

Full Length Research Paper

# Heritability, variance components and genetic advance of some yield and yield related traits in Ethiopian collections of finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes

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**Eighty-eight (88) finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm collections were tested using augmented randomized complete block design at Adet Agricultural Research Station in 2008 cropping season. The objective of this study was to find out heritability, variance components, variability and genetic advance for some yield and yield related agronomic characters. Statistically significant ( $p < 0.01$ ) difference was observed among the genotypes tested for important characters indicating the presence of variability. A considerable amount of variability among germplasms for the traits studied also indicated the usefulness of selection for these traits in the genetic material used for future improvement in finger millet. In addition, high genotypic coefficient of variation (GCV) was recorded for number tillers per plant (71.93), number of ears per plant (96.55), number of fingers per ear (85.48), finger length (94.48), biomass yield (87.67), and grain yield (78.17) and high phenotypic coefficient of variation (PCV) was similarly recorded for number tillers per plant (30.42), number of ears per plant (45.55), number of fingers per ear (24.88), finger length (26.18), biomass yield (85.56), and grain yield (29.87). High heritability coupled with high expected genetic advance as percent of mean was obtained for number of ears per plant (96.55, 90.59%), number of finger per ear (85.48, 43.81%), finger length (94.48, 50.95%), and days to heading (96.01, 14.13%), biomass yield (87.67, 154.52%), 1000 kernel weight (93.69, 37.70%), lodging susceptibility (98.92, 384.24%) and blast severity (87.60, 89.47%) indicating that the presence of more additive gene effects for potential crop improvement and so these characters could be improved through selection. This study reveals that greater yield response could be obtained through direct selection scheme in finger millet landraces.**

**Key words:** *Eleusine coracana*, finger millet, genotypic coefficient, phenotypic coefficient, variance, heritability, genetic advance, Ethiopia.

## INTRODUCTION

The presence of morpho-genetic variations in agronomic characters of a crop would be of considerable importance in determining the best method needed to improve the yield of that crop (Ojo et al., 2006). The magnitude of genetic variability present in base population of any crop species is also pivotal to crop improvement which must

be exploited by plant breeders for yield improvement (Idahosa et al., 2010).

Finger millet (*Eleusine coracana* (L.) Gaertn.) is one of the most important small millet grown in eastern and southern Africa. It serves as a subsistence and food security crop that is especially important for its nutritive

and cultural value. It is an important food crop in traditional low input cereal-based farming systems in Africa, and is of particular importance in upland areas of Eastern Africa, where it commands a high market price compared with other cereals (National Research Council, 1996). In Ethiopia, traditionally it is used for making bread, 'injera' mixed with tef, porridge, local beer 'tella' and a powerful distilled spirit 'areke' and a number of other uses. Finger millet grain has good taste and is an excellent dietary source of methionine (an amino acid lacking in the diets of hundreds of millions of the poor who live on starchy foods like cassava, plantain, polished rice, and maize meal) whose level ranges around 5% of protein; is of special benefit, notably for those who depend on plant foods for their protein.

Creation of genetic variability and selection for important traits is a crucial activity that any plant breeder should apply to achieve better yield and other desirable agronomic traits. However, to carry out effective selection, the information on available genetic variation among finger millet genotypes, the nature of component traits on which selection would be effective and the influence of environmental factors on each trait need to be known (Jaleta et al., 2011). Information on the nature and magnitude of variability and heritability in a population is one of the prerequisites for successful breeding program in selecting genotypes with desirable characters (Dudly and Moll, 1969). It is therefore, of great importance for breeders to know the heritability of the agronomical characters to improve the yield of the crop effectively.

According to Falconer and Mackay (1996), heritability is defined as the measure of the correspondence between breeding values and phenotypic values. Thus, heritability plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. It is the breeding value which determines how much of the phenotype would be passed onto the next generation (Tazeen et al., 2009). There is a direct relationship between heritability and response to selection, which is referred to as genetic advance. High genetic advance with high heritability estimates offer the most effective condition for selection (Larik et al., 2000). The utility of heritability therefore increases when it is used to calculate genetic advance, which indicates the degree of gain in a character obtained under a particular selection pressure. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection program. Knowledge of the extent and pattern of variability, heritability of the trait and genetic gain present in a population

of finger millet collections under diversified agro-climatic condition of Ethiopia is limited where finger millet is a major food crop and farmers commonly use their landraces. Hence, this study was done with the objective to assess the variability, heritability and genetic advance of grain yield and some of its related components to select a more desired trait that may contribute for the improvement of finger millet.

