IJPS INTERNATIONAL JOURNAL OF PLANT SCIENCES
e ISSN-0976-593X Volume **13** | Issue 1 | January, 2018 | 82-89

DOI: 10.15740/HAS/IJPS/13.1/82-89
Visit us - *www.researchjournal.co.in*

RESEARCH ARTICLE

Genetic diversity analysis for yield and yield components in foxtail millet [*Setaria italica* (L.) Beauv.]

■ **V. Thippeswamy, G.M. Sajjanar and Prabhakar**

SUMMARY

Genetic diversity analysis helps in identification of the diverse genotypes for hybridization purposes and to derive desirable segregants. Knowledge on the nature and magnitude of genetic diversity present in the crop species will play an important role in formulating a successful breeding programme. In this regard a field experiment was conducted to study the genetic diversity analysis for yield and yield contributing characters using 149 germplasm accessions of foxtail millet. Based on D^2 values, a total of 149 genotypes were grouped into 15 clusters, among these clusters, cluster I was the largest with 134 genotypes followed by cluster VIII with 2 genotypes whereas remaining 13 were solitary clusters. Maximum intra cluster distance among the genotypes was recorded by cluster I having 134 genotypes followed by cluster VIII with two genotypes. The maximum intra cluster distance in the cluster I indicated the genotypes in this cluster were relatively more diverse than the genotypes within other clusters. The maximum inter cluster distance was found between clusters IX and XIV followed by cluster VI and XIV, while it showed least distance between clusters II and cluster V followed by clusters III and VI, thus it can be concluded that, considerable diversity existed among 149 lines. The per cent contribution of yield and yield contributing characters to total divergence among nineteen characters were recorded. It showed that maximum contribution towards divergence was recorded by number of tillers per meter row length and 1000 seed weight followed by number of productive tillers/plant, days to maturity, days to 50% flowering, grain yield/hectare and plant height indicating the major role of these characters in building up diversity and differentiating inter cluster levels. All the 149 genotypes were spread over fifteen clusters and means were scored across the clusters for all the nineteen characters. Cluster IV with overall score of 78 across the nineteen characters secured first rank followed by cluster VI, cluster I and cluster IX indicating the presence of most promising genotypes in them and can be extensively used for further breeding programme to generate new material.

Key Words : Foxtail millet, Genetic diversity, D^2 values, Clusters, Yield contributing characters

How to cite this article : Thippeswamy, V., Sajjanar, G.M. and Prabhakar (2018). Genetic diversity analysis for yield and yield components in foxtail millet [*Setaria italica* (L.) Beauv.]. *Internat. J. Plant Sci.*, **13** (1): 82-89, **DOI: 10.15740/HAS/IJPS/13.1/82-89**.

Article chronicle : Received : 16.10.2017; **Revised :** 20.11.2017; **Accepted :** 03.12.2017

MEMBERS OF THE RESEARCH FORUM

Author to be contacted :
V. Thippeswamy, Department of Genetics and Plant Breeding, College of Agriculture (U.A.S.), Vijayapur (Karnataka) India
Email : swamyak9133@gmail.com

Address of the Co-authors:
G.M. Sajjanar and Prabhakar, Department of Genetics and Plant Breeding, College of Agriculture (U.A.S.), Vijayapur (Karnataka) India

Foxtail millet [*Setaria italica* (L.) Beauv.] ranks second in the total world production of millets and continue to have an important place in the world agriculture providing approximately six million tons of food to millions of people. Foxtail millet mainly grows on poor or marginal soils in temperate, subtropical and tropical Asia. China ranks 1st in foxtail millet production

in the world (4.6 mt), with productivity around 1.8 t/ha. In India, foxtail millet, with colloquial names *Kangni, Navane, Tenai, Korra* and *Rala*, is one of the oldest crops cultivated for straw and grain. In India it is cultivated in an area of 5 lakh hectares and the production of 2.9 million tons with productivity of 600 kg per hectare (Anonymous, 2012). At present, foxtail millet (*Setaria italica*) is cultivated on a limited area in Andhra Pradesh, Karnataka, Maharashtra, Tamil Nadu, Rajasthan, Madhya Pradesh, Uttar Pradesh and North eastern states.

