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Inheritance and Association of Quantitative Traits in Finger Millet (*Eleusine coracana* Subsp. *Coracana*) Landraces Collected from Eastern and South Eastern Africa

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Abstract: One hundred forty four finger millet landraces were collected from different regions of Ethiopia and some introduced from Eastern and south Eastern African (Kenya, Eritrea, Zambia and Zimbabwe) were planted with six improved varieties in RCBD design at Gute and Arsi Negele during 2011 cropping season to assess variability, heritability, genetic advance and association of quantitative traits. The analysis of variance indicated that the mean square due to location and genotype were highly significant (P#0.01) for all quantitative traits except ear weight for the latter case. Phenotypic coefficient of variation was higher than the corresponding genotypic and genotype by environment coefficient of variations for all traits. This implies, beside the genetic factors, environmental factors have high contributions for the variations observed. The higher heritability coupled with higher genetic advance noted for ear weight (71.14%), lodging index (53.49), finger length (41.94%), thousand grain weights (28.88) and grain yield per plant (26.34) indicated that the ease of phenotype based selection for the improvement of those traits. About 68.4% of the total traits association showed positive correlation. As obtained from path coefficient analysis, the higher and positive direct effect of productive tiller per plant (0.356) and thousand grain weight (0.285) and the positive direct effect of finger length, finger number, ear weight, number of grain per spikelet and culm diameter on grain yield indicated that any genetic improvement on those traits has positive contribution to improve productivity of finger millet.

Key words: *Eleusine coracana* % Heritability % Genetic advance % Path coefficient

INTRODUCTION

Finger millet [*Eleusine coracana* (L.) Gaertn.] is an important traditional food crop in many parts of Africa and Asia. In Africa, it is extensively grown in Uganda, Tanzania, Ethiopia, Kenya, Rwanda, Burundi, Zimbabwe, Zambia and Malawi [1, 2]. Finger millet (*Eleusine coracana* subsp. *Coracana)* and its putative wild ancestor (*E. coracana* subsp. *Africana)* are among the polyploidy [3]. It is extensively cultivated in the tropical and sub-tropical regions of Africa and India and is known to save the lives of poor farmers from starvation at times of extreme drought.

The major attributes of finger millet are therefore, its adaptability to adverse agro-ecological conditions with minimal inputs, tolerant to moisture stress, produced on marginal land where other crops cannot perform and tolerant to acidic soil and termite [4]. Moreover, it has high nutritional value and excellent storage qualities [5]. Therefore, finger millets represent one of the critical plant genetic resources for the agriculture and food security of poor farmers that inhabit arid, infertile and marginal lands.

In Ethiopia, finger millet utilization is deep-rooted in the culture of the people. The grain is used for making the native bread injera, porridge, cake, soup, traditional breakfast called “chachabsa”, malt, local beer and distilled spirit (Areki) alone or in mixture with teff, maize and barley. The straw is used for animal feed or roof thatching. The great merit of finger millet is that it can be stored for period of up to ten years or more without deterioration

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and weevil damage. Consequently, it has played an important role as reserve crop [6]. Nevertheless, its productivity is very low mainly due to lack of improved varieties, management technologies and other biotic and abiotic factors [7-9].

Improvement in any crop usually involves exploiting the genetic variability in specific traits. Simultaneous improvement of these traits depends on the nature and degree of association between traits. Heritability is of interest to plant breeders primarily as a measure of the value of selection for a particular character in various types of progenies and as an index of transmissibility. If the percentage is large, the character is heritable but if it is small, environment is correspondingly prominent in the character expression [10].

