



## Genetic Variability and Correlation Analysis in Global Composite Collection of Finger Millet (*Eleusine coracana* (L.) Gaertn)

A. Bharathi<sup>1</sup>\*, P. Veerabathiran<sup>1</sup>, C.L.L. Gowda<sup>2</sup> and H.D. Upadhaya<sup>2</sup>

<sup>1</sup>Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore

<sup>2</sup>International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad, Andhra Pradesh, India

**A global composite collection of finger millet germplasm which included ICRISAT core collection was evaluated for fifteen quantitative characters in augmented design with four control cultivars during 2007 rainy season. The objectives were to assess the variability and association between the characters related to yield. The genotypic variances were highly significant for all characters except plot yield. Plot yield exhibited the highest range (0.02 – 2.6 t ha<sup>-1</sup>). The phenotypic and genotypic coefficients of variations varied from 9.59 to 57.13% and 11.14 to 64.96% respectively. Heritability estimates ranged from 37.01% for single panicle weight to 98.34% for days to 50 percent flowering. Plot yield was strongly associated positively with productive tillers, number of fingers and days to 50 percent flowering. Generally, the result revealed the existence of variability for the characters studied in finger millet genotypes.**

**Key words:** Finger millet, genetic variability, correlation analysis.

Finger millet (*Eleusine coracana* (L.) Gaertn.) is one of the most important small millets grown in eastern and southern Africa. It is cultivated mostly as a rainfed crop in India for its valued food grains and its adaptability to wide range of geographical areas and agro-ecological diversity, mostly countries in Africa and Asia. Finger millet is highly nutritious as its grains contain 65- 75% carbohydrates, 5-8% protein, 15 -20% dietary fiber and 2.5-3.5% minerals (Chetan and Malleshi, 2007). Considering its importance in food and fodder security, adequate information on variability and interrelationship between yield and its attributes is meager in finger millet.

Information on nature and magnitude of variability present in a population due to genetic and non-genetic causes is an important prerequisite for systemic breeding programs to improve yield potential of the crop. So, proper evaluation of the extent of genetic variation available for the yield attributes will be of immense help to plant breeders. Information on the correlation co-efficients between grain yield with yield contributing traits is a prerequisite for improving yield. In formulating selection program for the improvement of yield in any crop, study on the relationship of yield with other traits would be of great value. It is a well established fact that the progress in improvement of a crop depends on the degree of variability in the desired characters in the base materials vis-à-vis germplasm collection. The present study was

undertaken to study the extent of variability present in 1000 finger millet germplasm and to assess the inter relationship between the characters related to yield.

### Materials and Methods

The global composite collection was developed from the entire collection of finger millet germplasm conserved in RS Paroda Genebank, International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad. It included Core collection of 622 accessions, National core collection, landraces and other wild relatives. It was evaluated along with four control cultivars viz., VR708, VL149, PR202 and RAU8 in an augmented design in 2007 rainy season at ICRISAT Centre, Patancheru, India. One of four control cultivars was repeated after every 9 test entries. Each plot consisted of a single 4 m long row on a ridge, in a ridge and furrow system. The distance between rows was 60 cm and between plants was 10 cm. A good crop stand was maintained following standard crop cultivation practices. Data on fifteen quantitative (days to 50% flowering, plant height, productive tillers, flag leaf blade length and width, flag leaf sheath length, peduncle length, panicle exertion, ear head length and width, number of fingers, length and width of longest finger, panicle weight and grain yield) traits were recorded following finger millet descriptors (IBPGR, 1985). Data for the quantitative traits were recorded on five representative plants from each row. Grain yield per plant was recorded on all plants in a plot and it was converted into grain yield per

\*Corresponding author email: bharat22880@yahoo.co.uk

hectare. The random model of residual maximum likelihood (REML) in GenStat 10 was used to analyze data of 15 quantitative characters. Mean, range, variance,  $h_2$  and phenotypic correlation were calculated for all characters.

