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ASSESMENT OF GENETIC DIVERSITY IN PROMISING FINGER MILLET [*ELEUSINE CORACANA* (L.) GAERTN] GENOTYPES

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ABSTRACT
An experiment with thirty five genotypes of finger millet carried out to study the nature and magnitude of divergence using Mahalanobis D^2 statistics, in randomized block design with three replication. The data for eleven important quantitative traits recorded from the genotypes raised. The variability study indicated high to moderate phenotypic and genotypic coefficient of variation accompanied by high heritability and genetic advance as per cent of mean for traits, grain yield per plant, harvest index, grain weight of main panicle, number of tillers per plant, flag leaf area, 1000-grain weight, number of fingers per panicle, panicle length and days to fifty per cent flowering, indicating their importance in selection for yield improvement. The 35 genotypes of finger millet were grouped into six clusters using Tocher's method. The genotypes in cluster IV and cluster VI, exhibited high degree of genetic diversity. Cluster III was suitable for grain yield per plant, 1000-grain weight, grain yield of main panicle and harvest index. Days to fifty per cent flowering and grain yield per plant contributed maximum towards genetic divergence.

INTRODUCTION

Finger millet locally known as "Ragi" or "Madua" (*Eleusine coracana* L.) is the most important among small millets and possesses the potentialities to be exploited to meet crying need of dry land farmers. This crop is a native of Africa (Abyssynian now known as Ethiopia center of origin) and belongs to the group *Chloridoideae*, tribe Ergrasetae and family *Gramineae*. Among the millet crops finger millet ranked fourth after the pearl millet, foxtail millet and proso millet. It is a self pollinated (allopolyploid) crop and the chromosome number of the species has been reported to be 2n = 4x = 36 and evolved from a cross between two diploid species *Eleusineindica* (AA) and *Eleusinefloccifolia* or *Elusinetristachya* (BB) as genome donars (Chennaveeraiah and Hiremath, 1973, 1974, Hilu and de Wet, 1976b, Hiremath and Salimath, 1992). The presence of genetic diversity and genetic relationships among genotypes is a prerequisite and paramount important for successful wheat breeding programme. Developing hybrid wheat varieties with desirable traits require a thorough knowledge about the existing genetic variability (Kahrizi *et al.*, 2010). The more genetic diverse parents, the greater chances of obtaining higher heterotic expression in F_1's and broad spectrum of variability in segregating population as already reported by earlier workers (Shekhawat *et al.*, 2001). Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization. Several genetic diversity studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (Shekhawat *et al.*, 2001, Daniel *et al.*, 2011). Jagadev *et al.* (1991) reported that the character contributing maximum to the divergence should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parents for hybridization.In views of these facts, the present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among finger millet genotypes for further utilization in breeding programme.

MATERIALS AND METHODS

The experiment was conducted in a randomized block design with three replication. The experimental materials were sown on 24th July, during *Kharif*, 2013 keeping plot size 3.0 m × 2.5 m. In each replication each genotype was grown in a plot of 3 rows of 3 meter length each with a spacing of 22.5 cm between rows and 10 cm between plants (within rows). In order to compare the genotype unbiaselly, uniform plant population was kept in each row. Ten random plants per genotype per replication were tagged to record observations on yield and yield attributing traits *viz*. days to fifty per cent flowering, plant height, flag leaf area, number of tillers per plant, numbers of fingers per panicle, panicle length, days to maturity, grain yield of main panicle,1000-grain weight, grain yield per plant and harvest index.

Flag leaf area was calculated by following formula (Mokhtarpour *et al.*, 2010).

