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Character Association and Path Analysis for Grain Yield and Yield Components in White Finger Millet (*Eleusine coracana* L. Gaertn) Germplasm

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ABSTRACT: White finger millet is generally low yielder when compared to brown finger millet but it is nutritionally superior and is desired for its use especially in bakery and other products. Grain yield is a complex trait and it is influenced by many independent traits. Therefore, the knowledge of association studies is beneficial to breeder for improvement of yield. Finger millet is the third most important millet after pearl millet and sorghum and occupies an estimated area of 1.23 million hectares in India. Grains of finger millet are known for having highest levels of calcium (250-350 mg/100g) in addition to quality protein (7-9%), dietary fibre (2-4%) and other mineral content (2.7%). The present study aimed at understanding the genetic relationships among various grain attributing traits in white finger millet germplasm lines. The study was conducted in alpha lattice design in two replications for the evaluation of ten quantitative traits in 52 germplasm lines of white finger millet in kharif 2022. The traits include days to 50% flowering, plant height, finger length, finger width, number of tillers, number of fingers, panicle weight, days to maturity, grain yield per plot and test weight. Association studies revealed that plant height, number of tillers per plant, panicle weight and test weight showed a positive significant association with grain yield per plot at both genotypic and phenotypic level respectively. Grain yield per plot exhibited negative significant association with days to 50% flowering and days to maturity at both genotypic and phenotypic level respectively. Path analysis revealed that panicle weight, test weight, plant height and finger width showed a positive significant direct effect on grain yield per plot at both genotypic and phenotypic level respectively. Correlation and path analysis concluded that the characters panicle weight, number of tillers per plant, plant height and test weight showed a true association with grain yield per plot and significant positive correlation with high positive direct effects. Hence direct selection of these traits will be beneficial.

Keywords: Finger millet, Correlation, Path analysis, Grain yield, Genotypic, Phenotypic.

INTRODUCTION

Finger millet (*Eleusine coracana* L. Gaertn.) commonly called as ragi belongs to the family Poaceae. The cultivated species is an allo-tetraploid ($2n = 4x = 36$) and it is believed that *E. coracana* originated from its related species, *E. indica*. It is a self-pollinated crop and breeding methods aims at developing improved genotypes with superior grain and stover yield.

In India, finger millet occupied an area of 1.21 million hectares with a production of 1.70 million tonnes (INDIASTAT, 2022). Whereas in Telangana, finger millet grows in an area of 1000 hectares with a production of 1650 tonnes (Directorate of Economics and Statistics, Telangana 2022).

The grains of finger millet range from brown to reddish brown due to tannins and flavonoids (Vadivoo *et al.*, 1998). The white grain finger millet is nutritionally comparable with coloured grained finger millet and is desired for its use especially in bakery and other food products (Ravishankar, 2019). Grains of finger millet are known for highest amount of calcium, iron, zinc, fiber and essential amino acids (Singh and Raghuvanshi 2012; Upadhyaya *et al.*, 2011; Ambuko *et al.*, 2014). The white grain types are also suited for malting purposes as well as other end-uses such as weaning foods, infant foods and malted milk foods etc. In addition to its nutritional benefits, finger millet is climate resilient and environment sustainable crop with great storage qualities (Ayyangar *et al.*, 1932). Despite its tremendous potential, the cultivation of white finger millet is limited with few cultivars released. With this background information, the current investigation was carried out using white finger millet germplasm lines with commercially available checks.

The genetic gain during selection mainly depends on the degree and direction of association between grain yield and its components. Path analysis splits the correlation coefficient into measures of direct and indirect effects and measures the direct and indirect contribution of each independent variable on dependent variable. Hence, correlation and path analysis are important for the identification of characters that contribute to grain yield for efficient genetic improvement (Dewey and Lu 1959; Lenka and Mishra 1953).

