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Role of Molecular Markers and Importance of SNP for the Development of Cotton Programs

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Abstract
Cotton is an important commercial cash crop and cultivated worldwide. It is very important for improvement of desirable traits for development of cotton crop. In this review paper we have discussed the overall Molecular markers and advance techniques with their utilization in cotton improvement programmers. Molecular markers have reliable results and performance increased research of cotton breeding programs. Molecular markers are used to analyze genomic variations, association mapping, fingerprinting and genetic diversity in cotton crop.SNP markers have many advantages for genotyping of large populations as compared to previous marker systems. It is more advance and efficient processing technique. With the help of SNP technique we get more accurate results as compared to other markers in a short time. Overall DNA markers are used in cotton include Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphism, with their history current development, implication and importance in cotton breeding.

Keywords
PCR Polymerase chain reaction
QTLs Quantitative trait loci
RAPD Random amplified polymorphic
DNA RFLP Restriction fragment length polymorphism
RIL Recombinant inbred line
SNPs Single nucleotide polymorphisms
SSR Simple sequence repeat

1 Background

Cotton (*Gossypium* spp.) is important economic major crop; it is grown in 80 countries all around the world in different ecological conditions (Kalivas et al., 201). Cotton is most cultivated important crop, it is provides oil and fiber around the worldwide (Zhang et al., 2007). Cotton is cultivated on large scale for production of fiber and according with three largest producer china, India and USA cotton crop is 3rd cultivated crop around the world (FAO. FAOSTAT). Total species of genus Gossypium present in world is 50 in which 5 (2n = 4x = 52) are tetraploid and remaining 45 species are diploids (2n=2x=26) ((Fryxell, 1992)). There are four cotton species use for cultivation in which upland cotton (*Gossypium hirsutum*) (AD_1 genome), (*Gossypium barbadense*) (AD_2 genome) from tetraploid species and Asian cotton, (*Gossypium arboreum*) (A_2 genome), *(Gossypium herbaceum)* (A_1 genome) from diploid species (Wendel et al., 1999. Upland cotton (*G. hirsutum*) and Pima (*G. barbadense*) are more used for cultivation and fiber production worldwide. In the U.S their total production accounts 95.5% for American Cotton and 4.5% for Pima cotton (USDA National Agriculture statistics Service 2013).

Molecular markers are increase the efficiency and speed of breeding programs. Various molecular markers are broadly used for analysis of genomic variations in plants, their association mapping as well as diagnostics, evolutionary studies analysis, fingerprinting, and also widely used for breeding applications. Among all of these markers, the new generation molecular markers called single nucleotide polymorphisms (SNPs) are most abundant, robust and feasible because of its availability in whole genome and that they play a key role in the induction of phenotypic variations.

SNP molecular markers are very important for marker assistant selection (MAS) due to highly prolific, solid and workable for robotic high production genotyping. SNP have many options to used different new technology methods for molecular crop genetics and breeding studies of plants (Steemers and Gunderson 2007; Alkan et al. 2011). SNP is mostly used for identification of gene in crop genetics and breeding group as prospective molecular markers (Rafalski et al., 2002). SNPs are used for study of genetic diversity in varieties to explain the origin, phylogeny and link genotypic variations with morphological characters (McNally et al., 2009). SNP molecular markers are commonly accessible for study of varying genes. The objectives of this review to explain role of molecular markers and importance of SNPs in genetics study of Cotton breeding.

2 Molecular markers in Cotton

Due to presence of genomic database molecular markers are easily developed (Andersen and Lubberstedt, 2003)

and plant breeders are used these molecular markers to find for heredity variation, genomic study, and marker assistant selection (Kalia et al., 2011). Mishra et al., 2014) recommend that the ideal molecular marker should have following traits.

1-High polymorphic is essential for genetic studies
2-Codominanace in which difference between homozygous and heterozygous of diploids species
3-Occurring in the genome
4-Selected neutral behavior
5- Cheap and fast
6- Data reset and easily exchange data between laboratories.

DNA Markers can divide into three main groups.

1. Low throughput hybridization based markers such as restriction fragment length polymorphisms (RFLPs)
2. Medium throughput, PCR based molecular markers in which include random amplification of polymorphic SSR and AFLP.
3. High throughput, Markers such as SNP, GBS and GIVAS.

