Journal of Innovative Agriculture: 8(1) : 21-26, 2021
DOI: 10.37446/jinagri/rsa/8.1.2021.21-26

Research paper

Genetic diversity studies for yield and quality traits in barnyard millet

Harshal E. Patil *[1], **Tanvi A. Darjib**[2], **Vikas Pali** [3]

[1]Hill Millet Research Station, Navsari Agricultural University, Waghai (Dangs) -394 730, India.
[2]Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat - 396 450, India.
[3]Hill Millet Research Station, Anand Agricultural University, Dahod, Gujarat, India.

Edited by
Gurunathan Selvakumar,
SRM College of Agricultural Sciences,
SRM Institute of Science and Technology,
India.

Received: 02 October 2020
Accepted: 11 February 2021
Published: 31 March 2021

***Correspondence**
Harshal E. Patil
harshpatil@nau.in

Assessments of genetic variability was carried out in a set of forty-one genotypes of Barnyard millet [*Echinochloa frumentacea* (Roxb.) Link] grown in a Randomized Block Design with three replications during the *Kharif*, 2019-2020 at Hill Millet Research Station, Navsari Agricultural University, Waghai, The Dangs. The basic objective of the experiment was to assess the extent of morphological variation as well as genetic divergence in the available barnyard millet germplasm, which will serve as base for future barnyard millet crop improvement programmes. Fourteen different characters related to seed yield were recorded and subjected to estimation genetic diversity of the genotypes. Studies pertaining to genetic divergence were also carried out using Mahalanobis D^2 statistics for forty-one barnyard millet genotypes and twelve clusters were formed. Clustering pattern of the genotypes was independent of their geographical distribution. Based on inter-cluster distance, cluster III and V showed the maximum distance followed by the distance between cluster III and IV. Therefore, it is concluded that the genotypes belonging to these clusters should be inter-crossed in order to generate more variability and improving grain yield in barnyard millet. On the basis of cluster means for different characters, it concluded that high yielding genotypes coupled with other important physiological traits *viz.,*days to 50 % flowering, days to maturity, plant height at maturity, productive tillers per plant, branches per panicle, panicle (finger) length, straw yield per plant, 1000 seed weight, protein content, Ca content, fat content, Fe content and Zn content could be selected as parents for hybridization programme from cluster III, IV, V, VI, VII, VIII, IX, X, XI and XII. Inter-crossing among the genotypes from these clusters might results in hybrids having high vigour which may further results in wide array of genetic variability for exercising effective selection. Analysis corroborated the absence of relationship between geographic origin and genetic diversity, as genotypes from the different area grouped into same clusters and the genotypes of same area were grouped in the different clusters. Therefore, breeder must evaluate their material for genetic diversity and should not merely depend on their geographical origin.

Key words: *barnyard millet, genetic diversity, yield characters, quality characters, quantitative characters*