MATERIAL AND METHODS

The present investigation was taken up with a set of 52 white finger millet germplasm lines during *kharif* 2022 in alpha lattice design in two replications at ICAR-Indian Institute of Millets Research Rajendranagar, Hyderabad. Plot size for each genotype is 1.35 square meter and spacing followed is 45 cm between rows and 15 cm between plants. All standard package of practices were followed to raise a good crop. Ten uniform and representative plants were tagged in each genotype in each replication and data was collected from those plants for days to 50% flowering, plant height, finger length, finger width, number of tillers per plant, number of fingers, panicle weight, days to maturity, grain yield per plot and test weight.

By using the method provided by Falconer (1996), the statistical analysis of the mean of 10 plants was performed to calculate the phenotypic and genotypic correlation coefficients. Fisher and Yates (1943) approach was used to evaluate the significance of correlation. The path analysis technique developed by Dewey and Lu (1959) can be used to breakdown complex correlation into direct and indirect effects at both genotypic and phenotypic levels were followed in the present study.

RESULTS AND DISCUSSION

A. Correlation Analysis

In order to develop a successful selection strategy for identification superior genotypes, the breeder has to be aware of the phenotypic and genotypic relationships between grain yield and its component characters as well as between the component characters themselves. In addition to selection of grain yield perse, indirect selection based on correlated component characters could be beneficial because grain yield is a complex trait and is influenced by many component traits.

The present study revealed the estimates of the genotypic and phenotypic correlation coefficient for each pair of characters given in Table 1. With a few exceptions, the magnitude of the genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, which indicating that there is an inherent relationship between the various traits. For almost all characters, the genotypic correlation coefficient and phenotypic correlation coefficient values are almost same, which indicating that there is a strong genetic relationship between the various traits.

Grain yield per plot showed positive significant association with plant height (0.48** and 0.46**), number of tillers per plant (0.57** and 0.44**), panicle weight (0.93** and 0.91**) and test weight (0.28** and 0.24**) and negative significant correlation with days to 50% flowering (-0.32** and -0.30**) and days to maturity (-0.29** and -0.26**).

Days to 50% flowering showed positive significant association with days to maturity (0.89** and 0.83**) and number of fingers (0.61** and 0.46**) and negative significant association with finger length (-0.63** and -0.59**), test weight (-0.45** and -0.42**), number of tillers per plant (-0.41** and -0.32**), grain yield per plot (-0.32** and -0.30**) and plant height (-0.37** and -0.35**) at both genotypic and phenotypic level respectively.

Plant height showed positive significant association with finger length (0.60** and 0.54**), grain yield per plot (0.48** and 0.46**), number of tillers per plant (0.43** and 0.30*), test weight (0.41** and 0.39**) and panicle weight (0.34** and 0.38**) and negative significant association with days to maturity (-0.32** and -0.31**) at both genotypic and phenotypic level respectively.

Finger length showed positive significant association with test weight (0.29** and 0.24**) and negative significant association with days to maturity (-0.55** and -0.51**) at both genotypic and phenotypic level respectively.

Finger width showed positive significant association with test weight (0.35** and 0.26**) and negative significant association with number of fingers (-0.51** and -0.41**) at both genotypic and phenotypic level respectively.

Number of tillers per plant showed positive significant association with grain yield per plot (0.57** and 0.44**) and panicle weight (0.52** and 0.37**) and negative significant association with days to maturity (-0.38** and -0.25**) at both genotypic and phenotypic level respectively.

Number of fingers showed positive significant association with days to maturity (0.56** and 0.45**) and negative significant association with test weight (-0.48** and -0.37**) at both genotypic and phenotypic level respectively. Panicle weight showed highest positive significant association with grain yield per plot (0.93** and 0.91**) at both genotypic and phenotypic level.

Days to maturity showed negative significant correlation with test weight (-0.36** and -0.30**) and grain yield per plot (-0.29** and -0.26**) and Test weight showed positive significant correlation with grain yield per plot (0.28** and 0.24*) at both genotypic and phenotypic level.

Characters such as plant height, number of tillers per plant, panicle weight and test weight showed a positive significant correlation with grain yield per plot at both genotypic and phenotypic level respectively. It revealed that there is a strong association between the characters and selection for one character will simultaneously bring improvement in another character. Similar results of positive significant correlation were obtained by Marefia *et al*. (2022); Anwar *et al*. (2022) for number of tillers and Lad *et al*. (2020) for number of tillers, plant height and test weight in finger millet.