Northern dry zone of Karnataka is the largest agro climatic zone of the state. Foxtail millet that was commonly grown and was part of balanced diet in earlier days in these areas has been replaced with other crops. In the current changing life style and food habits of people, consumption of nutrigrain cereals in the daily diet is poor due to lack of cultivation of nutrigrain cereals and availability of high yielding but less nutritious cereals in the last few decades. To meet out the nutrition demand of growing population, area under millets must be rejuvenated through millet policy. Attention has to be given to development of reliable production technologies specially the development of high yielding varieties. The presence of rich diversity for this crop (~6000 varieties) and existence of genetic potential of moderate to high productivity promise breaking the yield barriers.

Foxtail millet is a self-pollinated crop. Despite this reproductive behaviour, existence of thousands of varieties in the Centre of origin indicates their evolution mostly through natural selection. It needs to be assessed the genetic diversity between them. Proper identification of diverse genotypes for hybridization is most crucial and it offers the scope for generating potential genotypes that provide higher variability. It is reported from genetic diversity analysis that selection of genotypes from the most divergent clusters may exhibit a high heterosis. Therefore, hybridization between the genetically diverse parents in breeding programmes may produce large variability and better recombinants in the segregating generation. Hence, several workers studied genetic diversity within available germplasm.

Mahalanobis', D^2 statistics is an effective tool in quantifying the degree of genetic divergence at the genotypic level and provides measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis', 1928). Rao (1952) suggested the application of this technique for the assessment of genetic diversity in plant breeding.

Divergence analysis is performed to identify the diverse genotypes for hybridization purposes and clustering by D^2 statistic is useful in this matter. The genotypes grouped together are less divergent than the ones which fall into different clusters. Three important points are considered while selecting genotypes for hybridization purpose; i) Choice of the particular cluster from which genotypes are to be used as parents, ii) Selection of particular genotypes from selected cluster, iii) Relative contribution of characters towards total divergence.

MATERIAL AND METHODS

A field experiment was conducted to study the Genetic diversity analysis for yield and yield component traits in foxtail millet. The experiment was carried out at Regional Agricultural Research Station, Vijayapur, University of Agricultural Sciences, Dharwad during *Kharif* 2014-15 in a Randomized Block Design (RBD) with two replications. Each entry was planted in two rows of 3 m length with inter row spacing of 30 cm and intra row spacing of 10 cm. The crop was planted in medium black soil and the cultivation practices recommended for North Karnataka were followed to raise good crop of foxtail millet.

Experimental material used in the present study was comprised of 149 genotypes of foxtail millet including germplasm accessions, released varieties and local collections. Among these, 126 entries were obtained from the Project coordinating unit (small millets), All India Coordinated Small millet Improvement Project, Indian Council of Agricultural Research, GKVK, UAS, Bangalore. The check entries used were PS 4 (national check), HMT-100-1 (local check) and SiA 326 (state check). The observations were recorded on nineteen yield and yield contributing traits. The traits included days to panicle emergence, days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), panicle girth (mm), peduncle length (cm), number of tillers per meter row length, number of productive tillers per meter row length, number of productive tillers per plant, area of standard leaf (cm^2), stem thickness (cm), SPAD reading at flowering, SPAD reading at maturity, grain yield per plant (g), fodder yield per plant (g), grain yield per hectare (kg/ha), fodder yield per hectare (kg/ha) and 1000 grain weight (g).

RESULTS AND DISCUSSION

Genetic divergence analysis helps in assessing nature of diversity in order to identify the genetically diverse lines which can be used to create new variability through hybridization. With cluster analysis, the genotypes grouped into different clusters, intra and inter cluster distances serve as indices for selection of parents with diverse origin. Analysis of genetic divergence has been used (a) to quantify the genetic distance between the genotypes, (b) to identify promising types to initiate crossing programme.

In the present study, the genetic diversity among 149 genotypes for 19 characters was assessed by employing Mahalanobis's generalized distance (D^2) statistic. The mean values for the traits were utilized for calculating genetic distance between pairs of genotypes. The correlated unstandardized mean values (X) for all the genotypes for all quantitatively measured characters were transferred into the uncorrelated standardized values (Y). The generalised distance (D^2) was calculated for each pair of genotypes among 22,052 possible combinations. The results and discussion pertaining to genetic diversity analysis is presented below :

Genetic diversity :