Flag leaf area (cm^2) = flag leaf length (cm) x flag leaf width (cm)

Harvest index was calculated as per the formula (Huhn, 2008).

$$H.I. = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

Where,

Economic yield = Grain yield (g)

Biological yield = Total plant yield (g)

The data were analyzed using WINDOSTAT version 9.1 software for computation of analysis of variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2b) and clustering by Tocher's method

RESULTS AND DISCUSSION

In the present investigation, 35 diverse genotypes of finger millet were studied to assess their yield and yield related attributing characters. The analysis of variance clearly indicated that there was highly significant variation among the genotypes for all the traits studied. This in turn indicated that there was sufficient variability in the material studied, which could be utilized in further breeding programme. Similarly, Many earlier workers Karad *et al*. (2013), Reddy *et al*. (2013), Ulaganathan *et al*. (2013), Wolie *et al*. (2013), Surayanarayan *et al*. (2014) and Dapke *et al*. (2014) reported high variability for different traits in finger millet. Thus, it is implied that there was reasonably sufficient variability in material used for their study, which provides ample scope for selecting superior and desire genotypes by the plant breeder for further improvement.

The phenotypic variances (Table 1) for all the traits under studied were higher than the genotypic variances (Reddy *et al*., 2013). This may be due to the non-genetic factor which played an important role in the manifestation of these characters. Wide ranges of variance (phenotypic and genotypic) were observed in the experimental material for all the characters under investigation. The maximum phenotypic and genotypic variance exhibited by the traits, plant height, days to maturity, harvest index, days to fifty per cent flowering, grain yield per plant and flag leaf area. These findings were in accordance of Dhanpal *et al*. (2008) and Dinesh *et al*. (2010) reported grain yield per plant exhibiting the highest range and days to maturity showed the lowest range. In the present investigation, the genotypic and phenotypic coefficient of variation for grain yield per plant was found high. This result is in agreement with Shet *et al*. (2009) and Ulaganathan *et al*. (2013). The results showed that harvest index, grain yield of main panicle, 1000-grain weight, number of tillers per plant and flag leaf area exhibited very high GCV and PCV indicating the importance of this trait in evaluation and selection of the genotypes. In this study, the phenotypic and genotypic coefficient of variance was found moderate for number of fingers per panicle, panicle length, plant height and days to fifty per cent flowering. Similar results were also reported by Reddy *et al*. (2013) and Wolie *et al*. (2013). They found high GCV and PCV for respective traits. The genotypic and phenotypic coefficient of variation for days to maturity was found lowest. Karad *et al*. (2013) and Ganapathy *et al*. (2011) reported days to maturity exhibit the lowest GCV as well as PCV. These findings were clearly indicated that selecting genotypes through these traits will be effective. It is interesting to note that the differences between GCV and PCV values were minimum implying least influence of environment and additive gene effects indicating genotypes can be improved and selected for these characters for improvement of yield. The coefficient of variation indicated the extent of variability present in these characters and does not indicate the heritable portion. This could be ascertained from the heritability estimates, which in broad sense include both additive and non-additive gene effects and in narrow sense include the portion of heritable variation which is due to additive

Table 1: Estimates of variability parameter of yield and yield attributing traits in Finger millet

Sl. No	Characters	σ^2_g	σ^2_p	GCV	PCV	h^2 (Broad sense)%	GA as % of Mean
1	Plant height (cm)	108.01	150.86	10.70	12.64	71.60	18.64
2	Days to 50 per cent flowering	60.86	61.02	10.02	10.03	99.75	20.61
3	Flag Leaf Area(cm^2)	38.91	42.33	22.52	23.49	91.91	44.47
4	Numbers of Tillers per Plant	1.14	1.19	27.81	28.38	95.98	56.13
5	Panicle Length(cm)	1.85	1.91	15.42	15.64	97.14	31.30
6	Numbers of Finger per Panicle	1.47	1.52	17.06	17.36	96.49	34.52
7	Days to Maturity	96.96	97.78	8.56	8.60	99.16	17.57
8	Grain Yield of Main Panicle(gm)	1.55	1.60	28.72	29.18	96.87	58.23
9	1000 - Grain weight	0.48	0.50	20.81	21.37	94.85	41.76
10	Grain Yield per Plant(gm)	51.92	53.17	43.98	44.51	97.64	89.52
11	Harvest Index (%)	68.71	70.68	36.27	36.79	97.21	73.67

Where, σ^2_g = Genotypic variance σ^2_p = Phenotypic variance, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation h^2 = heritability, GA = Genetic Advance