Tanksely (1983) has been gave five features which differentiate DNA markers from morphological markers. The features are given below.

1- Checked genotypes from tissue at molecular level and from whole plant
2- There is a many naturally occurring alleles that present at many loci
3- Phenotypic neutrality
4- Alleles are codominat at many loci
5- Some epistatic effects are observed

2.1 Restriction Fragment Length Polymorphism (RFLP)

Many diverse molecular technique used in past for study of cotton Crop. The RFLP was first technique that used for cotton crop development. RFLP technique shows comparison of DNA sequence separately due to restriction enzyme. The different sizes of DNA fragments' are form from addition, deletions and substitutions of base among populations. Scientists used RFLPs markers for construction of genetic map of cotton (Ulloa and Meredith, 2000). The first genomic map of cotton was produced by using of 705 RFLP loci and distributed into 41linkage groups (Reinsich) et al., 1994). RFLP markers provide a saturated map of cotton plant genome. RFLP markers are not affected by environment or others genes and placed in linkage group due to its dominance.

Advantages of RFLP

The main benefit of RFLP is that it describes the naturally occurring variation in DNA of wide range of different plants. Polymorphism occurs when a single base pair addition or deletion in restriction site due to mutation.

Disadvantage of AFLP

Major disadvantage of RFLP needs a large quantity of DNA for every reaction. RFLP technique is expensive, labouirs and required a long time for analysis which reduces its use in marker assistant selection (Agarwal *et al*., 2008).

2.2 Randomly Amplified Polymorphic DNA (RAPD)

RAPD is a PCR based technique required small primers to speed up the random portions of the genome technology (Williams *et al*., 1990). RAPD is used for the accession profiling with primers that shows polymorphism about exact sequence information. The primers used for this technique should be free from palindromic sequence and have fourty percent GC content in fragments (Williams *et al*., 1990). RAPD markers were used for check the resistant of cotton varieties against jassids, mites and aphids (Geng *et al*., 1995). RAPD marker was used for produced a genetic map and checked the genetic diversity in cotton (Lu and Mayers, 2002)

RAPDs molecular markers are used for study of genetic diversity, gene mapping and finger printing (Zhang *et al*., 2008; Zahra *et al*., 2011). The main advantage of RAPD is that minuet amount of DNA needed for process analysis compared to AFLP. RAPD molecular markers were worked faster for polymorphism screening as compare to RFLP markers. RAPD molecular process is very easy for Bulk segregation analysis (BSA) to connect with regions of genome.

2.3 AFLP (Amplified Fragment Length Polymorphism)

AFLP techniques have been used for observed genotypic diversity in cotton crop (Zhang *et al*., 2005), and it was first developed by Vos *et al*., 1995). AFLP have four major steps which include Restriction digestion and ligation, of adapters, pre selective amplification, selective amplification and gel electrophoresis.

The advantage of AFLP is that it is reliable and efficiently works. There is no need of DNA sequence and information for analysis because AFLP has ability to analyze large number of polymorphic loci with a single primer on a single gel than the single sequence repeat and RFLPs (Russell *et al.,* 1997).AFLP is used for study of genetic diversity, DNA fingerprinting, genetic map, gene identification of desirable traits and phylogenetic

relationship.

2.4 SSR (Simple Sequence Repeat) (Microsatellites)

Simple sequence Repeat another common name is Microsatellites and it was first discovered in humans (Litt and Lutty, 1989). SSRs are advance and new type of DNA markers that speedup the work of cotton genomic mapping. Microsatellites markers are reliable and having higher possibility markers for study of phylogenetic in cotton (Zhang *et al*., 2008). The SSR markers and their map information can be found from cotton gene database website (www.cottongen.org/find/mappedmarkers). SSR markers have been used for observing the genetic diversity and analysis of closely related varieties (Liu *et al*., 2006).

