Full Length Research Paper

Correlation and path coefficient analyses of some yield related traits in finger millet (*Eleusine coracana* (L.) Gaertn.) germplasms in northwest Ethiopia

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The associations among yield components and their direct and indirect influence on the grain yield of finger millet were investigated. For this purpose, eighty-eight finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes were tested using an augmented randomized complete block experimental design with two replications at Adet Agricultural Research Center in 2008. Accordingly, phenotypic and genotypic correlations among the traits and their path coefficients were estimated. Grain yield was significantly correlated with its component characters like plant height (r_p=0.446** and r_g=0.574**), number of ears per plant (r_p=0.364** and r_g=0.443**), number of fingers per ear (r_p=0.329** and r_g=0.532**), finger length (r_p=0.361** and r_g=0.426**), biomass yield (r_p and r_g=0.839**), harvest index (r_p=0.336** and r_g=0.476**) and thousand kernel weight (r_p=0.225* and r_g=0.267*). Phenotypic path analysis showed biomass yield (0.835) and finger length (0.159), number of fingers per ear (0.016), and number of ears per plant (0.038) to exert positive direct effects on grain yield, while plant height, days to heading and days to maturity exhibited negative direct effects. Genotypic path analysis also revealed that biomass yield (2.240), number of tillers per plant (0.359) and finger length (0.242) exerted positive direct effects on grain yield. Thus, the correlation analysis showed plant height, number of ears per plant, number of fingers per ear, finger length, biomass yield, harvest index and 1000 kernel weight to be important yield components that can be used to improve the yield potential of finger millet genotypes.

Key words: Finger millet, path coefficient, yield related traits, correlation.

INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn.) is one of the most important small millets 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 and 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 sprit 'arekie' and a number of other uses. Finger millet has also a high-yielding potential though yields are variable (compared to other cereals) but are generally good and needs improvement.

Improvement in any crop usually involves exploiting the genetic variability in specific traits and associations among them. Simultaneous improvement of these traits depends on the nature and degree of association between traits (Mnyenyembe and Gupta, 1998). Knowledge of the

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Abbreviations: ANOVA, Analysis of variance; **PH,** plant height (gm); **TPP,** number of tillers per plant; **EPP,** number of ears per plant; **FL,** finger length (gm); **DH,** days to 50% heading; **DM,** days to 50% maturity; **BMY,** biomass yield per hectare (kg); **GY,** grain yield per hectare (kg); **HI,** harvest index; **TKW,** thousand kernel weight (gm); **LO,** lodging %; **HBL,** head blast severity; **df,** degrees of freedom; **CV%,** coefficient of variation; **BMYP,** biomass yield per plot (gm).

extent and pattern of variability and character association present in a population of a given crop is absolutely essential for further improvement of the crop. This may arise from linkage or from developmental genetic interaction, with or without a purely phenotypic component (Simmonds, 1986). To facilitate selection in breeding for high yield, therefore, it is logical to examine various components and give more attention to those having the greatest influence on yield. In correlation studies, it is customary to emphasize a large number of varieties and use the correlation to establish an index in deciding the direction of selection.

The ultimate expression of yield in crop plants is usually dependent upon the action and interaction of a number of important characters (Elias, 1992). This is due to the fact that in the integrated plant structure, most of the characters are interrelated with one another and often a change in one is likely to influence the other, so that the net gain obtained by selection of one may be counterbalanced or even negated by a simultaneous change in the other. Correlation, therefore, is helpful in determining the component characters of a complex trait, like yield. With more variables in correlation studies, indirect associations become more complex and important; consequently, a correlation study coupled with a path analysis is more effective tool in the study of yield attributing characters. Yield is a complex entity and is influenced by its various components directly as well as indirectly via other characters. For recommending the reliable selection indices, these effects and interrelationships must be analyzed (Singh et al., 1976). Such studies are useful in disclosing the magnitude and direction of these relationships between the different characters and yield as well as among the characters themselves. However, this information on finger millet collections under diversified environmental condition of Ethiopia is limited. Hence this study was done with the objectives of finding associations among finger millet traits and assessing the direct and indirect contribution of each trait to grain yield of finger millet.