Table 2: Clustering pattern of 35 genotypes of Finger millet on the basis of D^2 statistic

Cluster No.	No. of Genotypes within cluster	Genotypes in cluster
I	19	BR145,GPU85,BR64,PEH1201,KR1007-01,KMR126,BR105,PR202,IE4414,WN259,KMR128,PPR1012,PPR1010,DHFMV10-2,DHFMV78-2,IE4424,PR10-3,DHFMV26-2,RAU9
II	6	TNAU1226,VL368,PRM601,VL367,KMR340,TNAU1228
III	1	RAU8
IV	7	GPU84,VR708,PPR2773,WWN25,VL149,VL369,RAU3
V	1	BR 67
VI	1	IE 3575

Table 3: Cluster mean for eleven characters in Finger millet

Cluster No.	PH	DFF	FLA	NTP	PL	FP	DM	GYMP	TGW	GYP	HI
I	97.321	82.439	26.577	3.728	8.816	6.912	119.105	4.425	3.470	15.830	22.812
II	99.033	76.056	29.956	3.050	8.661	6.617	110.333	2.917	2.600	8.606	13.156
III	111.567	81.333	30.233	4.667	8.567	8.533	107.333	5.267	4.133	25.367	37.767
IV	93.614	65.810	26.200	4.686	9.143	7.881	104.095	5.181	3.386	23.405	28.662
V	102.767	65.667	28.633	2.600	10.133	7.467	127.000	3.567	3.067	11.500	20.600
VI	87.700	95.000	42.467	5.667	6.933	6.400	135.667	4.900	3.967	20.300	28.500

Abbreviations-
Plant Height (PH), Days to 50 per cent flowering (DFF), Flag Leaf Area (FLA), Number of Tillers per Plant (NTP), Panicle Length (PL), Number of Fingers per Panicle (NFP), Days to Maturity (DM), Grain Yield of Main Panicle (GYMP), 1000-Grain weight (TGW), Grain Yield per Plant (GYP), Harvest Index (HI)

Table 4: Mean intra and inter cluster distance (D^2) among six clusters in Finger millet

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Cluster I	177.59	393.63	269.31	1136.74	900.15	652.23
Cluster II		238.76	487.77	817.75	598.19	1372.51
Cluster III			0.00	727.34	953.27	1023.33
Cluster IV				347.97	571.19	2844.60
Cluster V					0.00	2366.60
Cluster VI						0.00

Table 5: Percentage contribution of eleven characters towards genetic divergence in Finger millet

Sl. No.	Source	Times Ranked 1st	Contribution %
1	PH	0	0.00
2	DFF	316	53.11
3	FLL	12	2.02
4	NTP	8	1.34
5	PL	36	6.05
6	NFP	17	2.86
7	DM	78	13.11
8	GYMP	20	3.36
9	TGW	6	1.01
10	GYP	71	11.93
11	HI	31	5.21

component (Lush, 1949). The knowledge of heritability is helpful in assessing merits and demerits of a particular trait as it enables the plant breeder to decide the course of selection procedure to be followed under a given situation.

In this study, heritability in broad sense for all the characters namely, days to fifty per cent flowering, days to maturity, grain yield per plant, harvest index, panicle length, grain yield of main panicle, number of fingers per panicle, number of tillers per plant, 1000-grain weight, flag leaf area and plant height were found high. High heritability value for these traits indicated that the variation observed was mainly under genetic control and was less influence by environment. So, these traits may be used as a selection criteria for yield improvement in confirmation with the result of earlier workers viz. Reddy *et al.* (2013), Ulaganathan *et al*. (2013) Wolie *et al*. (2013), Nandini *et al*. (2010), Shet *et al.* (2009) and Lush (1949). In the present investigation, the characters, namely grain yield per plant, harvest index, grain yield of main panicle, number of tillers per plant, flag leaf area, 1000-grain weight, number of fingers per panicle, panicle length and days to fifty per cent flowering have high heritability and genetic advance as per cent of mean. Hence, direct selection can be done through these characters for future improvement of genotypes for higher grain yield. Similar results were also reported by earlier workers Surayanarayan *et al*. (2014), Wolie *et al.* (2013), Ulaganathan *et al*. (2013), Shet *et al.* (2009). The high heritability associated with high genetic advance indicated, the variation was mostly due to additive gene effects. It indicates that if these characters are subjected to any selection scheme for exploiting fixable genetic variance, a wide adopted genotype can be developed. Plant height and days to maturity exhibited high heritability and moderate genetic advance as per cent of mean. These traits indicated that their manifestation is governed by both additive and non-additive genetic effects and therefore, selection should be practiced in later segregating generations *i.e*. by hybridization programme to exploit heritability. These findings were in accordance with Nandani *et al.* (2010).