Allard [11] indicated that the heritability values for quantitative traits are low mainly due to their sensitivity to environmental factors and genetic advance should be used along with heritability estimates in predicting the efficiency of selection and this high heritability values could be obtained with genotypes having small or large genetic variance but genetic progress would be larger with larger genotypic variance. According to Panes [12], high heritability associated with equally high genetic advance is chiefly due to the additive gene effect but if heritability is mainly due to dominance and epitasis; the genetic gain would be low. In general, genetic variability, heritability and genetic advance are pre-requisites for breeding program and provide opportunity to plant breeder for selecting high yielding genotypes or to combine or transfer genes having desirable traits [13]. Heritability and genetic advance are important factors to determine the success of selection in breeding programs. Pandey and Tiwari [14] indicated the importance of estimating heritability to know the inheritance of quantitative traits as it indicates the genetic gains that may be gained through selection.

Seed yield is a complex character and is considered as the ultimate product of its components. Hence, selection of superior genotypes based on grain yield is difficult due to the integrated structure of plant in which most of the characters are interrelated and being governed by a more number of genes. This necessitates a thorough knowledge on the nature of relationship prevalent between contributory characters and grain yield and the extent of genetic variability. Besides, determination of the interrelationships between various agronomic characters and their direct and indirect effect on grain yield may provide a clue for crop breeders in improving the productivity of the crop and also a pre- requisite to plan a meaningful breeding program. The path coefficient analysis is used to partition the correlation coefficients in to direct and indirect effects and to clarify the relationship between different morphological characters with the seed yield. In path coefficient analysis, grain yield is considered as dependent variable and the remaining traits are considered as independent variables [15]. Lenka and Mishra [16] have suggested scales for path coefficients in rice with values 0.00 to 0.09 as negligible, 0.10 to 0.19 low, 0.20 to 0.29 moderate and 0.30 to 0.99 high path coefficients. Therefore, the present investigation aims to assess the variability, heritability and genetic advance together with the relative contribution of different yield attributes to grain yield and their interrelationships.

MATERIALS AND METHODS

Field experiment was conducted at Arsi Negele research sub site (altitude of 1947 masl, N: 07°19"29.9' and E: 38°39"27.2) and Gute sub site (altitude of 1906 masl, E: 36°38"24.3' and N: 09°00"53.6') in 2011 main cropping season. 144 finger millet landrace collected from Ethiopia (Oromia, Amhara, Tigray, B/Gumuz and SNNP regional state), some introduced germplasms from Kenya, Eritrea, Zambia and Zimbabwe and 6 released varieties were used (Table 1). The design was RCBD with two replication and plot size was single row of 2m long and 50cm between row spacing. Each block was folded into two. Spacing between plants within row was adjusted to 10cm. Ten individual plants were selected randomly per plot, marked before heading and used as a sample for some of the measurable quantitative data collected. Data for quantitative morphological traits such as days to 50% heading, days to 50% maturity, plant height (cm), productive tiller number, finger length (cm), number of finger per main ear, number of grain per spikelet, culm diameter (cm), finger width (cm), lodging index (%), ear weight (g), thousand grain weight (g) and grain yield per plant (g) were recorded following finger millet descriptor [17]. Altitude classes of collection region were grouped in to eight based on the formula suggested by Agrawal [18]: $K = 1+3.32\log_{10}n$ and $W= (L-S)/K$, where K= number of class interval, W= width of class interval, L= the largest value, S= the smallest value and n= sample size (in this case the number of landraces used in the study).

Table 1: Regional and altitudinal distribution of F. millet landraces used for the study

		Altitude classes								
No.	Region/Country	#1241	1242-1382	1383-1523	1524-1664	1665-1805	1806-1946	1947-2087	# 2088	Sub total
1	Amhara/Ethiopia	0	0	0	1	2	16	9	4	32
2	B.Gumuz/Ethiopia	0	1	2	0	1	2	0	0	6
3	Eritrea	0	0	0	1	7	1	0	0	9
4	Kenya	0	0	4	3	0	0	0	0	7
5	Oromia/Ethiopia	0	3	9	4	5	8	2	3	34
6	SNNP/Ethiopia	0	0	3	1	0	0	1	1	6
7	Tigray/Ethiopia	0	0	4	6	4	8	2	3	27
8	Zambia	5	5	0	0	0	0	0	0	10
9	Zimbabwe	0	0	13	0	0	0	0	0	13
Sub total		5	9	35	16	19	35	14	11	144
Released Varieties										6
Grand total										150

Data Analysis

Analysis of Variance: The data collected for all quantitative character were subjected to analysis of variance (ANOVA) using Agrobase (2000) software [19].

