Hierarchical Cluster Analysis for Yield and Nutritional Traits in Elite Foxtail Millet Genetic Resources [*Setaria italica* (L.) Beauv.]

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Abstract:- Hundred genetic resources of foxtail millet were subjected to multivariate analysis through Wards' minimum variance method that grouped them into eleven clusters. Cluster III (16) was maximum followed by cluster VIII (14), cluster IX (12), cluster VII (11) and cluster V (10). The clusters IV, VI and XI comprised of eight genotypes each. Seven and five genotypes were grouped in clusters X and II, respectively. The cluster I registered as monogenotypic / solitary cluster. Considering the distribution of genotypes, it can be concluded that cross between SiA 3222 x SiA 3580 has good chance of generating heterotic hybrids or transgressive segregants, depending on the gene action controlling the traits.

Keywords:- Foxtail Millet, Genetic Divergence, Hierarchical Cluster Analysis, Wards' Minimum Variance.

I. INTRODUCTION

Millets refers to a group of annual grasses, belonging to the family *Poaceae* with tiny edible seeds that do not shatter readily at maturity. Ideally, these crops are amenable for climate resilent agriculture as they are tuned to adapt varying thermal-moisture regimes, scarce input conditions and serve diversified purposes as food, feed, fodder, biofuels and brewing. Among the six small millets, *Setaria italica* (L.) P. Beauv, popularly known as foxtail millet, chinese millet, german millet, hungarian millet and italian millet resembling a fox's tail in appearance *i.e.* a long panicle with soft, long and erect hairs ranks second in economic importance, next to finger millet in terms of global production. Being an annual C_4 autogamous diploid (2n=2x=18) with small genome size (~ 515 Mb), short duration and prolific seed bearing ability, this millet serves as a 'model species' in functional genomic studies. The grains of this millet are enriched with quality protein (leucine and methionine), β carotene, minerals (Ca, Fe, K, Mg and Zn), antioxidants, dietary fibre, phytochemicals, vitamins (B_1, B_2 and B_3) and possess low glycemic index, a requisite for healthy human diet (Murugan and Nirmalakumari, 2006).

The success of any plant breeding programme largely depends on the existence of diversity among the genotypes (Allard, 1960). Assessment of a large number of germplasm for genetic diversity assists in selection of divergent genotypes for hybridization programme.

Hierarchical cluster analysis of quantitative traits is used to measure the genetic divergence and to classify the genetic stock into distinct groups. Intercrossing between more divergent parents is expected to generate a broad spectrum of variability and selection to be adopted in the segregating generations. Accordingly, the present study was taken up in foxtail millet to understand the genetic diversity available in the genetic stocks.

II. MATERIAL AND METHODS

Field studies at Regional Agricultural Research Station, Nandyal, Andhra Pradesh utilizing hundred foxtail millet genetic resources were laid in a Augmented randomized complete block design (ARCBD) with four checks during *Kharif*, 2018 in order to study the genetic divergence by Wards' minimum variance method. The experiment was carried out at an altitude of 211.3 m above mean sea level, latitude of 18.29°N and longitude of 78.29°E at RARS, Nandyal, A.P. The net plot size was 40 x 3 m^2 with a recommended spacing of 22.5 cm x 10 cm. The data was collected on five randomly selected plants per genetic resource for 18 metric traits *viz.*, SCMR at 30 DAS, SCMR at 45 DAS, days to 50% flowering, plant height, panicle length, number of productive tillers /plant, days to maturity, number of grains / ear head, 1000 grain weight, protein, carbohydrate, calcium, magnesium, iron, zinc, copper, manganese and grain yield/ plant. Genetic divergence analysis was done following the hierarchical cluster analysis. This analysis was done for the 100 foxtail millet genetic resources and these genetic resources were grouped into eleven clusters using the Ward's minimum variance (Anderberg, 1993). The data obtained was subjected to analysis using JMP-14 version software.

