



## RESEARCH ARTICLE

### Studies on the genetic variability, heritability, and genetic advance of finger millet (*Eleusine coracana* L.) genotypes in northwestern Ethiopia

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#### ABSTRACT

Finger millet (*Eleusine coracana* L.) is vital in the farming systems of many parts of Ethiopia in which there is limited information on the genetic variability, heritability, and genetic advance. The major aim of the current research was to investigate variation and quantify variance components, including genetic advance, for common agronomic characters of finger millet, such as yield and related once. Eleven finger millet genotypes were assessed using RCBD with four replications at Pawe and manbuk/dangur for three years. mean squares of tested genotypes were highly significant ( $p < 0.001$ ) for the most important agronomic features, suggesting heterogeneity among tested finger millet genotypes. Heritability estimations ranged from 12.18 % for tillers per plant to 97.35 % for days to maturity. Overall, the results showed a significant level of character variability between genotypes, which may be used for future finger millet genetic improvement.

**Keywords:** Finger millet, Genetic advance, Heritability, Variability

#### INTRODUCTION

Finger millet (*Eleusine coracana* L.) is one of the most important cereal crops in the driest areas of the globe. The crop is sometimes called African millet or Ragi, a known self-pollinated tetraploid where  $2n=36$ . The name finger millet was coined from its morphological appearance of fingers/spikes which look like human fingers. Unlike the majority of cereal crops (wheat, rice, barley etc.) finger millet is relatively drought tolerant that can able to grow under harsh and

marginal agro-ecologies because of its nature of C4 photosynthesis system and adaptation. Regarding its utilization the crop is cultivated mainly for its grain to make certain traditional food items as well as the stalks for livestock feed, construction and fuel by many small-scale farmers globally, critically in Ethiopia, Uganda, India, Nepal and China (Birhanu, 2015). Many researchers have shown that finger millet has various health benefits like reducing

diabetes (Anitha et al., 2021), obesity (Gupta et al., 2017), osteoporosis (Maharajan et al., 2021 and Tsehay et al., 2006), anemia (Gupta et al., 2017), malaria and diarrhea (Assefa et al., 2013 and Vetriventhan et al., 2015). The presence of high calcium, iron and dietary fiber content and being gluten free makes the crop to have health values. It has been played a significant role as a nutritious millet for most rural populations in developing countries including Ethiopia. In general, according to Sharma et al., (2016) and Devi et al., (2014) the special properties of finger millet such as anti-tumorigenic, anti-diabetic, antioxidant and antimicrobial nature make the crop highly valued and important for utilization.

Arun Prabhu et al., (2008) described that the presence of genetic variability in the population and availability of diverse germplasm is the prerequisite for genetic improvement through conventional plant breeding approaches. In Ethiopia the crop is cultivated mostly as rain fed under a diverse production environment. This time there is a need for genetic enhancement of finger millet productivity in considering the demand for food purpose increased and decreasing area due to competing crops. According to Nethra et al., 2014 much work is needed to use the genetic diversity for crop improvement and increase utilization efficiency. Thus, the present study was done to assess the availability of variability in the studied finger millet genotypes and to estimate heritability as well as genetic advance under rain fed conditions.

## MATERIALS AND METHODS

### Experimental sites



**Figure 1.** Dangur/Manbuk and Pawe study areas. The experiment was carried out in two districts of the Metekel zone, namely Pawe and Dangur (Manbuk), for three consecutive years (2011 to 2013 main cropping seasons). Geographically, Pawe is located 575 km away from Addis Ababa with a latitude of 11°

15'N and a longitude of 36° 05' E at an elevation of 1150 MSL, and Manbuk is a town located at a latitude, longitude and elevation of 11° 17' N, 36° 13' E and 1200 MSL respectively. With the Nitisol type, the area has a single rain pattern, and the average annual rainfall is between 1500 mm and 1800 mm. The average annual low temperature is 16 °C, and the average annual high temperature is 32 °C.

### Experimental materials and design

A total of eleven finger millet genotypes (PWRFM-1 to PWRFM-10 and a standard check variety Baruda) which were advanced from preliminary yield trials were used. Randomized complete block design (RCBD) with four replications was deployed at two locations. Each plot has five rows with 0.75 m row spacing and row length of 3 m. For the purpose of plot management and data recording 1.5 m path was left between each block. Both urea and DAP fertilizer were used at the recommended rate of 100 kg/ha. The whole DAP was applied at once during sowing whereas split application was done for urea. The composition of essential elements in the DAP fertilizer are: Nitrogen=18% and Phosphate=46% as a basal dose of 100 kg/ha of urea (nitrogen=46%) as top dressing. Planting was done by hand drilling at the rate of 8 kg/ha and appropriate thinning was performed at the right time and the required number of populations was maintained. The remaining agronomic activities were applied uniformly as per the recommendations.

