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Variability Studies and Metroglyph Analysis in Foxtail Millet (*Setaria italica* L.) for Grain Yield Characters

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ABSTRACT

The present investigation was conducted with 20 Foxtail millet genotypes including one check during *kharif* (July-October 2021) at the Crop Research Farm (CRF), Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P., India. The objectives were to study the magnitude of variability for different traits among foxtail millet genotypes and to identify diverse parents for morphological and seed quality parameters in foxtail millet. The data were recorded on 12 quantitative traits. ANOVA revealed high GCV and PCV for test weight, flag leaf length, number of tillers plant^{-1}, grain yield plant^{-1}, number of productive tillers plant^{-1}, flag leaf width and peduncle length. High heritability coupled with high genetic advance as per cent of mean (h^2_b) (>60%) were recorded for test weight, number of tillers plant^{-1}, flag leaf length, grain yield plant^{-1}, number of productive tillers plant^{-1}, peduncle length, flag leaf width, flag leaf area, plant height and panicle length. Days to maturity, plant height, flag leaf area, peduncle length and panicle length were positively significant concerning grain yield plant^{-1}. Metroglyph analysis indicated significant variations among the 20 genotypes for twelve characters. The maximum number of genotypes falls in cluster I (14) followed by cluster II (4), cluster III (1) and cluster IV (1). The genotypes recorded high grain yield plant^{-1} fell into cluster I. The genotypes that recorded high index scores fell into different clusters that can be crossed to have maximum variability of a good combination of characters. Thus, the use of these genotypes in a further breeding program is suggested.

KEYWORDS: Foxtail millet, PCV, GCV, correlation analysis, metroglyph analysis

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1. INTRODUCTION

Foxtail millet (*Setaria italica* (L.) Beauv.) is a self-pollinating diploid crop with chromosome numbers, 2n=2x=18, classified under the Poaceae family and subfamily Panicoideae. It is a crop of the Neolithic era and is an important crop of dry land agriculture, grown more than 10,500 years ago in China. In terms of the total production of millet worldwide, foxtail millet rank second (Bala, 2004). In India, it is cultivated in Andhra Pradesh, Karnataka, Maharashtra and the Hilly Areas of Northern India. It is critical to develop ways to counteract the adverse consequences of climate change on agriculture and food security but one of the strategies can be growing climate-resilient crops, which have the ability to adapt to poor soil conditions. It is a crop with a limited lifespan that needs to be revitalized and prioritized in public plant breeding projects for agriculture. Foxtail is renowned for its capacity to withstand drought, quick recovery from delayed rain and early maturation. Additionally, it can withstand pests and illnesses and flourish in nutrient-poor soil (Hirano et al., 2011). Foxtail millet is high in micronutrients, has a low glycemic index, is high in dietary fiber and contains a variety of phytochemicals and phenolic compounds with therapeutic benefits. It has also recently gained recognition for its medical and health benefits, such as lowering blood glucose levels and regulating cholesterol in healthy and diabetic individuals. (Ghimire et al., 2018; Kamatar et al., 2014a; Kamatar et al., 2014b) It is a natural source of nutrients like calcium, zinc, iron, and other necessary elements for preventing malnutrition. 100 grams of foxtail millet grains contain protein (12.3 g), carbohydrate (60.9 g), fat (4.3 g), minerals (3.3 g), calcium (31 mg) and phosphorus (290 mg) (Anonymous).It also has a high photosynthetic efficiency and drought resistance under low fertility conditions (Dai et al., 2008, 2011).

Grain yield is a complex trait controlled by numerous genes and affected by the environment in the area (Owere et al., 2015). The seeds of these millets can be preserved for a long time without much loss of their quality characteristics such as nutrients and seed viability. Therefore, this is one of the best suitable crops for the recent dry farming programs thus, the improvement of this crop becomes imperative. Foxtail millet typically experiences anthesis around midnight and in the morning, however, this varies greatly depending on the environment (Malm and Rachie, 1971). The small millets nevertheless play a significant role in Indian agriculture, despite the declining acreage and productivity.

