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Molecular Markers in Cotton Improvement

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A B S T R A C T

Cotton is the very important commercial and cash crop, it is a very much necessary to improve the Superior agronomic traits to withstand against biotic and abiotic stress in the field and fiber qualities to meet requirement of advance spinning technology. Cotton improvement through conventional breeding is time consuming, in this context molecular markers found that efficient tool to accelerate the plant breeding program in cotton improvement. At present variety of molecular markers are available, choice of molecular marker depends on the user. This review article gives a over view of various molecular markers used in cotton include Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), Simple Sequence Repeats (SSR), Inter Simple Sequence Repeats (ISSR), Sequence Related Amplified Polymorphism (SRAP) and Single Nucleotide Polymorphism (SNP). These markers play a crucial role in crop improvement program like (a) Analysis of Genetic diversity in cotton, (b) Construction of linkage map, (c) QTL analysis agronomic and fiber related traits in cotton (d) Marker assisted selection (MAS).

Introduction

Cotton (*Gossypium* spp) is the world's most important natural and textile fiber crop, seeds are good source of vegetable oil and protein meal. Cotton is also called white gold because of economic importance, cotton alone contributes about 4% of national GDP. Cotton belongs to genus *Gossypium* familly Malvaceae and genus *Gossypium* comprised of fifty species out of which forty five are diploid (2n=2x=26) and five are tetraploid (2n=4x=52), they occur in semiarid and arid areas of Africa, Central and South America, Galapagos, Indian subcontinent, Australia, Arabia, and Hawaii (Fryxell, 1992). The cultivated cotton includes, two diploid A genome species (*G. arborium* and *G. herbacium*) and two allotetraploid AD genome species (*G. hirsutum* and *G. barbadense*) (Wendel *et al.*, 1999). In the world cotton is grown in an area of 33.1 million hectares producing 117 million bales with a productivity of 766 kg/ha (Dhruv, 2015). India ranks first in the world in terms of area under cotton cultivation 11.72 million

hectares and second in production with producing 372 lakh bales with a productivity of 541 kg/ha, Karnataka producing 15 lakh bales with a productivity of 464 kg/ha (Dhruv, 2015).

Plant breeders select the plants with desirable traits by looking at the phenotype. Most of these traits are polygenic in nature and many of them are influenced by environment. Although biometrical genetics provides the cumulative effects of the genetic loci involved in a polygenic trait but fails to identify locus involved in a particular trait. If the quantitative traits partition into individual genetic components by finding DNA marker closely linked to each trait, it would be easy to manipulate them efficiently and this would help to attain the desirable results quickly and more precisely (Preetha and Rveendren, 2008). These DNA markers will provide a information to the plant breeders to select desirable plants directly on the basis of genotype in the early stage itself, instead of waiting up to phenotype expression, where it is not possible through conventional breeding alone.

Generally aim of plant breeders is to improve Agronomically superior varieties or combining of interested traits present in different parental lines of cultivated species or their wild relatives. In order to combine all the favorable traits from different cultivars or related wild species for development of superior varieties through conventional breeding methods involve repeated backcrossing, selfing and testing which are time consuming and less precise processes as compared to direct selection of plants based on molecular processes (Preetha and Rveendren, 2008). Further conventional selection depends upon availability of lines with clear-cut phenotypic characters and accurate screening methods. The molecular marker techniques hasten the transfer of desirable genes from different varieties to background of single genotype and also introgress novel genes from related wild species into the local or popular genotypes, which would accelerate the generation of new varieties. In cotton there are different marker technologies are available ie., RFLPs, RAPDs, AFLPs, ISSRs, SSRs and SNPs, each marker have its own advantage and disadvantages. Tanksley (1983) listed five properties that distinguish molecular markers from morphological markers. These properties are (1) genotypes can be determined at the whole plant, tissue and/or cellular level (2) a relatively larger number of naturally occurring alleles exists at many loci, (3) phenotypic neutrality (4) alleles at many loci are codominant, (5) few epistatic or pleiotrophic effects are observed. In this brief background let us understand the role of particular marker in cotton improvement programme.

DNA marker techniques used in cotton

Restriction fragment length polymorphism (RFLP)

Restriction fragment length polymorphism was the first kind of DNA marker. It belongs to hybridization based marker, which employs cloned DNA sequences to probe specific regions of the genome for variations that are seen as changes in the length of DNA fragments produced by digestion with restriction endonucleases (Landry *et al.*, 1987). The main steps involve isolation of DNA, digestion with restriction enzymes (e.g., EcoRI, HindIII, DraI), separation of restricted fragments by agarose gel electrophoresis, transfer of fragments to nylon membrane, hybridization with probe and scoring of polymorphism by autoradiography.

RFLP was the first DNA marker used in crop improvement. Meredith (1992) in a study of

heterosis and varietal origins reported the first RFLP evaluation in upland cotton. Reinisch *et al.,* (1994) developed first RFLP based linkage map of 4675 cM length with 41 linkage groups by using 705 RFLPs in cotton. Reinisch *et al.,* (1994) reported that 46.2% of nuclear DNA probes detect RFLPs between *Gossypium hirsutum* and *Gossypium barbadense*, 64% are codominant in nature after that many scientists were used this markers in linkage map construction in cotton(Saranga *et al.,* 2001; Paterson *et al.,* 2003; Rong *et al.,* 2004 and Chee *et al.,* 2005). Yu *et al.,* 1997 used RFLP markers for genetic diversity study in different cotton species. Wright *et al.,* 1998, reported utility of RFLP markers in marker assisted selection (MAS) and RFLP linked to resistance allele for pathogen of bacterial blight was validated. RFLP markers are very complex and time and cost intensive technique which restricted it use, leading to development of less complicated techniques known as PCR base markers (Agarwal *et al.,* 2008).

Random amplified polymorphic DNA (RAPD)

RAPD is the oldest PCR-based molecular marker technique it involves 10 bp random primer (Williams *et al.,* 1990). It has many advantages over RFLP technique such as non-radioactive detection, it does not require prior sequence information, it required very small amount of genomic DNA, experimental simplicity and no need for expensive equipments beyond a thermocycler and a transilluminator (Rafalski, 1997). RAPD main disadvantage is that poor reproducibility (Jones *et al.,* 1997). RAPD profile varies within and between laboratories because it is influenced by many factors like DNA concentration, reproducibility of thermocycler profiles, primer quality and concentration, choice of DNA polymerase, and pipetting accuracy (Rafalski, 1997).

RAPD techniques have been used for many purposes in cotton including assessment of, diversity, genome mapping, phylogentic studies (Rahman *et al.,* 2002; Zhang *et al.,* 2002; He *et al.,* 2008; Rahman *et al.,* 2008; Rana and Bhat, 2004), genetic variations or diversity studies (Tatineni *et al.,* 1996 Chalmers *et al.,* 1992, Xu *et al.,* 2001 and Chaudhary *et al.,* 2010), DNA fingerprinting (Multani *et al.,* 1995) and determining the relationship between the genotypes of different and same species (Wajahatullah *et al.,* 1997), also used to evaluate the genetic relationship among cotton genotypes (Shu *et al.,* 2001), to identify the QTLs for stomatal conductance (Ulloaand Meredith, 2000), to construct linkage mapping and QTL analysis in cotton (Zhang *et al.,* 2003, Wang *et al.,* 2006 and Lin *et al.,* 2009). RAPDs were used to distinguish the cotton varieties resistant to jassids, aphids, and mites (Geng *et al.,* 1995). RAPD marker (R-6592) for the male sterility gene has been identified in cotton (Lan *et al.,* 1999).

Amplified fragment length polymorphism (AFLP)

AFLP technique was first developed by Vos *et al.,* 1995, this technique combines reliability of RLFP with the ease of RAPD. The process involves three simple steps: (1) restriction of genomic DNA and ligation of oligonucleotide adaptors, (2) pre and selective amplification of restriction fragments and (3) gel analysis of amplified fragments. Generally polymorphic fragments are detected as present or absent making it a dominant marker system but in soybean Maughan *et al.,* 1996 noticed codominant nature. The technique can be automated and allows the simultaneous analysis of many genetic loci per experiments. AFLP produces more polymorphic loci per primer than RFLPs, SSRs or RAPDs (Maughan *et al.,* 1996).

AFLP is an effective tool for the observation of genetic diversity (Murtaza *et al.,* 2006; Abdalla *et al.,* 2001; Rana *et al.,* 2005 and Li *et al.,* 2008), fingerprinting studies, and tagging of agronomic, seed and fiberquality traits (Zhong *et al.,* 2002; Rakshit *et al.,* 2010 and Badigannavar *et al.,* 2010). AFLP is a great valued technique for gene mapping studies due to their high abundance and random distribution throughout the genome (Vos *et al.,* 1995). A linkage map of cotton was developed using the AFLP and RAPD markers (Altaf *et al.,* 1997). AFLP markers have also been used for construction of linkage map and QTL analysis along with other markers (Y*u et al.,* 2007; Wang *et al.,* 2006; Lacape *et al.,* 2009;Samer *et al.,* 2015 and Cuming *et al.,* 2015) and map saturation in cotton (Zhang *et al.,* 2005 and Lacape *et al.,* 2003).