III. RESULTS AND DISCUSSION

Hierarchical cluster analysis through Ward's minimum variance method in 100 foxtail millet genetic resources, grouped them into 11 clusters, with the genotypes distribution in each cluster at random (Table 1) with the dendrogram delineated (Fig 1). The cluster means computed for 18 characters studied revealed existence of differences among the clusters. The highest cluster mean was recorded in number of grains per ear head (1690.945) and the lowest was in copper (1.262). Maximum cluster mean was recorded in cluster III (131.918) followed by cluster I (127.093). This showed the existence of maximum

genetic divergence among the genotypes in these clusters. Genotypes were grouped into clusters shown on the dendrogram. The dendogram divided the genotypes into 11 clusters and singleton as shown (Fig 1). Genotype SiA 3222, grouped as a singleton can used widely in breeding programmes to improve the yield levels. Similar result was published by Ayesha *et al.* (2019) for assessment of genetic diversity in foxtail millet genotypes.

The constellation plot depicting relationship for the 100 genetic resources was also shown (Fig 2). Clustering pattern divulged that majority of genotypes congegrated in cluster III (16) followed by cluster VIII (14), cluster IX (12), cluster VII (11) and cluster V (10). The clusters IV, VI and XI comprised of eight genotypes each. Seven and five genotypes were grouped in clusters X and II, respectively. The cluster I registered as monogenotypic / solitary cluster might have resulted due to geographic barriers preventing gene flow or intensive natural and human selection for diverse and adaptable gene complexes.

Estimates of genetic distance matrix was based on 18 metric traits for all pair wise combinations of $(100 \times 99)/2 = 4950$ for the 100 foxtail millet genotypes (data not shown). The observed genetic distance ranged from 2.455 (SiA3657and SiA 3085) to 12.029 (SiA 3222 and SiA 3580) pair wise combinations reflecting the wide diversity

among the genotypes. The genotypes with high genetic distance can be utilized directly as potent parents in breeding programmes to achieve improved yields.

The clusters obtained using Ward's method indicated that the highest genetic distance of 12.029 was between SiA 3222 and SiA 3580. Genotype SiA 3222, grouped as a singleton can be used widely in breeding programmes to improve the yield levels. Considering the distribution of genotypes, it can be concluded that cross SiA 3222 x SiA 3580 has enormous potential in generating heterotic hybrids or transgressive segregants.

REFERENCES

[1]. Allard, R.W. 1960. Principles of Plant Breeding. John Wiley and Sons Inc., New York. pp. 485.
[2]. Anderberg, M.R. 1993. Cluster Analysis for Application. Academic Press, New York.
[3]. Ayesha, M.D and Babu, D.R. 2019b. Genetic divergence studies in foxtail millet [*Setaria italica* (L.) Beauv.]. *Electronic Journal of Plant Breeding,* 10 (1): 18 – 29.
[4]. Murugan, R and Nirmala kumari, A. (2006). Genetic divergence in foxtail millet. (*Setaria italica* (L.) Beauv). *Indian Journal of Genetics*. 66(4):339- 340.

Cluster No.	No. of genotypes	Name of genotype (S)
I	1	SiA 3222
II	5	SiA 3323, SiA 3496, SiA 3409, SiA 3282 and SiA 3291
III	16	SiA 3657,SiA 3085 (C),SiA 2662, SiA 4155, SiA 2674, SiA 3737, SiA 3754, SiA 2745, SiA 3639, SiA 2579, SiA 3430, SiA 2737, SiA 3492, SiA 4107, SiA 3851 and SiA 3511
IV	8	SiA 3611, SiA 4027, SiA 3701, SiA 3429, SiA 3580, SiA 3498, SiA 4044 and SiA 3674
V	10	SiA 3627, SiA 3577, SiA 3588, SiA 3560, SiA 4013, SiA 3554, SiA 2850, SiA 1266, SiA 4005 and SiA 3469
VI	8	SiA 3559, SiA 3969, SiA 4180, SiA 3753, SiA 3513, SiA 4182, SiA 2844 and SiA 3281
VII	11	SiA 4061, Prasad (C) , SiA 4179, SiA 2856, SiA 3971, SiA 3423, SiA 3965, SiA 3972, Suryanandi (C), SiA 3516 and SiA 3038
VIII	14	SiA 4036, SiA 3697, SiA 2671, SiA 4020, SiA 2713, SiA 2663, SiA 3827, SiA 2667, SiA 3908, SiA 4016, SiA 3793, SiA 3422, SiA 2864 and SiA 3436
IX	12	SiA 2849, SiA 3462, SiA 3894, SiA 3419, SiA 3643, SiA 4009, SiA 3156 (C), SiA 3465, SiA 4114, SiA 4068, SiA 3749 and SiA 4141
X	7	SiA 805, SiA 3756, SiA 3413, SiA 3435, SiA 3499, SiA 3420 and SiA 4045
XI	8	SiA 2697, SiA 3855, SiA 4181, SiA 2757, SiA 4063, SiA 1244, SiA 2681 and SiA 4167

