

# STUDIES ON GENETIC ASSOCIATION AND INTER-RELATIONSHIPS AMONG YIELD AND QUALITY TRAITS IN FINGERMILLET (*ELEUSINE CORACANA* (L.) GAERTN.)

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## ABSTRACT

Experiment was conducted with 55 finger millet genotypes to study the genetic association among 14 yield and quality traits, and their direct and indirect effects on the yield. The genotypic correlation was generally of higher magnitude than phenotypic correlation indicating the associations are majorly due to genetic reason. Number of basal tillers (0.497), flag leaf length (0.393), number of fingers ear<sup>-1</sup>(0.467) and plant height (0.264) were positively and significantly associated with grain yield plant<sup>-1</sup> at genotypic level, indicating improvement in these traits will increase the yield. Negative and significant association at genotypic level was noticed with days to 50% flowering (-0.344) and negative but non-significant association with calcium content (-0.053). Plant height (0.264), number of basal tillers (0.498), flag leaf length (0.394), inflorescence width (0.254) and number of fingers ear<sup>-1</sup> (0.498) at genotypic level have positive direct effect on yield indicating importance of these characters in improvement of yield in finger millet.

## INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn.) commonly known as *ragi*, is an important cereal crop amongst the small millets and third in importance after sorghum and pearl millet in India. It is a nutritious food grain crop with a fair amount of protein (7.3g 100g<sup>-1</sup>) (Malleshi and Klopfenstein, 1998), dietary fibre (15–20%) (Chethan and Malleshi, 2007) and a rich source of calcium (Ca) (344mg 100g<sup>-1</sup>) (Gopalan *et al.*, 2002). Higher nutritional quality, higher multiplication rate, longer shelf life under ambient conditions and wide range of seasonal adaptation makes finger millet an ideal crop for use as a staple food and for famine reserve.

Yield is a complex character and dependent on many component characters. Hence it is necessary to have knowledge on the extent of association between yield and yield contributing characters. The study of relationships among quantitative traits is important for assessing the feasibility of joint selection of two or more traits and hence for evaluating the effect of selection for secondary traits on genetic gain of the primary trait under consideration (Kalpande *et al.*, 2015). Path analysis is necessary for better understanding of correlations among traits, which is a pathway for knowledge on specificity of the genetic material being studied (Arun Kumar, 2013).

In the present study, correlation and path analysis was used to work out the associations, direct and indirect effects of yield contributing characters on yield using 55 genotypes of finger millet.

## MATERIALS AND METHODS

### Plant material

The experimental material comprised of 55 diverse genotypes of finger millet was evaluated in a randomized block design with three replications. Each genotype was represented by two rows of three meter length and spaced 30×10 cm.

### Data recording

Five competitive plants were selected at random from each replication and observations were recorded on 14 quantitative traits *viz.*, days to 50% flowering (plot basis), plant height (cm), number of basal tillers, flag leaf length (mm), peduncle length (mm), inflorescence exertion (mm), inflorescence length (mm), inflorescence width (mm), length of finger (mm), width of finger (mm), number of fingers ear<sup>-1</sup>, seed protein content (%) (estimated by Microkjeldahl method), calcium content (mg/100g) (estimated by Versenate titration method) and grain yield plant<sup>-1</sup> (g).

### Data analysis

Genotypic and phenotypic correlations and path analysis were worked out as per the standard procedures (Snedecor and Cochran, 1967; Dewey and Lu, 1959), using the software 'WINDOSTAT version 9.2.

## RESULTS AND DISCUSSION

### Character association

Phenotypic and genotypic correlation coefficients in all possible combinations of the characters were presented in Table 1. Individually, the genotypic correlations were higher

**Table 1: Estimates of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients for 14 characters in finger millet genotypes**