Inter Simple Sequence Repeats (ISSR)

It allows the detection of polymorphism in inter SSR loci using primer (16–25 bp long) complimentary to a single SSR and anneal at either the 3' or 5' end (Khanam *et al.,* 2012), that can be di, tri, tetra or pentanucleotide (Reddy *et al.,* 2002). The technique of ISSR markers combines many benefits of AFLPs and SSRs with universality of RAPDs (Bornet *et al.,* 2001). Generally the sequence of ISSR primers is larger as compare to RAPD primers, allowing higher annealing temperature which outcomes greater reproducibility of bands than RAPDs (Reddy *et al.,* 2002, Culley *et al.,* 2000). Amplification of ISSRs also revealed larger fragments number per primer than RAPDs (Wang and Yi, 2002). Many earlier studies reported that ISSR markers were more informative than RAPDs for genetic diversity evaluation in different crop species (Nagaoka *et al.,* 1997; Galv´an *et al.,* 2003). The applications of ISSRs for different purposes depend on the diversity and frequencies of SSR within the particular genomes (Shi *et al.,* 2010). It is quickly being utilized by the research community in different areas of plant improvement, that is, in gene tagging, analysis of genetic diversity, and estimation of SSR motif (Blair *et al.,* 1999; Bornet *et al.,* 2002 and Sica *et al.,* 2005). ISSRs have been reported as quite useful markers for revealing polymorphism in cotton genotypes (Liu *et al.,* 2001).

Simple Sequence Repeats (SSR)

These are di-, tri-, tetra- or pentatandom repeats of nucleotide, scattered abundantly in both noncoding and coding regionsof a genome (Kalia *et al.,* 2011; Khanam *et al.,* 2012). Microsatellites are created from sphere where variants of repetitive DNA sequence are previously overrepresented (Tautz *et al.,* 1986). The loci of these markers are highly transferable about 50% across species (Saha and Jenkins, 2004). For SSRs analysis forward and reverse primers are employed in PCR reaction that anneal to the template DNA at the 5' and 3' ends. Short repetitive DNA sequences furnish the basis for multi allelic, co dominant PCR based molecular marker and found more polymorphic as compare to other DNA markers (Preetha and Raveendren, 2008; Khanam *et al.,* 2012). Due to their greater polymorphism, SSRs are considered as an important marker system in fingerprinting, analysis of genetic diversity (Qayyum *et al.,* 2009 and Arunita *et al.,* 2010), molecular mapping and marker assisted selection (Reddy *et al.,* 2001). According to Blenda *et al.,* (2006), there are various uses of microsatellites for plant breeders such as selective breeding improvement, genetic diversity estimation, introducing novel genes into breeding materials from exotic germplasm, cultivar protection, locating qualitative and quantitative trait loci.

Several methods have been pursued to develop SSR markers in cottons, including analysis of SSR-enriched small insert genomic DNA libraries (Kalia *et al.,* 2011; Udall *et al.,* 2006; Ince *et al.,* 2010; Richard *et al.,* 1995), SSR mining from ESTs (Shaheen *et al.,* 2009), and large-insert BAC derivation by end sequence analysis (Reddy *et al.,* 2002).Cotton researchers have explored simple sequence repeats (SSRs) for studies the phylogenetic and diversity analysis (He *et al.,* 2007; Lacape *et al.,* 2007)genetic mapping and QTL analysis for different traits (Guo *et al.,*2007; Lacape *et al.,*2009; Park *et al.,*2005; Xiao *et al.,*2009; Yu *et al.,* 2012, Michael *et al.,* 2014 and Tang, *et al.,* 2015), association mapping (Kantartzi and stewart, 2008).

Sequence related amplified polymorphism (SRAP)

SRAP marker technique was introduced by Li and Quiros (2001), this new marker technique preferentially amplifies ORFs through PCR by using two different primer pair. First one forward primer, which contains 17 base pairs, in that 14 nucleotide sequence rich in G and C in the 5'end and three selective bases in the 3'end.This primer amplifies preferentially exonic regions. The second one is reverse primer with 19 base pairs, contains a sequence of 16 nucleotide rich in A and T in the 5'end and three selective bases in the 3'end.This primer preferentially amplifies intronic regions and regions with promoters. This technique combines simplicity, reliability, moderate throughput ratio and facile sequencing of selected bands. Further, it targets coding sequences in the genome and results in a moderate number of co dominant markers. However, these techniques will not utilize any prior sequence information, and the markers generated are randomly distributed across the genome. In cotton this new marker technique is being used along with other markers (Lin *et al.,* 2005; He *et al.,* 2007; Lin *et al.,* 2009; Zhang *et al.,* 2009 and Yu *et al.,* 2007) for saturating the genome.

Single Nucleotide Polymorphism (SNP)

Variations of single nucleotide (A, T, C, G) in sequence of individual genome are known as single nucleotide polymorphism or SNPs (Agarwal *et al.,* 2008). These may occur in the non coding, coding and intergenic regions of the genome, so allowing the detection of the genes due to the variations in the sequences of nucleotides (Agarwal *et al.,* 2008) and these are either non synonymous or synonymous within the coding regions of the genome. Synonymous changes can alter mRNA splicing that result the changes in the phenotype of an individual (Richard *et al.,* 1995). The main advantage of SNP markers is to relate their ease of data management along with their flexibility, speed and cost-effectiveness. Bi-allelic SNP markers are straight forward to merge data across groups and create large databases of marker information, since there are only two alleles per locus and different genotyping platforms will provide the same allele calls once proper data has been performed.

SNP markers are important tool for linkage mapping, map based cloning and marker assisted selection due to the high level of polymorphism. The co dominant nature of SNPs makes these markers able to distinguish the heterozygous and homozygous alleles (Shaheen *et al.,* 2009). Because of high polymorphism nature SNPs were used to observe diversity, characterization, mapping and for construction of linkage map and QTL analysis in cotton (Michael *et al.,* 2014 and Hulse-Kemp *et al.,* 2015).

Recently, an international collaborative effort has developed 70K SNP chip based on Illumina Infinium genotyping assay

(Unpublished data; http://www.cottongen.org/node/1287616). This high-throughput genotyping assay will be a resource that will be used globally by public and private breeders, geneticists, and other researchers to enhance cotton genetic analysis, breeding, genome sequence assembly, and many other uses.

Important applications of molecular markers in cotton improvement

Genetic diversity studies in cotton

Success of breeding program depends on the understanding of genetic diversity within and among genetic resources of the available germplasm and enable plant breeders to choose parental sources that will generate diverse populations for selection. Characterization of genetic similarity among genotypes is a valuable source to select parental combinations for maintaining genetic diversity in a breeding program (Becelaere *et al.,* 2005). The knowledge of genetic relationships among plant genotypes helps to know the complexity available germplasm, to discover the differences in available genotypes and to build up useful conservation plans (Dahab *et al.,* 2013). Thus, evaluation based on the molecular markers can give valuable insight into the genetic structure of a plant population, which helps in the development of new varieties. There are manygenetic diversity studies have been carried out in cotton by employing different marker techniques e.g. amplified fragment length polymorphism (AFLP) (Abdalla *et al.,* 2001; Rana *et al.,* 2005; Li *et al.,* 2008), random amplified polymorphic DNA (RAPD) (Xu *et al.,* 2001; Chaudhary *et al.,* 2010) and simple sequences repeats (Qayyum *et al.,* 2009; Arunita *et al.,* 2010). A overview of some published genetic diversity studies by using molecular markers is depicted in Table 1.

Genetic linkage map construction in cotton

Genetic mapping (also known as linkage mapping or meiotic mapping) refers to the determination of the relative position and distances between markers along chromosomes. Genetic map distances between two markers are defined as the mean number of recombination events, involving a given chromatid, in that region per meiosis. Genetic linkage maps are fundamental for the localization of genes conferring biotic and abiotic stress tolerance. Genetic maps based on molecular markers have several advantages over classical maps. Genetic mapping can be developed by different mapping populations, but popularly F2, backcross and recombinant inbred lines these three populations were used for construction of genetic linkage map in plants(Paterson, 1996). Molecular map of the cotton genome was first constructed using 705 RFLP loci and partitioned into 41 linkage groups (Reinisch *et al.,* 1994). Many more cotton molecular maps have been developed and published. An overview of published genetic linkage maps in cotton is given in Table 2

QTL mapping for yield, yield contributing and fiber quality trait in cotton

The regions in genomes to have genes linked with a quantitative trait are known as quantitative trait loci, QTLs (Collard *et al.,* 2005), and the process of developing linkage maps and performing QTL analysis is referred to as QTL mapping (Paterson *et al.,* 1996 and Paterson *et al.,* 1996). QTL analysis stands on the principal of identifying a connection among phenotype and genotype of markers. The QTLs identified in cotton using different marker technologies are listed in table 3. These identified QTLs are the new avenue to accelerate the cotton improvement through marker assisted selection.