### Data collected and analysis

The common agronomic characters of finger millet which includes days to flowering, days to maturity, plant height, number of tillers per plant, number of fingers per plant, length of fingers, and stand count at harvest, lodging and grain yield were collected. The collected data were subjected for analysis of variance using SAS 9.3 software. The significance of the mean sum of squares for each character was tested against the corresponding error degrees of freedom using 'F' Test (Fisher and Yates, 1967). The components of variances were used to estimate genetic parameters like phenotypic and genotypic and environmental coefficient of variation (PCV, GCV and ECV) as per the procedure given by Burton and De Vane (1953) and Kumar et al., (1985). Heritability in the broad sense was calculated according to the formula given by Allard (1960) and expressed in percentage whereas genetic advance was estimated by using formula of Johnson et al., (1955).

## RESULTS AND DISCUSSION

### ANOVA for some agronomic traits of finger millet

The analysis of variance revealed the existence of highly significant differences ( $p < 0.001$ ) among genotypes for most of the studied characters such as days to maturity, plant height, number of fingers per plant, finger length, and grain yield except number of tillers per plant (NTPP) as shown in the present study. This indicating that the genotypes were highly variable. Similar results were reported by earlier researchers (Reddy et al., 2013; Ulaganathan and Nirmalakumari, 2015). The summary statistics of the results were presented in the **Table 1**.

### Mean and range estimation

In the present study, most of the characters studied showed a wide range of variability among the evaluated finger millet genotypes in which the ranges

between minimum and maximum mean performances were illustrated in Table 2. Characters like days to flowering ranged from 94 (Baruda) to 117 (PWRFM-3) with a mean value of 110, days to maturity ranged from 145 (Baruda) to 165 (PWRFM-6) with a mean value of 160. Likewise, number of tillers per plant and number of fingers per plant ranged from 4.9 (PWRFM-8) to 6.3 (PWRFM-2) and 8.8 (Baruda) to 11.5 (PWRFM-1) with a mean value of 5.5 and 10.4 respectively, while plant height varied from 95.6 cm (Baruda) to 126.5 cm (PWRFM-9), finger length varied from 7 cm (Baruda) to 15.7 cm (PWRFM-9) and grain yielding ability ranged from 19.1 q/ha (PWRFM-7) to 25.5 q/ha (Baruda) with a mean value of 107.8 cm, 12.2 cm and 21.9 q/ha respectively. Previous scholars Singamsetti et al., (2018), Mahanthesha et al., (2017), Kumari and Singh (2015) and Kumar et al., (2019) were found similar variations in their tested finger millet entries.

**Table 1.** Combined ANOVA for agronomic traits of Finger millet

Sources of variation	Df	Mean squares							
		DM	PHT (cm)	NTPP	NFPP	FL (cm)	GYD (q/ha)	SCTH	LODG
Year	2	2318**	763*	99.6**	359**	45.11**	293**	2060**	651
Location	1	41.76	5777**	0.01	435**	1.83	2589**	3818**	22866**
Replication	3	2.34	642	28.23**	5.0	3.60	135	87.46	208
Treatment	10	800**	2592**	3.34	14.64**	119.5**	101**	40.15	10063**
Error	247	10.86	182.8	3.15	6.03	3.44	30.75	45.31	314

Df=Degree of freedom, DM=Days to maturity, PHT=Plant height, NTPP=Number of tillers, NFPP=Number of fingers per plant, FL=Finger length, GYD=Grain yield, SCTH=Stand count at harvest, LODG=Lodging, DISE=Disease.

