

# Genetic Diversity and Genotype by Trait Analysis for Yield & Yield Attributing Traits in Foxtail Millet (*Setaria italica* (L.) Beauv.)

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**Abstract** – Twenty four foxtail millet genotypes including three checks were evaluated for understanding genetic diversity for yield and yield attributing traits. Out of seven principal components, PC1 and PC2 contributed 61.90% and 16.15% variation respectively. UPGMA method based cluster analysis arranged genotypes in four clusters with wide variation for yield traits. Cluster II(d) associated maximum genotypes with high grain yield, cluster II(c) represented three extra early maturing genotypes and cluster I(a) and I(b) contained genotypes each four respectively with high plant height, number of tillers/plant and fodder yield. The GT biplot analysis explained 78.05% of the total variation. Grain yield was positively associated with panicle length, plant height, days to maturity, days to 50% flowering and number of tillers/plant and negatively associated with fodder yield. Genotypes TNSI 267, SiA 3222, DhFTMV 2-5, SiA 3221, SiA 3159, SiA 3223, SiA 3163 and TNSI 309 have one or more extreme traits which may be useful as parents for development of varieties.

**Keywords** – Foxtail Millet, PCA, Genetic Diversity, GT Biplot.

## I. INTRODUCTION

Foxtail millet is one of the important ethnic small millet crops which provides staple food with good supplementary nutrients and protein. It is adapted for cultivation in dry climate with less resources. Foxtail millet is not thoroughly studied so far and germplasm is underutilized which resulted low productivity levels. The breeding effort for developing high yielding varieties followed through utilization of diverse germplasm, creation and exploitation of the genetic variation for different traits of economic importance is critical in crop improvement. [1].

The foxtail millet gene pool possesses huge diversity for various traits which can be exploited for yield, pest, disease resistance and improving resilience to climate change. Identification of trait specific parents, attempting crosses followed by selection is the basic approach to foxtail millet breeding. Precise information on the nature and degree of genetic diversity helps plant breeders in selecting the parents for targeted hybridization. Genetic divergence analysis helps the extent of diversity existing among selected genotypes. The cluster analysis is an appropriate method for determining relationship among genotypes, extent of genetic affinity or distance from each other [2]. In order to benefit from transgressive segregation, genetic distance between parents is necessary [3] that can be estimated by euclidean distance [4]. Principal component analysis (PCA) allows natural grouping of the genotypes and is precise indicator of

differences among genotypes. The main advantage of using PCA over cluster analysis is that each genotype can be assigned to one group only [5].

Relationships among traits of economic importance impact the breeding strategies along with selection procedure. If all breeding objectives were positively correlated, selection would be easy for a single trait. If all breeding objectives were either positively correlated or independently inherited, selection would not be too difficult either [6]. Strong negative genetic correlations between breeding traits often exist, which make breeding very challenging [7], [8]. The genotype-by-trait (GT) biplot is a statistical tool to evaluate cultivars based on multiple traits and identify lines that are superior. Entries identified for yield and yield attributed traits can be candidates for use as parents in breeding program [9]. The GT biplot analysis allows visualization of genetic correlation among traits [10] and help in understanding genotype by trait relationships. Hence, this study carried out to estimate the diversity among tested genotypes for yield and yield attributing traits and study the genotype and trait relationship by GT biplot analysis.

## II. MATERIALS AND METHODS

The plant material comprised of 21 elite entries and 3 checks pooled under All India Coordinated Small Millets Improvement Project (Table 1). These 21 foxtail millet genotypes along with 3 checks SiA 326, SiA 3156 and SiA 3085 were evaluated in randomized block design with 3 replications during crop season of 2014-15 at Regional Agricultural Research Station (ANGRAU), Nandyal, Andhra Pradesh (latitude of 18.29°N, longitude of 78.29°E and altitude of 211.3 m above mean sea level). These genotypes were sown in plots of 10 rows of 3 meter length with a row spacing of 30 cm. Standard crop production and protection measures were followed to raise healthy crop.