Based on D^2 values, a total of 149 genotypes were grouped into 15 clusters (Table 1 and Fig. 1). Among these clusters, cluster I was the largest with 134 genotypes followed by cluster VIII with 2 genotypes whereas remaining 13 were solitary clusters. The genotypes of the solitary clusters may be very unique and useful in breeding. In the present study the genotypes identified in solitary clusters were MLT-12-3 (cluster II), GS 27 (cluster III), SR 11 (cluster IV), MLT-12-9 (cluster V), GS 213 (cluster VI), MLT-12-10 (cluster VII), GS 510 (cluster IX), MLT-12-11/HMT-100-1 (cluster X), GS 17 (cluster XI), MLT-12-8 (cluster XII), GS 511 (cluster XIII), GS 35 (cluster XIV) and GS 338 (cluster XV). Similar studies were also reported by Murugan and Nirmalakumari (2006) in foxtail millet. They grouped seventy five genotypes into nine clusters, Selvarani and Gomathinayagam (2000) grouped fifty genotypes into six clusters, Maloo and Bhattachargee (1999) grouped forty genotypes into four clusters, Sheriff and Shivashankar (1992) grouped 225 genotypes into 33 clusters, and Nagarajan and Prasad (1980) grouped fifty genotypes into fifteen clusters.

In D^2 analysis scattering of genotypes is due to

Table 1 : Distribution of foxtail millet germplasm accessions into different clusters based on cluster analysis

Sr. No.	Cluster No.	Number of lines	Name of the genotype
1.	I	134	GS 5,GS 6, GS 8, GS 12, MLT-12-12, GS 18, GS 21, GS 26, GS 29, GS 42, GS 45, GS 47, GS 53, GS 56, GS 60, GS 62, GS 64, GS 71,GS 77, GS 78, GS 91, GS 94, GS 95, GS 96, GS 97, GS 103, GS 105, GS 106, GS 111, GS 121, GS 140, GS 158, GS 200, GS 203, GS 204, GS 205, GS 206, GS 208, GS 209, GS 210, GS 211, GS 212, GS 214, GS 215, GS 216, GS 218, GS 219, GS 220, GS 221, GS 222, GS 242, GS 243, GS 246, GS 248, GS 250, GS 256, GS 260, GS 264, GS 266, GS 271, GS 276, GS 280, GS 282, GS 285, GS 289, GS 293, GS 301, GS 310, GS 316, GS 335, GS 336, GS 337, GS 308, GS 343, GS 344, GS 352, GS 362, GS 363, GS 372, GS 377, GS 378, GS 379, GS 401, GS 403, GS 415, GS 426, GS 433, GS 499, GS 453, GS 461, GS 472, GS 478, GS 494, SiA 3156, SiA 3088, SiA 3085, Co7, SR 51, SiA 2644, SR 16, PS4, TNAU186, SiA 2622, SiA 2593, Lepakshi, K 3, SiA 326, Co5, Chitra, K2, Co 4, RS 118, K 221-1, H 1, H 2, Co 1, Co 2, FMGPM1, FMGPM2, FMGPM3, FMGPM4, FMGPM6, FMGPM7, FMGPM8, FMGPM9, FMGPM10, FMGPM11, MLT-12-1, MLT-12-2, MLT-12-4, MLT-12-5, MLT-12-6, MLT-12-7.
2.	II	1	MLT-12-3
3.	III	1	GS 207
4.	IV	1	SR 11
5.	V	1	MLT-12-9
6.	VI	1	GS 213
7.	VII	1	MLT-12-10
8.	VIII	2	Arjuna, FMGPM-5
9.	IX	1	GS 510
10.	X	1	MLT-12-11(HMT-100-1)
11.	XI	1	GS 17
12.	XII	1	MLT-12-8
13.	XIII	1	GS 511
14.	XIV	1	GS 33
15.	XV	1	GS 338

heterogeneity, genetic architecture of the population, past history of selection for development and degree of good combining ability of the parents evolved in particular genotype (Murty and Arunachalam, 1966).

In the present study, out of 15 clusters formed 12 were solitary clusters. The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes.

Maximum intra cluster distance among the genotypes was recorded by cluster I (20.45) having 134 genotypes followed by cluster VIII (13.51) with two genotypes (Table 2). The maximum intra cluster distance in the cluster I indicated the genotypes in this cluster were relatively more diverse than the genotypes within other clusters.

