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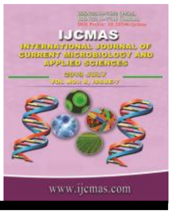

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Genetic Parameters of Yield and Quality Component Traits in Foxtail Millet [*Setaria italica* (L.) Beauv.]

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ABSTRACT

The present investigation was conducted to evaluate the sixty foxtail millet germplasm to access the nature and magnitude of genetic variability for yield and yield component traits. The experiment was laid out in Augmented Randomized Complete Block Design (ARCBD) at RARS, Lam, Guntur during *kharif*, 2018-19. The analysis of variance indicated significant differences for most of the traits *viz.*, days to 50% flowering, panicle length, productive tillers per plant, days to maturity, iron, zinc, copper, manganese, phosphorus and grain yield per plant indicating a high degree of variability in the material for these traits. Coefficient of variation studies indicated that the estimates of PCV were greater than the corresponding GCV estimates for all the traits indicating the influence of environment on expression of these traits. High PCV and GCV were recorded for panicle length, productive tillers per plant, protein, calcium, iron, zinc, copper, manganese, phosphorus, grain yield per plant. Moderate PCV and GCV recorded for days to 50% flowering, plant height, test weight and carbohydrate whereas days to maturity recorded low PCV and GCV. The estimates of heritability and genetic advance as per cent of mean were high for the traits, days to 50% flowering, plant height, panicle length, test weight, protein, carbohydrate, calcium, iron, zinc, copper, manganese and phosphorus indicating the probable operation of additive gene action in inheritance of these traits and simple selection may be sufficient to improve these traits.

Keywords

Foxtail millet, Variability, Heritability, Genetic advance and quality

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Introduction

Among the six small millets, Italian millet [*Setaria italica* (L.) Beauv.] is the most important crop next to finger millet. The naming of this taxon evolved as millet having panicles resembling a foxtail in appearance *i.e.*, long panicle with soft long and erect hairs (Upadhyaya *et al.*, 2008). It is the one of the world's oldest cultivated crop. Its domestication and cultivation is estimated to have occurred over 4000 years ago (Chang, 1973; Ho, 1975). It is having high nutritional value and is good source of β-carotene. It possess 12.3% protein, 4.7% fat, 60.6% carbohydrate and 3.2% ash. It also contains minerals (Fe, Zn, K, Ca, Mg), antioxidants, dietary fiber, phytochemicals, vitamins (thiamine, riboflavin, niacin) and possess low glycemic index (Rai, 2002). In view of several merits, this crop deserves attention in research. But it has received little research attention in the past and continued to be a neglected. The breeding effort for developing high yielding varieties through utilization of diverse germplasm, creation and exploitation of the genetic variation for different traits of economic importance is critical.

In any crop improvement programme, knowledge on available variability of various traits is necessary. Yield is quantitative trait and is a result of interactions between the component traits. Presence of wider spectrum of variability will enhance the chances of selecting a desired genotype. Besides genetic variability, knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted to progeny, thereby helps the breeder to employ a suitable breeding method to achieve the objective. Keeping the above points in view, the present investigation was carried out with the objective to estimate the extent of genetic variability, heritability and genetic advance.

Materials and Methods

The present investigation was carried out during *kharif*, 2018-19 at RARS, Lam, Guntur, Andhra Pradesh, which is located at 16.10^0 N latitude, 28.29^0 E longitude and 31.5 m altitude with 60 foxtail millet [*Setaria italica* (L.) Beauv.] germplasm including checks. The trial was laid out in a Augmented Randomized Complete Block Design (Federer, 1956) with four checks *viz.*, Suryanandi, Prasad, Co 7 and Krishnadevaraya in each block. Each genotype was grown in a two rows of 4 m length with a spacing of 22.5 cm between the rows and 10 cm between the plants. Data were collected on five randomly selected plants per treatment for plant height, panicle length, productive tillers per plant and grain yield per plant. However data on days to 50% flowering, days to maturity, test weight, protein, carbohydrate, calcium, iron, zinc, copper, manganese and phosphorus were recorded on plot basis. Phenotypic and genotypic coefficients of variation were calculated as per Burton (1952) and these PCV, GCV values were classified as described by Sivasubramanian and Menon (1973). Heritability (h^2) in the broad sense was computed as suggested by Hanson *et al.*, (1956) and heritability in the broad sense was categorized as per the classification given by Johnson *et al.*, (1955). The range of genetic advance as per cent of mean was classified and calculated based on the formula given by Johnson *et al.*, (1955).

Results and Discussion

The success of any breeding programme depends upon the quantum of genetic variability present in the population and the presence of a wider spectrum of variability will enhance the chances of selecting a desired genotype. The analysis of variance revealed significant variation among the genotypes for the traits *viz.*, days to 50% flowering, panicle length, productive tillers per plant, days to maturity, iron, zinc, copper, manganese, phosphorus and grain yield per plant (Table 1) indicating a significant amount of variability in the germplasm under study for these traits.