The complete euclidean distances were calculated by the UPGMA method and dendrogram was constructed to examine the relationships among different genotypes [11], [12]. Principal component analysis, cluster analysis and Genotype by trait Biplot was constructed from R programming Software Package [12], [13].

## III. RESULTS AND DISCUSSION

Results obtained from the experiment are described and discussed under the following heads.

### Principle Component Analysis

Principal component analysis (PCA) reveals the significance of the major contributor to the total variation at each axis of differentiation. The eigen values helps in determining the number of factors to be retained. Therefore, in this analysis the first factor retains the information contained in 2.0816 of the original variables (Table 2). The 7 principal components, PC1 to PC7 obtained from original data accounted for 100% of total variation. Among all principal components PC1 contributed 61.90% and PC2 contributed 16.15% to the total variation respectively. Characters with largest absolute value closer to unity within the first principal component influences the clustering more than those with lower absolute value closer to zero [14]. Accordingly, the major contributing traits for diversity in first principal component were days to maturity, plant height, panicle length, number of tillers/plant, fodder yield. Similarly, for second principal component (PC2) grain yield was major contributor for the diversity. The major contributing character for the diversity in the third principal component 3 (PC3) was days to 50% flowering, while fodder yield in principal component four (PC4), plant height in principal component five (PC5), number of tillers/plant and panicle length in principal component six (PC6) and days to maturity and panicle length in principal component 7 (PC7). However, one variable is selected from these identified groups depending on respective loadings. Hence, for the first group days to maturity is the best choice, which had the largest loading from PC1, grain yield for the PC2, days to 50% flowering for the third group and fodder yield for fourth, plant height for fifth group, number of tillers/plant for sixth group and panicle length for seventh group respectively.

### Cluster Mean Analysis

The dendrogram was generated to examine the relationships among different genotypes based on complete euclidean distances calculated by the UPGMA method is presented in Figure 1, mean values of the traits in each cluster studied are presented in Table 3 and the feature of each cluster is described below.

Looking at the dendrogram, it could be seen that 2 major clusters were formed, Cluster I and cluster II. Cluster I have 2 sub-clusters which could be named as 'a' and 'b'. Cluster 'a' consisted of 4 genotypes *viz.*, DhFtMV55-1, DHFT13-3, DhFtMV109-3 and DhFtMV2-5. The genotypes in this cluster had shown long days to 50% flowering, maximum days to maturity, high number of tillers/plant and maximum fodder yield. Similarly cluster 'b' comprised of 4 genotypes (TNSI309, DHFT33-3, TNSI306 and SiA 3223) which were characterized by maximum plant height, number of tillers/plant, panicle length and high fodder yield with medium grain yield. These genotypes possess high days to maturity with high number of tillers/plant and high fodder. Both cluster represented 33% of total genotypes with an equal representation of 16.5% for each cluster.

Cluster II have 2 sub-clusters 'c' and 'd'. Cluster 'c' comprised of 3 genotypes (SiA 3222, SiA 3221, SiA 3159) with characteristic feature of extra early days to 50%

flowering, days to maturity with moderate grain yield and less fodder yield. This cluster represented 13% of total genotypes. Cluster 'd' consisted of 13 genotypes *viz.*, SiA 3146, SiA 3162, TNSI 267, SiA 3164, SiA 3145, DHFT 33-3, SiA 3156(C), SiA 326 (C), SiA 3085 (C), SiA 3163, TNSI 266, SiA 3190, VMFC 329 ) with characteristic features of medium days to 50% flowering, days to maturity, number of tillers/plant, plant height with long panicle length and high grain yield and fodder yield. All check entries were clustered in this group showing high grain yield with medium fodder yield with narrow genetic base. This was the largest cluster with a representation of 54% of total genotypes. The cluster analysis showed that there was significant genetic variability among foxtail millet genotypes tested that indicated the presence of excellent opportunity to bring about improvement through hybridizing genotypes from different clusters. The extra early derivatives from cluster II(c) should be crossed with the genotypes of cluster IV to reduce the flowering time combined with high grain yield. High yielding genotypes from cluster IV could be further tested for their combining ability. Thus the genotypes present in different clusters can be hybridized to assemble desirable traits with higher heterotic potential.