As indicated by inter cluster D^2 values among 149 accessions of foxtail millet, the inter cluster distance was varied from 12.08 to 138.62. The maximum inter cluster distance was found between clusters IX and XIV (138.62), followed by cluster VI and XIV (132.8) (Table 2). While it showed least between clusters II and cluster V (12.08) followed by clusters III and VI (13.49). Thus, it can be concluded that, considerable diversity existed among 149 lines. For varietal improvement or selection of genotypes for crossing to obtain recombinants, we generally choose genetically diverse genotypes. Therefore, it would be reliable to choose genotypes belonging to distant clusters. The inter cluster distances estimated considering 19 characters were varied from

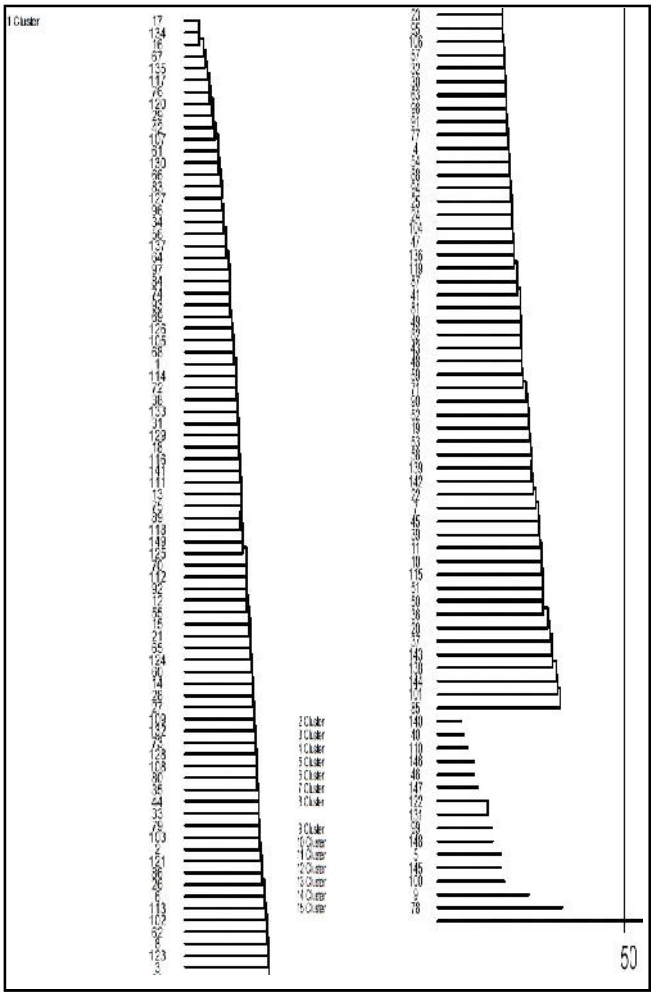


Fig. 1 : Diagrammatic representation of 15 clusters consisting of 149 foxtail millet lines

Table 2 : Average intra and inter cluster distances among 149 germplasm accessions of foxtail millet for yield and yield related traits

	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 XIII	Cluster XIV	Cluster XV
Cluster I	20.45	38.90	40.04	34.84	33.89	34.14	33.74	55.63	37.93	33.57	37.99	46.56	45.63	64.68	63.03
Cluster II		0.00	66.07	61.45	12.08	75.17	19.79	37.07	80.65	23.78	33.28	50.77	49.97	56.45	79.38
Cluster III			0.00	87.64	54.80	13.49	70.40	72.43	33.22	58.53	82.26	80.02	92.44	126.07	118.71
Cluster IV				0.00	51.34	77.93	37.19	72.06	88.43	40.51	49.84	29.88	38.08	36.69	53.03
Cluster V					0.00	63.42	25.40	46.05	72.88	19.87	38.13	43.91	67.61	56.73	81.30
Cluster VI						0.00	72.44	86.11	16.00	62.00	68.98	76.12	83.35	132.80	98.85
Cluster VII							0.00	62.81	72.67	30.21	55.73	25.47	43.53	52.75	65.28
Cluster VIII								13.51	86.21	44.17	52.25	83.31	77.06	73.13	89.97
Cluster IX									0.00	78.03	68.21	97.63	84.58	138.62	95.06
Cluster X										0.00	45.84	33.89	43.25	62.12	74.93
Cluster XI											0.00	64.74	39.10	54.66	66.15
Cluster XII												0.00	52.41	69.24	84.28
Cluster XIII													0.00	67.95	58.29
Cluster XIV														0.00	77.94
Cluster XV															0.00

12.08 (cluster II and V) to 138.62 (IX and XIV). These results suggest the presence of wide diversity between these clusters. The low inter cluster distance between II and V indicates that the genotypes MLT-12-3 and MLT-12-9 are closely related. It could be that common parents might be involved in derivating these genotypes.

The maximum inter cluster distance (138.62) was noticed between the clusters IX and XIV followed by between cluster VI and XIV (132.8), between III and XIV (126.07) and III and XV (118.71). The clusters, VI, III, XIV and XV also showed maximum intercluster distances with many clusters. Hence, genotypes belonging to these clusters are of prime importance in breeding for varietal improvement or selection of genotypes for crossing to obtain recombinants.