Marker-Assisted Selection (MAS)

Marker assisted selection (MAS) is a procedure by which a phenotype is selected on the basis of genotype of a marker (Collard *et al.,* 2005). Once the markers tightly linked to the genes have been detected, breeders may use particular DNA marker to identify the plants carry the genes (Young *et al.,* 1996). The effectiveness and cost of MAS are influenced by the marker technique; therefore, it must be selected carefully (Young *et al.,* 1996). During the past two decades, RAPDs techniques have been used for MAS for getting the glanded plants and glandless seeds in the interspecific population of G. sturtianum and other species. It was exposed that DNA markers connected to the major QTL (QTLFS1) for fiber strength could be utilized in MAS to increase fiber strength of commercial varieties in segregating populations (Zhang *et al.,* 2003). SSR markers namely CIR 316 tightly linked to Root knot nematod (RKN) resistant region on chromosome 11 and BNL 3661 marker tightly linked to RKN resistant region on chromosome 14.

Jenkins *et al.,* (2012) by using these SSR markers selected 11 homozygous plants for chromosome 11 and 14 from F2 population derived from RKN resistant genotype M 240 RNR ×susceptible cultivar FM966 instead of waiting up to F6-F8through conventional breeding. That selected plant confirmed resistance against the RKN. In cotton it is necessary to identify specific genes for particular traits like fiber length, strength, fineness...etc, to combine these genes from different genotypes through marker assisted selection. Some of identified genes for particular traits is depicted in Table 4.

Table.1 An overview of genetic diversity studies in cotton by using molecular markers

S. No.	Country	Population type	Markers used	References
1	India	150 G. hirsutum lines	50 SSR	Rajeev *et. al.,* 2014
2	India	Intraspecific cotton F1 hybrids and its parents	20 RAPD and 19 ISSR	Dongre et. al., 2012
3	USA	24 lines of cotton	270 SNP loci and 92 Indel	Van et. al., 2009
4	India	24 lines of *G. hirsutum*L.	6 AFLP primers	Rana et. al., 2005
5	USA	24 cultivars of *G. hirsutum*	88 SSR primers	Zhang et. al., 2005
6	Pakistan	31 *Gossypium*species, 3 subspecies and 1 interspecific hybrid	45 RAPD primers	Khan et. al., 2000

Table.2a Overview of published genetic linkage maps in cotton

S. No.	Cross parents	Mapping population		Markers	No. of mapped loci	Map Length (cM)	No.of LGs	Reference
Interspecifc crosses		**Types**	**SIZE**					
1.	*Gh*(palmeri) × *Gb* (K101)	F_2	57	RFLP	705	4675	41	Reinisch*et.al.*, 1994
2.	*Gh* (CAMD-E) × *Gb* (Sea Island Seaberry)	F_2	271	RFLP	261	3767	27	Jiang *et.al.*, 1998
3.	*Gh*(Deltapine 61) × *Gb* (Sea IslandSeaberry)	F_2	180	RFLP	-	3664	26	Jiang *et.al.*, 2000
4.	*Gh*(TM1) × *Gb* (3-79)	F_2	171	RFLP, RAPD and SSR	-	4766	50	Kohel *et.al.*, 2001
5.	*Gh*(Siv'on) × *Gb* (F-177)	F_2	430	RFLP	253	-	-	Saranga *et.al.*, 2001
6.	*Gh*(Siv'on) × *Gb* (F-177)	F_3	208	RFLP	-	-	-	Paterson *et.al.*,2003
7	(*Gh*(TM 1) × Gb (Hai7124)) × TM1	BC_1F_1	140	EST-SSR	624	5644.3	34	Han *et.al.*,2004,2006
8	*Gh* (Acala 44) × *Gb* (Pima S7)	F_2	94	AFLP, SSR, and RFLP	392	3287	42	Mei *et.al.*, 2004
9	*Gh*(Palmeri) × *Gb* (K101)	F_2	57	RFLP	2584	4447.9	26	Rong *et.al.*, 2004
10	(*Gh*(Tamcot 2111) × *Gb* (Pima S6))×Tamcot 2111	BC_3F_2	3662	RFLP	-	-	-	Chee *et.al.*, 2005
12	(*Gh*(Guazuncho 2) × *Gb* (VH8)) × Guazuncho 2	BC_1 and BC_2	200	SSR and RFLP	1306	5597	26	Lacape *et.al.*,2003, Lacape *et.al.*, 2005
13	*Gh*(Handan208) × *Gb* (Pima90)	F_2 and $F_{2:3}$	69	SSR, SRAP, RAPD, and REMAPs	1029	5472.3	26	Lin *et.al.*, 2005, He *et.al.*, 2007
14	*Gh*(TM1) × *Gb* (Pima 3-79)	RILs	183	EST-SSR	193	1277	19 + 11 LG	Park *et.al.*, 2005
15	*Gh*(7235) × *Gb*(TM-1)	F2 and $F_{2:3}$	163	SSR	86	666.7	21	Shen *et.al.*, 2005
16	*Gh*(TM1) × *Gb* (3-79)	RILs	183	SSR	433	2126.3	46	Frelichowski *et.al.*, 2006
17	*Gh*(CRI36) × *Gb* (Hai7124)	F_2	186	SSR, TRAP, SRAP, and AFLP	1097	4536.7	35	Yu *et.al.*, 2007
18	*Gh*(Handan 208) × *Gb* (Pima 90)	RILs	121	SSR	-	5472.3	26	He *et.al.*, 2008
19	*Gh*(Guazuncho 2) × *Gb* (VH8-4602)	RILs	140	SSR and AFLP	800	2044	26	Lacape *et.al.*, 2009
20	(*Gh*(KC3) × *Gb* (Suvin)) × KC3	BC_1F_1	62	SSR	57	911.6	19	Santoshkumarr *et.al.*, 2010
21	*Gh*(TM1) × *Gb* (3-79)	RILs	186	SSR and SNP	2072	3380	26	Yu *et al.*, 2012
22	*Gh*(SG 747) × *Gb* (Giza 75)	BILs	146	SSR	392	2,895	26	Yu *et al.*, 2013
23	*Gh*(TM-1) × *Gb* (NM24016)	RILs	98	SSR and SNP	841	2061	26	Michael *et al.*, 2014
24	*Gb*.doubled haploid line 3- 79 x *G. hirsutum*cv. Texas Marker- 1	F_2	118	SNP	19,198	4,439.6	0.23	Hulse-Kemp *et al.*, 2015
25	Giza 45 *(G. barbadense)* xTamcot Luxor *(G. hirsutum)*	F_2	60	AFLP, SSR, EST-SSR	210	3503.8	26	Samer *et al.*, 2015
26	*Gh*(TMS22) × *G.tomentosum*(WT936)	F_2	82	SSR	589	4259.4	52	Westengen *et al.*, 2005