INTRODUCTION

Barnyard millet [*Echinochloa frumentacea* (Roxb.) Link] is mainly grown in India, China, Japan, and Korea for human consumption as well as fodder (Upadhyaya et al., 2014). The crop is valued for its drought tolerance (Dwivedi et al., 2012), short growth period with superior nutrition value (Saleh et al., 2013). Globally, India is the biggest producer of barnyard millet, both in terms of area (0.146 m ha^{-1}) and production (0.147 mt) with average productivity of 1034 kg/ha during the last 3 years. In India, the crop is grown in Madhya Pradesh, Uttarakhand, Tamil Nadu, Andhra Pradesh, Karnataka, Maharashtra and Bihar. In Gujarat, barnyard millet is cultivated in the Dangs, Dediyapada and Valsad districts of south Gujarat. Barnyard millet has emerged as very important dual purpose feed and fodder crop. The grain can be consumed as whole grain or ground into flour which is used for porridge and various flat cakes or chapatis. Thus small millets are nutritionally rich staple food crop. But besides that they also provide good quality stover which is important for hill farming system, where fodder has become scarce in recent years. In fact the stover of barnyard millet is one of the best in terms of nutritional quality among all the existing small millet crops. Barnyard millet grains are nutritious and as similar to other millets, it is also an appropriate food for patients intolerant to gluten causing celiac disease or other forms of allergies/intolerance of wheat, as none of the millets are closely related to wheat, so they are appropriate foods for such patients. Barnyard millet contains of carbohydrate (65%), protein (11%), fat (3.9%), and crude fiber (13.6%). It is also an excellent source of minerals such as Iron (Fe) and Zinc (Zn) and antioxidative compounds, which makes the barnyard millet a nature's gift for the modern mankind who is engaged in sedentary activities. Its adaptability to wide range of geographical areas and agro-ecological diversity makes it more versatile. The availability of diverse genetic resources is a prerequisite for genetic improvement of any crop including finger millet. Besides the availability of genetic resources, their characterization is essential for effective utilization in crop improvement programs especially for quality improvement (Patil et al., 2018). Success of hybridization programme depends to a large extent upon the choice of suitable parents of diverse origin with the possibility of obtaining large frequency of transgressive segregants. The D^2 statistics is one of the powerful tools to assess the relative contribution of different component traits to the total diversity. Knowledge of genetic diversity among genotypes on the basis of divergence analysis usually helps a breeder in choosing diverse parents for breeding program. Therefore, the present investigation was undertaken to estimate the extent of genetic diversity in barnyard millet genotypes available in India.

MATERIALS AND METHODS

The experimental material consisted 41 barnyard millet genotypes collected from different locations across the country. The material was grown in simple randomized block design with three replications at Hill Millet Research Station, Navsari Agricultural University, Waghai, The Dangs, during kharif, 2019-20. All the recommended agronomic and cultural practices were followed for raising a healthy crop. Data were recorded on five randomly taken plants per replication of each genotype for twelve characters viz., Days to 50 % flowering, Days to maturity, Plant height at maturity (cm), Productive tillers per plant, Branches per panicle, Finger (Panicle) length (cm), Grain yield per plant (g), Straw yield per plant (g), 1000 Seed weight (g), Protein content (%), Fat content (%), Ca content (mg/100gm), Fe content (mg/100gm) and Zn content (mg/100gm). Genetic diversity was studied following as per Mahalanobis's (1936) D^2 statistics as extended by Rao (1952). On the basis of D2 values genotypes were grouped into different clusters according to Tocher's method. The parents having high genetic diversity are a basic requirement in any successful hybridization programme to get desirable character combination for selection of high yielding genotypes. Mahalanobis D2 statistics is the rational criterion for selecting such parents with high genetic divergence. Hence, to assess the genetic variability in this investigation forty-one genotypes of barnyard millet were evaluated for genetic divergence.

RESULTS AND DISCUSSION

Genetic divergence

Multivariate test using Wilk's criterion was carried out to test the difference among forty-one barnyard millet entries. Wilk's criterion was highly significant and eventually the differences among entries were also highly significant. Mahalanobis D2 statistic was computed between all possible pairs of forty-one barnyard millet genotypes and the genetic diversity present among the genotypes was assessed.

Clustering pattern: Distribution of genotypes into clusters

Forty-one genotypes of barnyard millet were grouped into twelve clusters by Tocher's method. The composition of clusters is given in Table 1. The results indicated that a maximum number of diverse genotypes (15 genotypes) appeared in cluster I followed by cluster II (9 genotypes), eight genotype appear in cluster III, while other nine clusters (IV to XII) were composed of single genotype. Genotypes of different geographical areas were fall in one group and also the genotypes of the same geographical area were clubbed into different groups indicating there is no formed relationship between geographical diversity and genetic diversity. Many workers have been arrived at similar conclusion for Satish et al. (2007); Kumar et al. (2010); Shinde et al. (2013); Suryanarayana et al. (2014); Patel et al. (2018) and Patel et al. (2020).