Table 1: Genotypic and phenotypic correlation among grain yield and component characters in 52 white finger millet germplasm lines.

Sr. No.	Characters		DFF	PH	FL	FW	NT	NF	PW	DM	TW	GY
1.	**DFF**	**G**	**1.00**	-0.37**	-0.63**	-0.38**	-0.41**	0.61**	-0.11	0.89**	-0.45**	-0.32**
		P	**1.00**	-0.35**	-0.59**	-0.30 **	-0.32 **	0.46**	-0.13	0.83**	-0.42 **	-0.30**
2.	**PH**	**G**		**1.00**	0.60**	0.11	0.43**	-0.05	0.34**	-0.32**	0.41**	0.48**
		P		**1.00**	0.54 **	0.11	0.30 *	-0.06	0.38 **	-0.31**	0.39**	0.46**
3.	**FL**	**G**			**1.00**	0.11	0.27 *	-0.15	0.00	-0.55**	0.29**	0.12
		P			**1.00**	0.12	0.17	-0.12	0.01	-0.51**	0.24**	0.11
4.	**FW**	**G**				**1.00**	-0.14	-0.51**	0.05	-0.23	0.35**	0.15
		P				**1.00**	-0.05	- 0.41**	0.08	-0.13	0.26 **	0.15
5.	**NT**	**G**					**1.00**	-0.12	0.52**	-0.38**	0.16	0.57**
		P					**1.00**	-0.03	0.37 **	-0.25 **	0.16	0.44**
6.	**NF**	**G**						**1.00**	0.12	0.56**	-0.48**	-0.02
		P						**1.00**	0.11	0.45**	-0.37 **	0.04
7.	**PW**	**G**							**1.00**	-0.06	0.07	0.93**
		P							**1.00**	-0.08	0.07	0.91**
8.	**DM**	**G**								**1.00**	-0.36**	-0.29**
		P								**1.00**	-0.30**	-0.26**
9.	**TW**	**G**									**1.00**	0.28**
		P									**1.00**	0.24*

Note: **DFF** = Days to 50% Flowering, **PH** = Plant Height, **FL** = Finger Length, **FW** = Finger Width, **NT** = Number of Tillers per plant, **NF** = Number of Fingers, **PW** = Panicle weight, **DM** = Days to Maturity, **TW** = Test Weight, **GY**= Grain Yield per plot.
G: Genotypic correlation P: Phenotypic correlation ** Significant at 1% level * Significant at 5% level

Days to 50% flowering (-0.32** and -0.30**) and days to maturity (-0.29**and -0.26) showed a significant negative correlation with grain yield per plot at both genotypic and phenotypic level respectively. The results of negative correlation are in accordance with Nandini *et al*. (2018); Bendi and Sarma (2016) for days to 50% flowering and Bezaweletaw *et al*. (2006) for days to maturity.

Correlation studies concluded that the characters panicle weight (0.93** and 0.91**), number of tillers per plant (0.57** and 0.44**), plant height (0.48** and 0.46**) and test weight (0.28** and 0.24**) showed higher values of positive correlation with grain yield. The results were in accordance with Kumari *et al.* (2018); Chavan *et al.* (2020); Lad *et al.* (2020). Therefore, while undergoing selection for grain yield traits, indirect selection of these correlated characters will aid in improvement of grain yield in white finger millet.

B. Path analysis

Ten characters were taken on the basis of genotypic and phenotypic correlation and partitioned into direct and indirect effects using grain yield per plot as a dependent variable. Table 2 gives the information about direct and indirect effects of nine variables on grain yield per plot in 52 germplasm lines of white finger millet.

Panicle weight (0.85 and 0.82), test weight (0.15 and 0.13), plant height (0.09 and 0.05) and number of tillers per plant (0.02 and 0.06) showed positive significant direct effect on grain yield per plot at both phenotypic and genotypic level. This revealed that there is a true relationship between the characters and direct selection for these traits would be rewarding for yield improvement. The similar results of positive significant direct effect were obtained by Anwar *et al*. (2022); Negi *et al.* (2016) for number of tillers per plant, Lad *et al.* (2020); Jyothsna *et al.* (2016) for plant height, Manjunath *et al*. (2013).