Table.2b Overview of published genetic linkage maps in cotton

	Intraspecific crosses	Type	Size	Markers	No. of mapped loci	Map Length (cM)	No.of LGs	Reference
1	*Gh*(HS46) × *Gh*(MARCABUCAG8US-1-88) F2 and F3 96 RFLP 120 865 31	F_2 and F_3	96	RFLP	120	865	31	Shappley *et al.*, 1998
2	*Gh*× *Gh*	$F_{2:3}$	569	RFLP	284	1502.6	47	Ulloa *et al.*, 2002
3	*Gh*(TM 1) × *G.anomalum*(7235)	F_2 and F_3	186	SSR and RAPD	-	-	-	Zhang *et al.*, 2003
4	*Gh (*Handan208) × *Gh*(Pima90)	F_2	129	SRAP	237	3030.7	39	Lin *et al.*, 2005
5	*Gh (*Acala 44) × *Gb*(Pima S7)	F_2	94	AFLP, SSR, and RFLP	392	3287	42	Mei *et al.*, 2004
6	*G. trilobum*(Skovsted)× *G. raimondii*(Ulbr)	F_2	62	RFLP	763	1493.3	13	Rong *et al.*, 2004
7	*Gh*(Yumian 1) × *Gh*(T586)	F_2 and $F_{2:3}$	117	SSR and AFLP	70	525	20	Zhang *et al.*, 2005
8	*Gh*(TM1) × *Gh*(7235)	RILs	258	SSR	110	810.07	22	Shen *et al.*, 2007
9	*Gh*(Zhongmiansuo12)× *Gh*(8891)	RILs	180	SSR, AFLP, RAPD, and SRAP	132	865.20	26	Wang *et al.*, 2006
10	*Gh*(L-70) × *Gh*(L-47)	RILs	76	EST-SSR	-	-	-	Abdurakhmonov *et al.*, 2007
11	*Gh*(7235) × *Gh*(TM-1)	RILs	207	SSR	156	1024.4	31	Shen *et al.*, 2007
12	*Gh*(Yumian 1) × *Gh*(T586)	RILs	270	SSR	19	96.2	1	Wan *et al.*, 2007
13	*Gh*(Deltapine) × *Gh*(Texas 701)	F_2	251	SSR	73	650.8	17	Guo *et al.*, 2008
14	*Gh*× *Gh*	4WC	273	SSR, EST-SSR	286	2113.3	56	Qin *et al.*, 2008
15	*Gh*(DH962) × *Gh*(Jimian5)	F_2	137	SRAP, SSR, RAPD and RGAP	471	3070.2	51	Lin *et al.*, 2009
16	*Gh (*HS 46) × *Gh (*MARCABUCAG8US-1-88)	RILs	188	SSR	125	965	26	Wu *et al.*, 2009
17	*Gh*(Yumian 1) × *Gh*(T586)	RILs	270	SSR and SRAP	604	3140.9	60	Zhang *et al.*, 2009
18	*Gb(Hai7124* × *Gb* (3-79)	F_2	124	SSR, EST-SSR, SNP	412	2108.34	52	Wang *et al.*, 2013
19	*Gh* (*Yumian 1* × *7235)*	RILs	180	SSR	1,540	2,842.06	26	Tang *et al.*, 2015
20	*Gh (Yesil* × *Nazilli 84)*	F_2	94	AFLP	240	2068.5	27	Cuming *et al.*, 2015

Table.3 List of QTLs identified in cotton

Sl.No.	Traits	Descriptor	Population		Marker (number and Type)	QTLs No.	Reference
			Type	Size			
1	Fiber quality	FS, FL, FF	F_2	171	216 RFLP, 139 RAPDs	13	Kohel *et al.*, 2001
		FS	F_2	186	217 SSRs, 800 RAPDs UBC and 1040 OPERON	2	Zhang *et al.*, 2003
		LY, LP, SW, NS, UQ, SF, FL, FE, FT, FF and IF	F_2	120	144 AFLPs, RFLPs and 150 SSRs	28	Mei *et al.*, 2004
		FS,FE, FF, FU and FL	F_2	200	448 RFLP	28	Zhang *et al.*, 2011
		FS, FE, FL, FU, LP and FF	F_2	117	290 SSRs and 9 AFLPs	16	Zhang *et al.*, 2005
		FF	$BC3F_2$	3,662	262 RFLPs	41	Draye *et al.*, 2005
		FL, FLU and SFC	$BC3F_2$	3,662	262 RFLPs	45	Chee *et al.*, 2005
		FS, FL, FF, FE	RILs	---	95 SSRs, 72 CSR	13	Park *et al.*, 2005
		FL, FS, FF and FE	F_2	—	1378 SSRs	39	Shen *et al.*, 2005
		FS, FL, FF, FMT, FE and SFI	RIL's	180	4106 SSRs, AFLPs, RAPDs and SRAPs	48	Wang *et al.*, 2006
		FS, FE, FU, FL and FF	RIL's	270	7508 SSRs, 384 SRAPs and 740 IT-ISJs	13	Zhang *et al.*, 2009
		FE, FL, FS, FF and FU	CP	172	16052 SSRs	63	Zhang *et al.*, 2012
		FE, FL, FS, FF and FU	RIL's	180	25,313 SSRs	62	Tang *et al.*, 2015
		, FL, FS, FE, FU and FC	F_2	94	123 AFLPs	43	Cuming *et al.*, 2015
2	Fiber and agronomical	SCY, LY, LP, BW, SI, FMT, PER, WF,WT, FF, FL, FE and FS	RIL's	188	141 SSRs	36	Wu *et al.*, 2009
		BW, LP, FF.ES, FU, DFF and DFN	F_2	60	50 EST, 18 EST-SSR, 36 SSRs and 64 AFLP	81	Samer *et al.*, 2015
3	Yield and fiber	SCY, LI, SI, LY, no. of seeds per boll, FS, FL and FF	F_2	69	834 SSRs, 437 SRAPs, 107 RAPDs, 16 REMAPs	57	He *et al.*, 2008
		FS, FL, FF, FE, LP, SI, NB, SCY and LY	RIL's	258	2131 SSRs	53	Shen *et al.*, 2007
		LI, SI, LY, SCY, NSB and FS	F_2	69	834 SSRs, 437 SRAPs, 107 RAPDs and 16 REMAPs	52	He *et al.*, 2007
		NB, BW, SI, LP, LI, SCY, LY, FL, FS, FF, FE and FU	4WC and inbred lines	280	6123 SSRs and EST-SSRs	31	Qin *et al.*, 2008
		SCY, LY, NB, BW, LP, SI, LI and FBN	RIL's and IF2	180	2675 EST-SSRs	111	Liu *et al.*, 2012
		PH, FBN, BW, LP, LI, SI, LY, FL, FS, FE, FF and FU	*G. hirsutum* accessions	81	121 SSRs	180	Zhang *et al.*, 2013
		SCY, LY,LI, BW, FL, FS, FU	BILs	146	2,041 SSRs	67	Yu *et al.*, 2013

NB: number of bolls per plant, BW: boll weight, SI: seed index, LP: lint percent, LI: lint index, SI: seed index, SCY: seed cotton yield per plant, LY: lint yield per plant, FL: fiber length, FS: fiber strength, FE: fiber elongation, FU: fiber uniformity ratio, FY: fiber yellowness, FF: fiber fineness, FMT: fiber maturity, PH: plant height, FBL: fruit branch length, FBN: fruit branch number, FBA: fruit branch angle, FLU: fiber length uniformity, SFC: short fiber content, FR: fiber reflectance, SW: seed weight, NS: number of seeds per bolls, UQ: upper quartile length, SF: short fiber content, FT: fiber tenacity, IF: immature fiber content, SFI: short fiber index, NSB: number of seeds per boll, Date of 1st Flowering (DFF), Node of 1st Fruiting Branch (FFN).

Table.4 Over view of specific genes identified in cotton for particular traits

Traits	Genes	Reference
Fiberstrength	qFs1	Zhang et al 2003
Fiberlength	qFL-D2-1	Wang *et al.*, 2006
CMS	Rf_1, Rf_2	Lan et al.1999 Liu et al.2003, Zhang et al.2005
GMS	ms_5, ms_6, ms_{15}	Chen *et al.*,2009
Fiber development	Li_1,Li_2,N_1,n_2,*Fz*,*ha* N_1, n_1, n_2	Rong *et al.*,2007
Leaf shape	L_2,P_1,Y_1	Song *et al.*,2005;Guo *et al.*,2006;
	t_1,T_1	Wright *et al.*,1999
Glandless	*gl1, gl2, gl3, gl4, gl5, and gl6*	Pauly, *1979*
Gladness	*Gl1* and *Gl2*	Lee, 1965; McCarty *et al.*,1996
Root-knot nematode resistance	rkn_1	Wang *et al.*,2006, Shen *et al.*,2006
Blight resistance	B_2,B_3,B_{12}	Wright *et al.*,1998
Fusarium resistance	*FWR*	Wang *et al.*,2009

In conclusion, marker mediated varietal fingerprinting and germplasm characterization Molecular Marker-Assisted Technologies for cotton Improvement appeared most common and most pervasive application with AFLP and SSR markers. Being cost effective, easy to handle and devoid of any radioisotope requirement, SSR and SNP markers are considered as the most suitable and reliable system for DNA fingerprinting. Marker-assisted selection has been successful for introgressing and pyramiding major-effect genes, however many challenges remain to be resolved before MAS can routinely provide added value for breeding very complex traits. Marker-assisted selections for qualitative traits appeared most successful after DNA fingerprinting while for quantitative characters, insect resistance genes and genes controlling QTL for abiotic stress tolerance, the success is limited. It is anticipated that application of markers will remain restricted in these areas till the allele-specific markers are available and the cost of marker analysis is reduced significantly. Although there have been numerous QTL mapping studies for a wide range of traits in cotton crop, relatively few markers have actually been implemented in breeding programs for cotton improvement. The rate, scale, and scope of uptake of MAS in public crop breeding program has continually lagged behind expectations. There are many technical and logistical factors that have hindered the speed and scope of MAS uptake. Steady progress and advancement in DNA markers will make it more attractive for molecular breeding and plant genetics and ultimately help in cotton improvement.

