Int.J.Curr.Res.Aca.Rev.2024; 12(8): 79-83

International Journal of Current Research and Academic Review
ISSN: 2347-3215 (Online) Volume 12 Number 8 (August-2024)
Journal homepage: http://www.ijcrar.com

doi: https://doi.org/10.20546/ijcrar.2024.1208.008

Trait Association and Path Coefficient Study for Yield and Yield Related Components of Finger Millet (*Eleusine coracana* L.) Genotypes in Northwestern Ethiopia

Tafere Mulualem Emrey*

Pawe Agricultural Research center, Pawe, Ethiopia

**Corresponding author*

Abstract

The present study was carried out for three years, from 2011 to 2013, during the main cropping season, with the goal of finding the relationships between yield-contributing traits and their direct and indirect effects on yield. The experiment was carried out using a randomized complete block design (RCBD) with four replications at two sites. Calculations made included correlation coefficient, direct and indirect effects using ten distinct genotypes and one standard check named, *Baruda*. The number of fingers per plant (rp = 0.409), stand count at harvest (rp = 0.468), and disease score (rp = -0.444) all had significant positive and negative phenotypic associations. Plant height (0.008), number of tillers per plot (0.053), number of fingers per plot (0.237), and finger length were all positively correlated with grain yield. Thus, from this study correlation and path coefficient analysis were critical in determining which attribute has a direct impact on the yield of finger millet genotypes.

Article Info

Received: 08 June 2024
Accepted: 22 July 2024
Available Online: 20 August 2024

Keywords

Character, Finger millet, Path analysis, Yield, Ethiopia.

Introduction

Finger millet (*Eleusine coracana* L.) is widely grown in dry and semi-arid regions of Africa and South Asia, and it comprises significant levels of seed protein, fiber, and minerals such as iron, calcium, and manganese (Upadhyaya *et al.,* 2011). It is one of the most important grain crops in northern Ethiopia, behind maize and sorghum. It is recognized as an ideal crop for changing people's dietary patterns due to its nutritional value, high photosynthetic efficiency, and resistance to biotic and abiotic stresses. Finger millet genetic potential is an invaluable resource for understanding their selection-based resilience to abiotic stresses. The direction and magnitude of the relationship between yield and related components are the most important factors influencing yield selection efficiency.

It's known that correlation only gives a relationship between two variables, whereas route coefficient analysis divides correlations into direct and indirect components using other standard qualities (Wright, 1921). In light of the aforementioned scenario, the current study was done to investigate character relationships among parameters in finger millet genotypes for yield improvement as a selection tool.

Materials and Methods

The experiment lasted three years and took place in two Metekel zone locations, Pawe and Manbuk. Pawe is located 575 kilometers from Addis Abeba at latitude 11° 15′ N and longitude 36° 05′ E at an elevation of 1150 masl, while Manbuk is a town at 11° 17′ N, 36° 13′ E, and 1200 masl, respectively. It has a Nitisol type having a single rainfall modality, with an average annual rainfall of 1500 mm to 1800 mm. The average annual low and high temperatures are 16 °C and 32 °C respectively.

A total of eleven finger millet genotypes (PWRFM-1 to PWRFM-10, advanced from preliminary yield experiments) and one standard check variety named, Baruda were utilized. A randomized complete block design (RCBD) with four replications was deployed. Each plot has five rows with 0.75m spacing and a row length of 3 m.

Each block was separated by a 1.5-meter corridor for plot management and data recording. Both urea and DAP fertilizer were applied at the recommended rate of 100 kg/ha. During sowing, the entire DAP was treated simultaneously, whereas the urea was sprayed in stages. The recommended agronomic practices were applied evenly in all plots as per the suggestions.