Days to 50% flowering (-0.03 and -0.04) and days to maturity (-0.28 and -0.18) showed negative significant direct effect on grain yield per plot at both genotypic and phenotypic level respectively shown in Fig. 1 and 2.

Finger width (0.07 and 0.07) and number of fingers (0.12 and 0.12) showed nonsignificant positive direct effect and finger length (-0.10 and-0.08) showed nonsignificant negative direct effect on grain yield per plot at both genotypic and phenotypic level respectively.

Among all the characters panicle weight (0.85 and 0.82) showed a highest positive direct effect on grain yield per plot. Highest positive direct effect of panicle weight on grain yield per plot is due to the highest indirect positive effect of number of tillers (0.44 and 0.31), plant height (0.29 and 0.31), number of fingers (0.10 and 0.09) and test weight (0.06 and 0.06). The characters panicle weight, number of tillers, plant height and test weight showed high positive significant direct effect on grain yield per plot. The results were in agreement with Bothikar *et al.* (2014); Lad *et al.* (2020); Anwar *et al.* (2022). It showed that direct selection of these characters is rewarding.

Table 2: Genotypic and phenotypic direct and indirect effects of different traits on grain yield in 52 white finger millet germplasm lines.

Sr. No.	Characters		DFF	PH	FL	FW	NT	NF	PW	DM	TW	GY
1.	**DFF**	**G**	**-0.03**	-0.01	-0.02	-0.01	-0.01	0.02	0.00	0.03	-0.01	-0.32**
		P	**-0.04**	0.02	0.03	0.01	0.01	-0.02	0.01	-0.04	0.02	-0.30**
2.	**PH**	**G**	-0.03	**0.09**	0.05	0.01	0.04	0.00	0.03	-0.03	0.04	0.48**
		P	-0.02	**0.05**	0.03	0.01	0.02	0.00	0.02	-0.02	0.02	0.46**
3.	**FL**	**G**	0.06	-0.06	**-0.10**	-0.01	-0.03	0.02	0.00	0.05	-0.03	0.12
		P	0.05	-0.05	**-0.08**	-0.01	-0.01	0.01	0.00	0.04	-0.02	0.11
4.	**FW**	**G**	-0.02	0.01	0.01	**0.07**	-0.01	-0.03	0.00	-0.02	0.02	0.15
		P	-0.02	0.01	0.01	**0.07**	0.00	-0.03	0.01	-0.01	0.02	0.15
5.	**NT**	**G**	-0.01	0.01	0.01	0.00	**0.02**	0.00	0.01	-0.01	0.00	0.57**
		P	-0.02	0.02	0.01	0.00	**0.06**	0.00	0.02	-0.01	0.01	0.44**
6.	**NF**	**G**	0.07	-0.01	-0.02	-0.06	-0.01	**0.12**	0.01	0.06	-0.06	-0.02
		P	0.06	-0.01	-0.01	-0.05	0.00	**0.12**	0.01	0.06	-0.05	0.04
7.	**PW**	**G**	-0.10	0.29	0.00	0.04	0.44	0.10	**0.85**	-0.05	0.06	0.93**
		P	-0.10	0.31	0.01	0.06	0.31	0.09	**0.82**	-0.06	0.06	0.91**
8.	**DM**	**G**	-0.25	0.09	0.15	0.07	0.11	-0.16	0.02	**-0.28**	0.10	-0.29**
		P	-0.15	0.06	0.09	0.02	0.05	-0.08	0.01	**-0.18**	0.05	-0.26**
9.	**TW**	**G**	-0.07	0.06	0.04	0.05	0.02	-0.07	0.01	-0.05	**0.15**	0.28**
		P	-0.05	0.05	0.03	0.03	0.02	-0.05	0.01	-0.04	**0.13**	0.24*

