

**GENETIC DIVERSITY ANALYSIS FOR YIELD AND
YIELD COMPONENTS IN FOXTAIL MILLET
[*Setaria italica* (L.) Beauv.]**

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Thesis submitted to the
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By
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CERTIFICATE

This is to certify that the thesis entitled “**GENETIC DIVERSITY ANALYSIS FOR YIELD AND YIELD COMPONENTS IN FOXTAIL MILLET [*Setaria italica* (L.) Beauv.]**” submitted by **Mr. THIPPESWAMY V.**, for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING**, to the University of Agricultural Sciences, Dharwad is a record of research work done by him during the period of his study in this University under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

**VIJAYAPUR
JULY, 2015**

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**Affectionately Dedicated to
My beloved Parents
And
Family**

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THIPPESWAMY V.

CONTENTS

Sl. No.	Chapter Particulars	Page No.
	CERTIFICATE	
	ACKNOWLEDGEMENT	
	LIST OF CONTENTS	
	LIST OF TABLES	
	LIST OF FIGURES	
	LIST OF PLATES	
	LIST OF ABBREVIATIONS	
	LIST OF APPENDICES	
I	INTRODUCTION	
II	REVIEW OF LITERATURE	
	2.1 Genetic divergence	
	2.2 Variability, heritability and genetic advance	
	2.3 Correlation studies	
	2.4 Nutrition and grain quality analysis	
III	MATERIAL AND METHODS	
	3.1 Experimental location	
	3.2 Experimental material	
	3.3 Methodology	
	3.4 Statistical analysis	
4.	EXPERIMENTAL RESULTS	
	4.1 Analysis of variance	
	4.2 Genetic diversity	
	4.3 Genetic variability parameters	
	4.4 Correlation coefficients	
	4.5 Variability for morphological traits	
	4.6 Screening genotypes for grain nutrients content	

5.	DISCUSSION	
	5.1 Analysis of variance	
	5.2 Genetic diversity analysis	
	5.3 Genetic variability parameters	
	5.4 Correlation coefficients	
	5.5 Varietal characterization for morphological traits	
	5.6 Superiority of genotypes for various traits	
	5.7 Screening genotypes for grain nutrients content	
6.	SUMMARY AND CONCLUSIONS	
	REFERENCES	
	APPENDIX	

LIST OF TABLES

Table No.	Title	Page No.
1.	Review of reports by various workers on the extent of variability, heritability and genetic advance for productivity traits in Foxtail millet	
2.	Review of reports by various workers on the nature of association between yield and yield components in Foxtail millet	
3.	Review of reports by various workers on associations among different components traits in Foxtail millet	
4.	Details on 149 germplasm lines of Foxtail millet used in the present study	
5.	Mean sum of squares for yield and its component traits in 149 germplasm accessions of Foxtail millet evaluated at Vijayapur during <i>kharif</i> 2014	
6.	Distribution of Foxtail millet germplasm accessions into different clusters based on cluster analysis	
7.	Per cent contribution of characters towards total divergence in 149 Foxtail millet germplasm accessions	
8.	Average intra and inter cluster distances among 149 germplasm accessions of Foxtail millet for yield and yield related traits	
9.	Cluster means of germplasm accessions of Foxtail millet in respect of a total of 19 characters and overall character wise score	
10.	Estimates of genetic variability parameters for productivity traits among 149 germplasm accessions of Foxtail millet	
11.	Phenotypic correlation co-efficients estimated between different traits using 149 germplasm accessions of Foxtail millet	
12.	Performance of selected genotypes of Foxtail millet for grain nutrients contents	
13.	Top 10 genotypes and their range of values for yield and yield components among 149 germplasm accessions of Foxtail millet evaluated during <i>kharif</i> 2014 at RARS, Vijayapur	

LIST OF FIGURES

Figure No.	Title	Between pages
1.	Diagrammatic representation of 15 clusters consisting of 149 Foxtail millet lines.	
2.	Per cent contribution of various characters towards total divergence in Foxtail millet germplasm accessions.	
3.	Phenotypic and genotypic coefficient of variation for 19 traits estimated using 149 germplasm accessions of Foxtail millet	
4.	Heritability and genetic advance as percent mean estimated for 19 characters using 149 germplasm accessions of Foxtail millet	

LIST OF PLATES

Plate No.	Title	Between pages.
1.	General view of experimental plot of Foxtail millet crop at maturity	
2.	Varietal differences for panicle (a) length, (b) girth	
3.	Varietal differences for awn length	
4.	Varietal differences for panicle compactness	
5.	Phenotypic diversity for panicle features	
6.	Varietal differences for grain colour	

LIST OF APPENDICES

Appendix No.	Title	Page No.
I.	Meteorological data for the year 2014 at Regional Agricultural Research Station, Vijayapur	
II.	Mean performance of 149 germplasm accessions of Foxtail millet evaluated during kharif season 2014 at RARS, Vijayapur	
III.	Characterization of Foxtail millet genotypes for qualitative traits	

LIST OF ABBREVIATIONS

GCV	:	Genotypic coefficient of variation
PCV	:	Phenotypic coefficient of variation
h^2_{bs}	:	Broad sense heritability
GA	:	Genetic advance
GAM	:	Genetic advance as per cent mean
S.Em. $\pm$	:	Standard error of mean
C. D	:	Critical difference at 5 % level of probability
C.V.	:	Coefficient of Variation
Max	:	Maximum
Min	:	Minimum
cm	:	Centimeter (s)
No.	:	Number (s)
g	:	Grams
kg	:	Kilograms
mt	:	Million tones
mha	:	Million hectare

I INTRODUCTION

Small millets have long cultivation history (3000-5000 years), were major food crops at one time, are highly resilient crops and assured harvests, can be used as catch crops, suitable for less fertile/native fertility soils, are infected with a fewer pests and diseases, grains highly nutritious and even superior to rice and wheat in certain constituents, are physiologically very efficient, wide adaptation and are reliable for harvest (Upadhyaya *et al.*, 2008). It is of interest to note that lower incidence of cardiovascular diseases, duodenal ulcer and hyperglycemia (diabetes) are reported among regular millet consumers. However, nationally, gradual decrease in area (55.35 lakh hectares in 1950-55 to 9.05 lakh hectares in 2008-09) and production (20.7 lakh tones in 1950-55 to 4.5 lakh tones in 2008-09) has been occurred over the years. The production of small millets is dependent on seasonal precipitation as they are mainly grown as rainfed *kharif* crops. The productivity enhancement is linked to adoption of improved cultivation package and this holds good to both rainfed and irrigated farming.

Foxtail millet (botanic name ***Setaria italica***, formerly as *Panicum italicum* L.) 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.

Foxtail millet has the longest history of cultivation among the millets, having been grown in China since sometime in the sixth millennium BC. China ranks 1st in foxtail millet production in the world (4.6 mt) with productivity around 1.8 t/ha. Total world production of foxtail millet is 6 million tonnes. Korea, Afghanistan, Japan, Syria, South Africa and India, are the other foxtail millet producing countries globally.

In India, Foxtail millet, with colloquial names *kangni*, *navane*, *tenai*, *korra* and *ralla*, is one of the oldest crops cultivated for straw and grain. In South India, it has been a staple diet among people for a long time from the *sangam* period. Known for its drought tolerance, it was once an indispensable crop of vast rainfed areas in semi-arid regions in India. It is cultivated in an area of 1.2 mha with a production of 0.57 mt and productivity of 0.47 t/ha (Anon., 2005). 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. The state Madhya Pradesh accounts for largest area (0.41 mha) and highest production (0.13 mt), followed by Chhattisgarh. With respect to productivity, Uttaranchal ranks first with 1.2t/ha, followed by Arunachal Pradesh with 0.957 t/ha. The popular high yielding varieties for different states are SiA 326, TNAU 186, Krishnadevaraya, Narasimharaya, Co-6, Co-7, HMT-100, TNAU 43 etc. In Karnataka, important foxtail millet growing districts are Koppal, Raichur, Haveri, Vijayapur, in north and Tumkur, Chitradurg, Mandya, Mysore and Chamrajnagar in south. Although few high yielding varieties are recommended for Karnataka (SiA 326, TNAU 186, PS-4 & HMT-100), but in many of these areas farmers are growing local genotypes.

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 genotypes) and existence of genetic potential of moderate to high productivity promise breaking the yield barriers.

It is evident now that, cultivated foxtail millet is highly variable within its primary centre of origin *i.e.*, China, and other secondary centers. In both China and other regions like Japan, Afghanistan, the crop has been in cultivation for more than 5000 years and isolated from each other. This isolation might have resulted in the emergence of two gene pools distinct from each other genetically and morphologically. In India, the crop being grown in different states, there is a need to assess the genetic diversity and variability within the Indian accessions. Genetic divergence analysis helps in identification of the diverse genotypes for hybridization purposes to derive desirable segregants. Knowledge on the nature and magnitude of

genetic variability present in the crop species will play an important role in formulating a successful breeding programme.

As yield is a complex character, is influenced by a number of yield contributing characters controlled by polygenes and also influenced by environment. Hence, it becomes necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance expressed as per cent mean.

Probing of structure of yield involves assessment of mutual relationship among various characters contributing to the yield. In this regard, correlation coefficients reveal the degree of association between different characters and thus aid in selection to improve the yield and yield attributing characters simultaneously.

As foxtail millet is an important millet crop with good nutritional quality, it is essential to study varietal differences for identification of genotypes with high nutrients content for their exploitation through value addition. Recent research studies conducted under NAIP at U.A.S Dharwad showed its scope for value addition.

Keeping these things in view the present study was planned with the following objectives.

Objectives

1. To assess the extent of genetic diversity and variability within germplasm accessions of foxtail millet for various quantitative and qualitative traits.
2. To study the association between yield and yield component traits among the genotypes.
3. To characterize the selected genotypes for grain nutrients content.

II REVIEW OF LITERATURE

The literature available on foxtail millet [*Setaria italica* (L.) Beauv] pertinent to the present study has been comprehensively reviewed under the following headings.

2.1. Genetic divergence

2.2 Variability, heritability and genetic advance

2.3 Correlation studies

2.4 Nutrition and grain quality analysis

2.1 Genetic divergence

Foxtail millet is a self pollinated crop. Despite this reproductive behavior, 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 to be 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.

Clusters separated by largest statistical distance (D^2) show maximum divergence (Singh and Chaudhary, 1977). Nagrajan and Prasad (1980) studied the genetic diversity in 50 genotypes of foxtail millet. A wide genetic diversity was revealed by the D^2 analysis where these genotypes partitioned into as many 15 clusters. The geographic distribution was not related to genetic diversity. Genotypes chosen from same eco geographic region were found scattered in different clusters. Based on average inter cluster distances, three clusters were found to be highly divergent from the others.

Li *et al.* (1995) reported cluster analysis of 2907 accessions of foxtail millet from 16 provinces, using nine morphological and agronomic descriptors. The results revealed the existence of high levels of variation for all characters observed among regions and suggested a multiple domestication hypothesis with the centers.

Li *et al.* (1996) analyzed phenotypic diversity of 2381 foxtail millet landraces of Chinese origin for seven qualitative traits and four quantitative traits. Hierarchical analysis of variance indicated that most of the variation was due to differences among characteristics. Only the diversity indices for leaf colour of seedlings, starch composition and 1000 grain weight showed significant differences among regions.

Maloo and Bhattachargee (1999) studied the genetic divergence in forty genetically and geographically diverse varieties of foxtail millet. The D^2 values ranged from 4.30 to 6058.21 and genotypes were grouped into four clusters, cluster I (28 varieties), II (9 varieties), III (2 varieties) and IV (1 variety). Characters contributing largely to the divergence were test weight, seed protein content, harvest index and seed yield/plant.

Murugan and Nirmalakumari (2006) studied genetic divergence in foxtail millet for eleven characters viz., days to 50 per cent flowering, plant height, number of productive tillers, ear length, ear weight, days to maturity, grain yield/plant, 1000 grain weight, straw yield/plant, harvest index and β carotene content (mg/100 g). The 75 genotypes evaluated were grouped into nine clusters. Cluster I had a maximum of 61 genotypes followed by cluster III with five genotypes. While cluster IV exhibited three genotypes and remaining cluster possessed one genotype each. The results revealed that genotypes from wide range of eco geographical areas assembled together to contribute a major cluster. The characters days to maturity, straw yield/plant, days to 50% flowering and thousand grain weight contributed maximum to diversity.

Nirmalakumari and Vetriventhan (2010) reported that cluster analysis of 741 accessions of foxtail millet was carried out using DARwin5 for yield and yield contributing traits. The population was grouped into nine clusters which shows wide range of variability in the population.

Reddy *et al.* (2006) collected and characterized the world's foxtail millet germplasm for morphological traits. They found that diversity for days to 50 per cent flowering was greater in germplasm accessions originating from Sri Lanka (55 to 135 days) while it was narrowest in Russian germplasm (30 to 50 days). Plant height varied from 20 cm to 215 cm, with accessions from China tending to be dwarf (20 cm) and those from India were taller (215 cm). Based on plant colour, accessions were classified into three classes: green (74.6%), pigmented (23.6%) and deep purple (1.8%).

Selvarani and Gomathinayagam (2000a) evaluated 50 genotypes of foxtail millet for their genetic divergence by D^2 analysis for a set of divergence characters including seed yield and four other metric traits. The genotypes were grouped into six clusters. Cluster V, VI and VII were identified as genetically more divergent based on inter cluster values.

Sheriff (1984) studied 225 genotypes for genetic divergence through multivariate analysis. The canonical variate 3 vector analysis *per se* accounted 56 per cent of the total variability. These genotypes are clustered into 46 clusters out of which 13 represented different geographic regions. The traits days to 50% flowering, days to maturity, number of productive tillers, panicle weight and panicle length, significantly contributed for the genetic diversity.

Sheriff (1992) studied the divergence among 20 varieties of finger millet grown across two environments using Mahalanobis D^2 statistics. Varieties were grouped into four clusters under rainfed and 11 under irrigated condition. Days to flowering, days to maturity, plant height, ear length, ear weight and grain weight contributed maximum to genetic diversity in both the environments.

Sheriff and Shivashankar (1992) studied genetic divergence in foxtail millet by analysing 225 genotypes by multivariate analysis using Mahalanobis D^2 statistics and canonical analysis. Both analyses suggested the existence of considerable divergence among the material. D^2 statistic resulted in 33 clusters. Genetic divergence has not been found to be related with geographical diversity. The

characters days to maturity, panicle weight and grain weight contributed for the maximum divergence which were confirmed by canonical analysis.

Upadhyaya *et al.* (2011) evaluated 155 accessions together for 21 descriptors at five agro ecologically diverse locations. The hierarchical cluster analysis of data using phenotypic distances resulted in 25 clusters, from each cluster, nearly 10% or a minimum of one accession was selected to form a mini core, which comprised of 35 accessions.

2.2 Genetic variability, heritability and genetic advance

2.2.1 Genetic variability

Economic traits, which are polygenically controlled and highly influenced by environment, determine the success in breeding programme through their genotypic variability. It is therefore, essential to partition the total variability into heritable and non heritable components. Knowledge on the magnitude of heritability coupled with nature and extent of variability in the breeding material gives an idea for effective genetic improvement through selection.

Amgai *et al.* (2011) evaluated five accessions of Nepalese foxtail millet for agro morphological characteristics. Days to heading and days to maturity varied from 33 to 56 and 59 to 87 days after germination respectively. Similarly, flag leaf length/breadth ratio, flag leaf sheath length, ligule length, peduncle length, peduncle exertion and plant height varied from 3.84 to 10.90, 5.47 to 9.84 cm, 0.1 to 0.2 mm, 10 to 22.57 cm, 2.7 to 13.58 cm and 41.67 to 120 cm, respectively and the thousand grain weight varied from 1.064 g to 2.172 g.

Basheeruddin and Sahib (2004) evaluated 15 genotypes of foxtail millet for yield and its components (days to 50 per cent flowering, plant height, productive tillers/plant and days to maturity). Plant height had the highest mean (132.6), genetic variability (233.74) and phenotypic variability (277.68). Heritability was highest for days to 50 per cent flowering (96.19%) while grain yield had the highest genotypic (31.13) and phenotypic (49.02) coefficient of variability and genetic advance as per cent of mean (40.60).

Islam *et al.*, (2012) evaluated seventy eight germplasm accessions of foxtail millet are evaluated. In this study, the coefficient of variation, heritability (broad sense), expected genetic advance and simple correlation coefficient were estimated. A wide range of variation was observed among the genetic stocks for quantitative characters like, plant height, number of tillers per plant, days to flowering, days to

maturity, panicle length, grain yield per plant and 1000 grain weight. High heritability associated with high genetic advance for number of tillers, panicle length and grain yield indicate additive gene effect for the characters. Significant positive correlation of grain yield with tiller number and 1000 grain weight showed that higher yield may be positive through selection of plants having more tillers and higher grain weight.

Lakshman and Guggari (2001) studied the genetic variability in foxtail millet for seven quantitative traits (days to 50 per cent flowering, plant height, days to maturity, number of productive tillers/plant, earhead length, grain yield and fodder yield) in 34 genotypes. High PCV and GCV were observed for grain yield, fodder yield, earhead length and productive tillers/plant. High heritability coupled with moderate genetic advance was observed for grain yield, earhead length and plant height, indicating the occurrence of additive gene effects for these characters. Earliness showed low estimates of genetic advance coupled with higher heritability, indicating the presence of non additive gene interaction.

Santhakumar (1999) studied correlation between 200 genotypes of foxtail millet for seven yield components. Grain yield was positively and significantly correlated with plant height, panicle length and fodder yield.

Selvarani and Gomathinayagam (2000b) studied the genetic variability in 50 genotypes of foxtail millet. The high level of GCV and PCV were estimated for number of productive tillers and grain yield per plant. Low GCV and PCV levels were obtained for days to 50 per cent flowering, plant height and days to maturity. The differences between GCV and PCV for these traits were low. High heritability estimates were observed in all traits, indicating that the characteristics were stable. The genetic advance was high for the number of productive tillers, grain yield/plant and plant height. High heritability and low genetic advance were recorded for days to 50 per cent flowering and days to maturity.

Upadhyaya *et al.* (2011) evaluated 155 accessions together with five controls (four common and one location-specific control) for 21 descriptors at five agro-ecologically diverse locations in India during 2008 rainy season. The experiment was conducted in an alpha design with three replications at Patancheru, and in an augmented design with one of the five controls repeated after every nine-test entries at other locations. A number of diverse germplasm accessions with agronomically (earliness and high grain yield) and nutritionally (high seed protein, calcium, iron and zinc) superior traits were identified for use in foxtail millet breeding. Literature available regarding variability studies in Foxtail millet is presented in Table 1.

Table 1. Review of reports by various workers on the extent of variability, heritability and genetic advance for productivity traits in foxtail millet

Sl. No.	Character studied	Materials used	PCV (%)	GCV (%)	h^2 (%)	GA (as% mean)	Reference
1.	Days to 50% flowering	78 genotypes. 741 genotypes. 78 genotypes 50 genotypes	 7.48 12.52 6.85	 6.11 12.42 6.09	77.5 66.60 98.4 85.66	9.9 11.79 25.38 9.02	Islam <i>et al.</i> , (2012) Nirmalakumari and Vetriventhan (2010) Brunda <i>et al.</i> , (2014) Selvarani and Gomathinayagam (2000b),
2.	Days to maturity	64 varieties 28 Genotypes 741 Genotypes 15 Genotypes 34 Genotypes 78 genotypes	----- 18.28 8.05 2.37 2.34 10.05	6.55 10.41 7.16 2.33 2.17 9.27	93.04 32.5 79.07 96.40 86.09 85.2	42.41 12.22 13.81 4.71 4.14 17.64	Sandhu <i>et al.</i> (1974) Chidambaram and Palanisamy (1995) Nirmalakumari and Vetriventhan (2010) Reddy and Reddy (2012) Prasanna <i>et al.</i> (2013) Brunda <i>et al.</i> (2014)

Table 1(contd..)

3.	Plant height	32 varieties	-----	-----	91.1	61.79	Athwal and Gian Singh (1966)
		64 varieties	-----	21.34	93.4	42.41	Sandhu <i>et al.</i> (1974)
		50 Genotypes	15.25	14.59	91.7	28.79	Nagarajan and Prasad (1980)
		28 Genotypes	16.53	9.10	30.9	10.32	Chidambaram and Palanisamy (1995)
		741 genotype	1.12	10.38	87.14	20.78	Nirmalakumari and Vetriventhan(2010)
		15 Genotypes	7.50	4.41	34.60	53.4	Reddy and Reddy (2012)
		34 Genotypes	5.54	5.42	95.59	10.92	Prasanna <i>et al.</i> (2013)
		78 Genotypes	8.25	7.66	85.8	14.58	Brunda <i>et al.</i> (2014)
4.	No. of productive tillers per plant	32 varieties	-----	-----	55.5	48.48	Athwal and Gian Singh (1966)
		64 varieties	-----	28.20	65.8	47.25	Sandhu <i>et al.</i> (1974)
		50 Genotypes	36.84	30.83	64.5	53.38	Nagarajan and Prasad (1980)
		28 Genotypes	39.47	22.27	32.0	26.02	Chidambaram and Palanisamy, (1995)
		741 Genotypes	27.85	25.85	86.12	34.97	Nirmalakumari and Vetriventhan(2010)
		15 Genotypes	16.29	15.17	86.70	29.12	Reddy and Reddy (2012)
		34 Genotypes	25.11	24.99	99	51.22	Prasanna <i>et al.</i> (2013)
		78 Genotypes	21.91	18.5	68.7	31.03	Brunda <i>et al.</i> (2014)

Table 1 (contd..)

5.	Panicle length	32 varieties	-----	-----	91.96	71.78	Athwal and Gian Singh (1966)
		64 varieties	-----	27.20	81.11	50.41	Sandhu <i>et al.</i> (1974)
		741	17.00	16.47	93.81	34.97	Nirmalakumari and Vetriventhan(2010)
		Genotypes	11.30	9.13	65.20	15.18	Reddy and Reddy (2012)
		15 Genotypes	16.44	15.17	84.64	28.75	Prasanna <i>et al.</i> (2013)
		34 Genotypes	15.45	12.57	66.2	21.08	Brunda <i>et al.</i> (2014)
		78 Genotypes					
6.	Panicle girth	78 Genotypes	9.41	8.09	73.9	14.32	Brunda <i>et al.</i> (2014)
7.	Grain yield/ plant	32 varieties	-----	-----	75.18	120.5	Athwal and Gian Singh (1966)
		64 varieties	-----	45.99	80.01	84.74	Sandhu <i>et al.</i> (1974)
		50 Genotypes	27.93	18.05	41.95	24.1	Nagarajan and Prasad (1980)
		28 Genotypes	35.29	9.31	7.00	5.08	Chidambaram and Palanisamy (1995)
		741	40.28	38.82	94.89	82.25	Nirmalakumari and Vetriventhan(2010)
		Genotypes	14.55	8.69	35.70	10.70	Reddy and Reddy (2012)
		15 Genotypes	42.94	42.16	96.41	85.28	Prasanna <i>et al.</i> (2013)
		34 Genotypes	23.23	21.89	88.8	7.036	Brunda <i>et al.</i> (2014)
		78 Genotypes					
8.	Grain yield per hectare	78 Genotypes	20.24	19.99	95.9	40.32	Brunda <i>et al.</i> (2014)

Table 1 (contd..)

9.	Test weight (g)	64 varieties	-----	45.99	80.01	84.74	Sandhu <i>et al.</i> (1974)
		34 Genotypes	15.47	15.09	95.13	30.33	Prasanna <i>et al.</i> (2013)
		78 genotypes	13.21	12.88	95.1	25.88	Brunda <i>et al.</i> (2014)
10.	Fodder yield (g)	50Genotypes	52.98	46.13	35.8	82.74	Nagarajan and Prasad (1980)
		28 Genotypes	41.15	21.78	26.50	22.47	Chidambaram and Palanisamy (1995)
		34 Genotypes	22.29	22.21	99.10	45.59	Reddy and Reddy (2012)
		15 Genotypes	15.09	19.5	39.70	22.33	Prasanna <i>et al.</i> (2013)
		78 Genotypes	41.65	21.66	97	23.20	Brunda <i>et al.</i> (2014)

PCV: Phenotypic coefficient of variation

GCV: Genotypes coefficient of variation

 h^2 : Heritability (broad sense)

GA: Genetic Advance

Table 2. Review of reports by various workers on the nature of association between yield and yield components in foxtail millet

Sl. No.	Characters	Nature of Association	Significant /non-significant	Phenotypic/ Genotypic	Reference
1	Days to flowering	Positive	S	G	Upadhyaya <i>et al.</i> (2011), Nirmalakumari and Vetriventhan (2010)
				P,G	Nagarajan and Prasad (1980)
			NS	G	Murugan and Nirmalakumari (2006)
				P,G	Sandhu <i>et al.</i> (1974)
				---	Chidambaram and Palanisamy (1995)
		Negative	NS	----	Singh and Rao(1980),
2	Days to maturity	Positive	S	G	Nirmalakumari and Vetriventhan(2010)
				P,G	Godawat and Gupta (1981)
				----	Singh and Rao (1980)
			NS	G	Murugan and Nirmalakumari (2006)
				----	Chidambaram and Palanisamy (1995)
		Negative	S	P, G	Dhagat <i>et al.</i> (1977), Reddy and Lakshmi (1991)
			NS	P,G	Sandhu <i>et al.</i> (1974)

Table 2 (contd...)

3	Plant height	Positive	S	P G	Sandhu <i>et al.</i> (1974), Gian Singh (1974), Upadhyaya <i>et al.</i> (2011) Murugan and Nirmalakumari (2006), Nirmalakumari and Vetriventhan (2010), Channappagaudar <i>et al.</i> (2008) Nagarajan and Prasad (1980)
		Positive	NS	P,G G P,G ----	Gian Singh (1974), Godawat and Gupta (1981) Godawat and Gupta (1981) Singh and Rao (1980) Chidambaram and Palanisamy (1995)
		Negative	S NS	G P P, G	Reddy and Lakshmi (1991) Reddy and Lakshmi (1991) Dhagat <i>et al.</i> (1977)
4	No. of productive tillers per plant	Positive	S	P G P,G	Sandhu <i>et al.</i> (1974), Gian Singh (1974), Nagarajan and Prasad (1980) Reddy and Lakshmi (1991), Murugan and Nirmalakumari (2006), Gian Singh (1974), Nirmalakumari and Vetriventhan (2010) Dhagat <i>et al.</i> (1977)
		Negative	S	---- P G	Chidambaram and Palanisamy (1995) Singh and Rao, Reddy and Lakshmi (1991) Nagarajan and Prasad (1980)

Table 2 (contd...)

5	Flag leaf Area	Positive	S	G	Dhagat <i>et al.</i> (1977)
			NS	P	Dhagat <i>et al.</i> (1977)
		Negative	NS	P, G	Reddy and Lakshmi (1991)
6	Panicle length	Positive	S	P	Gian Singh (1974), Sandhu <i>et al.</i> (1974)
				G	Murugan and Nirmalakumari (2006), Upadhyaya <i>et al.</i> (2011)
				P, G	Nirmalakumari and Vetriventhan(2010)
				----	Nagarajan and Prasad (1980), Godawat and Gupta (1981)
			NS	P	Singh and Rao (1980)
				G	Reddy and Lakshmi (1991)
				P, G	Gian Singh (1974), Sandhu <i>et al.</i> (1974)
		Negative	NS	G	Dhagat <i>et al.</i> (1977)
					Reddy and Lakshmi (1991)
7	Panicle weight	Positive	S	P	Reddy and Lakshmi (1991)
				G	Murugan and Nirmalakumari (2006), Upadhyaya <i>et al.</i> (2011)
				P, G	Dhagat <i>et al.</i> (1977)
				----	Chidambaram and Palanisamy (1995)
		Positive	NS	G	Reddy and Lakshmi (1991)

Table 2 (contd...)

8	Test weight	Positive	S	G	Godawat and Gupta (1981), Reddy and Lakshmi (1991)
				P, G	Dhagat <i>et al.</i> (1977)
			NS	P	Godawat and Gupta (1981), Reddy and Lakshmi (1991)
				G	Murugan and Nirmalakumari (2006)
				P, G	Sandhu <i>et al.</i> (1974)
9	Fodder yield	Positive	S	G	Murugan and Nirmalakumari (2006)
				---	Singh and Rao (1980),
			NS	P	Dhagat <i>et al.</i> (1977)
				---	Chidambaram and Palanisamy (1995)
		Negative	NS	G	Dhagat <i>et al.</i> (1977)
				---	Singh and Rao (1980)

S : Significant

P : phenotypic correlation coefficient

NS : Non significant

G : genotypic correlation coefficient

2.2.2 Heritability and genetic advance

Hanson *et al.* (1956) defined heritability in the broad sense as the ratio of genotypic variance to the total genetic variance in the non segregating populations. Heritability (h^2) measures the relative amount of heritable portion of the variability, while genetic advance (GA) indicates the amount of progress that can be expected with selection for a character. Johnson *et al.* (1955) reported that estimates of both heritability and genetic advance are more useful in the choice of selection method rather than heritability or genetic advance alone. High heritability coupled with high genetic advance indicates additive gene effect and improvement could be made for that character by simple selection based on the phenotypic performance.

The review of literature on heritability and genetic advance studied by several authors for various characters in foxtail millet is presented in Table 1.

2.3 Correlations

Correlation refers to the degree and direction of association between two or more variables. Correlation studies are useful in developing an effective basis of phenotypic selection in plant populations. Since, yield is a polygenically controlled character with low heritability; direct selection is not effective. Yield improvement could be achieved by indirect selection. Further, knowledge on genetic correlations among the characters contributing to the yield helps to adopt the most effective method of selection. By this way combinations of favourable characters could be brought together by minimizing the retarding effect of antagonistic relations.

2.3.1 Association of component characters with yield

Sandhu *et al.* (1974) reported positive significant association of yield with number of productive tillers per plant, plant height, ear length at phenotypic level and also reported positive non significant association of yield with days to 50%flowering and 1000 seed weight at phenotypic and genotypic level, with number of productive tillers per plant, plant height, ear length at genotypic level. The literature available on association of yield component characters with yield is presented in the Table 2.