## Results and Discussion

The genotypic variance values were highly significant for all characters except plot yield implying that the genotypes tested were highly variable (Table 1). Substantial variations in finger millet have

been also reported in previous studies (Prasada Rao *et al.*, 1994; Daba, 2000). The mean performance of most genotypes for characters days *viz.*, to 50 percent flowering, number of productive tillers, finger length and finger number and some accessions for plant height and grain yield exceeded the performance of the all four check varieties (data not shown). This situation ensured the existence of base population for improving the character of interest. The range and the mean for the fifteen finger millet characters studied are summarized in

**Table 1. Variability parameters for quantitative characters in global finger millet composite collection.**

Character	Genotypic variance	Mean	Range	GCV (%)	PCV (%)	$h_2$ (%)
Days to 50% flowering	69.2*	70.0	41 - 164	11.89	12.09	98.34
Plant height (cm)	120.7*	114.5	50 - 155	9.59	11.14	86.04
Productive tiller number	1.9*	3.7	1 - 18	14.63	20.18	72.49
Flag leaf blade length (mm)	2270.0*	333.2	100 - 600	14.30	17.68	80.88
Flag leaf blade width (mm)	12.5*	9.6	4 - 15	57.13	64.96	87.94
Flag leaf sheath length (mm)	84.0*	78.5	0-300	37.87	55.16	68.65
Peduncle length (mm)	1416.0*	192.9	0-360	25.47	29.2	87.22
Panicle exertion (mm)	109.0*	98.0	0-400	33.01	35.22	93.72
Ear head length(mm)	266.5*	87.7	10 - 200	26.14	29.56	88.43
Ear head width (mm)	71.2*	54.2	12 - 150	33.61	35.25	95.34
Number of fingers (numbers)	47.5*	71.3	10 - 200	26.14	37.6	69.52
Length of longest finger (mm)	61.51*	11.1	5 - 15	22.14	26.42	91.34
Width of longest finger (mm)	1.2*	7.9	2 - 22	9.96	12.85	77.5
Panicle weight (g)	15.7*	10.1	0.63 – 13.1	26.42	35.98	73.37
Plot yield (t ha <sup>-1</sup> )	4.8*	0.9	0.02 – 2.6	35.25	40.51	96.69

\*significant at 1% level

Table 1. Regardless of the variation in the relative magnitude of the range, the mean of the genotypes generally displayed considerable differences between the minimal and maximal values for all the traits evaluated.

Plot yield exhibited the widest range (0.02 – 2.6t ha<sup>-1</sup>) followed by finger length (10 – 200mm) and days to 50 percentage flowering (41 – 164 days) respectively. Relatively low range was recorded for leaf blade width and width of longest finger. Similar to the result of this study, a wide range of variations for plant height and productive tillers (Prasada Rao *et al.*, 1994) and for most traits studied (Daba, 2000), were reported. Such a broad diversity apparent among the finger millet genotypes tested would provide ample opportunities for the genetic improvement of the crop through selection directly from the landraces and/or following traits recombination through intra-specific hybridization of desirable traits.

Low phenotypic and genotypic variances were depicted by plant height, days to 50 percent flowering and width of longest finger and high PCV and GCV for other traits. This indicated the existence of immense inherent variability that remained unaltered by environmental conditions among the genotypes, which in turn was more useful for

exploitation in hybridization and/or selection. For all the 15 traits, the GCV and PCV ranged in the orders of 11.14 to 64.96% and 9.59 to 57.13 respectively. Generally, the PCV estimates were higher than the GCV showed that the apparent variation was not only due to genotypes but also to the influence of environment. Heritability which is the heritable portion of phenotypic variance is a good index of transmission of characters from parents to offspring (Falconer, 1981). In this study, heritability ( $h_2$ ) estimates ranged from 37.01% for single panicle weight to 98.34% for days to 50 percent flowering. Likewise, high heritability estimates for days to flowering and finger length were already reported (Daba, 2000). Similar results of high PCV and GCV were already observed (Abraham *et al.*, 1989).

Correlation provides information on the nature of relationship among characters. Grain yield is a complex trait controlled by many genes. The estimates of genotypic correlation coefficients are displayed in Table 2. The strongest positive association was observed between plant height with days to 50 percent flowering ( $rg=0.542$ ) while the strongest negative association between days to 50 percent flowering and number of panicle ( $rg=-0.101$ ). The high association of grain yield per plant with productive tillers was considered to occur due to

**Table 2. Phenotypic correlation coefficients between 15 quantitative traits in the global finger millet composite collection**