References

Abdalla, A.M., Reddy, O.U.K., El-Zik, K.M. and Pepper, A.E. 2001, Genetic diversity and relationships of diploid and tetraploid cottons revealed using AFLP. *Theor. Appl. Genet.*, 102: 222-229.

Abdurakhmonov, I.Y., Buriev, Z.T., Saha, S., 2007, Microsatellite markers associated with lint percentage trait in cotton, *Gossypium*hirsutum. *Euphytica*, 156(2): 141-156.

Agarwal, M., Shrivastava, N. and Padh, H. 2008, Advances in molecular marker techniques and their applications in plant sciences. *Pl. Cell Reports*, 27 (4): 617-631.

Altaf, M.K., Stewart, J.M.C.D., Wajahatullah, M. K., Zhang, J. and Cantrell, R. G., 1997, Molecular and morphological genetics of a trispecies F2 population of cotton, In Proceedings of the Beltwide Cotton Conferences, New Orleans, La, USA, vol. 1: 448-452.

Arunita, R., Rakshit, S., Santhy, V., Gotmare, V. P., Mohan, P., Singh, V.V., Singh, S., Singh, J., Balyan, H.S., Gupta P. K. and Bhat, S. R., 2010, Evaluation of SSR markers for the assessment of genetic diversity and fingerprinting of

*Gossypium*hirsutumaccessions. *J. Plant Biochem. Biotechnol.,* 19: 153-160.

Badigannavar, A. and Myers, G. 2010, Genetic analysis of AFLP markers associated with seed quality traits in upland cotton (*Gossypium*hirsutum). In Beltwide Cotton Conferences, New Orleans, La, USA.

Becelaere, G.V., Lubbers, E.L., Paterson, A. H., and Chee, P.W. 2005 Pedigree- vs. DNA marker-based genetic similarity estimates in cotton. *Crop Sci.,* 45: 2281–2287

Blair, M. W., Panaud, O. and McCouch, S. R., 1999, Inter-simple sequences repeat (ISSR) amplification for analysis of microsatellite motif frequency and fingerprinting in rice (Oryza sativa L.). *Theor. Appl. Genetics*, 98(5): 780-792.

Blenda, A., Scheffler, J., Scheffler, B., Palmer, M., Lacape, J., Yu, J. Z., Jesudurai, C., Jung, S., Muthukumar, S., Yellambalase, P., Ficklin, S., Staton, M., Eshelman, R., Ulloa, M., Saha, S., Burr, B., Liu, S., Zhang, T., Fang, D. and Main, D., 2006, CMD: a cotton microsatellite database resource for *Gossypium*genomics. *BMC Genomics*, 7: 132

Bornet, B. and Branchard, M., 2001, Nonanchored inter simple sequence repeat (ISSR) markers: reproducible and specific tools for genome fingerprinting. *Pl. Mol. Biol. Reporter,* 19(3): 209-215.

Bornet, B., Muller, C., Paulus, F. and Branchard, M., 2002, Highly informative nature of inter simple sequence repeat (ISSR) sequences amplified using tri- and tetra-nucleotide primers from DNA of cauliflower (Brassica oleracea var. botrytis L.). *Genome,* 45(5): 890-896.

Chalmers, K. J., Waugh, R., Sprent, J. I., Simons, A. J. and Powell, W., 1992, Detection of genetic variation between and within populations of Gliricidiasepium and G. maculata using RAPD markers. *Heredity,* 69: 465-472.

Chaudhary, L., Sindhu, A., Kumar, M., Kumar R. and Saini, M., 2010, Estimation of genetic divergence among some cotton varieties by RAPD analysis. *J. Plant Breed. Crop Sci.,* 2: 39–43.

Chee, P. W., Draye, X. and Jiang C. X., 2005, Molecular dissection of phenotypic variation between *Gossypium*hirsutum and *Gossypium*barbadense (cotton) by a backcross-self approach: III. Fiber length. *Theor. Appl. Genet.,* 111(4): 772-781.

Chen, D., Ding, G., Guo, W. and Zhang, T., 2009, Molecular mapping of genic male–sterile genes ms15, ms5 and ms6 in tetraploid cotton. *Plant Breed.*, 128: 193–198

Collard, B. C. Y., Jahufer, M. Z. Z., Brouwer, J. B., and Pang, E. C. K. An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: The basic concepts. *Euphytica*, 142: 169–196

Culley, T.M. and Wolfe, A.D. 2000, Population genetic structure of the cleistogamous plant species Viola pubescensAiton (Violaceae), as indicated by allozyme and ISSR molecular markers. *Heredity*, 86(5): 545-556.

Cuming, D. S., Altan, F., Akdemir, H., Tosun, Gurel, A. and Tanyolac, B., 2015, QTL analysis of fiber color and fiber quality in naturally green colored cotton (*Gossypium*hirsutumL.). *Turkish J. Field Crop*, 20(1): 49-58.

Dahab, A. A., Saeed, M. and Mohamed, B. B., 2013, Genetic diversity assessment of cotton (*Gossypium*hirsutumL.) genotypes from Pakistan using simple sequence repeat marker. *Australian J. Crop Sci.,* 7(2): 261–267.

Dhruv S., Cotton products annual report, India, USDA Foreign agricultural service, GAIN Report Number; IN5039, 2015.

Dongre, A. B., Raut, M. P., Paikrao, V. M. and S. S. Pande, 2012, Genetic purity testing of cotton F1 hybrid DHH-11 and parents revealed by molecular markers. *Int. Res. J. Biotechnol.*, vol. 3, no. 2, pp. 32–36, 2012.

Draye, X., Chee, P. and Jiang, C. X., 2005, Molecular dissection of interspecific variation between *Gossypium*hirsutum and G. barbadense by a backcross-self approach: II. Fiber fineness. *Theor. Appl. Genet.,* 111 (4): 764-771.

Frelichowski, J. E., Palmer, M. B. and Main, D., 2006, Cotton genome mapping with new microsatellites from Acala "Maxxa" BAC-ends. *Mol. Genet. Genom.* 275(5): 479-491.

Fryxell, P.A. 1992, A revised taxonomic interpretation of *Gossypium*L. (Malvaceae). *Rheedea*, 2: 108–165.

Galv´an, M. Z., Bornet, B., Balatti, P. A. and Branchard, M., 2003, Inter simple sequence repeat (ISSR) markers as a tool for the assessment of both genetic diversity and gene

pool origin in common bean (Phaseolus vulgaris L.). Euphytica, 132(3): 297-301.

Geng, C. D., Gong, Z. Z., Huang, J. Q., and Zhang, Z. C., 1995, Identification of difference between cotton cultivars (G. hirsutum) using the RAPD method. *Jiangsu J. Agric. Sci.*, 11: 21-24.

Guo, W. Z., Zhou, B. L., Yang, L. M., Wang, W. and Zhang, T. Z., 2006, Genetic diversity of landraces in *Gossypium*arboreumL. Race sinense assessed with simple sequence repeat markers, 48(9):1008–1017.

Guo, W., Cai, P. and Wang, C., 2007, A microsatellite-based, generich linkage map reveals genome structure, function and evolution in *Gossypium*. *Genet.*, 176(1): 527-541.

Guo, Y., McCarty, J. C., Jenkins, J. N. and Saha, S., 2008, QTLs for node of first fruiting branch in a cross of an upland cotton, *Gossypium*hirsutumL., cultivar with primitive accession Texas 701. *Euphytica*, 163(1): 113–122.

Han, Z. G., Guo, W. Z., Song, X. L. and Zhang, T. Z., 2004, Genetic mapping of EST-derived microsatellites from the diploid *Gossypium*arboreum in allotetraploid cotton. *Mol. Genetics and Genomics*, 272(3): 308–327.

Han, Z., Wang, C. and Song, Z., 2006, Characteristics, development and mapping of *Gossypium*hirsutumderived EST-SSRs in allotetraploid cotton. *Theoretical and Applied Genetics*, 112(3): 430–439.

He, D. H., Lin, Z. X. and Zhang, X. L., 2008, Dissection of genetic variance of fiberquality in advanced generations from an interspecific cross of *Gossypium*hirsutum and G. barbadense. *Pl. Breed.*, 127(3): 286-294.

He, D. H., Lin, Z. X., Zhang, X. L., Nie, Y. C., Guo, X. P., Zhang, Y. X. and Li, W., 2007, QTL mapping for economic traits based on a dense genetic map of cotton with PCR-based markers using the interspecific cross of *Gossypium*hirsutum Vs *Gossypium*barbadense. *Euphytica* 153(2): 181-197.