SSR markers are mostly found in eukaryotic genome but also occur in prokaryotes at low frequency. SSRs are used for study of association mapping, finding of QTLs of yield and fibers in Chinese cotton varieties and provides a good parents for develop a good accessions (Zhang *et al*., 2013). SSRs DNA markers are mostly used for construction of genetic map as compared to other markers. The main advantages of SSRs markers are simplicity and specificity. Microsatellite markers are linked with gene tightly and make a useful map. Jenkines *et al*., 2012) selected eleven most homozygous plants for chromosome eleven and fourteen from a F_2 population derived from cross of RKN resistant variety and susceptible variety FM966 by used of SSRs markers. These selected plats have confirmed resistant against RKN in F_2 generation, instead of waiting for F_6 and F_8 generation through conventional breeding. At that time round about 17,000 pairs of SSR primers have been developed from four cotton species *G. arboreum, G. raimondii*, *G. hirsutum* and *G. barbadense* for used as potential molecular markers (Blenda *et al*., 2006), (Frelichowski *et al*., 2006). By used of SSRs markers we identify specific traits genes such as fiber length, strength and fineness in early generation and these genes helpful in marker assisted selection. List of some identified genes of cotton is given in table no 1.

2.5 Genotyping by Sequencing (GBS)

Genotyping by sequencing technology is used for identification and genotyping of SNP molecular markers from a genome (Mir et al., 2013).GBS technique development is simple and has ability to reduce the intrication in genome (Elshire et al., 2011).

The multiplex libraries are developed for next generation sequencing by using of restriction endonuclease enzyme and with DNA barcoded adapters to detecting a section of genome from genotyping by sequencing (GBS).This technique has shown firstly in varieties and has ability to evolving huge markers (Elshire *et al*., 2011; Poland *et al*., 2012). The objective of functional genomics is to screening of good plants for development of crop by exchanging of phenotypic data between phenotype and genotype. From GBS firstly evolve large sequence variants and after that a complete genome sequencing (Poland and Trever, 2012). GBS is a best technique for study of populations because it is help in genetic mapping through which genomic selection can be done widely on large scale (Poland and Trever, 2012). This procedure has been used with some minor changes in protocol in cotton (*Gossypium hirsutum* L.) and sorghum (*sorghum bicolor*) species (Poland et al., 2012). Gore et al., 2014) contracted cotton genetic having eight hundreds fourty one SSR and SNP loci took the half tetraploid genome through SSR genotyping process and implementation of GBS

2.6 Association Mapping (GWAS)

Another name of association mapping is called linkage disequilibrium mapping and it was used for observed variation in multiplex characters through ancient and developmental process in population (M. Nordborg and S. Tavare, 2002). It was described relation of chromosomes among marker position and morphological position. Association mapping technology was generated in plants with transmutation, variation in gene, cross breeding and population selection (Hart and Clark, 1997).The Inherited traits allowing individual discretion of progenitors that permitting descendent for chromosomal mutation and transformation from this new advanced technique genome wide association mapping. The cotton genome required some markers for organize association mapping of complicated character which is reported for other crops (Barnaud et al., 2006). It is depend upon connection unbalance among chromosome position. Immensity connection of maternal combination and connection disequilibrium in gene bank allows suitable choice for genome wise association mapping (Lu *et al*., 2011).

All over the world scientists were used association mapping technology for study of cotton fibers related traits, parameters of yield and yield of cotton seed (Abdurakhmonov et al., 2008 and 2009). Association mapping has helped the scientists to check the variation found in germplasm. The development of SNP technique was made easy to study of whole genome, construction of genetic map and finding of desirable QTLs in plants (Waqas *et al*., 2014).

3 Discovery of SNP

Single nucleotide polymorphism (SNP) can be identified and used through different techniques which include Genotyping by sequencing(GBS), next generation sequencing technology (NGS) (Logan Young CJ, et al., 2015),

enzymatic and chemical mismatch assays, nucleotide amplification polymorphisms (SNAP), ligase chain reaction, Single Stranded confirmation polymorphism analysis (SSCP), Dideoxy fingerprinting, cleaved amplified polymorphic, sequence (CAPS) and derived CAPS (Gupta PK, 2001 and Lee.GA., 2009).

