

Molecular Marker Technology for Finger Millet Crop Improvement - An under-Utilized, Food and Nutritional

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Abstract

Finger millet, is a highly self-pollinated, allo-tetraploid crop believed to have been domesticated in East Africa, probably in the highland region that extends from Ethiopia to Uganda. It is known to save the lives of poor farmers from starvation at times of extreme drought. One of the major yield limiting factors is blast disease caused by *Magnaporthe grisea*. It is more nutritious than most cereal grains with respect to minerals, dietary fibre and amino acids. With the advancement of molecular marker technology, a lot of progress has been made in majority of the crops except neglected crops like small millets, such as finger millet, though it is highly nutritious crop. A considerable amount of work has been done for assessing the genetic diversity among finger millet germplasm using microsatellite and EST based microsatellite markers. The first genetic map of finger millet was also available using 82 SSR markers. The present review describes the application, status and future perspectives of molecular marker technology for finger millet crop improvement.

Keywords: Eleusine Coracana (L.); Microsatellite Markers; Expressed Sequence Tags; Quantitative Trait Loci

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Introduction

Finger millet, *Eleusine coracana* (L.) Gaertn, is a tetraploid crop ($2n = 4x = 36$; genome constitution AABB) belonging to the grass family Poaceae, subfamily Chloridoideae. It is highly self-pollinated, allo-tetraploid ($2n = 36$) crop derived from the wild tetraploid progenitor *E. coracana* subsp. *africana*. Cultivated finger millet (*E. coracana* subsp. *coracana*) is believed to have been domesticated in East Africa, probably in the highland region that extends from Ethiopia to Uganda, where populations of wild finger millet (subsp. *africana*) are particularly abundant. Based on inflorescence compactness and shape, finger millet germplasm is classified into races and sub races. Species *E. coracana* consists of two subspecies *africana* and *coracana*.

Finger Millet as a Food Security Crop

Finger millet is extensively cultivated in the tropical and sub-tropical regions of Africa and India and is known to save the lives of poor farmers from starvation at times of extreme drought. As a consequence, finger millet is the important cereal for many rural communities in marginal environments in eastern Africa, and India where they contribute significantly to the well-being of the local people. Of all the cereals and millets, finger millet has the highest amount of calcium (344 mg) and potassium (408 mg). It has higher dietary fibre, minerals, and sulphur containing amino acids compared to rice and wheat which are the major staple food crops of most of the world. There is an increase in the demand in other parts of the world because of its special characters like blood glucose

lowering, cholesterol lowering, anti-ulcerative, and wound healing properties. Despite its importance as a low input crop, its productivity in the region is limited to between 400 and 2,000 kg/ha [1]. One of the major yield limiting factors is blast disease caused by *Magnaporthe grisea* (anamorph *Piricularia grisea*). The average loss due to blast has been reported to be around 28-36%, and in certain areas yield losses could be as high as 80-90% [2]. Crop improvement through conventional breeding is slow, especially for traits controlled by quantitative gene action like disease resistance. Hence, the use of modern crop improvement tools such as genomics to transfer information about genes from model species to the species of interest and genetic mapping in order to identify genes controlling traits of interest.

Finger Millet as a Nutritional Security Crop

Ensuring food security ought to be an issue of great importance for a country like India where more than one-third of the population is estimated to be absolutely poor and one-half of all children malnourished in one way or another. According to the US National Research Council, 1996, finger millet grain is more nutritious than most cereal grains with respect to minerals, dietary fibre and amino acids. Finger millet grain contains various phenolic compounds, which due to their anti-oxidant properties, are potentially health promoting. In order to improve the nutritional status of finger millet crop, there is a need to explore the genetic diversity of finger millet and to evaluate its protein and essential amino acids using morpho-physiological and modern genomics tools. The chemical composition of finger millet grain is given in table 1.

