



Genetic Variability Analysis and Effect of Yield Attributing and Nutritional Traits on Productivity Improvement in Finger Millet (*Eleusine coracana* (L.) Gaertn)

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Finger millet is third in its importance with respect to area and production among millets in India after sorghum and pearl millet. Seven female lines were crossed with three testers during *rabi* 2009-2010 and the resultant 21 hybrids along with their parents were utilized for variability, correlation and path analysis during *kharif*, 2010. Estimates of phenotypic coefficients of variation (PCV) were slightly higher than genotypic coefficients of variation (GCV) for all the characters under consideration. The estimates of genotypic variances showed a considerable range of variation for most of the characters. Higher values of PCV and GCV were recorded for iron content, number of fingers per ear head and moderate value of PCV and GCV for the longest finger length, grain protein content and harvest index indicated large extent of genetic variability for these traits in the material. High heritability along with high genetic advance were observed for plant height, number of productive tillers per plant, number of fingers per ear head, longest finger length, grain protein content, harvest index and single plant grain yield, indicating involvement of additive gene action for these traits and phenotypic selection based on these traits in the segregating generations would likely to be more effective. However, the extent of contribution of a particular character to any dependent variable may not be judged from the genetic variation and correlation studies alone. Path analysis on grain yield showed that the harvest index and dry fodder yield had high positive direct effects and this revealed the true relationship of these traits with grain yield. Hence, direct selection for these traits would be rewarding for yield improvement.

Key words: Finger millet, Correlation, Path analysis, Heritability, Genetic advance, Gene action.

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Finger millet (*Eleusine coracana* (L.) Gaertn.) with $2n = 4x = 36$, belongs to the tribe Chloridae of the family Poaceae. It is a hardy crop with minimum disease and pest problems and assures reasonable economic return from adverse growing conditions (John Joel *et al.*, 2005). In development of improved varieties, recombination breeding occupies a predominant position in finger millet improvement programmes (Priyadharshini *et al.*, 2010). In addition, assessment of variability present in any crop species is the essential pre-requisite for formulating an effective breeding programme. The existing variability can be used further to enhance the yield level of the cultivars following appropriate breeding strategies (Patil *et al.*, 2012).

In the present investigation, for all the traits studied, the phenotypic co-efficients of variation were higher than the genotypic co-efficients of variation. Since heritability is also influenced by environment, the information on heritability alone may not help in pin pointing characters for enforcing selection. Nevertheless, the heritability estimates in conjunction with predicted genetic advance will be more reliable (Johnson *et al.*, 1955). Heritability

gives the information on the magnitude of quantitative characters, while genetic advance will be helpful in calculating suitable selection procedures. Correlation coefficient is a statistical measure to find out the degree (strength) and direction of relationship between two or more variables. However, contribution of particular character to any dependent variable may not be judged from the correlation studies alone (Shailaja *et al.*, 2010). It permits a critical look to recognize the special forces that are acting to produce a given correlation and its relative importance (Shet *et al.*, 2009). Correlation studies resolve the complex relations between important traits, which are of immense help in the selection of superior genotypes. So, the knowledge of association of different characters is the first hand information for any important breeding programme (Ganapathy *et al.*, 2011).

Therefore, the present investigation aims to assess the variability together with the relative contribution of different yield attributes to grain yield and their interrelationship.

Materials and Methods

The experimental material consisted of twenty

one hybrid combinations which were obtained by crossing seven lines (female) viz., CO (Ra) 14, RAU 8, PES 110, VR 708, GPU 28, GPU 48 and OEB 259 with a set of three testers (male) viz., PR 202, KM 252 and K 7 employed in line x tester mating design by adopting a spacing of 30x10 cm at Department of Millets, Tamil Nadu Agricultural University, Coimbatore during *rabi* 2009-2010. The F₁s along with ten parents were raised in a randomised complete block design with three replications during *kharif*, 2010. The observations on days to 50 per cent flowering, plant height (cm), number of productive tillers per plant, number of fingers per ear head, longest finger length (cm), thousand grain weight (g), grain protein (%), iron and zinc contents (mg/100g), harvest index (%), single plant dry fodder yield (g) and single plant grain yield (g) were recorded. Standard statistical procedures were used for the analysis of variance, genotypic and phenotypic coefficients of variation (Burton, 1952), heritability (Lush, 1940), genetic advance, correlation (Johnson *et al.*, 1955) and path analysis (Dewey and Lu, 1959).