Per cent contribution of characters towards divergence :

Among 19 characters studied, the maximum contribution towards divergence was recorded by number of tillers per meter row length (16.84%) and 1000 seed weight (12.07%) followed by number of productive tillers/plant (10.18%), days to maturity (8.68%), days to 50% flowering (7.03%), grain yield/ hectare (6.80%), plant height (5.74%) (Table 3 and Fig. 2) indicating the major role of these characters in building up diversity and differentiating inter cluster levels. Murugan and Nirmalakumari (2006) recorded the highest contribution of straw yield per plant, days to maturity and test weight towards divergence. Sheriff (1984) reported that traits days to 50% flowering, days to maturity, number of productive tillers, panicle weight and panicle length, significantly contributed for the genetic diversity. Sheriff and Shivashankar (1992) noticed that characters days to maturity, panicle weight and grain weight contributed for the maximum divergence. According to Maloo and Bhattacharjee (1999), characters contributing largely to the divergence were test weight, seed protein content, harvest index and seed yield/plant. Sheriff (1992) reported that days to flowering, days to maturity, plant height, ear length, ear weight and grain weight contributed maximum to genetic diversity in both the rainfed and irrigated environments.

The above results imply that in order to select genetically diverse genotypes, the material should be screened for the important traits *viz.*, number of tillers, test weight, days to maturity, days to 50% flowering, grain yield and plant height. These traits contribute to the economic cultivation of foxtail millet crop. Hence, screening for these traits contributes to improvement of foxtail millet.

Table 3 : Per cent contribution of characters towards total divergence in 149 foxtail millet germplasm accessions

Sr. No.	Characters	Contribution %
1.	Days to panicle emergence	2.88
2.	Days to 50% flowering	7.03
3.	Days to maturity	8.68
4.	Plant height (cm)	5.74
5.	Panicle length (cm)	2.31
6.	Panicle girth (mm)	3.58
7.	Peduncle length (cm)	2.37
8.	No of tillers/meter row length	16.84
9.	Number of productive tillers/meter row length	1.13
10.	Number of productive tillers/plant	10.18
11.	Area of standard leaf (cm^2)	2.49
12.	Stem thickness (cm)	2.27
13.	SPAD at 50% flowering	1.97
14.	SPAD at maturity	2.58
15.	Grain yield/plant (g)	4.41
16.	Grain yield/hectare (kg)	6.80
17.	Fodder yield/plant (g)	4.41
18.	Fodder yield/hectare (kg)	2.26
19.	1000 seed weight (g)	12.07
Total		100

Table 4 : Cluster means of germplasm accessions of foxtail millet in respect of a total of 19 characters and overall character wise score