Table 1. The distribution of forty-one genotypes of barnyard millet into seven different clusters on the basis of Mahalanobis D^2 statistics

Cluster	Total no. of genotypes	Genotypes
I	15	VL-173, VL-181, VL-207, VL-129, VL-172, VL-249, TNEF-182, WB-6, WB-7, WB-3, WB-8, KOPBM-46, KOPBM-18, KOPBM-33, KOPBM-43
II	9	WB-12, WB-13, WB-14, WB-9, WB-10, WB-11, WB-1, KOPBM-11, KOPBM-35
III	8	DHBM- 18-6, DHBM- 93-2, DHBM-99-6, DHBM-98-7, DHBM-97-4, DHB-23-3, TNEF-192, TNEF-198
IV	1	KOPBM-45
V	1	KOPBM-34
VI	1	WB-2
VII	1	KOPBM-5
VIII	1	KOPBM-47
IX	1	KOPBM-39
X	1	WB-4
XI	1	TNEF-188
XII	1	WB-5

Intra and Inter cluster distances

The intra and inter cluster distances (D) between all possible pairs of twelve clusters were computed and presented in table 2 as well as shown in figure 1. A study of the data revealed that the inter-cluster distance (D) ranged from 20.51 to 307.78. The maximum inter -cluster distance (D=307.78) was observed between cluster III and V followed by those between cluster III and IV (D=303.4). The minimum inter-cluster distance (D=20.51) was observed between cluster IV and V followed by the cluster VII and VIII (D=33.28). Intra-cluster distance (D) ranged from 0.00 to 63.36. At intra-cluster level, cluster I had the highest intra cluster distance (D=63.36) followed by cluster III (D=62.6) and cluster II (D=60.22) which involve 15, 8 and 9 genotypes, respectively. The intra-cluster distance within cluster IV, V, VI, VII, VIII, IX, X, XI and XII was zero (0) because these clusters were composed of only single genotype. The intra and inter cluster distances were considerably high revealing very interesting genetic diversity. The range of intra cluster distance was from 0.00 (monogenotypic clusters) to 63.36 (cluster I). Cluster I showed high intra cluster distance. Inter cluster distances indicated that the accessions included in the diverse clusters would be used in further crop improvement programme. Higher intra cluster distance indicates higher diversity among the genotypes. Similar results

Table 2. Average Intra and Inter-cluster distance for forty-one genotypes of barnyard millet

	Cluster I	**Cluster II**	**Cluster III**	**Cluster IV**	**Cluster V**	**Cluster VI**	**Cluster VII**	**Cluster VIII**	**Cluster IX**	**Cluster X**	**Cluster XI**	**Cluster XII**
Cluster I	63.36	123.15	158.9	100.96	94.6	167.53	90.59	80.23	97.44	95.4	101.21	120.77
Cluster II		60.22	152.75	138.17	145.41	103.51	126.98	117.3	140.24	147	185.48	109.66
Cluster III			62.6	303.4	307.78	240.65	241.08	244.14	251.13	224.58	123.54	143.81
Cluster IV				0	20.51	101.28	48.44	55.63	52.63	52.73	190.45	132.06
Cluster V					0	114.54	65.46	62.24	86.09	79.45	217.29	176.01
Cluster VI						0	114.39	120.93	162.62	107.07	297.58	116.42
Cluster VII							0	33.28	86.72	99.81	189.98	89.05
Cluster VIII								0	62.16	109.95	205.3	116.41
Cluster IX									0	58.44	145.46	136.41
Cluster X										0	136.72	145.41
Cluster XI											0	126.44
Cluster XII												0