**Table 2.** Mean performance of agronomic characters of Finger millet

Treatment	DF	DM	PHT (cm)	DISE	NTPP	NFPP	FL (cm)	LDG	GYD (q/ha)
PWRFM-1	114.00 <sup>c</sup>	163.37 <sup>abc</sup>	107.41 <sup>bcd</sup>	1.12 <sup>ab</sup>	5.2 <sup>b</sup>	11.54 <sup>a</sup>	12.04 <sup>b</sup>	12.58 <sup>b</sup>	21.74 <sup>bcd</sup>
PWRFM-2	107.83 <sup>e</sup>	163.04 <sup>bc</sup>	105.08 <sup>cde</sup>	1.20 <sup>a</sup>	6.33 <sup>a</sup>	10.83 <sup>abc</sup>	12.29 <sup>b</sup>	8.12 <sup>bc</sup>	25.01 <sup>a</sup>
PWRFM-3	117.58 <sup>a</sup>	163.79 <sup>ab</sup>	110.54 <sup>bc</sup>	1.16 <sup>ab</sup>	5.58 <sup>ab</sup>	11.2 <sup>ab</sup>	11.58 <sup>b</sup>	3.12 <sup>bc</sup>	19.59 <sup>cd</sup>
PWRFM-4	111.62 <sup>d</sup>	161.54 <sup>cd</sup>	97.54 <sup>ef</sup>	1.16 <sup>ab</sup>	5.29 <sup>b</sup>	10.75 <sup>abc</sup>	12.00 <sup>b</sup>	1.04 <sup>c</sup>	22.77 <sup>ab</sup>
PWRFM-5	114.91 <sup>bc</sup>	163.04 <sup>bc</sup>	103.00 <sup>cdef</sup>	1.20 <sup>a</sup>	5.66 <sup>ab</sup>	10.79 <sup>abc</sup>	12.20 <sup>b</sup>	2.29 <sup>c</sup>	22.37 <sup>abc</sup>
PWRFM-6	116.04 <sup>ab</sup>	165.20 <sup>a</sup>	114.87 <sup>b</sup>	1.20 <sup>a</sup>	5.79 <sup>ab</sup>	10.75 <sup>abc</sup>	12.33 <sup>b</sup>	2.91 <sup>bc</sup>	19.58 <sup>cd</sup>
PWRFM-7	115.41 <sup>bc</sup>	164.04 <sup>ab</sup>	101.20 <sup>def</sup>	1.12 <sup>ab</sup>	5.25 <sup>b</sup>	9.91 <sup>bcd</sup>	11.75 <sup>b</sup>	1.25 <sup>c</sup>	19.17 <sup>d</sup>
PWRFM-8	111.75 <sup>d</sup>	160.58 <sup>d</sup>	99.50 <sup>ef</sup>	1.16 <sup>ab</sup>	4.91 <sup>b</sup>	9.54 <sup>cd</sup>	11.50 <sup>b</sup>	0.83 <sup>c</sup>	21.61 <sup>bcd</sup>
PWRFM-9	106.00 <sup>f</sup>	154.75 <sup>e</sup>	126.58 <sup>a</sup>	1.00 <sup>b</sup>	5.45 <sup>ab</sup>	10.04 <sup>bcd</sup>	15.70 <sup>a</sup>	46.79 <sup>a</sup>	21.55 <sup>bcd</sup>
PWRFM-10	106.00 <sup>f</sup>	155.7 <sup>e</sup>	124.33 <sup>a</sup>	1.00 <sup>b</sup>	5.37 <sup>ab</sup>	10.33 <sup>abc</sup>	15.25 <sup>a</sup>	49.79 <sup>a</sup>	22.43 <sup>abc</sup>
Baruda	94.66 <sup>g</sup>	145.95 <sup>f</sup>	95.62 <sup>f</sup>	1.00 <sup>b</sup>	5.20 <sup>b</sup>	8.83 <sup>d</sup>	7.00 <sup>c</sup>	44.87	25.47 <sup>a</sup>

Mean	110.53	160.09	107.79	1.12	5.46	10.41	12.15	15.78	21.93
CV	2.83	2.05	12.54	26.89	32.47	23.59	15.28	47.23	25.27
LSD (5%)	1.78	1.87	7.68	0.17	1	1.39	1.05	10.08	3.15

### ***Estimation of variance components***

The genotypic and phenotypic coefficient of variations (GCV and PCV) were calculated from the mean squares and the classification as high, medium and low was done as suggested by Deshmukh et al., (1986). This implies GCV and PCV values roughly more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be medium or moderate. Based on this category, both plant height and finger length exhibited high level of GCV and PCV with a value of 22.7%, 25.9% and 44.3%, 46.8% respectively. High phenotypic coefficient of variability were recorded by characters number of tillers per plant, number of fingers per plant, grain yield and disease score with a values of 32.75%, 27.48%, 31.69% and 22.7% respectively (Table 4). Genotypic coefficient of variability (GCV) ranged from 3.99% for number of tillers per plant to 312.8% for lodging whereas the phenotypic coefficient of variability (PCV) values ranged from 9.01% for days to maturity to 332.4% for lodging. In addition, PCV value was generally higher than their corresponding GCV values for all the characters considered (Table 3). PCV value was low only for days to maturity. Genotypic coefficient of variability (GCV) values was low for days to maturity (8.77%) and number of tillers per plant (3.99%); medium for number of fingers per plant (14.09%), grain yield (19.11%) and disease (17.11%). The high GCV values of these characters showed the possibility of improving these traits through simple selection.