Characters / Clusters	Days to panicle emergence	Days to 50% flowering	Days to maturity	Plant height (cm)	Panicle length (cm)	Panicle girth (mm)	Peduncle length (cm)	No. of tillers / meter row length	Number of productive tillers/meter	Number of productive tillers/plant
Cluster I	55.92 (4)	60.40 (4)	90.42 (7)	137.90 (4)	15.73 (5)	12.38 (9)	14.67 (6)	43.50 (3)	41.88 (4)	6.99 (3)
Cluster II	59.50 (10)	64.00 (10)	87.50 (3)	96.00 (14)	10.58 (15)	9.37 (13)	11.17 (12)	14.50 (14)	12.50 (15)	1.84 (11)
Cluster III	58.50 (9)	63.50 (9)	92.50 (10)	135.67 (5)	15.59 (6)	12.01 (11)	17.50 (1)	43.50 (3)	42.00 (3)	12.50 (2)
Cluster IV	49.00 (2)	55.00 (2)	93.50 (11)	142.34 (2)	20.59 (2)	14.65 (3)	15.75 (2)	31.00 (7)	32.00 (7)	4.84 (5)
Cluster V	58.00 (8)	61.00 (7)	86.00 (2)	114.17 (12)	14.25 (11)	8.83 (14)	11.17 (12)	19.50 (12)	18.50 (13)	3.83 (7)
Cluster VI	60.00 (11)	64.00 (10)	90.00 (6)	156.50 (1)	17.08 (3)	12.42 (8)	13.25 (8)	56.00 (2)	55.00 (2)	12.67 (1)
Cluster VII	57.50 (7)	61.00 (7)	95.50 (12)	114.50 (11)	15.00 (8)	9.35 (13)	11.17 (12)	25.00 (10)	23.50 (11)	2.67 (10)
Cluster VIII	57.25 (6)	60.75 (6)	89.00 (5)	57.25 (15)	15.55 (7)	12.77 (7)	15.58 (3)	36.00 (5)	35.25 (6)	5.25 (4)
Cluster IX	61.00 (12)	64.50 (11)	88.50 (4)	141.67 (3)	14.92 (9)	12.12 (10)	15.25 (4)	73.50 (1)	73.00 (1)	12.67 (1)
Cluster X	57.00 (5)	62.00 (8)	94.00 (11)	121.84 (10)	16.67 (4)	13.73 (4)	14.17 (7)	24.00 (11)	21.00 (12)	3.50 (8)
Cluster XI	57.00 (5)	61.00 (7)	78.00 (1)	129.34 (9)	14.67 (10)	15.52 (2)	12.84 (9)	34.50 (6)	31.00 (8)	4.17 (6)
Cluster XII	57.00 (5)	60.00 (3)	92.50 (9)	132.67 (8)	23.50 (1)	13.03 (5)	12.67 (10)	18.50 (13)	17.50 (14)	4.17 (6)
Cluster XIII	59.50 (10)	62.50 (8)	93.50 (10)	134.33 (6)	10.83 (14)	18.30 (1)	15.75 (2)	26.50 (9)	24.50 (10)	3.00 (9)
Cluster XIV	42.00 (1)	48.00 (1)	89.00 (5)	108.67 (13)	13.34 (12)	12.85 (6)	14.84 (5)	28.50 (8)	26.00 (9)	1.00 (12)
Cluster XV	55.00 (3)	60.50 (5)	91.00 (8)	133.67 (7)	12.59 (13)	11.96 (12)	11.67 (11)	43.00 (4)	41.50 (5)	4.83 (5)

Table 4 (Contd…)