MATERIALS AND METHODS

Experimental site and Design

The experiment was conducted on eighty-eight finger millet germplasms including the local and standard checks collected from the institute of biodiversity in 2008 at Adet representing the agro-ecology of finger millet growing areas of Gojam, 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 Gojam in 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°C 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 had two rows of 0.75 m apart and drilled in 5 m row length. The plot area was 7.5 m^2 (0.75 m × 2 rows × 5 m) and the distance between blocks 0.75 m. The seed and fertilizer rates used

were 10 kg ha^{-1} and 46/41 kg ha^{-1} N/P$_2$O$_5$, respectively. Half the rate of urea and all DAP was applied at planting time while half of the rate of urea at tilling or after first weeding. Hand-weeding was practiced twice starting from 35 days after planting depending on the weed infestation. 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.

Analysis of variance (ANOVA)

The mean value of the recorded data was subjected to ANOVA using the statistical analysis procedures of Sharma, 1998.

Estimation of phenotypic and genotypic correlations

Phenotypic and genotypic correlations between yield and yield related traits were estimated using the method described by Miller et al. (1958):

$$rp_{xy} = \frac{Covp_{xy}}{\sqrt{Vp_x Vp_y}}$$

where, r_{pxy}, phenotypic correlation coefficient between characters x and y; Cov_{pxy}, phenotypic covariance between characters x and y; Vp_x, phenotypic variance for character x; Vp_y, phenotypic variance for character y.

$$rg_{xy} = \frac{Covg_{xy}}{\sqrt{Vg_x Vg_y}}$$

where, rg_{xy}, Genotypic correlation coefficient between characters x and y; $Covg_{xy}$, genotypic covariance between characters x and y; Vg_x, genotypic variance for character x; Vg_y, genotypic variance for character y.

The coefficients of correlations at phenotypic level were tested for their significance by comparing the value of correlation coefficient with tabulated r-value at g-2 degrees of freedom. However, the coefficients of correlations at genotypic level were tested for their significance using the formula described by Robertson (1959) as indicated:

$$t = \frac{(rg_{xy})}{SEg_{xy}}$$

The calculated 't' value was compared with the tabulated 't' value at g-2 degree of freedom at 5% level of significance, where, g = number of genotypes.

Table 1. Analysis of variance of thirteen quantitative characters of eighty-eight finger miller genotypes.

Source of variation	Df	Mean square						
		PH	TPP	EPP	FPE	FL	DH	DM
Block	3	52.99	3.42	34.06	0.17	0.04	4.52	11.15
All entries	87	94.54	4.85*	27.58**	3.04**	3.05**	67.38**	31.65**
Test varieties	83	95.81	3.69*	17.42**	2.75**	2.64**	56.10**	29.38*
Checks	3	152.41	25.75**	254.73**	2.83*	14.66**	298.62**	98.17**
Checks vs. varieties	1	184.31	38.93**	189.45**	28.16**	2.14**	309.88**	20.86
Error	9	43.44	1.36	0.95	0.44	0.16	2.69	6.85
Total	99	88.64	4.49	25.36	2.72	2.70	59.59	28.77
CV (%)		7.59	16.11	8.46	9.51	6.07	1.43	1.55

Source of variation	Df	Mean square					
		BMY	GY	HI	TKW	Lodging	HBL
Block	3	3672216.00	225169.00	0.031	0.13549	6.770	15.85
All Entries	87	42703311.44**	332888.00**	0.184	0.40561**	673.14**	248.10**
Test Varieties	83	4121534.00	283348.00*	0.163	0.28597**	357.41**	232.39**
Checks	3	3983331.00	1412120.00**	0.801**	1.28904**	6695.80**	332.26**
Checks vs. Varieties	1	17480766.00	1206981.00**	0.018	7.68528**	8810.46**	1300.00**
Error	9	5266293.00	72657.00	0.097	0.02984	7.250	30.77
Total	99	38117.18	305966.00	0.171	0.363263	592.41	221.31
CV (%)		30.05	13.95	24.49	5.30	6.73	17.46

*, Significant at p< 0.05; **, significant at p<0.01. PH, plant height (gm); TPP, number of tillers per plant; EPP, number of ears per plant; FL, finger length (gm); DH, days to 50% heading; DM, days to 50% maturity; BMY, biomass yield per hectare (kg); GY; grain yield per hectare (kg); HI, harvest index; TKW, thousand kernel weight (gm); LO, lodging %; HBL, head blast severity; df, degrees of freedom; CV%, coefficient of variation.