Table 3. Review of reports by various workers on associations among different components traits in Foxtail millet

SI. No.	Characters	Nature of association	Significant/ non-significant	References
1. Association of No. of productive tillers with				
a.	Days to flowering	Positive Negative	NS NS	Sandhu <i>et al.</i> (1974) Nagarajan and Prasad (1980) Chidambaram and Palanisamy (1995) Singh and Rao (1980)
c.	Days to maturity	Positive Negative	S NS	Sandhu <i>et al.</i> (1974) Sandhu <i>et al.</i> (1974), Reddy and Lakshmi (1991) Singh and Rao (1980), Chidambaram and Palanisamy (1995), Reddy and Lakshmi (1991) Dhagat <i>et al.</i> (1977)
d.	Flag leaf area	Positive Negative	NS S	Dhagat <i>et al.</i> (1977) Reddy and Lakshmi (1991)
e.	Panicle length	Positive Negative	S NS S NS	Gian Singh (1974), Nagarajan and Prasad (1980) Singh and Rao (1980) Dhagat <i>et al.</i> (1977) Sandhu <i>et al.</i> (1974) Nagarajan and Prasad (1980) Reddy and Lakshmi (1991) Navale and Harinarayana (1987) Sandhu <i>et al.</i> (1974) Gian Singh (1974)

Table 3 (contd...)

f.	Panicle weight	Positive Negative	S NS S	Singh and Rao (1980) Chidambaram and Palanisamy (1995) Reddy and Lakshmi (1991)
g.	Straw weight	Positive Negative	S NS S NS	Singh and Rao (1980) Murugan and Nirmalakumari (2006) Chidambaram and Palanisamy (1995) Dhagat et al. (1977) Nagarajan and Prasad (1980) Nagarajan and Prasad (1980) Dhagat et al. (1977)
h.	Test weight	Positive	S NS	Sandhu et al. (1974), Cill and Randhawa (1975) Dhagat et al. (1977), Reddy and Lakshmi (1991)
2. Association of days to 50 % flowering with:				
a.	Days to maturity	Positive Negative	S NS NS	Sandhu <i>et al.</i> (1974), Cill and Randhawa (1975) Chidambaram and Palanisamy (1995) Singh and Rao (1980)

Table 3 (contd...)

b.	Plant height	Positive	S NS	Sandhu <i>et al.</i> (1974), Cill and Randhawa (1975) Nagarajan and Prasad (1980) Sandhu <i>et al.</i> (1974) Singh and Rao (1980) Chidambaram and Palanisamy (1995)
c.	Panicle length	Positive Negative	S NS NS	Sandhu <i>et al.</i> (1974) Nagarajan and Prasad (1980) Sandhu <i>et al.</i> (1974) Singh and Rao (1980)
d.	Panicle weight	Positive Negative	NS NS	Chidambaram and Palanisamy (1995) Singh and Rao (1980)
e.	Straw weight	Positive Negative	S NS NS	Nagarajan and Prasad (1980) Murugan and Nirmalakumari (2006) Chidambaram and Palanisamy (1995) Singh and Rao (1980)
f.	Test weight	Negative	NS	Sandhu <i>et al.</i> (1974)
g.	Grain yield	Positive	S	Nirmalakumari and Vetriventhan(2010)
3. Association of plant height with:				
a.	Days to maturity	Positive	S NS	Dhagat <i>et.al.</i> (1977), Reddy and Lakshmi (1991) Sandhu <i>et al.</i> (1974), Godawat and Gupta (1981) Singh and Rao (1980), Chidambaram and Palanisamy (1995)
b.	Flag leaf area	Positive	NS	Dhagat <i>et al.</i> (1977), Reddy and Lakshmi (1991)

Table 3 (contd...)

c.	Panicle length	Positive	S	Sandhu <i>et al.</i> (1974), Gian Singh (1974), Dhagat <i>et al.</i> (1977), Nagarajan and Prasad (1980), Godawat and Gupta (1981), Reddy and Lakshmi (1991) Singh and Rao (1980)
		Negative	NS S	Sandhu <i>et al.</i> (1974, Gian Singh (1974) Navale and Harinarayana (1(1987)
d.	Panicle weight	Positive	NS	Reddy and Lakshmi (1991) Chidambaram and Palanisamy (1995), Singh and Rao(1980)
e.	Straw weight	Positive	S NS	Murugan and Nirmalakumari (2006) Dhagat <i>et al.</i> (1977), Nagarajan and Prasad (1980) Chidambaram and Palanisamy (1995) Singh and Rao (1980)
f.	Test weight	Positive	NS	Dhagat <i>et al.</i> (1977), Godawat and Gupta (1981)
		Negative	NS	Sandhu <i>et.al.</i> (1974), Reddy and Lakshmi (1991)
4. Association of days to maturity with:				
a.	Flag leaf area	Positive	S NS	Dhagat <i>et al.</i> (1977) Reddy and Lakshmi (1991)

Table 3 (contd...)

b.	Panicle length	Positive	S NS	Sandhu <i>et al.</i> (1974) Singh and Rao (1980) Sandhu <i>et al.</i> (1974) Dhagat <i>et al.</i> (1977), Godawat and Gupta (1981) Reddy and Lakshmi (1991)
c.	Panicle weight	Positive Negative	S NS	Singh and Rao (1980) Reddy and Lakshmi (1991)
5. Association of leaf Area with:				
a.	Panicle length	Positive	S NS	Dhagat <i>et.al.</i> (1977) Reddy and Lakshmi (1991) Reddy and Lakshmi (1991) Dhagat <i>et.al.</i> (1977)
c.	Straw yield	Positive	NS	Dhagat <i>et al.</i> (1977)
d.	Test weight	Positive	S	Dhagat <i>et al.</i> (1977)
6. Association of Panicle length with:				

Table 3 (cond...)

b.	Fodder yield	Positive	S NS	Dhagat <i>et al.</i> (1977) Murugan and Nirmalakumari (2006) Nagarajan and Prasad (1980) Singh and Rao (1980) Dhagat <i>et al.</i> (1977)
c.	Test weight	Positive Negative	S NS NS	Dhagat <i>et al.</i> (1977) Godawat and Gupta (1981) Reddy and Lakshmi (1991) Sandhu <i>et al.</i> (1974)
7. Association of panicle girth with:				
a	Plant height	Positive	S	Gian Singh (1974) Velazco and Rimieri (2012)
b	Grain yield per plant	Positive	S	Gian Singh (1974) Velazco and Rimieri (2012)
c	Panicle length	Positive	S	Velazco and Rimieri (2012)
d	Test weight	Negative	S	Velazco and Rimieri (2012)
8. Association of peduncle length with:				
a	Panicle emergence	Positive	S	Upadhyaya <i>et al.</i> , (2011)

Table 3 (cond...)

9. Association of 1000 seed weight with:				
a	Days to flowering	Negative	NS	Islam <i>et al.</i> , (1990)
b	Plant height	Negative	S	Islam <i>et al.</i> , (1990)
c	Tiller number	Positive	S	Islam <i>et al.</i> , (1990)
d	Panicle length	Positive	S	Islam <i>et al.</i> , (1990)
e	Grain yield	Positive	S	Islam <i>et al.</i> , (1990)

S : Significant

NS : Non significant

2.3.2 Association among yield component characters

Nagarajan and Prasad (1980) studied 50 genotypes of foxtail millet and reported positive significant association of number of productive tillers per plant with days to 50% flowering at phenotypic and genotypic levels, ear length at phenotypic level; positive non significant association with plant height at phenotypic level and negative non significant association with plant height and ear length at genotypic level, negative significant association with ear length and straw yield at genotypic level. The reviews on the association among the yield component characters are presented in Table 3.

2.4 Nutrition and grain quality analysis

Grains of millets are the storehouses of many chemical components including nutrients, phytochemicals, and non nutritive plant protective functional constituents. The nutritive value of millets is comparable to other cereals with slightly higher contents of protein and minerals (Gopalan *et al.*, 2002).

Millets in general contain 4.5 to 6.3 per cent of crude fibre (Gopalan *et al.*, 2002). The crude fibre content reported in kodo millet was 6.3 per cent followed by little millet (5.73%) and proso millet with 5.51 per cent (Malleshi and Desikachar, 1985 and Kulkarni *et al.*, 1992). Thus, minor millets are good store houses of nutrients with varietal differences evident within the species.

In a study by Ravindran (2003) grain samples of six varieties of common millet (*Panicum miliaceum*), three varieties of finger millet (*Eleusine coracana*) and four varieties of foxtail millet (*Setaria italica*) were analyzed for their proximate composition, mineral composition and phytate and oxalate contents. The average protein content of common millet, finger millet and foxtail millet were 14.4, 9.8 and 15.9%, respectively. The crude fibre content of the millets ranged from 3.2 to 4.7%. In general, the mineral contents were high compared with those of other common cereal grains. The oxalate contents (21–29 mg/100 g dry weight) of the millets were low.

A significant variation in calcium content of five minor millets was recorded with values ranging from 12.36 to 29.17 mg/100 g and little millet was reported to contain 12.36 mg calcium (Kulkarni *et al.*, 1992). Veena *et al.*, (2005) reported that the calcium and iron content of barnyard millet varieties ranged from 17.1 to 32.7 and 1.2 to 1.5 mg/100g seed, respectively.

Studies have indicated that the protein content of little millet ranged from 7.70 to 12.50 per cent. The protein content in foxtail, kodo, proso and barnyard millet were reported to be ranging between 9.70 to 13.70, 8.50 to 10.50, 9.00 to 10.50 and 9.50 to 12.00 per cent, respectively with varietal differences within species as reported by several investigators (Kulkarni *et al.*, 1992, Hadimani and Malleshi, 1993, Mogra *et al.*, 1998, Kulkarni and Naik, 1999 and 2000, Itagi, 2003, and Veena *et al.*, 2005).

Varietal differences in nutrient composition within the species of minor millets were reported by several investigators. Studies indicated that little millet genotypes recorded a moisture content of 8.56 to 12.34 per cent. It was also reported that proso millet recorded a high moisture content ranging from 10.60 to 15.00 per cent, followed by foxtail millet, kodo millet and barnyard millet with values of 10.70, 11.5, 10.20 and 9.53 per cent, respectively (Kulkarni *et al.*, 1992, Kulkarni and Naik, 1999 & 2000, Itagi, 2003 and Veena *et al.*, 2005).

Mandelbaum *et al* (1996) studied on two species of *Echinochloa* millets and their direct wild ancestor species were analyzed for proximate composition, and amino acid, calcium, and iron content. The protein, calcium, and iron content of the four species were comparable to or greater than in other major cereals. Calcium was higher in each of the wild species than their domesticated counterpart. Essential amino acid values for the three species analyzed were generally higher than the FAO/WHO standards, except for lysine. The results indicate a wide variation in the content of examined nutrients and suggest that there is opportunity for improvement in the nutritional value of the *Echinochloa* millets *via* selective cross breeding of wild and domesticated species.

Sridevi *et al.* (2011) studied antioxidant contents and antioxidant activity of cereals of both cooked and enriched foods. The highest polyphenol content was observed in common sorghum for whole grains and cooked. Whereas, for enriched foods the highest polyphenol was observed in foxtail millet and similar results were also observed for phytic acid. The highest zinc and copper content was found to be highest in foxtail millet. The highest manganese content was observed to be in common sorghum.

Varietal differences in foxtail millet were studied by various workers and reports are given below. In addition to foxtail millet, the nutritional analysis reports in other minor millets individually are also reviewed.

2.4.1 Foxtail millet

Choudhury *et al.* (2011) estimated crude fat and crude fibre contents of foxtail millet. The results revealed that crude fat and crude fiber contents were significantly lower than raw millet in both the yellow and purple varieties, while the carbohydrate and energy values were significantly higher. In malted samples, crude protein and fat contents were significantly lower than in raw millet in both the varieties, whereas the carbohydrate contents were higher.

In Foxtail millet, 21 varieties recorded a fat content ranging from 2.3 to 5.9 per cent, followed by Proso (2.1 to 5.2%), little (3.10 to 3.7%) and Kodo millet (1.1 to 3.3%) as reported by several investigators (Malleshi and Desikachar, 1985; Sahu, 1987; and Kumar and Parmeshwaran, 1998).

Kamara *et al.* (2009) examined the chemical composition and physicochemical properties of two varieties defatted foxtail millet flour grown in China. The seeds were obtained, milled and sieved to produce flour the flours were tagged DFMFW and DFMFY for defatted foxtail millet flour white and defatted foxtail millet flour yellow, respectively. The protein contents of DFMFW and DFMFY were 11.92 and 11.39, respectively. DFMFY had higher mineral elements, ash and fat content than DFMFW. A low bulk density (0.27 and 0.23 g mL⁻¹) and also low in total phenolic assay (0.56 and 0.72 mg) was observed for both DFMFW and DFMFY, respectively.

Phillip and Maloo (1996) evaluated 40 diverse varieties of foxtail millet for their iron content. The varieties were classified into high, moderate, and low iron content categories. High genetic variability for grain Fe content was reported in many crops.

Prasanna *et al.* (2013) studied 18 Indian genotypes foxtail millet for 13 characters during *kharif* and *rabi*. The association of protein and calcium content and carotene with grain yield is negative.

Seetharam *et al.* (1983) noted that the variability available for protein content in foxtail millet ranged from 7.16 to 15.73 per cent and identified the sources with high protein for both direct exploitation and use in breeding. Kumar and Parmeswaran (1998) studied the

characterization of storage protein from selected varieties of foxtail millet. Protein content of grain of foxtail millet was 91.7, 105.2 and 112.0 g/kg in Cv. CO 6, TNAU 172 and TNAU 173, respectively. Tyagi and Rawat (2004) developed an induced mutant cultivar of foxtail millet *i.e.*, PS4. It was high in protein content (13.15%) than its parents SIA 2616 (12.25%) and the control SiA 326 (12.22%).

2.4.2 Finger millet

Barbeau and Hilu, (1995) examined two wild and eight domesticated cultivars of finger millet and reported that wide variations were observed in the protein (mean values ranged from 7.5 to 11.7%).

Chemical composition of finger millet revealed that total carbohydrate content of finger millet has been reported to be in the range of 72 to 79.5 per cent (Singh and Raghuvamshi, 2011). Finger millet had nearly 7% protein but large variations in protein content from 5.6 to 12.70 per cent were reported. The total ash content was higher in finger millet than in commonly consumed cereal grains. The ash content has been found to be nearly 1.7 to 4.13 per cent in finger millet. Calcium content of 36 genotypes of finger millet ranged from 162 to 487 mg.

Finger millet is the richest source of calcium and iron. Barbeau (1993) analysed two wild and eight domesticated cultivars of finger millet to determine their proximate composition, calcium, iron and amino acid content. Wide variations were observed in the protein (mean values ranged from 7.5 to 11.7%), calcium (376 to 515 mg/100 g), and iron (3.7 to 6.8 mg/100 g) content of the wild and domesticated cultivars. A wild progenitor of finger millet, *E coracana* subsp. *africana* was significantly higher in protein, calcium and iron than of the domesticated accessions analyzed. The wild species was also found to be higher in lysine and five other essential amino acids.

Shimelis and Mulugeta (2009) studied on three improved finger millet varieties (Tadesse, Padet, Boneya) and six local varieties. The local varieties included were labeled PBR (pawe brown) 1, PBR 2 & PBR 3, PBL (pawe black) 1, PBL 2 & PBL 3, and analyzed for chemical composition. The protein content was higher in boneya (10.50 g/100g) followed by padet (9.86 g/g) and the PBL 1 had lowest content. Moisture was highest in PBL 3 and lowest in boneya. Ash was higher in PBL 2 & 3 and lowest in boneya.

Singh and Srivastava (2006) reported that the iron content of 16 finger millet varieties ranged from 3.61 mg/100g to 5.42 mg%. Zheng Li *et al.* (2006) developed the new foxtail millet germplasm with super early maturity and high iron content (Super early maturation No. 2). The iron content of the millet of super early maturation No. 2 was 54.10 mg/kg which was 62 per cent higher than the average iron content of foxtail millet varieties of China.

Upadhyaya, *et al.* (2011) evaluated finger millet core germplasm for grain nutrients and agronomic traits revealed a substantial genetic variability for grain Fe, Zn, calcium (Ca) and protein contents. The accessions rich in nutrient contents were identified and their agronomic diversity assessed. The accessions rich in Zn content have significantly higher grain yield potential than those rich in Fe and protein content. Grain nutrient specific accessions and those contrasting for nutrient contents were identified for use in strategic research and cultivar development in finger millet.

2.4.3 Little millet

Nambi *et al.* (2012) reported that among the 18 accessions of little millet which were analyzed, maximum proximate content of moisture (MSSRF BD2), protein (MSSRF BD2), carbohydrate (MSSRF BD11), total ash (MSSRF BD9), fiber (MSSRF BD18), fat (MSSRF BD12), and energy (MSSRF BD12), were listed. High mineral content of calcium (MSSRF BD8), iron (MSSRF BD1), magnesium (MSSRF BD14), phosphorus, (MSSRF BD14), potassium (MSSRF BD15) and zinc (MSSRF BD6) were observed.

Nazneen *et al.* (2013) reported that little millet whole grains contain, zinc, copper, manganese and iron contents ranged from 0.24 to 0.50 mg\100g, 0.24 to 0.58 mg\100g, 0.08 to 0.16 mg\100g and 1.28 to 3.05 mg\100g, respectively. The antioxidant activity in whole millet grain ranged from 19.06 to 24.33 per cent in millets.

Roopa *et al.* (2013) found that local little millet had higher moisture (11.43%) and fat (4.97%), while variety Sukshema possessed higher protein (8.96%), carbohydrate (70.47%), starch (59.19%) and zinc (2.03 mg\100g). Functional properties indicated that the water (0.88 g\g) and oil (0.66 g\g) absorption capacity and swelling power (7.73 g\g) were higher and least gelatinization capacity (9.07%) was in Sukshema.

2.4.4 Barnyard millet

The crude fibre content of the barnyard millet was 9.8 g /100g. Barnyard millet is the richest source of fibre. Dietary fibre content was fairly high with soluble and insoluble fractions ranging between 3.5 to 4.6 per cent and 6.1 to 10.5 per cent as reported by Veena *et al.* (2005). Barnyard millet contains 65.5 mg/100g of carbohydrate content. The amount of iron present in the grains of the barnyard millet is 2.9 mg/100g.

Jun Young Kim *et al.* (2011) studied 13 barnyard millet genotypes and reported that IT 153600 exhibited the highest total protein ($14.75 \pm 1.7\%$).

Veena *et al.* (2005) revealed that the amount of calcium present in nine barnyard millet varieties ranged between 1.2 – 1.5 mg 100 g⁻¹, crude fibre in the range of 5.35 to 7.90 per cent and highest fat content with varietal differences ranging between 3.20 to 9.84 per cent.

2.4.5 Pearl millet

Basahy (1996) analyzed the proximate composition, minerals, amino acid profiles, grain protein contents of *Pennisetum typhoides* (Burm.f.) Stapf & Hubbard. The crude protein was 12.3%, fat 5.3% and ash 2.4%. The grains contained similar amounts of phosphorus, calcium and iron as compared to some Indian and African millets. In general, the results indicated that this grain has a good nutritive value.

Mustafa and Magdi (2008) studied the proximate composition, sugars, amino acids profile of pearl millet. Results showed that pearl millet is a good source of carbohydrate (67.26%) and protein (14.52%) and lipid was least (5.77%) but considerably higher lipid content and crude fiber compared to sorghum ($2.17\% \pm 0.03$). Sugars detected in pearl millet seed were glucose (1.2 g/100g), maltose (1.37 g/100g) and fructose (1.2 g/100g). Pearl millet is rich in glutamic acid (23.12%), leucine (10.89%), alanine (8.13%) and aspartic acid (7.78%) but deficient in lysine (2.35%).

Velu *et al.* (2008) conducted an experiment in 52 pearl millet hybrids. He reported that the grain Fe content among hybrids ranged from 52.1 to 87.5 mg/kg in the rainy season, whereas it ranged from 41.7 to 86.2 mg/kg in summer season.

III MATERIAL AND METHODS

A field experiment was conducted to study the genetic diversity and variability within germplasm accessions of foxtail millet for yield and yield contributing characters, and varietal differences for nutritional quality parameters. The details on the material used and techniques adopted for analysis and interpretation are described here under.

3.1 Experimental location

The experiment was carried out at Regional Agricultural Research Station, Vijayapur, University of Agricultural Sciences Dharwad during *Kharif* 2014. The research station is situated in the northern dry zone of Karnataka between 16°49'N latitude, 75°43'E longitude and at an altitude of 593 meters above the mean sea level, with an average annual rainfall of 590.7 mm. The soil type and climatic conditions are well suited for foxtail millet cultivation.

3.2 Experimental material

Experimental material for the present study was comprised of 149 genotypes of foxtail millet. Among these, 126 were obtained from the Project Coordinating unit (small millets), All India Coordinated Small Millet Improvement Project, Indian council of agricultural research, GKVK, UAS, Bangalore, 11 local collections (from Koppal district of Karnataka), and 12 genotypes from ARS, Hanumanamatti, Karnataka. These genotypes are listed in Table 4. The variety PS 4 was used as national check, HMT-100-1 as local check and SiA 326 as state check.

3.3 Methodology

3.3.1 Experimental design and layout

The experimental material was planted during *Kharif* 2014 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. Overview of experimental plot laid out is shown in plate 1.

3.3.2 Cultivation practices

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.

Table 4. Details on 149 germplasm lines of foxtail millet used in the present study

Sl. No.	Genotype	Source of collection
1	GS 5	AICMIP, UAS (B)
2	GS 6	AICMIP, UAS (B)
3	GS 8	AICMIP, UAS (B)
4	GS 12	AICMIP, UAS (B)
5	GS 17	AICMIP, UAS (B)
6	GS 18	AICMIP, UAS (B)
7	GS 21	AICMIP, UAS (B)
8	GS 26	AICMIP, UAS (B)
9	GS 33	AICMIP, UAS (B)
10	GS 35	AICMIP, UAS (B)
11	GS 39	AICMIP, UAS (B)
12	GS 42	AICMIP, UAS (B)
13	GS 45	AICMIP, UAS (B)
14	GS 47	AICMIP, UAS (B)
15	GS 53	AICMIP\, UAS (B)
16	GS 56	AICMIP, UAS (B)
17	GS 60	AICMIP, UAS (B)
18	GS 62	AICMIP, UAS (B)
19	GS 64	AICMIP, UAS (B)
20	GS 71	AICMIP, UAS (B)
21	GS 77	AICMIP, UAS (B)
22	GS 78	AICMIP, UAS (B)
23	GS 91	AICMIP, UAS (B)
24	GS 94	AICMIP, UAS (B)
25	GS 95	AICMIP, UAS (B)
26	GS 96	AICMIP, UAS (B)
27	GS 97	AICMIP, UAS (B)
28	GS 103	AICMIP, UAS (B)
29	GS 105	AICMIP, UAS (B)
30	GS 106	AICMIP, UAS (B)

Table 4. (Contd...)

Sl. No.	Genotype	Source of collection
31	GS 111	AICMIP, UAS (B)
32	GS 121	AICMIP, UAS (B)
33	GS 140	AICMIP, UAS (B)
34	GS 158	AICMIP, UAS (B)
35	GS 200	AICMIP, UAS (B)
36	GS 203	AICMIP, UAS (B)
37	GS 204	AICMIP, UAS (B)
38	GS 205	AICMIP, UAS (B)
39	GS 206	AICMIP, UAS (B)
40	GS 207	AICMIP, UAS (B)
41	GS 208	AICMIP, UAS (B)
42	GS 209	AICMIP, UAS (B)
43	GS 210	AICMIP, UAS (B)
44	GS 211	AICMIP, UAS (B)
45	GS 212	AICMIP, UAS (B)
46	GS 213	AICMIP, UAS (B)
47	GS 214	AICMIP, UAS (B)
48	GS 215	AICMIP, UAS (B)
49	GS 216	AICMIP, UAS (B)
50	GS 218	AICMIP, UAS (B)
51	GS 219	AICMIP, UAS (B)
52	GS 220	AICMIP, UAS (B)
53	GS 221	AICMIP, UAS (B)
54	GS 222	AICMIP, UAS (B)
55	GS 242	AICMIP, UAS (B)
56	GS 243	AICMIP, UAS (B)
57	GS 246	AICMIP, UAS (B)
58	GS 248	AICMIP, UAS (B)
59	GS 250	AICMIP, UAS (B)
60	GS 256	AICMIP, UAS (B)

Table 4. (Contd...)

Sl. No.	Genotype	Source of collection
61	GS 260	AICMIP, UAS (B)
62	GS 264	AICMIP, UAS (B)
63	GS 266	AICMIP, UAS (B)
64	GS 271	AICMIP, UAS (B)
65	GS 276	AICMIP, UAS (B)
66	GS 280	AICMIP, UAS (B)
67	GS 282	AICMIP, UAS (B)
68	GS 285	AICMIP, UAS (B)
69	GS 289	AICMIP, UAS (B)
70	GS 293	AICMIP, UAS (B)
71	GS 301	AICMIP, UAS (B)
72	GS 310	AICMIP, UAS (B)
73	GS 316	AICMIP, UAS (B)
74	GS 335	AICMIP, UAS (B)
75	GS 336	AICMIP, UAS (B)
76	GS 337	AICMIP, UAS (B)
77	GS 308	AICMIP, UAS (B)
78	GS 338	AICMIP, UAS (B)
79	GS 343	AICMIP, UAS (B)
80	GS 344	AICMIP, UAS (B)
81	GS 352	AICMIP, UAS (B)
82	GS 362	AICMIP, UAS (B)
83	GS 363	AICMIP, UAS (B)
84	GS 372	AICMIP, UAS (B)
85	GS 377	AICMIP, UAS (B)
86	GS 378	AICMIP, UAS (B)
87	GS 379	AICMIP, UAS (B)
88	GS 401	AICMIP, UAS (B)
89	GS 403	AICMIP, UAS (B)
90	GS 415	AICMIP, UAS (B)

Table 4. (Contd...)

Sl. No.	Genotype	Source of collection
91	GS 426	AICMIP, UAS (B)
92	GS 433	AICMIP, UAS (B)
93	GS 449	AICMIP, UAS (B)
94	GS 453	AICMIP, UAS (B)
95	GS 461	AICMIP, UAS (B)
96	GS 472	AICMIP, UAS (B)
97	GS 478	AICMIP, UAS (B)
98	GS 494	AICMIP, UAS (B)
99	GS 510	AICMIP, UAS (B)
100	GS 511	AICMIP, UAS (B)
101	SiA3156	AICMIP, UAS (B)
102	SiA3088 (S.Nandi)	AICMIP, UAS (B)
103	SiA 3085	AICMIP, UAS (B)
104	Co7	AICMIP, UAS (B)
105	SR51 (P.Kangini)	AICMIP, UAS (B)
106	SiA 2644 (Srilakshmi)	AICMIP, UAS (B)
107	SR16 (Meera)	AICMIP, UAS (B)
108	PS 4	AICMIP, UAS (B)
109	TNAU 186	AICMIP, UAS (B)
110	SR11 (Gavari)	AICMIP, UAS (B)
111	SiA 2622 (Na.Raya)	AICMIP, UAS (B)
112	SiA 2593 (Kr.d.Raya)	AICMIP, UAS (B)
113	Lepakshi	AICMIP, UAS (B)
114	K 3	AICMIP, UAS (B)
115	SiA 326 (Prasad)	AICMIP, UAS (B)
116	Co 5	AICMIP, UAS (B)
117	Chitra	AICMIP, UAS (B)
118	K2	AICMIP, UAS (B)
119	Co4	AICMIP, UAS (B)
120	RS118	AICMIP, UAS (B)

Table 4. (Contd...)

Sl. No.	Genotype	Source of collection
121	K221-1	AICMIP, UAS (B)
122	Arjuna	AICMIP, UAS (B)
123	H1	AICMIP, UAS (B)
124	H2	AICMIP, UAS (B)
125	Co1	AICMIP, UAS (B)
126	Co2	AICMIP, UAS (B)
127	FMGPM-1	Koppala (D) Local collection
128	FMGPM-2	Koppala (D) Local collection
129	FMGPM-3	Koppala (D) Local collection
130	FMGPM-4	Koppala (D) Local collection
131	FMGPM-5	Koppala (D) Local collection
132	FMGPM-6	Koppala (D) Local collection
133	FMGPM-7	Koppala (D) Local collection
134	FMGPM-8	Koppala (D) Local collection
135	FMGPM-9	Koppala (D) Local collection
136	FMGPM-10	Koppala (D) Local collection
137	FMGPM-11	Koppala (D) Local collection
138	MLT-12-1 [Co 6 x GS 1919 (4-5)]	ARS, Hanamanamatti
139	MLT-12-2 [Co 5 x PS 4 (35-1)]	ARS, Hanamanamatti
140	MLT-12-3 [Co 6 x GS 145 (55-3)]	ARS, Hanamanamatti
141	MLT-12-4 [Co 5 x PS 4 (2-3)]	ARS, Hanamanamatti
142	MLT-12-5 [Co 5 x GPUS 30 (109-3)]	ARS, Hanamanamatti

Table 4. (Contd...)

143	MLT-12-6 [Co 5 x GS 199 (2-5)]	ARS, Hanamanamatti
144	MLT-12-7 [Co 5 x PS 4 (2-5)]	ARS, Hanamanamatti
145	MLT-12-8 [GPUS 26 x Co 7 (5-6)]	ARS, Hanamanamatti
146	MLT-12-9 [GPUS 26 x Co 7 (5-3)]	ARS, Hanamanamatti
147	MLT-12-10 [GPUS 26 x Co 7 (77-3)]	ARS, Hanamanamatti
148	MLT-12-11 (HMT-100-1)	ARS, Hanamanamatti
149	MLT-12-12 (SiA 326)	ARS, Hanamanamatti



Plate 1. General view of experimental plot of foxtail millet crop at maturity

3.3.3 Climatic conditions

The monthly meteorological data of 2014-15 obtained from Agro-meteorology department of Regional Agricultural Research Station, Vijayapur, University of Agricultural Sciences, Dharwad, with regard to temperature, relative humidity, rainfall and number of rainy days during the course of investigations is presented in Appendix I.

3.3.4 Field Observations recorded

The observations were recorded on both qualitative and quantitative characters. The list of parameters and procedures followed to record the observations in 149 genotypes on each trait are summarized below. From each entry in each replication, three randomly selected plants were tagged for recording observations on all the quantitative characters. Mean of three plants for each of quantitatively measured characters was worked out and used for statistical analysis.

3.3.4.1 Productivity traits

Observations on the following yield and yield component characters were recorded at appropriate stages of plant growth.

3.3.4.1.1 Days to panicle emergence

The observation on days to panicle emergence was recorded as number of days taken from sowing to the complete panicle emergence from the boot leaf.

3.3.4.1.2 Days to 50% flowering

The observation on days to 50% flowering was recorded as number of days taken from sowing to the day on which fifty percent of the plants initiated anthesis in each entry.