In the present investigation, 35 genotypes (including checks) were grouped into six clusters on the basis of D^2 statistics (Table 2). On the basis of inter or intra-cluster distance dendrogram (Fig. 1) of 35 finger millet genotypes were obtained. Cluster I had maximum number of genotypes (19) viz. BR145, GPU85, BR64, PEH1201, KR1007-01, KMR126, BR105, PR202, IE4414, WN259, KMR128, PPR1012, PPR1010, DHFMV10-2, DHFMV78-2, IE4424, PR10-3, DHFMV26-2 and RAU9. Cluster IV had seven genotypes viz. GPU84, VR708, PPR2773, WWN25, VL149, VL369, and RAU3. Cluster II had six genotypes viz. TNAU1226, VL368, PRM601, VL367, KMR340 and TNAU1228 while Cluster III, V and VI were solitary, comprising single genotypes each namely RAU8, BR67 and IE3575 respectively. The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating that there was no formal relationship between geographical diversity and genetic diversity. Similar studied based on D^2 statistic was also performed by Dhanpal *et al.* (2008), Dinesh *et al.* (2010), Wolie *et al.* (2013). The genetic drift and selection in different environment could cause greater diversity than geographical distance (Patel and Patel, 2012).

Different clusters comprises unique feature for different

Table 6: Diverse finger millet genotypes based on genetic distance and superior *per se* performance for the traits under investigation

Sl. No.	Characters	Cluster	Suitable Parents in Cluster	*Per se* Performance
1	Plant Height (cm)	VI	IE3575*	87.7
2	Days to 50 per cent flowering	V	BR67*	65.67
3	Flag Leaf Area (cm²)	VI	IE3575*	42.46
4	Number of tillers per Plant	VI	IE3575*	5.66
5	Panicle Length (cm)	V	BR67*	10.13
6	Number of Fingers per Panicle	III	RAU8	8.53
7	Days to Maturity	IV	RAU3*	90.67
8	Grain Yield of Main Panicle (gm)	III	RAU8	5.27
9	1000 - Grain Weight (gm)	III	RAU8	4.13
10	Grain Yield per Plant (gm)	III	RAU8	25.37
11	Harvest Index %	III	RAU8	37.76