Path coefficient analysis

The direct and indirect effects of yield related traits on yield per plot was worked out through path coefficient analysis. The analysis was done following the method suggested by Dewey and Lu (1959). The formula was as follows:

$$r_{ij} = P_{ij} + \sum r_{ik} p_{kj}$$

where, r_{ij}, Mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient; P_{ij}, component of direct effects of the independent character (i) and dependent (j) as measured by the path coefficient and; $\sum r_{ik} p_{kj}$, summation of components of indirect effect of a given independent character (i) on the given dependent character (j) via all other independent characters (k).

Residual effect was estimated by the formula:

$$\sqrt{1 - R^2}$$

where, $R^2 = \sum p_{ij} r_{ij}$

P_{ij}, Component of direct effects of the independent character (i) and dependent character (j) as measured by the path coefficient;

r_{ij}, mutual association between the independent character (i) and dependent character (j) as measured by the correlation coefficient.

RESULTS

Analysis of variance

The result of ANOVA of thirteen yield related traits for the eighty-eight genotypes is presented in Table 1. The ANOVA showed significant differences (p<0.05) among the tested genotypes for all the characters except for plant height and biomass yield indicating the presence of variability which can be exploited through selection.

Association of characters:

Estimates of phenotypic and genotypic correlation coefficient between each pair of characters are presented in Table 2. The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except few cases, which indicate the presence of inherent association among various characters.

Grain yield per plot showed positive and significant phenotypic association with plant height, number of ears

Table 2. Phenotypic (upper value) and genotypic (lower value) correlation coefficients yield related traits for the 88 finger millet genotypes.

Trait		TPP	EPP	FPE	FL	DH	DM	BMYP	HI	TKW	LO	HBL	GY
PH	pcc	0.093	0.278**	0.387**	0.366**	0.071	0.012	0.550**	-0.156	-0.022	0.073	0.067	0.446**
	gcc	0.192	0.349**	0.529**	0.424**	0.075	-0.033	0.820**	-0.283**	-0.040	0.095	0.054	0.574**
TPP	pcc		0.258*	-0.025	0.337**	0.121	0.151	0.087	0.066	-0.104	0.234*	-0.043	0.105
	gcc		0.426**	0.107	0.475**	0.168	0.272*	0.166	0.235*	-0.181	0.323**	-0.205	0.254*
EPP	pcc			0.257*	0.144	-0.213*	-0.062	0.307**	0.100	-0.222*	0.275*	0.399**	0.364**
	gcc			0.373**	0.148	-0.250*	-0.117	0.413**	0.109	-0.250*	0.301**	0.571**	0.443**
FPE	pcc				0.148	-0.061	-0.069	0.333**	-0.006	-0.250*	0.042	0.233*	0.329**
	gcc				0.221*	-0.121	-0.121	0.633**	-0.080	-0.334**	0.053	0.477**	0.532**
FL	pcc					0.007	0.144	0.258*	0.191	-0.163	0.393**	-0.019	0.361**
	gcc					0.006	0.149	0.339**	0.222*	-0.177	0.404**	0.028	0.426**
DH	pcc						0.494**	0.102	-0.433**	-0.207	-0.248*	-0.528**	-0.155
	gcc						0.604**	0.116	-0.568**	-0.234*	-0.276*	-0.809**	-0.223*
DM	pcc							0.237*	-0.221*	-0.129	-0.218*	-0.365**	0.099
	gcc							0.297**	-0.304**	-0.176	-0.235*	-0.572**	0.087
BMYP	pcc								-0.215*	-0.215*	-0.064	0.058	0.839**
	gcc								-0.067	-0.275**	-0.091	0.084	0.839**
HI	pcc									0.000	0.325**	0.133	0.336**
	gcc									0.011	0.387**	0.287**	0.476**
TKW	pcc										-0.064	-0.082	0.225*
	gcc										-0.074	-0.103	0.267*
LO	pcc											0.242*	0.124
	gcc											0.305**	0.133
HBL	pcc												-0.138
	gcc												-0.242*

*, ** Significant at p<0.05 and p<0.01, respectively. 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; BMYP, biomass yield per plot (gm); GY, grain yield per plot (gm); HI, harvest index; TKW, thousand kernel weight (gm); LO, lodging %; HBL, head blast severity %.

per plant, number of fingers per ear, finger length, biomass yield, harvest index and 1000 kernel weights. At genotypic level, grain yield per plot had also positive and high correlation with plant height, number of tillers per plant, number of ears per plant, number of fingers per ear, finger length, biomass yield, harvest index and 1000 kernel weight except for days to maturity and lodging susceptibility.