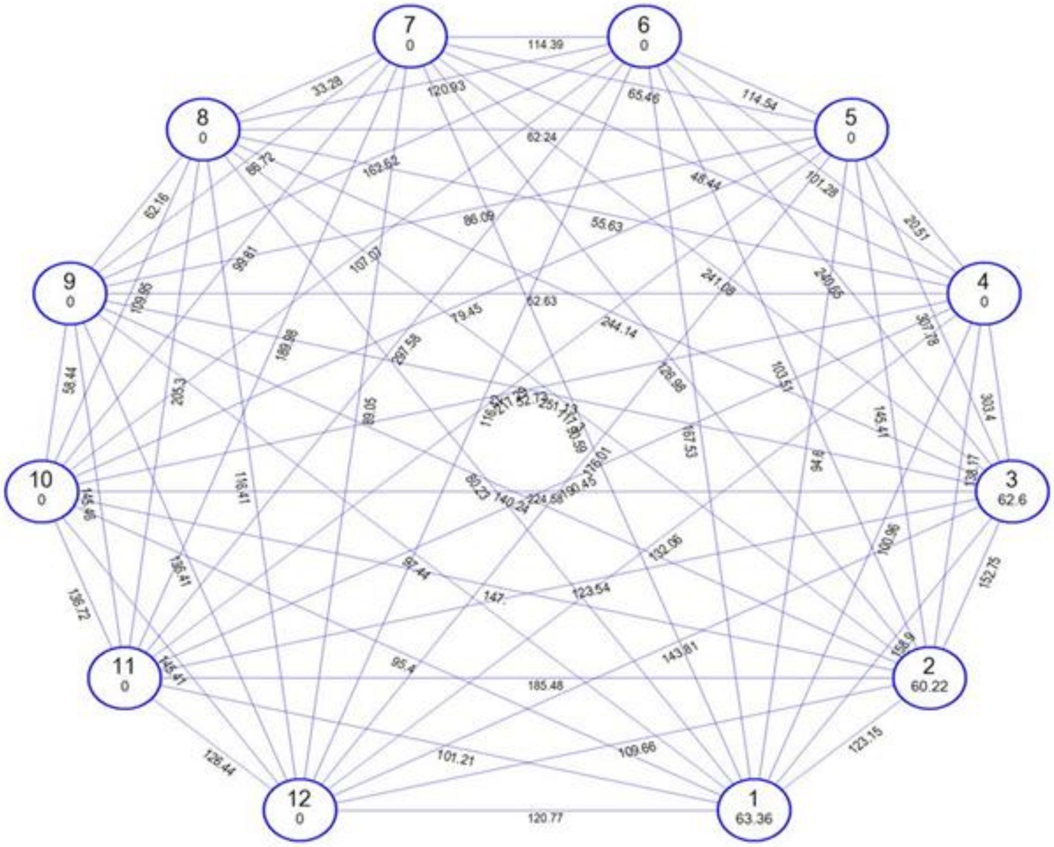

Figure 1. Clustering pattern in barnyard millet genotypes based on morphological character

were revealed by Karad and Patil (2013); Suryanarayana *et al.* (2014); Saundaryakumari and Singh (2015); and Patel *et al.* (2020). From the results of this investigation, it was found that number of clusters contained at least one genotype with the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits. From the results, it could be concluded that inter-crossing genotypes from cluster IV, V, VI, VII, VIII, IX, X, XI and XII might result in wide array of variability for exercising effective selection. In heterosis breeding, genotypes of diverse groups are known to play very important role of potential parents and when each genotype of different clusters are inter crossed, which are likely to produce heterotic combinations.

Contribution of various characters towards genetic divergence

The analysis for estimating the contribution of various characters towards the expression of genetic divergence indicated that the traits *viz.,*

Table 3. Contribution of fourteen characters under study towards total divergence

Sr. No.	Characters	No. of times ranked first	Percentage contribution towards divergence
1.	Days to 50% flowering	60	7.32
2.	Days to maturity	12	1.46
3.	Plant height at maturity (cm)	39	4.76
4.	Productive tiller per plant	1	0.12
5.	Branch per panicle	29	3.54
6.	Panicle (Finger) length (cm)	55	6.71
7.	Grain yield per plant	0	0
8.	Straw yield per plant	2	0.24
9.	1000 seed weight	3	0.37
10.	Protein content (%)	49	5.98
11.	Fat content (%)	24	2.93
12.	Ca content (mg/100g)	103	12.56
13.	Fe content (mg/100g)	290	35.37
14.	Zn content (mg/100g)	153	18.64
	Total	820	100