### Genotype by trait (GT) biplot

The biplot (Figure 2) displays the relationship of 24 foxtail millet lines for 7 traits. The GT biplot of the mean performance of the foxtail millet genotypes explained the 78.05 % of the total variation of the standardized data. In GT biplot, a vector drawn from origin to each trait facilitates the visualization of interrelationships among traits. The vector length of the trait measures the magnitude of its effects on the yield [15]. The polygon view of GT biplot is best to visualize the interaction pattern between genotypes and traits, provided the biplot should explain a sufficient amount of the total variation. The correlation coefficient between any 2 traits is approximated by the cosine of the angle between their vectors [9]. On this premise, 2 traits are positively correlated if the angle between their vectors is an acute angle ( $< 90^\circ$ ) while they are negatively correlated if their vectors are an obtuse angle ( $> 90^\circ$ ) [16].

Across the 24 tested foxtail millet genotypes grain yield was positively associated with panicle length, plant height, days to maturity, days to 50% flowering and number of tillers/plant and negatively associated with fodder yield. In regular breeding programs taller genotypes are not preferred. Panicle length, days to 50% flowering, days to maturity and number of tillers/plant are positively associated to grain yield. Grain yield was negatively associated to fodder yield due to photosynthate partition mechanism (Figure 2).

The distance between genotype and the biplot origin is a unique measure of the genotype (i.e., how it differs from an "average" genotype), which is a hypothetical genotype that has an average level for all traits and is represented by the biplot origin [10]. Therefore, genotypes TNSI 267, SiA 3222, DhFTMV 2-5, SiA 3221, SiA 3159, SiA 3223, SiA 3163 and TNSI 309 with long vectors are those that have extreme values for one or more traits (Figure 3). Such

genotypes may or may not be superior, but they may be useful as parents for some useful traits.

#### IV. CONCLUSION

The cluster analysis showed that there is significant genetic variability among tested foxtail millet genotypes that indicates the presence of excellent opportunity to bring about improvement through hybridizing genotypes from different clusters. The extra early genotypes need further improvement regarding panicle length and grain yield. The GT biplot showed that the grain yield was positively associated with panicle length, number of tiller/plant, days to 50% flowering and days to maturity.

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Table 1. Tested genotypes of foxtail millet and their pedigree.

S.No.	Genotype	Pedigree	Source
1	SiA3146	SiA 2871 x PS 4	RARS (ANGRAU), Nandyal, Andhra Pradesh
2	SiA3145	SiA 2871 x SiA 3075	RARS (ANGRAU), Nandyal, Andhra Pradesh
3	SiA3163	Srilakshmi x SiA 1482	RARS (ANGRAU), Nandyal, Andhra Pradesh
4	SiA3222	SiA 3075 x SiA 326	RARS (ANGRAU), Nandyal, Andhra Pradesh
5	SiA3162	SiA 2644 x SiA 1482	RARS (ANGRAU), Nandyal, Andhra Pradesh
6	SiA3190	SiA 2622 x SiA 3075	RARS (ANGRAU), Nandyal, Andhra Pradesh
7	SiA3164	SiA 2644 X SiA 1435	RARS (ANGRAU), Nandyal, Andhra Pradesh
8	SiA3223	Selection from GS 96	RARS (ANGRAU), Nandyal, Andhra Pradesh
9	SiA3221	SiA 3075 X Ise 379	RARS (ANGRAU), Nandyal, Andhra Pradesh
10	SiA3159	Srilakshmi x SiA 1378	RARS (ANGRAU), Nandyal, Andhra Pradesh
11	VMFC329	Selection from Ise 663	ARS (ANGRAU), Vizianagaram, Andhra Pradesh
12	TNSI267	Co 5x SiA 3052	TNAU, Coimbatore, Tamilnadu
13	TNSI266	Selection from IE 17330	TNAU, Coimbatore, Tamilnadu
14	TNSI306	SiA 306 X Co 5	TNAU, Coimbatore, Tamilnadu
15	TNSI309	Co 5 x GS 2154	TNAU, Coimbatore, Tamilnadu
16	DhFtMV333	SiA 326 x Co 5	ARS, Hanumanamatti, Karnataka
17	DHFT33-3	Co 5 x PS 4 (2-5)	ARS, Hanumanamatti, Karnataka
18	DhFtMV109-3	Co 5 XGPUS-30	ARS, Hanumanamatti, Karnataka
19	DhFtMV55-3	Co 6 x GS 145	ARS, Hanumanamatti, Karnataka
20	DhFtMV2-5	Co 5 X PS 4	ARS, Hanumanamatti, Karnataka
21	DHFT13-3	Co 6 X GS 1919 (2-5)	ARS, Hanumanamatti, Karnataka
22	SiA326 (C)	PLS from Nallamallakorra	RARS (ANGRAU), Nandyal, Andhra Pradesh
23	SiA 3085 (C)	Selection from SiA 2644	RARS (ANGRAU), Nandyal, Andhra Pradesh
24	SiA3156(C)	Selection from SiA 2871	RARS (ANGRAU), Nandyal, Andhra Pradesh

