The Pharma Innovation Journal 2022; 11(11): 1858-1863

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; 11(11): 1858-1863

www.thepharmajournal.com
Received: 21-09-2022
Accepted: 24-10-2022

Vikas Pali
Agricultural Research Station, Anand Agricultural University, Dahod, Gujarat, India

Harshal E Patil
Hill Millet Research Station, Navsari Agricultural University, Waghai (Dangs), Gujarat, India

Mayur P Ramani
Directorate of Research, Anand Agricultural University, Anand, Gujarat, India

Corresponding Author:
Vikas Pali
Agricultural Research Station, Anand Agricultural University, Dahod, Gujarat, India

Genetic diversity assessment in finger millet (*Eleusine coracana* L.) genotypes for yield and yield contributing traits

Vikas Pali, Harshal E Patil and Mayur P Ramani

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 percent 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 50% 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, yield of main panicle and harvest index. Days to 50% flowering and grain yield per plant contributed maximum towards genetic divergence.

Keywords: Genetic diversity, fingermillet, mahalanobis D^2

Introduction
Fingermillet (*Eleusine coracana* (L.) Gaertn) belongs of family Poaceae with species Coracana. The cultivated *E. coracana*is a tetraploid (2n = 4X = 36); has morphological similarities to both *E. indica* (L.) Gaertn. (2n = 18) and *E. Africana* (O.) Byrne (2n = 36). It is an important cereal crop amongst the small millets and third in importance among millets in the country in area and production after sorghum and pearl millet. Finger millet is a valued food grain crop and mostly cultivated in rainfed condition in India. Finger millet is more versatile crop due to its adaptability to wide range of geographical areas and agro-ecological diversity. In India, it is cultivated on 1.8 million ha with a production of 2.19 million tonnes and average productivity of 1489 kg per ha. Major finger millet growing states in India are Karnataka followed by Uttrakhand, Maharashtra, Tamil Nadu, Andhra Pradesh, Orissa, Gujarat, Jharkhand and Bihar (Directorate of Economics and Statistics, GOI, 2010-11).
Finger millet is an important cereal because of its excellent storage properties and the nutritive value of the grains. Fingermillet is a good source of calcium and dietary fiber and consumed both in native and processed form (Gopalan *et al*., 1989; Rao and Murlikrishna, 2001) [12, 32].
Finger millet grain can be stored for several years without storage pest infestation which makes it a perfect food grain commodity. It is also a good source of mineral nutrients like Calcium, Iron, Phosphorus, Zinc and Potassium. The fingermillet crop residues are excellent source of dry matter for livestock especially in dry season so; its grains are used for human consumption. Finger millet straw contains up to 61 percent total digestible nutrients makes good fodder. The most important tropical cereals among finger millet is very adaptable and thrives at higher elevations. (Vilas*et al*., 2015) [40].
Genetic variability and diversity play very important role inany crop improvement programme. If we using higher diverse parents they produced higher heterosis in progeny and more chance of getting transgressive segregation. Breeder has to identify diverse parents having high genetic variability for combining desirable characters for develop improved crop variety over existing cultivated variety. Due to multivariate analysis to study morphologically complex, individuals and measuring the degree of divergence between different populations. Multivariate technique is useful for analyzing multiple measurements on each individual under study. Among the multivariate techniques, principal component analysis (PCA) have been very important in selecting genotypes for breeding program that meet the objective of a plant breeder.

Materials and Methods

The experiment was conducted at two locations at Agricultural Research Station, Anand Agricultural University, Dahod and Hill Millet Research Station, Navsari Agricultural University, Waghai and pooled data were used for statistical analysis using 35 finger millets genotypes in randomized block design with three replications during *kharif*, 2020. The data of eleven different characters *viz.*, days to 50% flowering, plant height, flag leaf area, number of tillers per plant, number of fingers per panicle, panicle length, days to maturity, grain yield of main panicle, 1000 grain weight, grain yield per plant and harvest index were taken from five plants and only selected plants from each replication.