The trait, days to 50% flowering ranged from 24 days (Ise 719) to 65 days (Ise 1129) with a mean of 47.36 days. Plant height ranged from 57.20 cm (Ise 1563) to 151.40 cm (Ise 1647) with a mean of 120.35 cm. For panicle length the range is from 8.10 cm (Ise 1320) to 26.09 cm (Ise 49 and Ise 1511) with a mean of 17.06 cm. Productive tillers per plant ranged from 1.00 (Ise 388, Ise 1037) to 6.63 (Ise 663) with a mean of 3.27. Days to maturity ranged from 58 (Ise 719) to 97 days (Ise 1129) with a mean of 80.81 days. Test weight ranged from 1.97 g

(Ise 1320) to 3.98 g (Ise 1511) with a mean of 2.71 g. For grain yield per plant, the range is from 1.14 g (Ise 1312) to 18.54 g (Ise 1511) with a mean of 6.67 g.

Further, the quality traits registered following ranges. Protein content in the studied genotypes ranged from 6.21g (Ise 238) to 19.43g (Ise 758) with a mean of 11.39 g. Similarly, the ranges were 43.25 g (Ise 1320) to 82.14 g (Ise 1511) with a mean of 63.55 g for carbohydrate; 10.20 mg (Ise 398) to 22.60 mg (Ise 1299) with a mean of 15.76 mg for calcium; 1.18 mg (Ise 1458) to 5.23 mg (Ise 1320) with a mean of 2.22 mg for zinc; 0.12 mg (Ise 1458) to 2.43 mg (Ise 1454) with a mean around 0.89 mg for copper; 0.26 mg (Ise 1151) to 1.55 mg (Ise 1299) with a mean of 0.77 mg for manganese and 0.11 g (Ise 999 and Ise 1610) to 0.43 g (Ise 1209) with a mean of 0.27 g for phosphorus.

The phenotypic coefficient of variations (PCVs) and genotypic coefficient of variations (GCVs) were estimated and presented in table 2. High PCV and GCV were recorded for panicle length (25.45 and 22.31), productive tillers per plant (46.36 and 35.30), protein (23.69 and 22.28), calcium (21.49 and 20.51), iron (40.66 and 38.21), zinc (28.34 and 27.87), copper (38.99 and 37.34), manganese (39.39 and 37.71), phosphorus (30.83 and 30.29) and grain yield per plant (43.40 and 38.00), respectively. Similar results were indicated by Gurunadharao *et al.,* (1984) and Sirisha *et al.,* (2009) for panicle length; Jyosthna *et al.,* (2016) and Smita *et al.,* (2016) for productive tillers per plant; Jadhav *et al.,* (2015) in finger millet for protein; Prasanna *et al.,* (2013), Johar (2015) and Banu *et al.,* (2017) for calcium; Brunda (2014) and Banu *et al.,* (2017) for both iron and zinc; Brunda (2014) for both copper and manganese; Ayesha *et al.,* (2019) for phosphorus; Banu *et al.,* (2017), Kavya *et al.,* (2017) and Ayesha *et al.,* (2019) for grain yield per plant. This high PCV and GCV indicate the presence of higher magnitude of variability in germplasm for the respective traits. The higher GCV value indicates the majority of variation within each traits was genetic in nature. Hence, selection will be effective.

Moderate PCV and GCV were recorded for days to 50% flowering (17.23 and 13.90), plant height (17.23 and 13.90), test weight (17.80 and 16.93) and carbohydrate (11.61 and 11.24), respectively. Similar results for days to 50% flowering were indicated by Brunda *et al.,* (2014) and Ayesha *et al.,* (2019); for plant height by Banu *et al.,* (2017) and Kavya *et al.,* (2017); for test weight by Brunda *et al.,* (2014), Smita *et al.,* (2016) and Banu *et al.,* (2017). While, contrary result for carbohydrate *i.e.,* low PCV and GCV were reported by Kavya *et al.,* (2017) and Ayesha *et al.,* (2019). These moderate estimates of PCV and GCV revealed that the presence of moderate variation among the genotypes studied for these traits. Low PCV and GCV were recorded by days to maturity. These results are in accordance with those of Prasanna *et al.,* (2013), Ashok *et al.,* (2016) and Ayesha *et al.,* (2019) for days to maturity, indicating less variation among the genotypes studied.

Further, the genotypic coefficients of variation were lesser than the phenotypic coefficients of variation for all the characters studied, indicating that there is influence of environment on expression of these traits.

Appropriate selection and consistency in the performance of selected traits in succeeding generations depends on the magnitude of heritable variation present in relation to observed variation. The estimates of heritability revealed that except for the trait, number of productive tillers per plant (58.00%) all the remaining traits were found to have high magnitude of heritability.