Hulse-Kemp, A. M., Jana, L., Joerg, P., Hamid, A., Ramesh, B., David, D. F., James, F., Marc, G., Steve Hague, L. L., Hinze, K. J., Kochan, P. K., Riggs, J. A. S., Joshua, A. U., Mauricio, U., Shirley, S. W., Qian-Hao, Z., Sumit, K. B., Archana, B., John. J. B., Robert, L. B., Michel, C., Michael, A. G., David, B. H., Md, S. I., Johnie, N., Jenkins, D. C. J., Jean-Marc, L, Danny, J. L., Richard, G. P., Alan, E., Pepper, J. A., Poland, Krishan, M. R., Samir, V. S., Sunil Kumar, S., Andrew, S., Jen, M., Taylor, F. W., Scott, M. Y., Xiuting, Z., Cindy, T., Lawley, M. W., Ganal, A. V. W. and David, M. S., 2015, Development of a 63K SNP array for cotton and high-density mapping of intra and inter-specific populations of *Gossypium* spp. G3: *Genes, Genomes, Genetics.* doi: 10. 1534/g3. 115. 018416.

Ince, A. G., Karaca, M. and Onus, A. N. 2010, CAPS-microsatellites: use of CAPS method to convert non polymorphic microsatellites into useful markers. *Mol. Breed.*, 25(3): 491-499.

Jenkins, N, J., Jack, M. C., Martin, J. W., Russel, H., Osman, A. G., Franklin, C. and Dewayne, D., 2012, SSR Markers for Marker Assisted Selection of Root Knot nematod (Meladogyne incognita) Resistant plant in cotton (*Gossypium*hirsutum L). *Euphytica* 183: 49-54

Jiang, C. X., Chee, P. W., Draye, X., Morrell, P. L., Smith, C. W. and Paterson, A. H., 2000, Multilocus interactions restrict gene introgression in interspecific populations of polyploidy *Gossypium*(cotton). *Evolution*, 54(3): 798-814.

Jiang, C. X., Wright, R. J., El-Zik, K. M. and Paterson, A. H., 1998, Polyploid formation created unique avenues for response to selection in *Gossypium*(cotton). *Proc. Nat. Acad. Sci. USA.*, 95(8): 4419-4424.

Kalia, R. K., Rai, M. K., Kalia, S., Singh, R. and Dhawan, A. K. 2011, Microsatellite markers: an overview of the recent progress in plants, *Euphytica*, 177(3): 309-334.

Kantartzi, S. K., Stewart, J., Mc, D., 2008, Association analysis of fibertraits in *Gossypium*arboreum accessions. *Plant breed.*, 127: 173-179.

Khan, M. Q., Awan, S. I. and Mughal, M. M., 2005, Estimation of genetic parameters in spring wheat genotypes under rainfed conditions. *Indian J. Biol. Sci.*, 2: 367-370

Khan, S. A., Hussain, D., Askari, E., Stewart, J. M., Malik, K. A. and Zafar, Y., 2000, Molecular phylogeny of *Gossypium*species by DNA fingerprinting. Theoretical and Applied

Genetics, vol. 101, no. 5- 6, pp. 931–938, 2000.

Khanam, S. A., Sham, J. L., Bennetzen, and Aly, M. A. M., 2012, Analysis of molecular marker-based characterization and genetic variation in date palm (Phoenix Dactylifera L.). Aust. J. *Crop Sci.*, 6(8): 1236-1244.

Kohel, R. J., Yu, J., Park Y. H. and Lazo, G. R., 2001, Molecular mapping and characterization of traits controlling fiber quality in cotton. *Euphytica*, 121(2): 163-172.

Lacape, J. M., Jacobs, J., Arioli, T., Derijcker, R., Forestier, N. C., Llewellyn, D., Jean, J., Thomas, E. and Viot, C., 2009, A new interspecific, *Gossypium*hirsutum x G. barbadense, RIL population: towards a unified consensus linkage map of tetraploid cotton. *Theor*. *Appl Genet.*, 119: 281-292.

Lacape, J. M., Nguyen, T. B. and Thibivilliers, S., 2003, A combined RFLP-SSR-AFLP map of tetraploid cotton based on a *Gossypium*hirsutum × *Gossypium*barbadense backcross population. *Genom.*, 46(4): 612-626.

Lacape, J. M., Nguyen, T. B., Courtois, B., Belot, J. L., Gib, M., Gourlot, J. P, Gawryziak, G., Roques, S. and Hau, B., 2007, QTL analysis of cotton fiber quality using multiple *Gossypium*hirsutum × *Gossypium*barbadense backcross generations. *Crop Sci.*, 45: 123-140.

Lacape, J. M., Nguyen, T. B., Courtois, B., Belot, J. L., Gib, M., Gourlot, J. P, Gawryziak, G., Roques, S. and Hau, B., 2005, QTL analysis of cotton fiber quality using multiple *Gossypium*hirsutum × *Gossypium*barbadense backcross generations. *Crop Sci.*, 45: 123-140.

Lan, T. H., Cook, C. G. and Paterson, A. H., 1999, Identification of a RAPD marker linked to male fertility restoration gene in cotton (*Gossypium*hirsutum L.). *J. Agri. Genom.*, 1: 1-5.

Landry, B. S., Kesseli, RV, Farrara B, Michelmore RW (1987) A genetic map of lettuce (Lactuca sativa L.) with restriction fragment length polymorphism, isozyme, disease resistance and morphological markers. *Genetics*, 116: 331-337.

Lee, J.A. 1965. The genomic allocation of the principal foliar-gland loci in *Gossypium*hirsutum and *Gossypium*barbadense. *Evol.* 19: 182-188.

Li, G. and Quiros, C. F., 2001, Sequence – related amplified polymorphism(SRAP), a new marker system based on a simple PCR reaction : its application to mapping and gene tagging in Brassica. *Theor. Appl. Genet.*, 103: 455-461.

Li, Z., Wang, X., Zhang, Y., Zhang, G., Wu, L., Chi, J. and Ma, Z., 2008, Assessment of genetic diversity in glandless cotton germplasm resources by using agronomic traits and molecular markers. *Front. Agric. Chin.*, 2: 245–252.

Lin, C. H., Yeakley, J. M., McDaniel, T. K. and Shen, R., 2009, Medium to high-throughput SNP genotyping using VeraCodemicrobeads, DNA and RNA Profiling in Human Blood. Humana Press, New York, 129-142

Lin, Z., He, D., Zhang, X., Nie, Y., Guo, X., Feng, C. and Stewart, J. M. C. D., 2005, Linkage map construction and mapping QTL for cotton fiberquality using SRAP,,SSR and RAPD. *Plant Breeding*, 124 : 180-187.

Liu, B. and Wendel, J. F., 2001, Intersimple sequence repeat (ISSR) polymorphisms as a genetic marker system in cotton. *Mol. Ecol. Notes*, 1: 205-208.

Liu, R. and Meng, J., 2003, MapDraw: a microsoft excel macro for drawing genetic linkage maps based on given genetic linkage data. Hereditas (Beijing), 25: 317-321.

Liu, R., Wang, B. and Guo, W., 2012, Quantitative trait loci mapping for yield and its components by using two immortalized populations of a heterotic hybrid in *Gossypium*hirsutum L. *Molecular Breeding*, 29(2): 297–311.

Maughan, P. J., Seghai, M. A., Maroof, G. R., Buss. andHuestis, G. M., 1996, Amplified fragment length polymorphism in soyabean: species diversity, inheritance and near -isogenic line analysis. *Theor. Appl. Genet.*, 93: 392-401.

McCarty, J. C., Hedin, P. A. and Stipanovic, R. D., 1996, Cotton *Gossypium*spp. plant gossypol contents of selected Gl2 and Gl3 Alleles. *J Agric and Food Chem*. 44: 613-616.

Mei, M., Syed, N. H. and Gao, W., 2004, Genetic mapping and QTL analysis of fiber-related traits in cotton (*Gossypium*), *Theor. Appl. Genet.*, 108(2): 280–291.

Meredith, W. R., 1992, RFLP association with varietal origin and heterosis. In: Proc. Beltwide Cotton Conf. (ed. D. Herber), Nashville, TN. pp. 607.

Michael, A., Gore., Fang, D. D., Jesse, A., Poland., Zhang, J., Richard, G., Percy., Roy, G., Cantrell., Gregory, T. and Alexander, E. L., 2014, Linkage map construction and quantitative trait locus analysis of agronomic and fiber quality traits in cotton. *Pl. Genom.*, 7(1): 213-215

Multani, D. S. and Lyon, B. R., 1995, Genetic fingerprinting of Australian cotton cultivars with RAPD markers. *Genom.*, 38(5): 1005-1008.

