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Use of Molecular Markers in Improvement of Cotton for Agronomic Traits

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Abstract
Upland Cotton (*Gossypium spp)* is known as the largest natural fiber and vegetable oil source worldwide, to increase the superiority of agronomic traits withstand contrary abiotic and biotic stress in the field and fiber/yield qualities to fulfill all the necessity of advance spinning technology. Upland cotton increase through conventional plant breeding is a time consuming; present circumstance molecular markers established that effective tools to speed up the plant breeding programme for cotton improvement. Especially accentuate is given to application, obstacles, and perspectives of marker-assisted breeding since it appears to be more hopeful in falsify novel gene that are used in the cotton germplasm. The development of system quantitative breeding/genetics in molecular marker-helps for breeding programme would be necessary requirement to understand its role in cotton. While the same time, the function of genetic engineering and in vitromutagenesis cannot be used out in genetic melioration of cotton. In the demonstrate variety of molecular markers are useable, option of molecular marker depends on the users. The critique article gives a over view of versatile molecular markers used in cotton possess, Inter simple sequence repeats (ISSR), Random Amplified polymorphic DNA (RAPD), Amplified fragment length polymorphism (AFLP), Restriction fragment length polymorphism (RFLP), Sequence Related Amplified Polymorphism (SRAP), Single Nucleotide Polymorphism (SNP), and Simple sequence repeats (SSR), Above all molecular markers act a vital role in for betterment of crop improvement programme such as (a) Construction of linkage Map (b) Investigation of genetic diversity in cotton, (c) Marker Assisted Selection (MAS) (d) QTL investigation for agronomic and fiber related traits in cotton.
Keywords: Molecular marker, Single nucleotide polymorphism, Cotton Improvement, GWAS, QTL.

INTRODUCTION

Upland cotton is a most crucial natural fiber crop cultivated in subtropical and moderate zones of atleast about 80 different countries of the world. The cotton fiber is used directly for raw material in textile, industrial and for cotton seed oil as a spin-off, (Li *et al*., 2014). Upland cotton incorporate atleast 50 approved species belongs to 8 genome groups (Wendal and Grover, 2015). From them 4 cotton species, such as *G.hirsutum L, G.barbadence, G.herbaceum, and G.arborium* had been cultivated for domesticated purpose. Whereas *Gossypium hirsutum L.* (2n=4x=52), the size of genome is 2.5 Gega bite; (li *et al*., 2015; 2014; Wendal and Grover, 2015). In addition, to specify the genetic base makes the productivity of cotton susceptible to attack different insect pests, any other fungal or any other disease. That is autochthonic to tropical and subtropical regions and existence cultivated on every continent of all over the world. In the world cotton crop is grown in an area of 35.1 million hectares producing 117 million bales with a productivity of 766 kg/ha (Dhruv, 2015). On the discipline that the quantitative traits divides into mortal genetic factors by finding deoxyribonucleic acid molecular marker closely connected with each others, that is very simple to control them expeditiously and this also helps to achieve the suitable results speedily and more exactly (Preetha and Rveendren 2008). Investigation of microsatellite or simple sequence repeats loci is high pragmatic due to of their duplicability transferability, co-dominant in nature (Ghaffari and Hasnaouri, 2013). In prescribe to compound all the favorable traits from different varieties are associate with wild species for evaluation of superior varieties through conventional breeding methods involve repeated backcrossing, testing and selfing they are time consuming and low exact processes as comparison to direct excerpt of plants basis on molecular procedures, (Preetha and Rveendren, 2008). SSR markers had been extremely used for the observation of genetic diversity, supervise of the introgression of novel alleles, quantity trait loci mapping, cultivars shelter, and choice of breeding (Rahman *et al*., 2008, Blenda *et al*., 2006, and Zhao *et al*., 2014,).

The immense majority of agronomical factors in upland cotton, as qualitative and quantitative traits, are controlled by many genes with little effects. Quantitative trait loci are effective tools which had been commonly used to detect the genetic architecture in quantitative factors. And it is also highly affected for using in marker assisted selection in crop breeding programmes. Diachronic markers, such as Simple sequence repeats (SSR), Amplified fragment length polymorphism (AFLP), and Restriction fragment length polymorphism (RFLP), had played a vital role in previous studies in QTL mapping in cotton. large number of interspecific and intraspecific genetic maps had been established and used in quantitative trait loci mapping by genetic linkage analysis in *G.hirsutum L* (Zhang *et al*., 2013; Yu *et al*., 2015; Wang *et al*., 2015a; Jamshed *et al*., 2016; and Fang *et al*., 2014). Linkage analysis can skim a minute quantitative trait loci and palace the quantitative trait loci in high regions (Powell and Mackay 2007; and Cavanagh *et al*., 2008). The using of high technology, such as single nucleotide polymorphism arrays and sequence, amend the firmness of molecular genetics maps and the accuracy of Quantitative trait loci mapping. high concentration of genetic linkage maps holding a high numbers of Single nucleotide polymorphisms or excision or addition polymorphism molecular markers had been observed on the basis of mixed type molecular markers, single nucleotide polymorphism are important locus (Wang *et al*., 2015; Yu *et al*., 2012; Zhang *et al*., 2016; Hulse-Kemp *et al*., 2015). Linkage with the physical genetic maps of *G. hirsutum L*. (Zhang *et al*., 2015; Li *et al*., 2015; Wang *et al*., 2012; Li *et al*., 2014). The tools which provides the content for fine mapping, identification of gene functional exploration, candidate gene, and Marker assisted selection (Zhu *et al*., 2016; Ma *et al*., 2016).