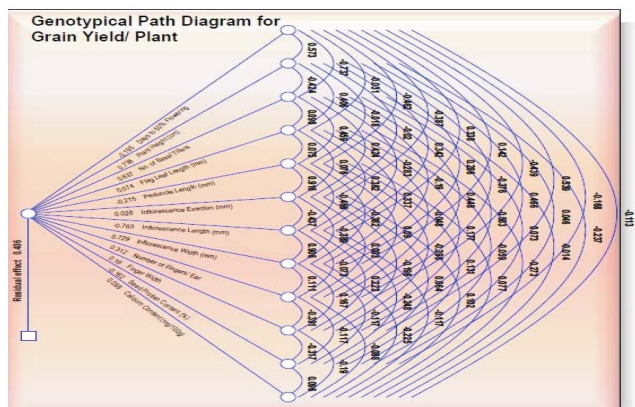
Character	DTF	PlHt	NBT	FLL	Ped L	InfEx	InfL	InfW	NFE	FinL	FinW	Seed PC	Cal C	GYP
DTF	1	0.573**	-0.737**	-0.031	-0.462**	-0.387**	0.338**	0.142	-0.439**	0.306**	0.539**	-0.168	-0.113	-0.344**
PlHt	0.533**	1	-0.424**	0.406**	-0.018	-0.02	0.342**	0.286**	-0.376**	0.335**	0.466**	0.046	-0.237*	0.264**
NBT	-0.677**	-0.371**	1	0.098	0.459**	0.424**	-0.283**	-0.19	0.448**	-0.233*	-0.583**	0.073	-0.014	0.497**
FLL	-0.02	0.343**	0.085	1	0.075	0.076	0.362**	0.337**	-0.048	0.402**	0.177	-0.059	-0.273**	0.393**
Ped L	-0.396**	0.077	0.386**	0.092	1	0.916**	-0.466**	-0.382**	0.09	-0.434**	-0.398**	0.131	0.077	0.213
InfEx	-0.348**	0.038	0.365**	0.06	0.843**	1	-0.437**	-0.389**	0.003	-0.405**	-0.196	0.064	0.102	0.186
InfL	0.323**	0.295**	-0.261**	0.351**	-0.413**	-0.404**	1	0.906**	-0.073	0.997**	0.223*	-0.248*	-0.117	0.06
InfW	0.121	0.237*	-0.143	0.331**	-0.309**	-0.346**	0.853**	1	0.111	0.896**	0.167	-0.117	-0.225*	0.254**
NFE	-0.350**	-0.279**	0.352**	0.019	0.054	0.023	-0.03	0.149	1	-0.051	-0.391**	-0.117	-0.088	0.467**
FinL	0.291**	0.299**	-0.206	0.391**	-0.378**	-0.371**	0.982**	0.832**	0.001	1	0.187	-0.226*	-0.104	0.101
FinW	0.406**	0.355**	-0.388**	0.179	-0.263**	-0.139	0.192	0.206	-0.201	0.153	1	-0.317**	-0.19	0.101
Seed PC	-0.159	0.036	0.082	-0.032	0.146	0.059	-0.233*	-0.079	-0.071	-0.215	-0.204	1	0.096	-0.016
Cal C	-0.111	-0.219*	-0.016	-0.231*	0.067	0.095	-0.113	-0.206	-0.072	-0.1	-0.139	0.09	1	-0.053
GYP	-0.295**	0.228*	0.462**	0.302**	0.187	0.147	0.068	0.248**	0.373**	0.094	0.069	-0.016	-0.22	1

\*, \*\* Significance at 5 (P = 0.005) and 1 (P = 0.001) percent level of significance, respectively.