The common agronomic characters of finger millet were recorded, including days to flowering, days to maturity, plant height, number of tillers per plant, number of fingers per plant, finger length, harvest stand count, lodging, and grain yield. The collected data were subjected to SAS 9.3 to analyze variance components. The 'F' Test was used to determine the importance of each character's mean sum of squares in comparison to the corresponding error degrees of freedom (Fisher and Yates, 1967). The correlation was evaluated using the method proposed by Miller *et al.,* (1958), and the path coefficient analysis, which was first proposed by Wright (1921) and defined by Dewey and Lu (1959), allows for the partitioning of the correlation coefficient into direct and indirect effects of various characteristics.

The dependent variable, which aids in determining the cause-and-effect relationship as well as successful selection. The genetic correlations were further partitioned into direct and indirect effects using path coefficient analysis, as stated by Dewey and Lu (1959).

Results and Discussion

Correlation coefficient estimates of yield and related agronomic characters

It's clear that grain yield is the result of the multiplicative interactions of many more characters known as yield components, or super characters. Results of the present study identifying relevant yield components and understanding how they interact with yield and one another is critical in variety development. In this regard, the correlation coefficient, which provides a symmetrical measure of the degree of link between two variables or characters, helps us comprehend the nature and scope of the relationship between yield and yield-related components.

The genotypic correlation coefficients between diverse traits frequently had the same sign and nature as the phenotypic correlation coefficients in the experiment. However, genotypic correlations were greater than their phenotypic counterparts. Misra *et al.,* (2008); Ali *et al.,* (2013) and Suryanarayana *et al.,* (2014) all reported higher estimates of genotypic correlation than phenotypic correlation coefficients between yield and yield-related characters in finger millet.

The current study discovered significant positive and negative phenotypic associations between grain yield, number of fingers per plant (rp = 0.409), stand count at harvest (rp = 0.468), and disease score (rp = -0.444). Significant positive features at both genotypic and phenotypic levels included plant height with finger length (rg = 0.391, rp = 0.817), days to maturity with days to 50% flowering (rg = 0.943, rp = 0.762), and number of fingers per plant with days to maturity (rg = 0.743, rp = 0.469).

This discovery is consistent with previous findings published by Arya *et al.,* (2017); Bhasker *et al.,* (2017); Negi *et al.,* (2017) and Singh *et al.,* (2018). Disease score, on the other hand, displayed a substantial negative phenotypic relationship with the number of fingers and tillers per plant (rp = -0.200 and -0.667 respectively).

Similarly, the number of tillers had a significant positive phenotypic correlation with the number of fingers per plant (rp = 0.234). The current discovery is corresponding with the results of Muduli *et al.,* (2012); Eric *et al.,* (2016); Arya *et al.,* (2017) and Singh *et al.,* (2018).

Nevertheless, correlation studies only provide information about the relationship and not about the source of the association, therefore the data produced can be deceptive when identifying yield components.

As a result, path coefficient analysis is a method for dividing the observed correlation coefficient into direct and indirect effects of yield contributing components on grain yield, This offering a clear picture of character correlations to help build an effective selection strategy.

Table.1 Estimated genotypic and phenotypic correlation coefficients for several agronomic traits of finger millet

Characters		DF	DM	PHT	DS	NTPP	NFPP	FL	LODG	STCN	YD
DF	r_g	1	0.943^{***}	0.033	0.727	0.115	0.695	0.306	-0.791^{**}	-0.782^{**}	-0.561
	r_P	1	0.762^{***}	0.131	-0.155	0.184^{**}	0.414^{***}	0.273^{***}	-0.488^{***}	-0.002	-0.081
DM	r_g		1	-0.038	0.839^{**}	0.325	0.743^{**}	0.288	-0.844	-0.599	-0.430
	r_P		1	0.105	-0.213^{**}	0.332^{***}	0.469^{***}	0.252^{***}	-0.400^{***}	0.049	0.011
PHT	r_g			1	-0.404	0.220	0.236	0.817^{**}	0.528	-0.297	-0.138
	r_P			1	-0.472^{***}	0.082	0.510^{***}	0.391^{***}	0.354^{***}	0.252^{***}	0.275
DS	r_g				1	0.419	0.539	-0.112	-0.936^{***}	-0.248	-0.421
	r_P				1	-0.200^{**}	-0.667^{***}	-0.096	-0.181^{**}	-0.362^{***}	-0.444^{***}
NTPP	r_g					1	0.439	0.195	-0.143	0.186	-0.111
	r_P					1	0.234^{***}	0.115	-0.021	-0.014	0.100
NFPP	r_g						1	0.393	-0.446	-0.310	-0.072
	r_P						1	0.150	0.101	0.390^{***}	0.409^{***}
FL	r_g							1	0.190	-0.338	-0.215
	r_P							1	0.097	-0.005	0.006
LODG	r_g								1	0.408	0.425
	r_P								1	0.207^{**}	0.231^{**}
STCN	r_g									1	0.610
	r_P									1	0.468^{***}

