



## Research Article

# Characterization of foxtail millet germplasm collections for yield contributing traits

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### Abstract

The evaluation of 741 germplasm accessions including some varieties was done during *rabi*, 2008-2009 at Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore to determine the genetic variability, correlation and path analyses of yield and its components. Data were recorded on various morphological traits such as days to 50 per cent flowering, plant height (cm), total number of tillers, number of productive tillers, panicle length (cm), days to maturity and grain yield per plant. Considerable diversity was observed for all accessions studied for all seven characters. Highest heritability, genotypic coefficient of variation and genetic advance as per cent of mean was recorded in grain yield per plant and the lowest was recorded in days to 50 per cent flowering. In the present study, all seven characters studied exhibited highly significant positive correlations with grain yield. The path analysis revealed that direct effect of days to 50 per cent flowering on grain yield was positive and negligible. Direct effect of number of productive tillers on grain yield was positive and high. Panicle length showed moderate positive direct effect on grain yield and negligible indirect effects through other traits studied. This study indicates that, great yield advantage could be achieved by using germplasm with more productive tillers, medium panicle length and medium duration. A 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.

### Key words:

Foxtail Millet; germplasm; variation; grain yield; correlation; path analysis

### Introduction

Foxtail millet (*Setaria italica* (L.) Beauv) is one of the oldest crops cultivated for food grain, hay and pasture. It has the longest history of cultivation among the millets, having been grown in China since sometime in the sixth millennium BC. The geographical origin of foxtail millet based on cytological studies indicated that wild ancestor of foxtail millet is *S. viridis* (Li *et al.* 1945). According to Vavilov (1926), the principal center of diversity for foxtail millet is East Asia, including China and

Japan. Several hypotheses concerning the origin and domestication of foxtail millet have been proposed (Kawase and Sakamoto, 1984; Nguyen van and Pern-s, 1985; Vavilov, 1926; de Wet *et al.*, 1979). A multiple domestication hypothesis (de Wet *et al.*, 1979) is widely accepted. Foxtail millet ranks second in the world's total production of millets and is an important staple food for millions of people in southern Europe and Asia (Marathe, 1993). Foxtail millet is an annual grass with slim, vertical, leafy stems which can reach a height of 120-200 cm (4-7 feet). The seedhead is a dense, hairy panicle and 5-30 cm long. The small seeds, around 2 mm in diameter, are encased in a thin, papery hull which is easily removed after threshing. Seed color varies greatly between genotypes. Morphology and anthesis behaviour make foxtail millet one of the most

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difficult species to cross pollinate. Foxtail millet is largely self-pollinated, with cross pollination averaging about 4 per cent (Li *et al.* 1935). The inflorescence is a spike with short side branches bearing spikelets and bristles. Each spikelet consists of a pair of glumes that embrace two minute flowers (about 1 mm in length); the lower one sterile and the upper one bisexual, with three stamens and a long oval smooth ovary with two long styles, that terminate in a brush like stigma (Hector, 1936). From one to three bristles develop at the base of each spikelet (Vinall, 1924). Anthesis in foxtail millet generally takes place near midnight and in the morning, but varies significantly with the environment (Malm and Rachie, 1971). The rate of anthesis is generally favoured by low temperature and high humidity. The accessions were classified into races and subraces on the basis of inflorescence morphology (Prasada Rao *et al.* 1987). There is wide genetic diversity available in foxtail millet, and characterizing these resources is a prerequisite for the genetic improvement of its cultivars. Recognizing this, the Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University had assembled 741 collections of foxtail millet accessions including some varieties.

#### Material and Methods

The evaluation of germplasm accession was done during *rabi*, 2008-2009 at Department of Millets, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, which is situated at about 11°N latitude and 77°E longitude at an altitude of 427 metres above MSL. The average annual rainfall is around 700mm at Coimbatore. The 741 accessions including CO 5, CO 6 and CO 7 cultivated varieties were raised in Randomized Block Design with three replications. Each accession was accommodated in one row with row spacing of 30 cm and plant to plant spacing of 10 cm. Uniform and recommended cultural practices were followed to raise agronomically good managed crop. Data were recorded on various morphological traits such as days to 50 per cent flowering, plant height (cm), total number of tillers, Number of productive tillers, panicle length (cm), days to maturity and grain yield per plant as per descriptors of *Setaria italica* and *S. pumila* (IBPGR, 1985). For each accession five competitive plants in a row were tagged for taking observation in each replication. The present study was planned to characterise the germplasm materials for different yield and yield contributing traits, to study the variability parameters and to understand the association of various characters, their cause with yield and its components in foxtail millet. The estimation of mean, variance and standard error were worked out by adopting the standard methods (Panse and Sukhatme, 1964). The significance test was