Analysis of Phenotypic and Genotypic Coefficient of Variation: The variability of each quantitative trait was estimated by simple statistical measures such as mean, range, phenotypic and genotypic variances and coefficient of variation. The PCV and GCV values of less than 10%, 10%-20% and greater than 20% are considered to be low, intermediate and high, respectively [13]. The phenotypic and genotypic variation and coefficient of variation were calculated following the formula suggested by Singh and Chaundhary [15] and Allard [11] as follows;

Genotypic Variance ($*^2_g$):

$*^2_g = (MS_g - MSgl)/rl$

Where,

Ms_g = Mean square of genotype,
Msgl is the mean square due to genotype by environment interaction,

l = number of locations and
r = number of replications

Genotype by environment interaction variance ($*^2_{gl}$):

$*^2_{gl} = (MSgl-MS_e)/r$

Where MSgl is the mean square due to genotype by environment interaction and

Ms_e = Combined error mean square ($*^2_e$)

Phenotypic Variance ($*^2_p$):

$*^2_p = *^2_g + (*^2_{gl}/l) + (*^2_e/rl)$

Estimates of coefficient of variation were obtained as follows

Phenotypic Coefficient of Variation (PCV):

$PCV = \frac{\sqrt{d^2 p}}{\bar{x}}$ x 100 where, PCV = phenotypic coefficient of variation, $*^2_p$ = phenotypic variance and 0 = population mean for the trait considered.

Genotypic Coefficient of Variation (GCV):

$GCV = \frac{\sqrt{d^2 g}}{\bar{x}}$ x 100 where, GCV = genotypic coefficient of variation, $*^2_g$ = genotypic variance 0 = population mean for the trait considered

Environmental Coefficient of Variations (ECV):

$ECV = \frac{\sqrt{d^2 e}}{\bar{x}}$ x 100

Genotype by Environment Interaction Coefficient of Variation (GECV):

$GECV = \frac{\sqrt{d^2 g^l}}{\bar{x}}$ x 100 Where, $*^2_{gl}$ = genotypic x environment variance 0 = population mean for the trait considered

Broad Sense Heritability (H^2) and Genetic Advance: Broad sense heritability was estimated according to the suggestion of Allard [11]. Heritability per location is calculated by dividing genotypic variances by phenotypic variance:

$$H^2 = (*^2_g/*^2_p) \times 100,$$

Where $*^2_{g=}$ genotypic variance and $*_p = {}^2$phenotypic variance.

When heritability is calculated for combined analysis of two locations, the phenotypic variance combined over location was used.

Hence,

$$H^2 = (*^2_g/*^2_p) \times 100,$$

Where $*^2_{p=} *^2_g + (*^2_{gl}/l) + (*^2_e/rl)$

Expected genetic advance under selection assuming a selection intensity of 5% was computed following the formula developed by Allard [11] as:

$$GA = (K)\ (*_p)\ (H^2),$$

Where

GA = Expected genetic advance,

K = Selection differential that varies depending up on the selection intensity and stands at 2.056 for selecting 5% of the genotypes,

$*_p$ = Phenotypic standard deviation and

H^2 = Heritability (in broad sense).

Genetic advance as percent of mean was obtained as;

$$GA\ (\%\ of\ mean) = \left(\frac{GA}{\bar{x}}\right) \times 100\%:$$

Where

GA = Genetic advance,

0 = Population mean for the trait considered

Estimation of Correlation Coefficient: The Pearson's correlation coefficient between all possible pairs of quantitative traits were tested for their significance using MINITAB14 [20] computer software.