Grain yield per plot had negative genotypic and phenotypic correlation with days to heading and head blast severity while it is significant with head blast severity (Table 2). Muhammad et al. (2004) also reported

negative association of grain yield with days to flowering on chick pea.

Path coefficient analysis

The nine characters were taken on the basis of genotypic and phenotypic correlations and partitioned into direct and indirect effects using grain yield as a dependent variable. The phenotypic path analysis (Table 3) revealed that, biomass yield, finger length, number of ears per plant, and number of fingers per ear exerted positive

Table 3. Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level of yield related traits in finger millet genotypes.

Trait	PH	TPP	EPP	FPE	FL	DH	DM	BMYP	TKW	r_P
PH	-0.074	0.000	0.011	0.006	0.058	-0.017	0.000	0.460	0.001	0.446
TPP	-0.007	0.000	0.010	0.000	0.054	-0.028	-0.001	0.072	0.006	0.105
EPP	-0.020	0.000	0.038	0.004	0.023	0.050	0.001	0.256	0.013	0.364
FPE	-0.028	0.000	0.010	0.016	0.023	0.014	0.001	0.278	0.014	0.329
FL	-0.027	0.000	0.005	0.002	0.159	-0.002	-0.001	0.215	0.009	0.361
DH	-0.005	0.000	-0.008	-0.001	0.001	-0.234	-0.005	0.085	0.012	-0.155
DM	-0.001	0.000	-0.002	-0.001	0.023	-0.115	-0.010	0.198	0.007	0.099
BMYP	-0.041	0.000	0.012	0.005	0.041	-0.024	-0.002	0.835	0.012	0.839
TKW	0.002	0.000	-0.008	-0.004	-0.026	0.048	0.001	-0.180	-0.058	-0.225

Residual, 0.2072;

direct effect on grain yield. However, plant height, days to heading, days to maturity and 1000 kernel weights had negative direct effect on grain yield. Plant height, days to heading, days to maturity and thousand kernel weights contributed to grain yield mainly via their high and positive indirect effect with biomass yield.

The result also revealed that all characters included in the path analysis except 1000 kernel weight contributed negatively to grain yield indirectly via plant height. While in the reverse direction, all the characters had positive indirect effect to grain yield via thousand kernel weight.

Genotypic path analysis (Table 4) also revealed that biomass yield, number of tillers per plant, finger length and thousand kernel weight exerted positive direct effect on grain yield while days to heading, days to maturity, number of ears per plant, plant height and number of fingers per ear had negative direct effects on grain yield.

Number of ears per plant, which otherwise had the highest and positive genotypic correlation with grain yield, recorded negative and low direct effect. Its high indirect effect via biomass yield may be the cause of the genotypic correlation with grain yield. All the characters in the genotypic path exhibited a positive indirect effect of the grain yield via number of tillers per plant, finger length and biomass yield except 1000 kernel weight which was negative to grain yield via these characters.

DISCUSSION

The fact that the tested genotypes showed significant difference (P< 0.05) for most of the characters in the analysis of variance indicates that the presence of variability which can be exploited through selection (Table 1).

It is commonly known that grain yield is the result of many characters which are interdependent and breeders always look for genetic variation among these characters to select desirable types that are highly associated among them and with grain yield. The analysis of the

relationship among these characters and their association with grain yield is also essential to establish selection criteria (Singh et al., 1990).

The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except few cases. A similar finding was also reported by Hussain et al. (2003) on pearl millet.

The study showed that grain yield per plot had positive and significant genotypic association with plant height, number of tillers per plant, number of ears per plant, number of fingers per ear, finger length, biomass yield, harvest index and 1000 kernel weight. This indicates that increase in these characters may result in increase in grain yield. Singh et al. (1990) and Tazeen et al. (2009) found that grain yield correlated positively with, biomass, and harvest index. Sharathbabu et al. (2008) found association with finger number and finger length on white ragi while Nandini et al. (2010) found association with plant height, tiller number and 1000 kernel weight on finger millet. Therefore, any improvement of these characters would result in a substantial increment on grain yield of finger millet.

Grain yield per plot had negative genotypic and phenotypic correlation with days to heading. Similarly, Bezaweletaw et al. (2006), found finger millet grain yield per plant to be significantly negatively correlated to days to heading and days to maturity. However, Singh et al. (1990) found positive association of days to 50% heading and days to maturity with grain yield in chickpea.