Flag leaf area was calculated by following formula (Mokhtarpur *et al.*, 2010) [25]

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

Harvest index was calculated as per the formula (Huhn, 2008) [16]

$$\text{Harvest Index} = \frac{\text{Economic Yield}}{\text{Biological Yield}} \times 100$$

Where

Economic yield = Grain yield (g)
Biological yield=Total plant yield (g)

Results & Discussion

In the present investigation, 35 diverse genotypes of fingermillet 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. 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) [22], Reddy *et al.* (2013) [33], Ulaganathan *et al.* (2013) [39], Wolie *et al.* (2013) [41], Suryanarayan *et al.* (2014) [38] and Dapke *et al.* (2014) [6] 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) [33]. 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 experiment 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 50% flowering, grain yield per plant and flag leaf area. These findings were in accordance of Dhanpal *et al.* (2008) [8] and Dinesh *et al.* (2010) [9] 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) [35] and Ulaganathan *et al.* (2013) [39]. The results showed that harvest index, grain yield of main panicle, 1000-grain weight, and 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 50% flowering. Similar results were also reported by Reddy *et al.* (2013) [33] and Wolie *et al.* (2013) [41].

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) [22] and Ganapathy *et al.* (2011) [11] 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 board sense include both additive and non-additive gene effects and in narrow sense include the portion of heritable variation which is due to additive component (Lush, 1949) [23]. 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 50% 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) [33], Ulaganathan *et al.* (2013) [39] Wolie *et al.* (2013) [41], Nandini *et al.* (2010) [26], Shet *et al.* (2009) [35] and Lush (1949) [23]. 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 50% 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 Suryanarayan *et al.* (2014) [38], Wolie *et al.* (2013) [41], Ulaganathan *et al.* (2013) [39] and Shet *et al.* (2009) [35]. The high heritability associated with high genetic advance indicated, the variation was mostly due to additive gene effects. It indicated 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) [26].

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 dendogram (Fig. 1) of 35 finger millet genotypes were obtained. Cluster I had maximum number of genotypes (19) *viz.* PCGF 36, DFM 1101, DN 7, DN 11, DN 9, DFM 1105, PCGF 31, DN 2 DN 4, DN 10, DFM 1106, IFM 1101, DN 14, DN 8, DFM 1058, DN 12, DFM 1019, DFM 1051 and DN 1, Cluster IV had seven genotypes *viz* PCGF 35, DFM 4009, PCGF 41, DFM 4055, DN 6, DFM 4010 and DFM 4059. Cluster II had six genotypes *viz.* PCGF 47, DFM 1023, DFM 4112, PCGF 44, DN 6 and DFM 1028 while Cluster III, V and VI were solitary, comprising single genotypes each namely DM 13, DN 5 and IFM 1110 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 statistics was also performed by Dhanpal *et al.* (2008) [8], Dinesh *et al.* (2010) [9], Wolie *et al.* (2013) [41], and Patil *et al.* (2017) [30]. The genetic drift and selection in different environment could cause greater diversity than geographical distance (Patel and Patel, 2012) [29].

Different clusters comprises unique feature for different 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) [41]. 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 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) [41], Dinesh *et al.* (2010) [9] and Jadhav *et al.* (2014) [17]. They also suggested that genotypes of most diverse cluster may be used as parents in hybridization programmes to develop high yielding varieties. The 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 50% flowering followed by days to maturity, grain 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. A similar observation was recorded by Wolie *et al.* (2011) [41].

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. DN 5 grouped in cluster V exhibited earliness in days to 50% flowering based on cluster mean (lowest) and significantly superior *per se* performance. These genotypes also exhibited superiority for panicle length with highest cluster mean and superior *per se* performance. IFM 1110 showed highest flag leaf area and tillers per plant based cluster mean and *per se* performance. The genotypes namely DFM 4059 and DFM 4055 were selected from cluster IV for earliness in days to maturity based on cluster (lowest) and significantly superior per se performance. DM 13 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. Gentoype DM 13 (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 IFM 1110 from cluster VI was selected as suitable parent for flag leaf area and number of tillers per plant, whereas the genotypes namely DFM 4059 and DFM 4055 were selected from cluster IV for earliness in days to maturity based on 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) [22], Daniel *et al.* (2011) [7] and Kahrizi *et al.* (2010) [21], Savankumar *et al.* (2017) [34] and Patro *et al.* (2018) [31].