3.3.4.1.3 Days to maturity

The number of days taken from sowing to the day on which the grains matured and ready for harvest was recorded as days to maturity.

3.3.4.1.4 Plant height (cm)

Height of the plant from ground level to the tip of the matured panicle was measured and expressed in centimeters.

3.3.4.1.5 Total number of tillers per meter row length

Total numbers of tillers produced were counted in a meter row length in each entry.

3.3.4.1.6 Number of productive tillers per meter row length

Number of productive tillers was counted in a meter row length in each entry.

3.3.4.1.7 Number of productive tillers per plant

The number of productive tillers was counted in each of the three randomly selected plants and average is calculated and recorded.

3.3.4.1.8 Panicle length (cm)

The length of the panicle in each of the three randomly selected plants was measured from base to the tip of the panicle and expressed in centimeters.

3.3.4.1.9 Panicle girth (mm)

The breadth was recorded at the point of maximum width of the panicle of the three randomly selected plants was measured and expressed in centimeters.

3.3.4.1.10 Peduncle length (cm)

The length of the peduncle was measured from base of the boot leaf of the three randomly selected plants was measured and expressed in centimeters.

3.3.4.1.11 Area of standard leaf (cm²)

Length and width of the 3rd leaf of the three randomly selected plants was measured from top of the plant and leaf area is calculated and expressed in centimeter square.

3.3.4.1.12 Stem thickness (mm)

Stem thickness of the plant of the three randomly selected plants was measured at the middle of the plant stand from the ground and expressed in millimeters.

3.3.4.1.13 SPAD reading at 50% flowering

SPAD reading at 50% flowering observation was recorded from the three randomly selected plants. This observation was measured at the third leaf from top of the plant at the time of 50% flowering. SPAD reading was taken at three spots, top, middle and lower portion of the leaf and the average of three spots reading were recorded.

3.3.4.1.14 SPAD reading at maturity

SPAD reading at maturity observation was recorded from the three randomly selected plants. This observation was measured at the third leaf from top of the plant at the time of

maturity. SPAD reading was taken at three spots, top, middle and lower portion of the leaf and the average of three spots reading were recorded.

3.3.4.1.15 Grain yield per plant (g)

Grains harvested from each of the three randomly selected plants of each entry were threshed, dried, cleaned and weighed. The grain yield per plant is expressed in grams.

3.3.4.1.16 Grain yield per hectare (kg)

Grains harvested from each plot is threshed, dried, cleaned and weighed. The grain weight was recorded per plot and later converted and expressed in kg/hectare.

3.3.4.1.17 Straw weight per plant (g)

The weight of straw of each of the randomly selected plants in each entry was recorded after sun drying to a constant weight. Then the mean straw weight of the 3 plants was computed and expressed in grams.

3.3.4.1.18 Straw weight per hectare (kg)

Straw weight in gross plot of each entry was recorded after sun drying to a constant weight and expressed in kg/hectare.

3.3.4.1.19 Test weight (g)

The weight of 1000 seeds drawn from each entry was recorded and expressed in grams.

3.3.4.2 Morphological traits

Observations on following morphological traits were recorded.

3.3.4.2.1 Anther colour

Scored as; 0. Purple to deep purple, 1. Orange and white orange mixture.

3.3.4.2.2 Awn length

Scored as; 1. Long, 2. Medium, 3. Short.

3.3.4.2.3 Awn colour

Scored as; 0. Coloured, 1. Normal.

3.3.4.2.4 Panicle compactness

Scored as; 1. Compact, 2. Medium, 3. Loose.

3.3.4.2.5 Stem and leaf pigmentation

Scored as; 0.Green, 1. Pigmented.

3.3.4.2.6 Grain colour

Scored as; 1. Black, 2. Red, 3. Yellow, 4. White.

3.3.4.3 Grain nutrients content

A total of 25 genotypes from the list of 149 germplasm accessions were used for estimation of grain nutrients content viz., protein content, and grain micronutrients (calcium, iron and zinc) content. Total protein was estimated in selected genotypes using Micro Kjeldhal Distillation Method (A.O.A.C, 1070). About 3-5 gram of dry seed was randomly drawn from each of the genotype were powdered. One gram of powder was accurately weighed using electronic balance and subjected to digestion. Total nitrogen in the seed obtained after titration was multiplied with the factor 6.25 to arrive at protein content and expressed in percentage. Grain micronutrients (calcium, iron and zinc) were estimated using Atomic Absorption Spectrophotometer (AAS) using mineral solution which was made using diacid mixture.

3.4 Statistical analysis

The data on individual mean for each trait was processed with the help of various standard statistical procedures as mentioned below.

3.4.1 Analysis of variance (ANOVA)

The data on mean values for all the characters were analyzed for the variance following randomized block design as per the outline presented below.

Sl. No.	Source of variation	d.f.	MSS	Cal F
1	Replication	(r -1)	M1	
2	Genotypes	(g -1)	M2	$e^2 + g^2$
3	Error	(r -1)(g -1)	M3	e^2
	Total	rg-1	M1 + M2 + M3	

Where,

r = Number of replications

g = Number of total genotypes

The standard error was calculated as

$$\text{S.Em.} = \sqrt{\frac{\text{EMSS}}{r}}$$

The significance of the differences among all the genotypes was tested by 'F' test using the error variance. Further, standard error of means ($\text{SEm}_{\pm}$), critical difference (CD) and co-efficient of variation (CV) were worked out using appropriate formulae to facilitate the comparison of means of genotypes in ANOVA table. After testing for significance of the differences among the means of different genotypes for each character, further computations were done as detailed below.

3.4.2 Genetic diversity analysis

3.4.2.1 Multivariate analysis using D^2 statistics

Mahalanobis (1936) D^2 - statistic was used for assessing of the genetic divergence between genotypes.

The generalized distance between any two populations is defined as,

$$D^2 = Y_{ij}\beta_i\beta_j$$

Where,

Y_{ij} = The reciprocal matrix to the common dispersion matrix

β_i = The difference between the two mean values of the two populations for i^{th} character ($\mu_{i1} - \mu_{i2}$)

β_j = The difference between the mean values of the two populations for the j^{th} character ($\mu_{j1} - \mu_{j2}$)

μ = Vector mean values for all the characters

The formula for the estimation of distance, D^2 from samples

$$D^2 p = d_1 (S-1) d$$

Where,

$D^2 p$ = Square of the distance considering P values.

$$d_1 = (X_{i1} - X_{i2})$$

X = Vector for mean values of all the characters

S - 1 = inverse of variance covariance matrix

Formula for computation of D values, which requires inversion of the matrix, becomes complicated especially when the numbers of variables under consideration are large.

Therefore, the original correlated un-standardized variables (X_i) were transformed to standardized uncorrelated variables (Y_i) so that the computation of D^2 values reduce to simple summation of squares of the differences between values of transformed variables of the two population *i.e.*, $D^2 i$.

From the newly transformed uncorrelated variables, the square of the distance was computed using the following formula.

$$D^2 = (Y_{i1} - Y_{i2})^2$$

Where,

Y_{i1} = Vector of transformed mean values, for first genotype

Y_{i2} = vector of transformed mean values, for second genotype

The square root of the D^2 values gives the generalized distance (D) between the two populations. The D^2 values were arranged in a matrix form. The significance of D^2 values between any populations was tested using the following formula.

$$F = \frac{(n_1 + n_2 - p - 1)}{(n_1 + n_2 - 2) P} \times \frac{(n_1 n_2) D^2}{(n_1 + n_2)}$$

This computed F values was compared with table F value at 5 per cent and 1 percent levels of significance with P (number of characters) and $(n_1 + n_2 - p - 1)$ degrees of freedom.

3.4.2.2 Clustering of the D^2 values

All the $n(n-1)/2$ D^2 values were clustered as follows: The two genotypes having the lowest D^2 value between them were selected and a third genotype which had on an average the smallest D^2 value from the first two, was added. Similarly, fourth was chosen which showed, the smallest average D^2 value from the first three. If at any stage increase in D^2 values because of the addition of a new genotype exceeded the average of those already included, then that genotype was taken out. The genotypes that are included already in that group were considered as the first cluster. The procedure is repeated for other genotypes omitting those that are already included in the former cluster.

The average distance of all the genotypes within the cluster (intracluster distance) and average distance between any two clusters (intercluster distance) were calculated.

3.4.2.3 Contribution of individual characters towards genetic divergence

The character contribution towards genetic divergence was computed using method given by Singh and Chaudhary (1977). In all the combinations, each character is ranked on the basis of $d_i = y_i^j - y_i^k$ values.

Where,

d_i = mean deviation

y_i^j = mean value of the j^{th} genotype for the i^{th} character and

y_i^k = mean value of the k^{th} genotype for the i^{th} character.

Rank '1' is given to the highest mean difference and rank p is given to the lowest mean difference

Where,

P is the total number of characters.

Finally, another Table giving information on, number of times that each character appeared in the first rank is prepared and per cent contribution of characters towards divergence was calculated.

3.4.3 Identification of superior genotypes

The working collections were assessed for identification of superior genotypes and compared with the different check varieties included in the study. The following CD values were used for the comparison.

Where CD is calculated using these $SEd \times t$ at 5 % or 1 % level

SEd (between means of a check and test variety) = $EMS (1+1/b+1/c+1/bc)$

3.4.4 Estimation of Genetic parameters

The different genetic parameters should be estimated in order to evaluate and assess the genetic variability among the germplasm accessions of Foxtail millet by adopting following formulae.

3.4.4.1 Estimation of variance components

Genotypic and phenotypic components of variance were estimated with the help of following formulae.

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{MSS (treatment)} - \text{MSS (error)}}{\text{Number of replications}}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \text{MSS (error)}$$

3.4.4.2 Co-efficient of variation:

Both genotypic and phenotypic coefficients were computed for each character as per the method suggested by Burton and De Vane (1953).

$$\text{Genotypic coefficient of variability (GCV)} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variability (PCV)} = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

σ_g = Genotypic standard deviation

σ_p = Phenotypic standard deviation

$\bar{X}$ = General mean of character

GCV and PCV values were categorized as low, moderate and high values as suggested by Sivasubramanian and Menon (1973), which is as follows:

- 1-10 per cent : Low
 10.1-20 per cent : Moderate
 20.1 per cent and above : High

3.4.4.3 Heritability (h^2)

Heritability in broad sense was computed as the ratio of the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed in terms of percentage.

$$\text{Heritability } (h^2) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The heritability percentage was low, moderate and high as given by Robinson *et al.* (1949).

- 0-30 per cent : Low
 30.1-60 per cent : Moderate
 60.1 per cent and above: High

3.4.4.4 Genetic advance (GA)

Genetic advance was estimated by using the formula given Johnson *et al.* (1955).

$$GA = h^2 k \sigma_p$$

Where,

h^2 = Heritability in broad sense

k = Selection differential which is equal to 2.06 at 5 % intensity of selection (Lush, 1940)

σ_p = Phenotypic standard deviation

3.4.4.5 Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

$\bar{X}$ = General mean of the character

Genetic advance as per cent mean was categorized as low, moderate and high as given by Johnson *et al.* (1955).

It is as follows,

0-10	Per cent	: Low
10.1-20	Per cent	: Moderate
20.1	per cent and above	: High

3.4.5 Correlation analysis

The correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components.

Phenotypic correlations were computed by using the formula given by Weber and Morthy (1952).

$$r = \frac{\text{Cov}(xy)_p}{\sigma_{p_x} \times \sigma_{p_y}} \times 100$$

Where,

r = Correlation coefficient

Cov (xy) = Covariance between the characters 'x' and 'y'

σ_{p_x} and σ_{p_y} = Phenotypic variance of the character 'x' and 'y' respectively

Correlation coefficients were compared against 'r' values given in Fisher and Yates (1963) table at (n-2) degrees of freedom at the probability levels of 0.05 and 0.01 to test their significance.

IV EXPERIMENTAL RESULTS

The present study was conducted at the Regional Agricultural Research Station, Vijayapur during the *Kharif* season of 2014, to assess genetic diversity and variability, and degree of association using 149 genotypes of Foxtail millet. The observations were recorded on days to panicle emergence, days to 50 percent flowering, days to maturity, plant height (cm), panicle length (cm), panicle girth (cm), 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 (cm²), 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. A total of 25 selected genotypes were screened for grain nutrient contents (protein, iron, zinc & calcium).

The data recorded were subjected for variability analysis, genetic diversity analysis using Mahalanobis D² statistic and phenotypic correlation analysis. The data were analyzed using WINDOSTAT (version 9.2). The results obtained are presented under the following headings.

4.1 Analysis of variance

4.2 Genetic diversity

4.3 Genetic variability parameters

4.4 Correlation coefficients

4.5 Variability for morphological traits

4.6 Screening genotypes for grain nutrients content

4.1 ANALYSIS OF VARIANCE

The analysis of variance for yield and yield attributing characters of 149 accessions of foxtail millet revealed that mean sum of squares were highly significant for all the characters studied indicating the presence of sufficient amount of variability for days to panicle emergence, days to 50 percent flowering, days to maturity, plant height, panicle length, panicle girth, peduncle length, 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, stem thickness, SPAD reading at flowering, SPAD

Table 5. Mean sum of squares for yield and its component traits in 149 germplasm accessions of foxtail millet evaluated at Vijayapur during *kharif* 2014

Sl. No.	Character	Replication	Treatment	S.Em±	CV (%)	CD@5%	CD@1%
1	Days to panicle emergence	3.22	17.74**	1.94	4.91	5.43	7.17
2	Days to 50% flowering	4.11	15.75**	1.35	3.17	3.78	5.00
3	Days to maturity	1.78	16.33**	1.48	2.32	4.14	5.46
4	Plant height (cm)	10.53	400.95**	7.27	7.57	20.32	26.84
5	Panicle length(cm)	0.86	8.44**	1.48	13.34	4.14	5.46
6	Panicle girth (mm)	1.67	4.20**	0.94	10.72	2.63	3.47
7	Peduncle length (cm)	17.17	10.46**	1.75	16.92	4.88	6.44
8	No of tillers/meter row length	180.62	237.90**	4.83	16.06	13.50	17.83
9	Number of productive tillers/meter row length	310.12	237.09**	5.95	20.54	16.62	21.95
10	Number of productive tillers/plant	6.53	10.48**	1.18	24.42	3.30	4.36
11	Area of standard leaf (cm ²)	1116.71	178.99*	6.81	15.31	19.02	25.12
12	Stem thickness (cm)	0.97	9.11**	1.54	16.80	4.31	5.69
13	SPAD at 50% flowering	33.37	24.18**	2.81	9.87	7.85	10.37
14	SPAD at maturity	59.19	29.14**	3.11	17.21	8.70	11.48
15	Grain yield/plant (g)	166.10	113.61**	5.50	24.90	15.38	20.31
16	Grain yield/hectare (kg)	165628.80	591672.65**	279.84	25.40	782.05	1032.68
17	Fodder yield/plant (g)	1168.12	2803.17**	22.91	24.90	64.02	84.54
18	Fodder yield/hectare (kg)	901.08	1359655.06**	746.46	17.68	1519.74	2006.80
19	1000 seed weight (g)	0.02	0.18**	0.17	6.66	0.47	0.62

*Significant at 5% probability

** Significant at 1% probability

reading at maturity, grain yield per plant, fodder yield per plant, grain yield per hectare, fodder yield per hectare and 1000 grain weight. The results obtained are presented in Table 5.

4.2 GENETIC DIVERSITY

Genetic divergence in the population, especially in respect of the character in which improvement is sought for, is a pre requisite for successful plant breeding work. Genetic divergence along with genetic variability is of greatest interest to the breeder as they play vital role in distinguishing genotypic response as groups in framing a successful breeding programme. 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.

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 pertaining to genetic diversity is presented below.

4.2.1 Group constellations

A method suggested by Tocher (Rao, 1952) was used to group accessions into different clusters based on D^2 values. The 149 genotypes were grouped into 15 clusters. The distribution pattern into various clusters is given in Table 6 and depicted in Fig. 1. Among the 15 clusters, cluster I was the largest with 134 accessions, followed by cluster VIII comprising 2 accessions. Remaining clusters, viz., cluster II, III, IV, V, VI, VII, IX, X, XI, XII, XIII, XIV and XV were solitary in nature comprising of one genotype each.

Cluster I was having highest number of genotypes i.e. 134 genotypes which includes 91 germplasm lines (GS series), 25 varieties, 10 locally collected foxtail millet germplasm and 8 MLT lines. Cluster VIII was having 2 genotypes viz., Arjuna, FMGPM-5. While, remaining genotypes grouped in 13 solitary clusters viz., MLT-12-3 (II), GS 27 (III), SR 11 (IV), MLT-12-9 (V), GS 213 (VI), MLT-12-10 (VII), GS 510 (IX), MLT-12-11 [HMT-100-1(X)], GS 17 (XI), MLT-12-8 MLT-12-8 (XII), GS 511 GS 511 (XIII), GS 33 (XIV) and GS 338 (XV).

Table 6. Distribution of foxtail millet germplasm accessions into different clusters based on cluster analysis

Sl. 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

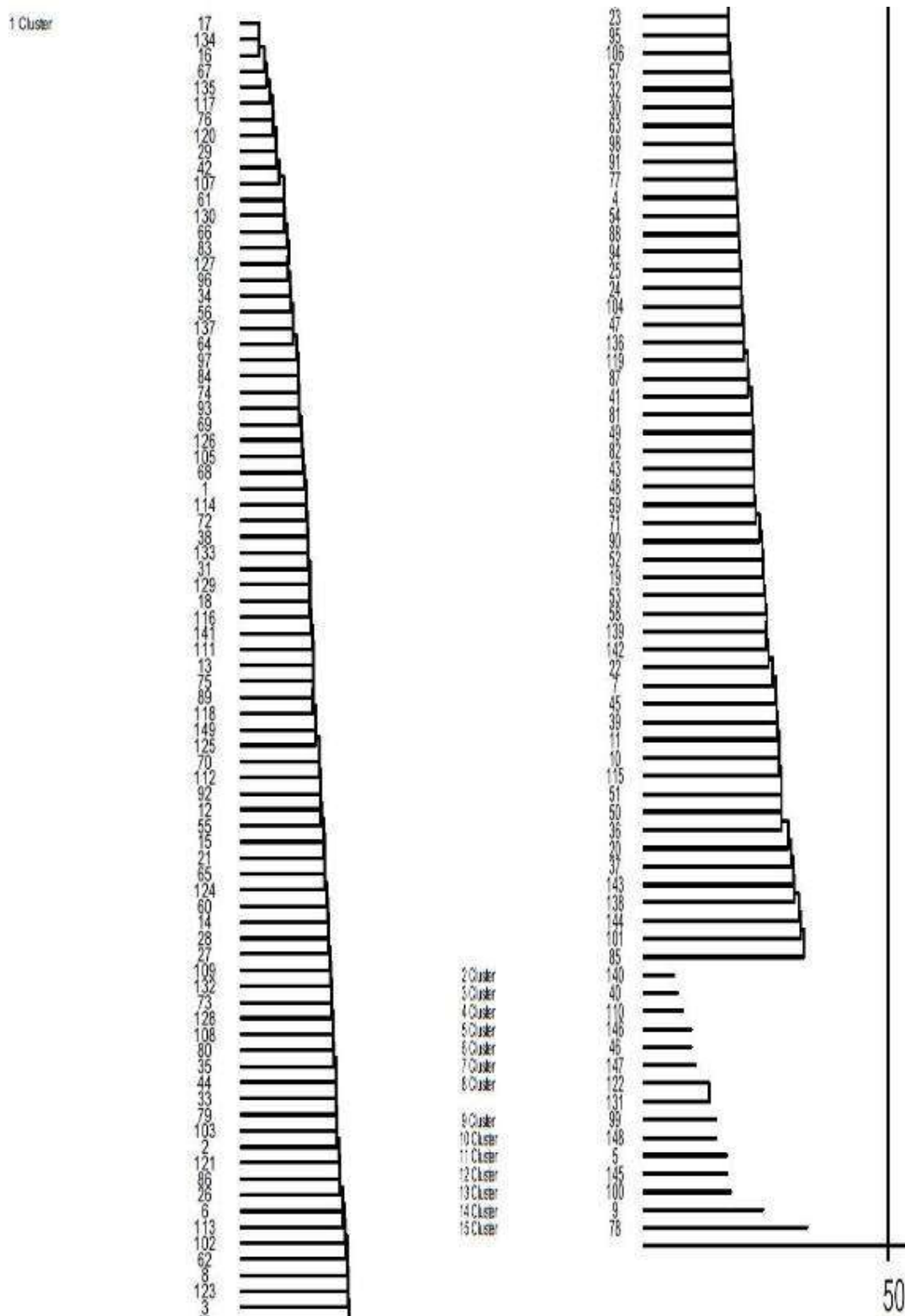


Fig 1: Diagrammatic representation of 15 clusters consisting of 149 foxtail millet lines.

4.2.2 Percent contribution of characters towards divergence

Out of 19 characters studied in germplasm accessions of foxtail millet, 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%), fodder yield/plant (4.41%), grain yield/plant (4.41%), panicle girth (3.58%), days to panicle emergence (2.88%), SPAD at maturity (2.58%), area of standard leaf (2.49%), peduncle girth (2.37%), panicle length (2.31%), stem thickness (2.27%), fodder yield/hectare (2.26%) fodder yield/hectare (2.26%), SPAD at 50% flowering (1.97%) and number of productive tillers/meter row length (1.13%). The results are presented in Table 7 and Fig. 2.

4.2.3 Intra and inter cluster distances

The average D^2 values of intra and inter cluster distances are given in Table 8. Among 15 clusters, maximum intra cluster distance among the genotypes was recorded by cluster I (20.45) followed by cluster VIII (13.51). Since there is one genotype in each of clusters II, III, IV, V, VI, VII, IX, X, XI, XII, XIII, XIV, XV, the intra cluster divergence was found to be zero.

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 (138.62) was noticed between the clusters IX and XIV followed by between cluster VI & XIV (132.8), between III & XIV (126.07) and III & XV (118.71). The lowest inter cluster distance was noticed between clusters II and V (12.08) followed by between clusters III and VI (13.49). Cluster IX and XIV were most diverse clusters intercluster distance of 138.62. Cluster XV was the most distant cluster with as many cluster showed maximum inter cluster distance with it.

Cluster I (with intracluster distance of 20.45) which comprised of 134 accessions (GS 5,GS 6, GS 8, GS 12, MLT-12-12 (SiA 326), 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

Table 7. Per cent contribution of characters towards total divergence in 149 foxtail millet germplasm accessions

Sl. No.	Character	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

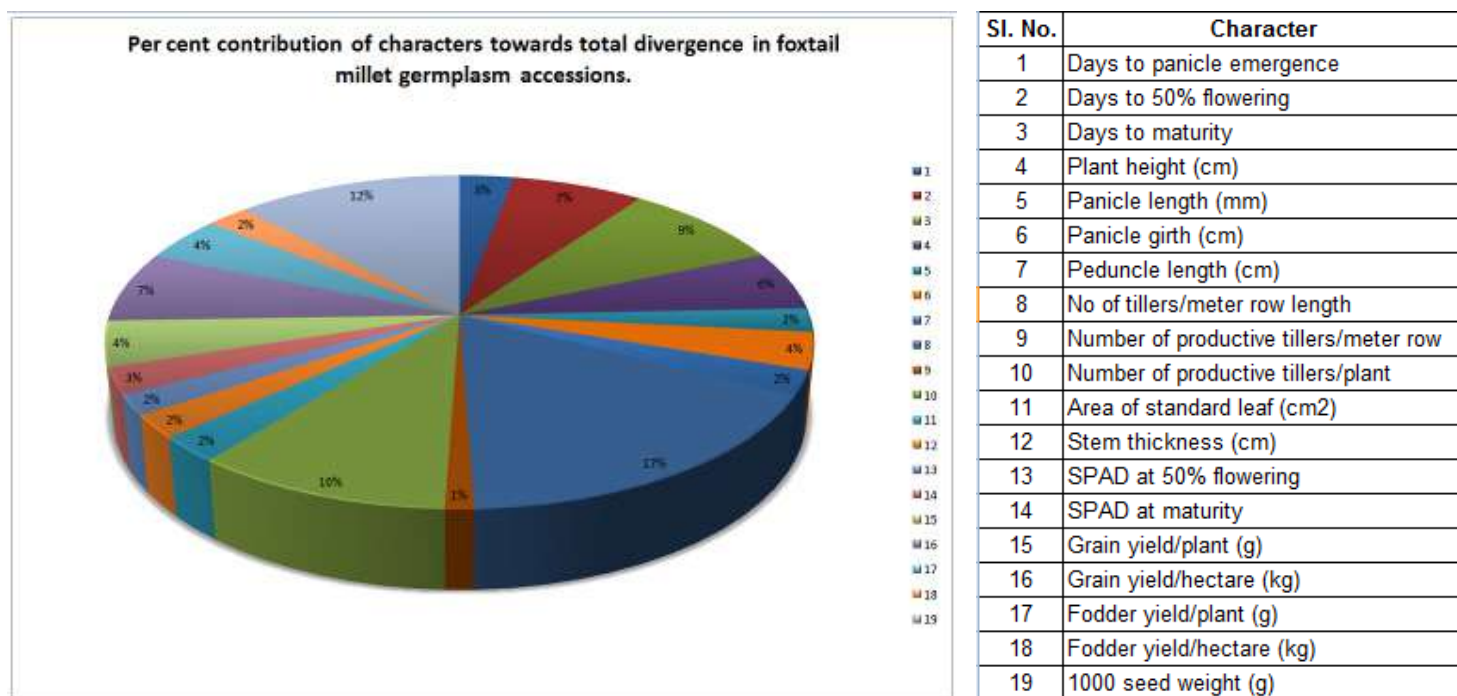


Fig. 2 Per cent contribution of various characters towards total divergence in foxtail millet germplasm accessions.

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) was the largest cluster. The cluster was diverse from all the clusters XV, XIV, VIII, XIII, XII, III, II, XI, IV, VI, V, IX, VII and X with D^2 values of 63.03, 64.68, 55.63, 45.63, 46.56, 40.04, 38.9, 37.99, 34.84, 34.14, 33.89, 37.93, 33.74 and 33.57, respectively.

Cluster II, a solitary cluster having the genotype MLT-12-3 was closely related to cluster V, VII and X with D^2 values of 12.08, 19.79 and 23.78, respectively. Whereas, it was diverse from other clusters like IX, XV, VI, III, IV, XIV, XII, XIII, VIII, II and XI with D^2 values of 80.65, 79.38, 75.13, 66.07, 61.45, 56.45, 50.77, 49.97, 37.07, 38.9 and 33.28, respectively.

Cluster III, a solitary cluster having the genotype GS 207 was closely related to VI with D^2 value 13.49. Whereas, cluster III was diverse from XIV, XV, XIII, IV, XI, XII, VII, II, X, V and IX with D^2 values of 126.07, 118.71, 92.44, 87.64, 82.26, 80.02, 70.4, 66.07, 58.53, 54.8 and 33.22, respectively.

Cluster IV, a solitary cluster having the genotype SR 11 was closely related to XII with D^2 value 29.88. Whereas, cluster IV was diverse from IX, III, VIII, VI, II, XV, V, XI, X, XIII, VII, XIV and I with D^2 values of 88.43, 87.64, 72.06, 77.93, 61.45, 53.03, 51.34, 49.84, 40.51, 38.08, 37.19, 36.69 and 34.84, respectively.

Cluster V, a solitary cluster having the genotype MLT-12-9 was closely related to II, X and VII with D^2 values 12.08, 19.87 and 25.4, respectively. Whereas, cluster V was diverse from XV, IX, XIII, VI, III, XIV, IV, VIII, XII, XI and I with D^2 values of 81.31, 72.88, 67.61, 63.42, 54.8, 53.73, 51.34, 46.05, 43.91, 38.13 and 33.89, respectively.

Cluster VI, a solitary cluster having the genotype GS 213 was closely related to III and IX with D^2 values of 13.49 and 16.0, respectively. Whereas, cluster VI was diverse from XIV, XV, VIII, XIII, IV, XII, VII, II, XI, V, X, and I with D^2 values of 132.8, 98.85, 86.11, 83.35, 77.93, 76.12, 75.17, 68.98, 63.42, 62.0 and 34.14, respectively.

Cluster VII, a solitary cluster having the genotype MLT-12-10 was closely related to clusters II, V, XII with D^2 values of 19.79, 25.4 and 25.47, respectively. Whereas,

cluster VII was diverse from clusters IX, VI, III, XV, VIII, XI, XIV, XIII, IV, I and X with D^2 values of 72.67, 72.44, 70.4, 65.28, 62.81, 55.73, 52.75, 43.53, 37.19, 33.74 and 30.21, respectively.

Cluster VIII (with intra cluster distance of 13.5) having two genotypes (Arjuna and FMGPM-5) was diverse from clusters XV, IX, VI, XII, XIII, XIV, III, IV, VII, I, XI, V, X and II with D^2 values of 89.97, 86.21, 86.11, 83.31, 77.06, 73.13, 72.43, 72.06, 62.81, 55.63, 52.25, 46.05, 44.17 and 37.07, respectively.

Cluster IX, a solitary cluster having the genotype GS 510 was closely related to cluster VI with D^2 value of 16.0. Whereas, cluster IX was diverse from clusters XIV, XII, XV, IV, VIII, XIII, II, X, V, VII, XI, I and III with D^2 values of 138.62, 97.63, 95.06, 88.43, 86.21, 84.58, 80.65, 78.03, 72.88, 72.67, 68.21, 37.93 and 33.22, respectively.

Cluster X, a solitary cluster having the genotype MLT-12-11(HMT-100-1) was closely related to clusters V and II with D^2 values of 19.87 and 23.78, respectively. Whereas, cluster X was diverse from clusters IX, XV, XIV, VI, III, XI, VIII, XIII, IV, XII, I and VII with D^2 values of 78.03, 74.93, 62.12, 62.0, 58.53, 45.84, 44.17, 43.25, 40.51, 33.89, 33.57 and 30.21, respectively.

Cluster XI, a solitary cluster having the genotype GS 17 was diverse from clusters III, VI, IX, XV, XII, VII, VIII, XIV, IV, X, XIII, V, I and II with D^2 values of 82.26, 68.98, 68.21, 66.15, 64.74, 55.73, 54.66, 52.25, 49.84, 45.84, 39.1, 38.13, 37.99 and 33.28, respectively.

Cluster XII, a solitary cluster having the genotype MLT-12-8 was closely related to clusters VII and IV with D^2 values 25.47 and 29.88. This cluster was diverse from clusters IX, XV, VIII, III, VI, XIV, XI, XIII, II, I, V and X with D^2 values of 97.63, 84.28, 83.31, 80.02, 76.12, 69.24, 64.74, 52.41, 50.77, 46.56, 43.91 and 33.89, respectively.