**Table 2: Genotypic path coefficient analysis for 14 characters in finger millet.**

Character	DTF	PlHt	NBT	FLL	Ped L	InfEx	InfL	InfW	NFE	FinW	Seed PC	Cal C
DTF	-0.195	-0.112	0.144	0.006	0.09	0.076	-0.066	-0.028	0.086	-0.105	0.033	0.022
PlHt	0.423	0.738	-0.313	0.3	-0.013	-0.015	0.252	0.211	-0.278	0.344	0.034	-0.175
NBT	-0.47	-0.27	0.637	0.062	0.293	0.27	-0.18	-0.121	0.285	-0.371	0.047	-0.009
FLL	-0.002	0.03	0.007	0.074	0.006	0.006	0.027	0.025	-0.004	0.013	-0.004	-0.02
Ped L	0.1	0.004	-0.099	-0.016	-0.215	-0.197	0.1	0.082	-0.019	0.086	-0.028	-0.017
InfEx	-0.011	-0.001	0.012	0.002	0.026	0.028	-0.012	-0.011	0	-0.005	0.002	0.003
InfL	-0.258	-0.261	0.216	-0.276	0.355	0.333	-0.763	-0.692	0.056	-0.17	0.19	0.09
InfW	0.104	0.209	-0.139	0.246	-0.278	-0.284	0.661	0.729	0.081	0.122	-0.085	-0.164
NFE	-0.137	-0.117	0.14	-0.015	0.028	0.001	-0.023	0.035	0.312	-0.122	-0.037	-0.028
FinW	0.086	0.075	-0.093	0.028	-0.064	-0.031	0.036	0.027	-0.063	0.16	-0.051	-0.03
Seed PC	0.027	-0.007	-0.012	0.01	-0.021	-0.01	0.04	0.019	0.019	0.051	-0.162	-0.016
Cal C	-0.011	-0.023	-0.001	-0.027	0.008	0.01	-0.011	-0.022	-0.009	-0.019	0.009	0.098
GYP	-0.344	0.264	0.498	0.394	0.213	0.186	0.06	0.254	0.468	-0.016	-0.053	-0.246

Residual effect = 0.406, Bold items denotes direct effect; Where, DTF = Days to 50% flowering, PlHt = Plant height, NBT = Number of basal tillers, FLL = Flag leaf length, Ped L = Peduncle length, InfEx = Inflorescence exertion, InfL = Inflorescence length, InfW = Inflorescence width, NFE = Number of fingers ear<sup>-1</sup>, FinL = Finger length, FinW = Finger width, Seed PC = Seed protein content, Cal C = Calcium content, GYP = Grain yield plant<sup>-1</sup>.



**Figure 1: Genotypic path diagram showing direct and indirect effects of 14 characters on grain yield plant<sup>-1</sup> in 55 finger millet genotypes.**

in magnitude than phenotypic correlations, indicating that the apparent associations are largely due to genetic reason.

Number of basal tillers (0.497\*\*, 0.462\*\*), flag leaf length (0.393\*\*, 0.302\*\*), inflorescence width (0.254\*\*, 0.248\*\*) and number of fingers ear<sup>-1</sup> (0.467\*\*, 0.373\*\*) showed high positive and significant correlation with grain yield plant<sup>-1</sup> both at genotypic and phenotypic levels. Traits peduncle length (0.213, 0.187), inflorescence exertion (0.186, 0.147), inflorescence length (0.060, 0.068), finger length (0.101, 0.094) and finger width (0.101, 0.069) exhibited non significant

positive relationship with grain yield plant<sup>-1</sup>. Whereas days to 50% flowering (-0.344\*\*, -0.295\*\*) showed negative and significant association with grain yield plant<sup>-1</sup> both at genotypic and phenotypic levels. The traits seed protein content (-0.016, -0.053) and calcium content (-0.016, -0.022) showed negative non-significant association with grain yield plant<sup>-1</sup> at both genotypic and phenotypic levels. These results were in accordance with findings of Gowda *et al.* (2008), Kadam *et al.* (2009), Priyadarshini *et al.* (2011).

**Path coefficient analysis**

The direct and indirect effects of 14 characters on grain yield are presented in Table 2. Path analysis revealed that plant height (0.738) had highest positive direct effect on grain yield plant<sup>-1</sup> followed by inflorescence width (0.729) and number of basal tillers (0.637) indicating its role in simultaneous selection, while selecting genotypes with high grain yield.

The trait plant height had positive indirect effects via days to 50% flowering (0.423), flag leaf length (0.300), inflorescence length (0.252), inflorescence width (0.211) and finger width (0.344). Inflorescence width had positive indirect effects via inflorescence length (0.661), plant height (0.209) and days to 50% flowering (0.104). And the trait, number of basal tillers showed positive indirect effects through peduncle length (0.293), inflorescence exertion (0.270), number of fingers ear<sup>-1</sup> (0.285) and flag leaf length (0.062). Hence, direct selection for these traits would be rewarding for yield improvement, which will also reduce the undesirable effect of the component

traits studied. Similar findings were reported by Kadam *et al.* (2009), Andualem and Tadesse (2011), Ganapathy *et al.* (2011), Priyadharshini *et al.* (2011) and Dinesh kumar *et al.* (2014).

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