carried out by referring to the 'F' table given by Snedecor (1961). Phenotypic variance and genotypic variance estimated according to the formula given by Lush (1940). Heritability ( $h^2$ ) in the broad sense was calculated according to Lush (1940). Genetic advance was expressed as percentage of mean by using the formula suggested by Johnson *et al.* (1955). The genotypic correlation between yield and its component traits and among themselves was worked out as per the methods suggested by Johnson *et al.* (1955). The correlation coefficient was partitioned into direct and indirect causes according to Dewey and Lu (1959).

#### Results and Discussion

##### Studies on variability among accessions

Genetic variability studies provide basic information regarding the genetic properties of the population based on which breeding methods are formulated for further improvement of the crop. These studies are also helpful to know about the nature and extent of variability that can be attributed to different causes, sensitive nature of the crop to environmental influences, heritability of the characters and genetic advance that can be realized in practical breeding. Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing characters enforcing selection. Nevertheless, the heritability estimates in conjunction with the predicted genetic advance will be more reliable (Johanson *et al.*, 1955). Heritability gives the information on the magnitude of inheritance of quantitative traits, while genetic advance will be helpful in formulating suitable selection procedures.

In the present investigation seven quantitative characters were considered for working out variability and character association among themselves. The estimation of mean, variance and standard error was worked out by adopting the standard methods (Panse and Sukhatme, 1964). The data showing continuous variation were subjected to statistical analysis to determine mean, standard deviation, standard error, variance, co efficient of variability. Results of important quantitative characters are summarized in Table I. The estimates on genotypic co-efficient of variation, phenotypic co-efficient of variation, heritability, genetic advance as per cent of mean are furnished in Table II.

Days to 50 per cent flowering ranged from 37 to 70 days with coefficient of variability of 6.87 per cent. Plant height varied from 57 to 185 cm with a mean height of 139.89 cm and with CV 10.82 per cent. Total number of tillers varied from 3 to 19 with CV of 2.62 per cent. Number of productive tillers ranged

from 3 to 15.05 with a mean of 7.27 and CV was 27.69 per cent. Panicle length varied from 10 to 34 cm with a mean of 18.60 cm and CV of 17.44 per cent. Days to maturity ranged from 80 to 101 days in the accessions evaluated. The CV observed was 47.28 per cent with mean of 89.38. Seed yield per plant showed a wide range of 3.31 to 107.46 g with a mean of 34.75 g. Maximum CV (40.16 %) was observed for this character (Table I).

In the present study, all the traits showed narrow difference between phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) except days to 50 per cent flowering, indicating the low effect of environment and greater role of genetic factors on the expression of the traits. The values of phenotypic co-efficient of variation varied from 7.48 to 40.28 per cent. The highest magnitude of phenotypic coefficient of variation was recorded by grain yield per plant (40.28 %) followed by total number of tillers (30.61 %). The lowest phenotypic coefficient of variation was recorded in days to 50 per cent flowering (7.48 %). The values of genotypic coefficient of variation obtained in respect of various yield and yield contributing characters ranged from 6.11 to 38.82 per cent. The highest genotypic coefficient of variation was recorded in grain yield per plant (38.82 %) followed by total number of tillers (28.09 per cent). The lowest genotypic coefficient of variation was recorded in days to 50 per cent flowering (6.11 %). High GCV and PCV estimates were recorded for three traits namely total number of tillers, number of productive tillers and grain yield per plant. The traits plant height and panicle length showed moderate values.

