

Insight in the Utilization of Marker Assisted Selection in Cotton (A Review)

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Abstract Upland cotton represents the most important, and natural fiber crop in the world. Limitations in conventional breeding program for genetic improvement is due to the lack of knowledge about yield productivity and fiber quality traits. The use of molecular markers for the detection and exploitation of DNA polymorphism is one of the significant developments in the field of molecular genetics. The availability of reference genome of *G. raimondii* L., *G. arboreum* L., and next generation sequencing, routed it on the fast track for exploring the variability among genotypes of cotton. There is no molecular marker available which can fulfill all the requirements of cotton scientists. Plant breeders should utilize genomics in the breeding programs for effective selection of potential parents for certain traits. The genomic research work could use quantitative trait loci mapping, genome wide associations and next generation sequencing strategies. This review highlights the recent developments of various molecular markers for analyzing genetic diversity, constructing linkage maps and genomics tools which will assist in marker assisted selection in cotton.

Keywords Cotton; Genome; Genetic diversity; DNA marker; SSR; SNP; GBS; MAS; GWAS

1 Abbreviations

RFLP (Restriction fragment length polymorphism), AFLP (Amplified fragment length polymorphism), RAPD (Random amplified polymorphic DNA), ISSR (Inter simple sequence repeat), SCAR (Sequence characterized amplified regions), SSR (Simple sequence repeat), STS (Sequence tag sites), ESTs (Express sequence tags), CAPS (Cleavage amplified polymorphic site), SNP (Single nucleotide polymorphism), GBS (Genotyping by sequencing), MAS (marker assisted selection), GWAS (Genome wide association studies)

2 Introduction

Cotton (*Gossypium* spp.) being the world most widely sown fiber crop, has an important share in global economy (Cuming et al., 2015) and being a significant contributor of oilseed with an approximate utilization of about 115 million bales (Waqas et al., 2014). Cotton is cultivated by more than 80 countries in the world (Sunilkumar et al., 2006; Abdurakhmonov et al., 2012) on 32-34 million hectares (2010/11 to 2012/2013) with annual total production of 25.65 million metric tons (MT) (forecast for 2013/14, USDA report, 2013). Wendel et al., (2009); Grover et al. (2014) has described 52 different *Gossypium* species including 7 tetraploid (AD) and 45 diploid differentiated into eight genomes (A-G and K). Moreover, allotetraploid *Gossypium hirsutum* L. ($2n=4x=52$) is the most prominent, which accounts for over 95% of the world crop while *G. arboreum* and *G. herbaceum* together share 2% cotton on global level (Zhang et al., 2008).

Molecular marker is a specific DNA portion with a known position on the chromosome (Kumar, 1999), or a gene whose phenotypic expression is frequently easily distinguished and used to detect an individual (King and Stansfield, 1990; Schulmann, 2007). Genetic markers are divided into three groups: (1) morphological markers which themselves have phenotypic characters; (2) biochemical markers, having allelic variants of enzymes called isozymes; and (3) DNA markers, which show sites of variation in DNA (Joshi and Nguyen 1993; Winter and Kahl, 1995; Jones et al., 1997; Gupta et al., 1999). DNA markers are having the property of polymorphism which is based on the differentiation of homozygotes and heterozygotes (Roychowdhury et al., 2014). Molecular markers are more authentic