Yield being quantitative in nature is a complex trait with low heritability and depends upon several other components with high heritability (Santhakumar, 1999).The ability to improve yield in any crop requires knowledge of the correlation coefficient between grain yield and features that contribute to yield; research on this link would be highly beneficial. The objectives were to study the magnitude of variability for different traits among foxtail millet genotypes and to identify diverse parents for morphological and seed quality parameters in foxtail millet.

2. MATERIALS AND METHODS

Twenty genotypes of foxtail millet namely TNSi 380, IIMR FxM-6, IIMR FxM-7, CRS FXM-3, CRS FXM-4, IIMR FXM-8, IIMR FXM-9, IIMR FXM-10, IIMR FXM-11,GPUF 16, TNPSi 382, TNSi 385, DHFt 20-3, DHFt-20-153, SiA 4201, SiA 4213, BUFTM 82, BUFTM 98, SiA 3156, DHFt 109-3(check) were collected from the Unit of All India Coordinated Research Project 2021 (AICRP) on small millets and were grown in a randomized block design (RBD) during *kharif* (July-October 2021) at Crop Research Farm (CRF) of the Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P , located at 25.57°N latitude, 81.51°E longitude and 98 meters above sea level. This region has a subtropical climate. Each genotype was sown in 10 rows of 3 m length witha spacing of 22.5×10 cm^2. Five plants were randomly selected from each genotype in each replication (leaving the first two border rows from four sides, in order to avoid sampling error) to record observation on days to 50% flowering, days to maturity, plant height, flag leaf length, flag leaf width, flag leaf area, number of tillers $plant^{-1}$, number of productive tillers $plant^{-1}$, peduncle length, panicle length, test weight, grain yield $plan^{-1}$. According to Panse and Sukhatme's, 1964, the mean values were subjected to statistical analysis to create an analysis of variance for each character. According to Burton and De Vane, 1953, the phenotypic, genotypic and environmental coefficients of variation, and heritability estimate were computed. The genetic advance was evaluated using the Johanson et al., 1955 approach. The genotypic and phenotypic correlation coefficient between yield and its component traits and among themselves was worked out as per the methods suggested by Al Jibouri et al., 1958. Metroglyph and index score methods advocated by Anderson, 1957 were used for the analysis of morphological characters in different crop species.

3. RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed highly significant differences among the genotypes, for twelve characters studied. Mean sum of square for genotypes, environments and genotype×environment was significant given in (Table 1). Genetic parameters of variation for yield and its components are given in (Table 2). Estimation of

Table 1: Analysis of Variance (ANOVA) among 20 genotypes for 12 quantitative traits of foxtail millets

Sl. No.	Features	Mean sum of square		
		Replication	Treatment	Error
		(d.f=2)	(d.f=19)	(d.f=38)
1.	Days to fifty percent flowering	28.7240	47.983**	13.726
2.	Days to maturity	15.20	46.929*	20.568
3.	Plant height (cm)	107.0250	826.96**	77.897
4.	Flag leaf length (cm)	5.9620	280.339**	4.73
5.	Flag leaf width (cm)	0.0050	0.407**	0.016
6.	Flag leaf Area (cm)	55.8870	580.764**	50.085
7.	Number of tillers plant^{-1}	0.0230	0.668**	0.008
8.	Number of productive tillers plant^{-1}	0.0030	0.526**	0.017
9.	Peduncle length (cm)	0.2860	15.187**	0.502
10.	Panicle length (cm)	3.5830	16.651**	1.976
11.	Test weight (g)	0.0150	0.793**	0.008
12.	Grain yield plant^{-1} (g)	0.0040	2.322**	0.065

* and ** indicates significant at (p=0.05) and (p=0.01) level significance respectively