Cluster XIII, a solitary cluster having the genotype GS 511 was diverse from clusters III, IX, VI, VIII, XIV, V, XV, XII, II, I, VII, X, XI and IV with D^2 values of 92.44, 84.58, 83.35, 77.06, 67.95, 67.61, 58.29, 52.41, 49.97, 45.63, 43.53, 43.25, 39.1 and 38.08, respectively.

Cluster XIV, a solitary cluster having the genotype GS 35 was diverse from clusters IX, VI, III, XV, VIII, XII, XIII, I, X, V, II, XI, VII and IV with D^2 values of 138.62, 132.8, 126.07, 77.94, 73.13, 69.24, 67.95, 64.68, 62.12, 56.73, 56.45, 54.66, 52.75 and 36.69, respectively.

Table 8. Average intra and inter cluster distances among 149 germplasm accessions of foxtail millet for yield and yield related traits

[illegible]

Cluster XV, a solitary cluster having the genotype GS 338 was diverse from clusters III, VI, IX, VIII, XII, V, II, XIV, XI, X, VII, I, XIII and IV with D^2 values of 118.71, 98.85, 95.06, 89.97, 84.28, 81.31, 79.38, 77.94, 74.93, 66.15, 65.28, 63.03, 58.29 and 53.03, respectively.

4.2.4 Cluster mean analysis

The cluster means in respect of 19 characters studied in 149 foxtail millet genotypes and overall character wise score across the 15 clusters are presented in Table 9. Highest ranking was recorded by cluster IV (rank 1) followed by cluster VI (rank 2), cluster I (rank 3), cluster IX (rank 4) and cluster XI (rank 5). Least ranking was recorded by cluster II (rank 15) followed by cluster VII (rank 14), cluster V (rank 13), cluster X (rank 12) and cluster XIV (rank 11).

The results indicated substantial variation present among clusters grouped according to D^2 analysis. Based on the range of means, it was possible to know the characters influencing divergence. In the accessions of the present study, low days to panicle emergence was occurred in the clusters XIV and IV (below 50 days) and cluster IX had highest days to panicle emergence (above 60 days), while remaining clusters had moderate days to panicle emergence indicating the wide range of genetic diversity available in the accessions. Minimum number of days to panicle emergence was observed in cluster XIV (42.00) followed by greater number of days to panicle emergence was observed in IX cluster (61.00).

For days to 50% flowering trait, low days to 50% flowering was occurred in the clusters XIV and IV (below 56 days) and cluster IX had highest days to 50% flowering (above 60 days). The mean values of the remaining clusters were intermediate. Minimum number of days to 50% flowering was observed in cluster XIV (48.00) followed by greater number of 50% flowering was observed in IX cluster (64.50).

For days to maturity trait, Cluster XI (78 days) had the early mature genotype, whereas, cluster VII (95.5 days) had the late maturing genotype. The clusters having genotypes maturing between 85-90 days were V, II, IX, VIII and VI. Remaining clusters were with mean values between above 90 days.

Highest mean for plant height (cm) was showed by cluster VI (156.50 cm) whereas lowest plant height was observed in cluster VIII (57.25 cm). While, other clusters were moderate in plant height. Thus, indicating a wide range of diversity existed for these traits.

Lowest panicle length (cm) was noticed in the cluster II (10.58 cm) followed by Cluster XIII whereas highest panicle length was observed in cluster XII (23.50 cm).

Cluster V had the genotype with lowest panicle girth (8.83 mm) and highest panicle girth (18.30 mm) was in cluster XIII.

The genotypes in the clusters II, V and VII (11.17 cm each) had the lowest peduncle length while genotype of cluster III (17.5 cm) had highest Peduncle length.

With respect to number of tillers per meter row length, lowest value was found for cluster II (14.50) whereas highest value was observed for clusters IX (73.50) followed by cluster VI (56.0).

With respect to number of productive tillers per meter row length, lowest value was observed for cluster II (12.50) whereas highest value was found out for cluster IX (73.0).

With respect to number of productive tillers per plant, lowest value was found out for cluster XIV (1.0) whereas highest value was found out for clusters VI and IX (12.67 each) followed by cluster III (12.0).

The genotype in the cluster II (44.52 cm²) had lowest standard leaf area while genotype of cluster XII (87.67 cm²) had highest standard leaf area.

For stem thickness trait, Cluster II (0.92 cm) had the lowest value genotype, whereas, cluster XV (3.09 cm) had the highest value genotype.

With respect to SPAD at flowering, lowest value was found out for cluster II (35.22) whereas highest value was found out for cluster IV (48.12). With respect to SPAD at maturity, lowest value was found out for cluster X (19.82) whereas highest value was found out for clusters XI (34.22) and VI (33.14).

With respect to grain yield per plant, Cluster II had the lowest yielding genotype with 14.94 gram per plant and the cluster IX had the highest yielding genotypes with mean grain yield of 44.93 gram per plant.

With respect to grain yield per hectare, Cluster II had the lowest yielding genotypes with 139.82 kg per hectare. The highest mean value for grain yield per hectare was observed for cluster IV (2553.71 kg per hectare) followed by cluster IX (2039.82 kg/ha).

Lowest fodder yield per plant was noticed in the cluster II (60 g) but the genotypes having higher fodder yield per plant belonged to cluster VI (227.50 g) and cluster IX (195.0 g).

Table 9. 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 9 (Contd...)

Characters Clusters	Area of standerd 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

Lowest fodder yield per hectare was noticed in the cluster X (703.71 kg) but the genotypes having highest fodder yield per hectare belonged to cluster IV and XIV (3388.89 kg/ha).

With respect to 1000 seed weight, cluster VII recorded the lowest test weight of 2.85 g, whereas cluster III recorded highest test weight of 4.20 g followed by cluster X (4.15 g) and cluster V (4.01 g).

4.3 GENETIC VARIABILITY PARAMETERS

Assessment of variability was done among the 149 germplasm accessions of foxtail millet. The mean values obtained for various traits of all accessions are given in Appendix II. The results pertaining to genetic parameters *viz.*, range, mean, genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2), genetic advance (GA) and genetic advance as per cent of mean (GAM) were calculated to estimate the extent of genetic variability for 19 characters and the results are presented in Table 10. Diagrammatic representation of GCV and PCV are presented in Fig. 3. Whereas, heritability estimates and genetic advance on per cent of mean were presented in Fig. 4.

4.3.1 Days to panicle emergence

Days taken for complete emergence of panicle out of flag leaf in 149 genotypes varied from 42 to 61 days with a mean value of 55.96 days. Among 149 genotypes, 47 genotypes were earliest for panicle emergence. Among them GS 33, GS 29, GS 301, SR 11 and GS 377 took 42, 46, 47, 49, and 50 days for panicle emergence, respectively.

There is a significant variation found for the trait. The phenotypic (6.35%) and genotypic (4.03%) co-efficient of variations for trait were low followed by moderate heritability of (40.31%) and genetic advance as percent mean showed low value of 5.28.

4.3.2 Days to 50 per cent flowering

Days taken for 50 per cent of the plants to initiate flowering among 149 genotypes was varied from 48 to 65 days with a mean value of 60.42 days. 54 genotypes were earliest to flower. Among them genotypes *viz.*, GS 33, GS 29, GS 377, FMGPM-1 and SR 11 recorded 48, 54, 54, 55 and 55 days, respectively taken for 50% flowering.

There was wide variation observed for the days to 50 per cent flowering. The estimates of phenotypic (5.16%) and genotypic (4.07%) co-efficient of variation were

recorded low but the broad sense heritability (62.26%) was found to be high, accompanied by low genetic advance as per cent mean of 6.62.

4.3.3 Days to maturity

Range of variation for days to maturity was from 78 to 95 days with a mean value of 90.37 days. During the crop growth GS 33 genotype was early to mature by taking minimum number of 78 days in the season. This was followed by GS 377, FMGPM-1 (84 days each) and GS 29 (85days). On the other hand, the genotypes viz., MLT-12-1, GS 460 and GS 220 were very late to mature by taking as much as 95 days each followed by K3 which took 94 days for maturity.

The estimates of PCV (3.56%), and GCV (2.7%) for days to maturity were low coupled with medium level heritability (57.68 %) but showed low genetic advance as percent mean of 4.23.

4.3.4 Plant height (cm)

The genotypes exhibited a wide variation for plant height ranging from 56.50 cm to 158.33 cm with a mean value of 136 cm. The genotype, FMGPM-5 (56 cm) was the dwarfest among 149 genotypes followed by Arjuna (58 cm) and MLT-12-3 (96 cm). The tallest plant was GS 78 which recorded the height of 158 cm which was followed by GS 213(156 cm) and FMGPM-2 (154 cm).

For plant height character, it was recorded medium PCV (11.71%) but it showed low GCV (8.93%) accompanied by medium heritability (58.25%) and medium genetic advance as per cent mean of 14.05.

4.3.5 Panicle length (cm)

Panicle length was ranged between 10.28 cm to 23.50 cm with a mean value of 16 cm. Among 149 genotypes, about 31 genotypes performed above average panicle length. Among 31 genotypes, MLT-12-8 (23 cm), GS 78 (21 cm) followed by SR 11 (21 cm) and GS 45 (19 cm) were superior when compared with the best check PS-4 (Plate 2). The lowest panicle length was recorded by the genotype GS 6 (10 cm) followed by GS 511 (11 cm).

Moderate estimate of PCV (16.14%) and low estimate of GCV (9.09%) were observed for panicle length. The estimates of heritability (31.71%) and genetic advance as per cent of mean (10.54) were recorded as moderate.



2(a)



2(b)

Plate 2. Varietal difference for panicle (a) length, (b) girth

4.3.6 Panicle girth (mm)

Considerable variation was observed among the genotypes in respect of trait as seen by mean values ranging between 8.82 and 18.29 mm among all genotypes. The average panicle girth was 12.41 mm. In the crop growth period, panicle girth was highest in the genotype GS 511 (18.29 mm) followed by SiA 3156 (16.06 mm) and GS 29 (15.91 mm) whereas the genotypes MLT-12-9 (8.82 mm), MLT-12-1 (9.22 mm) and MLT-12-2 (9.30 mm) recorded the lowest panicle girth (Plate 2).

Moderate estimate of PCV (13.9%) and low estimate of GCV (8.9%) accompanied by moderate heritability (40.80%) and genetic advance as per cent mean (11.71) were recorded for the trait panicle girth.

4.3.7 Peduncle length (cm)

Considerable variation was found for the peduncle length among the genotypes which was ranged between 8.67 to 21.33 cm and average value of 15 cm. Among all genotypes, GS 248 (21.33) showed highest peduncle length followed by GS 210 (20.6 cm) and GS 494 (20.25 cm) whereas the genotypes GS 377 (8.6 cm), MLT-12-1 (10 cm) and GS 401 (10.25 cm) recorded lowest peduncle length.

The genotypic (10.14%) and phenotypic (19.72%) coefficients of variation for peduncle length character were moderate values, heritability (26.45%) recorded low value while genetic advance as per cent mean was recorded moderate value of 10.75.

4.3.8 Number of tillers per meter row length

There was considerable amount of variation was observed for the trait. It ranged between 14 to 73.5 tillers with mean value of 42.52 tillers per meter row. Among all 149 genotypes, 76 entries showed above the average tiller numbers. Among them GS 510 (73 tillers) recorded highest number of tillers followed by GS 212 (66 tillers) and GS 352 (64 tillers). Whereas the genotypes MLT-12-7 (14 tillers), MLT-12-3 (15 tillers) and GS 35 (25 tillers) were observed with lowest number of tillers.

Computed data showed highest estimates of PCV (28.05%), GCV (22.99%), heritability (67.20%) and genetic advance as per cent of mean (38.83) recorded for the trait number of tillers per meter row length.

4.3.9 Number of productive tillers per meter row length

The range of values observed was 11.50 to 73.00 productive tillers per meter row length with mean value of 41. It was observed that for productive tillers, 111 genotypes significantly exceeded the best checks SiA 326 and PS 4. Among all

evaluated genotypes GS 510 (73 tillers), was found to be superior followed by GS 212 (64) and GS 352 (61) whereas MLT-12-5 (11), MLT-12-3 (12) and GS 35 (25) found to be inferior among all the genotypes for this trait.

High estimates of GCV (22.62%) and PCV (30.86%), moderate heritability (53.75%) and high genetic advance as per cent of mean of 34.17 were recorded for the trait.

4.3.10 Number of productive tillers per plant

Number of productive tillers per plant was ranged between 1.00 to 13.17. The mean number of productive tillers per plant observed was 6.84.

Among all the genotypes, 25 genotypes significantly exceeded the best check PS 4 while 97 genotypes exceeded the check SiA 326. Among the genotypes evaluated GS 71 (13 tillers), GS 213 (12) and GS 510 (12) found to have highest productive tillers per plant whereas GS 33 (1 tiller), MLT-12-3 (2 tillers), and GS 511 (3 tillers) had lowest number of tillers.

Computed data showed highest estimates PCV (37.67%), GCV (28.67%), heritability (57.95%) and genetic advance as per cent of mean (44.96) recorded for the trait

4.3.11 Area of standard leaf (cm²)

Wide range of variation was observed for standard leaf area (39.87 to 160.91 cm²) with mean leaf area of 62.87 cm². Among all genotypes, leaf area was found to be highest in the genotype SiA 326 with leaf area of 160.91 cm² followed by GS 215 (91.6 cm²) and MLT-12-8 (87.7 cm²) whereas MLT-12-1 (39.8 cm²) and GS 140 (45 cm²) were found to have lowest leaf area.

High estimates of phenotypic (25.46%) and moderate estimates genotypic coefficient of variation (10.69%) coupled with low heritability (17.63%) and low genetic advance as per cent mean (9.24) were recorded for the trait.

4.3.12 Stem thickness (cm)

There was considerable amount of variation was observed for the character. The range of variation was 0.92 cm to 3.00 cm with mean value of 1.30 cm. It was found that among all the genotypes, GS 338 (3.09 cm) found to have highest stem thickness followed by GS 250 (1.85 cm) and GS 362 (1.72 cm) where as the genotypes MLT-12-3 (0.92 cm), GS 207 (1.2 cm) and GS 140 (1.34 cm) found to have the lowest stem thickness.

High estimates of phenotypic (20.28%) and moderate estimates genotypic co efficient of variation (11.36%) were recorded coupled with moderate estimates of heritability (31.38%) and genetic advance as per cent mean (13.11) were recorded for the trait.

4.3.13 SPAD at 50% flowering

There was wide range of variation was observed for SPAD reading at 50% of flowering. The values were ranged from 31.02 to 48.12, and the mean SPAD value was 40.24. Genotype SR 11 showed highest SPAD value of 48.12 followed by GS 266 and GS 12 with SPAD value 48.1 and 48, respectively. Whereas, GS 415, MLT-12-1 and MLT-12-2 were recorded with lowest SPAD values of 31, 31.93, 33.5, respectively.

For SPAD at flowering trait, moderate estimates of phenotypic (11.11%) and low estimates genotypic coefficient of variation (5.09%) were recorded coupled with low estimates of heritability (21.02%) and genetic advance as per cent mean (4.81) were recorded. .

4.3.14 SPAD at maturity

There was considerable range of variation observed for SPAD reading at maturity. The values were ranged from 16.87 to 41.57 and the mean SPAD value for all the genotypes was found to be 25.57. Genotype SiA 3156 showed highest SPAD value of 41.57 followed by GS 17 and GS 77 with SPAD values of 34.22 and 33.22, respectively. Whereas the genotypes Co 4, GS 453 and GS 379 were recorded with lowest SPAD values 16.87, 18.03 and 18.80, respectively.

For SPAD reading at maturity trait, moderate estimates of phenotypic (19.26%) and low estimates genotypic co-efficient of variation (8.65%) were recorded coupled with low heritability (20.18%) and low genetic advance as per cent mean (8.01) recorded for the trait.

4.3.15 Grain yield per plant (g)

Grain yield per plant exhibited mean of 31.26 g and range of 14.94 g to 55.24 g. Among 149 lines, 69 genotypes have recorded the above mean yield values. A total of 87 genotypes showed superior performance compared with national check SiA 326 while 8 genotypes were found to be superior to PS 4. Among them genotypes GS 71 has recorded highest grain yield of 55.24 g/pl followed by GS 221 (50.42 g) and GS 78 (47.17 g).

Grain yield per plant was recorded high estimates of PCV (29.86%) and moderate GCV (16.47%) values, coupled with moderate heritability (30.44%) and moderate genetic advance as per cent of mean (18.72).

4.3.16 Grain yield per hectare (kg)

Wide range of variation was noticed for grain yield per hectare (139.81 kg/ha to 2717.5 kg/ha) with mean value of 1558.28 kg/ha. Among 149 lines, 23 genotypes recorded significantly higher grain yield per hectare when compared with national check PS-4 while 28 genotypes were found superior to best check MLT-12-12 (SiA326). Among them genotype SiA 3156 (2717 kg/ha) performed highest grain yield per hectare followed by SiA 2593 (2633 kg/ha) and Co 7 (2607 kg/ha) whereas MLT-12-3 (139.81 kg/ha), MLT-12-1 (212.9 kg/ha) and GS 21 (275.9 kg/ha) showed lowest yield.

It was recorded high estimates of PCV (39.25%), GCV (29.93%), heritability (58.14%) and genetic advance as per cent of mean (47.01) for the trait grain yield per hectare.

4.3.17 Fodder yield per plant (g)

The range of variation observed for the trait was 55 to 262.50 g per plant with mean value of 130.13 g. Among all 149 genotypes, 50 genotypes exceeded the best check SiA 326 while 55 genotypes exceeded the check HMT-100-1. Among them GS 71 (262 g) performed better followed by GS 216 (232 g) and GS 213 (227 g) whereas GS 377 (55 g) showed lowest fodder yield followed by GS 140 (57 g) and MLT-12-3 (60 g).

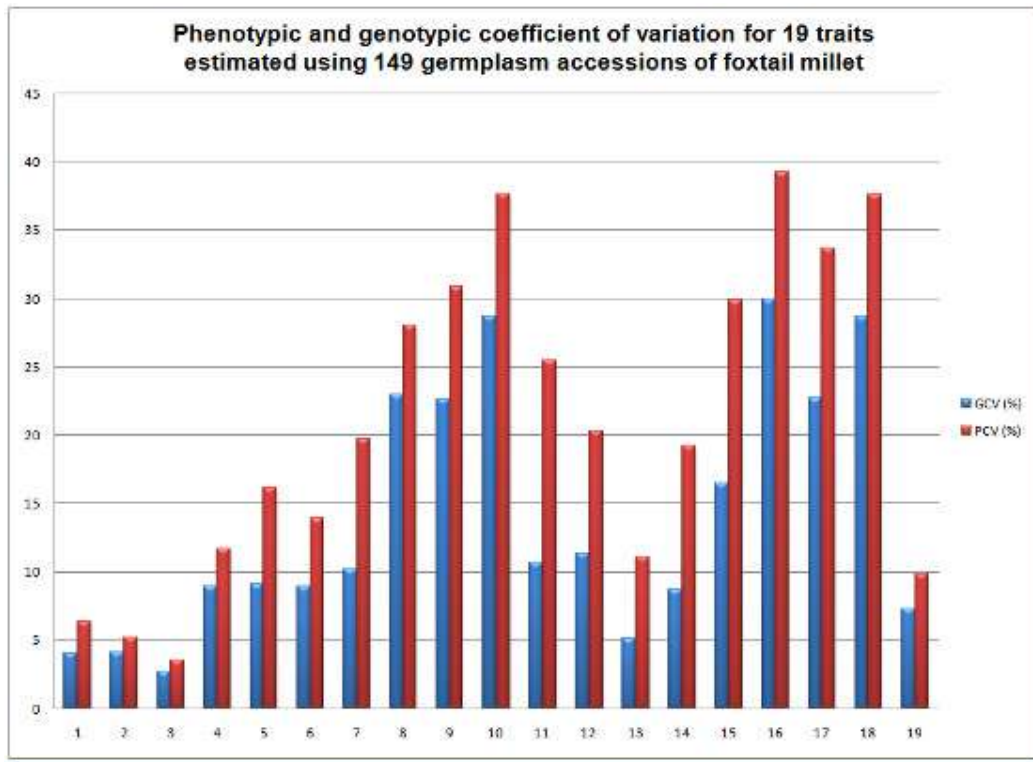
High estimates of phenotypic (33.73%) and genotypic co efficient of variation (22.75%) were recorded coupled with moderate heritability (45.51%) and high genetic advance as per cent mean (31.62) observed for the trait.

4.3.18 Fodder yield per hectare (kg)

There was wide range of variation observed for the trait. The values were ranged from 370.37 kg/ha to 5388.8 kg/ha with mean fodder yield of 2915.98 kg/ha. Among 149 lines, 72 genotypes showed better fodder yield. 50 genotypes exceeded the check MLT-12-12 (Sia326) whereas 136 genotypes exceeded the check HMT-100-1. Among them GS 363 (5388.8 kg/ha) was found to be superior followed by GS 510 (5222 kg/ha) and K 3 (5148 kg/ha). While, GS 21 (400 kg/ha), MLT-12-3 (518 kg/ha) and MLT-12-6 (870 kg/ha) were observed with lowest fodder yield.

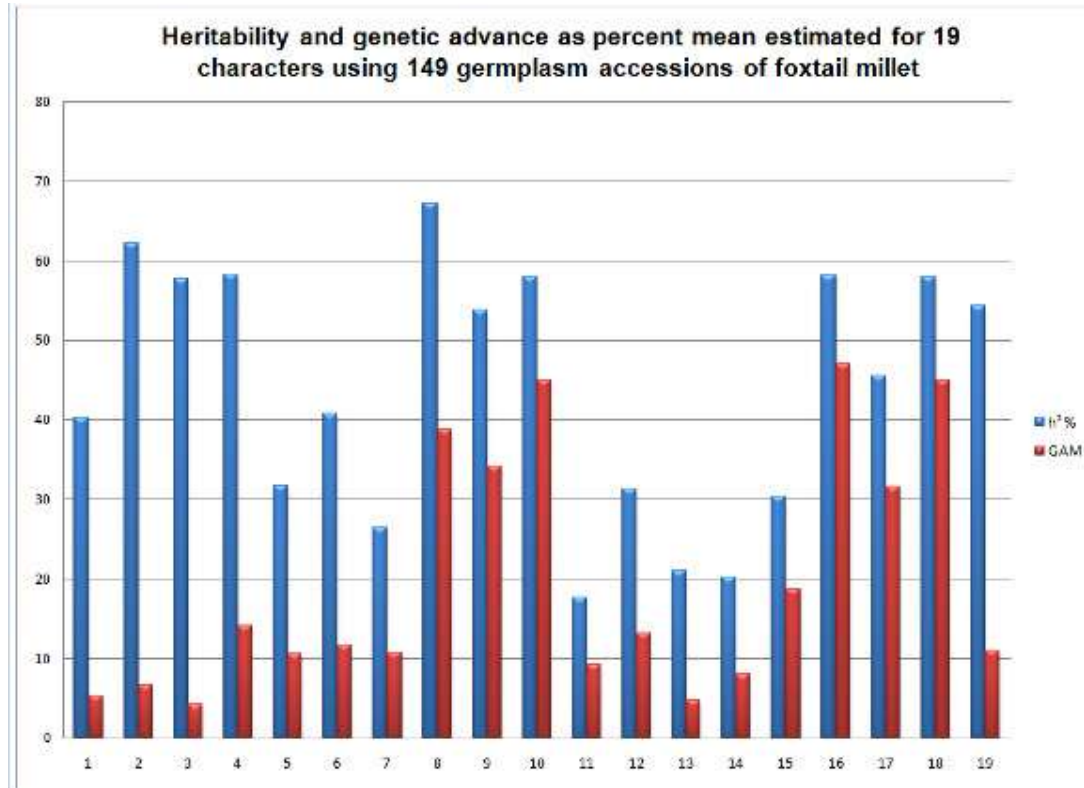
Table 10. Estimates of genetic variability parameters for productivity traits among 149 germplasm accessions of foxtail millet

Sl. No.	Character	Mean	Range		GCV (%)	PCV (%)	h ² %	GAM
			Max	Min				
1	Days to panicle emergence	55.96	42	61.00	4.03	6.36	40.31	5.28
2	Days to 50% flowering	60.42	48	65.00	4.07	5.16	62.26	6.62
3	Days to maturity	90.37	78	95.00	2.70	3.56	57.68	4.23
4	Plant height (cm)	135.94	56.5	158.33	8.94	11.71	58.25	14.05
5	Panicle length (mm)	15.69	10.28	23.50	9.09	16.14	31.71	10.54
6	Panicle girth (cm)	12.41	8.82	18.29	8.90	13.93	40.81	11.71
7	Peduncle length (cm)	14.59	8.67	21.33	10.14	19.72	26.45	10.75
8	No of tillers/meter row length	42.52	14	73.50	22.99	28.05	67.20	38.83
9	Number of productive tillers/meter row	40.95	11.5	73.00	22.62	30.86	53.75	34.17
10	Number of productive tillers/plant	6.84	1	13.17	28.67	37.67	57.95	44.96
11	Area of standard leaf (cm ²)	62.87	39.87	160.91	10.69	25.46	17.63	9.25
12	Stem thickness (cm)	1.30	0.92	3.00	11.36	20.28	31.38	13.11
13	SPAD at 50% flowering	40.24	31.02	48.12	5.09	11.11	21.02	4.81
14	SPAD at maturity	25.57	16.87	41.57	8.65	19.26	20.18	8.01
15	Grain yield/plant (g)	31.26	14.94	55.24	16.47	29.86	30.44	18.72
16	Grain yield/hectare (kg)	1558.28	139.81	2717.50	29.93	39.25	58.14	47.01
17	Fodder yield/plant (g)	130.13	55	262.50	22.75	33.73	45.51	31.62
18	Fodder yield/hectare (kg)	2915.98	370.37	5388.80	28.67	37.63	58.02	44.98
19	1000 seed weight (g)	3.54	2.85	4.44	7.28	9.86	54.42	11.06



Sl. No.	Legend
1	Days to panicle emergence
2	Days to 50% flowering
3	Days to maturity
4	Plant height (cm)
5	Panicle length (mm)
6	Panicle girth (cm)
7	Peduncle length (cm)
8	No of tillers/meter row length
9	Number of productive tillers/meter row
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	Grain yield/plant (g)
16	Grain yield/hectare (kg)
17	Fodder yield/plant (g)
18	Fodder yield/hectare (kg)
19	1000 seed weight (g)

Fig 3. Phenotypic and genotypic coefficient of variation for 19 traits estimated using 149 germplasm accessions of foxtail millet



Sl. No.	Legend
1	Days to panicle emergence
2	Days to 50% flowering
3	Days to maturity
4	Plant height (cm)
5	Panicle length (mm)
6	Panicle girth (cm)
7	Peduncle length (cm)
8	No of tillers/meter row length
9	Number of productive tillers/meter row
10	Number of productive tillers/plant
11	Area of standard leaf (cm2)
12	Stem thickness (cm)
13	SPAD at 50% flowering
14	SPAD at maturity
15	Grain yield/plant (g)
16	Grain yield/hectare (kg)
17	Fodder yield/plant (g)
18	Fodder yield/hectare (kg)
19	1000 seed weight (g)

Fig. 4 Heritability and genetic advance as percent mean estimated for 19 characters using 149 germplasm accessions of foxtail millet

High estimates of phenotypic (37.63%) and genotypic co-efficient of variation (28.67%) coupled with moderate heritability (58.02%) and high genetic advance as per cent mean (44.98) were recorded for the trait.

4.3.19 1000 seed weight (g)

Among the genotypes, values of 1000 seed weight were ranged between 2.85 to 4.44 grams. Further, mean seed weight was found to be 3.54 g. The genotype GS 95 showed highest test weight of 4.44g, followed by GS 308 (4.26g) and GS 207 (4.2g). On the other hand genotype MLT-12-10 showed lowest test weight of 2.85 g, followed by GS 426 and GS 200 with test weight of 2.88 and 2.92, respectively.

Low estimates of PCV (9.86%) and GCV (7.28%) values were recorded for test weight. Moderate estimates of heritability (54.42%) and genetic advance as per cent mean (11.06) were recorded for the trait.

4.4 CORRELATION COEFFICIENTS

Correlation is a measure which is used to find out degree and direction of relationship between two or more variables. In breeding programme, correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. The phenotypic correlations of grain yield and its component characters among 149 genotypes studied are presented in Table 11. The results on correlation coefficients between the traits are given below.

4.4.1 Days to panicle emergence

Days to panicle emergence was found to be significantly and positively correlated with days to 50% flowering ($r=0.88$), days to panicle maturity (0.87), number of productive tillers per plant (0.231) and fodder yield per plant (0.189). While it was found to be significantly and negatively correlated with panicle girth (-0.233), area of standard leaf (-0.243), stem thickness (-0.225), SPAD at 50% flowering (-0.274) and grain yield per hectare (-0.355). For other traits, it was non-significantly and negatively correlated with panicle length, peduncle length, number of tillers per meter row length, number of productive tillers per meter row length and fodder yield per hectare whereas it was non-significantly and positively correlated with plant height, SPAD at maturity, grain yield per plant and test weight.

4.4.2 Days to 50% flowering

Days to 50% flowering was found to be significantly and positively correlated with days to panicle emergence (+0.875), days to panicle maturity (+0.995), number of productive tillers per plant (+0.184), fodder yield per plant (+0.219) and 1000 seed weight (+0.185). It was found to be significantly and negatively correlated with area of standard leaf (-0.208), SPAD at 50% flowering (-0.253) and grain yield per hectare (-0.251). It was non-significantly and negatively correlated with panicle length, panicle girth, peduncle length, stem thickness and fodder yield per hectare while it was non-significantly and positively correlated with plant height, number of tillers per meter row length, number of productive tillers per meter row length, SPAD at maturity and grain yield per plant.

4.4.3 Days to maturity

Days to maturity was found to be significantly and positively correlated with days to panicle emergence (+0.871), days to 50% flowering (+0.995), number of productive tillers per plant (+0.177), fodder yield per plant (+0.213) and 1000 seed weight (+0.184). It was found to be significantly and negatively correlated with area of standard leaf (-0.206), SPAD at 50% flowering (-0.249) and grain yield per hectare (-0.246). It was non-significantly and negatively correlated with panicle length, panicle girth, peduncle length, stem thickness and fodder yield per hectare. While, it was nonsignificantly and positively correlated with plant height, number of tillers per meter row length, number of productive tillers per meter row length, SPAD at maturity and grain yield per plant.