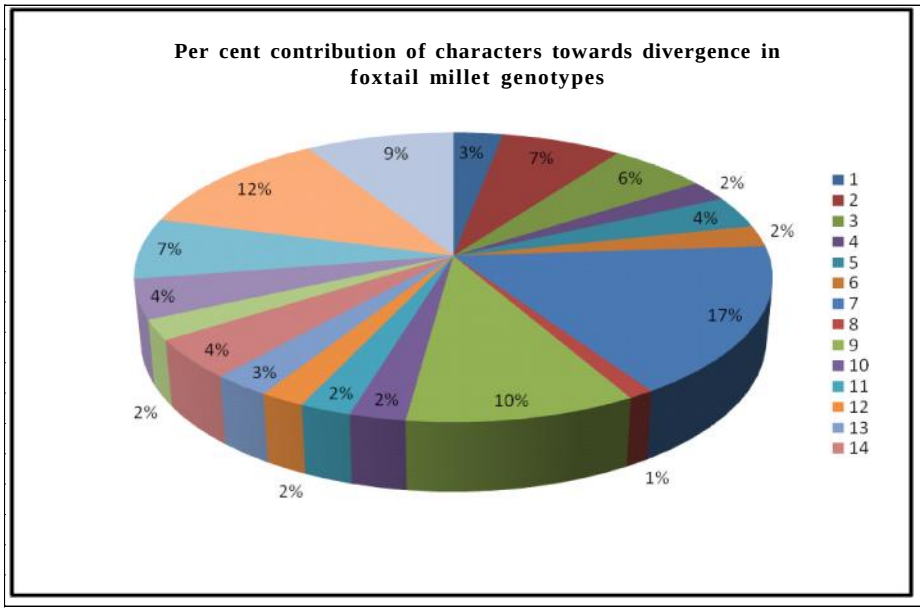
Characters / Clusters	Area of standard leaf (cm^2)	Stem thickness (cm)	SPAD at 50% flowering	SPAD at maturity	Grain yield/plant (g)	Grain yield/ hactare kg)	Fodder yield/ plant (g)	Fodder yield/ hectare (kg)	1000 seed weight (g)	Total score	Rank
Cluster I	62.96 (7)	1.29 (8)	40.24 (9)	25.55 (8)	31.86 (5)	1597.41 (5)	131.64 (5)	2993.99 (3)	3.55 (6)	105	3
Cluster II	44.52 (14)	.92 (15)	35.22 (15)	24.34 (9)	14.94 (15)	139.82 (15)	60.00 (15)	1907.41 (9)	3.49 (7)	231	15
Cluster III	55.67 (11)	1.02 (14)	38.72 (12)	29.27 (3)	32.28 (4)	775.00 (10)	142.50 (3)	3185.19 (2)	4.20 (1)	119	6
Cluster IV	78.87 (2)	1.70 (2)	48.12 (1)	25.85 (7)	31.21 (6)	2553.71 (1)	125.00 (6)	3388.89 (1)	3.29 (9)	78	1
Cluster V	45.35 (13)	1.11 (12)	43.09 (4)	21.02 (14)	17.32 (12)	314.82 (14)	67.50 (14)	703.71(13)	4.01 (3)	197	13
Cluster VI	68.93 (5)	1.27 (9)	40.72 (8)	33.14 (2)	40.63 (2)	1723.15 (3)	227.50 (1)	2925.93 (4)	3.97 (4)	91	2
Cluster VII	46.62 (12)	1.08 (13)	40.87 (6)	23.69 (10)	15.86 (13)	576.86 (13)	72.50 (13)	1259.26 (12)	2.85 (14)	207	14
Cluster VIII	60.13 (9)	1.29 (7)	36.22 (13)	23.57 (11)	23.90 (10)	1422.69 (8)	90.00 (12)	2620.37 (6)	3.79 (5)	145	9
Cluster IX	54.71 (11)	1.16 (11)	43.19 (3)	27.19 (6)	44.93 (1)	2039.82 (2)	195.00 (2)	1879.63 (10)	3.37 (8)	110	4
Cluster X	74.34 (3)	1.22 (10)	39.18 (10)	19.82 (15)	26.23 (7)	620.37 (12)	137.50 (4)	703.71 (14)	4.15 (2)	157	12
Cluster XI	62.42 (8)	1.47 (4)	39.15 (11)	34.22 (1)	34.69 (3)	1575.00 (6)	115.00 (9)	2796.30 (5)	3.37 (8)	118	5
Cluster XII	87.67 (1)	1.35 (5)	44.84 2()	27.55 (4)	17.36 (11)	696.30 (11)	122.50 (7)	2148.15 (8)	3.01 (11)	134	7
Cluster XIII	69.99 (4)	1.64 (3)	40.80 (7)	27.50 (5)	26.02 (8)	1459.26 (7)	95.00 (10)	2481.48 (7)	2.95 (13)	143	8
Cluster XIV	55.78 (10)	1.35 (6)	41.28 (5)	23.42 (12)	15.25 (14)	1149.08 (9)	92.50 (11)	3388.89 (1)	2.99 (12)	152	11
Cluster XV	65.87 (6)	3.00 (1)	35.44 (14)	22.03 (13)	24.43 (9)	1662.97 (4)	117.50 (8)	1277.78 (11)	3.11 (10)	149	10

Analysis of cluster means :

All the 149 genotypes were spread over fifteen clusters and means were scored across the clusters for all the nineteen characters (Table 4).

The highest cluster mean was given the first rank and the clusters possessing next best means were given second, third and so on upto sixteenth rank for all the traits except for days to 50 per cent flowering and days to maturity, for all these the lowest mean was given the first rank. Accordingly, cluster IV (SR 11) with overall score of 78 across the nineteen characters secured first rank followed by cluster VI (GS 213), cluster I, cluster IX (GS 510) indicating the presence of most promising genotypes in them and can be extensively used for further breeding programme to generate new material. Hence, apart from selecting genotypes from the clusters which have high inter cluster distance for hybridization, one can also think of selecting genotypes based on cluster mean values in respect to a particular character of interest.

Cluster IV (SR 11) was not only showed earliness in terms of panicle emergence as well as flowering but also high cluster means for majority of the traits. Similarly cluster XIV (GS 35) which is early in terms of panicle emergence as well as flowering showed maximum



	Legend
1	Days to panicle emergence
2	Days to 50% flowering
3	Days to maturity
4	Plant height
5	Panicle length (cm)
6	Panicle girth (mm)
7	Peduncle length (cm)
8	No of tillers/meter row length
9	Number of productive tillers/meter row length
10	Number of productive tillers/plant
11	Area of standard leaf (cm^2)
12	Stem thickness (cm)
13	SPAD at 50% flowering
14	SPAD at maturity
15	Fodder yield/plant (g)
16	Fodder yield/hectare (kg)
17	Grain yield/plant (g)
18	Grain yield/hectare (kg)
19	1000 seed weight (g)

Fig. 2 : Per cent contribution of various characters towards total divergence in foxtail millet germplasm accessions

distance with many of the clusters. This indicates that this genotype may be used in breeding for earliness. The early maturing cluster was XI (GS-17) may be used for crossing with genotypes of clusters III (GS 207), VI (GS 213), XIV (GS 35) and XV (GS 338) for which high genetic distance has been observed.