Results and Discussion

Analysis of variance revealed significant differences between the genotypes for all the characters studied. The estimates on genotypic coefficient of variation, phenotypic co-efficient of variation, heritability and genetic advance as per cent of mean for the traits under study are furnished (Table 1, Fig 1&2). In general, for all the traits studied, the phenotypic co-efficients of variation were higher than the genotypic co-efficients of variation. The values for genotypic co-efficients of variation obtained

for various yield, yield attributing and grain quality characters ranged from harvest index (2.66%) to iron content (49.48%). The high GCV was observed for iron content (49.48%), number of fingers per ear head (21.68%) and number of productive tillers per plant (20.69%). Moderate GCV was observed for longest finger length (14.02%). The lowest GCV was recorded for zinc content (8.51%), thousand grain weight (8.33%), single plant grain yield (8.19%), plant height (8.05%), protein content (7.15%), days to 50 per cent flowering (7.04%), single plant dry fodder yield (3.82%) and harvest index (2.66%). The results are in conformity with the findings of Satish *et al.* (2007) and Priyadharshini *et al.* (2011).

The values for PCV ranged from harvest index (3.17%) to iron content (49.48%). The highest magnitude of phenotypic co-efficient of variation was observed for iron content (49.48%), number of productive tillers per plant (24.95%) and number of fingers per ear head (24.20%). Moderate PCV was recorded for longest finger length (14.48%). The lowest PCV was recorded for single plant grain yield (8.84%), zinc content (8.54%), plant height (8.48%), thousand grain weight (8.35%), protein content (7.25%), days to 50 per cent flowering (7.13%), single plant dry fodder yield (4.81%) and harvest index (3.17%). The genotypic and phenotypic coefficients of variation indicated the extent of variability for different traits. Those results are in conformity with those of by Satish *et al.* (2007) and Priyadharshini *et al.* (2011).

Higher value of phenotypic coefficient of variation and genotypic coefficient of variation were recorded for iron content (49.48 and 49.48 % respectively) and

Table 1. Variability parameters for grain yield and yield attributing traits in finger millet

Trait	Mean	Range		GCV (%)	PCV (%)	h ₂ (%) (broad sense)	GA as per cent of mean
		Minimum	Maximum				
Days to 50 per cent flowering	60.30	51.33	68.67	7.04	7.13	97.53	14.33
Plant height (cm)	86.98	70.00	97.67	8.05	8.48	90.10	15.75
Number of productive tillers per plant	3.91	2.67	5.66	20.69	24.95	68.75	35.34
Number of fingers per ear head	6.55	4.00	8.66	21.68	24.20	80.26	40.01
Longest finger length (cm)	6.56	3.99	8.35	14.02	14.48	93.73	27.96
Thousand Grain weight (g)	2.39	2.08	2.90	8.33	8.35	99.43	17.11
Protein content (%)	8.36	7.22	10.02	7.15	7.25	97.38	14.54
Iron content (mg/100 g)	3.66	1.01	7.59	49.48	49.48	100.00	101.93
Zinc content (mg/100 g)	3.37	2.86	4.45	8.51	8.54	99.44	17.49
Harvest index (%)	40.06	38.01	41.71	2.66	3.17	70.07	4.58
Single plant dry fodder yield (g)	24.91	23.04	27.18	3.82	4.81	63.32	6.27
Single plant grain yield (g)	16.66	14.04	19.32	8.19	8.84	85.96	15.65

number of fingers per ear head (24.20 and 21.68 % respectively). High value of phenotypic coefficient of variation and genotypic coefficient of variation show that the genotypes exhibit much variation among themselves with respect to these characters. Further high phenotypic coefficient of variation and genotypic coefficient of variation for any characters indicated more scope for selection. Lowest value of phenotypic coefficient of variation and genotypic coefficient of variation were recorded for harvest index (%) (3.17 and 2.66 % respectively) and single plant dry fodder

yield (4.81 and 3.82 % respectively). Low values of phenotypic coefficient of variation and genotypic coefficient of variation indicate that the genotypes do not exhibit much variation among themselves with respect to these characters. Further low phenotypic coefficient of variation and genotypic coefficient of variation for any characters indicated less scope for selection. This was in agreement with the findings of Namita *et al.* (2008) and Punetha *et al.* (2011). The genotypic and phenotypic coefficients of variation indicated the extent of variability for different traits.