The GWAS is substitute tool for deleting quantitative trait loci and promising a genetic method to detection of some especial sites in plants parts (Saidou *et al*., 2014; Remington *et al*., 2001). Comparison to biparental genetic linkage mapping, Genome-wide association study had the reward of high-resolution, high price and no need for making a genetic population. Genome-wide association studies had been broadly used in studies of different plants, such as in the Rape and mustard, rice, maize. based on high database of discrepancy phenotypic and high concentration cultivars protecting the overall genome, the Genome-wide association studies is the effective and dominant for analyze genetic changes. Study the hindrance of population ascribes and surroundings changes, such as mixed linear model, general linear model, and Anderson test had been established using infrastructure, Relationship or other traits such as resultants changes to decrease mistakes (Yang *et al*., 2014; Liu *et al*., 2016). In last previous years, scientists have recognized many molecular markers loci colligate with plant characters, yield and fiber quality, resistance and yield by affiliation mapping using simple sequence repeats molecular markers (Liu *et al*., 2015; Nie *et al*., 2016; Abdurakhmonov *et al*., 2009), whileas, the molecular marker concentration and the representation population In this surveys was limited.

Tetraploid genome of upland cotton which is comparatively large and incorporate atleast 2200-3000 Mega byte of Deoxyribonucleic acid and morphological characterstics and RAPD, Crop Science, vol. no 36, no.1,pp. 186-192,1996). Interspecific Deoxyribonucleic acid polymorphism is too small in this species morphological characterstics and RAPD, Crop Science, vol, no,1, 36, pp. 186-192,1996, RFLP genetic diverseness in upland cotton,pp.81-101,Science Publishers, Enfield,

NH,USA,2001), that create it a ambitious crop for evaluation of markers. There is a huge demand for an high polymorphic marker on the condition of progress in crop breeding is to be creating using MAS plant breeding/techniques. In much quantity extraordinary reassessment had been written about the unlike classes of markers using in plants in construction of linkage map. The QTL analysis and MAS deoxyribonucleic acid markers, in Deoxyribonucleic acid-based molecular markers in plants species, pp. 39-57, Kluwer Academic Publishers, Dordrecht, the Netherland, 1994- marker engineering in *G.hirsutum*, Biotechnology and Molecular Biology reassessment, vol,3,no.2,pp. 32-45, 2008). The accusative of this review are as (a) analysis of the development of molecular marker technologies in cotton breeding and genetics, (b) genetic diverseness in the wild and cultivated cotton gene pools, and (c) An overview of QTL mapping and MAS activities in cotton.

Zhang *et al*., (2003) discovered eight markers connected with FS quantitative trait loci (QTLFS) which explicate more than 30% of the physical changes in a *G.anomalum* introgression line 7245. The quantitative trait loci was remains same in relative mapping of RIL and F2 population (Shen *et al*., 2005,2006,2007) it was offently used in Marker assisted selection plant breeding to increase fiber length (Guo *et al*., 2003). Conception of genetic molecular markers Mendal used phenotypic based genetic molecular markers research in his experiment estimate in the 19th century. Subsequently, genetic molecular markers formation of the hypothesis of genetic linkage map. (Reproduction plant cell, 2008 April; 27(4):617-31. The marker is delimited as a specific section of Deoxyribonucleic acid which is instance of the dissimilar at the genomic positions. The markers are not correlative with phonotypical manifestation of a trait. A schematic model of molecular markers in given in the figure 1.

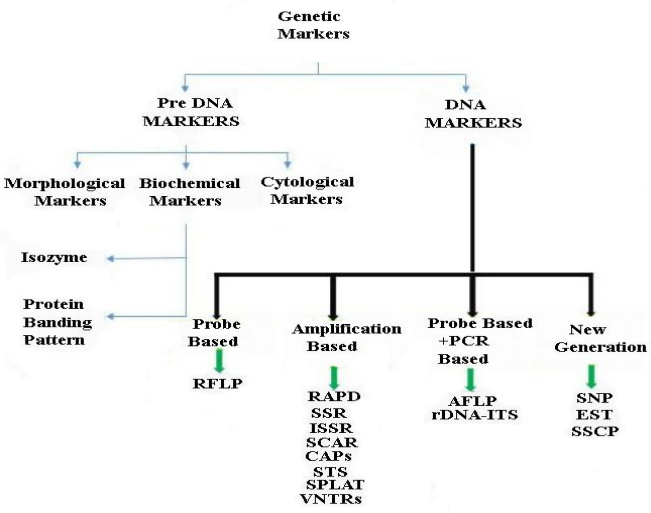

Fig. 1. Schematic model of molecular markers

Overview of marker methods

The release of Botstein *et al*., 1990, genetic linkage maps using RFLP was the only first described marker method in the spying of Deoxsiribonucleic acid polymorphism.

The basic marker methods can be divided into two classes: (a) Polymerize chain reaction- based method (b) Non Polymerize chain reaction based method or interbreeding based methods and the other one is PCR-based method.

Polymerize chain reaction-based method

Later the conception of Polymerize chain reaction technology (Faloona & Mullis 1987), a wide No of ideas for propagation of markers found on polymerize chain reaction were elaborate, principally because of its evident easiness and high certainly of success. Using of unsequenced primers overcome the restriction of anterior sequence information for Polymerize chain reaction investigation and easy to the evolution of genetic molecular markers for a motley of purpose. Polymerize chain reaction-based methods can foster sub grouped into two sub groups: (1) haphazardly primed Polymerize chain reaction-based methods or sequence nonspecific methods and the other one is (2) Targeted sequence polymerize chain reaction-based methods.

