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# Studies on genetic variability, character association and path analysis for yield and yield components in finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes

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#### Abstract

The present investigation was carried out to study the genetic variability parameters and nature of associations among the traits affecting grain yield in thirty finger millet genotypes. The estimates of genotypic and phenotypic coefficient of variation were high for number of productive tillers per plant and grain yield, moderate for days to 50% flowering, days to maturity, plant height and main ear length, whereas low GCV and high PCV was recorded for number of fingers per ear. High heritability coupled with high genetic advance was observed for most of the traits suggesting that they can be improved through direct selection due to predominant additive gene action. High heritability coupled with moderate genetic advance was observed for plant height and number of fingers per ear indicating the role of both additive and non-additive gene action. Correlation studies revealed that days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, main ear length, number of fingers per ear exhibited highly significant positive correlation with grain yield at phenotypic and genotypic level. Path coefficient analysis showed that number of fingers per ear (0.554) at genotypic level and number of productive tillers at phenotypic level (0.283) exerted maximum direct effect on grain yield (q/ha).

Keywords: Heritability, genetic advance, correlation and path analysis in finger millet

#### Introduction

Finger millet Eleusine coracana (L.) Gaertn.) is designated as climatic resilient crop receiving more attention in agricultural research and development. It is suitable to dry land areas, hill and tribal agriculture and contributed to nutritional security of tribal farming community as the grains are nutritionally superior to many cereals. Being rich in protein, iron and calcium, finger millet severs as an important staple food for rural populations. It is largely grown in southern states of India in an area of 1.02 M ha, with a production of 1.39 Mt and productivity of 1363 kg/ha (Anonymous, 2019)<sup>[2]</sup>. The amount of genetic variability present in the population will determine the breeding strategy to be adopted, in addition to the genetic variability, knowledge on heritability and genetic advance is also helpful to the breeder. Hence, it is necessary to have knowledge on genetic variability, heritability and genetic advance. The correlation studies simply measure the associations between yield and other traits, whereas path analysis permits the understanding of cause and effect of related characters. Grain yield is a complex trait, its expression depends upon the contribution and interrelationship of several component traits. Therefore, the present investigation was undertaken to study the relative contribution of different yield attributes to grain yield and their interrelationship by estimating correlation, path analysis to assess the direct and indirect effect of component characters on grain yield

#### **Material and Methods**

The experimental material consisting of 30 genotypes were laid out in Randomized Block Design (RBD) with three replications at Regional Agricultural Research Station, Chintapalle during *Kharif*, 2010. Each genotype was sown in 10 rows of 3 m length with a spacing of 22.5 cm between rows and 10 cm within a row by adopting all the recommended package of practices to raise a healthy crop. The observations were recorded on five randomly selected plants in each replication for plant height (cm), number of productive tillers per plant, main ear length (cm), number of fingers per ear and observations for days to 50% flowering, days to maturity and grain yield q/ ha were recorded on per plot basis.

Analysis of variance was done according to the procedure given by Panse and Sukhatme (1964) <sup>[10]</sup> phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953) <sup>[4]</sup>, heritability in broad sense as per Allard (1960) <sup>[1]</sup>. Genetic advance as per cent of mean estimated by using the formula suggested by Johnson *et al.* (1955) <sup>[8]</sup>. Correlation coefficients were worked out according to the formula suggested by Falconer (1960) <sup>[7]</sup> and direct and indirect effects were estimated as described by Dewey and Lu (1959) <sup>[5]</sup>

# **Results and Discussion**

The results of analysis variance for seven characters in thirty genotypes were presented in Table. 1. The analysis of variance revealed highly significant differences for the seven characters indicating the existence of sufficient amount of variability among the genotypes which can be exploited through selection.

The estimates of genotypic coefficient of variation were low for number of fingers per ear, moderate for days to 50% flowering, days to maturity, plant height and main ear length, whereas it was high for number of productive tillers per plant and grain yield (q/ha). Estimates of phenotypic coefficients of variation were moderate for days to 50% flowering, days to maturity, plant height, main ear length and number of fingers per ear, whereas high for number of productive tillers per plant and grain yield (q/ha).

Generally the estimates of phenotypic coefficients of variation were higher than the genotypic coefficients of variation, it indicates the variation was not only due to genotypes but also due to the influence of environment. Heritability (b) estimates were high for all the characters under study and ranged from 61.54 (plant height) to 98.83 (days to maturity) (Table. 2).

Genetic advance as percent of mean ranged from 13.77 (number of fingers per year) to 59.52 (number of productive tillers per plant), high estimates of genetic advance were reported for days to 50% flowering, days to maturity, number of productive tillers per plant, main ear length and grain yield (q/ha). High heritability coupled with high genetic advance was observed for these traits suggesting that they can be improved through direct selection due to predominant additive gene action in inheritance of these traits. Similar results were reported by Jyothsna *et al.*, (2016) <sup>[9]</sup> and Suryanarayana *et al.*, (2014) <sup>[13]</sup> in finger millet. High heritability coupled with moderate genetic advance was observed for plant height and number of fingers per ear indicating the role of both additive and non-additive gene action in inheritance of these traits and can be improved by population improvement method.

Correlation analysis revealed that the genotypic correlation coefficients in most of the traits were higher than their phenotypic correlation coefficients indicating the association is largely due to genetic reason. Days to 50% flowering, days to maturity, plant height, number of productive tillers per plant, main ear length, number of fingers per ear exhibited highly significant positive correlation with grain yield at phenotypic and genotypic level (Table.3). Selection for these characters would possibly be helpful in improving the yield potential of this crop. These results were in accordance with the findings of Anuradha *et al.*, (2013) <sup>[3]</sup>, Jyothsna *et al.*, (2016) <sup>[9]</sup> and Sneha *et al.*, (2019) <sup>[12]</sup>.