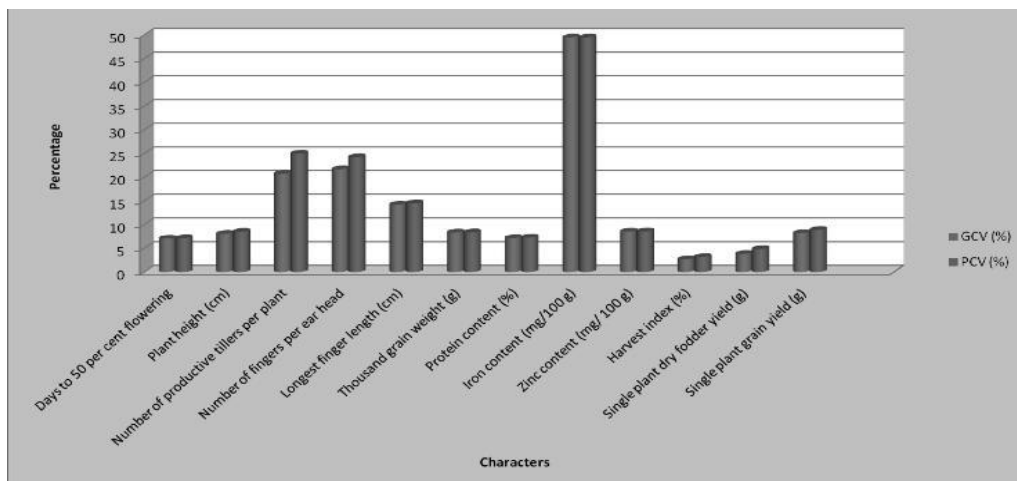


Fig. 1. Comparison of Genotypic Coefficient of Variation and Phenotypic Coefficient of Variation for yield and yield components in finger millet

High heritability coupled with low genetic advance, low heritability with high genetic advance or low heritability and low genetic advance offer less scope

for selection, as they were more influenced by environment and accounted for non-additive gene effects. High heritability coupled with high genetic

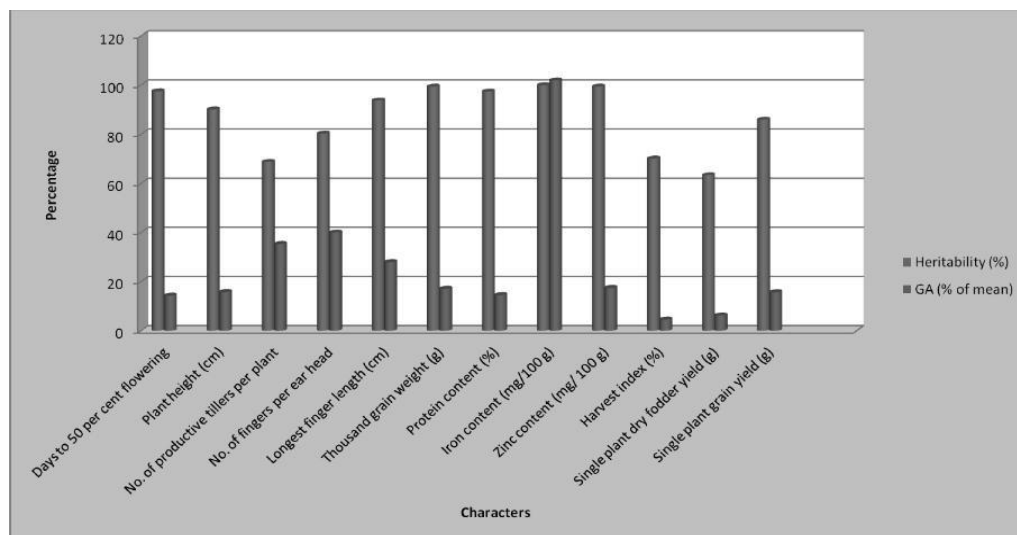


Fig. 2. Comparison of heritability in broad sense and genetic advance as per cent of mean for yield and yield components in finger millet

advance is indicative of greater proportion of additive genetic variance and consequently a high genetic

gain is expected from selection (Singh and Rai 1981). The characters having high heritability with

Table 2. Genotypic correlation coefficients among grain yield and their components in finger millet

TRAIT	FLOW	PH	PT	FNG	FLGTH	TGWT	PC	IRON	ZINC	HI	DFYP	GYP
FLOW	1.000	0.066	-0.050	0.149	0.057	0.195	0.261	0.033	-0.048	0.149	-0.177	-0.013
PH		1.000	0.274	0.473**	0.488**	-0.082	0.775**	0.201	-0.269	0.387 **	0.450 **	0.426 **
PT			1.000	0.089	0.107	0.033	0.253	0.356**	-0.103	0.848 **	0.936 **	0.909 **
FNG				1.000	0.613 **	0.050	0.533**	0.096	-0.221	0.250	0.344 *	0.281 *
FLGTH					1.000	0.027	0.404**	0.254	-0.285 *	0.126	0.367 **	0.261
TGWT						1.000	-0.010	0.043	-0.125	0.150	0.080	0.093
PC							1.000	0.246	-0.315 *	0.493 **	0.443 **	0.466 **
IRON								1.000	-0.358**	0.519 **	0.385 **	0.495 **
ZINC									1.000	-0.341 **	-0.150	-0.253
HI										1.000	0.908 **	0.973 **
DFYP											1.000	0.981 **
GYP												1.000

*Significant at 5 per cent level; **Significant at 1 per cent level.