Murtaza, N., 2006, Cotton genetic diversity study by AFLP markers. *Electron. J. Biot.*, 9(4): 456-460.

Nagaoka, T. and Ogihara, Y., 1997, Applicability of inter-simple sequence repeat polymorphisms in wheat for use as DNA markers in comparison to RFLP and RAPD markers. *Theor. Appl. Genet.*, 94(5): 597-602.

Park, Y. H., Alabady, M. S., Ulloa, M., Sickler, B., Wilkins, T. A., Yu, J., Stelly, D. M., Kohel, R. J., El-Shiny, O. M. and Cantrell, R. G., 2005, Genetic mapping of new cotton fiberloci using EST-derived microsatellites in an interspecific recombinant inbred (RIL) cotton population. *Mol. Genet. Genomics*, 274: 428-441.

Paterson, A. H., 1996. Making genetic maps. In: A.H. Paterson (Ed.), Genome Mapping in Plants, pp. 23-39. R. G. Landescompany, San Diego, California; Academic Press, Austin, Texas.

Paterson, A. H., Saranga, Y., Menz, M., Jiang, C. X. and Wright, R. J., 2003, QTL analysis of genotype × environment interactions affecting cotton fiber quality. *Theor. Appl. Genet.*, 106(3): 384-396.

Pauly, G., 1979,. Les glandes à pigments du cotonnier: aspects gènètiqueetsèlection des variètès glandless et high gossypol. *Cotton Fibres Trop*. 34:379-402.

Preetha, S. and Raveendren T. S., 2008 Molecular marker technology in cotton. *Biotechnology and Molecular Biology Review*, 3 (2): 032-045.

Qayyum, A., Murtaza, N., Azhar, F. M.and Malik, W., 2009, Biodiversity and nature of gene action for oil and protein contents in *Gossypium*hirsutumL. estimated by SSR markers. *J. Food Agric. Environ.*, 7: 590–593.

Qin, H., Guo, W., Zhang, Y. M. and Zhang, T., 2008, QTL mapping of yield and fiber traits based on a four-way cross population in *Gossypium*hirsutumL, Theor. Appl. Genet., 117(6): 883–894.

Rafalski, J. A., 1997, Randomly amplified polymorphic DNA (RAPD) analysis. In : DNA markers : Protocols, Applications and Overviews (eds. G.C.Anolles and P.M. Gresshoff), Wiley-Liss, Inc. USA, p. 364.

Rahman, M., Hussain, D. and Zafar, Y., 2002, Estimation of genetic divergence among elite cotton cultivars-genotypes by DNA finger printing technology. *Crop Sci.*, 42: 2137-2144.

Rahman, M., Yasmin, T., Tabassum, N., Ullah, I., Asif, M. and Zafar, Y., 2008, Studying the extent of genetic diversity among *Gossypium* arboretum L. genotypes/cultivars using DNA finger printing technology. *Genet.Resour. Crop Evol.*, 55: 331-339.

Rajeev, S., Shreekanth S. P., Ranganath, H. M., Srivalli, P., Manjula, S. M. and Pranesh K. J., 2014, Genetic Diversity Analysis in Cotton (*Gossypium*Hirsutum L.) Based on Morphological Traits and Microsatellite Markers. *Int. J.* Basic and Applied Biolog., Vol. 1, No. 1: pp. 19-22.

Rakshit, A., Rakshit, S. and Singh, J., 2010, Association of AFLP and SSR markers with agronomic and fiberquality traits in *Gossypium*hirsutum L. *J. Genet.*, 89(2): 155-162.

Rana, M. K. and Bhat, K. V., 2004, A comparison of AFLP and RAPD markers for genetic diversity and cultivar identification in cotton. *J. Pl. Biochem. Biotech.*, 13(1): 19-24.

Rana, M. K., Singh, V. P. and Bhat, K. V., 2005,Assessment of genetic diversity in upland cotton (*Gossypium*hirsutumL.) breeding lines by using amplified fragment length polymorphism (AFLP) markers and morphological characteristics. *Genet.Resour. Crop Evol.*, 52: 989–997

Reddy, M. P., Sarla, N. and Siddiq, E. A., 2002, Inter simple sequence repeat (ISSR) polymorphism and its application in plant breeding. *Euphytica*, 128(1): 9-17.

Reddy, U. K., Pepper, A. E., Abdurakhmonov, I., Saha, S., Jenkins, J. N., Brooks, T., Bolek, Y. and El-Zik, K. M., 2001, New dinucleotide and trinucleotide microsatellite marker resources for cotton genome *Res. J. Cotton* Sci, 5: 103-113.

Reinisch, J., Dong, J. M., Brubaker, C. L., Stelly, D. M., Wendel, J. F. and Paterson, A. H., 1994,

A detailed RFLP map of cotton, *Gossypium*hirsutum × *Gossypium*barbadense: chromosome organization and evolution in a disomic polyploid genome. *Genet.*, 138(3): 829- 884.

Richard, I. and Beckmann, J. S., 1995, How neutral are synonymous codon mutations. *Nat. genet.*, 10(3): 259.

Rong, J., Abbey, C., Bowers, J. E., Brubaker, C. L., Chang, C., Chee, P. W., Delmonte, T. A., Ding, X., Garza, J. J., Marler, B. S., Park, C., Pierce, G. J., Rainey, K. M., Rastogi, V. K., Schulze, S. R., Trolinder, N. L., Wendel, J. F., Wilkins, T. A., Williams-Coplin, T. D., Wing, R. A., Wright, R. J., Zhao, X., Zhu, L. and Paterson, A. H., 2004, A 3347-locus genetic recombination map of sequence-tagged sites reveals features of genome organization, transmission and evolution of cotton (*Gossypium*). *Genetics*, 166: 389-417.

Rong, J., Feltus, F. A., and Waghmare, V. N., 2007, Meta-analysis of polyploid cotton QTL shows unequal contributions of subgenomes to a complex network of genes and gene clusters implicated in lint fiber development. *Genetics*, 176(4): 2577–2588.

Russell, J., R., Fuller, D. and Macaulay, M., 1995, Direct comparison of levels of genetic variation among barley accessions detected by RFLPs, AFLPs, SSRs and RAPDs. *Theoretical and AppliedGenetics, 95(4): 714*–722.

Saha, S., Wu, J. and Jenkins, J. N., 2004, Breeding and genetics: effect of chromosome substitutions from *Gossypium*barbadense L. 3-79 into G. hirsutumL. TM-1 on agronomic and fiber traits. *J. Cotton Sci.*, 8(3): 162-169.

Samer, E. M. I., Sami, S. A., Abdel-Kader, Y. G. and Ebtissam H. A. H., 2015, Linkage map construction and detection of QTLs associated with earliness, fiber quality and yield in an inter specific cross between *Gossypium*hirsutum L. and *Gossypium*barbadense L. *Int. J. Advanced Res.*, 3(3): 637-649.

Santoshkumar.M., 2010, Genetic and quantitative trait loci analysis for yield and fiberquality traits in cotton (*Gossypium* spp.), M. S. thesis, Tamil Nadu Agricultural University, Coimbatore, India.

Saranga.Y., Menz, M., Jiang, C. X., Wright, R. J., Yakir, D. and Paterson, A. H., 2001, Genomic dissection of genotype x environment interactions conferring adaptation of cotton to arid conditions. *Genom. Res.*, 11(12): 1988-1995.

Shaheen, T., Asif, M. and Zafar, Y., 2009, Single nucleotide polymorphism analysis of MT-SHSP gene of *Gossypium*arboreum and its relationship with other diploid cotton genomes, G. hirsutum and Arabidopsisthaliana. *Pakistan J. Botany*, 41(1): 177-183.

Shappley, Z. W., Jenkins, J. N., Meredith, W. R. and McCarty, J. C., 1998, An RFLP linkage map of upland cotton, *Gossypium*hirsutumL. *Theor. Appl. Genet.*, 97: 756-761.

Shen, X. L., Guo, W., Lu, Q., Zhu, X., Yuan, Y. and Zhang, T., 2007, Genetic mapping of quantitative trait loci for fiberquality and yield trait by RIL approach in upland cotton. *Euphytica*, 155 (3): 371-380.

Shen, X., Guo, W. and Zhu, X., 2005, Molecular mapping of QTLs for fiber qualities in three diverse lines in Upland cotton using SSR markers, *Molecular Breeding*, 15(2):169–181.

Shi, A., Kantartzi, S., Mmbaga, M. and Chen, P., 2010, Development of ISSR PCR markers for diversity study in dogwood (Cornus spp.). *Agril. and Biol. J. of North America*, 1: 189-194.

Shu, B., K., Fenling, Z. Y., Yao, Z. G., Mei, Z. Q., Yuan, and Gang, W. X., 2001, Genetic diversity analysis of representative elite cotton varieties in three main cotton regions in China by RAPD and its relation with agronomic characteristics. *Scientia AgriculturaSinica*, 34: 597-603.

