,HR44,HR27,HR1,WN562,HR45,HR15, HR49, HR29,VL376,HR7,VL394,HR5,HR8
V	8	HR21,HR54,HR18,HR28,HR13,HR4,HR47,HR52
VI	1	BR14-27
VII	1	KMR704
VIII	2	HR43,HR48

Table.3 Intra (diagonal) and inter-cluster D^2 values among seven clusters in finger millet under moisture stress free environment

Clusters	I	II	III	IV	V	VI	VII
I	577.91	1465.51	903.78	1260.48	821.14	1010.14	1516.1
II	1465.51	510.14	2043.47	3130.41	2703.06	1936.02	1148.24
III	903.78	2043.47	0	873.57	1708.64	2231	3285.3
IV	1260.48	3130.41	873.57	741.23	1358.64	2408.84	3763.54
V	821.14	2703.06	1708.64	1358.64	0	617.16	1826.24
VI	1010.14	1936.02	2231	2408.84	617.16	0	1010.98
VII	1516.1	1148.24	3285.3	3763.54	1826.24	1010.98	0

Table.4 Intra (diagonal) and inter-cluster D² values among eight clusters in finger millet under terminal moisture stress environment

Clusters	I	II	III	IV	V	VI	VII	VIII
I	536.98	1023.44	1551.25	1502.82	1162.53	1423.49	1823.34	4306.52
II	1023.44	707.79	2419.4	1195.42	1706.39	1137.28	1373.49	2826.01
III	1551.25	2419.4	780.91	3480.8	2162.11	1252.06	1644.16	7828.66
IV	1502.82	1195.42	3480.8	880.01	2808.3	2373.62	2781.26	1938.55
V	1162.53	1706.39	2162.11	2808.3	1278.03	1907.19	2210.03	5718.33
VI	1423.49	1137.28	1252.06	2373.62	1907.19	0	227.75	4953.03
VII	1823.34	1373.49	1644.16	2781.26	2210.03	227.75	0	5177.83
VIII	4306.52	2826.01	7828.66	1938.55	5718.33	4953.03	5177.83	608.14

Table.5 Cluster mean values for different characters of finger millet genotypes under moisture stress free environment

Cluster	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅
I	77.3	109.8	96.1	3.0	7.3	7.1	3.3	30.0	31.3	26.4	7.0	8.8	84.3	32.3	25.4
II	61.4	92.7	77.3	3.2	7.5	6.9	3.2	31.0	27.3	23.5	7.0	8.6	82.7	35.2	23.9
III	71.0	102.20	113.0	3.2	6.3	7.5	3.2	20.3	36.3	30.3	8.2	5.3	82.6	28.6	17.1
IV	77.6	111.65	120.7	3.3	7.3	7.4	3.4	31.8	30.5	26.3	7.0	8.9	84.3	35.0	26.3
V	91.0	124.7	97.1	2.4	7.2	6.8	3.3	36.1	33.2	25.9	6.9	14.0	89.8	36.8	24.8
VI	85.0	125.0	80.0	4.2	7.2	7.9	3.9	25.8	23.6	21.9	6.5	9.1	85.6	39.6	20.5
VII	78.0	109.0	63.6	2.8	8.2	7.2	3.9	37.1	27.8	24.0	6.2	7.9	80.7	32.6	34.9

X₁=Days to 50% flowering X₅ = Finger length (cm) X₉= Root length (cm) X₁₃ = RWC (%)
 X₂= Days to maturity X₆ = Fingers/earhead X₁₀= Root volume (cc) X₁₄= SCMR reading
 X₃= Plant height (cm) X₇ = 1000 Seed weight (g) X₁₁= Root biomass (g) X₁₅ = Grain yield (g/plant)
 X₄ = Productive tillers/plant X₈=Harvest index (%) X₁₂ = Proline (µmole g⁻¹fr.wt)

Table.6 Cluster mean values for different characters of finger millet genotypes under terminal moisture stress environment

Clusters	X ₁	X ₂	X ₃	X ₄	X ₅	X ₆	X ₇	X ₈	X ₉	X ₁₀	X ₁₁	X ₁₂	X ₁₃	X ₁₄	X ₁₅
I	75.6	107.8	88.3	2.0	6.5	6.4	2.8	28.3	33.7	25.0	7.13	15.6	72.1	28.7	21.4
II	70.7	107.4	104.0	2.0	7.3	7.0	2.6	22.5	33.5	25.1	7.0	13.1	63.9	24.5	16.1
III	57.3	91.2	71.2	2.3	7.3	6.7	2.8	28.3	31.3	23.7	7.1	15.5	73.2	30.0	20.7
IV	74.5	108.3	116.7	2.2	6.7	7.0	2.8	29.7	33.7	26.1	7.1	16.2	75.4	31.3	21.1
V	79.7	112.7	78.4	2.0	7.4	7.4	2.8	23.8	27.5	24.3	6.8	12.6	62.0	24.7	17.5
VI	56.0	90.0	91.5	1.2	5.8	6.5	2.2	17.0	27.1	21.5	7.3	13.8	60.3	20.4	14.3
VII	56.5	88.6	92.4	2.4	12.0	8.1	2.0	21.9	31.9	14.2	6.8	10.1	52.4	19.5	11.8
VIII	82.5	114.0	148.7	2.1	7.23	7.5	2.7	28.1	24.2	23.0	7.1	13.2	64.5	26.0	22.4