Path Coefficient Analysis: The direct and indirect effects of yield related quantitative traits on grain yield per plant were calculated following the formula suggested by Dewey and Lu [21] as:

$$rij = Pij + G\ rikPkj$$

Where, r_{ij} is mutual association between the independent character (I) and dependent character (j) as measured by the correlation coefficient; Pij is the component of direct effects of the independent character (i) and dependent (j) as measured by the path coefficient and; G *rikpkj* is the summation of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent characters (k).

Residual effect, which determines how best the causal factor accounts for the variability of the dependent factor (grain yield), was estimated by the formula:

$\sqrt{1-R^2}$ Where R^2 = G *Pijrij*, *Pij* = Component of direct effects of the independent character (i) and dependent character (j) as measured by the path coefficient; *rij*, mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient.

RESULT

Analysis of Variance: The combined analysis of variance across locations showed significant location effects for all quantitative traits (Table 2). The genotype mean squares were also significant (P#0.01) for all quantitative traits except ear weight. Genotype by environment mean square was highly significant (P#0.01) for days to 50% maturity, total tiller number, productive tiller number, plant height, finger length, finger number, ear eight and lodging index, but none significant for days to 50% heading, number of grain per spikelet, culm diameter, finger width, thousand seed weight and grain yield per plant.

Phenotypic and Genotypic Coefficient of Variation: Comparatively maximum PCV values were observed for lodging index (44.5%), finger l ength (43.5%), grain yield per plant (33.85%), total number of tiller per plant (30.9%) and productive tiller number per plant (30.5%) and finger number (24.35%). Intermediate PCV values were observed for plant height, finger number per main ear, number of grain per spikelet, culm diameter, finger width and thousand grain weights. However, days to 50% heading and days to maturity exhibit very low PCV values, 3.003 and 9.153%, respectively.

Table 2: Mean squares for 14 quantitative traits of 144 finger millet landraces and 6 released varieties as obtained from combined ANOVA of the two locations (Gute and Arsi Negele)

Source of variation	df	DH	DM	TTN	PTN	PLHT	FL	FN
Location	1	4066.4**	11102.61**	3199.8**	3087.2**	47638.2**	28.12**	36.66**
Genotype	149	315.4**	89.26**	12.02**	11.48**	491.75**	15.1**	4.85**
G x E	149	51.24	44.13**	8.31**	8.20**	122.75**	2.45**	1.21**
Error	298	46.83	13.01	1.10	1.19	35.58	0.94	0.65
CV (%)		7.05	2.29	18.72	19.55	8.68	12.12	11.09
LSD (5%)		7.98	4.21	1.23	1.27	6.95	1.13	0.94
Mean		97.01	157.73	5.61	5.55	68.75	7.98	7.23
source of variation	df	EW	NGPS	CD	FW	TGW	GYPLN	LOG
Location	1	72.45**	134.6**	2129.8**	13.23**	0.02	28912.1**	228150**
Genotype	149	5.32*	1.07**	0.389**	0.08**	0.754**	182.79**	1546.25**
G x E	149	1.09**	0.34	0.32	0.05	0.20	111.90	642.79**
Error	298	0.74	0.37	0.27	0.05	0.17	53.61	82.50
CV (%)		32.44	12.21	22.01	28.72	18.52	35.85	20.57
LSD (5%)		1.00	0.71	0.61	0.26	0.49	8.54	10.59
Mean		2.65	4.39	2.37	0.79	2.26	20.42	44.15

KEY: df= degree of freedom, DH=days to50% heading, DM= days to maturity, TTN=Total tiller number, PTN= productive tiller number, PLHT= plant height, FL= finger length, FN= finger number, EW=ear width, NGPS=number of grain per spikelet, CD=culm diameter, EW= finger weight, TGW=thousand grain weight, GYPLN=grain yield per plant, LOG= lodging index

Table 3: Estimation of the different variances parameters, heritability and genetic advance for 14 major quantitative traits of 144finger millet landraces and 6 released varieties