Note: **DFF** = Days to 50% Flowering, **PH** = Plant Height, **FL** = Finger Length, **FW** = Finger Width, **NT** = Number of Tillers per plant, **NF** = Number of Fingers, **PW** = Panicle weight, **DM** = Days to Maturity, **TW** = Test Weight, **GY**= Grain Yield per plot
G: at genotypic level P: at phenotypic level
Genotypic residual effect = 0.2030, Phenotypic residual effect = 0.3169 ** Significant at 1% level * Significant at 5% level
Diagonal bold are direct effects

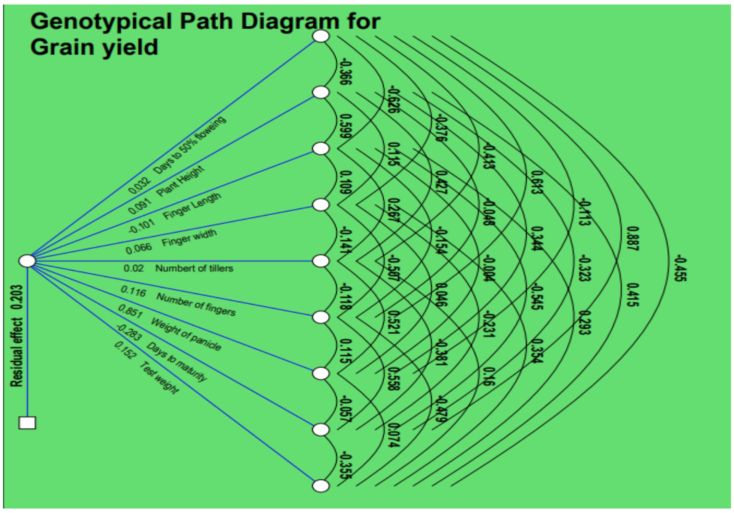

Fig. 1. Genotypic path diagram for grain yield.

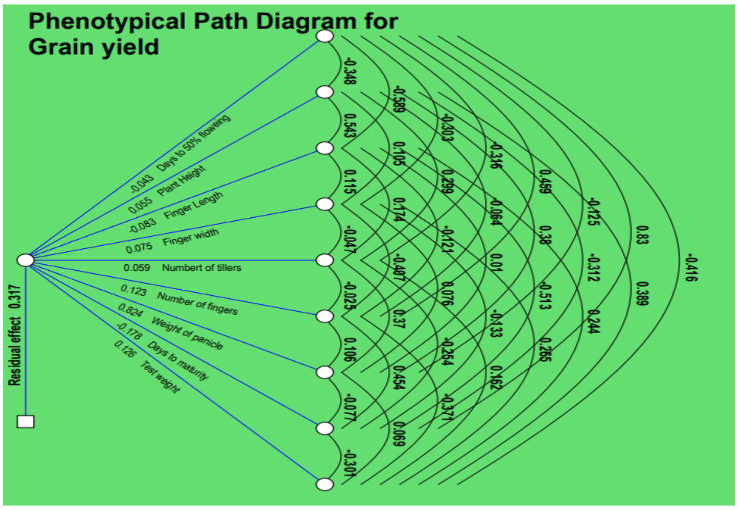

Fig. 2. Phenotypic path diagram for grain yield.

CONCLUSIONS

The current investigation of correlation analysis showed that panicle weight followed by the number of number of tillers per plant, plant height and test weight had a significant and positive association with grain yield per plot. Weight of panicle contributing more towards the grain yield per plot among all characters that have significant association.

According to path analysis, grain yield was significantly and positively affected by weight of panicle, number of tillers per plant, plant height and test weight.

The results of the present study of correlation and path analysis concluded that weight of panicle, number of tillers per plant, plant height and test weight had a significant positive and direct effect on grain yield per plot. Therefore, it is beneficial to put more focus on these traits in the selection process to increase the grain yield of white finger millet.

FUTURE SCOPE

The selection process is a crucial element in breeding programmes. In addition to correlated traits identified in the present study, future study will aim at identifying superior genotypes through multi-location trials for its direct selection as variety or as parents in breeding programs.

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