

Original Research Article

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Studies on Genetic Variability for Yield and Yield Contributing Traits in Finger Millet *Eleusine coracana* (L.) Gaertn

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Fifteen genotypes of finger millet were evaluated in a field study to assess the magnitude of genetic variability, heritability and genetic advance for yield and yield contributing traits. The analysis of variance revealed that there were significant differences among the entries for all the traits studied. A wide range of variation was recorded for plant height (cm), days 50% flowering, days to maturity, number of tillers per plant, number of fingers per year, length of finger (cm), test weight (g), yield per plant (g), straw yield per plant (g). The phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters studied which shows the influence of the environmental effect on the characters. High values for phenotypic coefficient and genotypic coefficient was recorded for yield per plant (g). High heritability and high genetic advance was recorded for iron content (mg/100g), yield per plant (g), calcium content (mg/100g) and test weight (g) indicating that these characters were controlled by additive gene effects. Selection based on these characters would be effective for future finger millet crop improvement program. Moderate heritability coupled with moderate genetic advance was observed for length of finger (cm) and protein content (%). Plant height (cm) showed low heritability as well as low genetic advance.

Introduction

Finger millet (*Eleusine coracana* L. Gaertn., $2n=4x=36$) belongs to the family *Poaceae*. Among millets it ranks third in importance after sorghum and pearl millets. Its wide adaptability to diverse environments and

cultural conditions makes it a potential food crop. It also contains sufficient amount of iron and rich source of calcium. Small millets comprise of Finger millet, Little millet, Foxtail millet, Kodo millet, Barnyard millet and Proso millet is an important group of dry land field crops. Finger millet occupies first place with

fifty percent of the area. Recently government of India declared millets as a 'Nutricereal' crops being a rich source of minerals in almost all types of millets. The availability of diverse genetic resources is a prerequisite for genetic improvement of any crop including finger millet. The basic information on the existence of genetic variability and diversity in a population and the relationship between different traits is essential for any successful plant breeding programme. Considering its importance in food and fodder security, adequate information on genetic variability between yield and its attributes is meager in finger millet. Systematic breeding efforts in this crop have so far been neglected. 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). Estimation of genetic parameters in the context of trait characterization is an essential component in developing high yielding varieties. Hence, an attempt was made to estimate the extent of variation for yield contributing traits in fifteen 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 this crop.

Materials and Methods

The field experiment was conducted on the field of Department of Agricultural Botany, College of Agriculture, VNMKV, Parbhani by taking three replications in Randomized Block Design during *Kharif*, 2017. Experimental material comprises of 13 different genotypes with 2 checks from different diverse sources of country. The materials was grown in randomize block design with three replications

30 cm spacing was kept between the rows while, 10 cm spacing was kept between the plants. The gross plot size was 2 m x 2 m and net plot size maintained was 1.50 x 1.60 m. All the agronomic practices were performed for better performance of the trial. The data was recorded in five random plants per entry in each replication viz., plant height (cm), days 50% flowering, days to maturity, number of tillers per plant, number of fingers per year, length of finger (cm), test weight (g), grain yield per plant (g), straw yield per plant (g), Protein content (%), Calcium content (mg/100g) and Iron content (mg/100g). 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

In the present investigation, 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. 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, sensitivity of crop to environment, heritability of the character and genetic advance. The analysis of variance showed a wide range of variation and significant differences for all the characters under study, indicating the presence of adequate variability for further improvement.

The analysis of variance revealed that the differences among the genotypes were significant for most of the characters under study. The genotypes were thus suitable for genetical studies, as their contribution to the genotypic sum of squares was significant for most of the characters.

The total variability in each of these characters could be partitioned into three components viz., phenotypic, genotypic and environmental. The phenotypic variance and genotypic variance was maximum for calcium content (mg/100g) and days to maturity. Genotypic and phenotypic variances were high for calcium content (mg/100g), followed by days to maturity, days 50% flowering plant height and harvest index (%), straw yield per plant indicating wide variability for these characters.

A wide range of variation was recorded for days to 50% flowering, plant height, days to maturity, straw yield per plant, calcium content (mg/100g), iron content (mg/100g) and harvest index (%). The estimates of phenotypic coefficient of variation ranged from 8.172 for Plant height (cm) to 24.690 for Iron content (mg/100g) and the corresponding values for genotypic coefficient of variation were 7.300 for Plant height (cm) to 0.890 for Iron content (mg/100g), respectively. Yield per plant (g) showed nearly high PCV and GCV values. Similarly, high genotypic and

phenotypic coefficient of variation was also found Yield per plant (g) by Abraham *et al.*, (1989). No. of fingers per year, Days 50% flowering and Straw yield per plant (g) showed moderate phenotypic coefficient of variation and genotypic coefficient of variation. In general, the differences between phenotypic coefficient of variation and genotypic coefficient of variations for most of traits were less indicating the ample scope for improvement through selection. Low values of phenotypic coefficient of variation and genotypic coefficient of variation were observed for plant height and No. of fingers per ear indicating narrow range of variability for these traits there by restricting the scope for selection.