### ***Estimation of broad sense heritability and genetic advance***

According to Falconer, (1981) heritability is the heritable portion of phenotypic variance, which would be a good index of the transmission of characters from parents to offspring. In the present study heritability in broad sense estimates ranged from 12.18% for number of tillers per plant to 97.35% for days to maturity (Table 3). Selection of characters would be fairly easy when the heritability of a character is measured very high such as 80% or more (Singh, 2001). This would be possible as a close correspondence between the genotypes and phenotypes due to the relatively small contribution of the environment to the genotype. Though, heritability of a character is low say 40% or less, this showed selection may be difficult or virtually impractical as a result of the masking effect of the environment.

Taking this into account and considered as a benchmark, heritability estimate was high (>80%) for days to maturity, plant height, finger length and lodging. The remaining quantitative characters showed moderate heritability (40 - 80%). These results were in agreement with previously studied by Reddy et al., (2013); Manoj Kumar et al., (2015); Ezeaku et al., (2015); Suryanarayana et al., (2014); Jyothsna et al., (2016) and Mahanthesha et al., (2017).

Genetic advance (GA) is another genetic component parameter that implies the improvement of characters using genetic values for the new population compared to the base population in one cycle of selection at a given selection intensity (Singh, 2001). In the current findings GA for grain yield was 8.62 q/ha which indicates that whenever we select the best 5% high yielding genotypes as parents, mean grain yield of progenies could be improved by 8.62 q/ha, that is mean genotypic value of the new population for grain will be improved from 21.93 to 33.55 q/ha. Similarly, it will be 5.51 for number of tillers per plant, 13.43 for number of fingers per plant, 23.22 cm for finger length and 158.25 cm for plant height (Table 3). On the other hand, the maximum genetic advance as percentage of mean (GAM) at 5% selection intensity was obtained for lodging (643.23%), finger length (91.15%), plant height (46.81) followed by grain yield (39.29). The minimum were recorded by number of tillers per plant (8.20%) and days to maturity (18.04%).

Johnson et al., (1955) has explained that the combination of high heritability estimates along with high genetic advance is usually helpful in predicting genetic gain under selection than heritability estimates alone. The present study reveals high heritability coupled with high expected genetic advances percent of mean of days to maturity, plant height, finger length and lodging susceptibility. These traits are predominantly under the control of additive gene actions and hence these characters can be improved by selection (Mohan Prem Anand et al., 2005). Characters such as number of fingers per plant, grain yield and disease showed moderate heritability with relatively higher genetic advance. So, these characters could be improved more easily than other characters. Similar findings were obtained by John et al. (2006).

**Table 3.** Genetic parameters of 11 Finger millet advanced lines

	DM	PHT	NTPP	NFPP	FL	GYD	LODG	DISE
$\sigma^2g$	197.285	602.3	0.0475	2.1525	29.015	17.5625	2437.25	0.037
$\sigma^2p$	208.145	785.1	3.1975	8.1825	32.455	48.3125	2751.25	0.065
GCV (%)	8.774	22.768	3.992	14.094	44.334	19.110	312.855	17.116
PCV (%)	9.012	25.995	32.750	27.478	46.888	31.695	332.398	22.720
ECV (%)	6.784	169.589	57.692	57.925	28.313	140.219	1989.861	2.500
H (%)	97.356	87.588	12.188	51.290	94.552	60.293	94.121	75.337
Mean(X)	160.09	107.79	5.46	10.41	12.15	21.93	15.78	1.12
GA	28.878	50.458	0.448	3.016	11.075	8.616	101.502	0.394
GAM	18.039	46.811	8.207	28.976	91.150	39.290	643.230	35.191

$\sigma^2g$  = Genotypic variance,  $\sigma^2p$ =Phenotypic variance, GCV= Genotypic coefficient of variability, PCV = Phenotypic coefficient of variability, H = Heritability, GA = genetic advances percent of mean, GAM = Genetic advances percent of mean.

## CONCLUSION

The nature of variability existing for a certain trait of interest is a key point for the better accomplishment and success of genetic improvement. A plant breeder should take into consideration the presence of genetic variability and its magnitude in the gene pool of a crop is most important for careful plant breeding programs. Variability in the given gene pool is essential for some traits that we need to improve, for example, disease resistance (blast in this case), varietal adaptability and effective selection. An effort was made in the current study to further substantiate the earlier limited studies that indicated Ethiopian finger millet genotypes having wide variability. Most of the characters studied showed a wide range of variability. This would be an indication of the existence of a large amount of variability and potential in the landraces to offer a particular trait of interest. Therefore, the use of genetic improvement of finger millet through hybridization and/or selection to boost the present finger millet production and productivity.

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## COMPETING INTERESTS

The authors declare that they have no competing interests

## DATA AVAILABILITY STATEMENT

The raw data used to support the findings of this study are available from the corresponding author upon request.

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