Table 2: Vector loadings and percentage explained variation by the 7 PCs.

Trait	Comp 1	Comp 2	Comp 3	Comp 4	Comp 5	Comp 6	Comp 7
DFE	-0.2710	0.0000	0.8640	-0.2050	-0.3480	0.1260	0.0000
PH	-0.4420	0.0000	0.1190	0.4150	0.5460	0.3890	0.4020
NTP	-0.4040	0.0000	-0.4620	-0.3170	-0.4350	0.5680	0.0000
PL	-0.4410	0.1740	-0.1220	-0.3940	0.0000	-0.6300	0.4540
DM	-0.4590	0.0000	0.0000	-0.2170	0.3950	0.0000	-0.7630
GY	0.0000	0.9210	0.0000	0.2380	-0.2550	0.0000	-0.1590
FY	-0.4020	-0.3270	0.0000	0.6530	-0.4090	-0.3330	-0.1360
Eigen value	2.0816	1.0632	0.9303	0.5518	0.4097	0.3496	0.2771
Individual percentage	0.6190	0.1615	0.1236	0.0435	0.0240	0.0175	0.0110
Cumulative variance	0.6190	0.7805	0.9041	0.9476	0.9716	0.9890	1.0000

DFE-Days to 50% flowering, PH-Plant height (cm), NTP-Number of tillers/plant, PL-Panicle length (cm), DM-Days to maturity, GY-Grain yield (kg/ha), FY-Fodder yield (kg/ha)

Table 3: Mean value of the traits in the 4 clusters.

Cluster		DFE	PH	NTP	PL	DM	GY	FY
Cluster 1(a)	Mean	47	157	4	20	84	3480	9429
	Max	52	167	4	21	87	3569	10000
	Min	42	150	4	19	75	3419	9074
Cluster 1(b)	Mean	41	152	4	19	84	3271	8066
	Max	47	168	4	21	86	3663	8395
	Min	35	143	4	18	83	3054	7716
Cluster 2(c)	Mean	36	107	2	13	59	3054	3159
	Max	40	113	3	14	60	4062	3457
	Min	33	100	2	12	58	2436	2809
Cluster 2(d)	Mean	45	142	3	19	78	4012	5677
	Max	50	160	4	21	83	5064	7716
	Min	37	120	2	14	60	3569	4630

DFE-Days to 50% flowering, PH-Plant height (cm), NTP-Number of tillers/plant, PL-Panicle length (cm), DM-Days to maturity, GY-Grain yield (kg/ha), FY-Fodder yield (kg/ha)