4.4.4 Plant height (cm)

For plant height, it was significantly and positively correlated with panicle length (+0.378), panicle girth (+0.234), peduncle length (+0.264), number of tillers per meter row length (+0.338), number of productive tillers per meter row length (+0.341), number of productive tillers per plant (+0.346), area of standard leaf (+0.254), stem thickness (+0.172), SPAD at 50% flowering (+0.248), SPAD at maturity (+0.327), fodder yield per plant (+0.474), fodder yield per hectare (+0.408), grain yield per plant (+0.454) and grain yield per hectare (+0.378). While none of the characters were significantly negatively correlated. It was non-significantly and positively correlated with panicle emergence, days to 50% flowering, days to maturity and 1000 seed weight but there was no character found non significantly and negatively correlated with the trait.

4.4.5 Panicle length (cm)

For panicle length, it was significantly and positively correlated with plant height (+0.378), panicle girth (+0.324), area of standard leaf (+0.381), stem thickness (+0.189), SPAD at 50% flowering (+0.287), SPAD at maturity (+0.296), fodder yield per plant (+0.389), fodder yield per hectare (+0.284), grain yield per plant (+0.327) and grain yield per hectare (+0.308). But there was no character found significantly and negatively correlated with the trait. Non significantly and positively correlated values were found for peduncle length, number of tillers per meter row length, number of productive tillers per meter row length, number of productive tillers per plant and 1000 seed weight, whereas it was non-significantly and negatively correlated with panicle emergence, days to 50% flowering and days to maturity.

4.4.6 Panicle girth (mm)

For panicle girth character, it was significantly and positively correlated with plant height (+0.234), panicle length (+0.324), area of standard leaf (+0.468), stem thickness (+0.465), SPAD at 50% flowering (+0.265), SPAD at maturity (+0.447), fodder yield per plant (+0.194), fodder yield per hectare (+0.335), grain yield per plant (+0.335) and grain yield per hectare (+0.398). It was found significantly and negatively correlated with days to panicle emergence (-0.233). Non-significantly and positively correlated values were found for peduncle length and 1000 seed weight whereas it was non-significantly and negatively correlated with days to 50% flowering, days to maturity, number of tillers per meter row length, number of productive tillers per meter row length and number of productive tillers per plant.

4.4.7 Peduncle length (cm)

For peduncle length, it was significantly and positively correlated with plant height (+0.264), area of standard leaf (+0.218) and test weight (+0.178). While there was no character found significantly and negatively correlated with the trait peduncle length. It was non-significantly and positively correlated with panicle length, panicle girth, number of tillers per meter row length, number of productive tillers per meter row length, number of productive tillers per plant, stem thickness, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare while it was non-significantly and negatively correlated with days to panicle emergence, days to 50% flowering and days to maturity.

4.4.8 Number of tillers per meter row length

For the trait, it was significantly and positively correlated with plant height (+0.338), number of productive tillers per meter row length (+0.986), number of productive tillers per plant (+0.563), fodder yield per plant (+0.404), fodder yield per hectare (+0.475), grain yield per plant (+0.442) and grain yield per hectare (+0.528). While there was no character found significantly and negatively correlated with the trait. It was non-significantly and positively correlated with days to 50% flowering, days to maturity, plant height, peduncle length, SPAD at 50% flowering, SPAD at maturity and 1000 seed weight while it was non-significantly and negatively correlated with days to panicle emergence, panicle girth, area of standard leaf and stem thickness.

4.4.9 Number of productive tillers per meter row length

For the trait, it was significantly and positively correlated with plant height (+0.341), number of tillers per meter row length (+0.986), number of productive tillers per plant (+0.573), fodder yield per plant (+0.408), fodder yield per hectare (+0.492), grain yield per plant (+0.448) and grain yield per hectare (+0.536). While there was no character found significantly and negatively correlated with the trait. It was non-significantly and positively correlated with days to 50% flowering, days to maturity, peduncle length, SPAD at 50% flowering, SPAD at maturity and 1000 seed weight while it was non-significantly and negatively correlated with days to panicle emergence, panicle girth, area of standard leaf and stem thickness.

4.4.10 Number of productive tillers per plant

For the trait, it was significantly and positively correlated with panicle emergence (+0.235), days to 50% flowering (+0.184), days to maturity (+0.177), plant height (+0.346), number of tillers per meter row length (+0.563), number of productive tillers per meter row length (+0.573), fodder yield per plant (+0.536), fodder yield per hectare (+0.257), grain yield per plant (+0.717) and grain yield per hectare (+0.193). While it was significantly and negatively correlated with stem thickness (-0.168). It was non-significantly and positively correlated with panicle length, peduncle length, SPAD at 50% flowering, SPAD at maturity and 1000 seed weight, while it was non-significantly and negatively correlated with panicle girth and area of standard leaf.

4.4.11 Area of standard leaf (cm²)

It was significantly and positively correlated with plant height (+0.254), panicle length (+0.381), panicle girth (+0.468), peduncle length (+0.218), stem thickness

(+0.402), SPAD at 50% flowering (+0.232), SPAD at maturity (+0.208), fodder yield per plant (+0.228), fodder yield per hectare (+0.288), grain yield per plant (+0.229) and grain yield per hectare (+0.329). Whereas it was significantly and negatively correlated with day to panicle emergence (-0.243), days to 50% flowering (-0.208) and days to maturity (-0.206). It was non-significantly and positively correlated with 1000 seed weight while it was non-significantly and negatively correlated with number of tillers per meter row length, number of productive tillers per meter row length and number of productive tillers per plant.

4.4.12 Stem thickness (cm)

It was significantly and positively correlated with plant height (+0.172), panicle length (+0.189), panicle girth (+0.465), SPAD at maturity (+0.161), standard leaf area (+0.402), fodder yield per hectare (+0.191) and grain yield per hectare (+0.213). While it was significantly and negatively correlated with days to panicle emergence (-0.225) and number of productive tillers per plant (-0.168). It was non-significantly and positively correlated with peduncle length, SPAD at 50% flowering, fodder yield per plant, grain yield per plant while it was non-significantly and negatively correlated with days to 50% flowering, days to maturity, number of tillers per meter row length, number of productive tillers per meter row length and number of productive tillers per plant and test weight.

4.4.13 SPAD at 50% flowering

SPAD at 50% flowering was found to be significantly and positively correlated with plant height (+0.248), panicle length (+0.287), panicle girth (+0.265), area of standard leaf (+0.232), SPAD at maturity (+0.320), fodder yield per plant (+0.182), fodder yield per hectare (+0.302), grain yield per plant (+0.216) and grain yield per hectare (+0.383). Whereas it was found to be significantly and negatively correlated with days to panicle emergence (-0.274), days to 50% flowering (-0.253) and days to maturity (-0.249). There was no trait found non-significantly and negatively correlated while it was non-significantly and positively correlated with peduncle length, number of tillers per meter row length, number of productive tillers per meter row length, number of productive tillers per plant, stem thickness and test weight.

4.4.14 SPAD at maturity

For SPAD at maturity, it was significantly and positively correlated with plant height (+0.327), panicle length (+0.296), panicle girth (+0.447), area of standard leaf (+0.208), stem thickness (+0.161), SPAD at 50% flowering (+0.320), fodder yield per

plant (+0.333), fodder yield per hectare (+0.412), grain yield per plant (+0.358), grain yield per hectare (+0.371) and 1000 seed weight (+0.215). However, there was no character found significantly and negatively correlated with this trait. While, it was non-significantly and positively correlated with days to panicle emergence, days to 50% flowering, days to maturity, peduncle length, number of tillers per meter row length, number of productive tillers per meter row length and number of productive tillers per plant and there was no character found non-significantly and negatively correlated with the trait.

4.4.15 Grain yield per plant (g)

For the trait, it was significantly and positively correlated with plant height (+0.454), panicle length (+0.327), panicle girth (+0.335), number of tillers per meter row length (+0.442), number of productive tillers per meter row length (+0.448), number of productive tillers per plant (+0.717), standard leaf area (+0.229), SPAD at 50% flowering (+0.216), SPAD at maturity (+0.358), fodder yield per plant (+0.626), fodder yield per hectare (+0.371) and grain yield per hectare (+0.391). while there was no character found significantly and negatively correlated with the trait. It was non-significantly and positively correlated with days to panicle emergence, days to 50% flowering, days to maturity, peduncle length, stem thickness and test weight while there was no character found non-significantly and negatively correlated with the trait.

4.4.16 Grain yield per hectare (kg)

For the trait, it was significantly and positively correlated with plant height (+0.378), panicle length (+0.308), panicle girth (+0.398), number of tillers per meter row length (+0.528), number of productive tillers per meter row length (+0.536), number of productive tillers per plant (+0.193), standard leaf area (+0.329), stem thickness (+0.213), SPAD at 50% flowering (+0.383), SPAD at maturity (+0.371), fodder yield per plant (+0.267), fodder yield per hectare (+0.823), grain yield per plant (+0.391) and test weight (+0.169). whereas it was significantly and negatively correlated with days to panicle emergence (-0.355), days to 50% flowering (-0.251) and days to maturity (-0.246). It was non-significantly and positively correlated with peduncle length while there was no character found non-significantly and negatively correlated with the trait

4.4.17 Fodder yield per plant (g)

For the trait, it was significantly and positively correlated with days to panicle emergence (+0.189), days to 50% flowering (+0.219), days to maturity (+0.213), plant

Table 11. Phenotypic correlation co-efficients estimated between different traits using 149 germplasm accessions of foxtail millet

	DPE	DFF	DM	PH	PL	PG	PDL	NOTPM	NOPTPM	NOPTPP	ASL	ST	S50PF	SM	FYPP	FYPH	GYPP	GYPH	SW
DPE	1.00	.875**	.871**	0.09	-0.06	-.233**	-0.04	-0.03	-0.04	.231**	-.243**	-.225**	-.274**	0.03	.189*	-0.14	0.04	-.355**	0.12
DFF		1.00	.995**	0.16	-0.02	-0.13	-0.02	0.02	0.02	.184*	-.208*	-0.12	-.253**	0.13	.219**	-0.05	0.05	-.251**	.185*
DM			1.00	0.15	-0.01	-0.14	-0.04	0.02	0.02	.177*	-.206*	-0.14	-.249**	0.13	.213**	-0.05	0.04	-.246**	.184*
PH				1.00	.378**	.234**	.264**	.338**	.341**	.346**	.254**	.172*	.248**	.327**	.474**	.408**	.454**	.378**	0.11
PL					1.00	.324**	0.03	0.10	0.10	0.15	.381**	.189*	.287**	.296**	.389**	.284**	.327**	.308**	0.14
PG						1.00	0.15	-0.06	-0.05	-0.09	.468**	.465**	.265**	.447**	.194*	.335**	.335**	.398**	0.08
PDL							1.00	0.03	0.04	0.11	.218**	0.05	0.06	0.11	0.09	0.08	0.14	0.12	.178*
NOTPM								1.00	.986**	.563**	-0.02	-0.09	0.10	0.08	.404**	.475**	.442**	.528**	0.05
NOPTPM									1.00	.573**	-0.02	-0.09	0.12	0.09	.408**	.492**	.448**	.536**	0.05
NOPTPP										1.00	-0.02	-.168*	0.12	0.12	.536**	.257**	.717**	.193*	0.11
ASL											1.00	.402**	.232**	.208*	.228**	.288**	.229**	.329**	0.10
ST												1.00	0.04	.161*	0.11	.191*	0.12	.213**	-0.04
S50PF													1.00	.320**	.182*	.302**	.216**	.383**	0.12
SM														1.00	.333**	.412**	.358**	.371**	.215**
FYPP															1.00	.350**	.626**	.267**	.214**
FYPH																1.00	.371**	.823**	.166*
GYPP																	1.00	.391**	0.14
GYPH																		1.00	.169*
SW																			1.00

Note: DPE: days to panicle emergence, DFF: days to 50% flowering, DM: days to maturity, PH: plant height(cm), PL: panicle length(cm), PG: panicle girth(mm), PDL: peduncle length(cm), NOTPM: number of tillers per meter row length, NOPTPM: number of productive tillers per meter length, NOPTPP: number of productive tillers per plant, ASL: standard leaf area(cm²), ST: stem thickness(cm), S50PF: SPAD reading at flowering, SM: SPAD reading at maturity, FYPP: Fodder yield per plant(g), FYPH: Fodder yield per hectare(kg), GYPP: grain yield per plant(g), GYPH: grain yield per hectare(kg) and SW: 1000 seed weight(g).

height (+0.474), panicle length (+0.389), panicle girth (+0.194), number of tillers per meter row length (+0.404), number of productive tillers per meter row length (+0.408), number of productive tillers per plant (+0.536), standard leaf area (+0.228), SPAD at 50% flowering (+0.182), SPAD at maturity (+0.333), fodder yield per hectare (+0.350), grain yield per plant (+0.626) and grain yield per hectare (+0.267) and test weight (+0.214). While there was no character found significantly and negatively correlated with the trait. It was non significantly and positively correlated with peduncle length and stem thickness whereas there was no character found non-significantly and negatively correlated with the trait.

4.4.18 Fodder yield per hectare (kg)

For the trait, it was significantly and positively correlated with plant height (+0.408), panicle length (+0.284), panicle girth (+0.335), number of tillers per meter row length (+0.475), number of productive tillers per meter row length (+0.492), number of productive tillers per plant (+0.257), standard leaf area (+0.288), stem thickness (+0.191), SPAD at 50% flowering (+0.302), SPAD at maturity (+0.412), fodder yield per plant (+0.350), grain yield per plant (+0.371), grain yield per hectare (+0.823) and test weight (+0.166). While there was no character found significantly and negatively correlated with the trait. It was non-significantly and positively correlated with peduncle length whereas it was non-significantly and negatively correlated with days to panicle emergence, days to 50% flowering and days to maturity.

4.4.19 Test weight (1000 seed weight in gram)

For the trait, it was significantly and positively correlated with days to 50% flowering (+0.185), days to maturity (+0.184), peduncle length (+0.178), SPAD at maturity (+0.215), fodder yield per plant (+0.214), fodder yield per hectare (+0.166) and grain yield per hectare (+0.169). While there was no character found significantly and negatively correlated with the trait. It was non-significantly and positively correlated with days to panicle emergence, plant height, panicle length, panicle girth, 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, SPAD at 50% flowering, and grain yield per plant whereas it was non-significantly and negatively correlated with stem thickness.

4.5 VARIABILITY FOR MORPHOLOGICAL TRAITS

All the lines were observed for various morphological characters like anther colour, awn length, awn colour, panicle compactness, stem and pigmentation, grain colour and panicle pigmentation. The observations recorded are presented in Appendix III.



Long



Medium



Short

Plate 3. Varietal differences for awn length



Compact



Medium



Loose



Plate 4. Phenotypic differences for panicle compactness



Plate 5. Phenotypic diversity for panicle features



Plate 6. Varietal differences for grain colour

4.5.1 Anther colour

Anther colour was recorded when anthesis occurred in 50 percent of the panicles. The genotypes were categorized as purple to deep purple, and orange and white orange mixture.

Among all the genotypes, GS 71, GS 111, GS 121, GS 204, GS 209, GS 212, GS 213, GS 243, GS 285, GS 461, SiA 3156 and FMGPM-9 were orange and orange white mixture coloured while rest of the genotypes were purple to deep purple.

4.5.2 Awn length

For awn length trait there was a wide range of variability found. For the trait, genotypes were categorized into 3 grades *viz.*, long, medium and short (Plate 3). Among all the 149 lines, 23 genotypes were long, 68 genotypes were medium while rest of 58 genotypes were short.

4.5.3 Awn colour

For awn colour, considerable range of variability was found. For the trait, genotypes were categorized into 2 grades *viz.*, coloured and normal. Among all the 149 lines, 5 genotypes were coloured while rest of the genotypes were normal.

4.5.4 Panicle compactness

With respect to yield of a genotype, panicle compactness plays an important role. For the trait, genotypes were categorized into 3 grades *viz.*, compact, medium and loose (Plate 5). Among all the 149 lines, 38 genotypes were compact panicles, 84 genotypes were medium while rest of 27 genotypes were having loose panicles.

4.5.5 Stem and leaf pigmentation

For stem and leaf pigmentation trait considerable range of variability was observed. For the trait, genotypes were categorized into 2 grades *viz.*, pigmented and normal green. Among all the 149 lines, 25 genotypes were pigmented while rests of the genotypes were normal green.

4.5.6 Grain colour

For grain colour, genotypes were categorized into 4 grades *viz.*, black, red, yellow and white (Plate 6). Among all the genotypes, GS 29, FMGPM-5 and FMGPM-10 were found black coloured, GS 276 found red coloured, GS 12, GS 96, GS 203, GS 216, GS 362 and Chitra showed white coloured whereas rest of the genotypes showed yellow colour.

4.6 SCREENING GENOTYPES FOR GRAIN NUTRIENTS CONTENT

Millet share a set of characteristics which make them unique amongst cereals. Millets grow under dry conditions, can cope with relatively poor soils and require few

external inputs. They are a staple food with superior nutritional qualities compared to other cereals. In the present study, 25 lines were chosen from the list of 149 genotypes of foxtail millet and were assessed for varietal differences for grain protein (%) and micronutrients (Zn, Fe, Ca) contents. The nutritional data is presented in Table 12 and the results are given below.

4.6.1 Grain protein content (%)

For grain protein content, wide range of variation was found for the trait. The extent of variation found for the character ranged from 6.2 per cent to 10.89 per cent with mean value of 8.53 percent.

Among all the 25 selected lines, 9 genotypes were performed better than all the three check varieties [PS 4, MLTB-12-11 (HMT-100-1), MLTB-12-12 (SiA 326)]. The top five entries were GS 95, GS 64, GS 12, GS 78 and GS 71 that showed highest protein content of 10.89(%), 10.13(%), 9.64(%), 9.49(%) and 9.32(%), respectively. While it was observed low protein content in genotypes GS 276(6.2%), followed by GS 511(7.28%) and SiA 2593(7.45%).

4.6.2 Grain Zinc content (mg/100g)

For grain Zn content it was found a wide range of variation. The range of variation observed for the trait was 2.29 to 11.4 (mg/100g), with a mean value of 4.40 (mg/100g).

Among all the 25 selected lines 5 genotypes performed better than all the three check varieties [PS 4, MLTB-12-11 (HMT-100-1), MLTB-12-12 (SiA 326)] viz., GS 121, GS 78, GS 71, GS 213 and GS 106, which showed Zn content of 11.4(mg/100g), 11.3(mg/100g), 9.22(mg/100g), 5.89(mg/100g) and 4.96(mg/100g), respectively. While low Zn content was recorded in GS 64(2.29 mg/100g), followed by SR 11(2.39 mg/100g) and FMGPM-9 (2.46 mg/100g).

4.6.3 Grain Iron content (mg/100g)

For grain Fe content there was a wide range of variation found. The extent of variation found for the micronutrient was ranged from 0.33 (mg/100g) to 16.26 (mg/100g) with mean value of 6.61(mg/100g).

It was found that among all the 25 selected lines, 18 genotypes were found superior to all the three check varieties [PS 4, MLTB-12-11 (HMT-100-1), MLTB-12-12 (SiA 326)]. Among these, the genotypes viz., GS 121 (16.26 mg/100g) and GS 78 (14.48 mg/100g) showed highest Fe content followed by GS 310 (14.13 mg/100g), GS 106 (11.42

mg/100g) and GS 64 (11.36 mg/100g). While, it was showed lowest Fe content for GS 510(0.33 mg/100g), followed by GS 29(1.16 mg/100g) and Co 7 (2.47 mg/100g).

4.6.4 Grain Calcium content (mg/100g)

Considerable amount of variation was observed for the Calcium content. The range of variation found among all the selected genotypes was 1.99 (mg/100g) to 22.69(mg/100g) with mean value of 8.61 (mg/100g).

It was found that among all the 25 selected lines, 7 genotypes performed better than all the three check varieties [PS 4, MLTB-12-11 (HMT-100-1), MLTB-12-12 (SiA 326)] viz., GS 78, GS 106, GS 12, GS 121, GS 95, GS 71 and TNAU 186 which showed Ca content of 22.69(mg/100g), 19.49(mg/100g), 16.76(mg/100g), 14.43(mg/100g), 13.23(mg/100g), 9.93(mg/100g) and 8.46(mg/100g) respectively. While, the lowest Ca content was noticed for GS 510(1.99 mg/100g), followed by GS 213(3.33 mg/100g) and GS 276 (4.93 mg/100g).

Table 12. Performance of selected genotypes of foxtail millet for grain nutrients contents

Sl. No.	Genotype	Protein (%)	Zn (mg/100g)	Fe (mg/100g)	Ca (mg/100g)
1	GS 12	9.64	4.33	8.46	16.76
2	GS 64	10.13	2.29	11.36	5.89
3	GS 71	9.32	9.22	7.83	9.93
4	GS 78	9.49	11.3	14.48	22.69
5	GS 95	10.89	3.56	5.39	13.23
6	GS 106	8.76	4.96	11.42	19.49
7	GS 121	8.67	11.4	16.26	14.43
8	GS 213	7.92	5.89	3.83	3.33
9	GS 29	8.27	3.86	1.16	6.33
10	GS 221	8.94	4.26	4.94	6.69
11	GS 276	6.20	3.86	8.29	4.93
12	GS 293	8.50	2.76	10.23	5.66
13	GS 310	8.94	3.46	14.13	6.93
14	GS 510	8.35	3.23	0.33	1.99
15	GS 511	7.28	2.99	5.11	5.49
16	SiA 3085	8.32	4.33	4.20	5.76
17	Co 7	8.59	3.36	2.47	5.83
18	SiA 2644	8.38	4.13	11.09	6.86
19	TNAU 186	7.89	3.53	4.06	8.46
20	SR 11	9.05	2.39	4.63	8.13
21	SiA 2593	8.53	2.63	2.91	6.56
22	FMGPM-9	7.45	2.46	4.69	7.69
23	PS 4	8.03	2.36	2.53	7.23
24	MLT-12-11(HMT-100-1)	7.16	4.33	2.70	6.99
25	MLTB-12-12 (SiA 326)	8.73	3.16	2.93	8.16

V DISCUSSION

Small millets being eco friendly crops are suitable for fragile and vulnerable agro ecosystems, and hence they should be preferred crops for climate change, organic cultivation and sustainable agriculture. Grains are nutritious even superior to rice and wheat in certain constituents. Grains are having quality protein, rich in minerals, dietary fibre, phyto chemicals and vitamins. Consumption of millets reduces the incidence of cardio vascular diseases, diabetes mellitus, obesity, constipation, and improves the overall health of people. Wheat and rice provide food security whereas millets provide both food and nutritional security. In spite of all these advantages unfortunately, millets cultivation and consumption has diminished a lot in the last 50 years. There is an urgent need to rejuvenate millets cultivation by development of high yielding varieties to meet nutritional food security demand in the current scenario of changing life style and food habits of people.

Foxtail millet is one of the millet crops which is highly nutritious and sustainable food crop grown under different climatic conditions. In general, foxtail millet is valued as a short duration crop which is fairly resistant to insect pests and diseases (Upadhyaya *et al.*, 2008), adaptable to varied soil and environmental conditions due to its high photosynthesis and water use efficiency. It has high nutritional and medicinal value and also it has low glycemic index (GI), which makes it as an ideal food for people suffering from diabetes (Anju and Sarita, 2010; Thathola *et al.*, 2010). Foxtail millet grains contain vitamins B1, B2, B6, C and E (Coulibaly and Chen, 2011). It can be cooked and eaten like rice, either as whole grain or broken; flour used for making porridge and puddings. Foxtail millet is also used as bird feed for feeding cage birds and the by-product of the foxtail millet is used as animal feed extensively in China (En *et al.*, 2008). At present, foxtail millet is regaining its value and emerging as important millet crop next to finger millet (ragi) after realizing the nutritional and health benefits and adaptability to changing climate.

Foxtail millet (*Setaria italica*) is one of the oldest crops cultivated in India for straw and grain. It was once an indispensable crop of vast rainfed areas in semi-arid regions in India due to its drought tolerance. At present, foxtail millet is cultivated on a limited area in Andhra Pradesh, Karnataka, Maharashtra, Tamil Nadu, Rajasthan, Madhya Pradesh, Uttar Pradesh and north eastern states. In Karnataka, Foxtail millet growing districts are Koppal,

Raichur, Haveri, Vijayapur, districts in north and Tumkur, Chitradurg, Mandya, Mysore and Chamrajnagar in South. Although few high yielding varieties are recommended for Karnataka (SIA 326, TNAU 186, PS-4 & HMT-100-1) but in many of these areas farmers are growing local genotypes. In Northern dry zone of Karnataka, foxtail millet that was commonly grown and was part of balanced diet in earlier days in these areas has been replaced with other crops. Hence, in daily diet nutrigrains like foxtail millet has occupied poor share. Therefore, to recover the area under foxtail millet in dry land areas, it is essential to pay attention to development of reliable production technologies specially the development of high yielding varieties. The presence of rich global diversity available for this crop and existence of genetic potential of moderate to high productivity promise breaking the yield barriers.

The selection of genetically diverse parents for hybridization programme is most crucial for generating genetic variability in the crop. Hence, it needs to be assessed genetic diversity, the nature and magnitude of variability in the available foxtail millet germplasm. The precise information on the nature and degree of genetic variability, heritability, genetic advance, correlation among various traits that contribute towards seed yield and genetic divergence would help the breeder in identifying the appropriate genotypes. It is also desired to screen the available germplasm for grain nutritional composition to identify the germplasm accessions with high nutrients content for their subsequent use in breeding programme to develop high yielding nutrigrain foxtail millet, and to identify among existing high yielding varieties with high nutrients content for their commercial exploitation through value addition.

Genetic variability studies for the identification of trait-specific germplasm accessions for various agronomic and nutritional traits are lacking in foxtail millet, and are hence seldom used in breeding (Upadhyaya *et al.*, 2011). Therefore, an effort has been made to procure and study the mini set of germplasm accessions along with the varieties released for different states from Project Co-ordinating unit (small millets), All India Co-ordinated Small millets Improvement Project, ICAR, GKV, Bangalore, also few local collections from present large foxtail millet growing area of Northern dryzone of Karnataka (Koppal district). The present study was aimed to assess the genetic variability and genetic diversity among

these germplasm collections for various quantitative traits; to characterize the selected genotypes for grain nutrients content; and to study the association between various traits.

A total of 149 genotypes (involving germplasm lines, released varieties, advanced lines and local collections) formed the experimental material. Among these, 100 germplasm lines and 26 varieties were obtained from PC Unit (small millets), GKVK, UAS, Bangalore, 11 local collections (from Koppal district of Karnataka), and 12 genotypes from ARS, Hanumanamatti, Karnataka. These lines were evaluated during late *kharif* 14-15 in a replicated trial in RBD design at Regional Agricultural Research Station, Vijayapur for yield and yield traits.

The observations were recorded on days to panicle emergence, days to 50% flowering, days to maturity, plant height (cm), panicle length (cm), panicle girth (cm), 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 (cm²), 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. Also, all the lines were observed for various morphological characters like anther colour, awn length, awn colour, panicle compactness, stem and leaf pigmentation, glume colour and panicle pigmentation. A total of 25 selected genotypes were screened for grain nutrients (protein, iron, zinc & calcium) content.

The data recorded on various traits were subjected to Mahalanobis's D² statistical analysis, variability analysis and correlation coefficient analysis. The results obtained are discussed below in the light of available literature under following headings.

5.1 Analysis of variance

5.2 Genetic diversity analysis

5.3 Genetic variability parameters

5.4 Correlation coefficients

5.5 Varietal characterization for morphological traits

5.6 Superiority of genotypes for various traits

5.7 Screening genotypes for grain nutrients content

5.1 ANALYSIS OF VARIANCE

The analysis of variance done using a total of 149 genotypes revealed that significant differences were observed all the traits studied including yield and yield components and non significant differences existed between the replications (Tale 5). This indicates the presence of considerable amount of variability in the material under study for yield and yield component traits.

5.2 GENETIC DIVERSITY ANALYSIS

Genetic diversity analysis in general helps in assessing nature of diversity in order to identify specific parents for realizing useful recombinants in breeding programme of self pollinating crops like foxtail millet. Of the several methods available, Mahalanobis generalized distance estimated by D^2 statistic (Rao, 1952) is a unique tool for discriminating population considering a set of parameters together rather than infusing from indices based on morphological similarities and phylogenic relationships.

Several workers have followed Mahalanobis D^2 statistic on a wide range of crop species to measure the genetic distance among the available breeding material and to identify characters responsible for such divergence. In the present study, D^2 analysis has been applied to assess the diversity available among available germplasm lines of foxtail millet for 19 quantitatively measured traits. 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.

5.2.1 Genetic diversity

Based on D^2 values, a total of 149 genotypes were grouped into 15 clusters (Table 6). 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 (2000a) 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 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 9). 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 (Table 9). While it showed least between clusters II and cluster V followed by clusters III and VI, 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 12.08 (cluster II & V) and to 138.62 (IX and XIV). These results suggest the presence of wide diversity between these clusters. The low inter cluster distance between II & 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 & XIV (132.8), between III & XIV (126.07) and III & 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.

5.2.2 Percent 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 7 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 Bhattachargee (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.

5.2.3 Analysis of cluster means

All the 149 genotypes were spread over sixteen clusters and means were scored across the clusters for all the nineteen characters (Table 8).

The highest cluster mean was given the first rank and the clusters possessing next best means were given second, third and so on up to 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 was showed maximum 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) & 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/m 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) were 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/m row length, number of productive tillers/m row length, number of productive tillers/plant, grain yield (g/pl) 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).

5.3 GENETIC VARIABILITY PARAMETERS

Effectiveness of selection depends on the magnitude of genetic variability for a particular character. Productivity traits, which are polygenically controlled and highly influenced by environment, determine the success in breeding programme through their genotypic variability. It is therefore, essential to partition the total variability into heritable and non heritable components. Knowledge on the magnitude of heritability coupled with nature and extent of variability in the breeding material gives an idea for effective genetic improvement through selection. Though heritability estimates are the true indicators of genetic potentiality of the genotypes as a tool for selection (Johanson *et al*, 1955), but the changes in the level of heritability due to fluctuation of the environmental factors detracted from total dependence on such estimates. However, heritability estimates when considered in conjunction with the predicted genetic gain form a reliable tool in selection. They indicate the expected genetic advance of a character in response to the certain selection pressure imposed on them. High heritability coupled with high genetic advance indicates additive gene effect and improvement could be made for that character by simple selection based on the phenotypic performance.

In the present study, the genotypes showed a wide range of variation for majority of the characters. Wide range of variation provides ample scope for selection of superior and desired genotypes by the plant breeders for further improvement in these characters. Based on estimates obtained, variability and heritability studied for yield and yield related traits (Table 10) are discussed under following sections.