Table 4. Cluster means for fourteen characters in forty-one genotypes of barnyard millet

	Days to 50% flowering	**Days to maturity**	**Plant height at maturity (cm)**	**Productive tiller per plant**	**Branch per panicle**	**Panicle (Finger) length (cm)**	**Grain yield per plant**	**Straw yield per plant**	**1000 seed weight**	**Protein content (%)**	**Fat content (%)**	**Ca content (mg/100g)**	**Fe content (mg/100g)**	**Zn content (mg/100g)**
Cluster I	60.27	92.47	157.44	3.31	6.62	17.15	158.51	469.7	4.62	9.32	4.24	10.59	7.48	5.41
Cluster II	63	93.93	152.04	3.16	6.9	19.09	159.96	492.8	4.1	8.49	4.51	9.41	6.4	6.39
Cluster III	52.58	83.71	148.96	3.08	7.71	16.81	147.63	405.9	4.46	8	4.61	9.26	5.83	4.5
Cluster IV	72.33	104	160.33	3.93	7.1	17.53	143	432.6	4.7	9.13	3.77	10.2	8.13	6.48
Cluster V	68.67	100	164.33	3.07	6.13	18.4	135	408.3	3.63	8.97	3.27	10.3	8.43	6.43
Cluster VI	68.33	105	183.33	3.27	7.03	21.4	188	480	2.76	6.5	4.53	8.9	7.21	6.4
Cluster VII	69.33	100.67	120.33	3.33	7.3	20.4	135	408	5.17	8.83	5.13	10.03	8.04	6.08
Cluster VIII	63.33	95.33	164.67	4.07	6.9	19.4	184.33	523	5.5	9.27	5.43	9.9	8.13	6.33
Cluster IX	67.33	98	166.67	3.67	7.43	9.93	155.33	469.6	5.2	8.8	5.37	10.17	7.9	6.2
Cluster X	68	103	183.33	3.47	7.53	15.07	158	353.3	4.08	7.53	4.6	11.3	7.75	5.61
Cluster XI	59.67	30	128	4.07	7.93	12.27	130.33	456.6	4.58	10.87	3.57	11.03	6.55	4.47
Cluster XII	69	101	128	3.93	7.67	17.6	194	383.3	3.91	10.87	4.63	8.87	6.15	5.48

Fe content (35.37%), Zn content (18.66%), Ca content (12.56%), days to 50% flowering (7.32%), panicle length (6.71%), protein content (5.98%), plant height at maturity (4.76%), branches per panicle (3.54%), fat content (2.93%), days to maturity (1.46%), 1000 seed weight (0.37%), straw yield per plant (0.24%), productive tiller per plant (0.12%) and grain yield per plant (0%) contributed much towards genetic divergence in the present material under study (table 3). Those accounted nearly 100 % of total divergence available in the genotypes. In the present study, Fe content, Zn content, Ca content, days to 50% flowering, panicle (finger) length and protein content contributed much towards total genetic divergence. Plant height at maturity, branches per panicle, Fat content, days to maturity, 1000 seed weight, straw yield per plant, productive tillers per plant and grain yield per plant in the present material had low contribution to the divergence (table 3). Similar results were earlier obtained in this regard by Saundaryakumari and Singh (2015) for Days to 50% flowering and panicle length; Nirubana *et al.* (2017) for days to 50% flowering, Zn content and Fe content and Patel *et al.* (2018) for Ca content and Zn content (figure 3).