## MATERIALS AND METHODS

### Experimental site and design

The experiment was conducted on 88 collections of finger millet germplasm including the local and standard checks obtained from the Ethiopian Institute of Biodiversity and Conservation in 2008 at Adet Agricultural Research Center, Northwest Ethiopia. Adet is located at a longitude from 37° 28' 38" to 37° 29' 50" E and latitude from 11° 16' 19" to 11° 17' 28" N in northern highlands of Ethiopia with an average altitude of 2240 masl with average annual rainfall of 1177 mm during the study and the annual minimum and maximum temperatures varied from 24.3 to 26.6°C and 8.49°C to 11.0°C, respectively. The experimental design used was augmented randomized complete block design of four blocks.

Each accession was assigned to plots of 5 m long double and sown 0.75 m apart and drilled in the row length. The seed and fertilizer rates used were 10 and 46/41 kg ha<sup>-1</sup> N/P<sub>2</sub>O<sub>5</sub>, respectively. Hand-weeding and normal management practices were followed. Data collection was done on plant and plot basis as; plant height (cm), number of effective tillers per plant, number of ears per plant, number of fingers per ear, finger length (cm) were recorded on plant basis while days to flowering, days to maturity, biomass yield per plot (g), grain yield per plot (g), harvest index per plot (%), thousand kernel weight (g), lodging susceptibility and blast severity were recorded on plot basis. Five plants were selected at random for data record on plant basis.

### Statistical data analysis

#### Estimation of magnitude of variation

The mean value of the recorded data was subjected to analysis of variance (ANOVA) using the statistical analysis procedures of Sharma (1998). The phenotypic and genotypic variances were also estimated according to the method suggested by Burton and De Vane (1953) using the formula:

$$\sigma^2_g = \frac{(MS_g - MS_e)}{r}$$

$$\sigma^2_P = \sigma^2_g + \sigma^2_e$$

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**Abbreviations:** PH, Plant height (cm); TPP, number of tillers per plant; EPP, number of ears per plant; FL, finger length (cm); DH, days to 50% heading; DM, days to 50% maturity; BMY, biomass yield per hectare; GYPH, grain yield per hectare(kg); HI, harvest index (%); TKW, thousand kernel weight(g); LO, lodging (%); HBL, head blast severity; DF, degree of freedom; SEM, standard error of mean; CV, coefficient of variation (%); s<sup>2</sup><sub>p</sub>, phenotypic variance; s<sup>2</sup><sub>g</sub>, genotypic variance; PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation; h<sup>2</sup>, broad sense heritability; GA, expected genetic advance; GAM, genetic advance as percent of the mean.

$$\sigma_e^2 = MS_e$$

Where,  $\sigma_g^2$  = genotypic variance,  $\sigma_p^2$  = phenotypic variance,  $\sigma_e^2$  = environmental variance,  $MS_g$  = Mean square due to genotypes/accessions,  $MS_e$  = Error mean square, and  $r$  = number of replications

The coefficient of variations at phenotypic and genotypic level variation was estimated using the formula adopted by Johnson et al. (1955) as:

$$PCV = \left[ \frac{\sigma_p}{\bar{x}} \right] \times 100$$

$$GCV = \left[ \frac{\sigma_g}{\bar{x}} \right] \times 100$$

$$ECV = \left[ \frac{\sigma_e}{\bar{x}} \right] \times 100$$

Where,  $\sigma_p$  = phenotypic standard deviation ( $\sigma_g + \sigma_e$ ),  $\sigma_g$  = genotypic standard deviation,  $\sigma_e$  = Environmental standard deviation, and  $\bar{x}$  = Grand mean for the characteristic x; PCV, GCV, and ECV = phenotypic, genotypic and environmental coefficient of variation, respectively.