The understanding of cotton genome is possible by using of new genomics technologies for development of American cotton. The next generation sequencing (NGS) is no expensive new rapid technique for genome sequencing and transcriptome, to enable the discovery of single nucleotide polymorphism (SNP), RNA sequencing, gene expression and high throughput genotyping from sequencing studies in plants. However due to limited DNA polymorphism within the cotton species, the used of SSR or SNP markers are restricted for plant breeding and genotyping. Single sequence repeat (SSR) markers were used for construction of genetic map and observed genetic diversity in plants; their numbers are limited in a genome. SNP molecular markers are most present in plants even species are limited to their genetic diversity (Ganal MW *et al*., 2009) .In cotton the development of first SNP markers were slow and expensive and few SNP markers have been developed (Udall JA*, et al*,. 2006),(Van Deynze A, *et al.,* 2009). The development of next generation sequencing (NGS) technique sequencing has become rapid and cheap and it is used for identifying large number of SNP markers (Byers RL, *et al*., 2012), (Lacape JM, *et al*., 2012),(Gore MA, *et al*., 2012) . On other hand development of new cotton genome resources was very important

The development of first NGS based SNP in cotton through method of genome reduction on restriction site (GR-RSC) by using two varieties from Upland cotton (*G. hirsutum*) and two verities from Pima cotton (*G. barbadense*) (Byers *et al*., 2012). GBS technique has used to discover several million of SNPs, a major problem in this technique is large number of missing data.

3.1 Introduction

Variation occurs at a single nucleotide position in DNA sequence of chromosome between two accessions is known as Single nucleotide polymorphism. In other short word SNP is polymorphism which occurs within two DNA samples and difference between single bases by addition, deletion, transversion, transition of chromosome (Ayeh *et al.*, 2008; Hearne *et al*., 2008). SNP markers are extremely reliable directly furnish phenotype (Batley and Edwards, 2007). They are the easiest type of markers as having minor heredity entity as alone base and can produce large number of markers. SNP markers are mostly found in plants and animals. SNPs are commonly assigned and connected with morphological changes used as marker. Lindbeld *et al*., 2000) SNPs play an important role in creations of phenotypic variation by DNA polymorphism in genome of plants, animals and humans. According to international working group of SNP 1.42 million of SNPs are found in human genome and average one SNP is equal to 1.9kb (Sachidanandam *et al*., 2001). In addition to plants SNP polymorphism are present high density in genome (Ching *et al*., 2002).The rice genome have 0.64 SNP per one kb (Jeong *et al*., 2013), in addition tomato genome was observed 6.1 SNP per one in a complete genome (Kim *et al*., 2014).

The first genetic map of cotton was published in 1994. SNP markers have been identified by world scientists for study of gene mapping, phylogenetic analysis and genetic diversity in Gossypium genome (Deynze *et al*., 2009). SNPs were identified in many species include Arabidopsis thaliana (Jander *et al*., 2002), many in cultivated crops like maize (Ching *et al*., 2002), wheat (Ablet *et al*., 2006) and in human beings (Sachidanandam *et al*., 2001)

SNPs have been detected in many species including model species such as Arabidopsis thaliana (Jander *et al*., 2002), many field crops like maize (Ching *et al*., 2002), wheat (Ablet *et al*., 2006) and in humans (Sachidanandam *et al*., 2001). SNP offer high speed and effective genotyping by using next generation sequencing technique. Two genes are ms5 and ms6 to control male sterility in cotton. Four SNP markers were identified from gene of male sterility and male fertility lines. These identified SNP markers were used for separation of male sterility and fertility lines in cotton (Feng *et al*., 2015).

3.2 Importance of SNP

The use of SNP markers in breeding programs has been growing at a faster pace and so is the development of technologies and platforms for the discovery and screening of SNPs in many crops. SNP markers have become extremely popular in plant molecular genetics due to their genome-wide abundance and amenability for high to ultra high throughput detection platforms. Unlike earlier marker systems, SNPs made it possible to create saturated, if not, supersaturated genetic maps, thereby enabling genome-wide tracking, fine mapping of target regions, rapid association of markers with a trait, and accelerated cloning of gene QTLs of interest.

SNP markers are important tool for linkage mapping, map based cloning and marker assistant selection due to the high level of polymorphism. SNPs dominate nature enable the markers to distinguish homozygous and heterozygous alleles (Shaheen *et al*., 2009). Due to high polymorphism rate SNP markers were to measure the gene mapping, genetic diversity, and construction of genetic map, and analysis for QTL in cotton (Michael *et al*., 2014 and Hulse Kemp *et al*., 2015).

Based on international collaboration struggle has developed 70K depend upon illumina genotyping assay (unpublished data: http//www.cttongen.org/node/1287616).This will be a source of high genotyping assay will be

used by cotton breeder, researcher and geneticists' worldwide to increased genome configuration and cotton breeding.

