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GENETIC VARIATION AND MORPHOLOGICAL DIVERSITY IN FOXTAIL MILLET

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Abstract: Foxtail millet accessions were evaluated for extent genetic variation and Morphological diversity for seed yield and yield attributes. Days to 50% flowering, Plant height, and seed yield per plant showed grater variability. Phenotypic coefficient of variation and genotypic coefficient of variation were high for plant height, Tillers per plant and length of inflorescence. High heritability with high Genetic advance as percent mean were found for Days to 50% flowering and seed yield. Fifty two accessions were grouped into three clusters, cluster III with 20genotypes, cluster II with 17 and cluster I with 20 genotypes. The genotypes ISe 204, GS 2137, Sia 147, Ise 40, ISe318, Sia 3156, Sia326 and Sia 2847 were selected from different cluster and used for foxtail millet improvement programme
Keywords: Genotypes, Variability, Foxtail millet, Diversity.

INTRUDUCTION

Foxtail millet is one of the oldest crop cultivated for food grain and fodder for livestock. Foxtail millet grains are highly nutritious with good quality protein, rich in minerals, dietary fibre, phyto- chemicals and vitamins (Thiamin, Riboflavin Niacin). It is known for drought tolerant and grown well in where soil, climate and other condition are less favorable. In India it is grown in semiarid regions of Andra Pradesh, Karnataka, Maharashtra, Tamil Nadu, Rajasthan, Madhy Pradesh, Uttar Pradesh and North Eastern states of our country. It was once an essential crop grown and consumed extensively as daily food in rainfed areas but now the crop is replaced by rice crop due to many irrigation projects. In Karnataka Foxtail millet is grown mainly in arid and semi-arid regions of Bellary, Chithradurga, Gadag, Haveri, Dharwad, Raichur, Gulberga and Koppal. The farmers of these regions were growing local land races of foxtail millet which are low yielding with long duration. Hence there is need for development of High yielding Verities of foxtail millet. In the present study, evaluation and characterizing the genetic resources was undertaken which is the prerequisite for foxtail millet improvement programme.

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MATERIAL & METHODS

Field experiment was carried out at Agricultural Research Station, Bellary, Karnataka. Fifty two accessions of foxtail millet from All India Coordinated Small Millet Improvement Project, ZARS, Bangalore were used as plant material for the study. Accessions were sown in Randomized complete Block design along with check and evaluated in field during *kharif 2013.* The sowing was taken in last week of July 2013 and crop was raised with protective irrigation. The soil of experimental site was Black cotton soil and the recommended NPK fertilizer dose was applied (30:15:15 Kg/ha). The spacing between plant to plant 10cm and row to row 30cm was maintained. At the time of maturity five plants selected at random from each genotype were tagged in each replication and observations on quantitative traits were recorded and the average of these five plants for each quantitative character was made to compute mean for further analysis. The observations viz., Days to 50% flowering, Plant Height (CM), Tillers per plant Length of Inflorescence (cm) and Seed yield (g/plant) were recorded. Data was analyzed with different statistical packages like DSAAT, TNAU STAT, PASTA (Ward's cluster) and Excel.

RESULT AND DISCUSSION

Genetic Variability

Analysis of variance (Table 1) revealed all the genotypes exhibited significant difference in respect of Days to 50% flowering, Plant height and seed yield indicating the presence of genetic variability and the choice of the material for the investigation is appropriate. One of the ways to appreciate the extent of variability is to examine the range, which reflects the extent of phenotypic variability in respect of the trait under consideration, encompassing genotypic, environmental and interaction components. In the present study, the Foxtail millet genotypes exhibited considerable amount of variation for characters Days to 50% flowering, Plant height and seed yield. High range values indicate good scope for selection for any trait of interest for the breeder to exercise his selection.

Although range can provide a preliminary idea about the variability, it has to be confirmed by the magnitude of variance. Further, for comparing the variability of one character with another, coefficient of variation which is independent of unit of measurement is preferred. The phenotypic coefficient of variation and genotypic coefficient of variation were low to high for characters. As expected, the PCV values were greater than the GCV values for all the characters indicating considerable influence of environment on the expression of these characters under field conditions. The difference between GCV and PCV

values was more for plant height, Tillers per plant and Length of Inflorescence indicating that selection based on phenotypic observations may not be very effective for these traits (Table 2). In general, the PCV and GCV were quite high for plant height, Tillers per plant and Length of Inflorescence, indicating that there is greater scope for selection for improvement of these characters. Contrary to the above days to 50 per cent flowering PCV and GCV values were low. High heritability coupled with high genetic advance as per cent of mean was observed for days to 50 per cent flowering, plant height and seed yield suggesting that these characters are under the control of additive genes and phenotypic selection for these characters may be effective. These results are in agreement with the results obtained in Foxtail millet by Goopalreddy *et al*. (2006). High heritability and High genetic advance were observed for the Days to 50% flowering and Seed yield per plant. The heritability is high for these characters and selection differential is always constant.