Traits	Mean	$*^2_g$	$*^2_p$	$*^2_e$	$*^2_{gl}$	GCV	ECV	G x ECV	PCV	H^2 (%)	GA	GA (%)
Days to 50% heading	97.010	66.040	78.850	46.830	2.205	8.377	7.054	1.531	9.153	83.754	15.291	15.762
Days to 50% maturity	157.300	11.283	22.315	13.010	15.560	2.135	2.293	2.508	3.003	50.560	4.911	3.122
Total tiller number	5.610	0.928	3.005	1.103	3.604	17.167	18.721	33.838	30.900	30.865	1.100	19.609
Productive tiller number	5.550	0.820	2.870	1.187	3.507	16.316	19.631	33.740	30.524	28.571	0.995	17.931
Plant height (cm)	68.750	92.250	122.938	35.578	43.586	13.970	8.676	9.603	16.128	75.038	17.106	24.881
Finger length	7.980	3.163	3.775	0.942	0.754	22.285	12.162	10.881	24.348	83.775	3.347	41.937
Finger number per ear	7.230	0.910	1.213	0.647	0.282	13.194	11.125	7.338	15.230	75.052	1.699	23.501
Ear weight (g)	2.650	1.058	1.330	0.737	0.177	38.806	32.396	15.854	43.519	79.511	1.885	71.143
Number of grain per spike	4.390	0.170	0.268	0.371	0.010	9.392	13.875	2.220	11.781	63.551	0.676	15.394
Culm diameter(cm)	2.370	0.018	0.098	0.273	0.024	5.582	22.046	6.468	13.175	17.949	0.115	4.862
Finger width (cm)	0.790	0.006	0.020	0.051	0.003	9.805	28.586	6.329	17.901	30.000	0.087	11.042
Thousand grain weight (g)	2.260	0.138	0.188	0.176	0.012	16.408	18.563	4.847	19.160	73.333	0.653	28.888
Grain yield per plant(g)	20.420	17.673	45.648	53.600	34.150	20.587	35.853	26.440	33.087	38.715	5.378	26.336
Lodging percentage	44.150	225.863	386.563	82.500	280.150	34.040	20.573	37.911	44.533	58.428	23.619	53.497

KEY: $*^2_{g=}$ genotypic variation, $*^2_p$=phenotypic variation, $*^2_e$=environmental variance, $*^2_{gl=}$genotype by location variance ĢCV=genotypic coefficient of variation, G *x* ECV=genotype by environment coefficient of variation, ECV= environmental coefficient of variation, PCV=phenotypic coefficient of variation, H^2= heritability in broader sense, GA=genetic advance and GA % =genetic advance as percentage of mean

An estimates of genotypic coefficient of variation (GCV) were lowest for traits such as days to heading, days to maturity, number of grains per spikelet, culm diameter and finger width. Intermediate GCV values were observed for plant height, total number of tiller per plant, proactive tiller number per plant, finger number per main ear and thousand grain weights. The highest genotype *x* environment interaction coefficient of variation (G x ECV) was obtained for lodging index (37.9%), total number of tiller per plant (33.8%), productive tiller number per plant (33.7%) and grain yield per plant (26.44%). Those traits also have higher GCV value. The G x ECV values for most of the traits considered in this study were found to be less than the GCV values.

Broad Sense Heritability (H^2) and Genetic Advance: Estimates of heritability (H^2) ranged from 17.95% for culm diameter to 83.78% for finger length (Table 3). Hence, the highest heritability estimates were observed for finger length (83.78%), days to heading (83.75%) and ear weight (79.51%). About 64.3% of the traits considered in the current study have heritability percentage greater than 50%. However, the heritability value was not accompanied by genetic advance. Genetic advance was least for days to maturity (3.122%) and highest for ear weight (71.14%). Relatively higher heritability followed by higher genetic advance were recorded for ear weight, lodging index, finger length, thousand grain weight and grain yield per plant. Days to maturity, culm diameter, finger weight,

Table 4: Pearson correlation coefficient for 14 quantitative traits of 144 finger millet populations and 6 improved varieties