*, ** significant at 5% and 1% levels, respectively, r_g=genotypic correlation, r_p=phenotypic correlation, DF=Days to 50% flowering, DM=Days to maturity, PHT= Plant height, DS=Disease score, NTPP= No. of tillers per plant, NFPP= No. of fingers per plant, FL=Finger length, LODG=Lodging, STCN=Stand count

Table.2 Phenotypic Path coefficient analysis demonstrating the direct (diagonal and bold) and indirect (off diagonal) effects of several features on grain yield in finger millet

Characters	DF	DM	PHT	DS	NTPP	NFPP	FL	LODG	STCN	YD
DF	**-0.207**	-0.016	0.001	0.031	0.010	0.098	0.002	0.002	-0.001	-0.081
DM	-0.158	**-0.021**	0.001	0.042	0.018	0.111	0.002	0.002	0.015	0.011
PHT	-0.027	-0.002	**0.008**	0.094	0.004	0.121	0.002	-0.001	0.077	0.275^{***}
DS	0.032	0.005	-0.004	**-0.198**	-0.011	-0.158	-0.001	0.001	-0.110	-0.444^{**}
NTPP	-0.038	-0.007	0.001	0.040	**0.053**	0.056	0.001	0.000	-0.004	0.100
NFPP	-0.086	-0.010	0.004	0.132	0.013	**0.237**	0.001	0.000	0.118	0.409^{***}
FL	-0.057	-0.005	0.003	0.019	0.006	0.036	**0.006**	0.000	-0.001	0.006
LODG	0.101	0.009	0.003	0.036	-0.001	0.024	0.001	**-0.004**	0.063	0.231
SCNT	0.000	-0.001	0.002	0.072	-0.001	0.093	-2.758	-0.001	**0.304**	0.468^{***}

*, ** significant at 5%and 1% levels, respectively, r_g=genotypic correlation, r_p=phenotypic correlation, DF=Days to 50% flowering, DM=Days to maturity, PHT= Plant height, DS=Disease score, NTPP= No. of tillers per plant, NFPP= No. of fingers per plant, FL=Finger length, LODG=Lodging, STCN=Stand count

Table.3 Genotypic Path coefficient analysis demonstrating the direct (diagonal and bold) and indirect (off diagonal) effect of several characteristics on grain yield in finger millet

Characters	DF	DM	PHT	DS	NTPP	NFPP	FL	LODG	STCN	YD
DF	**-2.804**	2.346	-0.032	0.150	-0.060	0.629	-0.008	-1.265	0.484	-0.561
DM	-2.644	**2.487**	0.037	0.173	-0.168	0.673	-0.008	-1.350	0.371	-0.430
PHT	-0.093	-0.095	**-0.974**	-0.083	-0.114	0.214	-0.021	0.844	0.184	-0.138
DS	-2.037	2.086	0.394	**0.206**	-0.217	0.488	0.003	-1.498	0.154	-0.421
NTPP	-0.323	0.809	-0.215	0.086	**-0.517**	0.398	-0.005	-0.229	-0.115	-0.111
NFPP	-1.947	1.847	-0.230	0.111	-0.227	**0.906**	-0.010	-0.713	0.192	-0.072
FL	-0.857	0.717	-0.796	-0.023	-0.101	0.356	**-0.026**	0.305	0.209	-0.215
LODG	2.217	-2.098	-0.514	-0.193	0.074	-0.404	-0.005	**1.601**	-0.253	0.425
SCNT	1.572	-1.070	0.134	-0.087	0.057	-0.065	0.006	0.681	**-0.619**	0.610