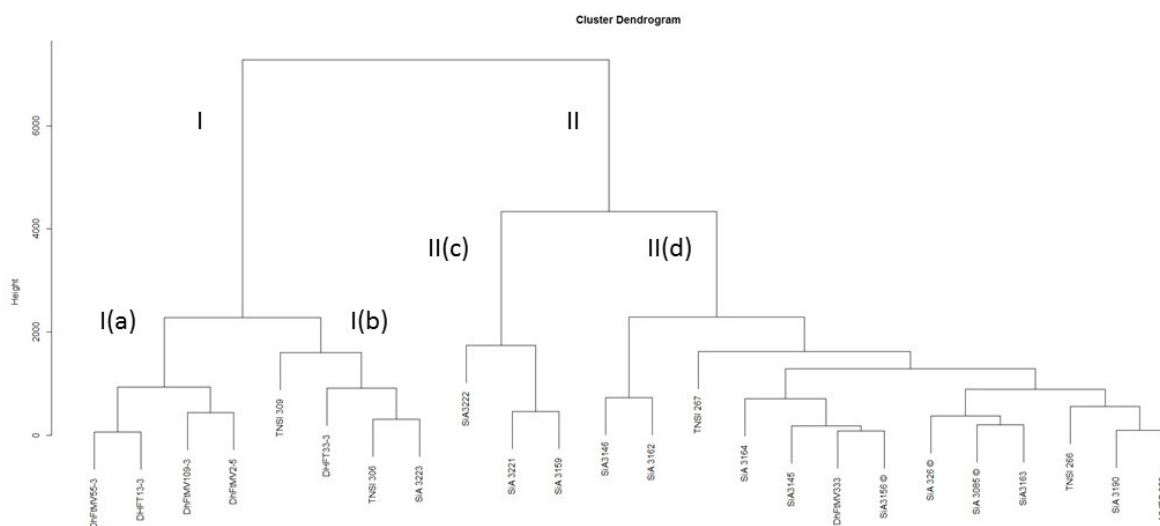


Fig.1. Dendrogram depicting genetic relationships among 24 foxtail millet genotypes.

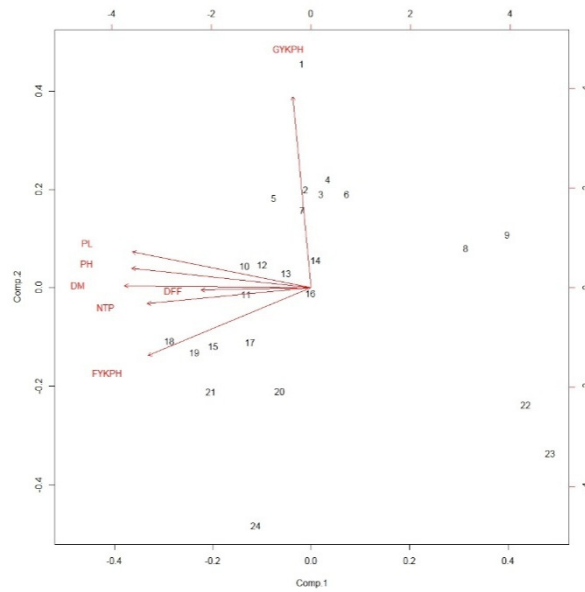


Fig.2. Genotype by trait (GT) biplot comprising of 24 foxtail millet genotypes studied for seven traits. DFF-Days to 50% flowering, PH-Plant height (cm), NTP-Number of tillers/plant, PL-Panicle length (cm), DM-Days to maturity, GY-Grain yield (kg/ha), FY-Fodder yield (kg/ha)