Cluster VI (GS 213) which showed high cluster mean for plant height, also showed high mean values for number of tillers/plant, number of tillers/meter row length, number of productive tillers/plant, number of productive tillers/m row length, fodder yield (kg/ha), grain yield (g/pl), grain yield (kg/ha), high SPAD values at both flowering and maturity.

For panicle length, clusters XII (MLT-12-8) followed by cluster IV (SR 11) recorded highest values. This cluster also showed highest value of area of standard leaf (cm^2) followed by SR 11 (cluster IV). For panicle girth, cluster XIII (GS 511) recorded highest value. This entry also showed high peduncle length.

The cluster IX (GS 510) which showed the highest number of tillers/m row length, number of productive tillers/m row length and number of productive tillers/plant, also showed high cluster means for grain yield (g/pl), grain yield (kg/ha) and fodder yield (kg/ha). For stem thickness, cluster XV (GS 338) recorded the highest value.

With respect to SPAD reading, the highest SPAD at both flowering and maturity stages was recorded by cluster XI (GS 17) followed by cluster VI (GS 213) and cluster III (GS 207). This indicates that these genotypes showed minimum reduction in chlorophyll content from flowering to maturity stage. Hence, these genotypes may be tested under moisture stress conditions for their stay-greenness/terminal drought tolerance.

For both grain yield per plant (g) and grain yield per hectare (kg), clusters IX (GS 510) and cluster IV (SR 11) recorded high value. These genotypes also showed high fodder yield per plant (g).

Highest values for fodder yield per plant were recorded by cluster VI (GS 213) followed by cluster IX (GS 510). These clusters also showed high means for number of tillers/meter row length, number of productive tillers/m row length, number of productive tillers/plant, grain yield (g/plant) and grain yield (kg/ha).

With respect 1000 seed weight, the clusters which recorded highest values (> 4.0 g) were III (GS 207), V (MLT-12-9) and X (MLT-12-11 or HMT-100-1).

In general the clusters, VI, III, XIV and XV showed maximum intercluster distances with many clusters. Hence, genotypes belonging to these clusters *viz*., GS 213, GS 27, GS 35, GS 338 is used in hybridization programme to widen the genetic base and hence used in varietal development. The genotypes identified for superiority for various traits *viz*., SR 11, GS 213, GS 511, GS 510 could be utilized for simultaneous transfer of multiple traits/genes in crop improvement programme.

REFERENCES

Anonymous (2012). Quarterly Bulletin of statistics 2012, FAO, pp. 12 30.

Mahalanobis, P.C. (1928). A statistical study at Chinese head measurement. *J. Asiatic Soc. Bengal.*, **25**: 301-307.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proceed. National Institute of Sci.*, (India), **2** (1) : 49-55.

Maloo, S.R. and Bhattacharjee, I. (1999). Genetic divergence in foxtail millet. Recent advances in management of arid ecosystem, In : Proceedings of a symposium held in India, March, 1997, pp. 155-158.

Murty, B.R. and Arunachalam, V. (1966). The nature of divergence in relationship to breeding system in some crop plants. *Indian J. Genet*., **26**: 188-189.

Murugan, R. and Nirmalakumari, A. (2006). Genetic divergence in Italian millet [(*Setaria italica* L.) Beauv]. *Indian J. Genet.*, **66**(4): 339-340.

Nagarajan, K. and Prasad, M.N. (1980). Studies on genetic diversity in foxtail millet [*Setaria italica* (L.) Beauv]. *Madras Agril. J.*, **67**(1): 28-38.

Rao, C.R. (1952). Advanced statistical methods in biometerical Research. New York, John Wiley and Sons.

Selvarani, M. and Gomathinayagam, S.P. (2000). Genetic diversity in foxtail millet [*Sataria italica* (L.) Beauv]. *Res. Crop.*, **1**(3): 410-412.

Sheriff, R.A. and Shivashankar, G. (1992). Genetic divergence in foxtail millet (*Setaria italica)*. *Indian J. Genet.*, **52**(1): 29-32.

Sheriff, R.A. (1992). Divergence analysis in finger millet (*Eleusine coracana* Gaertn.). *Indian J. Genet*., **52**(1): 72-74.