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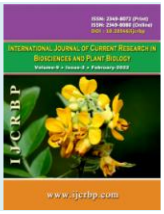

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Genetic variability, heritability and genetic advance studies in finger millet [*Eleusine coracana* (L.) Gaertn] genotypes in Mtekel zone, Northwestern Ethiopia

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Abstract

Finger millet is (*Eleusine coracana* L.) is a vital component in the farming systems of many parts of Ethiopia with limited information on variability, heritability and genetic advance. The aim for this study was to investigate the genetic variability, and find out heritability, variance components and genetic advance for some yield and yield related common agronomic traits. A total of 11 finger millet genotypes were tested using randomized complete block design (RCBD) at two locations i.e. Pawe and Manbuk in three consecutive years. The mean squares of genotypes were highly significant ($p<0.001$) for most important studied agronomic traits indicating the presence of variability. Heritability estimates ranged from 12.18% for number of tillers per plant to 97.35% for days to maturity. Overall, the results revealed the existence of high variability for the traits studied in the finger millet genotypes which can be utilized in the genetic improvement.

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Introduction

Finger millet [*Eleusine coracana* (L.)] is an important cereal crop in the semi-arid and tropical regions of the world. Also known as African millet or Ragi, it is a self-pollinated tetraploid ($2n = 36$) crop.Its name finger millet derived from the appearance of spikes/fingers which are arranged and appear like human fingers. Unlike other major cereals such as rice, wheat and barley, it is relatively drought-tolerant to grow under harsh and marginal agro-ecologies because of its C4 photosynthesis system and adaptation. Finger millet is grown mainly for its grain, which is utilized to make traditional food and drinks, while the stalks are used for livestock feed, construction and fuel by the small scale farmers globally, critically in Ethiopia, Uganda, India, Nepal and China (Birhanu, 2015). Finger millet has various human health benefits such as reducing diabetes (Anitha et al., 2021), obesity (Gupta et al., 2017), osteoporosis (Maharajan et al., 2021; Tsehaye et al., 2006), anemia (Gupta et al., 2017), malaria (Assefa et al., 2013 and Vetriventhan et al., 2015) and diarrhea (Assefa et al., 2013 and Vetriventhan et al., 2015). The health values of finger millet are linked to its high calcium, iron and dietary fiber content and being gluten-free. It serves as 'nutritious millet' for rural populations in developing countries like Ethiopia. More over its special properties like anti-tumerogenic, anti-diabetic, antioxidant and antimicrobial properties make this crop highly valued for its utilization (Sharma et al., 2016; Devi et al., 2014).

Genetic improvement through conventional breeding approaches depends mainly on the availability of the diverse germplasm and the amount of genetic variability present in the population (Arun Prabhu et al., 2008).

The crop is cultivated mostly as a rain fed crop in Ethiopia under diverse production environments. Considering increased demand for food purposes and decreasing area due to competing crops, there is immediate need for genetic enhancement of finger millet productivity. However, only a small fraction of genetic diversity is utilized in crop improvement program (Nethra et al., 2014). Hence the present study was carried out to assess the variability present in the studied finger millet genotypes and to estimate heritability as well as genetic advance under rain fed conditions.

Materials and methods

Experimental sites

The experiment was conducted at two districts of Metekel zone namely Pawe and Dangur (Manbuk) for three consecutive years (2011 to 2013 main cropping seasons. Geographically Pawe is located 575 kilometers away from Addis Ababa with a latitude of 11° 15′N and longitude of 36°05'E at an elevation of 1150 meters above sea level and Manbuk is a town located in a latitude, longitude and elevation of 11°17′N 36°13′E and 1200 meters above sea level respectively. The area has unimodal rain pattern and received annual rain fall which ranges from 1500mm to 1800mmand minimum and maximum mean annual temperature of 16° and 32°C respectively with Nitisol type.

