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GENETIC VARIABILITY FOR MORPHO-AGRONOMIC TRAITS IN CORE GERMPLASM COLLECTIONS OF FINGER MILLET (*Eleusine coracana* (L.) GAERTN)

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Abstract

The use of diverse germplasm is the key to success of crop improvement programmes. Unwieldiness of germplasm size which has restricted the researchers for accurate characterization and resulted in limited utilization of genetic resources in crop improvement programmes. A smaller (622 accessions) and manageable sub sets (known as core collections) which capture maximum variability of the entire global collections (5949 accessions) has been developed in finger millet. The relatively smaller size of the core collections could be effectively characterized for a number of economic traits. In the present investigation, 622 core finger millet germplasm accessions were evaluated for six quantitative characters. The results revealed substantial genetic variability for all the traits investigated. The contribution of genetic variability was greater in relation to environmental variability towards total variability for all the investigated traits among the germplasm accessions. These results are discussed in relation to the development of strategic genetic material for localizing genes controlling economic traits and designing suitable breeding and selection strategies for genetic improvement of finger millet.

Key Words: *Core accessions, finger millet, genetic variability.*

Introduction

In India, finger millet ranks 3rd among millets after sorghum and pearl millet (Anon, 2008). Wide adaptability, nutritional quality, dual-purpose (grain and dry fodder) nature of crop and high multiplication rate of finger millet makes it one of the ideal crops for use as a staple food crop and as an indispensable crop component in mixed crop-livestock system of farming prevalent in semi-arid tropics. The current on-farm finger millet productivity at 1.84 t ha^{-1} (Annon.2008) is considerably low compared to its potential of 2.68 t ha^{-1} (Annon. 2008) as realized in research stations under well managed conditions. One of the ways to break the productivity ceiling can be enhanced by use of diverse germplasm in crop improvement programmes. A core sub set of 622 finger millet accessions was developed which captures the maximum diversity present in the entire global collection of 5949 accessions being maintained at International Crops Research for Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India (Upadhyaya et al. 2006). Such core collections could be effectively evaluated and used in breeding programmes. These considerations prompted us to assess genetic variability for grain yield and its component traits in core finger millet collections.

Material and Methods

The material for the present study comprised of 622 core finger millet germplasm accessions procured from ICRISAT, Patancheru, India and four check varieties, PR 202, VR 708, GPU 28 and MR 2. The seeds of check varieties were procured from All India co-ordinated small millets improvement project, UAS, GKVK, Bengaluru. Twenty four days-old seedlings of 622 germplasm accessions and four check varieties were transplanted in the experimental plots of Zonal Agricultural Research Station (ZARS), Mandya, Karnataka on 1st August 2008 in an Augmented design. Recommended agronomic and plant protection practices were followed during crop growth period to raise a good crop. Ten competitive plants in each entry were labelled for recording data on six quantitative traits such as days to 50 per cent flowering, plant height, number of productive tillers $plant^{-1}$, number of fingers ear $head^{-1}$, 1000-grain weight and grain yield $plot^{-1}$.

Statistical Analysis

The mean values of six quantitative traits computed on sample plants in each accession and check varieties were subjected to statistical analysis. The analysis of variance (ANOVA) (Federer, 1961) was carried out to dissect total variability of the entries into sources attributable to genotype and error using the SPAD software developed by IASRI, New Delhi, India.

Results and Discussion

Analysis of Variance for Quantitative Traits

Mean squares due to accessions + checks, accessions *per se* and check varieties were significant for all the six quantitative traits under study (Table1). These results indicate substantial variability among germplasm accessions under study. Purushotham Rao (1992), Malali Gowda (1996) and Satish (2003) have also reported significant differences among large number of finger millet germplasm accessions.

Components of Quantitative Traits Variance

The total variation (phenotypic) of traits is attributable to genotype and environment assuming absence of interaction between them. The variation due to genotype can only be managed to suit to end-user needs. To compare variation of the accessions across six quantitative traits at phenotypic and genotypic levels, the phenotypic and genotypic variations were standardized to make them unit-free and expressed as phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV). Grain yield plot^{-1} was less variable both at phenotypic and genotypic levels compared to other traits among the germplasm accessions as indicated by its PCV and GCV estimates in relation to other traits. However, substantial range in the expression of germplasm lines for all the traits offer ample scope for selection of desirable lines for further use in genetic enhancement. Comparatively limited influence of weather variables on the expression of germplasm lines for most of the traits including grain yield as suggested by narrow difference between PCV and GCV has clearly reflected in higher broad-sense heritability (Table 2). Higher predicted genetic advance could be realized as the genetic variation among the germplasm accessions is solely attributable to genes acting additively, which cause greater resemblance between selected parents and their progeny.

The accessions contrasting for economic traits are useful in inheritance studies and developing trait-based mapping populations for chromosomal localization and molecular dissection of genes controlling the economic traits. DNA markers that are in near complete linkage disequilibrium with genomic regions affecting grain yield, would facilitate marker-assisted introgression of quantitative trait loci (QTLs) controlling grain yield into elite agronomic background. The accessions (IE 2322 and IE 6059) that are contrasting for plant height, number of productive tillers plant^{-1} and grain yield plot^{-1} are useful for developing multiple traits-based mapping population for molecular dissection, chromosomal localization and unravelling mode of action of genes controlling these traits simultaneously.

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Appendix:

Table 1: Analysis of variance (mean sum of squares) for 14 quantitative characters in finger millet core germplasm accessions (n =622).

Source of variation	df	Days to 50% flowering	Plant height (cm)	Number of productive tillers plant^{-1}	Number of fingers earhead^{-1}	1000 grain weight (g)	Grain yield Plot^{-1} (g)
Blocks	22	4.77**	0.40	1.10	0.37*	0.03**	41.9**
Accessions + Check varieties	625	1493.15**	128.65**	6.69**	16.80**	0.37**	47.40**
Accessions	622	1323.73**	98.90**	5.00**	15.05**	2.45**	32.90**
Check varieties	03	630.05**	249.10**	47.23**	5.14**	0.11**	428.21**
Accessions v/s Checks	01	1097.80**	256.87**	934.551**	1139.336**	15.67**	7910.78**
Error	66	5.23	7.90	0.76	0.17	0.01	18.58

Significant @ P = 0.05; ** = Significant @ P = 0.01

Table 2: Estimates of mean, components of variance, and genetic advance for different agronomic characters in finger millet core germplasm accessions (n = 622)

Characters	Mean ± SE	Range		Coefficient of variability		h^2 (broad sense) (%)	GA as per cent of mean (%)
		Lowest	Highest	PCV (%)	GCV (%)		
Days to 50% flowering	71.97 ± 0.22	50.88 (3025)	90.88 (4570)	50.11	42.84	85.50	13.64
Plant height (cm)	103.63 ± 0.39	68.26 (7072)	152.44 (2799)	98.49	90.87	92.26	17.83
Number of productive tillers $plant^{-1}$	5.07 ± 0.04	0.77 (2379)	10.44 (5999)	32.08	17.08	53.25	20.52
Number of fingers ear $head^{-1}$	7.53 ± 0.04	4.03 (7157)	14.28 (5563)	15.66	13.40	85.58	23.60
1000-grain weight (g)	2.46 ± 0.01	0.52 (4709)	3.73 (2872)	48.23	32.08	73.76	26.56
Grain yield $plot^{-1}$ (g)	0.42 ± 0.01	0.04 7128)	0.84 (5239)	6.78	4.41	65.07	43.83

Values in the parenthesis indicate accession numbers