Traits	DH	DM	TTN	PTN	PLHT	FL	FN	EW	FLL	NGPS	CD	FW	TGW	GYPL
DH	1.00	0.60**	-0.05	-0.04	0.38**	-0.26**	-0.01	0.28**	0.35**	0.08	0.16	0.09	-0.28**	-0.42**
DM		1.00	-0.16	-0.16	0.31**	-0.14	0.13	0.27**	0.34**	-0.07	0.18*	0.04	-0.07	-0.14
TTN			1.00	0.99**	0.16	0.38**	0.03	-0.51**	0.10	-0.08	-0.31**	-0.33**	-0.33**	0.28**
PTN				1.00	0.17*	0.38**	0.03	-0.51**	0.10	-0.09	-0.31**	-0.34**	-0.33**	0.28**
PLHT					1.00	0.33**	0.43**	0.02	0.61**	-0.08	0.31**	0.02	-0.11	0.13
FL						1.00	0.28**	-0.57**	0.28**	-0.14	-0.14	-0.34**	-0.24**	0.33**
FN							1.00	-0.02	0.27**	-0.13	0.10	-0.16	-0.23**	0.21**
EW								1.00	0.05	0.26**	0.48**	0.54**	0.43**	0.10
FLL									1.00	-0.10	0.17*	0.00	-0.16*	0.10
NGPS										1.00	0.14	0.03	0.15	0.04
CD											1.00	0.39**	0.33**	0.04
FW												1.00	0.33**	0.05
TGW													1.00	0.23**
GYPL														1.00

KEY: DH=days to heading, DM= days to maturity, TTN=Total tiller number, PTN= productive tiller number, PLHT= plant height, FL= finger length (cm), FN= finger number, EW=ear weight (g), NGPS=number of grain per spikelet, CD=culm diameter(cm), FW=finger width(cm), TGW=thousand grain weight(gram), GYPL=grain yield per plant(gram), LOG= lodging index, **= highly significant (P#0.01), *= significant (P#0.05)

Table 5: Estimate of direct (bold and diagonal) and indirect effect of 13 finger millet quantitative traits on grain yield per plant on the basis of phenotypic correlation

Traits	DH	DM	PTN	PLHT	FL	FN	CB	EW	NGPS	CD	TGW	LODG
DH	-0.386	0.087	-0.015	-0.040	-0.007	-0.001	-0.012	0.038	0.009	0.006	-0.079	-0.126
DM	-0.232	-0.144	-0.056	-0.032	-0.004	0.022	-0.001	0.037	0.004	0.007	-0.021	-0.080
PTN	0.016	-0.023	0.356	-0.017	0.010	0.006	0.001	-0.070	-0.038	-0.012	-0.093	0.113
PLHT	-0.147	0.045	0.059	-0.104	0.009	0.074	0.009	0.003	-0.014	0.011	-0.031	0.031
FL	0.102	-0.020	0.137	-0.034	0.027	0.048	0.015	-0.077	-0.052	-0.005	-0.069	0.199
FN	0.003	0.018	0.012	-0.045	0.008	0.171	0.013	-0.003	-0.020	0.004	-0.065	0.074
CB	0.082	-0.002	0.009	-0.016	0.007	0.039	0.056	-0.030	-0.027	0.002	-0.003	0.064
EW	-0.109	0.039	-0.182	-0.002	-0.015	-0.004	-0.012	0.136	0.079	0.018	0.121	-0.197
NGPS	-0.027	0.005	-0.108	0.012	-0.011	-0.027	-0.012	0.085	0.125	0.011	0.094	-0.148
CD	-0.060	0.025	-0.112	-0.032	-0.004	0.018	0.004	0.066	0.036	0.037	0.095	-0.096
TGW	0.107	-0.011	-0.116	0.011	-0.007	-0.039	-0.001	0.058	0.041	0.012	0.285	-0.085
LODG	0.168	-0.040	0.139	-0.011	0.019	0.044	0.012	-0.093	-0.064	-0.012	-0.083	-0.290

Residual effect=86.82%

KEY: DH=days to heading, DM= days to maturity, PTN= productive tiller number, PLHT= plant height, FL= finger length (cm), FN= finger number, CB=Culm branch, EW=ear weight (g), NGPS=number of grain per spikelet, CD=culm diameter (cm), TGW=thousand grain weight(gram), LOG= lodging index

number of grain per spikelet, days to heading, total tiller number and productive tiller number have lower percentage of genetic advance.