In the present investigation, high estimates of PCV (%), GCV (%), heritability and genetic advance as per cent of mean were observed for number of tillers/m row length, number of productive tillers/m row length, number of productive tillers/plant, grain yield per plant (g), grain yield per hectare (kg/ha), fodder yield per plant (g), and fodder yield per hectare (kg/ha).

5.3.1 Days to panicle emergence

The present study for days to panicle emergence showed that, there was low phenotypic and genotypic co-efficient of variation for the character. While it showed moderate heritability and moderate genetic advance as percent mean. Similar results were shown by Upadhyaya *et al.* (2011), and Cill and Randhawa (1975).

5.3.2 Days to 50 per cent flowering

For the trait, the analysis showed that the estimates of phenotypic and genotypic coefficients of variation were low. Similar results were shown by Brunda *et al.* (2014), Islam *et al.* (2012), Nirmalakumari and Vetriventhan (2010), Nirmalakumari *et al.* (2008), Lakshman and Guggari (2001), Selvarani and Gomathinayagam (2000b) and Reddy and Jhansilakshmi (1991a).

The study showed high heritability (62.26%) and low genetic advance as percent mean. The reviews pertaining to the study were reported by Brunda *et al.* (2014), Islam *et al.* (2012), Selvarani and Gomathinayagam (2000b), Reddy and Jhansilakshmi (1991a) and Lakshmanan and Guggeri (2001).

5.3.3 Days to maturity

Variability study showed that both PCV and GCV estimates were low. The studies related to same were reported by Nirmalakumari and Vetriventhan (2010), Reddy and Reddy (2012) and Prasanna *et al.* (2013) and Brunda *et al.* (2014). The heritability and genetic advance estimates were medium. Similar results were reported by Chidambaram and Palanisamy (1995), Brunda *et al.*, (2013).

5.3.4 Plant height (cm)

For plant height, the analysis revealed medium level of phenotypic coefficient of variation while it showed low genotypic coefficient of variation. The study pertaining to this observation was reported by Nirmalakumari and Vetriventhan (2010), Reddy and Reddy (2012), Prasanna *et al.* (2013) and Brunda *et al.* (2014).

Variability studies showed medium heritability (58.24%) in broad sense and also medium genetic advance as percent mean. The studies pertaining to the observation were reported by Chidambaram and Palanisamy (1995), Reddy and Reddy (2012), Prasanna *et al.* (2013), Nirmalakumari and Vetriventhan (2010) and Lakshman and Guggari (2001).

5.3.5 Panicle length (cm)

Moderate PCV and low GCV estimates were recorded for panicle length. The studies pertaining to the trait were reported by Reddy and Jhansilakshmi (1991a), Nirmalakumari and Vetriventhan (2010), Reddy and Reddy (2012), Prasanna *et al.* (2013) and Brunda *et al.* (2014).

Moderate estimates of heritability (40.80%) and genetic advance as percent mean were noticed for the trait. The studies related to the observation were reported by Reddy and Reddy (2012) and Prasanna *et al.* (2013).

5.3.6 Panicle girth (mm)

Moderate estimates of PCV and low GCV were observed for the trait. Similar results were obtained by Brunda *et al.*, (2014) and Upadhyaya *et al.* (2011). Variability study showed moderate heritability (40.80%) and genetic advance as per cent mean. The studies related to the observation were reported by Brunda *et al.* (2014) and Upadhyaya *et al.* (2011).

5.3.7 Peduncle length (cm)

Peduncle length showed moderate GCV and high PCV values with low heritability and moderate genetic advance as per cent mean. Similar results were obtained by Upadhyaya *et al.* (2011).

5.3.8 Number of tillers per meter row length

High variability in terms of GCV and PCV estimates were observed for number of tillers per meter row length. Similar findings have been reported in foxtail millet for number

of basal tillers by Nirmalakumari and Vetriventhan (2010), Nirmalakumari *et al.* (2008), Reddy and Jhansilakshmi (1991a) and Cill and Randhawa (1975).

Variability study also showed high heritability (67.02%) and high genetic advance as percent mean. The studies related to the character are reported for basal tillers by Nirmalakumari and Vetriventhan (2010), Nirmalakumari *et al.* (2008) and Upadhyaya *et al.* (2011).

5.3.9 Number of productive tillers per meter row length

High variability in terms of GCV and PCV estimates were observed for number of productive tillers per meter row length.. Similar results were reported by Reddy and Reddy (2012), Prasanna *et al.*(2013), Nagarajan and Prasad (1980), Chidambaram and Palanisamy, (1995), and Nirmalakumari and Vetriventhan(2010).

With respect to heritability (53.74%) it showed moderate value while it showed high genetic advance as percent mean. Similar results were obtained by Reddy and Reddy (2012), Prasanna *et al.* (2013), Nagarajan and Prasad (1980), Chidambaram and Palanisamy, (1995), Nirmalakumari and Vetriventhan (2010), Athwal and Gian Singh (1966) and Sandhu *et al.*(1974).

5.3.10 Number of productive tillers per plant

Number of productive tillers per plant in present study recorded high estimates of GCV, PCV. The studies pertaining to the observation is reported by Reddy and Reddy (2012), Prasanna *et al.* (2013), Nagarajan and Prasad (1980), Chidambaram and Palanisamy (1995), and Nirmalakumari and Vetriventhan (2010).

The variability study showed moderate value of heritability (57.95%) and high genetic advance as per cent of mean. Similar results were reported by Prasanna *et al.* (2013), Nagarajan and Prasad (1980), Chidambaram and Palanisamy (1995), Nirmalakumari and Vetriventhan (2010), Athwal and Gian Singh (1966), and Sandhu *et al.* (1974).

5.3.11 Area of standard leaf (cm²)

High estimates of phenotypic and moderate estimates genotypic co efficient of variation coupled with low heritability and low genetic advance as per cent mean (9.24) were recorded for the trait.

5.3.12 Stem thickness (cm)

The variability studies showed high estimates of phenotypic coefficient of variation, and moderate estimates genotypic co efficient of variation, heritability (31.37%) and genetic advance as per cent mean observed for the trait stem thickness.

5.3.13 SPAD at 50% flowering

SPAD reading at flowering is important trait for measuring photosynthetic rate of plant. There was a wide range of variation found for the character in terms of mean performance in all the lines. The variability studies showed moderate estimates of phenotypic and low estimates genotypic co efficient of variation, low heritability (21.02%) and low genetic advance as per cent mean were recorded for the trait.

5.3.14 SPAD at maturity

SPAD reading at maturity also important trait for measuring consumption rate of photosynthates at maturity. There was a wide range of variation found for the character in terms of mean performance in all the lines. For the character it showed moderate estimates of phenotypic co efficient of variation, and low estimates genotypic co efficient of variation, heritability (20.17%) and low genetic advance as per cent mean.

5.3.15 Fodder yield per plant (g)

High variability in terms of GCV and PCV were observed for the trait. Similar results were reported by Nagarajan and Prasad (1980), Chidambaram and Palanisamy (1995), Reddy and Reddy (2012), Prasanna *et al.* (2013) and Brunda *et al.*, (2014).

The variability study showed moderate heritability (45.51%) and high genetic advance as per cent mean recorded for the trait. The studies related the observation were shown by Prasanna *et al.* (2013) and Nagarajan and Prasad (1980) and Brunda *et al.* (2014).

5.3.16 Fodder yield per hectare (kg)

The variability study showed high estimates of phenotypic and high estimates genotypic co efficient of variation for fodder yield per hectare. The studies pertaining to the observation were reported by Nagarajan and Prasad (1980), Chidambaram and Palanisamy (1995), Reddy and Reddy (2012) and Prasanna *et al.* (2013). However, heritability estimates recorded for the trait were moderate (58.024%) and for genetic

advance as per cent mean, the estimates were high. Similar results were reported by Prasanna *et al.* (2013).

5.3.17 Grain yield per plant (g)

The variability studies showed high values of phenotypic co efficient of variation and moderate genotypic co efficient of variation. Similar results were reported by Nirmalakumari and vetriventhan (2010), Selvarani and Gomathinayagam (2000b) and Lakshman and Guggari (2001) and Brunda *et al.* (2014).

Moderate heritability (30.43%) and moderate genetic advance as per cent of mean estimates were observed for the trait. The studies pertaining to the observation were reported by Brunda *et al.* (2013), Nirmalakumari and Vetriventhan (2010), Reddy and Reddy (2012), Prasanna *et al.* (2013), Athwal and Gian Singh (1966), Sandhu *et al.* (1974), Nagarajan and Prasad (1980), and Chidambaram and Palanisamy (1995).

5.3.18 Grain yield per hectare (kg)

For the character, there was high variability in terms of GCV and PCV were observed. Similar results were reported by Upadhyaya *et al.* (2011), Nirmalakumari and vetriventhan (2010), Selvarani and Gomathinayagam (2000b) and Lakshman and Guggari (2001).

The variability studies showed high estimates of heritability (58.14%) and genetic advance as per cent of mean for grain yield per hectare trait. The studies pertaining to the observation were reported by Upadhyaya *et al.* (2011), Reddy and Reddy (2012), Prasanna *et al.* (2013), Athwal and Gian Singh (1966), Sandhu *et al.* (1974), Nagarajan and Prasad (1980), and Chidambaram and Palanisamy (1995).

5.3.19 Test weight (g)

For test weight, the analysis showed low phenotypic and genotypic co efficient of variation. The studies pertaining to the observation were reported by Prasanna *et al.* (2013).

The variability studies for the trait showed moderate estimates of heritability (54.42%) and genetic advance as per cent mean. Similar results were reported by Sandhu *et al.* (1974) and Prasanna *et al.* (2013).

5.4 CORRELATION COEFFICIENTS

The phenotype of a plant is the result of interaction of a large number of factors. Final yield is the sum of effect of several component factors. Amelioration of yield is the ultimate aim of the plant breeder in any crop improvement programme and this has to be achieved through gaining insight into the behavior of component characters that are associated with grain yield. Correlation studies provide information on the nature and extent of association between any two pairs of metric characters. Grafius (1959) opined that there may not be any gene for yield as such but operates only through its components. Correlation studies will help to identify the character to make selections for higher yield with a view to determine the extent and nature of relationship among the yield contributing characters.

The correlation coefficient helps a breeder in determining the degree and direction of selection and number of characters to be considered in improving the grain yield. Correlation coefficients not only denote the total association existing between a pair of characters which themselves are the result of the interaction between various features of the plant but also it measures the relationship existing between pair of characters. A dependent character is the result of interaction of many mutually associated component characters and change in any one component will disturb the whole network of cause and effect system.

Keeping these things in view correlation studies were estimated for yield and yield contributing traits.

In general, grain yield per plant and grain yield per hectare were positively significantly correlated with the traits plant height, panicle length, panicle girth, 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, SPAD at flowering, SPAD at maturity, fodder yield per plant and fodder yield per hectare. The magnitude of association was high for grain yield per plant with number of productive tillers per plant, fodder yield per plant followed by plant height. Hence, these component traits can be used as indirect selection criteria for grain yield.

Days to panicle emergence was found to be significantly and positively correlated with days to 50% flowering and days to maturity. The magnitude of association was very

high (0.87), which indicates that days to panicle emergence can be used as a criteria to identify early maturing types while screening large number of genotypes. While it was found to be significantly and negatively correlated with panicle girth, area of standard leaf, stem thickness, SPAD at 50% flowering and grain yield per hectare. These results are in support of the observations reported by Cill and Randhawa (1975).

Significant and positive correlation was recorded between days to 50% flowering with days to panicle emergence, days to panicle maturity, number of productive tillers per plant, fodder yield per plant and 1000 seed weight while significantly and negatively correlated with area of standard leaf, SPAD at 50% flowering and grain yield per hectare. It was non significantly and negatively correlated with panicle length, peduncle length, stem thickness, and fodder yield per hectare while it was non significantly and positively correlated with plant height, number of tillers per row length, number of productive tillers per meter row length, SPAD at maturity and grain yield per plant. Similar results were obtained by Brunda *et al.* (2014), Nirmalakumari and Vetriventhan (2010), Upadhyaya *et al.*

(2008), Basheeruddin and Sahib (2004), Santhakumar (1999), Chidambaram and Palanisamy (1995), Reddy and Jhansi Lakshmi (1991b), Islam *et al.* (1990) and Cill and Randhawa (1975).

Days to maturity was found to be significantly and positively correlated with days to panicle emergence, days to 50% flowering, number of productive tillers per plant, fodder yield per plant and 1000 seed weight. Whereas it was found to be significantly and negatively correlated with area of standard leaf, SPAD at 50% flowering and grain yield per hectare. It was non significantly and negatively correlated with panicle length, panicle girth, peduncle length, stem thickness and fodder yield per hectare. Similar results were reported by Brunda *et al.*, (2014), Sandhu *et al.* (1974), Chidambaram and Palanisamy (1995), Singh and Rao (1980), Cill and Randhawa (1975).

SPAD at 50% flowering was found to be significantly and positively correlated with plant height, panicle length, panicle girth, area of standard leaf, SPAD at maturity, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare while it is negatively significantly correlated with correlated with days to panicle emergence, days to 50% flowering and days to maturity.

SPAD at maturity was significantly and positively correlated with plant height, panicle length, panicle girth, area of standard leaf, stem thickness, SPAD at 50% flowering, fodder yield per plant, fodder yield per hectare, grain yield per plant, grain yield per hectare and 1000 grain weight.

High significant positive correlation observed between plant height character and panicle length, panicle girth, peduncle length, 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, stem thickness, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare. The studies pertaining to the observation are reported by Nirmalakumari and Vetriventhan (2010), Channappagoudar *et al.* (2008), Murugan and Nirmalakumari (2006), Ling *et al.* (2008), Basheeruddin and Sahib (2004), Santhakumar (1999), Reddy and Jhansi Lakshmi (1991a) and Reddy and Jhansi Lakshmi (1991b) and Islam *et al.* (1990).

For panicle length character, it was significantly and positively correlated with plant height, panicle girth, area of standard leaf, stem thickness, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare. Similar results were obtained by Nirmalakumari and Vetriventhan (2010), Upadhyaya *et al.* (2008), Sandhu *et al.* (1974), Nagarajan and Prasad (1980), Singh and Rao (1980), Murugan and Nirmalakumari (2006), Ling *et al.* (2008), Santhakumar (1999), Reddy and Jhansi Lakshmi (1991a), and Islam *et al.* (1990).

For panicle girth character, it was significantly and positively correlated with plant height, panicle length, area of standard leaf, stem thickness, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare. Studies pertaining to character were recorded by Brunda *et al.* (2014).

For peduncle length character, it was significantly and positively correlated with plant height, area of standard leaf and test weight.

With respect to number of tillers, all the three traits number of tillers per meter row length, number of productive tillers per meter row length and number of productive tillers per plant were highly significantly and positively correlated with each other, and also all these traits were significantly positively correlated with plant height, fodder yield per plant,

fodder yield per hectare, grain yield per plant and grain yield per hectare. Similar results were obtained by Nirmalakumari and Vetriventhan (2010), Channappagoudar *et al.* (2008), Upadhyaya *et al.* (2008), Islam *et al.* (1990), Reddy and Jhansi Lakshmi (1991b), Chidambaram and Palanisamy (1995).

Number of productive tillers per plant showed significant and positive correlation with panicle emergence, days to 50% flowering, days to maturity, plant height, number of tillers per meter row length, number of productive tillers per meter row length, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare while it was significantly and negatively correlated with stem thickness. Studies pertaining to character are recorded by Nirmalakumari and Vetriventhan (2010), Channappagoudar *et al.* (2008), Upadhyaya *et al.* (2008), Islam *et al.* (1990), Reddy and Jhansi Lakshmi (1991b), Chidambaram and Palanisamy (1995), Navale and Harinarayana (1987) and Brunda *et al.*, (2014).

Area of standard leaf was significantly and positively correlated with plant height, panicle length, panicle girth, peduncle length, stem thickness, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare whereas it was significantly and negatively correlated with panicle emergence, days to 50% flowering and days to maturity. Similar studies were conducted by Reddy and Lakshmi (1991) and Dhagat *et al.* (1977).

Stem thickness character was significantly and positively correlated with plant height, panicle length, panicle girth, SPAD at maturity, standard leaf area, fodder yield per hectare and grain yield per hectare while it was significantly and negatively correlated with days to panicle emergence.

Fodder yield per plant was significantly and positively correlated with panicle emergence, days to 50% flowering, days to maturity, plant height, panicle length, panicle girth, number of tillers per meter row length, number of productive tillers per meter row length, number of productive tillers per plant, Standard leaf area, SPAD at 50% flowering, SPAD at maturity, fodder yield per hectare, grain yield per plant and grain yield per hectare, and test weight. Similar results were recorded by Brunda *et al.* (2014), Murugan and Nirmalakumari (2006), Chidambaram and Palanisamy (1995), Singh and Rao (1980) and Nagarajan and Prasad (1980).

For the fodder yield per hectare trait, it was significantly and positively correlated with plant height, panicle length, panicle girth, number of tillers per meter row length, number of productive tillers per meter row length, number of productive tillers per plant, standard leaf area, stem thickness, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, grain yield per plant and grain yield per hectare, and test weight. Studies pertaining to character were reported by Murugan and Nirmalakumari (2006), Chidambaram and Palanisamy (1995), Singh and Rao (1980) and Nagarajan and Prasad (1980).

Grain yield per plant was significantly and positively correlated with plant height, panicle length, panicle girth, number of tillers per meter row length, number of productive tillers per meter row length, number of productive tillers per plant, standard leaf area, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, fodder yield per hectare, and grain yield per hectare. Same results were shown by Upadhyaya *et al.* (2011), Brunda *et al.*, (2014), Nirmalakumari and Vetriventhan (2010), Murugan and Nirmalakumari (2006), Chidambaram and Palanisamy (1995), Reddy and Lakshmi (1991), Godawat and Gupta (1981), Singh and Rao (1980) and Dhagat *et al.* (1977).

Grain yield per hectare trait showed significant and positive correlation with plant height, panicle length, panicle girth, number of tillers per meter row length, number of productive tillers per meter row length, number of productive tillers per plant, Standard leaf area, stem thickness, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, fodder yield per hectare, grain yield per plant and test weight. Whereas it was significantly and negatively correlated with panicle emergence, days to 50% flowering and days to maturity. Similar results were reported by Upadhyaya *et al.* (2011), Nirmalakumari and Vetriventhan (2010), Murugan and Nirmalakumari (2006), Chidambaram and Palanisamy (1995), Reddy and Lakshmi (1991), Godawat and Gupta (1981), Singh and Rao (1980) and Dhagat *et al.* (1977).

Test weight showed significant and positive correlation with days to 50% flowering, days to maturity, peduncle length, SPAD at maturity, fodder yield per plant, fodder yield per hectare and grain yield per hectare. The studies pertaining to the observation were reported by Reddy and Lakshmi (1991).

5.5 VARIETAL CHARACTERIZATION FOR MORPHOLOGICAL TRAITS

During the crop growth period observations were recorded in all the genotypes for some of the qualitative traits viz., anther colour (purple to deep purple, orange and white orange mixture), awn length (long, medium and short), awn colour (coloured and normal), panicle compactness (compact, medium and loose), stem and leaf pigmentation (pigmented and normal green) and grain colour (black, red, yellow and white). The seeds of foxtail millet are small and measure around 2mm in diameter. They are encased in a thin, papery hull which is easily removed upon threshing. Seed color can vary greatly between varieties grown.

For anther colour, eleven genotypes (GS 71, GS 111, GS 121, GS 204, GS 209, GS 212, GS 213, GS 243, GS 285, GS 461, SiA 3156 and FMGPM-9) showed orange and white orange mixture while remaining genotypes showed purple to deep purple colour. For awn length trait twenty three genotypes showed long awn, sixty eight genotypes showed medium length and while rest fifty eight genotypes showed short awn. For awn colour, five genotypes were coloured while rest of the genotypes are normal. For panicle compactness thirty eight genotypes were compact panicles, eighty four genotypes were medium while rest of twenty seven genotypes were having loose panicles. For stem and leaf pigmentation, twenty five genotypes were pigmented while rest of the genotypes were normal green. For grain colour, three genotypes showed black colour viz., GS 29, FMGPM-5 and FMGPM-10, one genotype showed red colour (GS 276), six genotypes showed white colour (12, GS 96, GS 203, GS 216, GS 362 and Chitra) and rest of the genotypes showed yellow colour. Similar characterization of genotypes was studied by Upadhyaya *et al.* (2011).

5.6 SUPERIORITY OF GENOTYPES FOR VARIOUS TRAITS

The top ten genotypes for each traits with their range of phenotypic values for yield and yield related traits are given Table 13. The promising genotypes identified with superiority for various traits were SR 11 (grain yield per hectare, early panicle emergence, flowering & maturity), panicle length, panicle girth, area of standard leaf, stem thickness, SPAD at flowering, GS 78 (grain yield per plant, fodder yield per plant and fodder yield per hectare plant height, panicle length, area of standard leaf, SPAD at maturity), GS 510 (Grain yield/plant, Fodder yield/plant, Fodder yield/hectare, Number of productive

tillers/meter row, Number of productive tillers/plant, Number of productive tillers/plant), GS 71 (Grain yield/plant, Fodder yield/plant, Number of productive tillers/meter row, Number of productive tillers/plant, Area of standard leaf). For earliness, promising ones were GS 33, GS 377 & GS 29 and test weight, promising ones were GS 95, GS 308, GS 207, GS 21 and HMT-100-1. Among the local collections, promising ones identified were FMGPM-11 (for grain yield per hectare and fodder yield per hectare), FMGPM-10 (for earliness), and FMGPM-2 (high plant height & panicle length). The number of diverse germplasm accessions with agronomically (earliness and high grain yield) superior traits was also identified in minicore collection for use in foxtail millet breeding (Upadhyaya *et al.*, 2011)

The superiority of genotypes for specific traits is discussed below.

GS 33 and GS 29 were the earliest with respect to panicle emergence. With respect to days to 50% flowering, fifty four lines showed early maturing when compared with the average. Among them GS 33, GS 29 and GS 307 were earliest to flower among all 149 genotypes. Regarding days to maturity, GS 33 was early to mature by taking minimum number of seventy eight days followed by genotypes, GS 377 and GS 29.

For plant height trait it exhibited a wide variation ranging from fifty six centimetres to one fifty eight centimeters. FMGPM-5 was with lowest plant height followed by Arjuna and MLTB-3 whereas the tallest plant found was GS 78 followed by GS 213.

For panicle length, thirty one genotypes performed better when compared to best check PS 4. Among them MLT-12-8 and GS 78 were having highest panicle length. For panicle girth, fifty five genotypes performed better when compared to national check PS 4. Among all the genotypes GS 511 showed highest panicle girth, and the genotypes SiA 3156 and GS 248 showed highest peduncle length.

For tillers per meter row length, one hundred nineteen genotypes performed better than best check PS 4 while 76 performed above average values. Among all the lines GS 510 showed highest number of tillers followed by GS 212.

For number of productive tillers per meter, it was found out that one hundred twelve genotypes significantly exceeded the best check PS 4, while sixty eight genotypes performed above average value. Among all the genotypes GS 510 showed highest number of productive tillers per meter followed by GS352.

Table 13. Top 10 genotypes and their range of values for yield and yield components among 149 germplasm accessions of Foxtail millet evaluated during *kharif* 2014 at RARS, Vijayapur

Sl. No.	Character	Genotypes	Range among top 10 genotypes.
1	Days to panicle emergence	GS 33, GS 29, GS 301, SR 11, GS 377, PS4, SiA 326, SiA 3088, GS 266, GS 403.	42-51
2	Days to 50% flowering	GS 33, GS 377, FMGPM-10, GS 29, GS 106, GS 266, GS 379, SR 11, SiA 326, GS 103.	48-55
3	Days to maturity	GS 33, GS 377, FMGPM-10, GS 29, GS 106, GS 266, SR 11, SiA 326, GS 103, GS 379.	78-85
4	Plant height (cm)	GS 78,GS 213,FMGPM-2,GS 64,GS 215,GS 264,GS 362,GS 95,GS 372,GS 310.	158.3-151.3
5	Panicle length (cm)	MLT B-8,GS 78,SR 11,GS 45,FMGPM-2,PS4,GS 415,SiA 3085,SiA 2593,GS 362.	23.5-18.4
6	Panicle girth (mm)	GS 511,SiA 3156,GS 29,GS 250,GS 17,GS 78,GS 12,FMGPM-6,SR 11,SiA 2644.	18.3-14.5
7	Peduncle length (cm)	GS 248,GS 210,GS 494,GS 208,SiA 326,GS 64,GS 206,MLT-12-12,FMGPM-6,GS 478.	21.3-18
8	No of tillers/meter row length	GS 510, GS 212, GS 352, GS 453,GS 106,GS 285, GS 8, GS 121, GS 246, GS 266.	73-57
9	Number of productive tillers/meter row	GS 510, GS 212, GS 352, GS 453, GS 285, GS 106, GS 121, GS 8, GS 246, GS 71.	73-56
10	Number of productive tillers/plant	GS 71, GS 213, GS 510, GS 207, GS 206, GS 218, GS 214, GS 211, GS 293, GS 221.	10-13
11	Area of standard leaf (cm ²)	SiA 326, GS 215, MLT-12-8, GS 362, GS 78, GS 71, H 1, GS 352, GS 96, SR 11.	78.8-160.9
12	Stem thickness (cm)	GS 338, GS 250 GS 362, SR 11 GS 35, GS 91, GS 511, GS 26, SiA 326, GS 401.	1.59-3.09
13	SPAD at 50% flowering	SR 11, GS 266, GS 12, SiA 326, SiA 3156, GS 78, GS 264, GS 121, GS 344, K 3.	45.17-48.12
14	SPAD at maturity	SiA 3156, GS 17, GS 77, GS 213, GS 78, GS 62, SiA 3085, TNAU 186, GS 215, GS 64.	32.37-41.57
15	Grain yield/plant (g)	GS 71, GS 221, GS 78, GS 18, GS 77, GS 510, GS 45, GS 206, PS4, GS 293.	43.36-55.24
16	Grain yield/hectare (kg)	SiA 3156, SiA 2593, Co7, GS 121, SR 11, GS 336, GS 64, GS 12, SiA 2644, FMGPM-11.	2314.8-2717.6
17	Fodder yield/plant (g)	GS 71, GS 216, GS 213, GS 94, GS 221, GS 78, GS 250, GS 510, Co 2, GS 210.	190-26
18	Fodder yield/hectare (kg)	GS 363, GS 510, K 3, FMGPM-11, Co7, GS 78, GS 121, GS 213, SiA 2644, GS 352.	4407-5388
19	1000 seed weight (g)	GS 95, GS 308, GS 207, GS 21, HMT-100-1, SiA 2622, GS 289, Co7, GS 218, GS 336.	4.04-4.44

For number of productive tillers per plant, twenty five genotypes performed superior to national check variety PS 4 while sixty one lines found superior to average mean value. Among all the lines GS 71 was having highest number of productive tillers per plant.

With respect to standard leaf area, SiA 326 was having largest leaf area followed by GS 215 and MLT-12-8. GS 338 found to have thickest stem followed by GS 250.

For SPAD reading at flowering, SR 11 was with the dark green leaves recorded highest SPAD value followed by GS 226. Whereas for SPAD reading at maturity, SiA 3156 showed highest SPAD value followed by GS 17.

However, with respect to percent reduction in SPAD values from flowering to maturity, the genotype SiA 3156 (10.83) showed lowest value followed by GS 215 (11.10) and GS 17(12.60) and the range of values among 149 genotypes was 10.83 to 60.69 percent and mean was 36.24. the results indicated that these genotypes maintained greenness of leaves even at maturity. The stay green genotypes play a role in moisture stress situations, hence these genotypes may be tested for terminal drought tolerance. The other genotypes which showed lowest value with respect to percent reduction in SPAD value from flowering to maturity were GS 343(16.60), GS 62(17.65), GS 213(18.65), H 2(18.90), SiA 3085(19.11), GS 77(20.44) and FMGPM-2(20.81).

For grain yield per plant sixty nine genotypes recorded above average mean value while nine lines performed superior to check variety PS 4. Among all lines GS 71 was recorded highest grain yield followed by GS 221. For grain yield per hectare, twenty five genotypes recorded significantly higher grain yield per hectare when compared with national check PS-4. It was found that variety SiA 3156 was the highest yielding variety among all the lines followed by SiA 2593.

For fodder yield per plant, fifteen lines showed high fodder yield per plant when compared to check variety PS 4 while fifty seven lines performed above average. Among all the genotypes GS 71 showed highest fodder yield per plant followed by GS 216. For fodder yield per hectare, seventy two genotypes showed better performance of above average mean value, among them GS 363 was superior followed by GS 510.

Among all lines, GS 95 recorded highest test weight followed by GS 308 and GS 207.

5.7 SCREENING GENOTYPES FOR GRAIN NUTRIENTS CONTENT

Foxtail millet grains are rich in protein, minerals (calcium, iron, potassium, magnesium, and zinc) and vitamins (Rai, 2002). It is not only widely used as an energy source for pregnant and lactating women, but also for sick people and children, and especially for diabetics. It reduces blood sugar concentration in women diabetics (Sema and Sarita, 2002). The grains have long shelf-life, a preferable attribute (Ravi *et al.*, 2010). It has been suggested to use foxtail millet protein as a food component to fight type 2 diabetes and cardiovascular diseases (Choi *et al.*, 2005). In spite of the foxtail millet being beneficial to health, it remained a neglected crop from the mainstream of crop improvement research compared to cereals such as maize (*Zea mays*), rice (*Oryza sativa*), wheat (*Triticum aestivum*), sorghum (*Sorghum bicolor*), and pearl millet (*Pennisetum glaucum*) (Upadhyaya *et al.*, 2011). Number of diverse germplasm accessions with agronomically (earliness and high grain yield) and nutritionally (high seed protein, calcium, iron and zinc) superior traits were identified by Upadhyaya *et al.*, (2011) in a minicore collection for use in foxtail millet breeding.

In the present study, 25 lines were chosen from the list of 149 genotypes of foxtail millet based on their diversity, superiority for various traits, and were assessed for varietal differences for grain protein (%) and micronutrients (Zn, Fe, Ca) contents. Among the genotypes, the two agronomically superior lines viz., GS 78 & GS 71 were found to be nutritionally superior also in terms grain nutrients content (protein & micronutrients). The genotype GS 78 was found superior for grain protein (%), zinc, iron and calcium content, and GS 71 grain protein (%), zinc and calcium content. The nutritional data is presented in Table 12 and the results are discussed below.