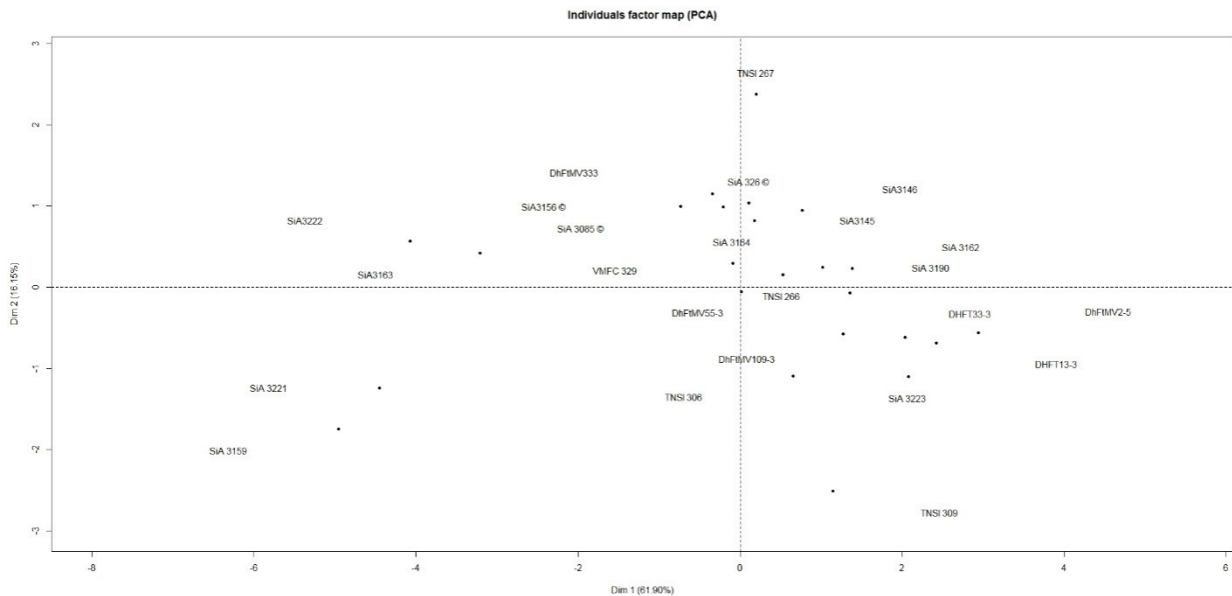


Fig.3. Scatter plot of first two principal components contributing 78.05% of the total variation for 7 quantitative traits in 24 foxtail millet genotypes.

### AUTHOR'S PROFILE



#### C V Chandra Mohan Reddy

*Title:* Scientist (Plant Breeding & Genetics)

*Organization & Address:* Regional Agricultural Research Station, Acharya NG Ranga Agricultural University, Nandyal, A.P.

*Contribution:* As Scientist of crop improvement, I am working in small millets includes foxtail millet under AICSMIP. In foxtail millet, 2 national varieties (SiA 3085 & SiA 3156) and one variety for Andhra Pradesh (Suryanandi) were released and the labeled seed is made available to seed agencies and farming community. The research results are being published in different peer reviewed journals of national and international recognition. At present I'm working as visiting scholar at WVSU, WV, US.



#### P. Pullibai

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*Contribution:* As Scientist of crop improvement, I am working in Tobacco under AINRP, small millets & millets (Sorghum). Pre-release culture in tobacco crop, Nandyala pogaku-1 (NBD 119), was popularized & submitted to the state variety releasing committee to release in Andhra Pradesh. Two bidi tobacco entries, NyBD 56 & 59, and two foxtail millets entries, SiA 3179 & SiA 3205, were proposed for multi-location evaluation under All India Coordinated Trials. Two sorghum entries, NJ 2647 & NJ 2446 and one small millet entry, SiA 3221 (extra early with 60 days maturity), were under minikit trials at farmers' field.



## J. Manjunath

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As Scientist of Plant Protection specialized in Entomology, I deeply involved in insect/pest response to climatic factors and formulating approaches for pest management to crops like foxtail millets, paddy, jowar, tobacco and sunflower. Artificial screening against pests of economic threshold was done for prerelease varieties like SiA 3085 & SiA 3156 in foxtail millet, Nandyalsenaga -1 in Chickpea and Nandyal Pogaku-1 in tobacco crop which were released recently. At present I am pursuing research on nano based molecules to accelerate pest control efficiency. My research results were published in recognized peer reviewed journals, booklets, brochures etc.

## P. Munirathnam

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*Contribution:* As head of small millets at RARS, Nandyal, I am instrumental in coordinating the release of foxtail millet varieties, SiA 3085, Suryanandi, SiA 3156 for A.P. as well as other states. Diverse and unique germplasm lines of foxtail millet are maintaining and characterized under AICSMIP. Crop production and protection technologies disseminated to growers towards enhancing productivity.