3.3 Advantages of SNP from others Markers

SNP markers were presented rapidly and efficiently genotyping of large scale by using a next generation sequencing technologies (NGS). SNPs have many advantages like easily accessible, data management, rapid, and flexibility cost. Biallic SNPs added data direct into group and make large database marker information because same type of data used from different genotyping places.

We first look the limitation of SSR marker before understanding of SNPs. SSR markers are laborious, time consuming, low output, high cost, not reliable and old technique. SSR images in genome create problems when identify gene. The management of a bioinformatics data of SNPs is easily handles as compare to SSRs markers. With high quality reference genome, SNP data and genome sequence enables a powerful analysis of entire SNP universe for every accession. The benefits of SNP markers were first, flexibility and cost effectiveness is range of genotyping platforms present to meet different need for different markers and cost of sample.

Early SNP technologies are depending upon amplified polymorphic sequence markers (CAPS) (Thiel *et al*., 2004) and allele specific amplification procedures. The life science companies have made investment to introduced latest genotyping platforms and sequencing for latest development in computer science, nanotechnology and automation. The range of multiplexed fixed assays is providing one million SNP loci per run. Through high throughput technologies running of hundreds of samples with low cost SNP assays per day. For these systems require a big investment at early stage the end output is that cost of per sample has reduced and genotype a breeding line is cheaper as compare to phenotype it. Another advantage is that many approaches are automatically in which usual routine staff has been freed to work more effectively in analyzing genotypic and phenotypic data management and using new devices for breeding and genetic applications. One of the main advantages of SNPs is that it is not gel based.

3.4 Uses of SNP in Cotton Research

SNP markers were used for construction of genetic map, finding of QTLs and genetic male sterility in cotton. Cotton varieties under cultivation have large, complex and homologous sub genomes. Genome A have chromosome from 1 to 13 and genome D have chromosome from 14 to 26.SNP markers are helpful to connecting with a gene in marker assistant selection (MAS) in genetic breeding of cotton. This discovery is provides information about candidate gene associate with complex traits will have unusual effects to descried genetically manipulation of connected gene to better desirable characters. The invention of SNP molecular markers will have big impact in master assistant selection of cotton breeding.

SNP molecular markers development are show new paradigm in marker assistant selection especially considering most commonly available genome sequence on gene pool. SNP molecular markers are usually associated with more than one candidate genes. The discovery of SNP molecular marks is difficult due to double set of chromosome in cotton. Mostly private seed companies are used SNP markers for marker assistant selection in corns and other crops.

4 Linkage mapping

Genetic maps are used for study of plant genome, transformation and marker assistant selection in plants to observed association with desirable traits.

The information get from plant genome are known as genetic linkage map. These genetic maps are used for identification of desirable gene, help in marker assistant selection of plants and cloning of plants. Marker assistant selection is used for development of resistant gene in crop breeding programs. Quantitative trait loci (QTL) are used to develop linkage map and run QTL analysis (Paterson *et al*., 1996a). Many important traits are check with marker process at same time by using F_2 population, recombinant inbred lines, and back cross population, isogonics lines and double haploids populations (Jiang *et al*., 2007).

World level scientists have developed a number of maps to map DNA markers and functional characters. The researchers at global level have constructed many linkage maps to map functional traits and markers. Five thousands markers in public database including with 3300 restriction fragment length polymorphism (RFLP),700 amplified length polymorphism(AFLP) and 1000 single sequence repeat (SSR) (Rehman *et al*., 2012) Published genetics maps details is given in table No: 01

5 QTL Mapping

The regions in which gene is present in genome and gene associated with a specific quantitative traits are called QTLs (Collard *et al.,* 2005). The process of construction linkage map and conduction QTL analysis to identify specific region associate with traits is known as QTL mapping (Paterson *et al*., 1996). For finding of QTLs used phenotypic data and a genotypic data of different populations. A quantitative traits locus (QTL) is successes from

process of crossing over which allows analysis of gene and markers in progeny.