Path coefficient analysis at genotypic level showed that number of fingers per ear (0.554) had maximum direct effect on grain yield (q/ha) followed by days to maturity (0.519), number of productive tillers per plant (0.386) and plant height (0.005) (Table. 4). Negative direct effect on grain yield were observed for days to 50% flowering (-0.263) and main ear length (-0.031). Indirect significant positive effects on grain yield were observed for days to 50% flowering (0.469), plant height (0.296), main ear length (0.292), number of productive tillers per plant (0.181), days to maturity (0.180) and number of fingers per ear (0.168). Considering the nature and magnitude of character association and their direct and indirect effects, it can be inferred that improvement of grain vield is possible through simultaneous manifestation of days to 50% flowering, plant height, main ear length, number of productive tillers per plant, number of finger per ear and days to maturity. These results are in accordance with the findings of Anuradha et al., (2013)<sup>[3]</sup>, Dinesh kumar et al., (2014)<sup>[6]</sup>, Jyothsna et al., (2016) [9], Shivangi Negi et al., (2017) [11] and Sneha et al., (2019)<sup>[12]</sup>.

**Table 1:** Analysis of variance for seven characters in 30 genotypes of finger millet

Source of variation	df							
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers per plant	Main ear length (cm)	Number of fingers per ear	Grain yield (Q/ha)
Replication	2	1.46	1.30	34.56	0.26	0.80	0.27	92.16
Treatments	29	224.13**	440.22**	488.43**	3.20**	3.78**	1.01**	272.54**
Error	58	1.76	1.73	84.21	0.12	0.23	0.14	38.52

Fable 2: Estimates of genetic variability	parameters for grain	yield and its attributes i	n 30 genotypes of finger millet
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Character		Range		<b>Coefficient of variation</b>			Heritability	Constis advance	Genetic advance as	
		Max	Mean	GCV	PCV	ECV	h <sup>2</sup> (b)	Genetic advance	percent of mean	
Days to 50% flowering		91.33	80.85	10.64	10.77	1.64	97.67	17.52	21.67	
Days to maturity	84.66	130.00	114.58	10.55	10.61	1.15	98.83	24.75	21.60	
Plant height (cm)	79.36	138.60	111.05	10.45	13.32	8.26	61.54	18.75	16.89	
Number of productive tillers per plant	1.73	6.60	3.30	30.66	35.54	10.89	88.78	1.96	59.52	
Main ear length (cm)	5.86	10.23	8.57	12.68	13.90	5.69	83.21	2.04	23.83	
Number of fingers per ear	5.06	8.40	6.51	8.23	10.14	5.92	65.93	0.89	13.77	
Grain yield Q/ha	22.91	52.63	37.74	23.40	28.60	16.44	66.94	14.88	39.44	

Table 3: Estimates of phenotypic and genotypic correlation coefficients for 7 characters in 30 finger millet genotypes

Characters		Days to 50%	Days to	Plant height	Number of productive	Main ear	Number of	Grain yield
		flowering	maturity	( <b>cm</b> )	tillers per plant	length (cm)	fingers per ear	Q/ha
Dava to 500/ flowering	rp	1.0	0.887**	0.301**	0.179	0.483**	0.293**	0.384**
Days to 50% howening	rg	1.0	0.904**	0.385*	0.174	0.536**	0.372**	0.465**
Deres ta maturita	rp		1.0	0.430**	0.330**	0.471**	0.259**	0.467**
Days to maturity	rg		1.0	0.572**	0.350**	0.520**	0.325**	0.583**
Dlant haight (am)	rp			1.0	0.215**	0.324**	0.083	0.340**
Plant height (Chi)	rg			1.0	0.273**	0.462**	0.055	0.322**
Number of productive	rp				1.0	-0.022**	-0.035	0.375**
tillers per plant	rg				1.0	-0.026**	-0.077	0.481**
Main our langth (am)	rp					1.0	0.393**	0.320**
Main ear lengur (cin)	rg					1.0	0.526**	0.382**
Number of fingers per	rp						1.0	0.347**
ear	rg						1.0	0.579**
Grain yield O/ha	rp							1.0
Grain yield Q/lia	rg							1.0

 $r_p$  = Phenotypic correlation coefficient  $g_p$  = Genotypic correlation coefficient

Table 4: Path coefficient analysis showing direct and indirect effects.

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of productive tillers per plant	Main ear length (cm)	Number of fingers per ear	Grain yield Q/ha
Dave to 50% flowering	-0.044	0.218	0.041	0.050	0.041	0.077	0.384**
Days to 50% nowering G	-0.263	0.469	0.002	0.067	-0.016	0.206	0.465**
Powe to maturity	-0.039	0.246	0.059	-0.093	0.040	0.068	0.467**
G	-0.238	0.519	0.003	0.135	-0.016	0.180	0.583**
Plant height (am)	-0.013	0.106	0.137	0.061	0.027	0.022	0.340**
G G	-0.101	0.296	0.005	0.105	-0.014	0.031	0.322**
Number of productive P	-0.008	0.081	0.030	0.283	-0.002	-0.009	0.375**
tillers per plant G	-0.046	0.181	0.001	0.386	0.001	-0.043	0.481**
Main con langth (cm)	-0.021	0.116	0.044	-0.007	-0.084	0.102	0.320**
G G G G G G	-0.141	0.270	0.002	-0.010	-0.031	0.292	0.382**
Number of fingers per P	-0.012	0.063	0.011	-0.009	0.033	0.261	0.347**
ear G	-0.098	0.168	0.000	-0.030	-0.016	0.554	0.579**

Residual effect = 0.323P = Phenotypic path coefficient G = Genotypic path coefficient

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