Genetic Diversity

The Fifty two accessions were grouped into 3 clusters (Table- 3 & Fig. 1). Of the 3 clusters, cluster III was the largest one comprising of 20 genotypes followed by cluster I with 17 genotypes and cluster II (15genotypes). As statement by Murthy and Arunachalam (1966), this none parallelism may be due to genetic drift and intense natural and human selection for diverse adaptive gene complexes under different environments causing greater diversity among genotypes rather than their geographic distances. Further, genotypes present in the more distanced clusters will serve as good sources of divergent genes which is very much required for breeding to exploit heterosis as reported by Gill *et al.* (1995) or and to get good transgressive segregants in the segregating population. Genotypes grouped into the same cluster presumably diverge little from one another as the aggregate of characters measured. Among the five characters studied, the seed yield showed the greater diversity as compared to Days to 50% flowering, Plant height and length of inflorescence (Fig.2). This is to mean that, if breeder's intention is to improve the seed yield per plant, we can select parents, which are highly divergent with respect to these characters. The genotypes ISe 204, GS 2137, Sia 147, Ise 40, ISe318, Sia 3156, Sia326 and Sia 2847 were selected from different clusters which will be used as parents for crossing programme for development of segregating populations.

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Table 1. Mean sum of squares for seed yield and its attributing characters in Foxtail millet

Source of Variation	DF	Days to 50% flowering	Plant height (cm)	Tillers per plant	Length of Inflorescence	Seed Yield (g/plant)
Replications	1	2.46	7.48	0.03	53.51	88.80
Genotypes	51	22.34**	360.08**	0.11	7.57	4398.3**
Error	51	0.25	148.19	0.10	4.86	209.80

Table 2. Mean, range and variability parameters for different quantitative characters in Foxtail millet

Sl.No	Characters	Mean	Range	PCV (%)	GCV (%)	h^2 (%) Bs	GAM (%)
1	Days to 50% flowering	53	48-58	6.37	6.3	97.8	370
2	Plant height (cm)	102.04	56.4-127.7	15.67	10.08	47.68	54
3	Tillers per plant	2	2-3	31.38	20.69	5.73	171
4	Length of Inflorescence (cm)	12.04	8.2-20.6	20.69	9.67	21.84	174
5	Seed Yield (g/plant)	168.58	78.0 -297.5	28.47	27.14	90.89	105

Table 3. Clustering Pattern of Foxtail millet accessions based on morphological traits

Cluster no.	No. of. Genotypes	Genotypes
I	17	Ise 204,Ise 144k,SiA2855,GS2143,SiA 2844,Ise 1204,Ise 792,Ise 1231,SiA 305,SiA 2846,GS 2184,SiA 2849,Ise 1054,Ise 174,GS 2137,Ise 779,Ise 9
II	15	Ise 143,Ise 54k,Ise 276B,Ise 348k,SiA2859,Ise 204,Ise 281,SiA 2856,SiA2859,Ise 33Ak,GS2143,SiA147,Ise 40,SiA 2854,Ise 138
III	20	Ise 1047,Ise 1057,GS1918,Sia 2847,Ise 1858,Sia 808,Ise 307,Ise 287A,Ise 317,Ise 278A,Ise 43K,Ise 260,Ise 74A,Ise 338K,Ise 1052,Ise 789,SiA326,Ise 1332,Ise 38K,Sia 3156(C)