The fiber quality traits are easily find through (QTL) mapping, and very helpful in revealing the genetic basis of various fiber quality characteristics and providing important information for improving cotton breeding strategies. Computer QTL Cartographer 2.5software is used for analysis of QTLs (Wang S, *et al*., 2005). List of identified QTLs are give in table No: 03

6 Conclusions

In this paper we have discussed about advance molecular markers how to use and its implications in cotton. In future DNA markers have important value for the development of cotton breeding programs. Molecular markers have increased the speed and efficiency of cotton development programs. In all of these DNA markers SNP is advance and reliable markers. DNA markers are helpful for finding of genetic source with simple methods. Thousands of SNPs are present in cotton varieties give a chance to discriminate from cultivated varieties of cotton all over the world. The SNPs will be dense markers of genomics variation for association mapping techniques, objectives is that correlating of genotypic variation with phenotypic characters and with breeding methods in cotton. The improvement of molecular markers will make more efficient for molecular study of plant genetics and plant breeding helpful in development of cotton.

Table No: 01 Published Genetic Maps using Interspecific population in Cotton

Strains name	Parentage		Population name	Total populaton	Name of Markers	Total loci	Map length (cM)	referances
G.h/ G.barbadnace	(Palmeri)	(k101)	F_2	57	RFLP	705	4675	Reinisch *et al*., 1994
G.h/ G.barbadnace	(CAMD-E)	(Sea Island Seaberry)	F_2	271	RFLP	261	3767	Jiang *et al*., 1998
G.h/ G.barbadnace	(Deltapine61)	(Sea Islandseaberry)	F_2	180	RFLP	-	3664	Jinag *et al*.,2000
G.h/ G.barbadnace	(TM1) ×	(3-79)	F_2	171	RFPL, RAPD and SSR	-	4766	Kohel et al., 2001
G.h/ G.barbadnace	(Sivon)	(F-177)	F_2	430	RFLP	253	-	Saranga *et al*., 2001
G.h/ G.h	(Sivon)	(F-177)	F_3	208	RFLP	-	-	Paterson *et al.,* 2003
G.h/ G.barbadnace	(TM1)	(Hai7124) × (TM1)	BC_1F_1	140	EST-SSR	624	5644.3	Han *et al*., 2004,2006
G.h/ G.barbadnace	(Acala 44)	(Pima S7)	F_2	94	AFLP,SSR and RFLP	392	3287	Mei *et al*., 2004
G.h/ G.barbadnace	(Palmeri)	(K101)	F_2	57	RFLP	2584	4447.9	Rong *et al*., 2004
G.h/ G.barbadnace	(Tamcot 2111) × (pima S6)	(Tamcot 2111)	BC_1F_2	3662	RFLP	-	-	Chee *et.al.,* 2005
G.h/ G.barbadnace	(Guazunch02) (VH8)	(Guazuncho 2)	BC_1 & BC_2	200	SSR and RFLP	1306	5597	Lacape *et al.,* 2003,2005
G.h/ G.barbadnace	(Handan208)	(Pima90)	F_2&$F_{2:3}$	69	SSR,SRAP, RAPD and REMAPs	1029	5472.3	Lin *et al*.,2005 He *et al*.,2007
G.h/ G.barbadnace	(TM1)	(Pima 3-79)	RILs	183	EST-SSR	193	1277	Park *et al*,. 2005
G.h/ G.barbadnace	(7235)	(TM-1)	F_2&$F_{2:3}$	163	SSR	86	666.7	Shen *et al*,.2005

Published Genetic Maps using Interspecific population in Cotton

Strains name	Parentage		Population name	Total population	Name of Markers	Total loci	Map length (cM)	referance
G.h/ G.barbadnace	(TM1)	(3-79)	RILs	163	**SSR**	433	2126.3	Frelichowski *et al.,* 2006
Gh/ G.barbadnace	(CR136)	(Hai7124)	F_2	183	SSR,TRAP,SRAP and AFLP	1097	4536.7	Yu *et al.*, 2007
G.h/ G.barbadnace	(Handan208)	(Pima 90)	RILs	186	SSR	-	5472.3	He *et al.*, 2007
G.barbadnace / G.barbadnace	(Guazunchо 2)	(VH8-4602)	RILs	121	SSR and AFLP	800	2044	Lacap *et al.*, 2009
G.h/ G.barbadnace	(KC3) × (Suvin)	KC3	BCIF1	140	SSR	57	911.6	Santoshkumar *et al.*, 2010
G.h/ G.barbadnace	(TM1)	(3-79)	RILs	62		2072	3380	Yu *et al.*, 2012
G.h/ G.barbadnace	(SG 747)	(Giza 75)	BILs	186	SSR and SNP	392	2895	Yu *et al.,* 2013
G.h/ G.barbadnace	(TM-1)	(NM24016)	RILs	146	SSR	841	2061	Michael *et al.*, 2014
G.barbadnace / G.hirsutumcv.	(Doubled haploids lines 3-79)	Texas Marker-1	F_2	98	SSR and SNP	19,198	4439.6	Hulse kemp *et al.*, 2015
G.barbadnace / G.h	(Giza 45)	Tamcot Luxor	F_2	118	SNP	210	3503.8	Samer *et al.*, 2015
G.h/ G.tomentosum	(TMS22)	(WT936)	F_2	60	AFLP,SSR and EST-SSR	589	4259.4	Westengen *et al.*, 2005
G.h/ G. *darwinii*	(CCRI 12-4)	*(5-7)*	F_2	188	SSR	2922	4176.7	Chen *et al.*, 2015
G.h/ G. Tomentosum	(CRI 12-2)	(P060I211)	F_2	188	SSR	3093	4365.3	Khan *et al.*, 2016