Pearson Correlation Coefficient: The result of analysis of phenotypic correlation coefficients based on the mean of 144 finger millet landraces and 6 released varieties for 14 quantitative traits showed that about 68.4% of the total traits showed positive correlation (Table 4). Finger length (0.33), finger number (0.21), thousand grain weight (0.23) and tiller number (0.28) has positive and significant (P# 0.01) correlation with grain yield per plant. Days to heading and days to maturity have negative correlation with grain yield per plant. Even if it is not significant, number of grains per spikelet has negatively associated with tiller number, finger length, finger number and plant height.

Path Coefficient Analysis: Path coefficient analyses showing direct and indirect effect of some morphological traits on grain yield per plant were given in Table 5. High and positive direct effects on grain yield per plant were obtained from productive tiller number (0.356) and moderate direct effect was obtained from thousand grain weight (0.285). Though none significant, traits such as number of grain per spikelet, culm diameter, finger length, finger number, culm branch and ear weight have positive direct effect on grain yield. Days to heading (-0.386), days to maturity (-0.144), lodging index (-0.290) and plant height (-0.104) have negative direct effect on grain yield. All morphological traits considered in this study have direct and indirect effect on grain yield with variable degree (Table 5).

DISCUSSION

The significant difference between genotypes for all quantitative traits except ear weight as observed from analysis of variance indicated that the landraces tested are highly variable and hence there is an opportunity for plant breeder to undertake further breeding activities. Similar results were reported in previous studies [6, 22-24]. Several authors also reported that the mean square due to location and genotypes were highly significant for quantitative traits considered in their study [25-28].

Phenotypic and genotypic coefficient of variation was very low for days to 50% heading and days to maturity. The most probable reason could be the phenotypic plasticity occurring in those traits is the main source of variation than the genetic variance [33]. Such result also indicated that selection is not effective for those traits because of the narrower genetic variability. Sharathbabu *et al*. [29] evaluated 19 white seeded finger millet genotypes and three standard checks and reported that very low value of PCV (6.46 and 8.34%) was observed for days to maturity and days to 50% heading, respectively. Low PCV and GCV were observed in the trait days to maturity for 230 finger millet germplasms [30]. Lower GCV values for days to heading and days to maturity were reported in different crops by several authors [6, 26, 27, 29, 30]. Most of the quantitative traits considered in this study had medium to high GCV values. This implies that there is a potential natural genetic variability among finger millet landraces and hence varietal improvement through conventional breeding.

About 64.3% of the traits considered in the current study have heritability percentage greater than 50%. However, the heritability value was not accompanied by genetic advance. Such result can be mainly due to dominance and epitasis [12]. The higher heritability followed by higher genetic advance recorded for ear weight, lodging index, finger length, thousand grain weight and grain yield per plant implied that the predominance of additive gene effects in controlling these traits, early and simple selection could be exercised due to fixable additive gene effects. Grain yield is largely dependent on those major traits and hence the result implies the possibility to increase the crop for its yielding capacity and its ability to resist lodging. High heritability coupled with high expected genetic gain may result due to high additive gene effect and thus selection applied on such traits lead to yield improvement [12].

Similarly, Ganapathy *et al*. [30] reported high heritability coupled with high genetic advance observed in finger length and seed yield per plant. John [34] also noted that high heritability coupled with high genetic advance as percentage of mean was observed for number of fingers per ear and ear weight. The lower percentage of genetic advance for days to maturity, culm diameter, finger weight, number of grain per spikelet, days to heading, total tiller number and productive tiller number in the present study implied that most of the variations for these traits were environmental and thus leading to low heritability and low expected genetic gains from selection. Similar results were reported for days to maturity in maize inbred-line by Ojo [35]. In the contrary, finger numbers per ear, days to 50% heading, plant height and productive tillers per plant were among traits with higher heritability and genetic advance [30].