Table 2: Estimation of genotypic and phenotypic variances

Sl. No.	Parameters	GCV	PCV	h^2 (Broad Sense)	Genetic advance	Genetic advance as % of mean 5%
1.	Days to fifty percent flowering	6.351	9.425	45.413	4.691	8.817
2.	Days to maturity	3.808	6.96	29.933	3.341	4.291
3.	Plant height (cm)	12.989	14.877	76.221	28.419	23.36
4.	Flag leaf length (cm)	28.532	29.258	95.104	19.255	57.32
5.	Flag leaf width (cm)	21.146	22.39	89.194	0.703	41.139
6.	Flag leaf area (cm)	16.166	18.312	77.934	24.187	29.399
7.	No. of tillers plant^{-1}	27.787	28.31	96.336	0.948	56.182
8.	No. of productive tillers plant^{-1}	26.421	27.738	90.729	0.808	51.843
9.	Peduncle length (cm)	21.063	22.116	90.707	4.341	41.325
10.	Panicle length (cm)	13.437	15.921	71.225	3.845	23.36
11.	Test weight (g)	35.654	36.179	97.117	1.038	72.38
12.	Grain yield plant^{-1} (g)	22.623	23.581	92.043	1.714	44.712

genotypic and phenotypic variances given in (Table 2). High PCV (>20) was recorded for test weight, flag leaf length, number of tillers plant^{-1}, grain yield plant^{-1}, number of productive tillers plant^{-1}, flag leaf width and peduncle length. Similar results have been reported by Pallavi et al., 2020 for test weight, flag leaf length, flag leaf width, and panicle length. While flag leaf area, panicle length and plant height had moderate PCV (10–20). The same trend was observed for GCV values except for days to 50% flowering (Shanthi et al., 2017) and days to maturity which recorded low GCV and PCV values (Nirmalakumari and Vetriventhan, 2010). All the traits exhibited narrow differences between PCV and GCV (Shingane et al., 2016, Chavan et al., 2019).

Selection for the traits with high heritability coupled with high genetic advance is likely to acquire more additive genes leading to further improvement. High heritability was observed for all the trait except for days to 50% flowering which had moderate heritability and days to maturity had low heritability. The genetic advance as % of mean recorded high for test weight, flag leaf length, number of tillers plant^{-1}, number of productive tillers plant^{-1}, grain yield plant^{-1}, peduncle length, flag leaf width, flag leaf area, panicle length, and plant height, except for days to 50% flowering and days to maturity. Similar results have been reported by Pallavi et al., 2020, for test weight, peduncle length, flag leaf width, flag leaf length, and panicle length. The characters like plant height, flag leaf length, flag leaf width, flag leaf area, number of tillers plant^{-1}, number of productive tillers plant^{-1}, peduncle length, panicle length, test weight, grain yield per plant^{-1} recorded high heritability and high genetic advance as % of the mean showing that the heritability is due to the additive gene effect, indicating that the differences are attributed to a high level of heritable variation and that selection would be efficient for enhancing these qualities. High heritability coupled with high genetic advance as % of mean were also reported in the earlier studies in foxtail millet for number of productive tillers plant^{-1} (Nagarajan and Prasad, 1980, Islam et al., 1989, Chidambaram and Palanisamy, 1995, Selvarani and Gomathinayagam, 2000), test weight (Gurunadha and Appu, 1984, Patil and Mohan Kumar, 1989, Nirmalakumari et al., 2008, Udamala et al., 2020), grain yield plant^{-1} (Islam et al., 1989, Selvarani and Gomathinayagam, 2000, Muhammed and Hussain, 2004, Nirmalakumari and Vetriventhan, 2010, Prasanna et al., 2013, Kavya, 2016).