Published Genetic Maps using Intraspecific population in Cotton

Strains name	Parentage		Population name	Total populaton	Name of Markers	Total loci	Map length (cM)	referance
G.h/ G.h	(LU28)	(Zhong 2013)	F_2	170	SNP	-	2480	Li et al., 2017
G.h/ G.h	(0-153)	(SGK9708)	RILs	196	SSR	997	4110	Jamshed *et al.*, 2016
G.h/ G.h	(Yesil)	(Nazilli 84)	F_2	94	AFLP	240	2068.5	Cuming *et al.,* 2015
G.h/ G.h	(Yumian1)	(7235)	RILs	180	SSR	1540	2842.06	Tang *et al.,* 2015
G.h/ G.barbadnace	(Hai7124)	(3-79)	F_2	124	SSR,EST-SSR and SNP	412	2108.34	Wang *et al.,* 2013
G.h/ G.h	(Yumian 1)	(T586)	RILs	270	SSR and SRAP	604	3140.9	Zhnag *et al.,* 2009
G.h/ G.h	(HS 46)	(MARCABUCAG8US-1-88)	RILs	188	SSR	125	965	Wu *et al.*, 2009
G.h/ G.h	(DH962)	(Jimian5)	F_2	137	SSR, SRAP, RAPD and RGAP	471	3070.2	Lin *et al.,* 2009
G.h/ G.h	(Deltapine)	(Texas 701)	F_2	251	SSR	73	650.8	Guo *et al.*, 2008
G.h/ G.h	(Yumina 1)	(T586)	RILs	270	SSR	19	96.2	Wan *et al.*, 2007
G.h/ G.h	(7235)	(TM-1)	RILs	207	SSR	156	1024.4	Shen *et al.*, 2007
G.h/ G.h	(L-70)	(L-47)	RILs	76	EST-SSR	-	-	Abdurakhmonov *et al.*, 2007
G.h/ G.h	(Zhongmian suo12)	(8891)	RILs	180	SSR, AFLP, RAPD and SRAP	132	865.20	Wang *et al.*, 2006
G.h/ G.h	(TM1)	(7235)	RILs	258	SSR	110	810.7	Shen *et al.,* 2007
G.h/ G.h	(Yumian 1)	(T586)	F_2 and $F_{2:3}$	117	SSR and AFLP	70	525	Zhang *et al.*, 2005

Published Genetic Maps using Intraspecific population in Cotton

Strains name	Parentage		Population name	Total populaton	Name of Markers	Total loci	Map length (cM)	Referance
G.trilobum/ G. raimondii	(Skovsted)	(Ulbr)	F_2	62	RFLP	763	1493.3	Rong *et al.,* 2004
Gh/ G.barbadnace	(Acala44)	(Pima S7)	F_2	94	AFLP,RFLP and SSR	392	3287	Mei *et al.*, 2004
G.h/ G.h	(Handan208)	(Pima90)	F_2	129	SRAP	237	3030.7	Lin *et al.,* 2005
Gh/ G.anomalum	(TM I)	*(7235)*	F_2 and F_3	186	SSR and RAPD	-	-	Zhang *et al.*, 2003
G.h/ G.h	*G.hirsutum*	*G.hirsutum*	4WC	273	SSR, EST-SSR	286	2113.3	Qin *et al.*, 2008