Traits	DF	PH	PTN	FLBL	FLBW	FLSL	PL	PE	EHL	EHW	LLF	WLF	NF	PW	PY
DF	-														
PH	0.542**	-													
PTN	-0.105**	-0.089**	-												
FLBL	0.044	0.245**	-0.059*	-											
FLBW	0.801**	0.132**	-0.031	0.143**	-										
FLSL	-0.218**	0.129**	0.0207	0.044	-0.081**	-									
PL	-0.309**	0.097**	-0.036	0.051*	-0.073*	0.230**	-								
PE	-0.197**	0.081**	-0.021	0.064*	-0.070*	0.112**	0.662**	-							
EHL	0.056*	0.184**	-0.042	0.166**	0.142**	-0.042	0.015	-0.082**	-						
EHW	0.028	0.064*	0.027	0.068**	0.210**	0.026	0.014	0.003	0.132**	-					
LLF	0.198**	0.199**	-0.051*	0.230**	0.051*	0.097**	-0.070	-0.062*	0.716**	0.066*	-				
WLF	0.203**	-0.019	-0.090**	0.108**	0.221**	-0.181**	0.090	-0.129**	0.060*	0.214**	0.032	-			
NF	-0.101**	-0.058*	0.083**	-0.005	0.084**	0.003	0.034	0.019	0.100**	0.304**	-0.049	-0.112**	-		
PW	0.299**	0.112**	-0.127**	0.053*	0.095**	-0.088**	-0.174**	-0.095**	0.102**	0.183**	0.147**	0.203**	0.066*	-	
PY	0.240**	0.550**	0.077*	0.188**	0.366**	-0.179**	-0.210**	-0.342**	0.337**	0.233**	0.583**	0.720**	0.025	0.575**	-

\* and \*\* significant at  $P = 0.05$  and  $0.01$  respectively. DF (days to 50% flowering), PH (plant height), PTN (productive tiller number), FLBL (flag leaf blade length), FLBW (flag leaf blade width), FLSL (flag leaf sheath length), PL (peduncle length), PE (panicle exertion), EHL (ear head length), EHW (ear head width), LLF (length of longest fingers), WLF (width of longest fingers), NF (number of fingers), PW (Panicle weight) and PY (plot yield).

favorable influence of the environment. Likewise, positive associations of grain yield per plant with productive tillers were reported (Daba, 2000). In contrast to the result of this study, significant and positive associations of grain yield per plant with days to ear head length and with plant height were also reported (Daba, 2000). Number of productive tillers per plant was the important yield contributing characters and need to be considered while framing selection criteria in finger millet breeding program (Sumathi *et al.*, 2006; Dagnachew *et al.*, 2012). Generally, the correlation results revealed that besides selection for plot yield, indirect selection for ear head length, days to 50 % flowering, finger number and productive tillers might lead to the improvement of grain yield per plant since they exhibited significantly positive correlation with the grain yield per plant.

### Conclusion

The success of genetic improvement in any character depends on the nature of variability present for that character. Variability in the population is important for disease resistance, varietal adaptability and effective selection. An effort was made in this study to assess the variability present in the global composite collection of finger millet. Regardless of the magnitude, all the characters studied showed wide range of variability. This ensured the existence of ample variability and potential in the composite collection to offer a particular character of interest. This could be employed in the genetic improvement of finger millet

through hybridization and/or selection. The correlation analysis clearly indicated apart from selection for grain yield; indirect selection for finger number and productive tillers could be applied in the improvement of finger millet.

### References

- Abraham, M.J., Gupta, A.S. and Sarma, B.K. 1989. Genetic variability and character association of yield and its components in finger millet in an acidic soil of Maghalaya. *Indian J. Agric. Sci.*, **59**: 579-581.
- Chetan S. and Malleshi, N.G. 2007. Finger millet polyphenols: Characterization and their nutraceutical potential. *American J. Food Technol.*, **2**: 582-592.
- Daba, C. 2000. Variability and Association among Yield and Related Traits in Finger Millet [*Eleusine coracana* (L) Gaertn]. M.Sc. thesis, Alemaya University.
- Falconer, D.S. 1981. *Introduction to Quantitative Genetics*, Ed. 2. Longmans Green, London/New York.
- IBPGR. 1985. Descriptors for Finger Millet. International Board for Plant Genetic Resources. Rome.
- Prasado Rao, K.E., de Wet, J.M.J., Gopal Reddy, V. and Mengesha, M.H. 1994. Diversity in the small millets collection at ICRISAT, pp.331- 345. In K.E. Riley, S.C. Gupta, A. Seetharam and J.N. Mushonga (eds.). *Advances in Small Millets. Inter. Sci.*, New York.
- Sumathi, P., John Joel, A. and Muralitharan, V. 2006. Inter trait association and path analysis in finger millet (*Eleusine coracana* L.Gaertn.). *Madras Agric. J.*, **93**: 115-119.
- Dagnachew, L., Tesfaye, K., Fetene, M. and Villiers, S.D. 2012. Inheritance and association of Quantitative Traits in Finger Millet (*Eleusine coracana* Subsp. *Coracana*), landraces collected from eastern and south eastern Africa, *Inter. J. Genetics*, **2**: 12-21.