The positive and significant association of biomass yield with plant height, number of ears per plant, number of fingers per ear, finger length and days to maturity, indicate that these traits can be improved simultaneously through selection. Harvest index showed positive and significant genotypic correlation with number of tillers per plant and finger length, which indicate increasing of these traits increase harvest index and grain yield too.

When more characters are involved in a correlation study, it becomes difficult to ascertain the characters

Table 4. Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level of yield-related traits in finger millet genotypes.

Trait	PH	TPP	EPP	FPE	FL	DH	DM	BMYP	TKW	r_g
PH	-1.203	0.069	-0.073	-0.175	0.102	-0.005	0.025	1.837	-0.004	0.574
TPP	-0.231	0.359	-0.089	-0.036	0.115	-0.011	-0.207	0.372	-0.018	0.254
EPP	-0.419	0.153	-0.209	-0.124	0.036	0.017	0.089	0.925	-0.024	0.443
FPE	-0.636	0.038	-0.078	-0.332	0.053	0.008	0.092	1.418	-0.033	0.532
FL	-0.510	0.170	-0.031	-0.073	0.242	0.000	-0.113	0.760	-0.017	0.426
DH	-0.090	0.060	0.052	0.040	0.001	-0.066	-0.459	0.260	-0.023	-0.223
DM	0.039	0.098	0.024	0.040	0.036	-0.040	-0.759	0.665	-0.017	0.087
BMYP	-0.986	0.060	-0.086	-0.210	0.082	-0.008	-0.225	2.240	-0.027	0.839
TKW	0.048	-0.065	0.052	0.111	-0.043	0.016	0.134	-0.617	0.098	-0.267

Residual, 0.0446.

which really contribute toward yield. On the basis of path analysis comprised nine out of the thirteen characters that are believed to have relationships with grain yield, biomass yield followed by finger length and ear number exerted positive direct effect on grain yield phenotypically in line with the results of Sharathbabu et al. (2008). This indicates improvement of these traits also improve the grain yield.

Plant height, days to heading, days to maturity and thousand kernel weights contributed to grain yield mainly via their high and positive indirect effect with biomass yield, that is, improving these traits also improve the biomass yield which indirectly improve the grain yield of finger millet. The phenotypic residual effect (0.2072) indicated that the characters included in the path analysis explained 79.28% of the phenotypic variation in grain yield (Table 3).

Genotypic path analysis also revealed that biomass yield followed by number of tillers per plant, finger length and thousand kernel weight exerted positive direct effect on grain yield. However, days to heading, days to maturity, number of ears per plant, plant height and number of fingers per ear had showed negative direct effects on grain yield (Table 4). Biomass yield, number of tillers per plant and finger length, which show positive genotypic correlation with grain yield, had also exerted considerable direct effects on grain yield. Number of ears per plant which otherwise had the highest and positive genotypic correlation with grain yield, recorded negative and low direct effect. Its high indirect effect via biomass yield may be the cause of the genotypic correlation with grain yield. The residual (0.0446) (Table 4) indicates that characters which are included in the genotypic path analysis explained 95.54% of the total genetic variations in grain yield.

Lenka and Mishra (1973) 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, 0.30 to 0.99 high and more than 1.00 as very high path coefficients. Accordingly, in this study, grain yield had

high direct positive phenotypic path coefficients (Table 3) with biomass and indirectly with plant height via biomass, respectively, while it had high direct positive genotypic path coefficient (Table 4) with number of tillers per plant and biomass yield. This implied that a small improvement in biomass and tiller number will result high improvement in the grain yield.

Conclusion

Correlation analysis showed that grain yield per plot had a positive and significant phenotypic and genotypic association with plant height, number of ears per plant, number of fingers per ear, finger length, and biomass yield and harvest index. Thus, these are important characters for finer millet improvement.

The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except for a few cases, which indicate the presence of inherent association among various characters.

Path analysis indicated that biomass yield, number of tillers per plant and finger length, number of ears per plant, and number of fingers per ear and 1000 kernel weights could be used as indirect selection criteria for better grain yield.

Thus, there is an opportunity to bring about improvement of the crop yield through direct and indirect selection as well as improving of these characters through hybridization using the germplasm collections in Ethiopia. This finding, being the result of one year and one location, it is recommended that the experiment be repeated at more locations and over more years to confirm the obtained results.

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