

Original Research Article

Studies on Genetic Variability for Yield and Yield Attributing Traits in Finger millet (*Eluesine coracana* L. Gaertn)

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ABSTRACT

Keywords

Variability, Heritability, Genetic advance, Yield attributing traits, Finger millet

Thirteen elite entries of finger millet were evaluated in a field study to assess the magnitude of genetic variability, heritability and genetic advance for yield and yield attributing traits. The analysis of variance revealed that there were significant differences among the entries for all the traits studied. The genetic parameters revealed that moderate to high variability coupled with high heritability and high genetic advance as per cent of mean were observed for days to 50% flowering, plant length (cm), number of tillers per plant, number of fingers per ear and main ear length (cm) suggesting the predominance of additive type of gene action in controlling these traits. These results indicating the operation of additive gene action in the inheritance of these traits and improvement of these characters is possible through simple selection.

Introduction

Eleusine coracana has several vernacular names all over the world, in India it is known as ragi. In English, it is known as finger millet. It is an important crop amongst the small millets and third important among millets in the country in area and production after sorghum and pearl millet. It is cultivated mostly as a rainfed crop for its valued food grains and its adaptability to wide range of geographical areas and agro-ecological diversity in India. Its chromosome number is $x = 9$. A subspecies of this genus, *E. coracana* subs. *coracana* is tetraploid in nature that has originated from

the uncultivated diploid subspecies *africana* (FAO, 2008). Finger millet is highly nutritious as its grain contain 65-75% carbohydrates, 5-8% protein, 15-20% dietary fibre and 2.5-3.5% minerals (Chetan and Malleshi, 2007). In India, it is staple crop that provides the food for millions of people. In India the overall cultivated region under finger millet was projected as 1299.7 million hectares with 2040.7 million tonnes production and 1570 kg/ha productivity. Whereas in Andhra Pradesh finger millet grown in 48.8 million hectares with 52.8 million tonnes production and 1128 kg/ha

productivity (Shukla *et al.*, 2015). In states like Tamil Nadu and Gujarat it has been grown mainly as irrigated crop. While, in the case of high yielding varieties the total production was estimated as 1614.53 thousand tonnes, *i.e.* 70.73% (Directorate of Millets Development, 2014). Finger millet is highly nutritious as its grain contains 65-75% carbohydrates, 5-8% protein, 15-20% dietary fibre and 2.5-3.5% minerals (Chetan and Malleshi, 2007). This estimated account further indicates the requirement for the encouragement of HYV to meet the aggressive global marketing setting. In order to achieve the expected targets there is need to develop the varieties with higher yield potential by breaking the existing yield plateau through utilizing more distant lines in the breeding programmes.

It is known that yield of finger millet is complex quantitative trait and under pleiotropic gene control at the same time it is highly influenced by environment and contributed by many other traits. Furthermore, selection based on only yield is misleading. For starting any crop improvement work, information about the genetic variability available in the population is a prerequisite. Presence of high variability in the genotypes of this crop offers much scope for its improvement (Poehlman, 1987). Success of hybridization and there after selection of desirable segregants of any crop depend largely on the selection of parents with high magnitude of genetic variability for different characters present in the plant population. Heritability and genetic advance are important selection parameters when considered together help the breeders in determining the traits having better corresponding between phenotypes and genotypes and are expected to give better response to selection (Binse *et al.*, 2016). Hence, an attempt was made to estimate the extent of variation for yield

contributing traits in 13 finger millet genotypes by studying the genetic parameters like phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance, which may contribute to formulation of suitable selection indices for improvement in the finger millet crop.

Materials and Methods

The study was conducted at Agriculture Research Station, Vizianagaram, Andhra Pradesh. The experimental site is located at an altitude of 74 m above mean sea level, latitude of 18.12°N and longitude of 83.42°E. Standard crop production and protection practices were followed to raise a healthy crop. Thirteen genotypes were evaluated in a Randomised Block Design with three replications during *kharif* 2015. Each plot consisted of ten rows of 3 meters length with a spacing of 22.5 × 10 cm. Observations were recorded on five plants for seven quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height, number of tillers per plant, number of fingers per ear, main ear length and grain yield. The data was recorded in five random plants per entry in each replication. The mean of all the plants for each trait under each replication was subjected to analysis (Panse and Sukhathme, 1967). The estimate of genotypic variance and phenotypic variance were worked out according to the method suggested by Johnson *et al.*, (1955) using mean square values from the ANOVA table. Phenotypic and genotypic coefficient of variance was calculated based on the method advocated by Burton *et al.*, (1952). Heritability percentage in broad sense was estimated as per the method described by Lush (1940) and traits were classified as having high, moderate and low heritability as per the method of Robinson *et al.*, (1949). Genetic advance was estimated according to

the method suggested by Johnson *et al.*, (1955), and expressed as percentage of mean. Traits were classified as having high, moderate or low genetic advance as per the method suggested by Johnson *et al.*, (1955).