#### **Estimate of heritability and expected genetic advance**

Heritability ( $h^2$ ) in broad sense for all characters was computed using the formula adopted by Allard (1960).

$$h^2 = \left[ \frac{\sigma_g^2}{\sigma_p^2} \right] \times 100$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,  $\sigma_g^2$  = genotypic variance,  $\sigma_p^2$  = Phenotypic variance,  $\sigma_e^2$  = error variance. Genetic advance as part of the mean (GA) for each character was computed using the formula by Allard (1960).

$$GA = (k) (\sigma_p) (h^2), \text{ and } GAM \text{ (as \% of the mean)} = \left[ \frac{(GA)}{\bar{X}} \right] \times 100$$

Where,  $k$  = selection differential (at 5% selection intensity),  $\sigma_p$  = phenotypic standard deviation,  $h^2$  = heritability and  $\bar{X}$  = grand mean.

## **RESULTS AND DISCUSSION**

### **Mean and range**

For each of the traits evaluated, the descriptive statistics including the extreme genotype mean values and the means together with their standard errors obtained on the basis of average data are summarized in Table 1. In general, finger millet genotypes showed wide range of variability for most of the characters and all the traits exhi-

bited broad spectrum of ranges between the maximum and minimum genotype mean values. For instance, days to heading ranged from 91 to 128 with a mean of 115 days to maturity ranging from 157 to 182 with a mean of 169. Similarly, number of tillers per plant and ears per plant ranged from 4 to 14 and 5 to 32, respectively while plant height varied from 63.8 cm to 111.5 cm with a mean height of 86.9 cm. Number of fingers per ear ranged from 5 to 14 with a mean of seven fingers per ear finger length of the test varieties varied from 3.9 to 12.3 cm with mean of 6.7cm.

Grain yielding ability ranged from 860.6 to 3781.5 kg ha<sup>-1</sup> with a mean of 1931.8 kg ha<sup>-1</sup> and that of thousand kernel weights ranged from 1.8 to 4.6 g with a mean weight of 3.3 g. The maximum yield obtained was 3781.5 kg ha<sup>-1</sup> followed by 3423.6 kg ha<sup>-1</sup>. Thus, it is possible to succeed in improving grain yield by direct selection.

Biomass yield ranged from 4266.7 to 15066.7 kg ha<sup>-1</sup> with a mean of yield of 7637.3 kg ha<sup>-1</sup> whereas harvest index varied from 15.3 to 40.8% with a mean of 25.3%. The range of variation was wide for the number of tillers and ears per plant, fingers per ear and finger length.

The result of analysis of variance on 13 quantitative characters for the genotypes is presented in Table 2. Mean square of all the characters studied, showed significant difference ( $P < 0.05$ ) among the tested genotypes except for plant height and biomass yield indicating the presence of variability which can be exploited through selection.

### **Estimates of variance components**

Grain yield, biomass yield, plant height, number of ears per plant, days to heading and maturity has exhibited high genotypic ( $s^2g$ ) and phenotypic ( $s^2p$ ) variances. Grain yield, biomass yield, number of ears per plant, number of tillers per plant, finger length, number of fingers per ear and blast severity exhibited high genotypic (GCV) and phenotypic (PCV) coefficient of variances (Table 3).

Phenotypic coefficient of variability (PCV) values ranged from 1.68% for harvest index to 188.55% for lodging, whereas the genotypic coefficient of variability (GCV) ranged from 1.18% for harvest index to 187.54% for lodging. In addition, PCV value was generally higher than their corresponding GCV values for all the characters considered (Table 3). According to Deshmukh et al. (1986), PCV and GCV 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. Based on this delineation, PCV value was low for days to maturity, days to heading and harvest index; medium for plant height, and thousand kernel weight; high for number tillers per plant, ears per plant, fingers per ear, finger length, biomass yield, grain yield and blast severity.