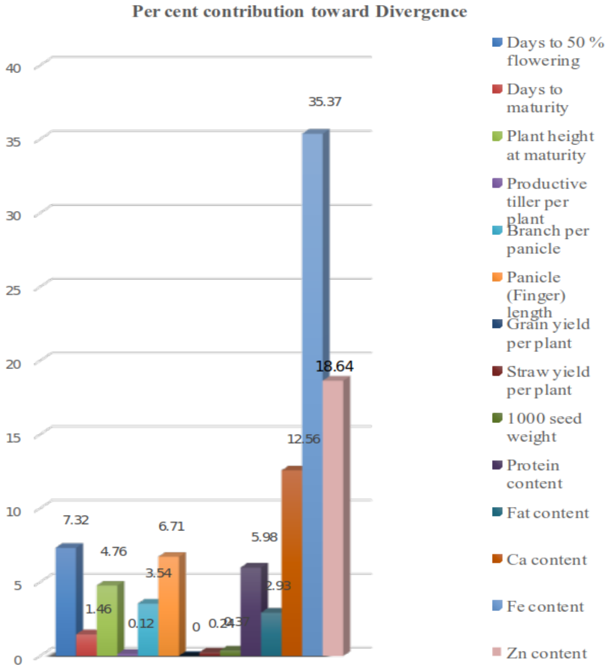

Figure 2. Contribution (%) of various traits of barnyard millet towards divergence

Cluster means for different characters

Cluster mean for all the fourteen characters are presented in table 4. The results clearly indicated appreciable difference among cluster means for most of the characters. As far as cluster means are concerned, Cluster I had the highest mean value for the character straw yield per plant. Cluster II had the highest mean value for the character number of straw yield per plant. Cluster III had the highest mean values for the characters *viz.,* grain yield per plant, plant height at maturity and straw yield per plant. Cluster IV had the highest mean value for straw yield per plant. Cluster V had the highest mean values for the traits *viz.,* straw yield per plant and plant height at maturity. Cluster VI had the minimum cluster mean values for traits *viz.,* 1000 seed weight, productive tillers per plant and fat content. Cluster VII had the highest mean values for the traits *viz.,* straw yield per plant, grain yield per plant, plant height at maturity. Cluster VIII had the highest mean values for straw yield per plant. Cluster IX had the minimum cluster mean values for productive tillers per plant, 1000 seed weight and fat content. Cluster X had the highest mean values for straw yield per plant. Cluster XI had the minimum cluster mean values for fat content, productive tillers per plant and Zn content. Cluster XII had the highest mean values for straw yield per plant, grain yield per plant and plant height at maturity. In general in regards with the cluster means concerned, for all the clusters the productive tillers per plant has recorded the minimum values for the cluster means while the straw yield per plant has recorded the highest values for the cluster means. On the basis of cluster means for different characters, it concluded that high yielding genotypes coupled with other important physiological traits *viz.,* days to 50% flowering, days to maturity, plant height at maturity, productive tillers per plant, branches per panicle, panicle length, straw yield per plant, 1000 seed weight, protein content, Ca content, fat content, Fe content and Zn content could be selected as parents for hybridization programme from cluster I, II, III, IV, V, VI, VII, VIII, IX, X, XI, and XII intercrossing genotypes from these clusters might results in hybrids having high vigour and may further results in wide array of genetic variability for exercising effective selection. Similar results were earlier reported in small millets by Sheriff and Shivshankar (1992), Saundaryakumari and Singh (2015); Nirubana *et al.* (2017), Patel *et al.* (2017), Patil *et al.* (2017) and Patel *et al.* (2020) .

CONCLUSION

For a successful breeding programme, the diversity of parents is very important, since the crosses made between the parents with maximum genetic divergence would more likely to yield desirable recombinants in segregating generations. Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. Improvement of existing varieties is a continuous process in plant breeding. For a plant breeder, single character is not of so much importance as the combined merit of a number of desirable traits become more important when he is concerned with a complex trait like yield. So, for improving yield, selection of parents based on a number of characters having quantitative divergence is required.

COMPETING INTERESTS

The authors declare that they have no competing interests.

ETHICS APPROVAL

Not applicable.