FLOW – Days to 50 per cent flowering; FLGTH – Longest finger length; ZINC – Zinc content; PH - Plant height; TGWT – Thousand grain weight; HI – Harvest index; PT – Number of productive tillers per plant; PC – Protein content; DFYP – Single plant dry fodder yield; FNG – Number of fingers per ear head; IRON- Iron content; GYP – Single plant grain yields

low genetic advance as per cent of mean appeared to be controlled by non-additive gene action and selection for such characters may not be effective (Singh and Singh 2007). The genotypes recorded high heritability values for all the characters under

study. Iron content recorded the maximum heritability followed by zinc content (99.44%) and thousand grain weight (99.43%). Genetic advance as per cent of mean ranged from single plant dry fodder yield (6.27%) to iron content (101.93%) studies

Table 3. Direct (diagonal, bold) and indirect effects of eleven characters on grain yield per plant at genotypic level in finger millet

TRAIT	FLOW	PH	PT	FNG	FLGTH	TGWT	PC	IRON	ZINC	HI	DFYP	Genotypic 'r' with grain yield
FLOW	-0.0276	0.0009	-0.0002	-0.0056	-0.0042	-0.0047	-0.0075	-0.0004	-0.0047	0.0961	-0.0678	-0.0130
PH	-0.0018	0.0138	0.0001	-0.0180	0.0366	0.0020	-0.0222	0.0029	-0.0089	0.2488	0.1727	0.4260**
PT	0.0013	0.0038	0.0004	-0.0033	0.0080	-0.0008	-0.0072	0.0052	-0.0034	0.5456	0.3595	0.9090**
FNG	-0.0041	0.0065	0.0004	-0.0380	0.0460	-0.0012	-0.0153	0.0014	-0.0073	0.1611	0.1319	0.2810*
FLGTH	-0.0015	0.0067	0.0005	-0.0233	0.0751	-0.0006	-0.0116	0.0037	-0.0094	0.0813	0.1410	0.2610
TGWT	-0.0054	-0.0011	0.0002	-0.0018	0.0020	-0.0244	0.0002	0.0006	-0.0041	0.0964	0.0309	0.0930
PC	-0.0072	0.0107	0.0001	-0.0203	0.0303	0.0002	-0.0287	0.0036	-0.010	0.3171	0.1703	0.4660**
IRON	-0.0009	0.0027	0.0001	-0.0036	0.0190	-0.0010	-0.0070	0.0148	-0.0118	0.3343	0.1479	0.4950**
ZINC	0.0013	-0.0037	-0.0005	0.0084	-0.0214	0.0030	0.0090	-0.0053	0.0331	-0.2196	-0.0576	-0.2530
HI	-0.0041	0.0053	0.0003	-0.0095	0.0094	-0.0036	-0.0141	0.0076	-0.0113	0.6438	0.3486	0.9730**
DFYP	0.0048	0.0062	0.0004	-0.0130	0.0276	-0.0019	-0.0127	0.0057	-0.0049	0.5843	0.3841	0.9810**

Residual Effect =0.4124 ;FLOW – Days to 50 per cent flowering; FLGTH – Longest finger length; ZINC – Zinc content; PH - Plant height; TWGT – Thousand grain weight HI – Harvest index; PT – Number of productive tillers per plant ;PC – Protein content; DFYP – Single plant dry fodder yield; FNG – Number of fingers per ear head; IRON- Iron content; GYP – Single plant grain yield

are presented in (Table 1 and Fig 2). Iron content (101.93%) recorded the highest genetic advance followed by number of fingers per ear head (40.01%), number of productive tillers per plant (35.34%) and longest finger length (27.96 %). Moderate genetic advance was recorded for zinc content (17.49%), thousand grain weight (17.11%), single plant grain yield (15.65%), protein content (14.54%) and days to 50 per cent flowering (14.33%). The lowest genetic advance was recorded by single plant dry fodder yield (6.27%). High genetic advance indicated that these characters are governed by additive genes and selection will be rewarding for improvement of

these traits. The above findings support the results of Shet *et al.* (2009) and Priyadarshini *et al.* (2011).