Genotypic coefficient of variability (GCV) values were low for plant height, days to maturity, days to heading

**Table 1.** Ranges, means and standard errors of means (SEM) for 13 quantitative traits of 88 finger millet germplasms.

Trait	Minimum value	Maximum value	Average/mean value	SEM ( $\pm$ )
PH	63.8	111.5	86.89	0.95
TPP	4.0	14.0	7.24	0.21
EPP	5.0	32.0	11.53	0.52
FPE	5.0	14.0	7.01	0.16
FL	3.9	12.3	6.67	0.17
DH	91	128	114.87	0.75
DM	157	182	169.14	0.54
BMY	4266.7	15066.7	7637.33	207.39
GY	860.58	3781.48	1931.82	56.99
HI	15.31	40.82	25.49	0.45
TKW	1.80	4.60	3.26	0.06
LO	0.286	89.714	13.76	2.99
HBL	20.0	77.78	31.77	1.44

PH, Plant height (cm); TPP, number of tillers per plant; EPP, number of ears per plant; FL, finger length (cm); DH, days to 50% heading; DM, days to 50% maturity; BMY, biomass yield per hectare; GYPH, grain yield per hectare(kg); HI, harvest index (%); TKW, thousand kernel weight(g); LO, lodging (%); HBL, head blast severity; SEM, standard error of mean.

**Table 2.** Mean squares from analysis of variance of 13 quantitative characters of 88 finger millet germplasms.

Trait	Mean square							(CV)
	Block (DF=3)	Entries (DF=87)	Varieties (DF=83)	Checks (DF=3)	Checks vs. Varieties (DF=1)	Error (DF=9)	Total (DF=99)	
PH	52.99	94.54	95.81	152.41	184.31	43.44	88.64	7.59
TPP	3.42	4.85*	3.69*	25.75**	38.93**	1.36	4.49	16.11
EPP	34.06	27.58**	17.42**	254.73**	189.45**	0.95	25.36	8.46
FPE	0.17	3.04**	2.75**	2.83*	28.16**	0.44	2.72	9.51
FL	0.04	3.05**	2.64**	14.66**	2.14**	0.16	2.70	6.07
DH	4.52	67.38**	56.10**	298.62**	309.88**	2.69	59.59	1.43
DM	11.15	31.65**	29.38*	98.17**	20.86	6.85	28.77	1.55
BMY	3672216.0	42703311.44**	4121534.0	3983331.00	17480766.00	5266293.0	38117.18	30.05
GY	225169.00	332888.00**	283348.00*	1412120.00**	1206981.00**	72657.00	305966.0	13.95
HI	0.031	0.184	0.163	0.801**	0.018	0.097	0.171	24.49
TKW	0.13549	0.40561**	0.28597**	1.28904**	7.68528**	0.02984	0.363263	5.30
Lodging	6.770	673.140**	357.410**	6695.800**	8810.460**	7.250	592.410	6.73
HBL	15.850	248.103**	232.390**	332.260**	1300.000**	30.770	221.308	17.46

\*Significant at probability level of 0.05 and \*\*significant at probability level of 0.01. DF, Degree of freedom; CV, coefficient of variation (%).

and harvest index; medium for thousand kernel weight; high for number of tillers per plant, number of ears per plant, number of fingers per ear, finger length, biomass yield, grain yield and blast severity (Table 3). The high GCV values of these characters suggest that the possibility of improving these trait through selection.

The difference between PCV and GCV values was high for plant height, number of tillers per plant, number of fingers per ear, biomass yield, grain yield and blast severity indicating the influence of environment on these characters. However, this difference was low for number of ears per plant, finger length, days to heading, days to maturity, thousand kernel weights, harvest index and lodging suggesting minimal influence of environment on

the expression of the characters, thereby having the highest estimates of heritability. Similar result was found by Yucel et al. (2006) for days to flowering, plant height and harvest index.

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

Estimates of heritability in broad sense ranged from 48.97% for harvest index to 98.92% for lodging (Table 3). According to Singh (2001), if heritability of a character is very high, say 80% or more, selection for such characters could be fairly easy. This is because there would be a close correspondence between the genotype and the

**Table 3.** Estimates of phenotypic ( $s^2_p$ ), genetic ( $s^2_g$ ) variance, phenotypic (PCV) and genotypic (GCV) coefficients of variation, heritability (H), genetic advance (GA) and GA as percentage of mean (GAM) of 13 traits of 88 finger millet germplasms.