Table 1:- Clustering pattern of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes by Ward's minimum variance method

Cluster	SCMR at 30 DAS	SCMR at 45 DAS	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of prod. tillers /plant	Days to maturity	No of Grains / ear head	1000 grain wt (g)	Protein (g/100g)	Carbohydrate (g/100g)	Calcium (mg/100g)	Magnesium (mg/100g)	Iron (mg/ 100g)	Zinc (mg/ 100g)	Copper (mg/ 100g)	Manganese (mg/ 100g)	Grain yield/ plant (g)	Mean
1	46.625	65.906	32.094	109.960	14.526	1.035	60.156	1816.662	2.501	12.886	63.022	32.122	12.003	4.411	1.622	0.983	1.688	9.469	127.093
2	41.848	50.111	42.694	134.940	12.366	2.401	77.956	1765.994	2.015	13.593	58.611	21.669	12.076	8.330	2.762	0.952	2.110	5.656	125.338
3	48.216	52.928	44.948	158.848	18.441	3.459	83.756	1812.746	3.135	13.996	59.794	23.828	14.412	14.501	2.980	1.113	2.265	15.154	131.918
4	45.105	49.512	46.469	150.861	17.866	4.024	82.875	1660.770	2.762	13.228	55.845	25.396	22.272	20.720	3.119	1.856	2.443	9.963	123.060
5	45.479	54.429	44.719	154.944	17.926	3.977	83.681	1666.348	3.081	15.047	65.304	25.227	23.341	11.423	4.770	1.047	2.685	12.396	124.212
6	47.422	54.025	45.782	154.495	17.842	3.972	81.062	1646.173	2.921	13.691	65.408	21.485	11.946	10.016	5.615	0.992	3.424	12.256	122.140
7	47.265	52.698	42.327	137.578	15.057	3.522	79.832	1652.522	2.891	14.312	59.268	27.504	14.691	10.602	3.140	1.330	2.258	11.426	121.012
8	47.062	51.965	47.523	149.650	17.868	4.632	82.299	1603.519	2.977	13.271	69.321	24.854	12.879	7.869	2.646	1.017	2.027	12.321	119.650
9	46.763	58.655	44.367	148.830	18.798	3.316	82.737	1561.049	2.972	14.997	62.415	22.720	12.666	7.565	2.720	1.111	2.111	9.850	116.869
10	42.112	55.277	45.451	145.213	17.764	5.300	81.120	1678.254	2.790	14.459	54.205	21.775	16.598	8.693	2.821	0.890	2.238	7.759	122.373
11	47.117	53.653	45.250	149.714	18.621	3.985	83.656	1736.364	2.983	14.440	62.520	22.360	11.236	8.919	2.586	2.592	2.115	10.796	126.606
Mean	45.910	54.469	43.784	145.003	17.007	3.602	79.921	1690.945	2.821	13.993	61.428	24.449	14.920	10.277	3.162	1.262	2.306	10.641	

Table 2:- Mean values of eleven clusters estimated by Ward's minimum variance method in 100 foxtail millet [*Setaria italica* (L.)Beauv.] genotypes