Results and Discussion

The basic objective of any breeding and bio-engineering program is the improvement of crop yield and quality. The measurement and evaluation of variability are essential steps in drawing meaningful conclusions from a given set of phenotypic observations (Reddy and Reddy, 2011; Joshi *et al.*, 2007). The genetic variability of a metric trait can be studied through the use of various statistical parameters like mean, range, variance components and coefficients of variation. Analysis of variance for the eleven selected characters indicated that the genotypic mean square values were highly significant for all characters, implying that the entries tested were highly variable. Substantial variation among finger millet entries has also been reported in previous studies (Naik *et al.*, 1994; Prasada Rao *et al.*, 1994; Daba, 2000).

The thirteen genotypes of finger millet studied in the present investigation differed statistically for all the characters studied.

Analysis of variance revealed highly significant differences among the genotypes for all the characters, indicating presence of sufficient amount of variability among the varieties (Table 1). Thus, there is ample scope for selection of different quantitative characters for finger millet improvement. Mean, range, variability, heritability and genetic advance as per cent mean for seven characters were presented in Table 2. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the modifying effect of the environment in association with the characters at genotypic level. The genetic parameters revealed that moderate PCV coupled with moderate GCV for characters days to 50% flowering (14.69 and 14.63), plant height (15.69 and 13.41), number of fingers per ear (13.43 and 10.20), number of tillers plant (16.50 and 12.07) and main ear length (14.01 and 12.14). Days to maturity (8.10 and 7.99) showed low PCV coupled with low GCV. Grain yield per plant (20.72 and 4.05) showed high PCV coupled with low GCV. Low values of phenotypic coefficient of variation and genotypic coefficient of variation were observed for days to maturity indicating narrow range of variability for these traits there by restricting the scope for selection.

Table.1 Analysis of variance for yield and yield components among 13 genotypes of Finger millet (*Eluesine coracana* L. Gaertn)

Source	Replications	Treatments	Error
Degree of freedom	2	12	24
Mean Sum of Squares			
Days to 50% flowering	0.240	211.679**	0.841
Days to maturity	3.266	140.342**	1.838
Plant height (cm)	98.506	271.730**	42.281
Number of tillers per plant	0.004	0.290**	0.088
Number of fingers per ear	0.809	1.958**	0.525
Main ear length (cm)	0.090	2.096**	0.297
Grain yield per plot (kg)	0.730	1.623**	0.150

(** Significant at 1 per cent level)

Table.2 Mean, Variability, Heritability and Genetic advance as per cent of mean for yield and yield attributing traits of Finger millet (*Eluesine coracana* L. Gaertn)

Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as percent of mean (5% level)
		Minimum	Maximum	PCV%	GCV%		
Days to 50% flowering	70.16	57.33	83.67	14.69	14.63	99.20	30.02
Days to maturity	104.06	89.00	111.67	8.10	7.99	97.41	16.25
Plant height (cm)	79.82	62.00	95.00	15.69	13.41	73.07	23.62
Number of tillers per plant	2.63	1.13	3.33	16.90	12.07	53.53	18.19
Number of fingers per ear	8.29	6.95	10.10	13.43	10.20	57.69	15.97
Main ear length (cm)	7.802	6.97	10.53	14.01	12.14	75.13	21.68
Grain yield per plot (kg)	1.90	1.60	2.41	20.72	4.05	3.8	1.63

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

Similarly low values of PCV and GCV for days to maturity were observed by Reddy *et al.*, 2013.

Heritability which is the heritable portion of phenotypic variance is a good index of transmission of characters from parents to offspring (Falconer, 1981). The estimates of heritability and genetic advance can be utilized for the prediction of genetic gain, which indicates the genetic improvement that would result from the selection of best individuals. High broad sense heritability coupled with high genetic advance as percent of mean for traits *viz.*, days to 50% flowering (99.20 and 30.02), plant height (73.07 and 23.62) and main ear length (75.13 and 21.68). Days to maturity (97.41 and 16.25) and number of fingers per ear (57.69 and 15.97) showed high heritability with moderate genetic advance as percent of mean. These results were in accordance with Reddy *et al.*, (2013), Manoj Kumar *et al.*, (2015), Ezeaku *et al.*, (2015), Suryanarayana *et al.*, (2014), Jyothsna *et al.*, (2016) and

Mahanthasha *et al.*, (2017). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.*, 1955). High heritability with high genetic advance (as percentage of the mean) was observed for days to 50% flowering and number of tillers per plant as found by Reddy *et al.*, (2013). Such conditions were most likely caused by additive gene action, thereby, reflecting the efficiency of selection for the improvement of these traits. According to Panse (1957), if the heritability is mainly owing to non-additive gene effect, the expected genetic advance would be low and if there is additive gene effect, a high genetic advance may be expected.

Present investigation suggested that there is adequate variability present in the material studied. The genotypes VR 1094 and VR 900 were identified as best genotypes for

grain yield per plot. Phenotypic coefficient of variation estimate was slightly higher than the genotypic coefficient of variation for all the traits, indicating low environmental influence on the expression of all the traits. The genetic parameters revealed that moderate GCV, PCV coupled with high heritability and high genetic advance as percent of mean were observed for days to 50% flowering, plant height and main ear length. These results indicating the operation of additive gene action in the inheritance of these traits and improvement of these characters is possible through simple selection.

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