Days to 50 per cent flowering and days to maturity showed low GCV and PCV. The heritability values for different yield and yield contributing characters ranged from 66.60 to 94.89 per cent. Highest heritability was observed for grain yield per plant (94.89 %) followed by panicle length (93.81 %). Days to 50 per cent flowering showed high heritability with low genetic advances as per cent of mean indicating the non-additive type of gene action. Hence selection for this may not be rewarding. The lowest heritability was recorded in days to 50 per cent flowering (66.60 %). In the present study, the values of genetic advance as per cent of mean ranged from 11.79 to 82.25 per cent. Grain yield per plant recorded the highest genetic advance as per cent mean (82.25 %) and days to 50 per cent flowering exhibited low genetic advance as per cent of mean (11.79 %) (Table 2).

### Studies on association of quantitative characters among the accessions

Grain yield is a complex character and jointly determined by a number of other yield related traits. An insight into the association between grain yield and other correlated traits helps to improve the efficiency of selection. In general, the correlation between yield and other characters as well as among the component characters will vary with the genotype handled by the breeder. In the present investigation, the genotypic correlation between pairs of characters have been studied to identify the component traits that are closely related to grain yield in 741 accession including varieties. All seven characters studied *viz.*, total number of tillers (0.489), number of productive tillers (0.413), panicle length (0.331), plant height (0.256), days to 50 per cent flowering (0.144) and days to maturity exhibited highly positive correlations with grain yield per plant (Table 3). It could be observed on pursuing Table III that most of the characters had positive inter correlations with each other. Days to 50 per cent flowering recorded positive and significant inter correlation with days to maturity (0.540), plant height (0.390) and panicle length (0.182). Days to maturity had positive and significant inter correlation with plant height (0.267) and panicle length (0.083). Plant height showed positive significant correlation with panicle length (0.438). Total number of tillers has significant correlation with number of productive tillers (0.780) and number of productive tillers had highly significant negative correlation with panicle length (-0.200).

The path analysis takes into account the cause and effect relationship between the variables by partitioning the association into direct and indirect effects through other independent variables. The partitioning of genotypic correlation coefficient of different components with grain yield into direct and indirect effects was done and the results are presented in Table IV. The path analysis revealed that direct effect of days to 50 per cent flowering on grain yield was positive but negligible (0.064). It would be inferred that selection should be in positive side for this trait increase the yield. The indirect effect of days to 50 per cent flowering through number of productive tillers (-0.024) was negative and negligible. The direct effect of days to maturity on grain yield was also low and positive (0.013). Days to maturity showed negligible positive and/or negative indirect effect through other traits *viz.*, days to flowering, plant height, total number of tillers, total productive tillers and panicle length. The direct effect of plant height on grain yield was positive and low (0.113). The indirect contribution by plant height was positive and low through panicle length (0.122). Total number of tillers recorded a negligible

and positive direct effect on grain yield (0.079). This trait expressed high positive indirect effect through number of productive tillers (0.343); negative indirect effects through plant height (-0.002) and panicle length (-0.007) were negligible indirect effect on grain yield. The direct effect of number of productive tillers on grain yield was positive and high (0.437). Panicle length showed moderated positive direct effect on grain yield and negligible indirect effect through other traits.

A cluster analysis of 741 accessions of foxtail millet was carried out using DARwin5 for yield and yield contributing traits. The populations were grouped into nine clusters (Fig. 1). The results revealed the existence of high levels of variation for all characters observed.

### Conclusion

There is wide genetic diversity available in foxtail millet, and characterizing these resources is a prerequisite for the genetic improvement of its cultivars (Gopal Reddy *et al.* 2006). The characterization and evaluation are the important prerequisites for effective utilization of germplasm and also to identify sources of useful genes. So, an effort was made for detailed evaluation of 741 accessions including varieties for seven yield and yield contributing characters. The highest genotypic coefficient of variation and genetic advance as per cent of mean was recorded in grain yield per plant and the lowest was recorded in days to 50 per cent flowering. Heritability gives the information on the magnitude of inheritance of quantitative traits, while genetic advance will be helpful in formulating suitable selection procedures. The heritability values for different yield and yield contributing characters ranged from 66.60 to 94.89 per cent. Days to 50 per cent flowering showed high heritability with low genetic advances as per cent of mean indicating the non-additive type of gene action. Hence selection for this may not be rewarding. The highest heritability and genetic advance as per cent of mean were observed for grain yield per plant and lowest heritability was recorded in days to 50 per cent flowering.