Sica, M., Gamba, G., Montieri, S., Gaudio, L. and Aceto, S., 2005, ISSR markers show differentiation among Italian populations of Asparagusacutifolius L. *BMC Genet.*, 6, article 17.

Song, X. L., Wang, K., Guo, W. Z., Han, Z. G., Zhang, T. Z., 2005, Quantitative trait loci mapping of leaf morphological traits and chlorophyll content in cultivated tetraploid cotton. *ActaBotanicaSinica*, 47(11): 1382-1390.

Tang, S., Zhonghua, T., Tengfei, Z., Fang, X., Liu, F., Liu, D., Zhang, J., Liu, D., Wang, S. Zhang, K., Shao, Q., Tan, Z., Andrew, H. P. and Zhang, Z., 2015, Construction of genetic map and QTL analysis of fiber quality traits for Upland cotton (*Gossypium*hirsutum L.). *Euphytica*, 201:195–213.

Tanksley, S. D., (1983). Molecular markers in plant breeding. *Plant Mol. Biol. Rep.,* 1 : 3-8.

Tatineni, V., Cantrell, R. G. and Davis, D. D., 1996, Genetic diversity in elite cotton germplasm determined by morphological characteristics and RAPDs. *Crop Sci.,* 36(1): 186-192.

Tautz, D., Trick, M. and Dover, G. A. 1986, Cryptic simplicity in DNA is a major source of genetic variation. *Nat.,* 322(6080): 652-656.

Udall, J. A., Swanson, J. M. and Haller, K., 2006, A global assembly of cotton ESTs. *Genom. Res.,* 16(3): 441-450.

Ulloa, M. and Meredith, W. R., 2000, Genetic linkage map and QTL analysis of agronomic and fibertraits in an intraspecific population. *J. Cotton Sci.,* 4 (3): 161-170.

Ulloa, M., Meredith, W. R., Shappley, Z. W. and Kahler, A. L., 2002, RFLP genetic linkage maps from four F2: 3 populations and a join map of *Gossypium*hirsutum L. *Theor. Appl. Genet.*, (104): 200-208.

Van, D. A., Stoffel, M. K., Lee, Thea, A. W., Alexander, K., Roy, G. C., Zohn, Z. Y., Russel, J. K. and David, M. S., 2009, Sampling nucleotide diversity in cotton. *BMC Plant Biol.*, vol. 9, article 125,.

Vos, P., Hogers, R. and Bleeker, M., 1995, AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Res.,* 23(21): 4407-4414.

Wajahatullah, M. K. and Stewart, J. M., 1997, Genomic affinity among *Gossypium* subgenus Sturtia species by RAPD analysis.In Proceeding of the Belt wide Cotton Conference, National Cotton Council, p. 452, Memphis, Tenn, USA.

Wang, C. B., Guo, W. Z., Cai, C. P. and Zhang, T. Z., 2006, Characterization, development and exploitation of EST derived microsatellites in *Gossypium*raimondii Ulbrich. *Chin. Sci. Bull.,* 51: 557-561.

Wang, J. B. and Yi, C., 2002, ISSR markers and their applications in plant genetics. 24(5): 613-616.

Weeden, N., G. Timmerman & J. Lu, 1994. Identifying and mapping genes of economic significance. *Euphytica*, 73: 191–198.

Wendel J. F., Small R. L., Cronn R. C. and Brubaker C. L., Genes, jeans and genomes: reconstructing the history of cotton, in : van Raamsdonk L.W.D., Den Nijs J. C. M., 1999, Plant evolution of man-made habitats-Proceedings of VIIth *Int.* symposium of the *Int.* organization of plant biosystematists, Hugo de Vries Laboratory, Amsterdam, Netherlands.

Westengen, O. T., Huam, Z. and Heun, M., 2005, Genetic diversity and geographic pattern in early SouthAmerican cotton domestication," *Theoretical and Applied Genetics,* 110(2): 392–402.

Williams, J., Kubelik, A., Liviak, J. L., Rafalski, J. A., Tingey, S. V., 1990, DNA polymorphism amplified by random primers are useful as genetic markers. *Nucleic acid Res.,* 18: 6531-6535.

Wright, R. J., Thaxton, P. M., El-Zik, K. M. and Paterson, A. H., 1998, D-subgenome bias of Xcmresistance genes in tetraploid*Gossypium* (cotton) suggests that polyploid formation has created novel avenues for evolution. *Genetics,* 149(4): 1987-1996.

Wright, R. J., Thaxton, P. M., El-Zik, K. M. and Paterson, A. H., 1999, Molecular mapping of genes affecting pubescence of cotton. *J. Heredity*, 90(1): 215–219.

Wu, J., Gutierrez, O. A., Jenkins, J. N., McCarty, J. C. and Zhu, J., 2009, Quantitative analysis and QTL mapping for agronomic and fiber traits in an RI population of upland cotton, *Euphytica*, 165(2): 231–245.

Xiao, J., Wu, K., Fang, D. D., Stelly, D. M. and Yu, J., 2009, New SSR markers for use in cotton (*Gossypium* spp.) improvement.J. Cotton Sci. 13: 75- 157.

Xu, Q. H., Zhang, X. L. and Nie, Y. C., 2001, Genetic diversity evaluation of cultivars (G. hirsumtumL.) from the Changjiang river valley and Tellow river valley by RAPD markers.Acta Genet.Sin.,28: 683–690

Young, N.D., 1996. QTL mapping and quantitative disease resistance in plants. Annu Rev Phytopathol 34: 479–501

Yu, J. W., Yu, S. X., Lu, C. R., Wang, W., Fan, S. L., Song, M. Z., Lin, Z. X., Zhang, X. L. and Zhang, J. F., 2007, High-density linkage map of cultivated allotetraploid cotton based on SSR, TRAP, SRAP and AFLP markers. *J. Integr Plant Biol.*, 49: 716-724.

Yu, J. Z., Kohel, R. J., Fang, D. D., Cho, J., Van Deynze, A., Ulloa, M., Hoffman, S. M., Pepper, A. E., Stelly, D. M., Jenkins, J. N., Saha, S., Kumpatla, S. P., Shah, M. R., Hugie, W. V. and Percy, R. G., 2012, A high density simple sequence repeat and single nucleotide polymorphism genetic map of the tetraploid cotton genome. *G3,* 2 (1): 43-58.

Yu, X., Wang. H., Zhong, W., Bai, J., Liu, P. and He, Y., 2013, QTL mapping of leafy heads by genome resequencing in the RIL population of Brassica rapa. *PloS One*, 8(10): e76059.

Yu, Z. H., Park, Y. H., Lazo, G. R. and Kohel, R. J., 1997, Molecular Mapping of the Cotton Genome.Agron, Abstracts, ASA, Madison, Wis, USA

Zhang, K., Zhang, J. and Ma, J., 2012, Genetic mapping and quantitative trait locus analysis of fiber quality traits using a three-parent composite population in upland cotton (*Gossypium*hirsutum L.). *Molecular Breeding*, 29(2): 335–348.

Zhang, M., McCarty, J. CJenkins, J. N. and Saha, S., 2002, Assessment of day-neutral backcross populations of cotton using AFLP markers. *J. Cotton Sci.*, 6(2): 97-103.

Zhang, T. Z., Yuan, Y. L., Yu, J., Guo, W. Z. and Kohel, R. J., 2003, Molecular tagging of a major QTL for fiberstrength in upland cotton and its marker assisted selection. *Theor. Appl. Genet.*, 106: 262-268.

Zhang, T., Qian, N. and Zhu, X., 2013, Variations and transmission of QTL alleles for yield and fiber qualities in upland cotton cultivars developed in China, *PLoS ONE*, 8(2): ID e57220.

Zhang, Y., Wang, X, F., Li, Z. K., Zhang, G. Y. and Ma, Z. Y., 2011, Assessing genetic diversity of cotton cultivars using genomic and newly developed expressed sequence tag-derived microsatellite markers," *Genetics and Molecular Res.*, 10(3): 1462–1470.

Zhang, Z. S., Xiao, Y. H. and Luo, M., 2005, Construction of a genetic linkage map and QTL analysis of fiber-related traits in upland cotton (*Gossypium*hirsutum L.). *Euphytica*, 144(1-2): 91-99.

Zhang, Z., Hu, M., Zhang, J., Liu, D., Zheng, J., Zhang, K., Wang, W. and Wan, Q., 2009, Construction of a comprehensive PCR-based marker linkage map and QTL mapping for fiber quality traits in upland cotton (*Gossypium*hirsutum L.). *Mol. Breed.*, 24 (1): 49-61.

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