Table.1 Analysis of variance for grain yield and quality component characters in foxtail millet [*Setaria italica* (L.) Beauv.]

Sources of variations	d.f	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Prod tillers/ plant	Days to maturity	Test weight (g)	Protein (g/100g)	Carbohydrate (g/100g)
		Mean sum of squares							
Block	4	33.094	305.972	38.649	1.847	30.726	0.415	33.466	173.099
Entries	63	80.904*	153.660	26.746*	2.104*	66.171	0.211	6.926	39.518
Checks	3	31.333	0.221	292.063*	0.414	0.802	0.032	0.837	4.262
Genotypes	59	84.684*	331.839	16.031*	1.675*	77.195*	0.211	6.818	52.742
Checks vs. Genotypes	1	7.163	0.004	1.071	32.475*	0.832	0.772	31.582	0.617
Error	12	12.508	754.953	1.366	0.358	30.520	0.200	1.560	25.304

Sources of variations	d.f	Calcium (mg/100g)	Iron (mg/100g)	Zinc (mg/100g)	Copper (mg/100g)	Manganese (mg/100g)	Phosphorus (g/100g)	Grain yield/ Plant (g)
		Mean sum of squares						
Block	4	12.410	4.327	0.204	0.189	0.067	0.002	65.789
Entries	63	8.195	1.967*	0.530*	0.229*	0.093*	0.012*	22.351*
Checks	3	0.249	0.179	0.068	0.036*	0.003	0.004	80.206*
Genotypes	59	10.764	2.165*	0.396*	0.183*	0.086*	0.007*	23.216*
Checks vs. Genotypes	1	2.738	4.327	9.807*	3.550*	0.760*	0.316*	1.008
Error	12	7.658	0.199	0.034	0.006	0.007	0.002	0.882

* Significant at 5% level
** Significant at 1% level

Table.2 Estimates of variability, heritability and genetic advance as per cent of mean for grain yield and quality components in foxtail millet [*Setaria italica* (L.) Beauv.]

S. No.	Character	Mean	Range		Coefficient of variation		Heritability (broad sense) (%)	Genetic advance as % of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	47.36	24.00	65.00	19.98	19.25	92.90	38.22
2	Plant height (cm)	120.35	57.20	151.40	17.23	13.90	65.10	23.10
3	Panicle length (cm)	17.06	8.10	26.09	25.45	22.31	76.90	40.31
4	Productive tillers/plant	3.27	1.00	6.63	46.36	35.30	58.00	55.36
5	Days to maturity	80.81	58.00	97.00	9.73	9.27	90.90	18.21
6	Test wt (g)	2.71	1.97	3.98	17.80	16.93	90.40	33.16
7	Protein (g/100g)	11.39	6.21	19.43	23.69	22.28	88.50	43.17
8	Carbohydrate (g/100g)	63.55	43.25	82.14	11.61	11.24	93.70	22.42
9	Calcium (mg/100g)	15.76	10.20	22.60	21.49	20.51	91.10	40.32
10	Iron (mg/100g)	3.74	0.14	5.32	40.66	38.21	88.30	73.97
11	Zinc (mg/100g)	2.22	1.18	5.23	28.34	27.87	96.70	56.44
12	Copper (mg/100g)	0.89	0.12	2.43	38.99	37.34	93.40	75.00
13	Manganese (mg/100g)	0.77	0.26	1.55	39.39	37.71	91.60	74.37
14.	Phosphorus (g/100g)	0.27	0.11	0.43	30.83	30.29	96.60	61.32
15.	Grain yield/plant (g)	6.67	1.14	18.54	43.40	38.00	86.10	77.00

Heritability estimates alone cannot give a better idea in selecting suitable breeding method. So in order to fulfill the requirement we have also estimated genetic advance in addition to the heritability. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone and these will also give a better picture for having an idea of gene action involved. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance.

High heritability coupled with high genetic advance as per cent of mean was noted for days to 50% flowering, plant height, panicle length, test weight, protein, carbohydrate, calcium, iron, zinc, copper, manganese, phosphorus and grain yield per plant indicating probable operation of additive gene action in inheritance of these traits and simple selection is sufficient to improve these traits.

These results were accordance with Ayesha *et al.*, (2019), Ashok *et al.*, (2016), Kavya *et al.*, (2017), Banu *et al.*, (2017), Smita *et al.*, (2016) and Brunda (2014). High heritability coupled with moderate genetic advance as per cent of mean was observed for days to maturity indicating the operation of both additive and non-additive gene action indicating that simple selection will not be rewarding in improving this trait.

Similar results were earlier reported by Jyothsna *et al.*, (2016) for days to maturity. While moderate heritability coupled with high genetic advance as per cent of mean was observed for productive tillers per plant indicating the operation of both additive and non-additive gene action and hence simple selection may not be rewarding. These findings are in accordance with those of Jyothsna *et al.*, (2016 for productive tillers per plant.

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