Understanding of the interaction of the traits among themselves and with the economic yield is of great use in plant breeding. Correlation studies provide information on the nature and extent of association between any two metric traits and it would be possible to bring out genetic upgradation in one trait that could be efficiently utilized in selection of the other trait of a pair also. The path analysis takes into account the cause and effect relationship between the variables by partitioning the association into direct and indirect effects through other independent

variables. In the present study, all seven characters studied exhibited highly positive correlation with grain yield per plant. It can be inferred that selection should be in positive side for all the traits studied which in turn automatically increase the grain yield. The path analysis revealed that direct effect of days to 50 per cent flowering on grain yield was positive and negligible. The direct effect of days to maturity and plant height on grain yield was low and positive. Total number of tillers recorded a negligible and positive direct effect on grain yield. Panicle length showed moderate positive direct effect on grain yield and negligible indirect effect through other traits *viz.*, days to flowering, days to maturity and plant height. The direct effect of number of productive tillers on grain yield was positive and high. These indicate the true relationship of number of productive tillers and panicle length with grain yield. Hence, direct selection for these traits could be rewarding for the improvement of grain yield.

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**Table 1. Summary of statistics on different yield and yield contributing traits in foxtail millet**

Particulars	Days to 50 % flowering	Days to maturity	Plant height (cm)	Total number of tillers	Number of productive tillers	Panicle length (cm)	Grain yield (g)
Mean	60.09	89.38	139.90	8.61	7.27	18.60	34.45
Minimum	37.33	80	57.00	3.00	3.00	10.00	3.31
Maximum	70.00	101.00	185.00	19.00	15.05	34.00	107.46
Standard Deviation	4.13	6.88	15.13	2.62	2.01	3.24	13.84
Variance	17.07	47.28	228.96	6.88	4.05	10.52	191.45
CV (%)	6.87	7.69	10.82	30.45	27.69	17.44	40.16
Standard Error	0.15	0.25	0.56	0.10	0.07	0.12	0.51

**Table 2. The estimates on genotypic co-efficient of variation, phenotypic co-efficient of variation, heritability, genetic advance as per cent of mean**

Characters	PCV (%)	GCV (%)	$h^2$ % (broad sense)	GA as % of mean
Days to 50 % flowering	7.48	6.11	66.60	11.79
Days to maturity	8.05	7.16	79.07	13.81
Plant height (cm)	11.12	10.38	87.14	20.78
Total number of tillers	30.61	28.09	84.18	62.14
Number of productive tillers	27.85	25.85	86.12	56.39
Panicle length (cm)	17.00	16.47	93.81	34.97
Grain yield (g)	40.28	38.82	94.89	82.25

**Table 3. Genotypic correlation coefficients between grain yield per plant and component characters**

Characters	Days to 50 % flowering	Days to maturity	Plant height	Total number of tillers	Number of productive tillers	Panicle length	Grain yield
Days to 50 % flowering	1.000	0.540**	0.390**	0.021	-0.054	0.182**	<b>0.144**</b>
Days to maturity		1.000	0.267**	-0.023	-0.020	0.083**	<b>0.091**</b>
Plant height			1.000	-0.021	-0.015	0.438**	<b>0.256**</b>
Total number of tillers				1.000	0.780**	-0.026	<b>0.413**</b>
Number of productive tillers					1.000	-0.200**	<b>0.489**</b>
Panicle length						1.000	<b>0.331**</b>

\*,\*\* significant at 5% and 1% level respectively.

**Table 4. Direct (diagonal) and indirect effects of six characters on grain yield**

Characters	Days to 50 % flowering	Days to maturity	Plant height	Total number of tillers	Number of productive tillers	Panicle length	Genotypic correlation with Grain yield
Days to 50 % flowering	<b>0.064</b>	0.007	0.044	0.002	-0.024	0.051	0.144**
Days to maturity	0.035	<b>0.013</b>	0.030	-0.002	-0.009	0.023	0.091**
Plant height	0.025	0.004	<b>0.113</b>	-0.002	-0.007	0.122	0.256**
Total number of tillers	0.001	0.000	-0.002	<b>0.079</b>	0.343	-0.007	0.413**
Number of productive tillers	-0.003	0.000	-0.002	0.062	<b>0.437</b>	-0.006	0.489**
Panicle length	0.012	0.001	0.050	-0.002	-0.009	<b>0.279</b>	0.331**

\*,\*\* significant at 5% and 1% level respectively. Residual value : 0.42



