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Genetic variability studies in nutritional improvement in finger millet [*Eleusine coracana* (L.) Gaertn]

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ABSTRACT : Finger millet [*Eleusine coracana* (L.) Gaertn] or *Ragi* is an important food crop in Africa and south Asia. Finger millet is commonly called as "nutritious millet" as the grains are nutritiously superior to many cereals providing fair amount of protein, minerals, calcium and vitamins in abundance to the people. The protein of finger millet is considered to be biologically complete" as in the case of milk. Combining ability studies are useful in classifying the parental lines in terms of their hybrid performance. It also helps in identifying the parents suitable for hybridization programme and deciding suitable breeding methodology. The line x tester analysis is one, which helps to find out combining ability of parents for yield and yield attributes.

KEY **W**ORDS : Finger millet, Nutritious millet, Combining ability, Molecular markers

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Ragi is considered as one of India's best dry land crops and most of it is produced without supplemental water. The plant is both adaptable and resilient, survives on lateritic soils, withstands some salinity and has a few serious diseases or pests. India only a very small fraction of the total available germplasm collection has been used in the national breeding programmes (Ramakrishna *et al.,* 1996). The project coordination cell on small millets in India has an exhaustive collection more than 6000 accessions representing the entire global distribution of finger millet. Other major collections are held by International Institutions such as ICRISAT in India (5000 accessions), the National Farming Research Station in Kenya (1500 accessions), the Gene Bank in Kenya (1000 accessions), the Plant Genetic Resource Centre in Ethiopia (1000 accessions) and the University of Georgia in USA (1500 accessions). A number of non-governmental organizations such as Green Foundation in India also maintain finger millet collections (Ramakrishna *et al.,* 1996). In recent years, crop improvement programme includes the molecular analysis for the reliability.

RESEARCH PROCEDURE

Seven lines *viz.*, CO (Ra)14, RAU 8, PES 110, VR 708, GPU 28, GPU 48 and OEB 259 were crossed with three testers *viz.*, PR 202, KM 252 and K 7 of diverse genetic architecture in a line x tester mating design resulting in twenty one hybrids. All the twenty one hybrids along with their parents and a check CO (Ra)14 were included in a Randomized Complete Block Design. The characters studied for yield and yield attributing traits were, days to 50 per cent flowering, plant height, number

of productive tillers per plant, number of fingers per ear head, longest finger length, thousand grain weight, harvest index, single plant dry fodder yield and single plant grain yield.

Varietal improvement for yield may, therefore, is achieved through better understanding of the genetic architecture of the crop. The inheritance of grain yield being more complex as evidenced from the studies made in other crops like wheat, rice, *Ragi*, etc., Therefore, it is suggested that this approach should be reviewed and reoriented, so as to formulate breeding programmes for yield, by which choice of the parents is based not only on desirable agronomic characters but also on phenotypic stability, combining ability, genetic diversity and genetic analysis of yield and its component characters. The use of the concepts of combining ability helps in choosing proper parents for hybridization.

RESEARCH ANALYSIS AND REASONING

The information on genetic diversity, which helps in choosing parents for generation of new varieties, needs continuous evaluation of germplasm for useful characters, which in earlier days was solely based on the available morphological data. Morphological traits/ markers reflect not only the genetic composition of the cultivar, but also the interaction of the genotype with the environment in which it is expressed and hence, the descriptions based on morphological information for the calculation of genetic distance. Advances in molecular biology have provided descriptions based on DNA markers (Shailaja *et al.*, 2010).

In the preset study, fifteen primers amplified in finger millet and produced seventeen alleles were polymorphic. The number of markers produced by different primers ranged from 3 to 4. Among the primers, UGEP 10 produced maximum number of bands.

The data of SSR markers was analysed using Sequential Hierarchial and Nested (SHAN) clustering methods of the NTSYS-pc programme (Rolf, 2001) based on Jaccard's similarity co-efficient with an unweighted pair group method with arithmetic average (UPGMA). The SSR marker profiles resulted in three clusters at nearly 57 per cent similarity.

Cluster I was constituted by four genotypes *viz*., VR 708, KM 252, K7 and CO (Ra) 14. The cluster II comprised of 3 genotypes *viz*., PES 110, OEB 259 and GPU 48. Cluster III consisted of 3 genotypes PR 202, RAU 8 and GPU 28. So, the diverse parents PES 110 and CO (Ra) 14 can be used for crossing programme.Similar results were reported by Priyadhashini (2010), the parents CO (Ra) 14 and TNAU 1039 are the diverse and they are very much useful for crossing programme.

The extent of genetic diversity of 10 parents of finger millet was estimated using SSR markers. A total of 23 polymorphic alleles were generated by the 15 primers. Out of 15 primers, 10 were polymorphic primers. Among the primers, UGEP 10 gave higher number of SSR fragments. Similarity indices for all pair wise combinations among the 10 parents were presented in Table 1. The similarity index values were computed as a ratio of number of similar bands to the total number of bands in each pair wise comparison of all the 10 parents. The similarity index was highest (0.92) between KM 252 and VR 708. The least similarity index (0.31) was observed between PR 202 and CO (Ra) 14. Cluster analysis was performed on similarity co-efficient matrices calculated from SSR

Table 1: Similarity matrix of ten parents using SSR markers in finger millet

Parents	VR 708	KM 252	PES110	GPU48	OEB 259	K 7	CO(Ra)14	PR 202	RAU 8	GPU 28
VR 708	1									
KM 252	0.92	1								
PES 110	0.66	0.53	1							
GPU48	0.66	0.54	0.69	1						
OEB 259	0.46	0.38	0.84	0.54	1					
K 7	0.69	0.77	0.77	0.62	0.61	1				
CO(Ra)14	0.61	0.69	0.38	0.54	0.38	0.62	1			
PR 202	0.46	0.38	0.59	0.84	0.69	0.38	0.31	1		
RAU 8	0.62	0.54	0.38	0.54	0.38	0.54	0.32	0.46	1	
GPU 28	0.54	0.38	0.38	0.54	0.38	0.54	0.32	0.69	0.84	1

markers to generate a dendrogram of 10 parents. The similarity ranged from 0.45 to 0.92. As a whole the 10 genotypes were grouped into 3 clusters at 57 per cent similarity levels. Cluster I was constituted by four genotypes *viz*., VR 708, KM 252, K 7 and CO (Ra) 14. The cluster II comprised of 3 genotypes *viz*., PES 110, OEB 259 and GPU 48. Cluster III consisted of 3 genotypes PR 202, RAU 8 and GPU 28.

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