The correlation between yield and yield contributing and nutritional characters in finger millet was studied for twenty one hybrids and ten parents. The nature and the extent of association that existed between the grain yield and its components were studied. The results on genotypic correlation studies are presented (Table 2). At genotypic level, plant height,

number of productive tillers, number of fingers per ear head, iron content, dry fodder yield and harvest index recorded significant positive correlations with grain yield. All other characters recorded non significant association with the grain yield. These results are in conformity with those of Krishnappa *et al.* (2009) and Mishra *et al.* (2008) for number of productive tillers and harvest index. Basavaraja and Sheriff (1991) reported for finger length. Regarding the inter correlation between yield attributes, days to 50 per cent flowering had significant positive association with plant height and thousand grain weight as observed by Anantharaju (2001) and Sumathi *et al.* (2006) for plant height in finger millet. The trait plant height was positively and significantly inter correlated with days to 50 per cent flowering, number of productive tillers per plant and finger length (Anantharaju, 2001).

From this study, it could be inferred that genotypic level of selection for high yield would be effective through positively associated characters viz., plant height, number of productive tillers, number of fingers per ear head, protein content, iron content, dry fodder yield and harvest index.

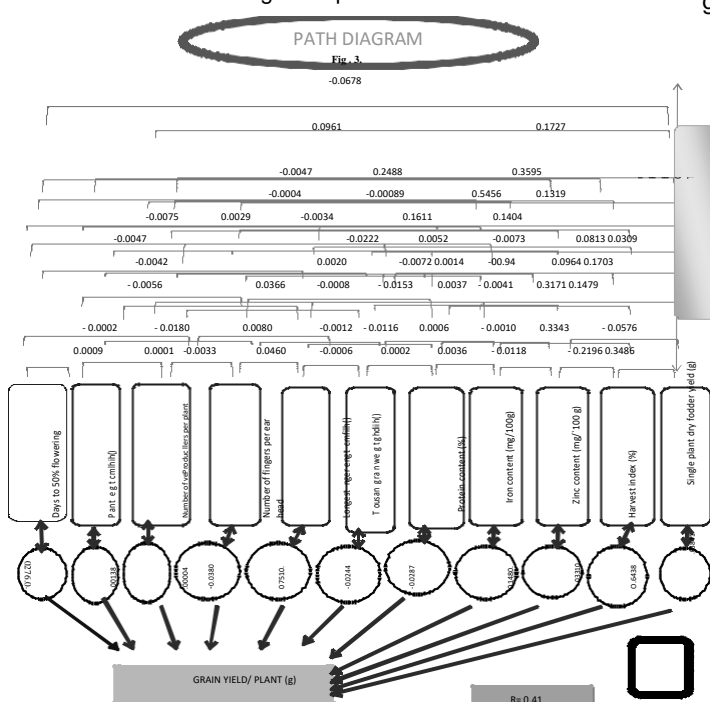


Fig. 3. Path diagram

Our results confirmed the findings of Bezaweleaw *et al.* (2006).

In the present study, path analysis on grain yield revealed that harvest index and dry fodder yield had high positive direct effects and the true relationships of these traits with grain are presented (Table 3 and Fig 3). Hence, direct selection for these traits could be practiced to reduce the undesirable effect of other component traits studied. Similar results were reported by Chunilal *et al.* (1996) for harvest index and Bezaweleaw *et al.* (2006) for productive tillers.

Regarding the indirect effect of component traits on grain yield, productive tillers followed by dry fodder yield, harvest index, plant height, iron content, protein content and number of fingers per ear head, were found to be low and negligible. The residual effect value of 0.412 showed that the additional characters could be included in future to formulate the selection indices for the improvement of grain yield in finger millet. Our results are also in conformity with the findings of Priyadarshini *et al.* (2010)

The genetic improvement in finger millet is possible through selection exercised for those characters which showed high values of phenotypic coefficient of variation and genotypic coefficient of variation, heritability, genetic advance, correlation and path analysis. In this study, the positive direct effect of thousand grain weight, finger number and productive tillers on grain yield per plant and their significantly positive association at genotypic level with grain yield per plant revealed that these characters were the major contributors to grain yield per plant. This will provide an opportunity to select better recombinants for various characters and thereby creating large variability for these characters in the future generations. However, characters predominantly controlled by additive gene action would be amenable to conventional breeding methods (Roy and Senapati, 2012).

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