DNA molecular markers techniques used in cotton
Random Amplified Polymorphic DNA (RAPD)

The Random amplified polymorphism deoxsiribonucleic acid technique is different polymerize chain reaction amplification of genomic DNA. It deducts DNA polymorphosis create by rearrangement of excision at or among oligonucleotide primer connecting with genome using little random oligonucleotide order (Williams *et al*., 1991). Random Amplified Polymorphism DNA this is the basic Polymerize chain reaction-based molecular marker method it regards 10 bp primers (Williams *et al*., 1990). In this method has many reword over restriction fragment length polymorphism method such as no radioactive sleuthing, this also did not demand anterior sequence information, it mandatory very small measure of genomic DNA, observation chasteness and there is no need for costly tool beyond a thermo cycler and a transilluminator (Rafalski, 1997). The major disfavor of random amplified polymorphism DNA is a method had been used for high purpose in upland cotton possess appraisal of, genome mapping, diversity, and phylogenic studies(He *et al*., 2008, Rehman *et al*., 2002: Zhang *et al*., 2002: Bhat and Rana *et al*., 2004: Rahman *et al*., 2008), hereditary changes or diverseness studies (Chalmers *et al*., 1992, Xu *et al*., 2001; Tatineni *et al*., 1996; and Choudary *et al*., 2010), Deoxyribonucleic acid Multani *et al*., (1995) determines the association between the genotypes of various and same species Wajahatullah *et al*., (1997), he also estimate the

genetic/hereditary association between cotton varieties Shu *et al*., (2001), to recognized the quantitative trait loci for stomatal conductance Ulloaand Meredith, (2000), to manufacture linkage mapping and QTL analysis in *G.hirsutum L* (Wang *et al*., 2006, Lin *et al*., 2009, and Zhang *et al*., 2003). Random amplified polymorphic profile varies within and between laboratories because that is influenced by many factors such as DNA denseness, reproducibility of thermo cycler profiles, primer quality and density, selection of DNA polymerase, (Rafalski, 1997). Random amplified polymorphic was used to differentiate the cotton genotypes immune to aphid, mites, and jassids (Geng *et al*., 1995). Random amplified polymorphism DNA molecular marker R-6592 for male infertility gene had been established in *G.hirsutum L* (Lan *et al*., 1999). The DAF method regards using of individual arbitrary primers smaller than 10 nucleic acids for elaboration (Bassam and Caetano-Anolles, 1993).

Restriction fragment length polymorphism (RFLP)

Restriction fragment length polymorphism was the first kind of Deoxyribonucleic acid marker. In restriction fragment length polymorphism is discovered by hybridization a chemically labeled Deoxyribonucleic acid analysis. In southern blot compilation by restriction ecdonucleases, consequence in different fragment profile. That inhabitant to hybridization based molecular markers that are used for cloned DNA sequences to analysis a specific regions of the genome for changing that are realize as changes in the length of Deoxyribonucleic acid fragment produce by digestion with restriction ecdonucleases (Landry *et al*., 1987).

RFLP was the initiative DNA molecular marker previously employed for crop betterment. Meredith *et al*., (1992) in a study of heterosis and varietal origins described that first restriction fragment length polymorphism rating in cotton (*G.hirsutum L*. Reinisch *et al*., 1994), described first RFLP based linkage map had 41 linkage with 4675 cm length with groups by using 700 RFLPs in cotton, (Chee et al., 2005, Paterson et al., 2003, Saranga et al., 2001: and Rong et al., 2004). The method is not broadly used because it is wasting of time, demand costly and radioactive/toxic reagents and expect high quantity and large quality genomic DNA. Yu *et al*., 1997, Used RFLP markers for genetic diversity studies in different *G.hirsutum* species. Reinisch *et al*., (1994) described that 46.2% of nuclear DNA analysis discover RFLPs among *G.hirsutum and G. barbadense*, 64% are highly dominant in nature than that many researchers were used that markers in constructing of linkage map in upland cotton. Wright *et al*., 1998, described utility of restriction fragment length polymorphism markers in marker help for selection (MAS) and RFLP connect to resistance allele for disease of bacterial blight was formalize. The demands of anterior sequence knowledge for probe multiplication improve the complex methodology. These restrictions led to the formulation pair of small technically complex techniques called as polymerize chain reaction-based methods.

Single Nucleotide polymorphism (SNP) Markers and Population

Usually Genome-wide association studies had been used to diagrammatic quantitative factors in plants species (Lu *et al*., 2015; Street and Ingvarsson, 2011; Zhao *et al*., 2011; Crowell *et al*., 2016; and Atwell *et al*., 2010). The ability of Genome-wide association studies primarily consists of 4 components; the profuseness of genetic diverseness, acquired the maker concentration and stastical techniques. The *G.hirsutum* varieties accumulation originally from china had high levels of phenotypic and genotypic diversity. The accessions of 503 shroud the 5 cotton development zones in china. From them a little accessions were acquaint mainly from SN and from America, like as Stoneville and Coker Deltapine, that are the beginner of upland cotton breeding programmes in china and had implication contribute in cotton yield.

The closely high sample size guaranteed enough genetic variability, and the size was like to the Genome-wide association studies used for A. thaliana (Zhao *et al*., 2005), Brassica napus (Xu *et al*., 2016), Oryza sativa (Famoso *et al*., 2011; Crowell *et al*., 2016), and Zea mays (Wen *et al*., 2014; Li *et al*., 2013a). The phonotypical variability associated with the environment upset the dependability of qualitative trait loci mapping. Multi environment plan and indifferent forecasting are practical manners to amend for this mistake. There are 4 sites for the factors analysis Hubei and Huanggang (HG, E115.77°, N29.45°); Yuanyang, Henan province (YY, E114.98°, N34.04°) Xijiang, Shihezi (SHZ, E84.92°, N42.28°); and korla, Xijiang (KX, E76.04°, N43.66°) are situated in the 3 major cotton zones in china. In improver, the 4 situations belong to 4 climatic divisions, BSK (cold and arid steppe), (hot temperate zones whereas the air is humid), Cwa (Desert & warm temperate regions), and Bwk (Arid desert and cold), (Du and Chen, 2006). Their are huge dissimilarities in geographic level and climate between these zones. There are sixteen agronomic traits having high phenotypic variability and stability herebility are suitable to expose their genetic foundation. The single nucleotide polymorphism array approach is dependable, effective and richly for genotyping. Upland cotton SNP 63K array, the first single nucleotide polymorphism for upland cotton, was established from pairs which symbolize inauspicious, possess *G.hirsutum G.barbadence, G.tomentosum, G.mustelinum, G.armouriannum* and *G.long* calyx (Hulse-Kemp *et al*., 2015). The array demonstrates high polymorphism which is (50.19%) in a cotton panel comparison with single sequence repeats markers (Wang *et al*., 2015, and Li *et al*., 2016). The common values concentration of polymorphic Single

nucleotide polymorphisms was ISNP/0.32 cM, equal to two hundred kilo byte in the phonotypical diagram that accomplishes the demand for Genome-wide association studies mapping.