The complicated characteristic of grain yield was influenced by a number of different yield related factors. The effectiveness of selection can be increased by having a better understanding of the relationship between grain yield and other linked qualities. In general, the genotype the breeder is working with will affect the association between yield and other characters as well as among the component characters. The genotypic correlation between character pairs has been examined in the current work to pinpoint the constituent features of 20 genotypes of foxtail millet that are most closely associated with grain yield. The magnitude of the genotypic correlation coefficient for all the characters was higher than their corresponding phenotypic correlation coefficient (Table 3). The grain yield plant^{-1} was significantly and positively correlated with plant height, flag leaf area, peduncle length and panicle length(In earlier studies similar results have been reported by Murugan and Nirmalakumari, 2006, for peduncle length and panicle length. Nirmalakumari and Vetriventhan, 2010, Pallavi et al., 2020, reported similar result for panicle length and plant height). Plant height recorded positive and significant correlation with flag leaf length, flag leaf area, panicle length and grain yield plant^{-1}. Flag leaf area recorded positive and

Table 3: Genotypic correlation coefficient for grain yield and component characters of foxtail millets

Parameters	D 50% F	DTM	PH (cm)	FLL (cm)	FLW (cm)	FLA (cm)	NTP	NPTP	Pedu L (cm)	P L (cm)	TW (g)	GYP (g)
D 50% F	1.0000	0.397*	0.289*	0.1465	0.0901	0.1791	0.1723	0.1969	- 0.391*	0.280*	-0.1657	0.1813
DTM		1.0000	0.324*	0.1087	0.1785	0.2377	0.1336	0.1842	- 0.381*	0.348*	-0.0579	0.1818
PH (cm)			1.0000	0.299*	-0.1353	0.409*	0.0496	0.0156	0.2148	0.556**	0.2220	0.422**
FLL (cm)				1.0000	-0.1026	0.1623	-0.1216	-0.1066	0.0359	0.279*	-0.0197	0.2260
FLW (cm)					1.0000	0.2244	-0.0844	-0.0107	- 0.258*	-0.1076	-0.1245	0.1069
FLA (cm)						1.0000	0.0451	-0.0452	0.301*	0.535**	0.0084	0.710**
NTP							1.0000	0.913**	- 0.1593	-0.0065	-0.0907	0.0889
NPTP								1.0000	- 0.300*	-0.0649	-0.1618	-0.0056
Pedu L (cm)									1.0000	0.1991	0.1829	0.347*
P L (cm)										1.0000	-0.0703	0.599**
TW (g)											1.0000	0.0973

D 50% F: days to 50% flowering, DTM: days to maturity, PH: plant height, FLL: flag leaf length, FLW: flag leaf width, FLA: flag leaf area, NTP: number of tillers plant^{-1}, NPTP: number of productive tillers plant^{-1}, Ped L: peduncle length, PL: panicle length, TW: test weight, GYP: grain yield plant^{-1}; * and ** indicates significant at 5% and 1% level significance respectively;

significant correlation with peduncle length and panicle length. Peduncle length recorded positive and significant correlation with flag leaf area and grain yield plant^{-1}. Panicle length recorded positive and significant correlation with days to 50% flowering, days to maturity, plant height, Flag leaf area, flag leaf length and grain yield plant^{-1}.

The scattered diagram revealed that four group could be distinguished based on morphological variation. (Figure 1). The index scores and signs used for twelve characters for Metroglyph analysis were presented in (Table 4). Cluster I was represented by fourteen genotypes with high plant height and moderate flag leaf area and the genotypes are TNSi 380, IIMR FxM–6, CRS FXM4, IIMR FXM–8, IIMR FXM–9, IIMR FxM–11, GPUF 16, TNPSi 382, TNSi 385, DHFt 20 - 3, SiA 4213, BUFTM 82, BUFTM 98, DHFt 109–3 (Check). Cluster II was represented by four genotypes and moderate plant height with moderate flag leaf area and the genotypes are CRS FXM 3, IIMR FxM–10, DHFt–20–153, SiA 3156. Cluster III was represented by one genotype having low plant height with moderate flag leaf area and the genotype is IIMR FxM–7 and this genotype exhibits earlier days to 50% flowering, days to maturity and medium grain yield plant^{-1} Cluster IV is represented by one genotype with moderate plant height and high flag leaf area and the genotype is SiA 4201, this genotype also recorded high for grain yield plant^{-1}. The majority of the genotypes showed high plant height and moderate flag leaf area. The frequency diagram showed the index score ranged from 17 (IIMR FxM–7)-29 (SiA 4201), (Verma et al., 2001). It indicates that germplasm lines were having variations and it is interesting to note that high grain yield plant^{-1} genotype were found with the highest index score. Among the 20 genotypes lines, the genotypes, SiA 4201, GPUF 16, BUFTM 98 and TNPSi 382 were observed as high grain yielders and identified for higher index scores. The findings of the present study suggested that genotypes in the different clusters can be used for crossing programme for harnessing maximum variability of character.