Note: Bold figures indicate minimum and maximum values in each characte
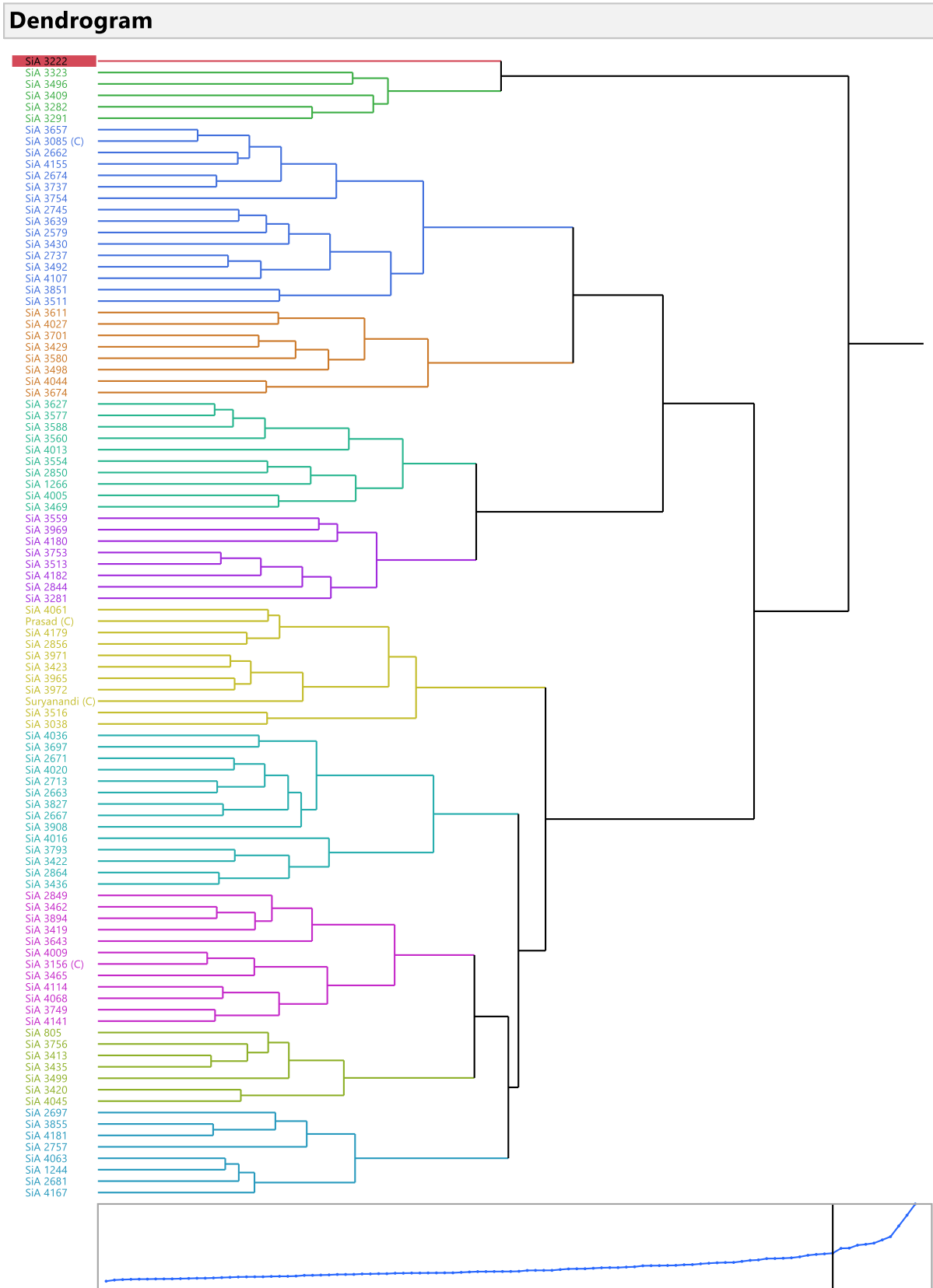
Fig. 1:- Dendrogram showing relationship of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes in 11 clusters based on Euclidean^2 distance