Amplified fragment length polymorphism (AFLP)

The AFLP technique was previously discovered by a namely Vos *et al*., 1995; this method was based on three procedure regard three steps: (1) gel analysis amplified fragment, (2) Restriction of genome DNA and ligation of oligo nucleotide adopters, (3) pre and selective amplification of restriction fragment. This method compound dependability of restriction length fragment polymorphism with the simpleness of random amplified polymorphic DNA. Usually polymorphic fragment are perceived as presence or absence devising it a prevalent marker system, but in case of soya bean Maughan *et al*., 1996, detect co-dominant nature. This method can be automation and permit the Co-Occurrent analysis of many genetic loci per observations. Amplified Fragment Length Polymorphism (AFLP) creates more polymorphic loci per primer than SSRs RAPDs Maughan *et al*., (1996). AFLP is an effectual tool for the noticed the genetic diversity (Murtaza *et al*., 2006; Abdalla *et al*., 2002; Li *et al*., 2008; and Rana *et al*., 2005) finger printing studies, and tagging of agronomic, fiber and seed quality traits (Rakshit *et al*., 2010; Badigannavar *et al*., 2010; and Zhong *et al*., 2002). AFLP is most important method for mapping of gene studies due to their high copiousness and random distribution end to end the genome (Vos *et al*., 1995). An association relationship map of upland cotton was discovered using the AFLP and Random fragment Length DNA markers (Altaf *et al*., 1997). Amplified fragment length polymorphism molecular markers had also been used for constructing of linkage map and QTL analysis in addition with other markers Yu *et al*., 2007; Wang *et al*., 2006; Cuming *et al*., 2015; Lacape *et al*., 2009; and samer *et al*., 2015 and map saturation in *G.hirsutum L.* (Lacape *et al*., 2003, and Zhang *et al*., 2005).

Primers are also used for Amplified fragment length polymorphism analysis. Amplified fragment are perceived on denaturing polyacrylamide gels using an automation Amplified length fragment DNA sequence with the fragment option (Sun and Huang *et al*., 1999). The arrival of highly through orders technology, and high information on Deoxyribonucleic acid sequences for the genomes in different plant kingdoms had been created in Arabidopsis Genome opening 2000; Yu *et al*., 2002. Different crops species had been created and thousand of sequences had been comment as purport useable of genes using hefty bioinformatics tools. In prescribe to associate Deoxyribonucleic acid sequence knowledge with specific phenotypes.

Microsatellite Marker Methods

The microsatellite based markers are small tandem reiterate or easy succession reiterate are flat repeating of too small 1-5 nucleotide theme, that happen as interspersed insistent components in many eukaryota genomes (Renz & Tautz 1984). Unevenness in the tandemly repetition units are primarily is due to maroon concurrently with Deoxyribonucleic acid reproduction where the reiterate permit matching via addition or deletion of iterates (Tautz and Schlotterer 1992). Equally slippage in reproduction is much similarly than point variations, microsatellite loci tend to be hyper variable.

The Polymerize chain reaction elaboration protocols used for microsatellites and is used sets or primers sets along one fluorolabelled or radiolabelled primer. Estimation of unmarkered Polymerize chain reaction product is carrying out using gel agarose. Using of microsatellite primers and laser sleuthing (such As., automation sequencer) in genotyping process had importantly amended (Wenz *et al*., 1998). Whileas, because of the maximum cost of the tag that is essential for to conduct by primers. Schuelke (2000) acquaint a process in which 3 primers are used for the elaboration rewords primer that demonstrates easy and little costly. Microsatellites are favorably famous genetic molecular markers due to of their predominant inheritance; high copiousness, extraordinary extent of allelic diverseness, and the simpleness of appraise simple sequence repeats size change by polymerize chain reaction along sets of primers. The duplicability of microsatellite markers that can be used expeditiously by many scientists in their laboratories to create coherent information (Maroof Saghai *et al*., 1994). The specific microsatellites-based molecular markers had been described from different plants species such as Lettuce (Lactuca sativa L.), and barley (Hordeum vulgare L.), (Saghai Maroof *et al*., 1994), (Van de wiel *et al*., 1999), and rice (Oryza sativa L.) (Tanksley and Wu *et al*., 1973).

Single nucleotide polymorphism (SNP)

Change of individual nucleotides (A, T, C, and G) in order of single genome is known as SNP (Agarwal *et al*., 2008). The Corn has single nucleotide polymorphism per 59-119 bp (Ching *et al*., 2002), whereas humans had an approximate 1 single nucleotide polymorphism 1,000 per bp (Sachidanandam *et al*., 2001). Single nucleotide polymorphisms discovery was high costly when based on sangar sequencing; so that have become costly effective with the use of different NGS technologies (Varshney *et al*., 2009, Metzker 2010). The Single nucleotide polymerize are commonly more predominant. In the coding or noncoding zones of the genome. Main advantage of single nucleotide polymorphism markers is to associate their simpleness of data management in addition with their flexibleness, speed and cost potency. It may present in coding, noncoding and intergenic zones of the genome, permit the espial of the genes is due to the changes in the order of nucleotides

(Agarwal *et al*., 2008) and they are either non synonymous inside the coding zones. Synonymous variation can modify MRNA splicing that consequence the variation in the phenotype of a single (Richard *et al*., 1995). Bi-allelic single nucleotide polymorphism markers are straight forward to unite data across groups and make big databases of marker information, there are only two alleles per locus and different genotyping platforms will provide the like allele calls once suitable data had been accomplish. And the other single nucleotide polymorphism genotyping engineering like as genotyping by in order (Sonah *et al*., 2013; Elshire *et al*.,2011) can be simultaneously indentify and genotype the Single nucleotide polymorphism molecular markers or the identified markers can be used to sum more markers to genotyping assay (Davey *et al*., 2011).