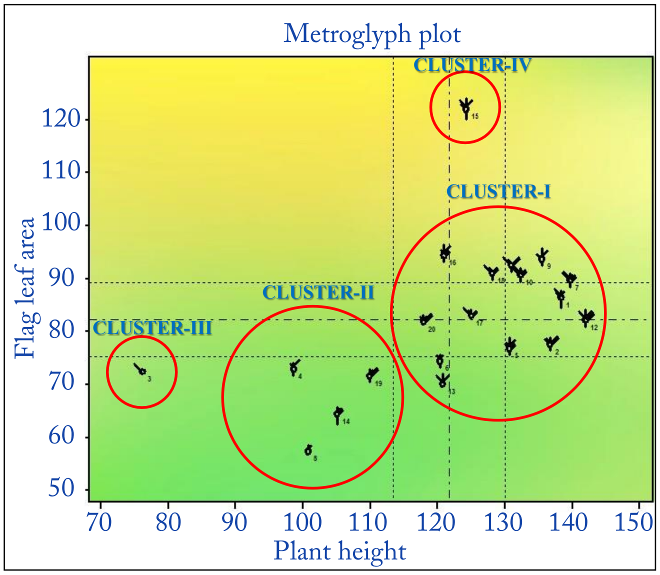

Figure 1: Scattered diagram of metroglyph analysis of 20 Foxtail millet genotypes

Table 4: Index score and signs used for 12 characters for Metroglyph analysis of 20 genotypes of foxtail millet

Character	Range of mean	Score 1	Sign	Score 2	Sign	Score 3	Sign
		Value <		Value from - to		Value >	
Days to 50% flowering	43.33 - 59.33	49.21	○	49.21 - 57.2	♀	57.20	♀
Days to maturity	65.33 - 83.67	73.89	○	73.89 - 81.81	♁	81.81	♁
Plant height (cm)	76.15 - 141.91	105.05	○	105.05 - 138.26	б	138.26	б
Flag leaf length (cm)	23.63 - 67.66	23.93	○	23.93 - 43.26	ծ	43.26	ծ
Flag leaf width (cm)	1.4 - 2.9	1.34	○	1.34 - 2.08	ծ	2.08	ծ
Flag leaf area (cm)	57.38 - 122.02	68.36	○	68.36 - 96.19	♂	96.19	♂
No. of tillers plant^{-1}	0.67 - 2.33	1.22	○	1.22 - 2.16	○	2.16	○
No. of productive tillers plant^{-1}	0.67 - 2.13	1.14	○	1.14 - 1.98	○	1.98	○
Peduncle length (cm)	6.14 - 14.76	8.25	○	8.25 - 12.75	♂	12.75	♂
Panicle length (cm)	11.47 - 20.59	14.10	○	14.1 - 18.82	⦸	18.82	⦸
Test weight (g)	0.5 - 2.47	0.92	○	0.92 - 1.95	○–	1.95	○–
Grain yield plant^{-1} (g)	2.4 - 5.8	2.95	○	2.95 - 4.71	–○	4.71	–○

4. CONCLUSION

A wide spectrum of variation can be observed for yield and its traits in foxtail millet. The correlation analysis revealed that flag leaf area, panicle length, plant height, days to maturity, and peduncle length are highly significant and positively associated with grain yield plant^{-1} hence the direct development and selection of these traits can increase grain yield. The genotypes grouped into Cluster I and Cluster II are good because of the maximum grain yield, maximum flag leaf area and highest index score. Further, these two cluster genotypes can be utilized in the breeding programme for the selection of elite genotypes.

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