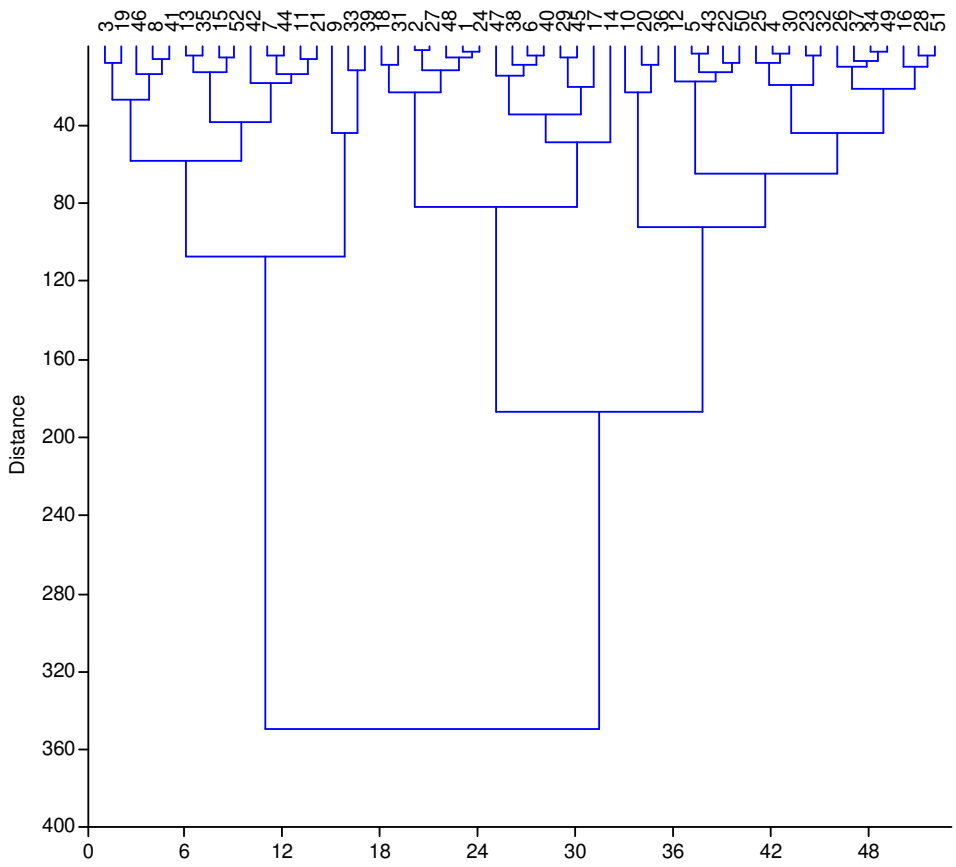

Fig.1: Clustering pattern of Foxtail Millet Accessions based on Ward's Analysis

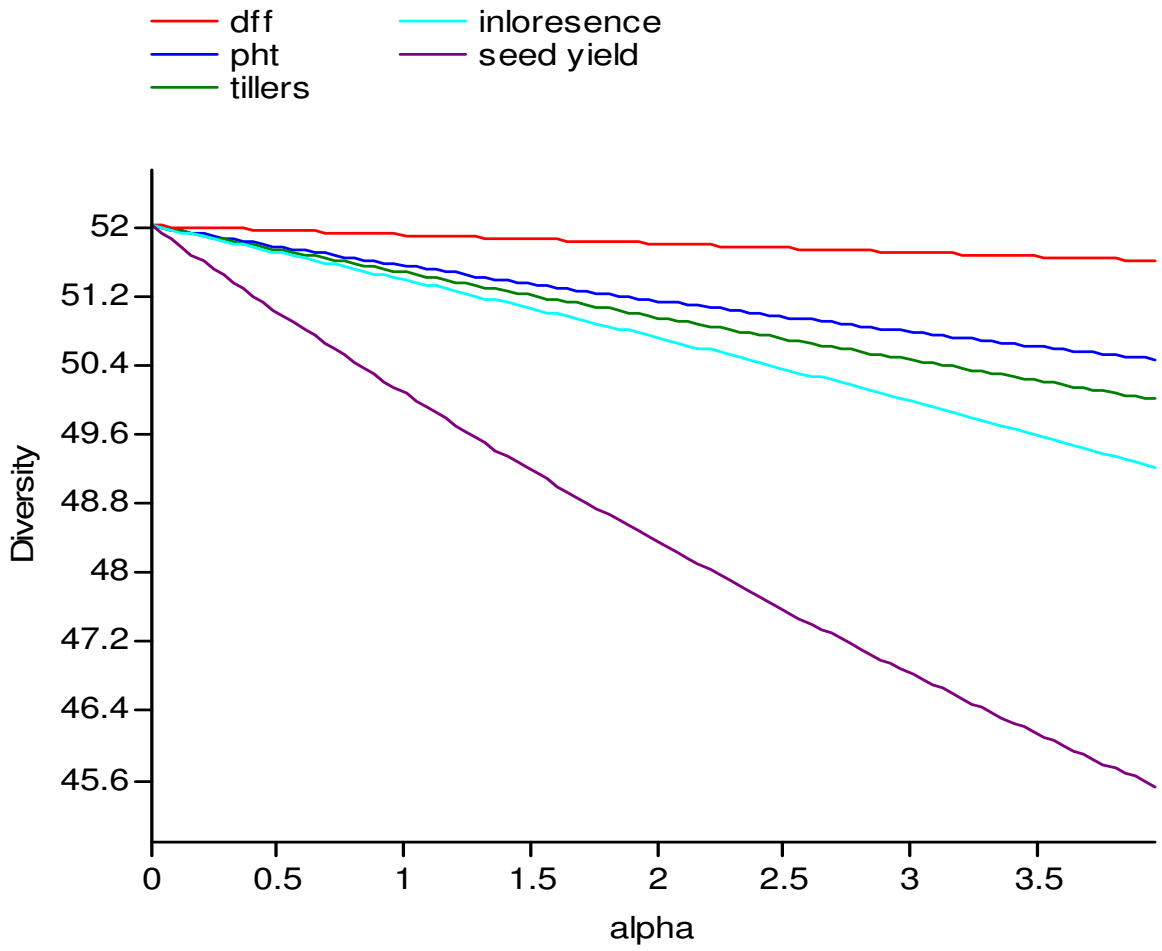

Fig.2: Contribution of traits for Diversity in Foxtail Millet Accessions