5.7.1 Grain protein content (%)

Among 25 genotypes screened, the wide range was observed (6.2-10.89%). GS 95 (10.89%) showed highest protein content followed by GS 64, GS 12, GS 78, GS 71. A total 9 genotypes were performed better than all the three check varieties (PS 4, HMT-100-1, SiA 326). Seetharam *et al.* (1983) noted that the variability available for protein content in foxtail millet ranged from 7.16 to 15.73 per cent and identified the sources with high protein for both direct exploitation and use in breeding. Kumar and Parmeswaran (1998) studied the characterization of storage protein from selected varieties of foxtail millet. Protein

content of grain of foxtail millet was 91.7, 105.2 and 112.0 g/kg in Cv. CO 6, TNAU 172 and TNAU 173, respectively. Ravindran (2003) reported the average protein content of foxtail millet was 15.9%.

5.7.2 Grain Zinc content (mg/100g)

For grain Zn content, the range of values observed was 2.29-11.4 mg/100g. GS 121 showed highest Zn (11.4 mg/100g) content followed by GS 78, GS 71, GS 213 and GS 106, which were better than all the three check varieties (PS 4, HMT-100-1, SiA 326).

5.7.3 Grain Iron content (mg/100g)

For grain iron content, the range of values observed was 0.33 to 16.26 mg/100g. Among 25 genotypes, GS 121 (16.26 mg/100g) showed highest Fe content followed by GS 78, GS 310, GS 106 and GS 64. A total of 18 genotypes were found superior to all the three check varieties (PS 4, HMT-100-1, SiA 326).

Phillip and Maloo (1996) evaluated 40 diverse varieties of foxtail millet for their iron content. The varieties were classified into high, moderate, and low iron content categories.

5.7.4 Grain Calcium content (mg/100g)

For grain calcium content, the range of values observed among the varieties was 1.99 to 22.69 mg/100g. GS 78 showed highest Ca (22.69 mg/100g) content followed by GS 106, GS 12, GS 121, GS 95, GS 71 and TNAU 186, which were better than all the three check varieties (PS 4, HMT-100-1, SiA 326).

A significant variation in calcium content of five minor millets was recorded with values ranging from 12.36 to 29.17 mg/100 g and little millet was reported to contain 12.36 mg calcium (Kulkarni *et al.*, 1992). Veena *et al.*, (2005) reported that the calcium and iron content of barnyard millet varieties ranged from 17.1 to 32.7 and 1.2 to 1.5 mg/100g seed, respectively.

Future line of work

1. 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 may be used in hybridization programme to widen the genetic base and hence used in varietal development.

2. 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.
3. The genotypes identified for their superiority for specific traits like early maturity (GS 35), plant height (GS 213), no. of tillers (GS 510), high SPAD values (GS 17, GS 213 & GS 207), panicle length (MLT-12-8 & SR 11), Panicle girth (GS 511), test weight (GS 207, MLT-12-8, HMT-100), grain yield (SR 11 & GS 510) and fodder yield/plant (SR 11 & GS 35) may be utilized in breeding for specific traits.
4. The genotypes which showed minimum reduction in chlorophyll content in terms of percent reduction in SPAD values from flowering to maturity (SiA 3156, GS 215, GS 17, GS 343 & GS 62) may further be tested for stay-green/terminal drought tolerance under moisture stress conditions.
5. The genotypes recorded with high protein, iron, zinc and Ca content may be further utilized in breeding for these nutritional traits.
6. The two agronomically superior lines viz., GS 78 & GS 71 were found to be nutritionally superior also in terms grain nutrients content (protein & micronutrients) may be utilized in value addition.
7. The genotypes with colored grains may be tested for anti-oxidants content and hence tested for keeping quality of processed grains.
8. The promising genotypes identified in the present study viz., SR 11, GS 213, GS 511, GS 510, GS 78, GS 71, GS 35, FMGPM-11 may be tested along with check varieties in large scale multilocation trials.

VI SUMMARY AND CONCLUSION

The present study was aimed to assess the genetic variability and genetic diversity among foxtail millet germplasm collections for various qualitative and quantitative traits; to characterize the selected genotypes for grain nutrients content; and to study the association between various traits. A total of 149 genotypes (involving germplasm lines, released varieties, advanced lines and local collections) formed the experimental material. Among these, 100 germplasm lines and 26 varieties were obtained from Project Co-ordinating Unit (small millets), GKVK, UAS, Bangalore, 11 local collections made (from Koppal district of Karnataka), and 12 genotypes from ARS, Hanumanamatti, Karnataka. These lines were evaluated during *kharif* 2014 in a replicated trial in RBD design at Regional Agricultural Research Station, Vijayapur for yield and yield traits.

The observations were recorded on 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 (cm²), 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. Also, all the lines were observed for various morphological characters like anther colour, awn length, awn colour, panicle compactness, stem and leaf pigmentation and grain colour. A total of 25 selected genotypes were screened for grain nutrient contents (protein, iron, zinc and calcium).

The data recorded on various traits were subjected to Mahalanobis D² statistical analysis, variability analysis and correlation coefficient analysis. The results pertaining to the investigation are briefly summarized below.

6.1 Analysis of variance

The analysis of variance revealed that significant differences were observed for all the traits studied including yield and yield components indicating the presence of considerable amount of variability in the material under study for various traits.

6.2 Genetic diversity analysis

In the present study, D² analysis was applied to assess the diversity available among available germplasm lines of foxtail millet for 19 quantitatively measured traits. 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%).

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. The genotypes identified in solitary clusters were MLT-13-3 (cluster II), GS 27 (cluster III), SR 11 (cluster IV), MLT-13-9 (cluster V), GS 213 (cluster VI), MLT-13-10 (cluster VII), GS 510 (cluster IX), MLT-12-11 (cluster X), GS 17 (cluster XI), MLT-12-8 (cluster XII), GS 511 (cluster XIII), GS 35 (cluster XIV) and GS 338 (cluster XV).

Maximum intra cluster distance among the genotypes was recorded by cluster I (20.45) followed by cluster VIII (13.51). The inter cluster distances were varied from 12.08 to 138.62. 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.

All the 149 genotypes were spread over fifteen clusters and means were scored across the clusters for all the nineteen characters. 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 these as most promising genotypes that can be extensively used for further breeding programme to generate new material. The solitary clusters identified based on high cluster means for various traits were, cluster XI (GS-17) for early maturity; VI (GS 213) for plant height; XII (MLT-12-8) and IV (SR 11) for panicle length; IX (GS 510) for number of tillers/m row length, number of productive tillers/m row length, number of productive tillers/plant; XI (GS 17), VI (GS 213) and III (GS 207) for SPAD at both flowering and maturity stages; IX (GS 510) and IV (SR 11) for both grain yield per plant and grain yield per hectare; VI (GS 213) and IX (GS 510) for fodder yield per plant; and III (GS 207), V (MLT-12-9) and X (HMT-100-1) for 1000 seed weight (> 4.0 g).

6.3 Genetic variability parameters

High GCV and high PCV estimates were observed for number of tillers per meter row length, number of productive tillers per meter row length, number of productive tillers per plant, fodder yield per plant, fodder yield per hectare, grain yield per hectare, low PCV and low GCV were recorded for days to panicle emergence, days to 50 per cent flowering, days to maturity, test weight, high PCV and moderate GCV were observed for area of standard leaf, stem thick ness, grain yield per plant, moderate PCV and low GCV for panicle length, panicle girth, SPAD at 50% flowering, SPAD at maturity, plant height, and moderate PCV and high GCV estimates were observed for peduncle length.

Estimates of high heritability and high genetic advance over mean were recorded for number of tillers per meter row length, grain yield per hectare; moderate heritability and high genetic advance over mean observed for number of productive tillers per meter row length, number of productive tillers per plant, fodder yield per plant, fodder yield per hectare; moderate heritability and moderate genetic advance for days to panicle emergence, days to maturity, plant height, panicle length, panicle girth, stem thickness, grain yield per plant, test weight; high heritability and low genetic over mean observed for days to 50 per cent flowering; low heritability and low genetic advance over mean was recorded for area of standard leaf, SPAD at 50% flowering, SPAD at maturity; and low heritability and medium genetic advance over mean was recorded by peduncle length.

6.4 Correlation coefficients

In general, grain yield per plant and grain yield per hectare were positively significantly correlated with the traits plant height, panicle length, panicle girth, 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, SPAD at flowering, SPAD at maturity, fodder yield per plant and fodder yield per hectare. The magnitude of association was high for grain yield per plant with number of productive tillers per plant, fodder yield per plant followed by plant height. Hence, these component traits can be used as indirect selection criteria for grain yield.

Days to maturity was found to be significantly and positively correlated with days to panicle emergence, days to 50% flowering, number of productive tillers per plant, fodder yield per plant and 1000 seed weight.

SPAD at maturity was significantly and positively correlated with plant height, panicle length, panicle girth, area of standard leaf, stem thickness, SPAD at 50% flowering, fodder yield per plant, fodder yield per hectare, grain yield per plant, grain yield per hectare and 1000 grain weight.

High significant positive correlation observed between plant height character and panicle length, panicle girth, peduncle length, 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, stem thickness, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare.

For peduncle length character, it was significantly and positively correlated with plant height, area of standard leaf and test weight.

With respect to number of tillers, all the three traits number of tillers per meter row length, number of productive tillers per meter row length and number of productive tillers per plant were highly significantly and positively correlated with each other, and also all these traits were significantly positively correlated with plant height, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare.

Area of standard leaf was significantly and positively correlated with plant height, panicle length, panicle girth, peduncle length, stem thickness, SPAD at 50% flowering, SPAD at maturity, fodder yield per plant, fodder yield per hectare, grain yield per plant and grain yield per hectare whereas it was significantly and negatively correlated with panicle emergence, days to 50% flowering and days to maturity.

Test weight showed significant and positive correlation with days to 50% flowering, days to maturity, peduncle length, SPAD at maturity, fodder yield per plant, fodder yield per hectare and grain yield per hectare.

6.5 Varietal characterization for morphological traits

During the crop growth period observations were recorded in all the genotypes for some of the qualitative traits. The distribution among 149 genotypes for these traits is as follows: anther colour (11 orange and white orange mixture and 138 purple to deep purple colour), awn length (23 long: 68 medium: 58 short), awn colour (5 coloured: 144 normal), panicle compactness (38 compact: 84 medium: 27 loose), stem and leaf pigmentation (25 pigmented: 124 normal green) and grain colour (3 black: 1 red: 6 white: 139 yellow).

6.6 Superiority of genotypes for various traits

The promising genotypes identified with superiority for various traits were SR 11 (grain yield per hectare, early panicle emergence, flowering and maturity), Co 7 (panicle length, panicle girth, area of standard leaf, stem thickness, SPAD at flowering), GS 78 (grain yield per plant, fodder yield per plant and fodder yield per hectare plant height, panicle length, area of standard leaf, SPAD at maturity), GS 510 (grain yield/plant, fodder yield/plant, fodder yield/hectare, number of productive tillers/meter row, number of productive tillers/plant, number of productive tillers/plant) and GS 71 (Grain yield/plant, Fodder yield/plant, Number of productive tillers/meter row, Number of productive tillers/plant, Area of standard leaf). For earliness, promising ones were GS 33, GS 377 and GS 29 and test weight, promising ones were GS 95, GS 308, GS 207, GS 21 and HMT-100-1. Among the local collections, promising ones identified were FMGPM-11 (for grain yield per hectare and fodder yield per hectare), FMGPM-10 (for earliness) and FMGPM-2 (high plant height and panicle length).

6.7 Screening genotypes for grain nutrients content

In the present study, 25 lines were chosen from the list of 149 genotypes of foxtail millet and were assessed for varietal differences for grain protein (%) and micronutrients (Zn, Fe, Ca) contents. The range of values for grain nutrients content among the genotypes observed was for protein (6.2-10.89%), zinc content (2.29-11.4 mg/100g), iron content (0.33 to 16.26 mg/100g) and calcium content (1.99 to 22.69 mg/100g). Among the genotypes, the two agronomically superior lines viz., GS 78 and GS 71 were found to be nutritionally superior also in terms of grain nutrients content (protein and micronutrients). The genotype GS 78 was found superior for grain protein (%), zinc, iron and calcium content, and GS 71 grain protein (%), zinc and calcium content.

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APPENDIX I. Meteorological data for the year 2014 at Regional Agricultural research Station Vijayapur

Month	Air Temperature		Relative Humidity		Wind Speed (KMPH)	Sunshine Duration (h)	Total Rainfall (mm)	Rainy Days	Pan Evaporation (mm/day)
	Max (C)	Min (C)	AM (%)	PM (%)					
January	29.7	15.2	79	37	5.0	8.3	0.0	0	4.1
February	31.7	16.1	66	33	5.3	9.0	6.4	1	5.5
March	34.5	20.1	61	29	5.8	8.8	27.4	2	6.8
April	38.0	22.7	56	24	7.2	7.6	27.0	2	8.1
May	37.6	22.9	75	31	9.9	7.8	68.6	4	7.8
June	35.0	22.7	81	43	16.7	7.6	54.4	4	7.2
July	30.1	21.6	88	64	15.4	3.4	151.6	7	4.4
August	30.2	21.3	89	63	11.8	5.5	245.7	8	4.3
September	30.7	21.1	88	56	10.4	5.9	59.4	4	4.2
October	31.9	19.6	84	48	4.9	7.7	65.3	4	4.3
November	30.4	15.6	85	42	4.0	7.8	15.0	3	3.6
December	29.0	13.0	83	41	3.6	7.8	16.0	2	3.5

APPENDIX II. Mean performance of 149 germplasm accessions of foxtail millet evaluated during kharif season 2014 at RARS, Vijayapur

Sl. No.	Genotypes	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/m row	No. of prod. Tillers/m row	No. of prod. Tillers /plant
1	GS 5	55.00	60.00	90.00	129.50	16.78	13.01	14.92	51.00	49.50	6.67
2	GS 6	57.50	61.00	91.00	117.33	10.28	10.63	13.08	43.00	41.50	6.83
3	GS 8	56.00	58.50	88.50	121.67	12.17	10.75	12.33	59.00	57.00	7.17
4	GS 12	53.50	57.50	87.50	135.33	17.50	14.90	13.17	37.00	35.50	5.50
5	GS 17	57.00	61.00	91.00	129.33	14.67	15.52	12.83	34.50	31.00	4.17
6	GS 18	58.50	61.50	91.50	134.17	16.55	13.10	14.58	32.00	31.00	9.00
7	GS 21	57.50	61.00	91.00	128.33	16.50	11.14	14.50	43.50	41.50	8.50
8	GS 26	55.50	60.50	90.50	135.17	14.58	13.82	12.17	55.50	53.50	5.33
9	GS 33	42.00	48.00	78.00	108.67	13.33	12.85	14.83	28.50	26.00	1.00
10	GS 35	53.50	58.50	88.50	124.17	15.17	12.57	16.92	25.00	26.50	4.50
11	GS 29	46.50	55.00	85.00	132.67	15.50	15.91	14.25	41.00	38.50	7.00
12	GS 42	57.50	61.50	91.50	129.83	13.50	11.52	14.83	52.00	50.00	8.83
13	GS 45	55.00	59.50	89.50	138.17	19.50	13.80	14.17	44.50	42.50	7.33
14	GS 47	52.50	57.00	87.00	130.50	15.17	10.19	13.08	35.00	34.00	6.50
15	GS 53	54.00	59.50	89.50	140.33	16.67	10.49	14.50	56.50	47.00	10.20
16	GS 56	53.50	59.00	89.00	140.17	14.33	12.83	16.83	45.50	44.50	6.33
17	GS 60	53.00	59.00	89.00	140.00	17.08	12.68	15.08	51.50	51.00	7.33
18	GS 62	57.00	61.50	91.50	126.17	14.12	13.70	13.17	46.50	45.50	8.65
19	GS 64	57.50	64.50	94.50	153.17	14.63	11.91	19.42	54.00	52.00	7.83
20	GS 71	59.00	61.00	91.00	144.67	18.25	14.01	14.47	57.00	56.00	13.17
21	GS 77	56.00	59.50	89.50	136.67	17.17	13.03	12.24	37.50	36.00	8.00
22	GS 78	54.50	63.50	93.50	158.33	21.42	15.05	10.75	49.50	47.00	8.00
23	GS 91	56.00	63.00	93.00	127.83	14.12	14.36	13.82	37.00	34.00	6.67

APPENDIX II (contd...)

Sl. No.	Genotypes	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/m row	No. of prod. Tillers/m row	No. of prod. Tillers /plant
24	GS 94	55.50	61.00	91.00	139.00	16.88	11.16	15.17	46.50	42.00	4.17
25	GS 95	54.50	62.00	92.00	152.00	17.83	14.21	17.42	51.00	49.50	6.17
26	GS 96	54.00	59.50	89.50	148.00	15.58	12.50	17.17	38.00	37.00	6.00
27	GS 97	54.00	59.50	89.50	131.00	14.25	13.76	15.92	37.00	35.50	8.30
28	GS 103	53.50	55.50	85.50	132.67	15.25	12.95	16.25	34.00	32.50	7.33
29	GS 105	53.50	58.50	88.50	132.00	13.33	10.98	14.25	54.00	52.50	8.00
30	GS 106	52.00	55.00	85.00	132.67	17.00	13.19	15.32	61.00	58.50	7.00
31	GS 111	57.00	60.00	90.00	138.33	15.58	13.04	13.75	31.50	31.00	4.67
32	GS 121	56.00	59.50	89.50	147.00	18.00	12.94	12.00	59.00	58.50	8.33
33	GS 140	57.00	59.50	89.50	127.00	11.58	10.79	16.33	44.50	42.50	6.17
34	GS 158	57.50	63.00	93.00	134.00	12.83	10.88	16.17	45.00	44.00	5.67
35	GS 200	53.50	59.00	89.00	135.33	17.17	12.33	12.58	53.00	52.50	6.67
36	GS 203	60.50	64.50	94.50	143.17	15.08	12.39	14.75	54.00	52.50	9.17
37	GS 204	60.00	65.00	95.00	145.17	16.67	10.03	17.25	47.50	47.00	10.30
38	GS 205	59.00	63.50	93.50	129.17	15.00	10.71	13.08	36.50	35.50	8.00
39	GS 206	54.00	58.00	86.00	131.33	12.08	11.28	18.67	44.00	43.00	12.33
40	GS 207	58.50	63.50	93.50	135.67	15.58	12.01	17.50	43.50	42.00	12.50
41	GS 208	59.00	63.00	93.00	149.67	14.50	10.94	19.92	48.00	45.50	8.17
42	GS 209	56.00	59.50	89.50	138.33	15.08	10.82	15.92	44.50	40.50	9.00
43	GS 210	60.00	64.00	94.00	147.17	17.08	13.02	20.67	43.00	40.50	7.50
44	GS 211	58.50	61.00	91.00	144.50	15.42	13.47	15.17	50.50	49.00	11.00
45	GS 212	58.00	61.00	91.00	139.33	15.00	11.25	11.83	66.00	64.00	10.17
46	GS 213	60.00	64.00	94.00	156.50	17.08	12.41	13.25	56.00	55.00	12.67

APPENDIX II (contd...)

Sl. No.	Genotypes	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/m row	No. of prod. Tillers/m row	No. of prod. Tillers /plant
47	GS 214	59.00	64.00	94.00	150.83	16.67	11.99	14.17	45.50	47.50	11.17
48	GS 215	58.50	62.50	92.50	152.33	17.17	12.98	16.67	34.00	33.00	6.17
49	GS 216	58.00	61.00	91.00	144.50	15.83	11.61	14.33	53.00	49.50	10.17
50	GS 218	58.00	62.00	92.00	141.50	16.00	11.84	17.08	51.00	49.50	11.83
51	GS 219	59.00	62.50	92.50	130.33	17.75	11.70	13.58	29.00	29.00	9.83
52	GS 220	60.50	65.00	95.00	131.83	13.33	12.07	11.75	43.00	40.50	10.33
53	GS 221	58.00	61.50	91.50	138.50	14.53	11.02	12.08	54.50	54.00	10.50
54	GS 222	59.50	62.50	92.50	142.33	14.92	9.98	11.50	56.50	55.00	7.33
55	GS 242	56.00	59.50	89.50	130.50	15.92	12.04	13.58	48.50	46.50	8.00
56	GS 243	58.50	62.00	92.00	146.00	15.77	10.89	17.17	53.00	50.00	8.17
57	GS 246	54.00	62.50	92.50	123.50	12.17	11.61	15.92	58.00	56.50	6.00
58	GS 248	54.00	58.00	88.00	148.00	18.00	11.83	21.33	33.00	32.50	8.50
59	GS 250	55.00	59.00	87.00	148.33	17.42	15.89	16.58	35.00	33.00	5.50
60	GS 256	56.00	62.50	92.50	140.33	14.33	13.25	15.58	44.50	43.50	6.50
61	GS 260	58.50	61.00	91.00	151.33	17.50	12.56	16.00	35.50	35.50	7.83
62	GS 264	60.00	63.50	93.50	152.17	16.25	12.57	17.75	40.50	45.50	6.00
63	GS 266	51.50	55.00	85.00	142.50	16.67	11.96	17.58	57.50	56.00	5.50
64	GS 271	58.50	61.00	91.00	143.83	13.17	10.80	14.08	40.50	39.00	5.83
65	GS 276	55.00	58.50	86.50	146.33	15.33	12.86	16.92	32.50	31.50	4.00
66	GS 280	58.50	61.50	91.50	135.17	17.00	12.34	12.50	45.00	44.00	7.67
67	GS 282	55.00	59.50	89.50	143.00	15.75	11.47	15.92	43.50	43.00	7.33
68	GS 285	54.00	60.50	90.50	134.17	17.00	11.06	12.17	59.50	59.00	8.33
69	GS 289	57.00	62.50	92.50	142.00	16.67	10.99	12.67	48.50	46.50	7.17

APPENDIX II (contd...)

Sl. No.	Genotypes	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/m row	No. of prod. Tillers/m row	No. of prod. Tillers /plant
70	GS 293	55.00	60.50	90.50	138.33	13.67	12.26	12.83	50.50	50.50	10.83
71	GS 301	47.50	56.00	86.00	125.83	13.92	11.49	15.75	55.00	53.50	5.50
72	GS 310	57.00	61.50	91.50	151.33	15.58	12.32	14.33	45.50	43.50	5.33
73	GS 316	60.50	64.50	94.50	136.67	17.75	12.46	14.83	39.50	38.50	4.67
74	GS 335	54.00	58.50	88.50	144.67	17.05	12.89	14.50	38.50	36.50	6.33
75	GS 336	53.50	58.00	88.00	143.67	17.08	13.24	16.33	47.50	46.00	6.17
76	GS 337	53.50	56.50	86.50	136.33	16.58	12.64	13.00	49.50	47.50	7.83
77	GS 308	57.50	61.00	91.00	127.67	16.17	11.89	12.17	36.00	34.50	6.83
78	GS 338	55.00	60.50	90.50	133.67	12.58	11.96	11.67	43.00	41.50	4.83
79	GS 343	57.00	62.50	92.50	148.50	17.50	11.00	17.25	53.50	52.50	8.33
80	GS 344	55.50	62.50	92.50	146.33	13.75	13.86	16.08	33.00	31.50	4.50
81	GS 352	57.50	64.50	94.50	141.67	16.58	13.56	12.58	64.00	61.50	8.33
82	GS 362	59.00	61.50	91.50	152.00	18.42	12.61	14.25	47.50	31.00	5.33
83	GS 363	56.50	60.00	90.00	143.17	16.58	12.17	15.00	51.50	51.00	8.83
84	GS 372	56.00	60.00	90.00	151.33	16.17	13.44	14.67	39.50	38.00	9.83
85	GS 377	50.00	54.50	84.00	105.17	14.17	12.06	8.67	38.00	36.50	4.00
86	GS 378	54.00	57.50	87.50	141.33	17.58	11.57	12.83	31.00	30.00	5.50
87	GS 379	52.00	55.00	85.50	134.67	17.00	12.91	15.58	29.00	28.50	5.67
88	GS 401	56.00	60.50	90.50	138.50	17.92	13.93	10.25	32.00	31.50	4.50
89	GS 403	51.50	55.50	85.50	132.17	15.75	12.52	15.50	44.00	43.00	6.00
90	GS 415	59.00	63.00	93.00	122.83	18.75	11.12	14.00	33.00	31.00	4.33
91	GS 426	55.00	60.00	90.00	134.17	15.25	10.41	15.25	42.00	41.00	9.67
92	GS 433	58.50	63.00	93.00	139.00	15.92	11.00	10.92	49.50	46.50	6.33

APPENDIX II (contd...)

Sl. No.	Genotypes	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/m row	No. of prod. Tillers/m row	No. of prod. Tillers /plant
93	GS 499	58.50	63.00	93.00	140.17	16.17	10.65	12.33	49.00	47.50	4.67
94	GS 453	54.00	56.00	86.00	123.50	15.50	11.10	12.17	63.50	60.00	8.00
95	GS 461	57.50	65.00	95.00	144.17	18.25	12.48	13.33	50.50	50.00	7.17
96	GS 472	56.50	59.50	89.50	145.00	14.75	12.85	15.50	41.50	38.00	8.00
97	GS 478	57.50	61.50	91.50	140.67	17.17	13.66	18.00	37.50	36.50	6.00
98	GS 494	58.00	61.00	91.00	146.67	15.50	11.57	20.25	36.00	33.50	6.33
99	GS 510	61.00	64.50	94.50	141.67	14.92	12.12	15.25	73.50	73.00	12.67
100	GS 511	59.50	62.50	92.50	134.33	10.83	18.29	15.75	26.50	24.50	3.00
101	SiA 3156	53.50	59.00	89.00	133.50	17.33	16.06	13.00	41.00	39.50	4.67
102	SiA 3088	51.00	56.50	86.50	122.83	15.88	12.90	17.75	43.50	42.00	5.67
103	SiA 3085	53.00	57.50	87.50	137.83	18.67	13.09	13.00	41.50	41.00	6.67
104	Co7	56.00	63.50	93.50	148.33	16.83	13.49	13.00	57.00	54.00	7.17
105	SR 51	55.50	60.50	90.50	146.17	16.92	11.49	15.25	49.50	47.00	6.83
106	SiA 2644	57.00	63.50	93.50	148.17	17.75	14.54	12.33	40.00	39.50	5.67
107	SR 16	55.50	60.50	90.50	135.67	15.00	12.21	12.58	51.00	52.50	7.00
108	PS4	50.50	57.50	86.50	139.33	18.75	12.74	14.75	33.00	32.50	8.83
109	TNAU 186	51.50	56.50	86.50	140.50	14.08	13.80	14.17	49.00	48.50	5.50
110	SR 11	49.00	55.00	85.00	142.33	20.58	14.65	15.75	31.00	32.00	4.83
111	SiA 2622	54.00	59.00	89.00	150.17	18.17	13.47	13.25	42.00	40.00	6.17
112	SiA 2593	54.00	57.50	87.50	133.00	18.50	12.98	14.42	55.50	52.00	9.00
113	Lepakshi	60.00	62.50	92.50	145.00	14.67	13.17	13.67	32.50	31.50	6.83
114	K 3	60.00	64.50	94.50	148.33	16.92	12.07	14.08	53.00	52.50	6.83
115	SiA 326	50.50	55.00	85.00	137.00	12.67	13.70	19.67	32.50	32.50	4.67

APPENDIX II.(cond...)

Sl. No.	Genotypes	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/m row	No. of prod. Tillers/m row	No. of prod. Tillers /plant
116	Co5	59.50	62.50	92.50	147.50	14.75	13.52	15.92	40.50	40.00	10.00
117	Chitra	57.50	61.00	91.00	138.17	15.67	11.48	16.58	51.50	50.50	6.33
118	K2	54.50	57.50	87.50	131.00	12.67	11.24	14.42	40.00	38.50	5.67
119	Co 4	52.00	55.50	85.50	139.33	13.25	12.22	11.58	47.50	45.50	5.50
120	RS 118	54.50	58.50	88.50	142.83	15.42	10.89	13.33	44.50	43.50	7.83
121	K 221-1	55.00	60.00	90.00	134.00	14.42	12.77	12.33	29.50	28.00	7.33
122	Arjuna	58.00	62.50	92.50	58.00	16.67	12.35	15.75	41.00	41.00	3.50
123	H 1	52.00	56.50	86.50	134.50	16.17	14.29	14.92	44.50	43.50	4.33
124	H 2	57.00	62.00	92.00	146.67	14.00	12.73	13.75	35.00	35.00	4.00
125	Co 1	55.50	60.50	90.50	142.50	15.75	12.85	17.50	37.50	36.00	4.67
126	Co 2	55.50	60.00	90.00	133.33	16.08	12.63	16.17	44.50	39.50	5.50
127	FMGPM-1	58.50	62.50	92.50	144.33	15.50	12.94	17.08	43.50	42.50	8.33
128	FMGPM-2	56.00	62.00	92.00	154.17	18.83	14.21	17.17	32.00	32.00	6.67
129	FMGPM-3	54.00	60.00	90.00	132.33	15.50	13.71	11.83	41.00	40.00	9.17
130	FMGPM-4	56.50	60.00	90.00	149.17	14.75	12.73	16.00	42.00	41.00	5.50
131	FMGPM-5	56.50	59.00	89.00	56.50	14.42	13.19	15.42	31.00	29.50	7.00
132	FMGPM-6	55.00	63.00	93.00	145.17	16.33	14.78	18.33	43.00	42.50	3.83
133	FMGPM-7	55.50	59.50	89.50	127.33	13.67	11.94	16.33	35.50	34.00	5.00
134	FMGPM-8	54.50	60.50	90.50	137.00	16.75	12.55	13.50	50.00	48.50	7.67
135	FMGPM-9	54.00	59.00	89.00	148.17	17.08	12.48	15.58	43.50	41.50	7.33
136	FMGPM-10	53.50	54.50	84.50	124.50	13.83	10.05	11.33	45.50	44.00	6.17
137	FMGPM-11	57.00	60.50	90.50	144.00	15.92	14.01	15.50	46.00	45.50	7.17
138	MLT-12-1	60.00	65.00	95.00	107.67	10.92	9.22	10.00	24.50	22.00	2.83

APPENDIX II. (contd...)