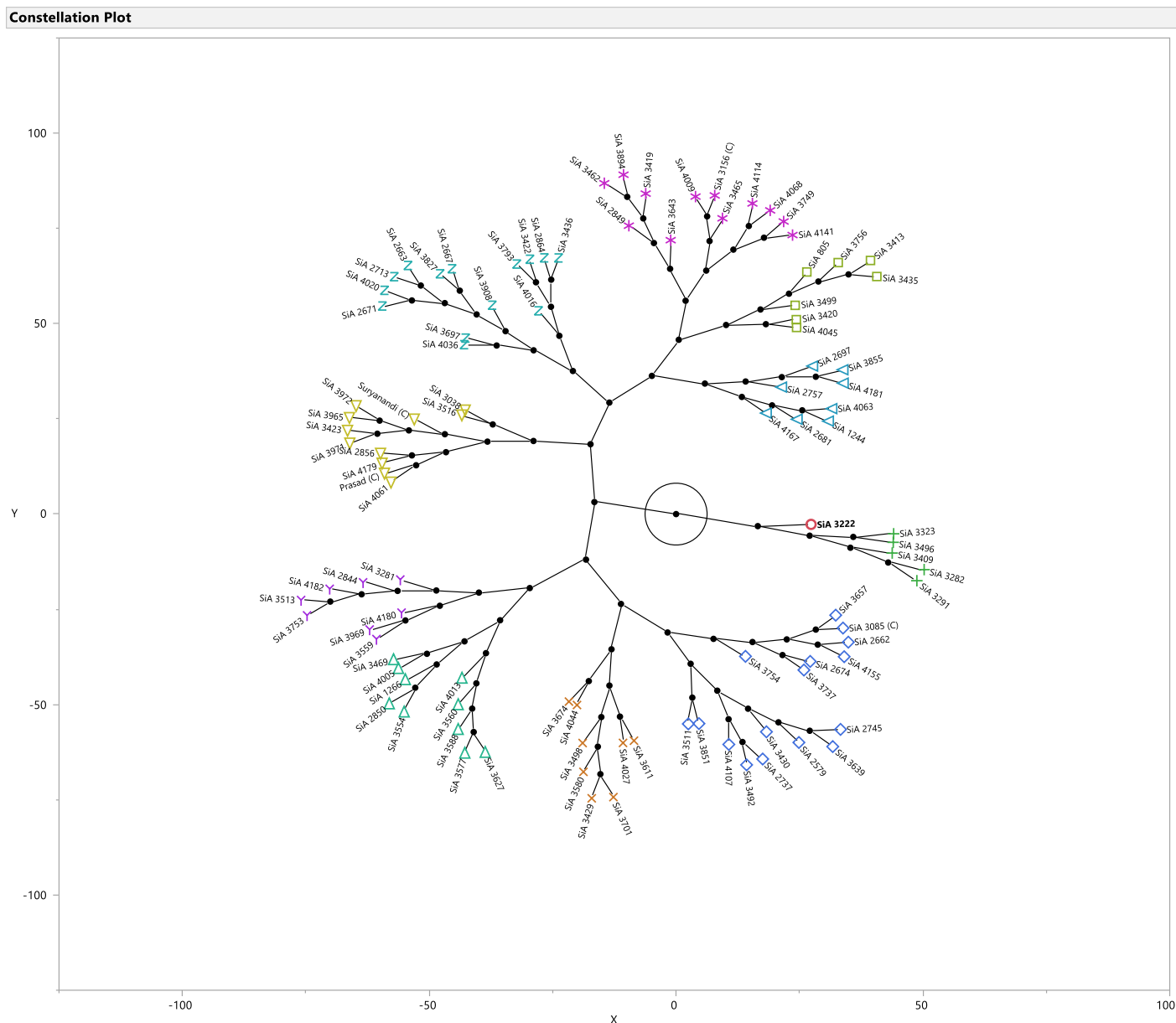
Constellation Plot

Fig. 2:- Constellation plot of 100 foxtail millet [*Setaria italica* (L.) Beauv.] genotypes into 11 clusters based on Euclidean^2 distances