Single nucleotide polymorphism markers are significant tool for linkage mapping, map based marker and cloning helps to selection due to the high level of polymorphism. Co-dominant nature of SNP creates those markers capable to differentiate the homozygous and heterozygous alleles (Shaheen *et al*., 2009). Because of maximum polymorphism nature SNP was used to detect diversity, enactment, and mapping and for constructing of linkage map and QTL analysis in upland cotton (Hulse-kemp *et al*., 2015, and Michael *et al*., 2014).

In the recent, an international collaborative endeavor has developed 70K Single nucleotide polymorphism chip basis on genotyping essay unpublished data; http//www.cottongen.org/node/1287616. These huge throughput genotyping assays are the resources it can be used globally by private as well as public cotton plant breeders, Scienticists, and other geneticists to increase cotton genetic investigation. These are suitable to use their functions, including rapid recongnization of cultivars and constructing of ultra-high concentration genetic linkage map.

Progress in Marker Methods

In molecular markers the technical promotion as well genome based find had lead to the enhancement of molecular marker methods. The plant cell genomes such as mitochondrial DNA and chloroplast DNA had been progressively utilize to study genetic phylogenetic and structure association in plants. According to uniparental manner of contagion, mitochondrial genomes and chloplast showing different shape of genetic distinction comparison to nuclear genes (Provan *et al*., 1999). Therefore, overall apprehensions of plant species distinction and development, three interconnected genomes have been viewed, in improver to nuclear microsatellites, Molecular marker methods based on the mitochondrial and chloroplast had also been evolved. Improvement in orders engineering and accessibility of a growing number of expresses sequence tag sequence had create direct investigation of genetic changes of the Deoxsiribonucleic acid orders (Sleimani *et al*., 2003, Buetow *et al*., 1999).

Actually the estimation of plastid organelle provide information of plants which are comprehensive to those receive from the nuclear genome. Various studies had described that chloroplast microsatellites lie on relatively small and number of mononucleotide extend such as (dA) n9 9dT) are omnipresent and polymorphic factors of chloroplast DNA (Powell *et al*., 1995). The genome based on markers visible genetic continuity and disparateness between taxa with rebuff physiological dissimilarities, which did not discover by nuclear deoxsiribonucleic acid markers as in the genetic breeding and interchange has vague, the manifest of previous demographic shape (Wolfe *et al*., 1987). Corresponding of orders in genome create it potential to comparison of allele in the plant species and analyze phylogenetic relationship in taxa which had deviate for hundreds years (Provan *et al*., 1999). The chloroplasts microsatellites are now decent steadfastly conventional as a huge-resolution tools for analyze shape of cytoplasmic change in a huge range of plants kingdom (Provan *et al*., 2001). The organelles are especially effectual markers for studying the pairing systems, gene stream for both seeds and pollen, and unapparent decent. The organelles microsatellite basis markers had been used for the espial of introgression and crossing (Bucci et al., 1998). The analysis of the genetic multifariousness (Clark *et al*., 2000) diverseness of plant species (Shaw *et al*., 2005; Parducci *et al*., 2001). The primer orders flanking organelles genomes. Generally endeavor to plan applicability primers to magnify chloroplast have consequence in a pair of microsatellite primers which purpose at amplifying cpsimple sequence reaction zones (Gardner and Weising 1999). Mainly the primer sets developed from T or A single nucleotide reiterate (n=10) indentified in the nicotiana organelles genome, were usable as genomic markers in the Cruciferae, Solanaceae and Actinidiaceae, (Staub and Chung 2003). The applicability primers for the elaboration of organelles in grasses family (Poaceae) had also been established (Provan *et al*., 2004).

A mitochondrial microsatellite in demarcation to carnal mtDNA calculates 319 MDa (Sedaroff *et al*., 1981). In improver to huge size and shape, the plant mtdeoxiribonuclei acid is qualified by molecular heterogeneousness discovered as sort of spherical chromosomes which change in shape and relative copiousness. In all plants species, genomes are commonly used for phyletic analysis because of a huge percentage of succession shakeup (Sederoff *et al*., 1981). Whatever, mitochondrial diversity associate to succession rearrangement testify helpful in population distinction of yearn and fir taxa (Sperisen *et al*., 2001; Soranzo *et al*., 1999). Mitochondrial reiterate had been used for sequestration population (Rajendrakumar *et al*., 2007).

Sequence Characterized Amplified Regions (SCAR)

In prescribe to use markers recognized by caprice marker analysis such as (RAPD,AFLP, etc.) for mapping based cloning, in individual locus moldiness be recognize unambiguously. Furthermore, the caprice marker methods are reasonable to vary in the reaction weather. In sequence to the space among the capability to receive associated markers to a gene of involvement in a short time and the usage of these markers for mapping cloning and for mundane screening processes, Sequence characterized Amplified regions marker method was discovered and employ. The SCAR are polymerize chain reaction based markers that symbolise genomic deoxyribonucleic acid fragment at genetically determine loci that are recognized by polymerize chain reaction elaboration using sequence particular oligonucleotide primers (McDermott *et al*., 1994; and paran and Michelmore 1993).

Etymologizing of Sequence characterized amplified regions regard propagate the amplified products of arbitrary marker methods that contrive particular primer sets of 15-30 bp that magnify individual main tie of the shapes alike propagate fragment. The polymorphism is either hold as the present or absent of elaboration of the tie or can involve in polymorphism change over prevalent caprice primed marker loci into predominant sequence characterized amplified regions markers. As sequence characterized Amplified regions are principally determined genetically, these are used for phonotypical as well as for genetic molecular markers. Predominant sequence characterized amplified regions are much informative are dominant primed markers; equally so these also be used to screen puddle genomic collections by polymerize chain reaction and for physiological map (Stephen and Chelkowski 2001), determining locus specificity (Michelmore and Paran 1993), equally relative map (Guo *et al*., 2003) and similar studies between comparative plant kingdoms.