Sl. No.	Genotypes	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/m row	No. of prod. Tillers/m row	No. of prod. Tillers /plant
139	MLT-12-2	57.50	63.00	93.00	109.83	10.83	9.30	12.33	20.50	18.00	4.33
140	MLT-12-3	59.50	64.00	94.00	96.00	10.58	9.37	11.17	14.50	12.50	1.83
141	MLT-12-4	58.00	61.00	91.00	132.17	16.83	12.57	12.83	34.00	30.50	6.50
142	MLT-12-5	59.50	63.00	93.00	117.17	13.42	11.64	13.92	15.00	11.50	3.83
143	MLT-12-6	58.50	64.00	94.00	125.50	14.00	11.15	13.50	15.50	13.00	3.17
144	MLT-12-7	59.50	63.00	93.00	118.33	15.67	12.45	11.50	14.00	12.50	3.50
145	MLT-12-8	57.00	60.00	90.00	132.67	23.50	13.03	12.67	18.50	17.50	4.17
146	MLT-12-9	58.00	61.00	91.00	114.17	14.25	8.82	11.17	19.50	18.50	3.83
147	MLT-12-10	57.50	61.00	91.00	114.50	15.00	9.35	11.17	25.00	23.50	2.67
148	MLT-12-11	57.00	62.00	92.00	121.83	16.67	13.73	14.17	24.00	21.00	3.50
149	MLT-12-12	58.50	62.50	92.50	130.17	13.58	12.42	18.50	33.50	31.50	5.67
Mean		55.96	60.42	90.37	135.93	15.69	12.41	14.59	42.52	40.95	6.84
C.V.		4.91	3.17	2.32	7.57	13.34	10.72	16.92	16.06	20.54	24.42
S.E.		1.94	1.35	1.48	7.27	1.48	0.94	1.75	4.83	5.95	1.18
C.D @ 5%		5.43	3.78	4.14	20.33	4.14	2.63	4.88	13.5	16.62	3.3
C.D.@ 1%		7.17	5	5.46	26.84	5.46	3.47	6.44	17.83	21.95	4.36

APPENDIX II (contd...)

Sl. No.	Genotypes	Area of standard leaf (cm ²)	Stem thickness (cm)	SPAD @ 50% flowering	SPAD @ maturity	Fodder yield/plant (g)	Fodder yield/hectare (kg)	Grain yield /plant (g)	Grain yield /hectare (kg)	1000 Seed Weight (g)
1	GS 5	76.14	1.23	40.26	28.77	115.00	4092.59	31.34	2164.81	3.85
2	GS 6	58.72	1.10	41.28	27.02	147.50	3981.48	24.96	1615.74	3.47
3	GS 8	66.19	1.23	34.35	19.95	95.00	3444.44	29.45	1750.00	3.04
4	GS 12	76.33	1.50	48.05	28.37	135.00	3796.30	34.79	2390.74	3.71
5	GS 17	62.42	1.48	39.15	34.22	115.00	3703.70	34.69	1575.00	3.37
6	GS 18	61.83	1.15	37.40	25.37	152.50	2537.04	46.89	1589.07	3.56
7	GS 21	51.93	1.27	37.93	23.78	182.50	370.37	36.19	275.93	4.15
8	GS 26	63.18	1.63	36.37	22.27	137.50	2703.70	33.60	1648.15	3.27
9	GS 33	55.78	1.35	41.28	23.42	92.50	2759.26	15.25	1149.07	2.99
10	GS 35	78.80	1.67	33.90	23.67	135.00	2703.70	25.54	1109.26	3.30
11	GS 29	65.14	1.48	43.09	27.27	97.50	2259.26	41.56	1465.74	3.27
12	GS 42	52.94	1.11	34.98	22.43	102.50	1592.59	28.97	1007.41	3.46
13	GS 45	66.02	1.46	38.55	24.98	157.50	2324.07	44.76	1487.96	3.73
14	GS 47	57.35	1.47	42.95	20.28	135.00	1944.44	31.12	1201.85	3.68
15	GS 53	74.09	1.18	43.87	28.22	135.00	3814.81	41.89	2184.26	3.52
16	GS 56	55.34	1.29	38.30	23.47	115.00	2925.93	29.87	1698.15	3.68
17	GS 60	57.98	1.40	42.48	27.75	160.00	2925.93	32.84	1927.78	3.36
18	GS 62	59.60	1.11	40.13	33.05	110.00	3407.41	38.74	1782.41	3.35
19	GS 64	56.27	1.33	43.17	32.37	160.00	3981.48	33.46	2418.52	3.94
20	GS 71	82.08	1.26	44.40	25.40	262.50	4129.63	55.24	2249.07	3.33
21	GS 77	66.39	1.43	41.75	33.22	167.50	1629.63	46.59	1254.63	3.42
22	GS 78	82.49	1.58	46.02	33.10	202.50	4703.70	47.17	1895.37	3.36
23	GS 91	62.83	1.65	42.62	30.82	100.00	2555.56	32.78	1212.04	3.21

APPENDIX II (contd...)

Sl. No.	Genotypes	Area of standard leaf (cm ²)	Stem thickness (cm)	SPAD @ 50% flowering	SPAD @ maturity	Fodder yield/plant (g)	Fodder yield/hectare (kg)	Grain yield /plant (g)	Grain yield /hectare (kg)	1000 Seed Weight (g)
24	GS 94	67.38	1.31	44.33	23.27	217.50	3407.41	26.20	1575.00	3.65
25	GS 95	75.06	1.32	44.60	29.10	177.50	3425.93	35.61	2235.19	4.44
26	GS 96	79.02	1.38	42.25	19.20	115.00	2907.41	31.39	1522.22	3.49
27	GS 97	72.07	1.40	33.90	24.42	167.50	2629.63	39.27	1600.93	3.90
28	GS 103	70.23	1.40	41.45	23.45	112.50	2722.22	31.85	1793.52	3.78
29	GS 105	56.34	1.15	37.28	22.53	110.00	2555.56	27.55	1697.22	3.37
30	GS 106	71.46	1.21	44.43	20.78	127.50	3092.59	31.63	2101.85	3.41
31	GS 111	57.58	1.53	38.10	20.02	105.00	2925.93	23.73	1404.63	3.64
32	GS 121	66.37	1.16	45.88	27.48	107.50	4462.96	38.84	2581.48	3.84
33	GS 140	45.87	1.03	34.88	18.85	57.50	1851.85	25.04	1131.48	3.61
34	GS 158	52.55	1.13	35.18	22.48	90.00	2944.44	26.92	1846.30	3.65
35	GS 200	72.53	1.28	36.82	24.40	120.00	3240.74	35.14	1878.70	2.92
36	GS 203	59.45	1.17	36.20	23.65	175.00	1435.19	25.92	681.67	3.18
37	GS 204	53.80	1.17	42.28	27.38	177.50	3759.26	27.95	1654.63	3.65
38	GS 205	57.20	1.19	43.15	22.50	147.50	2629.63	30.63	1325.00	3.86
39	GS 206	59.20	1.57	39.33	20.08	80.00	3555.56	44.55	1508.33	3.26
40	GS 207	55.67	1.02	38.72	29.27	142.50	1888.89	32.28	775.00	4.20
41	GS 208	58.02	1.08	41.80	25.33	102.50	3037.04	30.57	1474.07	3.17
42	GS 209	63.66	1.14	39.33	26.38	142.50	2648.15	37.12	1506.48	3.24
43	GS 210	62.73	1.29	42.13	27.35	190.00	2425.93	33.59	1219.44	3.86
44	GS 211	71.79	1.36	40.18	26.97	172.50	2194.44	42.64	1241.67	3.51
45	GS 212	60.13	1.27	37.32	22.37	157.50	2537.04	33.87	838.89	3.58
46	GS 213	68.93	1.28	40.72	33.13	227.50	4444.44	40.62	1723.15	3.97

APPENDIX II (contd...)

Sl. No.	Genotypes	Area of standard leaf (cm ²)	Stem thickness (cm)	SPAD @ 50% flowering	SPAD @ maturity	Fodder yield/plant (g)	Fodder yield/hectare (kg)	Grain yield /plant (g)	Grain yield /hectare (kg)	1000 Seed Weight (g)
47	GS 214	67.24	1.33	44.03	23.85	185.00	3629.63	38.89	1820.37	3.66
48	GS 215	91.69	1.35	36.48	32.43	145.00	2222.22	31.93	1112.96	3.73
49	GS 216	59.18	1.14	39.78	26.50	232.50	2231.48	35.61	1281.48	2.96
50	GS 218	50.92	1.19	42.60	26.16	130.00	2185.19	40.75	1058.33	4.05
51	GS 219	69.19	1.17	38.97	22.53	120.00	2037.04	21.97	437.22	3.72
52	GS 220	49.80	1.04	42.67	21.68	155.00	1796.30	40.42	1029.63	3.28
53	GS 221	46.73	1.17	39.63	22.30	217.50	2333.33	50.42	1400.93	3.19
54	GS 222	50.63	1.14	37.25	24.05	175.00	2129.63	36.33	1133.33	3.47
55	GS 242	59.11	1.18	38.73	24.13	167.50	2611.11	34.52	762.96	3.46
56	GS 243	59.65	1.21	36.80	24.45	117.50	2611.11	26.93	1445.37	3.54
57	GS 246	54.47	1.17	38.90	21.98	130.00	3648.15	28.40	1744.44	3.90
58	GS 248	74.82	1.39	37.00	23.53	157.50	2185.19	43.05	1023.15	3.54
59	GS 250	75.81	1.85	41.30	32.27	200.00	3518.52	40.24	1674.07	3.80
60	GS 256	55.04	1.45	41.17	24.80	122.50	1611.11	23.77	1040.74	3.38
61	GS 260	58.97	1.27	39.25	27.33	145.00	3259.26	34.74	1524.07	3.54
62	GS 264	66.31	1.48	45.92	30.85	170.00	3777.78	35.77	1564.81	3.91
63	GS 266	56.08	1.24	48.10	25.48	102.50	2472.22	24.18	1942.59	3.34
64	GS 271	63.41	1.21	36.25	19.65	132.50	2944.44	29.17	1303.70	3.48
65	GS 276	55.37	1.38	38.70	28.48	112.50	2870.37	20.10	1329.63	3.33
66	GS 280	60.53	1.22	43.37	25.50	110.00	3407.41	34.84	1827.78	3.27
67	GS 282	54.08	1.25	41.17	24.30	125.00	2481.48	27.80	1515.74	3.22
68	GS 285	64.03	1.22	41.17	23.82	110.00	2574.07	28.30	1737.04	3.59
69	GS 289	56.20	1.26	38.58	27.95	130.00	3703.70	30.95	1940.74	4.10

APPENDIX II (contd...)

Sl. No.	Genotypes	Area of standard leaf (cm ²)	Stem thickness (cm)	SPAD @ 50% flowering	SPAD @ maturity	Fodder yield/plant (g)	Fodder yield/hectare (kg)	Grain yield /plant (g)	Grain yield /hectare (kg)	1000 Seed Weight (g)
70	GS 293	53.46	1.23	41.25	27.77	150.00	3870.37	43.36	2014.81	3.52
71	GS 301	57.01	1.26	42.27	27.22	97.50	2888.89	30.62	1842.59	3.13
72	GS 310	64.32	1.36	40.63	24.73	147.50	4277.78	30.45	2131.48	3.93
73	GS 316	59.93	1.34	36.30	23.02	95.00	2685.19	23.59	1154.63	3.39
74	GS 335	69.89	1.37	41.92	25.05	112.50	2703.70	26.66	1856.48	3.58
75	GS 336	66.24	1.38	44.08	25.28	132.50	3833.33	32.55	2544.44	4.04
76	GS 337	68.78	1.21	44.83	26.93	145.00	2666.67	33.57	1778.70	3.40
77	GS 308	65.76	1.11	42.50	26.55	137.50	3944.44	29.68	1895.37	4.26
78	GS 338	65.87	3.01	35.43	22.03	117.50	3000.00	24.43	1662.96	3.11
79	GS 343	65.24	1.26	36.53	30.53	167.50	2777.78	37.75	1648.15	3.85
80	GS 344	69.27	1.44	45.20	28.17	105.00	2777.78	29.06	1674.07	3.87
81	GS 352	79.07	1.31	40.47	24.33	182.50	4407.41	33.19	2165.74	3.75
82	GS 362	82.84	1.72	35.45	27.32	140.00	3370.37	31.72	1953.70	3.52
83	GS 363	59.36	1.27	38.87	27.13	162.50	5388.89	31.19	2262.04	3.49
84	GS 372	69.62	1.27	38.27	24.12	135.00	3111.11	43.03	1624.07	3.86
85	GS 377	58.47	1.15	40.98	19.20	55.00	1870.37	16.08	1161.11	3.17
86	GS 378	77.83	1.36	39.35	25.75	145.00	3037.04	23.69	1220.37	3.37
87	GS 379	69.97	1.22	43.25	18.80	100.00	2740.74	27.25	1670.37	3.25
88	GS 401	61.09	1.60	35.70	23.38	127.50	2388.89	30.93	1490.74	3.30
89	GS 403	61.80	1.21	43.75	25.15	115.00	2925.93	28.75	1913.89	3.64
90	GS 415	60.57	1.18	31.02	19.60	87.50	1740.74	28.72	1053.70	3.22
91	GS 426	57.53	1.10	39.33	23.58	110.00	2833.33	28.39	1830.56	2.88
92	GS 433	69.59	1.20	34.88	19.97	80.00	3722.22	25.46	1342.59	3.50

APPENDIX II (contd...)

Sl. No.	Genotypes	Area of standard leaf (cm ²)	Stem thickness (cm)	SPAD @ 50% flowering	SPAD @ maturity	Fodder yield/plant (g)	Fodder yield/hectare (kg)	Grain yield /plant (g)	Grain yield /hectare (kg)	1000 Seed Weight (g)
93	GS 499	61.98	1.23	37.52	24.20	75.00	1629.63	22.83	1912.96	3.62
94	GS 453	54.33	1.05	44.23	18.03	110.00	2333.33	29.18	1647.22	3.28
95	GS 461	70.09	1.44	37.05	27.12	145.00	3388.89	32.92	1730.56	3.24
96	GS 472	47.99	1.19	43.50	29.52	115.00	3055.56	40.11	1619.44	3.70
97	GS 478	69.55	1.22	42.48	31.57	132.50	2574.07	37.05	1892.59	3.47
98	GS 494	59.66	1.12	40.50	22.80	97.50	2444.44	28.84	1225.93	3.12
99	GS 510	54.71	1.16	43.18	27.18	195.00	5222.22	44.93	2039.81	3.37
100	GS 511	69.98	1.65	40.80	27.50	95.00	2296.30	26.02	1459.26	2.95
101	SiA 3156	71.30	1.47	46.62	41.57	167.50	3925.93	32.90	2717.59	4.01
102	SiA 3088	65.12	1.53	38.35	25.50	90.00	2907.41	26.67	1880.56	3.53
103	SiA 3085	73.85	1.30	40.65	32.88	162.50	3851.85	38.08	2255.56	3.65
104	Co7	56.34	1.36	44.82	26.13	162.50	4851.85	30.06	2607.41	4.06
105	SR 51	66.04	1.36	35.67	20.67	147.50	3166.67	31.92	1466.67	3.56
106	SiA 2644	71.02	1.34	41.32	25.90	157.50	4425.93	28.18	2387.96	3.44
107	SR 16	52.66	1.08	37.25	28.92	135.00	3740.74	33.55	1979.63	3.37
108	PS4	78.06	1.40	44.98	24.27	172.50	3648.15	43.65	2006.48	3.68
109	TNAU 186	67.58	1.19	42.67	32.52	102.50	4370.37	32.70	2141.67	3.24
110	SR 11	78.87	1.70	48.12	25.85	125.00	3944.44	31.21	2553.70	3.29
111	SiA 2622	69.91	1.52	42.80	30.70	140.00	3555.56	32.04	1900.00	4.11
112	SiA 2593	71.39	1.32	44.32	23.47	125.00	4166.67	38.92	2633.33	3.45
113	Lepakshi	75.38	1.30	39.95	24.72	145.00	1203.70	39.81	676.85	3.58
114	K 3	60.00	1.30	45.17	31.25	150.00	5148.15	29.98	2050.00	3.69
115	SiA 326	160.91	1.62	47.12	26.28	115.00	3333.33	29.42	1961.11	3.68

APPENDIX II (contd...)

Sl. No.	Genotypes	Area of standard leaf (cm ²)	Stem thickness (cm)	SPAD @ 50% flowering	SPAD @ maturity	Fodder yield/plant (g)	Fodder yield/hectare (kg)	Grain yield /plant (g)	Grain yield /hectare (kg)	1000 Seed Weight (g)
116	Co5	62.59	1.31	38.57	28.08	160.00	3833.33	37.79	1394.44	3.49
117	Chitra	64.57	1.28	41.52	27.23	97.50	3370.37	26.25	1679.63	3.59
118	K2	54.18	1.15	39.15	24.60	130.00	2574.07	25.38	1453.70	3.96
119	Co 4	49.42	1.08	42.92	16.87	90.00	3000.00	22.50	1710.19	3.32
120	RS 118	62.01	1.26	40.12	25.45	142.50	2777.78	27.43	2024.07	3.36
121	K 221-1	64.62	1.31	41.73	28.43	122.50	3500.00	32.18	1991.67	3.99
122	Arjuna	62.58	1.31	35.95	22.87	90.00	2796.30	22.61	1434.26	3.99
123	H 1	80.99	1.37	38.65	24.70	100.00	3148.15	29.24	1840.74	3.40
124	H 2	57.78	1.15	35.37	28.68	107.50	4351.85	23.77	1627.78	3.50
125	Co 1	66.51	1.20	36.02	23.40	112.50	2111.11	24.95	1234.26	4.02
126	Co 2	61.52	1.20	35.42	23.25	192.50	3037.04	24.70	1689.81	3.34
127	FMGPM-1	60.98	1.28	43.25	28.95	122.50	2657.41	35.42	1621.30	3.70
128	FMGPM-2	66.36	1.52	39.08	30.95	107.50	3759.26	33.93	1962.04	3.64
129	FMGPM-3	64.62	1.33	36.83	25.93	92.50	3000.00	34.06	1861.11	3.55
130	FMGPM-4	53.84	1.13	40.93	25.03	110.00	3259.26	29.73	1851.85	3.31
131	FMGPM-5	57.69	1.27	36.48	24.27	90.00	2444.44	25.19	1411.11	3.60
132	FMGPM-6	72.42	1.40	37.03	25.50	100.00	3518.52	30.36	1870.37	3.76
133	FMGPM-7	59.08	1.10	37.82	25.60	125.00	2851.85	22.41	1971.30	3.73
134	FMGPM-8	61.37	1.29	39.50	27.27	155.00	2407.41	36.24	1742.59	3.74
135	FMGPM-9	55.05	1.27	41.72	31.83	127.50	3944.44	35.53	1623.15	3.32
136	FMGPM-10	51.84	1.09	42.73	26.67	85.00	2796.30	24.94	1541.67	3.73
137	FMGPM-11	66.42	1.36	36.85	26.58	162.50	4944.44	35.80	2314.81	3.81
138	MLT-12-1	39.87	1.09	31.93	22.95	85.00	935.19	15.27	212.96	3.18

APPENDIX II (contd...)

Sl. No.	Genotypes	Area of standard leaf (cm ²)	Stem thickness (cm)	SPAD @ 50% flowering	SPAD @ maturity	Fodder yield/plant (g)	Fodder yield/hectare (kg)	Grain yield /plant (g)	Grain yield /hectare (kg)	1000 Seed Weight (g)
139	MLT-12-2	40.48	1.10	33.53	21.07	67.50	1009.26	17.28	225.00	3.51
140	MLT-12-3	44.52	0.92	35.22	24.33	60.00	518.52	14.94	139.81	3.49
141	MLT-12-4	53.96	1.30	42.55	26.85	80.00	3314.81	30.18	1087.04	3.55
142	MLT-12-5	51.86	1.13	40.90	21.93	72.50	1000.00	18.75	220.37	3.69
143	MLT-12-6	50.15	1.15	44.55	22.42	75.00	870.37	18.35	307.41	3.17
144	MLT-12-7	54.57	1.34	39.35	24.60	77.50	1148.15	18.99	362.96	3.18
145	MLT-12-8	87.71	1.36	44.83	27.55	122.50	2074.07	17.36	696.30	3.01
146	MLT-12-9	45.34	1.11	43.08	21.02	67.50	1000.00	17.32	314.81	4.01
147	MLT-12-10	46.62	1.08	40.87	23.68	72.50	1129.63	15.86	576.85	2.85
148	MLT-12-11	74.33	1.23	39.18	19.82	137.50	1370.37	26.23	620.37	4.15
149	MLT-12-12	55.81	1.14	39.87	23.83	112.50	1407.41	25.98	908.33	3.49
Mean		63.54	1.3	40.24	25.57	130.13	2921.2	31.26	1558.28	3.54
C.V. (%)		15.31	16.8	9.87	17.21	24.9	17.68	24.9	25.4	6.66
S.Em.±		6.81	1.54	2.81	3.11	22.91	746.46	5.5	279.84	0.17
C.D @ 5%		19.02	4.31	7.85	8.7	64.03	1519.74	15.38	782.05	0.47
C.D.@ 1%		25.12	5.69	10.37	11.48	84.54	2006.8	20.31	1032.68	0.62

APPENDIX III. Characterization of foxtail millet genotypes for qualitative traits

Sl. No.	Genotypes	Awn length	Awn colour	Panicle compactness	Grain colour	Stem pigmentation	Anther colour
1	GS 5	2	1	2	3	0	0
2	GS 6	1	1	3	3	0	0
3	GS 8	2	1	3	3	0	0
4	GS 12	2	1	2	4	0	0
5	GS 17	1	1	2	3	0	0
6	GS 18	1	1	2	3	0	0
7	GS 21	3	1	2	3	0	0
8	GS 26	2	1	2	3	0	0
9	GS 33	2	1	2	3	1	0
10	GS 35	2	1	2	3	0	0
11	GS 29	3	1	1	1	0	0
12	GS 42	3	0	2	3	1	0
13	GS 45	2	1	2	3	0	0
14	GS 47	2	1	2	3	0	0
15	GS 53	2	1	2	3	0	0
16	GS 56	3	1	2	3	0	0
17	GS 60	2	1	1	3	0	0
18	GS 62	3	1	2	3	0	0
19	GS 64	2	1	2	3	0	0
20	GS 71	3	1	2	3	0	1
21	GS 77	2	1	1	3	0	0
22	GS 78	3	1	2	3	0	0
23	GS 91	2	1	2	3	0	0
24	GS 94	2	1	1	3	1	0
25	GS 95	2	1	1	3	0	0
26	GS 96	2	1	3	4	0	0
27	GS 97	1	1	2	3	0	0
28	GS 103	2	1	2	3	0	0
29	GS 105	3	1	2	3	0	0

APPENDIX III (Contd..)

Sl. No.	Genotypes	Awn length	Awn colour	Panicle compactness	Grain colour	Stem pigmentation	Anther colour
30	GS 106	1	1	1	3	0	0
31	GS 111	2	1	2	3	0	1
32	GS 121	2	1	2	3	0	1
33	GS 140	1	1	2	3	0	0
34	GS 158	2	1	3	3	0	0
35	GS 200	2	1	2	3	0	0
36	GS 203	3	1	2	4	0	0
37	GS 204	3	1	1	3	0	1
38	GS 205	2	1	2	3	0	0
39	GS 206	1	1	1	3	0	0
40	GS 207	3	1	2	3	0	0
41	GS 208	2	1	2	3	0	0
42	GS 209	3	1	2	3	0	1
43	GS 210	3	1	2	3	0	0
44	GS 211	3	1	2	3	0	0
45	GS 212	2	1	2	3	0	0
46	GS 213	3	1	3	3	0	1
47	GS 214	2	1	3	3	0	1
48	GS 215	2	1	3	3	0	0
49	GS 216	3	1	3	4	0	0
50	GS 218	3	1	2	3	0	0
51	GS 219	3	0	2	3	0	0
52	GS 220	3	1	2	3	0	0
53	GS 221	3	1	2	3	0	0
54	GS 222	3	1	2	3	0	0
55	GS 242	2	1	1	3	0	0
56	GS 243	3	1	2	3	1	1
57	GS 246	1	1	3	3	0	0
58	GS 248	2	1	1	3	0	0
59	GS 250	1	1	3	3	1	0

APPENDIX III (Contd..)

Sl. No.	Genotypes	Awn length	Awn colour	Panicle compactness	Grain colour	Stem pigmentation	Anther colour
60	GS 256	2	1	1	3	0	0
61	GS 260	2	1	1	3	0	0
62	GS 264	2	0	2	3	1	0
63	GS 266	3	1	1	3	0	0
64	GS 271	3	1	3	3	1	0
65	GS 276	2	0	1	2	0	0
66	GS 280	3	1	3	3	0	0
67	GS 282	2	1	2	3	1	0
68	GS 285	2	1	1	3	1	1
69	GS 289	2	1	1	3	1	0
70	GS 293	2	1	2	3	1	0
71	GS 301	1	1	2	3	0	0
72	GS 310	2	1	2	3	0	0
73	GS 316	3	1	2	3	0	0
74	GS 335	3	1	1	3	0	0
75	GS 336	2	1	1	3	0	0
76	GS 337	2	1	1	3	0	0
77	GS 308	3	1	2	3	0	0
78	GS 338	1	1	2	3	0	0
79	GS 343	3	1	3	3	1	0
80	GS 344	1	1	3	3	1	0
81	GS 352	3	1	2	3	0	0
82	GS 362	1	1	3	4	0	0
83	GS 363	2	1	3	3	0	0
84	GS 372	1	1	2	3	0	0
85	GS 377	3	1	2	3	0	0
86	GS 378	2	1	2	3	0	0
87	GS 379	2	1	1	3	0	0
88	GS 401	2	1	2	3	0	0
89	GS 403	2	1	1	3	0	0

APPENDIX II (Contd..)

Sl. No.	Genotypes	Awn length	Awn colour	Panicle compactness	Grain colour	Stem pigmentation	Anther colour
90	GS 415	3	1	1	3	0	0
91	GS 426	3	1	2	3	0	0
92	GS 433	3	1	2	3	0	0
93	GS 499	3	1	2	3	0	0
94	GS 453	3	1	3	3	1	0
95	GS 461	3	1	1	3	0	1
96	GS 472	3	1	2	3	0	0
97	GS 478	3	1	2	3	0	0
98	GS 494	3	1	2	3	0	0
99	GS 510	2	1	2	3	0	0
100	GS 511	1	1	3	3	1	0
101	SiA 3156	2	1	2	3	1	1
102	SiA 3088	1	1	3	3	0	0
103	SiA 3085	3	1	1	3	1	0
104	Co7	3	1	2	3	1	0
105	SR 51	2	1	3	3	0	0
106	SiA 2644	3	1	2	3	1	0
107	SR 16	2	1	2	3	1	0
108	PS4	2	1	1	3	0	0
109	TNAU 186	2	1	1	3	1	0
110	SR 11	1	1	1	3	0	0
111	SiA 2622	2	1	1	3	1	0
112	SiA 2593	3	1	1	3	0	0
113	Lepakshi	3	1	1	3	0	0
114	K 3	3	1	2	3	0	0
115	SiA 326	1	1	3	3	0	0
116	Co5	3	1	2	3	0	0
117	Chitra	2	1	2	4	0	0
118	K2	1	1	2	3	0	0
119	Co 4	3	1	1	3	0	0

APPENDIX III (Contd..)

Sl. No.	Genotypes	Awn length	Awn colour	Panicle compactness	Grain colour	Stem pigmentation	Anther colour
120	RS 118	3	1	3	3	0	0
121	K 221-1	2	1	3	3	0	0
122	Arjuna	2	1	3	3	0	0
123	H 1	2	1	2	3	0	0
124	H 2	1	1	2	3	0	0
125	Co 1	2	1	2	3	0	0
126	Co 2	3	1	2	3	0	0
127	FMGPM-1	1	1	2	3	0	0
128	FMGPM-2	3	1	2	3	0	0
129	FMGPM-3	3	1	1	3	0	0
130	FMGPM-4	2	1	2	3	1	0
131	FMGPM-5	2	1	1	1	0	0
132	FMGPM-6	2	1	2	3	0	0
133	FMGPM-7	2	1	3	3	1	0
134	FMGPM-8	1	1	3	3	0	0
135	FMGPM-9	2	1	2	3	0	1
136	FMGPM-10	3	1	2	1	1	0
137	FMGPM-11	1	1	3	3	0	0
138	MLT-12-1	3	1	1	3	0	0
139	MLT-12-2	2	1	1	3	0	0
140	MLT-12-3	2	1	1	3	0	0
141	MLT-12-4	2	1	2	3	0	0
142	MLT-12-5	2	1	2	3	0	0
143	MLT-12-6	3	1	1	3	1	0
144	MLT-12-7	3	1	2	3	0	0
145	MLT-12-8	2	1	3	3	0	0
146	MLT-12-9	2	1	2	3	0	0
147	MLT-12-10	3	1	1	3	1	0
148	MLT-12-11	3	0	2	3	0	0
149	MLT-12-12	2	1	2	3	0	0

GENETIC DIVERSITY ANALYSIS FOR YIELD AND YIELD COMPONENTS IN FOXTAIL MILLET [*Setaria italica* (L.) Beauv.]

THIPPESWAMY V

2015

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ABSTRACT

Foxtail millet is known for nutritional and medicinal value and has tremendous scope for its value addition in future. There is need to strengthen the genetic makeup of the crop for future breeding programme. Therefore, present investigation was carried out to assess genetic diversity, variability and association studies using 149 foxtail millet germplasm lines for various yield and yield component traits, and to study varietal differences for grain nutrients content (protein, Fe, Ca and Zn) among 25 selected genotypes.

Based on D^2 values, a total of 149 genotypes were grouped into 15 clusters. Among these cluster I was the largest with 134 genotypes followed by cluster VIII with 2 genotypes, remaining 13 were solitary clusters. Inter cluster distances were ranged from 12.08 to 138.62. Highest inter cluster distance was obtained between cluster IX and XIV. Among the traits, number of tillers per meter row length (16.84%) contributed maximum towards the genetic divergence. The genotypes of solitary clusters which secured overall high ranking across thirteen characters were SR 11, GS 213, GS 511 and GS 510.

High estimates of GCV (22.99), PCV (28.05), heritability (67.20) and genetic advance (38.83) were observed for number of tillers per meter row length. In general, grain yield per plant and grain yield per hectare were positively significantly correlated with the traits viz., plant height (0.454 and 0.378), panicle length (0.327 and 0.308), panicle girth (0.335 and 0.398), number of tillers per meter row length (0.442 and 0.528), SPAD at flowering (0.216 and 0.383), SPAD at maturity (0.358 and 0.371) and fodder yield per plant (0.626 and 0.267).

The range of values was observed for grain micronutrients viz., calcium (1.99-22.69 mg/100g), iron (0.33-16.26 mg/100g), zinc (2.29-11.4 mg/100g), and grain protein (6.2 to 10.89%).