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

S. No	Characters	$\sigma^2 g$	$\sigma^2 p$	GCV	PCV	h^2(Broad sense) %	GA as % of mean
1	Plant height (cm)	107.05	149.36	10.74	12.60	71.67	18.78
2	Days to 50% flowering	61.10	62.12	10.12	10.23	98.36	20.31
3	Flag leaf area (cm^2)	38.51	42.70	21.00	22.95	90.19	43.67
4	Number of tillers per plant	1.16	1.21	28.01	29.08	95.87	55.63
5	Panicle length (cm)	1.90	1.96	16.05	16.34	96.93	31.00
6	Number of finger per panicle	1.51	1.54	17.66	18.16	98.05	35.42
7	Days to maturity	95.20	96.38	8.50	8.56	98.77	16.87
8	Grain yield of main panicle (gm)	1.60	1.63	29.12	29.88	98.15	60.10
9	1000- Grain weight	0.50	0.52	21.01	21.77	96.15	43.56
10	Grain yield per plant (gm)	52.41	53.37	44.38	44.91	98.20	90.00
11	Harvest index (%)	66.51	69.18	36.77	37.09	95.28	72.27

Where, σ^2_g= Genotypic variance, σ^2_p = Penotypic 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 statistics

Cluster No.	No. of genotypes within cluster	Genotypes in cluster
I	19	PCGF 36, DFM 1101, DN 7, DN 11, DN 9, DFM 1105, PCGF 31, DN 2 DN 4, DN 10, DFM 1106, IFM 1101, DN 14, DN 8, DFM 1058, DN 12, DFM 1019, DFM 1051, DN 1
II	6	PCGF 47, DFM 1023, DFM 4112, PCGF 44, DN 6, DFM 1028
III	1	DM 13
IV	7	PCGF 35, DFM 4009, PCGF 41, DFM 4055, DN 6, DFM 4010, DFM 4059
V	1	DN 5
VI	1	IFM 1110

Table 3: Cluster mean of eleven characters in Finger millet

Cluster No.	PH	DFF	FLA	NTP	PL	NFP	DM	GYMP	TGW	GYP	HI
I	96.12	81.30	26.77	3.80	8.92	6.96	118.50	4.53	3.56	15.95	22.94
II	98.53	75.25	29.68	3.08	8.77	6.72	109.23	2.98	2.70	8.72	13.28
III	110.26	80.23	31.03	4.81	8.70	8.65	106.83	5.47	4.25	25.48	37.89
IV	92.51	64.33	27.00	4.76	9.33	7.96	103.19	5.35	3.46	23.51	28.80
V	101.81	64.36	28.23	2.68	10.31	7.58	126.20	3.68	3.20	11.62	20.73
VI	86.56	94.20	43.26	5.79	7.02	6.50	134.46	5.00	4.02	20.52	28.64

Abbreviations

Plant Height (PH), Days to50% 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).

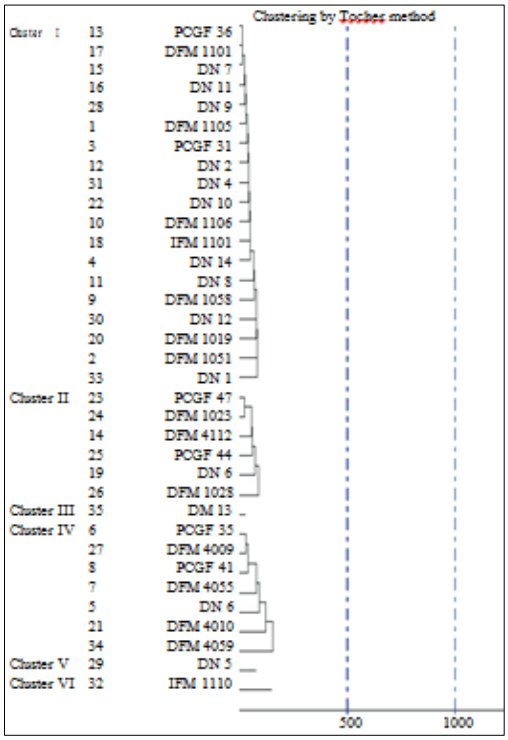

Fig 1: Clustering pattern of 35 finger millet genotypes on the basis of D^2 statistics by Tocher's method

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	176.39	392.53	268.91	1137.34	901.05	653.03
Cluster II		237.86	488.10	818.35	597.12	1373.21
Cluster III			0.00	728.14	954.33	1024.10
Cluster IV				348.25	572.10	2845.20
Cluster V					0.00	2367.30
Cluster VI						0.00

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

S. No.	Source	Times Ranked 1st	Contribution %
1	PH	0	0.00
2	DFF	310	51.20
3	FLL	12	2.02
4	NTP	9	1.50
5	PL	38	6.20
6	NFP	19	3.00
7	DM	78	13.11
8	GYMP	22	3.86
9	TGW	7	1.10
10	GYP	76	12.80
11	HI	31	5.21

Conclusion

In the present study, 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, yield of main panicle and harvest index. Days to 50% flowering and grain yield per plant contributed maximum towards genetic divergence.