Cleaved Amplified Polymorphic Sequence (CAPS)

Cleaved amplified polymorphic sequence marker technique which provide a technique to used the Deoxyribonucleic acid sequences of mapped Restriction Fragment Length polymorphism markers to evolve polymerize chain reaction based markers because obviate the tiresome DNA blotting (Konori Nitta and 2005). Consequently CAPS is also known as polymerizing chain reaction RFLP markers (Ausubel and Konieczny 1993). The cleaved amplified polymorphic sequences decode the RFLP caused by single base variation such as SNAs, insertion/deletions that alter restriction endo nuclease identification sites in PCR amplicons (Ausubel and Konieczny 1993; Chelkowski and Stephen 2001). Actually the CAPS assays the execute, by digest locus-specific polymerize chain reaction with single or many restriction enzymes, comply by detachment of the digested deoxsiribonucleic acid on gels polyacrylamide basis of sequence information usable in databank of genomic Restriction amplified polymorphism DNA bands. Cleaved amplified polymorphic sequence analysis is versatile and can be connected with one SCP, RAPD, SSCP, SCAR, and ALFP, analysis to improve the possibleness of determination ,DNA polymorphisms, the cleaved amplified polymorphic sequence the molecular markers are predominant and locus particular and had been used to differentiate among plants which are heterozygous and homozygous for genes (Ausubel and Konieczny 1993). Therefore, Cleaved amplified polymorphic sequence demonstrate helpful as well as useful for genotyping, levels molecular identification studies (Spaniolas *et al*., 2006, Yu and Weiland 2003), the sequence based identification is not executable. The method is restricted by changes that make a restriction enzyme identification site. (Amasino 1998) suggest a discrepancy of the cleavage amplified polymorphic sequence method is known as dCAPS. The derived cleaved amplified polymorphism sequence analysis, a restriction enzyme acknowledgement site, that possess the single nucleotide polymorphism, is acquaint in the polymerize chain reaction product through primer consisting single or more than one not desirable to template deoxyribonucleic acid (Neff *et al*., 1998). That alter polymerize chain reaction product is than subjected to present or absent of the single nucleotide polymorphism is determined by the consequence restriction shape. This method is cheaper and easy, and used the omnipresent engineering of polymerize chain reaction, agarose gel and restriction digestion analysis. This method demonstrates helpful for variation or segregating population and based on propagating a copy of genotypes in plants species (Haliassos *et al*., 1989).

Randomly Amplified Microsatellite Polymorphisms (RAMP)

Randomly amplified microsatellite polymorphism (RAMP) microsatellite based markers demonstrate a high range of allelic polymorphism but these are too much costly and labour expenditures. Meanwhile in the other side Random amplified polymorphism DNA markers are cheaper but display small range of allelic polymorphism. To correct for the failing of both two sources, a method namely as randomly amplified microsatellite polymorphism was established (Wu *et al*., 1994). This method regard a radio labeled primer lie of a 3 repeats and 5 anchors which is used for to magnify genomic DNA in the present or absent of Random amplified polymorphism DNA primers. So the boiling temperatures of the anchored primers are offently 10-15C higher than the Random amplified polymorphism DNA primers therefore at high temper expeditiously, whilemean in polymerize chain reaction oscillation at small annealing temperatures both anchored microsatellite and Random amplified polymorphism DNA primers would temper. The polymerize chain reaction plan was alter like

as that there is switching among low and high tempering temperatures in the reaction. Many fragment receive with Randomly amplified microsatellite polymorphism primers alone vanish when Random amplified polymorphism DNA primers are enclosed, and different shapes are receive with the similar RAMP primers and different Random amplified polymorphism DNA showing that restriction amplified polymorphism DNA primers contend with Randomly Amplified Microsatellite Polymorphisms primer in the low tempering temperature cycle. Randomly amplified microsatellite polymorphisms had been used in studies of the cultivars of peach (Cheng *et al*., 2001).

Target Region Amplification Polymorphism (TRAP)

TRAP method (Vick and Hu 2003) is an efficient and rapid polymerize chain reaction-based method that is used for bioinformatics tools and explicit sequence tag (EST) database knowledge to create polymorphic markers. These methods use two primers (nucleotide 18 in ranges) to create markers. Among of the primers, the rigid primer, is intentional from the aim explicit sequence tag sequence in the database; and the other one primer with At- or Gc to temper with a exon or intron. While the target region amplification polymorphism method used to create markers for specific gene sequence, that is helpful for germplasm genotyping and creating markers colligate with suitable for agronomic factors, plant breeding for marker assisted breeding (Hu *et al*., 2005). The technique had been efficaciously used in fingerprinting in cabbage genotypes (Hu *et al*., 2005), in calculating genetic diversity to mapping quantitative trait loci in wheat intervarietals recombinant inbred species (Liu *et al*., 2005).

Transposable elements-based molecular markers

Actually the transposable elements are the mobile genetic components able to modification their level in the genome. These are observed proximally previous 60 years in corn. There are two wider sections of transposable components, each with characterstics properties (Finnergan 1988). In section I or retro elements, such as retrotransposons, small interspaced nuclear components, and large interspaced nuclear components, these component encoded mRNA arbitrates markers. So in every transposition event generate a duplicate copy of the transposon whereas the original duplicate copy remains entire at the presenter site. In demarcation, section ii it lies of Deoxsiribonucleic acid transposon that changes their emplacement by a 'paste or cut' mechanics (Grzebelus 2006). That means they expunge themselves from the presenter site and regenerate themselves at the accepter site.