Heritability which is the heritable portion of phenotypic variance is a good index of transmission of characters from parents to offspring (Falconer, 1981). The heritability values for different yield and yield attributing traits ranged from 59.6% to 91.6 %. In the present investigation the traits yield per plant (g), iron content (mg/100g), length of finger (cm), days to 50% flowering, days to maturity and calcium content (mg/100g) traits showed high heritability. Moderate heritability was noted in trait plant height, test weight (g) and protein content (%). The heritability estimates low for No. of tillers per plant, No. of fingers per ear and Harvest index (%). High heritability indicates the amenability of the traits in the selection process. Likewise, high heritability estimates for days to flowering and maturity (Dhagate *et al.*, 1972) and length of finger (cm) (Daba, 2000). In present study, the values of genetic advance as percent of mean ranged from 0.577 to 123.750. Calcium content (mg/100g) recorded highest genetic advance as percent of mean (123.750). High heritability coupled with high genetic advance as per cent of mean was registered for Calcium content (mg/100g), days to maturity and days to 50% flowering.

Table.1 Analysis of variance for yield and yield contributing characters in finger millet

Sr. No	Characters	Mean sum of Squares		
		Replication	Treatment	Error
1	Plant height (cm)	1.870	197.369	15.358
2	Days 50% flowering	3.800	215.819	13.633
3	Days to maturity	18.20	407.51	27.70
4	No. of tillers per plant	0.179	0.484	0.089
5	No. of fingers per ear	0.108	1.757	0.167
6	Length of finger (cm)	0.347	4.112	0.206
7	Test weight (g)	0.044	1.606	0.130
8	Yield per plant (g)	0.549	14.468	0.429
9	Straw yield per plant (g)	0.979	19.258	1.587
10	Harvest index (%)	19.160	81.168	8.286
11	Protein content (%)	0.089	7.999	0.784
12	Calcium content (mg/100g)	1150.344	14206.959	978.435
13	Iron content (mg/100g)	1.585	67.536	2.666
	D.F	2	14	28

Table.2 Components of variation for yield attributing characters in finger millet

Sr. No	Characters	Phenotypic variance	Genotypic variance	Environmental variance
1	Plant height (cm)	76.029	60.670	15.360
2	Days 50% flowering	81.029	67.395	13.633
3	Days to maturity	154.305	126.605	27.700
4	No. of tillers per plant	0.221	0.132	0.089
5	No. of fingers per ear	0.697	0.530	0.167
6	Length of finger (cm)	1.508	1.302	0.206
7	Test weight (g)	0.622	0.492	0.130
8	Yield per plant (g)	5.108	4.680	0.429
9	Straw yield per plant (g)	7.477	5.890	1.587
10	Harvest index (%)	32.580	24.294	8.286
11	Protein content (%)	3.189	2.405	0.784
12	Calcium content (mg/100g)	5387.941	4409.509	978.433
13	Iron content (mg/100g)	24.289	21.623	2.666

Table.3 Genetic variability parameters for yield and yield attributing traits in finger millet

Sr. No	Characters	Mean	Range	PCV (%)	GCV (%)	Heritability (%)	Genetic Advance	Genetic Advance as % of mean
1	Plant height (cm)	106.702	122.4-98.73	8.172	7.300	79.8	14.333	13.433
2	Days 50% flowering	79.733	91-63	11.290	10.296	83.2	15.423	19.344
3	Days to maturity	116.466	129-96	10.666	9.661	82.0	20.996	18.027
4	No. of tillers per plant	2.253	3-1.6	20.854	16.104	59.6	0.577	25.618
5	No. of fingers per ear	7.311	9.6-6.2	11.418	9.960	76.1	1.309	17.898
6	Length of finger (cm)	6.895	9.40-4.40	17.810	16.546	86.3	2.184	31.667
7	Test weight (g)	3.464	5.36-2.24	22.759	20.243	79.1	1.285	37.091
8	Yield per plant (g)	9.896	14.91-6.37	22.837	21.858	91.6	4.265	43.097
9	Straw yield per plant (g)	21.810	28.487-19.28	12.538	11.128	78.8	4.437	20.345
10	Harvest index (%)	43.203	50.51-31.897	13.212	11.409	74.6	8.768	20.294
11	Protein content (%)	9.518	12.30-7.58	18.760	16.292	75.4	2.774	29.147
12	Calcium content (mg/100g)	349.793	421.63-219.37	20.985	18.984	81.8	123.750	35.378
13	Iron content (mg/100g)	19.961	27.170-9.623	24.690	23.295	89.0	9.038	45.278

Moderate heritability coupled with moderate genetic advance was observed for plant height and Iron content (mg/100g) indicating the presence of both additive and non additive gene action in the inheritance of this trait. No. of tillers per plant showed low heritability as well as low genetic advance besides narrow range of variability restricting the scope for improvement through selection. Low heritability coupled with low genetic advance for the trait indicated that this trait is controlled by environmental effects and simple selection would be ineffective. 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). 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. Taking into consideration the amount of variability, heritability and genetic advance as per cent of mean in the present study it may be concluded that selection would be effective in number of fingers per ear head, ear head yield, ear head length, days to 50% flowering, number of productive tillers per plant and grain yield for

developing high yielding varieties.

It is concluded that yield is controlled by both GCV and PCV also to use appropriate selection procedure for improvement of the characters in general and yield in particular since high heritability coupled with high genetic advance reveals the presence of lesser environmental influence and prevalence of additive gene action in their expression. High heritability with low genetic advance was indicated the influence of non additive gene action. The heritability provide the information on the magnitude of inheritance of quantitative characters, but it does not indicate the magnitude of genetic gain obtained by selection of best individual from the best population. So, heritability along with genetic advance is more useful for selection than the heritability alone.

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