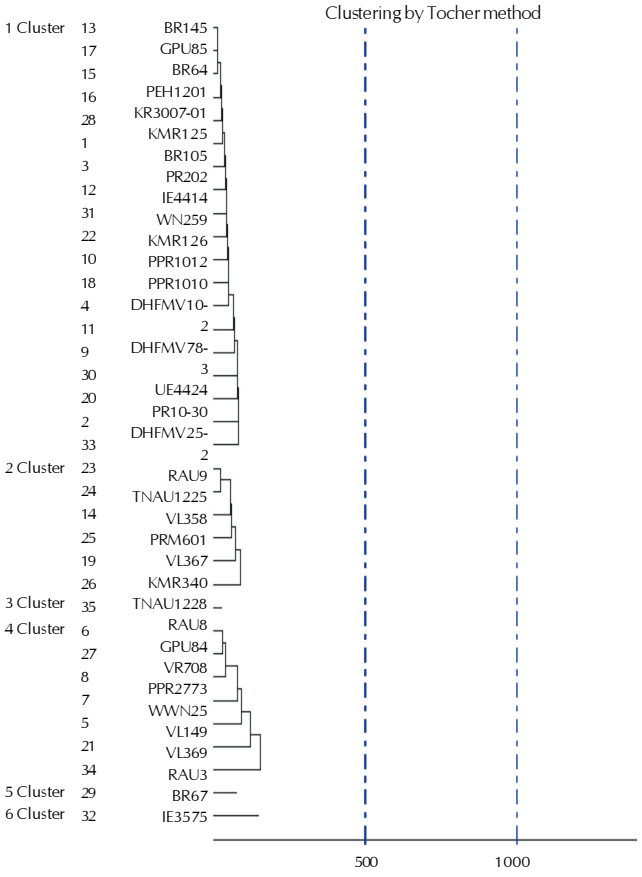

Figure 1: Clustering pattern of 35 finger millet genotypes on the basis of D^2 statistics by Tocher's method

characters under investigation. Cluster III had the maximum mean value for fingers per panicle, grain yield of main panicle, 1000-grain weight, grain yield per plant and harvest index. Cluster V was suitable for early flowering and panicle length whereas, cluster IV for early maturity. Cluster VI may be selected as a donor for dwarfness. Cluster VI had the genotype with the highest mean value for flag leaf area and number of tillers per plant. Therefore, these clusters may be chosen for transferring the traits having high mean values through hybridization programme. Selection of genotypes based on cluster mean for the better exploitation of genetic potential also reported by Wolie *et al.* (2012). The highest intra cluster distance (Table 4) was observed in cluster IV followed by cluster II and cluster I indicating differences in genotypes within cluster. Least intra cluster distance was found in cluster I indicating that close resemblance between the genotypes presented in this cluster. The genotypes in cluster IV and cluster VI due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses may be attempted between genotypes in cluster V and VI and cluster I and IV. The lowest inter cluster distance was observed between cluster I and III followed by cluster I and II and cluster II and III showing these clusters were relatively less divergent and crossing between them cannot produce vigorous offspring (F_1 progenies). These results of genetic diversity study were in agreement with the finding of Wolie *et al.* (2013) and Dinesh *et al.* (2010). They also suggested that genotypes of most diverse cluster may be used as parents in hybridization programmes to develop high yielding varietiesThe selection and choice of parents mainly depends upon contribution of characters towards divergence. The maximum contribution in the manifestation of genetic divergence was exhibited by days to fifty per cent flowering followed by days to maturity, gain yield per plant, panicle length, harvest index, grain weight of main panicle, fingers per panicle, flag leaf area, number of tillers per plant and 1000-grain weight suggesting scope for improvement in these characters. In other words, selection for these characters may be rewarding. Similar observation was recorded by Wolie *et al.* (2011).

In the present study, 35 diverse genotypes were grouped into various cluster and suitable diverse genotypes were selected based on their cluster mean superiority and per se performance for different characters. BR67 grouped in cluster V exhibited earliness in days to fifty per cent flowering based on cluster mean (lowest) and significantly superior per se performance. This genotypes also exhibited superiority for panicle length with highest cluster mean and superior per se performance. IE3575 showed highest flag leaf area and tillers per plant based cluster mean and per se performance. The genotypes namely RAU3 and WWN25 were selected from cluster IV for earliness in days to maturity based on cluster mean (lowest) and significantly superior per se performance. RAU8 have highest cluster mean for number of fingers per panicle, grain yield of main panicle, 1000-grain weight, grain yield per plant and harvest index with superior per se performance. Genotype

RAU 8 (cluster III) was found genetically diverse and superior for fingers per panicle, grain yield of main panicle, 1000-grain weight, grain yield per plant and harvest index. The genotype IE 3575 from cluster VI was selected as suitable parent for flag leaf area and number of tillers per plant, whereas the genotypes namely RAU3 and WWN25 were selected from Cluster IV for earliness in days to maturity based on cluster mean (lowest) and significantly superior per se performance. The genotypes in cluster IV and cluster VI due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme for getting high yielding recombinants. Similar inter varietal crosses may be attempted between genotypes in cluster V and VI and cluster II and V. Similar observation was recorded by karad *et al.* (2013),Daniel *et al.* (2011) and Kahrizi *et al.* (2010)

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