Based on the diagrammatical features, transposons are be foster sub classified into sub sections, super families, subfamilies, and families' basis on the structure and orientation of clear reading produced upon insertion (Grzebelus 2006). Large genomes and the retrotransposons are the basic unit of insistent deoxyribonucleic acid (Bennetzen and Kumar 1999) incorporates 35-55% from the total genome. Based on geomorphologic administration and fatty acid similarities between their encoded rearward transcriptases, retrotransposons also split into 3 classes. The long terminal repeats are mention to as the copia and gypsy like retrotransposons. And the 3rd one part of retrotransposons, the line-1 like or non-long terminal repeats retrotransposons, deficiency of TR and coded proteins with importantly few similarity to the retrovirus.

The retrotransposons Gypsy like (Suoniemi *et al*., 1998) and copia like (Kumar *et al.,* 1996; Voytas *et al*., 1992) are demonstrated all over the kingdom plantae. Retrotransposons provide a very good chance to evolve marker system (Kalender *et al*., 1999) explained, protected orders and new inspectional polymorphisms created by replication ally are the predominant members. And the new intromission assist organizing intromission events temporally in a decent (Shimamura *et al*., 1997) so that are helpful for a ascertain pedigree and phylogenetic (Hafez et al., 2006). In the inter retrotransposons amplified polymorphism, DNA among retrotransposons microsatellite magnifies polymorphism (REMAP) regard elaboration of fragment that lies between retrotransposon intromission location and a microsatellite site. RBIP discover loci filled by or hollow of a retrotransposon.

RNA-based molecular markers

The SSCP analysis of RT-Polymerize chain reaction merchandize are be used to appraise the manifestation condition (bearing and comparative quantity) of much alike homologus gene sets from a polyploidy genome. Repeated trial demonstrates that cDNA-SSCP dependably split copy transcripts with 98% sequence observed (Adam and Cronn 2003). This method had been used to increase remarkable penetration into the globular frequency of still in natural and synthetic polyploidy.

Ribonucleic acids fingerprinting by randomly primed polymerize chain reaction the RAP-polymerized chain reaction methods (Welsh *et al*., 1992) require fingerprinting of ribonucleic acid populations using randomly select primer at small Strictness for 1st and 2nd strand cDNA synthesis comply by polymerize chain reaction elaboration of cDNA population. This method demand nano grams of overall ribonucleic acid and is insensible by small percentage of genomic Deoxyribonucleic acid pollution. Derivative polymerize chain reaction fingerprints are discovered for RNAs among the similar tissue isolated from different mortal and for RNAs among different tissues from the similar mortal. The single-specific different disclose because of to sequence polymorphisms and these are helpful for genetic map of genes. These tissue-particular different discover are helpful as well as for study of different

gene manifestation. CDNA-Amplified fragment length polymorphism is a novel ribonucleic acid fingerprinting method to exhibit different explicit genomes (Bachem *et al*., 1996). The way possess digestion of cDNAs by two restriction enzymes comply by ligation of oligo nucleotide adaptors and polymerize chain reaction elaboration used primers complementary to the adopter succession with increasing the select nucleotides (Bachem *et al*., 1998). The cDNA-Amplified fragment length polymorphism method is a high rigorous and reproducible than RAP-Polymerize chain reaction (Pardee and Liang 1992). In demarcation to interbreeding-based methods, like as cDNA micro arrays, cDNA-Amplified fragment length fragment can differentiate among high homogenous allele from single gene species. So no demand of any pre-existing orders knowledge in cDNA- Amplified fragment length polymorphism, so that is meaningful as a tool for the designation of novel process colligate alleles (Yaa *et al*., 2007; Van der Hoveven *et al*., 1996; and Akihiro *et al*., 2006). Designation of stress-regulated alleles had been a most important procedure of cDNA- Amplified fragment length polymorphism (Mao *et al*., 2004).

Impact of Molecular Marker Methods

When the coming of marker, it is present potential to create direct inferences about genetic diverseness and relationships between organisms at the Deoxyribonucleic acid level without the contradictory effects of the surroundings to pedigree records. The genetic analysis of living organism's population and species for taxonomic, ecological studies enormously profited from the evolution of different markers methods. An oblivious trouble that commonly originate is, how to select the superlative proper DNA marker between the infinite of different markers methods. Generally, the selection of a marker method had to be a compromise among dependability and simple investigation, stastical confidence and ability of discloser polymorphisms (Table 1).

The start molecular marker technology which was used for physiological map of plant genome was Restriction fragment length polymorphism. The method demand anterior sequence knowledge and is costly. With the innovation of Polymerize chain reaction engineering, marker methods like as AP-PCR, Amplified fragment length polymerization, Restriction amplified polymerization DNA, were established. These methods are so fast, cheaper and don't demand anterior sequence information. Methods like as AFLP and RAPD had been every day used for genetics population (Althoff *et al*., 2007) and for crop breeding progremmes. These can be used for marking a physiological factor to a genetic factor (Agarwal *et al*., 1992). In same manner to change haphazardly primed Polymerize chain reaction products in genomics, The sequence characterized amplified regions method was intentional. Microsatellite marker method used the inters as well as intra mortal changes in simple sequence reiterate region for fingerprinting analysis.

Many marker methods are used to appraise the genetic diversity to construct a physical map of the genome being studies. Physical map of the connected markers assist in affiliation of the physical space to the genetical space among them. Association of the form to constructing of genetic linkage maps by emplacement of various polygenic and monogenic factors to particular zones of the plant species. The restricted genomes are kilo bases to several mega bases. After that the apart by pulse field gel electrophoresis and investigated by southern blot interbreeding using analysis incorporate of relatively linked markers. If analysis symbolize two markers hybridizes to the similar fragment, and the size of fragment is taken to be high space between the two markers.