Acknowledgement

Authors wish to acknowledge Director of Research & Dean PG Studies, Anand Agricultural University, Anand for providing necessary facilities and other supports for smooth conduction of the research work.

References

1. Arunachalam V. Genetic distance in plant breeding. Indian J. Genetics and Plant Breeding 1981;41:226-236
2. Arunkumar B. Genetic variability, character association and path analysis studies in sorghum (*Sorghum bicolor* Moench). The Bioscan. 2013;8(4):1485-1488.
3. Athwal DS, Singh G. Variability in Kagni adaptation and genotypic and phenotypic variability in four environments. Indian J Gent. and Pl Breed. 1966;26:153-161.
4. Channaveeraiah MS, Hiremath SC. Genome relationship of *Eleusine tristachya* and *Eleusine floccifolia*. J Cytology and Genetics. 1973;8:1-5.
5. Channaveeraiah MS, Hiremath SC. Genome analysis of *Eleusine coracana.* Electronic J Plant Breeding. 1974;1(4):747-751.
6. Dapke JS, Shah DS, Pawar GN, Dhembre VM, Kumar M. Genetic variability and character association over environment in pearl millet (*Pennisetum Glaucum* L.) under dryland conditions of Gujarat. The Bioscan. 2014;9(2):863-867.
7. Daniel H, Mebrahtom M, Tsige G. Genetic divergence analysis on some bread wheat genotypes grown in Ethiopia. J Central Eur. Agric. 2011;12(2):344-352
8. Dhanpal AP, Selvi B, Govindaraj M. Variability and Multivariate analysis in Finger millet (*Eleusine coracana*) germplasm for yield Characters. Crop Research. 2008;36(1, 2, 3):218-223.
9. Dinesh K, Vikrant T, Ramesh BB, Sukram, P. Genetic diversity in fingermillet (*Eleusine coracana* L.). Crop Improvement. 2010;37(1):25-28.
10. Food and Agriculture Organization. http://www/FAO.ORG/ 2004; FAOSTAT database
11. Ganapathy S, Nirmalakumari A, Muthiah AR. Genetic variability and interrelationship analysis for Economic traits in Finger Millet Germplasm. World J Agricultural Sciences. 2011;7(2):185-188.
12. Gopalan C, Ramasastri BV, Balasubramanian SC. Nutritive value of Indian food, National Institute of Nutrition; Hyderabad, India; c1989. p. 204.
13. Gopalan C, Ramasastri BV, Balasubramanian SC. Nurtitive values of Indian foods. National Institute of Nutrition, Indian Council of Medical Research. Hyderabad; c2002.
14. Hiremath SC, Salimath SS. The 'A' genome donor of *Eleusine coracana* (L) Gaertn (Gramineae). Theoretical & Applied Genetics. 1992;84:747-745.
15. Hittalmani S. Development of high yielding, disease resistant, drought tolerant Finger millet (*Eleusine coracana* Gaertn). Progress Report of the Mc Knight Foundation Funded Project. University of Agricultural Sciences; GKVK, Bangalore; c2004.
16. Huhn M. Comments on the calculation of mean harvest indices. J Agronomy and Crop Science. 2008;165(2-3):85-90.
17. Jadhav R, Babu DR, Ahamed L, Rao VS. Assessment of genetic divergence in Finger millet [*Eleusine coracana* (L.) Gaertn.] for yield and yield contributing traits. Intl. J Food. Ferment. Technol. 2014;4(2):113-120.
18. Jagadev PN, Shamal KM, lenla L. Genetic divergence in rape mustard. Indian J Genet & Plant Breed. 1991;51:465-466.
19. Jain AK, Dhagat NK, Tiwari AS. Genetic divergence in finger millet. Indian J Genet & Plant Breed. 1981;41:346-348.
20. Johnson HW, Robison HF, Comstock RE. Estimates of genetic and environmental variability in soybean. Agronomy J. 1955;47:314-318.
21. Kahrizi D, Maniee M, Mohammadi R, Cheghamirza K. Estimation of genetic parameters related to morpho-agronomic traits of durum wheat (*Triticum turgidum var. durum*). Biharean Biologist. 2010;4(2):93-97.
22. Karad SR, Patil JV, Kale AA. Study of genetic diversity in finger millet (*Eleusine coracana* L.) genotypes using RAPD markers. International J Integrative sciences, Innovation and Technology 2013;2(4):31-36.
23. Lush JL. Heritability of quantitative characters in farm animals. Proceedings of 8th Congress of Genetics and Heriditas. 1949;35:356-375.