X₁=Days to 50% flowering X₅ = Finger length (cm) X₉= Root length (cm) X₁₃ = RWC (%)
 X₂= Days to maturity X₆ = Fingers/earhead X₁₀= Root volume (cc) X₁₄= SCMR reading
 X₃= Plant height (cm) X₇ = 1000 Seed weight (g) X₁₁= Root biomass (g) X₁₅ = Grain yield (g/plant)
 X₄ = Productive tillers/plant X₈=Harvest index (%) X₁₂ = Proline (µmole g⁻¹fr.wt)

Table.7 Contribution of different characters towards genetic divergence in finger millet under moisture stress free environment

Sl. No.	Characters	No. of first rank	Contribution %
1	Days to 50% flowering	829	11.07
2	Days to maturity	72	1.18
3	Plant height (cm)	537	10.06
4	Productive tillers/plant	0	0
5	Finger length (cm)	7	0.11
6	Fingers/earhead	18	0.75
7	1000 seed weight (g)	201	3.29
8	Harvest index (%)	97	1.59
9	Root length (cm)	72	1.18
10	Root volume (cc)	49	0.8
11	Root biomass (g)	0	0
12	Proline ($\mu\text{mole g}^{-1}$ fr.wt)	6	0.1
13	RWC (%)	248	3.46
14	SCMR	916	15.64
15	Grain yield (g plant^{-1})	3053	50.77

Table.8 Contribution of different characters towards genetic divergence in finger millet under terminal moisture stress environment

Sl. No.	Characters	No. of first rank	Contribution %
1	Days to 50% flowering	819	11.07
2	Days to maturity	646	10.74
3	Plant height (cm)	343	7.79
4	Productive tillers/plant	0	0
5	Finger length (cm)	2	0.03
6	Fingers/earhead	7	0.11
7	1000 seed weight (g)	241	3.95
8	Harvest index (%)	154	2.59
9	Root length (cm)	103	1.59
10	Root volume (cc)	23	0.38
11	Root biomass (g)	0	0
12	Proline ($\mu\text{mole g}^{-1}$ fr.wt)	5	0.08
13	RWC (%)	713	10.81
14	SCMR	14	0.23
15	Grain yield (g plant^{-1})	3035	50.63

Under terminal moisture stress (TMS), as far as cluster means are concerned, cluster I had the highest mean value for root length and the lowest mean for fingers per ear head. Cluster III had lowest mean for plant height. Cluster

IV had the highest mean values for harvest index, root volume, proline, RWC and SCMR. Cluster V had the highest mean value for 1000 seed weight. Cluster VI had the highest mean value for root biomass. Cluster

VII had highest mean values for productive tillers per plant, finger length and fingers per ear head. Cluster VIII had highest mean values for days to fifty per cent flowering, days to maturity, plant height and grain yield, while it showed lowest mean for root length. Equivalent results have also been reported by Anteneh *et al.*, (2019), Kandel *et al.*, (2019) and Swamynatham *et al.*, (2020).

The relative contribution of different characters towards genetic divergence under MSF and TMS are depicted in Table 7 and Table 8. Out of the total contribution of different characters towards genetic divergence under non-stress environment, grain yield (50.77%) showed maximum contribution towards genetic diversity. The other characters *viz.*, SCMR (49.23%), days to 50% flowering (11.07%), plant height (10.06%), RWC (3.46%), 1000 seed weight (3.29%), harvest index (1.59%), days to maturity (1.18%), root length (1.18%), root volume (0.8%), fingers per ear (0.75%), finger length (0.11%) and proline (0.1%) contributed towards genetic divergence under MSF environment. This indicates the presence of variability for these traits among the studied genotypes. Analogous results were reported by Saundarya Kumari and Singh (2015) for grain yield per plant.

While under terminal moisture stress (TMS), grain yield (50.63%) showed maximum contribution towards genetic diversity. The other characters *viz.*, days to 50% flowering (11.07%), RWC (10.81%), days to maturity (10.74%), plant height (7.79%), 1000 seed weight (3.95%), harvest index (2.59%), root length (1.59%), root volume (0.38%), SCMR (0.23%), fingers per ear (0.11%), proline (0.08%) and finger length (0.03%) contributed towards genetic divergence under TMS environment. Therefore, these characters should be given due importance. Inter-cluster distances indicated that the

accessions included in the diverse clusters would be used in further crop improvement programme. Subramanya and Ravikumar (2020) reported collaborative result for grain yield per plant and days to fifty per cent flowering.

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