REFERENCES

Dwivedi, S.; Upadhyaya, H.; Senthilvel, S.; Hash, C.; Fukunaga, K.; Diao, X.; Santra, D.; Baltensperger, D. & Prasad, M. (2012). Millets: Genetic and Genomic Resources. *Plant Breeding reviews, 35:* 247-375.

Karad, S. R. & Patil, J. V. (2013). Assessment of genetic diversity among Finger millet (*Eleusine coracana* L.) genotypes. *International journal of integrative sciences, innovation and technology, 2 (4):* 37-43.

Kumar, D., Tyagi, V., Ramesh, B. & Pal, S. (2010). Genetic diversity in finger millet (*Elusine coracana* L.) *Crop Improvement*, *37 (1):* 25-28.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Nat. Inst. of Sci. of India, 2:* 49-55.

Patel S. N., H. E. Patil, H. M. Modi & Joydeep Singh Th. (2018). Genetic Variability Study in Little Millet (*Panicum miliare* L.) Genotypes in relation to yield and quality Traits. *Int.J.Curr.Microbiol.App.Sci., 7 (6):* 2712-2725.

Patel S. N., Patil, H. E., Patel S. P. & Patel U. M. (2017). Genetic Diversity Study in Relation to Yield and Quality Traits in Little Millet (*Panicum miliare* L.). *Int. J. Curr. Microbiol. App. Sci., 7 (6):* 2702-2711.

Patel Sayam.; Patil, H. E.; Pali, V. & Patel, B. K. (2020). Genetic diversity analysis in Finger millet [*Eleusine coracana* (L.) Gaertn.]. *Journal of Pharmacognosy and Phytochemistry, 9 (1):* 677-680.

Patil H. E., B. K. Patel & S. N. Patel. (2017). Assessment of Genetic Diversity in Finger millet (*Eleusine coracana* L.) through Multivariate Analysis Approach. *International Journal of Economic Plants, 4 (4):* 148-151.

Patil H. E., Patel B. K., Vavdiya P. & Pali V. (2018). Breeding for quality improvement in Small Millets: A Review. *International Journal of Genetics*, *10 (9):* 507-510.

Rao, C. R. (1952). Advanced Statistical Methods in Biometrical Research, John Willy and Sons, Inc., New York, pp. 390.

Saleh, A.S.M.; Zhang, Q.; Chen, J. & Shen, Q. (2013). Millet Grains: Nutritional Quality, Processing, and Potential Health Benefits. *Comprehensive Reviews in Food Science and Food Safety 12 (1):* 281-295.

Satish, D., Shanthakumar, G., Salimath, P. M. & Gangaprasad, S. 2007. Genetic diversity for productivity traits in finger millet. *International J. Plant Sci*., *2 (2):* 34-37.

Saundaryakumari and Singh, S. K. (2015). Assessment of genetic diversity in promising finger millet (*Eleusine coracana* L.) genotypes. *International Quarterly Journal of Environmental Sciences, 10 (2):* 825-830.

Sheriff, R. A. & Shivashankar, G. 1992. Genetic divergence in Foxtail Millet (*Setaria italica* L.*) Indian J. Genet., 52(1):* 29-32.

Suryanarayana, L., Sekhar, D. & Rao, V. D. (2014). Genetic variability and divergence studies in finger millet (*Eleusine coracana* (L.) Gaertn.). *International Journal of Current Microbiology and Applied Sciences, 3 (4):* 931-936.

Nirubana, V.; Ganesamurthy, K.; Ravikesavan, R. & Chitdeshwari, T. (2017). Genetic diversity studies in kodo millet (*Paspalum scrobiculatum* L.) Germplasm Accessions Based on Biometrical and Nutritional Quality Traits. *International Journal of Current Microbiology and Applied Sciences*, *6 (10):* 832-839.

Upadhyaya, H.; Dwivedi, S. & Singh, S. (2014). Forming core collections in barnyard, kodo and little millets using morpho-agronomic descriptors. *Crop Science*, *54:* 1-10.