*, ** significant at 5%and 1% levels, respectively, r_g=genotypic correlation, r_p=phenotypic correlation, DF=Days to 50% flowering, DM=Days to maturity, PHT= Plant height, DS=Disease score, NTPP= No. of tillers per plant, NFPP= No. of fingers per plant, FL=Finger length, LODG=Lodging, STCN=Stand count

Generally, path analysis differs from basic correlations in that it identifies the cause and their relative importance, whereas the latter just assesses mutual association and ignores causality, as discussed in Wright (1921) and Dewey and Lu (1959).

Phenotypic and genotypic Path-coefficient Analysis

As mentioned above path coefficient analysis is essentially a standardized partial regression coefficient that separates the correlation coefficient into measurements of direct and indirect effects (Singh and Narayanan, 1993). This technique provides data to assist the indirect selection for genetic yield improvement.

In the current study, the genotypic correlation coefficient was divided into direct and indirect effects using path-coefficient analysis. Table 2 summarizes the phenotypic direct and indirect impacts of yield-related variables on yield. As illustrated in the table below, plant height (0.008), number of tillers per plot (0.053), number of fingers per plot (0.237), finger length (0.006), and stand count at harvest (0.034) all exhibited a positive phenotypic direct effect on grain yield.

On the other hand, traits such as days to flowering, days to maturity, disease score, and lodging all had a negative direct impact on grain yield. Stand count at harvest had the largest and most beneficial phenotypic direct effect on grain output (0.304), followed by the number of fingers per plot (0.237). Hence, these traits are more likely to be used in future selection procedures to boost grain yield. Similarly, Table 3 shows the genotypic direct and indirect impacts of yield-contributing traits on grain yield. Thus, days to maturity (2.487), illness score (0.206), number of fingers per plot (0.906), and lodging (1.601) all had a favorable genotypic direct effect on grain yield. On the other hand, characteristics such as days to flowering, plant height, number of tillers per plot, finger length, and stand count all had a negative genotypic direct effect on grain output.

Days to maturity (2.487) had the highest and most positive genotypic direct, followed by lodging, number of fingers per plant, and disease score, which were 1.601, 0.906, and 0.206, respectively (Table 3). These results confirm the previous findings of Ganapathy *et al.,* (2011); Anuradha *et al.,* (2013); Kumar *et al.,* (2014); Jyothsna *et al.,* (2016) and Negi *et al.,* (2017).

Conclusion

The genotypic correlation was often similar and larger in magnitude than the equivalent phenotypic correlation coefficients. Correlation and path analysis revealed that the number of tillers per plot, number of fingers per plot, and finger length had a greater influence on grain yield than any other parameter. As a result, it would be worthwhile to prioritize these characteristics in the selection program to increase grain output in finger millet.

Acknowledgments

The author thanks the McKnight Foundation for financial support to carry out the research, as well as the sorghum and millet research teams for technical assistance during field experiments.

References

Ali, K., Ramesh, B., Gangwar, L. K., Imran, M. and Kam-boj, G. (2013). Variability, heritability and correlation among agro-morphological traits in Finger millet (*Eleusine coracana* (L.) Gaertn). Progress. Res, 8(1): 95-98.

Anuradha N, Udaya B K, Patro T, Sharma N. (2013). Character association and path analysis in finger millet (*Eleusine coracana* L. Gaertn.) accessions belongs to late maturity group. In. J of Food, Agric. and Vet. Sci. 3(3):113115.

Arya R, Bhatt A, Kumar V, Singh D P. (2017). Correlation analysis of some growth, yield and quality parameters of barnyard millet germplasm. J. of Pharmacognosy and Phytochemistry. 6(5):1426-1429.