Trait	$s^2_p$	$s^2_g$	PCV (%)	GCV (%)	$h^2$ (%)	GA	GAM
PH	94.54	51.1	11.19	8.23	54.05	10.83	12.46
TPP	4.852	3.49	30.42	25.80	71.93	3.26	45.08
EPP	27.5815	26.63	45.55	44.76	96.55	10.45	90.59
FPE	3.04149	2.6	24.88	23.00	85.48	3.07	43.81
FL	3.0482	2.88	26.18	25.44	94.48	3.4	50.95
DH	67.379	64.69	7.15	7.00	96.01	16.23	14.13
DM	31.6506	24.8	3.33	2.94	78.36	9.08	5.37
BMY	42703311.44	37437018.44	85.56	80.11	87.67	11801.51	154.52
GY	332888	260231	29.87	26.41	78.17	929.13	48.10
HI	0.18378	0.09	1.68	1.18	48.97	0.43	1.70
TKW	0.40561	0.38	19.54	18.91	93.69	1.23	37.70
LO	673.14	665.89	188.55	187.54	98.92	52.87	384.24
HBL	248.10299	217.33	49.58	46.40	87.60	89.47	89.47

$s^2_p$ , Phenotypic variance;  $s^2_g$ , genotypic variance; PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation;  $h^2$ , broad sense heritability; GA, expected genetic advance; GAM, genetic advance as percent of the mean.

phenotype due to the relative small contribution of the environment to the phenotype. Although, for characters with low heritability, say 40% or less, selection may be considerably difficult or virtually impractical due to the masking effect of environment. Considering this benchmark, heritability estimate was high (>80%) for number of ears per plant, number of finger per plant, finger length, days to heading, biomass yield, thousand kernel weight, lodging susceptibility and blast severity. It was moderate (40 to 80%) for the remaining quantitative characters.

Genetic advance under selection (GA) refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001). Estimates of GA for grain yield was 929.13 kg ha<sup>-1</sup> indicating that whenever we select the best, 5% high yielding genotypes as parents, mean grain yield of progenies could be improved by 929.13 kg ha<sup>-1</sup>, that is, mean genotypic value of the new population for grain yield will be improved from 1931.33 to 2860.46 kg ha<sup>-1</sup>. In the same way, it will be 21.98 for number of ears per plant, 19438.84 kg ha<sup>-1</sup> for biomass yield, 25.92% for harvest index, 10.07 cm for finger length, and 10.08 for number of fingers per ear (Table 3).

Maximum genetic advance as percentage of mean (GAM) at 5% selection intensity was recorded for lodging susceptibility (384.24%), biomass yield (154.52%) number of ears per plant (90.59%) followed by blast severity (89.47), and finger length (50.95%). It was minimum for harvest index (1.70%) and days to maturity (5.37%).

According to Johnson et al. (1955), high heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone. The present study reveals high heritability coupled with high expected genetic advance

as percent of mean for number of ears per plant, number of finger per plant, finger length, and days to heading, biomass yield, thousand kernel weight, lodging susceptibility and blast severity; moderate heritability with relatively higher genetic advance for grain yield, number of tillers per plant, and grain yield. Therefore, these characters could be improved more easily than the other characters.

## Conclusion

The PCV and GCV values were high for number of tillers per plant, number of ears per plant, number of fingers per ear, finger length, biomass yield, grain yield, lodging and blast severity suggesting the possibility of improving these traits through selection. The difference between PCV and GCV values was high for plant height, number of tillers per plant, number of fingers per ear, biomass yield, and grain yield and blast severity indicating high influence of the environment on the expression of these characters.

High heritability coupled with high expected genetic advance as percent of mean for number of ears per plant, number of finger per plant, finger length, and days to heading, biomass yield, thousand kernel weight, lodging susceptibility and blast severity; moderate heritability with relatively higher genetic advance for grain yield, number of tillers per plant, and grain yield. Therefore, these characters could be improved more easily than the other characters.

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