24. Mahalanobis PC. On the generalized distance in statistics. Proceedings of National Institute of Science India. 1936;2:49-55.
25. Mokhtarpour H, BSC Saleh G, Selamat AB, Asadi, MA, Kamkar B. Non-destructive estimation of maize leaf area, fresh weight and dry weight using leaf length and leaf width. Communications in Biometry and Crop Science. 2010;5(1):19-26.
26. Nandini B, Ravishankar CR, Mahesha B, Shailaja H, Kalyana MKN. Study of correlation and path analysis in F_2 population of finger millet. International J Plant Sciences. 2010;5(2):602-605.
27. National Reseacrh Council. Finger millet In: Lost crops of Africa. National Academy of Science; c1996. p. 39-57.
28. Panse VG. Genetics of quantitative characters in relation to plant breeding. Indian J Genet & Plant Breed. 1942;2:318-327.
29. Patel JN, Patel NK. Genetic diversity in *Vigna radiata* (L.) Wilczek. Life Science Leaflets. 2012;11:53-56.
30. Patil HE, Patel BK, Patel SN. Assessment of genetic diversity in finger millet (*Eleusine coracana* L.) through multivariate analysis approach. Int. J Econ. Pl. 2017;4(4):148-151.
31. Patro TSSK, Ashok S, Divya M, Rani YS, Triveni U. Assessment of genetic diversity using principal component analysis in finger millet. Front. In Crop Improv. 2018;6(1):34-37.
32. Rao MV, Murlikrishna G. Non-starch polysaccharides and bound phenolic acids from native and malted fingermillet (Ragi, *Eleusine coracana*, Indaf-15). Food Chem. 2001;72:187-189.
33. Reddy CVCM, Reddy PVRM, Munirathnam P, Jayarame G. Studies of genetic variability in yield and yield attributing traits of finger millet [*Eleusine coracana* (L.) gaertn]. Indian J Agricultural Research. 2013;47(6):549-552.
34. Savankumar NP, Harshal EP, Raj CP. Genetic diversity study in finger millet (*Eleusine coracana* L.) genotypes: amultivariate analysis approach. Int. J Pure App. Biosci. 2017;5(5):183-189.
35. Shet RM, Jagadeesha N, Lokesh GY, Gireesh C, Gowda. Genetic variability in segregating generation of interspecific hybrids of finger millet (*Eleusine coracana* (L.) Gaertn). Environment and Ecology. 2009;27(3):1013-1016.
36. Shekhawat US, Vijay P, Singhania DL. Genetic divergence in barley (*Hordeum vulgare* L.). Indian J Agric. Res. 2001;35(2):121-123.
37. Suryakumar M, Rsamasamy P, Shanmugasundaram P. Cluster analysis in finger millet genotypes. Madars Agricultural J. 1988;85(3/4):150-153.
38. Suryanarayana L, Sekhar D, Rao NV. Genetic variability and divergence studies in finger millet (*Eleusine coracana* (L.) Gaertn.). Current Microbial Applied Science. 2014;3(4):931-936.
39. Ulaganathan V, Nirmalakumari A. Phenotypic selection of elite genotypes based on genetic analysis in finger millet [*Eleusine coracana* (L.) Gaertn] germplasm. Plant Archives. 2013;13(2):1003-1008.
40. Vilas A, Tonapi B, Bhat V, Kannababu V, Elangovan M, Umakanth AV. Millet Seed Technology: Seed Production, Quality control & Legal compliance; c2015. p. 92-93.
41. Wolie A, Dessalegn T, Belete K. Heritability, variance components and genetic advance of some yield and yield related traits in Ethiopian collections of finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes. Afr. J Biotechnol. 2013;12(36):5529-5534.