Bhasker K, Shashibhushan D, Krishna M, Bhave M. H. V. (2017). Correlation and path analysis for grain yield and it components in pearl millet (*Pennisetum glaucum* (L). R.Br.). Bull. Env. Pharmacol. Life Sci. 6(1):104-106.

Dewey, D. R. and K. H. Lu. (1959). A correlation and path coefficient analysis of components of crescent wheat grass seed production. Agro. J. 51: 515-518.

Eric M O, Pangirayi T, Paul S, Mwangi G, Rathore A. (2016). Correlations, path coefficient analysis and heritability for quantitative traits in finger millet landraces. Philippine J of Sci. 145(2):197-208.

Fisher, R. A., & Yates. (1967). Statistical Tables for Biological Agricultural and Medical Research Olivar and Boyd, Edington.

Ganapathy S, Nirmalakumari A, Muthiah A R. Genetic variability and interrealationship analysis for economic traits in finger millet germplasm. World J of Agrilc. Sci.2011; 7(2):185-188.

Jyothsna S, Patro T S S K, Ashok S, Sandhya Rani Y, Neeraja B. (2016). Studies on Genetic Parameters, Character Association and Path Analysis of Yield and its Components in Finger Millet (*Eleusine coracana* (L.) Gaertn.). Int. J Theoretical & App. Sci. 8(1):25-30.

Kumar D, Tyagi V, Ramesh B. (2014). Path coefficient analysis for yield and its contributing traits in finger millet. In. JAdvanced Res. 2(8):235-240.

Miller, P. A., C. Williams, H. F. Robinson and R. E. Comstock. (1958). Estimates of genotypic and Environmental variances and co-variances in upland cotton and their implications in selection. Agric. J.50:126 –131.

Misra, R. C., Sahu, P. K., Pradhan, B., Das, S. and Mishra, C. H. P. (2008). Character association, path-coefficient and selection indices in Finger millet (*Eleusine coracana*). Enviro. and Eco, 26(1): 166-170.

Muduli K C, Pradhan K, Dash G B, Misra R C. (2012). Association analysis among micro mutant lines in finger millet (*Eleusine coracana* Gaertn.). Environment & Ecology. 30(2):343-347.

Negi S, Bhatt A, Kumar V. (2017). Character association and path analysis for yield and its related traits in finger millet (*Eleusine coracana* (L.) Gaertn.) Genotypes. J. of Applied and Natural Sci. 9(3):1624-1629.

Singh O, Gowthami R, Singh K, Shekhawat N. (2018). Assessment of inter-characters associations in the germplasm of pearl millet over five years in hot arid climate of Rajasthan, India. Int. J Curr. Microbiol. App. Sci. 7(1):3133-3149.

Singh P, Narayanan S. S. (1993). Biometrial techniques in plant breeding. Kalyani Publishers, New Delhi.

Suryanarayana, L., Sekhar, D. and Rao, N. V. (2014). Inter relationship and cause-effect analysis in Finger millet (*Eleusine coracana* (L.) Gaertn) genotypes. Int. J. of Curr. Micro. and App. Sci, 3: 937-941.

Upadhyaya H. D, Ramesh S, Sharma S, Singh S. K, Varshney S. K, Sarma N. D, Ravishankar C. R, Narasimhudu Y, Reddy V. G, Sahrawat K. L, Dhanalakshmi T. N. (2011). Genetic diversity for grain nutrients contents in a core collection of finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm. Field Crops Research, 121(1):42-52.

Wright S. (1921). Correlation and causation. Journal of agricultural research. 20(7):557-85.22

How to cite this article:

Tafere Mulualem Emrey. 2024. Trait Association and Path Coefficient Study for Yield and Yield Related Components of Finger Millet (*Eleusine coracana* L.) Genotypes in Northwestern Ethiopia. *Int.J.Curr.Res.Aca.Rev.* 12(8), 79-83. doi: https://doi.org/10.20546/ijcrar.2024.1208.008