About 68.4% of the total traits association showed positive and this positive correlation could be resulted from the presence of common genetic elements that controls the characters to the same direction. Positive significant correlation due to effect of genes can be the result of the presence of strong coupling linkage between their genes or the characters may be the result of pleiotropic genes that control these characters in the same direction [36]. The positive and significant correlation coefficient observed between finger length, finger number, thousand-grain weight and tiller number with grain yield per plant implied that there is an implication to combat the low yielding ability of finger millets through conventional improvement of those traits. Sharathbabu *et al*. [29] reported that grain yield per plant had strong positive association with finger number per ear and ear weight per plant across all locations and hence, simultaneous selection for these traits will be more reliable to develop high yielding genotypes in finger millet. Similar result were also noted by Ayana [37].

Days to heading and days to maturity have negative correlation with grain yield per plant. As observed from the field and the data, most of late maturing finger millet genotypes have open ear type, narrow finger width, few spikelets per finger and lower grain per spikelet. As tillering capacity increases, number of fertile floret per spikelet, finger width, ear weight and thousand grain weights would decreases. This can probably be explained as the available resources were used up in the production of profuse vegetative growth as the expense of material production that should be stored in the seeds. In addition, the different genes or pleiotrophic genes that have dominance on the character may control the character in different directions [36]. Studies on different crops also reported that days to maturity has negative correlation to grain yield [38, 39].

Even if it is not significant, number of grains per spikelet has negatively associated with tiller number, finger length, finger number and plant height. Finger millet landraces that have characteristics of wild relatives do have narrow finger width, long plant height, late maturing, high in tillering capacity and longer in finger length but few in number of spikelet per finger, lower seed number per spikelet and lower in grain yield. As observed from path coefficient analysis, the higher and positive direct effect of productive tiller per plant and thousand grain weight; and the positive direct effect of finger length, finger number, ear weight, number of grain per spikelet and culm diameter on grain yield indicated that any genetic improvement on those traits has positive contribution to improve productivity of finger millet.

In line with the present study, Sharathbabu *et al.* [29] reported that number of productive tillers per plant have positive direct influence on grain yield per plant. Das *et al*. [40] reported that selection for hundred seed weight in *Jatropha* could increase grain yield as it has positive correlation and positive direct effect on grain yield. The negative direct effect on grain yield observed from days to heading, days to maturity, lodging index and plant height could probably gave a clue that improvement for grain can be attained if breeder use finger millet genotypes that have early maturing characters and optimum plant height that can resist lodging. In other words, genetic and environmental factors that delays the maturity of the crop and increase plant height and lodging index should be given due attention in variety improvement procedures.

In line with this study, Wolie and Dessalegn [41] found that plant height, days to heading and days to maturity had negative direct effect on grain yield, but they have positive indirect effect on grain yield mainly through their high and positive indirect effect with biomass yield. All quantitative traits considered in the present study have direct and indirect effect on grain yield in variable degrees. This indicates that phenotypic and genotypic decrement or increments of those traits have direct or indirect contribution for the decrease or an increase of grain yield. Singh and chaundhary [15] suggested that indirect effect seem to be the cause of correlation and hence, these indirect causal factors (traits) should be considered simultaneously for selection.

CONCLUSIONS

Varietal improvement for grain yield is mainly dependent upon the extent of genetic variability present in the population. Accordingly, the significant variation between genotypes for most of the quantitative traits considered in the present study implied that the presence of diversified finger millet landraces in Ethiopia in particular and East and south eastern Africa in general. It also indicates that the possibility to improve productivity of this hard tolerant crop to cope-up with dramatic change of climate and edaphic factors. The higher heritability followed by higher genetic advance recorded for grain yield and yield related traits such as ear weight, finger length and thousand grain weight; the positive association of those and other traits on grain yield would give a clue for area of focus to improve productivity of the crop.

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