Table 1: The chemical composition of finger millet grain

Nutrients							
Major nutrients (g/100g)		Minerals (mg/100g)		Vitamins (mg/100g)		Amino acids (g/100g)	
Moisture	12.0	Calcium	358.0	Vitamin A	6.0	Essential amino acids	
Carbohydrate	74.0	Chlorine	84.0	Thiamine	0.2	Phe	6.2
Protein	7.3	Copper	0.5	Riboflavin	0.1	His	2.6
Fat	1.3	Iodine	10.0	Niacin	1.0	Ile	5.1
Total dietary fibre	22.0 ^b	Iron	9.9	Vitamin C	1.0	Leu	13.5
Ash	2.6	Magnesium	140			Lys	3.7
		Manganese	1.9			Met	2.6
		Molybdenum (µg)	2.0			Thr	5.1
		Phosphorous	250.0			Val	7.9
		Potassium	314.0			Trp	1.3

Application of Molecular Marker Technology for Finger Millet Crop Improvement

With the advancement of molecular marker technology, a lot of progress has been made in majority of the crops except neglected crops like small millets, such as finger millet, though it is highly nutritious crop. In major cereal crops, molecular markers have been using for several studies like genetic diversity, QTL mapping, Association mapping and

marker assisted breeding studies [3, 4]. However, in case of finger millet, these are at initial stages and need to focus at large scale. There are very few reports available on the assessment of genetic diversity among finger millet at the national and international level.

Salimath et al. [5] reported molecular diversity of 20 finger millet accessions by using isozyme, RFLP and RAPD.

Sixteen isozyme loci and 15 RFLP loci showed uniformity among the accessions indicating less genetic diversity among the accessions. Weisinget al. [6] made an attempt to identify the transferability of 210 SSR markers from major cereal crops (wheat, rice, maize, and sorghum) to *E. coracana* and more than half (57%) of the SSR primers screened, generated reproducible cross-species or cross-genus amplicons. They described that the transfer rate of SSR markers was correlated with the phylogenetic relationship or genetic relatedness. Babu et al. [7] reported the diversity of 32 finger millet genotypes, using 50 RAPD markers and reported a total 529 loci of which 479 loci (91%) were polymorphic and informative to differentiate the accessions and do cluster analysis. Recently, Dida et al. [8] reported the population structure of 79 finger millet accessions with 45 SSR markers and identified significant difference of plant architecture and yield in Asian and African subpopulation.

Linkage Mapping Studies in Finger Millet

Dida et al. [1] generated a genetic map of the tetraploid finger millet (*Eleusinecoracana* subsp. *coracana*) genome ($2n = 4x = 36$) by using RFLP, AFLP, EST and SSR markers. The maps span 721 cM on the A genome and 787 cM on the B genome and cover all 18 finger millet chromosomes, at least partially. They have developed a set of 82 SSR markers by using methylation-sensitive restriction enzymes and mapped thirty-one SSRs. They have developed a total of 18 major linkage groups with seven or more markers were formed at LOD 11. Srinivasachary et al. [9] studied the comparative genomic analysis of finger millet and rice genomes through molecular markers and showed that 85% synteny present between these two crops.

EST Based SSR Markers for Finger Millet Crop Improvement

Microsatellites or Simple Sequence Repeat (SSR) markers have been useful for integrating the genetic, physical and sequence-based physical maps in plant species, and simultaneously have provided molecular breeders with an efficient tool to link phenotypic and genotypic variation. The

disadvantages of SSR markers are that they are often tedious and costly cloning and enrichment procedures required for their generation. Microsatellites developed from Expressed Sequence Tags (ESTs), popularly known as EST-SSRs or genic microsatellites, represent functional molecular markers as a putative function for a majority of such markers can be deduced by database searches and other in-silico approaches.

Functional markers based molecular characterization of resistance gene analogs encoding NBS-LRR disease resistance proteins in finger millet (*Eleusinecoracana*) by Panwar et al. [10], described the analysis of a large collection of finger millet genotypes for association of NBS sequences with the blast disease resistance and susceptibility caused by *Magnaporthe grisea*. Panwar et al. [11] studied Comparison of RAPD, SSR and cytochrome P450 gene based markers with respect to calcium content in finger millet. The genotypes of finger millet collected from different districts of Uttarakhand constitute a wide genetic base and clustered according to calcium contents. Recently, Kumar et al. [12] used SSR, RAPD markers and protein profiles based analysis to differentiate *Eleusinecoracana* genotypes differing in their protein content. In their study, significant negative correlation ($r = -0.69^*$) was found between the protein and calcium content of finger millet genotypes.

Future Perspectives

Though there is an improvement in the involvement of molecular marker technology for finger millet crop, still there are many challenges when compared to the other major cereal crops like rice. There is an urgent need to develop the linkage maps of finger millet chromosomes and then identification of QTLs will play a major role in identifying the QTLs of important agro-morphological characters influencing the quality, biotic and abiotic stress characters. Fine mapping of the important genes will pave the way for marker assisted selection to introgress the genes into locally well adapted germplasm for higher yield and quality improvement.

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