Experimental materials and design

A total of 11 finger millet genotypes which were advanced from preliminary yield trial were used using a randomized complete block design with four replications at two locations (Table 1). Each plot has five rows with 0.75m row spacing and row length of 3m. For plot management and data collection 1.5m path was left between each block. Both urea and DAP fertilizer were applied at the recommended rate of 100 kg/ha. The whole DAP was applied at once during sowing whereas split application was done for urea. Fertilizer application was carried out 100 kg/ha of DAP (Nitrogen=18% and Phosphate=46%) as a basal dose, and 100 kg ha-1 of urea (nitrogen=46%) as top dressing. Sowing was done by hand drilling at the seed rate of 8 kg/ha and thinning applied at the right time and the required number of population was maintained. All the remaining agronomic practices were applied uniformly as per the recommendations.

Data collected and analysis

The common agronomic traits of finger millet such as days to flowering, days to maturity, plant height, number of tillers, number of fingers, 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 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 DeVane (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 Johnson et al., (1955) formula. Statistical analysis was done as indicated below in Table 2.

Results and discussion

Analysis of variance for some agronomic traits of finger millet

The present investigation has shown that 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).

This indicating that the genotypes were highly variable. Substantial variation was also reported by earlier workers (Reddy et al., 2013; Ulaganathan and

Nirmalakumari, 2013 and 2015). All the summary statistics were presented in Table 3.

Estimates of mean and range

The performance of most populations for the characters evaluated and their ranges including mean values are summarized in Table 4. In general, finger millet genotypes showed wide range of variability for most of the studied characters and all the traits exhibited broad spectrum of ranges between the maximum and minimum genotype mean values.

For instance, days to flowering ranged from 96 to 117 with a mean of 110 days to maturity ranging from 145 to 165 with a mean of 160. Similarly, number of tillers per plant and fingers per plant ranged from 4.9 to 6.3 and 8.8 to 11.5, respectively while plant height varied from 95.6 cm to126.5 cm with a mean height of 107.8 cm. Finger length of the test varieties varied from 7cm to 15.7 cm with mean of 12.5cm whereas grain yielding ability ranged from 19.1 q/ha to 21.5 q/ha with a mean of 21.9 q/ha.

Estimates of variance components

Only Plant height and finger length exhibited both high genotypic and phenotypic coefficient of variability (GCV and PCV). On the other hand, number of tillers per plant, number of fingers per plant, grain yield and disease recorded only high phenotypic coefficient of variability (PCV) with a value of 32.75%, 27.48%, 31.69% and 22.7% respectively (Table 5). 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 5).

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 or moderate. Based on this delineation, PCV value was low only for days to maturity. Genotypic coefficient of variability (GCV) values were 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%)(Table 5). The high GCV values of these characters suggest that the possibility of improving these trait through simple selection.

Estimation of heritability in broad sense and genetic advance

Heritability is the heritable portion of phenotypic variance is a good index of transmission of characters from parents to offspring (Falconer, 1981). Estimates of heritability in broad sense ranged from 12.18% for number of tillers per plant to 97.35% for days to maturity (Table 5). 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 phenotype due to the relative small contribution of the environment to the phenotype. Though, 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 bench-mark, heritability estimate was high (>80%) for days to maturity, plant height, finger length and lodging. It was moderate (40 to 80%) for the remaining quantitative traits.

Genetic advance (GA) is another genetic component parameter which 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 8.62 q/ha indicating that whenever we select the best, 5% high yielding genotypes as parents, mean grain yield of progenies could be improved by 8.62q/ha, that is, mean genotypic value of the new population for grain yield will be improved from 21.93 to 33.55q/ha. Similarly, it will be 5.51 for number of tillers per plant, 13.43 for number of fingers per plant, 23.22cm for finger length and 158.25 cm for plant height (Table 5). Maximum genetic advance as percentage of mean (GAM) at 5% selection intensity was recorded for lodging (643.23%), finger length (91.15%), plant height (46.81), followed by grain yield (39.29%). It was minimum for number of tillers per plant (8.20%) and days to maturity (18.04%).

High heritability estimates along with the high genetic advance is usually more helpful in predicting gain under selection than heritability estimates alone (Johnson et al., 1955).

Table 1. Studied experimental materials of finger millet.