Table No:02 Details list of Identified QTLs with different traits in Cotton

Sr.no	Traits	Details of traits	Population type	Total population	Total and type of markers	Total QTLs	Referance
1	Earliy maturity	FT, FBP, WGP,HNFFB, NFFB and PH.A	F_2	170	3978 SNP	47	Li et al., 2017
2	Salt traits	RL,SH,CHL,SFW,SDW,RFW	F_2	188	1295 SSR	11	Oluoch *et al.*,2016
	Fiber	FL,FU,FM,FE and FS	RILs	196	851 SSR	165	Jamshed *et al.*, 2016
		FS,FL and FF	F_2	171	216 RFLP and 139 RAPDs	13	Kohael *et al.*, 2001
		FL, FS, FE and FC	F_2	94	123 AFLPs	43	Cuming *et al.*, 2015
		FE, FL, FS, FF, and FU	RILs	180	25, 313 SSRs	62	Tang *et al.*, 2015
		FE, FL, FS, FF and FU	CP	172	16052 SSRs	63	Zhang *et al.*, 2012
		FS,FE,FF,FU and FL	F_2	200	448 RFLP	28	Zhang *et al* 2011
		FS, FE, FU, FL and FF	RILs	270	7508 SSRs, 384 SRAPs and 740 IT-ISJs	13	Zhang *et al.*, 2009
		FS, FL, FF, FMT, FE and SFI	RILs	180	4106 SSRs, AFLPs, RAPDs and SRAPs	48	Wang *et al.*, 2006
4	Fiber and Morphological	BW,LP,FF,ES,FU,DFF and DFN	F_2	60	64 AFLP, 36 SSRs, 50 EST,18 EST-SSRs	81	Samer *et al.*, 2015
		SCY, LY, LP, BW, SI, FMT, PER, WF, WT, FF, FL, FE and FS	RILs	188	141 SSRs	36	Wu *et al.*, 2009
5	Yield and fiber	SCY, LY, LI, BW, FL, FS and FU	BILs	146	2041SSRs	67	Yu *et al.*, 2013
		PH, FBN, BW, LP, LI, SI, LY, FL, FS, FE, FF and FU	*Gh*(varieties)	81	121SSRs	180	Zhang *et al.*, 2013
		SCY, NB, BW, LP, SI, LI and FBN	RILs and IF_2	180	2675 EST-SSR	111	Liu *et al.*, 2012
		NB, BW, SI, LP, LI, SCY, LY, FL, FS, FF, FE and FU	4WC and inbred lines	280	6123 EST-SSRs and SSRs	31	Qin *et al.*, 2008

Flowering time (FT), Period from first flower blooming to first boll opening (FBP), Number of bolls per plant (NB), Boll weight (BW), Seed index (SI), Lint percentage (LP), Lint index (LI), Seed index (SI), Seed cotton yield per plant (SCY), Lint yield per plant (LY), Fiber length (FL), Fiber strength (FS), Fiber elongation (FE), Fiber uniformity ratio (FU), Fiber yellowess (FY), Fiber fineness (FF), Fiber maturity (FMT), Fruiting branch length (FBN), Fruit branch number (FBN), Fruit branch angle (FBA), Fiber length uniformity (FLU), Short fiber content (SFC), Fiber reflectance (FR), Seed weight (SW), Number of seeds per boll (NS), Upper quartile length (UQ), Short fiber content (SF), Fiber tenacity (FT), Immature fiber content (IF), Short fiber index (SFI), number of seeds per boll (NSB), Date of first Flowering (DFF), Node of first fruiti ng branch (FFN), (HFFN), Plant height (PH), Period of growth and development (WGP)

Table No: 03

Identified genes in Cotton with Different traits

Traits	Genes	References
Fiber length	qFs1	Zhang *et al.*, 2003
Fiber strength	QFL – D2-1	Wang *et al.*, 2006
Fiber development	Li_1, Li_2, N_1, n_2, Fz, haN1, N_1, N_2	Rong *et al.*, 2007
Blight resistance	B_2, B_3, B_{12}	Wright *et al.*, 1998
CMS	Rf_1, RF_2	Lan *et al.*, 1999 and Liu *et al.*, 2003
GMS	ms_5, ms_6, ms_{15}	Chen *et al.*, 2009

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