Treatment	Sources	Remark
PWRFM-1	Advanced from PYT	From landrace collection
PWRFM-2	"	
PWRFM-3	"	
PWRFM-4	"	
PWRFM-5	"	
PWRFM-6	"	
PWRFM-7	"	
PWRFM-8	"	
PWRFM-9	"	
PWRFM-10	"	
Baruda	Standard check	

Table 2. Formulas used to calculate variances and other components

Variances	Formula
Genotypic variance (σ^2g)	$\sigma^2g = (MSg - MSe) / r$
Phenotypic variance (σ^2p)	$\sigma^2p = \sigma^2g + \sigma^2e$
Genotypic coefficient of variation (GCV)	GCV =($\sqrt{}$ σ^2g/X)100
Phenotypic coefficient of variation (PCV)	PCV =($\sqrt{}$ σ^2p/X)100
Environmental coefficient of variation (ECV)	ECV = (σ^2e/X)100
Broad-sense heritability (H2)	($H^2=(\sigma^2g) / (\sigma^2p) *100$
Genetic advance (GA)	$GA = \sigma p*H*K$
Genetic advance as % of the mean(GAM)	GAM = (GA/X)*100

MSg=Mean square of genotype, MSe=Mean square of error, X=Treatment Mean, K=Selection intensity constant at 5% K=2.056, σ^2e=MSe, σ p=phenotypic standard deviation

Table3. Combined ANOVA for some 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 4. Mean performance of some of the studied agronomic characters of finger millet.

Treatment	DF	DM	PHT (cm)	DISE	NTPP	NFPP	FL (cm)	LDG	GYD(q/ha)
PWRFM-1	114c	163.37abc	107.41bcd	1.12ab	5.2b	11.54a	12.04b	12.58b	21.74bcd
PWRFM-2	107.83e	163.04bc	105.08cde	1.2a	6.33a	10.83abc	12.29b	8.12bc	25.01a
PWRFM-3	117.58a	163.79ab	110.54bc	1.16ab	5.58ab	11.2ab	11.58b	3.12bc	19.59cd
PWRFM-4	111.62d	161.54cd	97.54ef	1.16ab	5.29b	10.75abc	12b	1.04c	22.77ab
PWRFM-5	114.91bc	163.04bc	103cdef	1.2a	5.66ab	10.79abc	12.2b	2.29c	22.37abc
PWRFM-6	116.04ab	165.2a	114.87b	1.2a	5.79ab	10.75abc	12.33b	2.91bc	19.58cd
PWRFM-7	115.41bc	164.04ab	101.2def	1.12ab	5.25b	9.91bcd	11.75b	1.25c	19.17d
PWRFM-8	111.75d	160.58d	99.5ef	1.16ab	4.91b	9.54cd	11.5b	0.83c	21.61bcd
PWRFM-9	106f	154.75e	126.58a	1b	5.45ab	10.04bcd	15.70a	46.79a	21.55bcd
PWRFM-10	106f	155.7e	124.33a	1b	5.37ab	10.33abc	15.25a	49.79a	22.43abc
Baruda	94.66g	145.95f	95.62f	1b	5.2b	8.83d	7c	44.87	25.47a
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

Table 5. Genetic parameters of 11 finger millet advanced lines.

Parameters	DM	PHT	NTPP	NFPP	FL	GYD	LODG	DISE
σ^2g	197.285	602.3	0.0475	2.1525	29.015	17.5625	2437.25	0.037
σ^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

σ^2g=Genotypic variance,^{2}p=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

Fig.1: Dangur/Manbuk and Pawe study areas.

The present study reveals high heritability coupled with high expected genetic advances percent of mean for days to maturity, plant height, finger length and lodging susceptibility. Moderate heritability with relatively higher genetic advance for, number of fingers per plant, grain yield and disease. Thus, these characters could be improved more easily than the other characters.

The better accomplishment and success of genetic improvement in any trait depends on the nature of variability existing for that trait. Hence, an insight into the magnitude of variability present in the gene pool of a crop is of utmost important to a plant breeder for starting careful plant breeding program. Variability in the population is important for disease resistance for example, blast in this case, varietal adaptability and effective selection.

An effort was made in this study to further substantiate the earlier limited studies that indicated Ethiopian finger millet of having wide variability. Regardless of the magnitude, most of the characters studied showed wide range of variability.

This ensured the existence of large amount of variability and potential in the landraces to offer a particular trait of interest. This could be employed in the genetic improvement of finger millet through hybridization and/or selection to boost the current finger millet production and productivity.

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Conflict of interest statement

Authors declare that they have no conflict of interest.

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