A Biotic Stress

Cotton yield is damaged by different abiotic factors that cause about 72% decrease of cotton yield (Saranga *et al*., 2009). Between them salinity and drought these two factors are that effectually effect on cotton production, and it's a big problem so generate improved tolerance cotton verities against these stresses. However, some MAPK cascades factors had been described in different crops. Two Kinases, such as GhMKKI and GHMKKS had been described in accentuate resistance in upland cotton (Lu *et al*., 2013, Zhang *et al*., 2012). Over dominant of GhMKKI in nicotiana amend which toleratrate to drought and salt stresses, showing an intensified scavenging capacity and highly minded behavior of antioxidant enzymes (Lu *et al*., 2013). In other studies, a drought hypersensitive variant of a positive MAPK kinase gene had been recognize in Oryza sativa (Ning *et al*., 2010). Conversely, the oscpk 12 changes in RNAi plants were highly sensible to high salinity and accumulated vigorous water compare to wild species plants (Asano *et al*., 2012). The protected WRKY domain act significant rules in different morphological methods by connecting to W-box the booster zones of target alleles (Somssich and Ulker 2004; Wang *et al*., 2015; Ruston *et al*., 2010). Described a stress reactive GmWRKY27, WRKY gene, reduce ROS level and enhance drought and salt tolerance in transgenic Glycine max roots. The GmWRKY27 acts with GmMYB174, that is turn, acts in performing to decrease booster activity and gene manifestation of GmNAC29 (Wang *et al*., 2015). Subsequent analysis demonstrates that GhWRKY17 includes in stress responses in ABA (Sun *et al*., 2015, and Yan *et al*., 2014). Glycine max GmNAC2, NAC TF, was established as a negative regulator in the abiotic stress, (Ramegowda *et al*., 2012, and Jin *et al*., 2013). Isolated a stress reactive NAC gene, EcNACL, from finger *Pennisetum glaucum*. In upland cotton such as MAP3k gene extremely regulates defence but arbitrate decrease

tolerance to Abiotic and biotic stress in transgenic tabacum (Chen *et al*., 2015).

Biotic factors

The biotic stresses are due to disease, weeds, pathogens, and insects hold with different levels of intensity, they generally decreased the plant population in crops (Borem and Fritsche-Neto, 2012). Between the various biotic factors, the cotton breeding against pest immune remains the basic aim. Due to shortage of resistant cotton genotypes creates a most severe disease to regulate cotton yield (Chang *et al*., 2008). And the cotton leaf curl virus is also one of them a serious disease in cotton that because decrease or reduces cotton production, it has been reported that resistant against cotton leaf curl virus is bestow one superior and two dominant gene by (Rahman *et al*., 2005). To stimulate the resistance against insects, using of insect herbivores to resistance against insect herbivores.

Table 1 comparing of diverse aspects of frequently used molecular marker methods.

	Abundance	Reproducibility	Degree of polymorphism	Locus specificity	Technical requirement	Quantity DNA required	Major application
RFLP	High	High	Medium	Yes	High	High	Physical mapping
PAPD	High	Low	Medium	No	Low	Low	Gene Tagging
SSR	Medium	Medium	Medium	No	Medium	Low	Genetic Diversity
SSCP	Low	Medium	Low	Yes	Medium	Low	SNP Mapping
CAPS	Low	High	Low	Yes	High	Low	Allelic Diversity
SCAR	Low	High	Medium	Yes	Medium	Low	Gene tagging & Phy- Map
AFLP	High	High	Medium	No	Medium	Medium	Gene tagging
IRAP/ PREMAP	High	High	Medium	Yes	High	Low	Genetic Diversity
RAMPO	Medium	Medium	Medium	Yes	High	Low	Genetic Diversity

Restriction fragment length polymorphism (RLFP), Random amplified polymorphic DNA (RAPD), Simple sequence repeats (SSR), Single strand conformational Polymorphism (SSCP), Cleaved amplified polymorphic sequence (CAPS), Sequence characterized amplified region (SCAR), Amplified fragment length polymorphism (AFLP), IRAP/REMAP inter-retro transposon amplified polymorphism Retrotransposon-microsatellite amplified polymorphism (IRAP/REMAP).

Major applications of molecular markers for betterment of cotton improvement

Genetic diversity surveys in upland cotton

Breeding program achiever depends on the apprehension of genetic diversity among and between genetic available germplasm and enable for breeders to select parental sources which will create diverse populations for selection. Portrayal of genetic similarity between genotypes is sources to select parental combining for keep genetic diversity in a plant breeding progamme (Beccelaere *et al*., 2005). The information of genetic relationships between plant genotypes used to know the complexity, to detect the comparison in available genotypes and to make up utile conservation plants (Dahab *et al*., 2013). Therefore, rating based on the markers that give meaningful that is useful in the evolution of new genotypes. There are many genetic diversity surveys had been carry out in cotton by using of different markers methods such as, RAPD (Choudary *et al*., 2010; Xu *et al*., 2001), AFLP (Rana *et al*., 2004; Lie *et al*., 2008; Abdalla *et al*., 2001) simple sequence repeats (Arunita *et al*., 2010; Qayyum *et al*., 2009). A overview of some published genetic diversity surveys by using molecular markers is described in Table-1.

Genetic Linkage map building in upland cotton

Genetic linkage mapping (is cognize as meiotic mapping or linkage mapping) mentions to the finding of the relative level and space among markers with chromosomes. The genetic map space among two markers is described as the mean No of recombination happens; regard a given chromatid, in this zone per meiosis. Genetic linkage maps are basic for the localization of genes conferring biotic and abiotic stress tolerance. The genetic linkage map bases on markers have much reward 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

constructing of genetic linkage map in plants (Paterson, 1996). The molecular map of the upland cotton genome was first manufactured by using 705 Restriction fragment length polymorphism loci and separate into 41 linkage groups (Reinish *et al*., 1994). Many more cotton molecular maps had been constructed and published. A summary of published genetic linkage maps in upland cotton is given in (Table-2).

QTL Map for Fiber and Yield Quality Trait Contributing in Cotton

The zones in genomes to have genes connected with a qualitative trait are called as QTLs (Collard *et al*., 2005), and the producer of evolving genetic linkage maps and playacting QTLs analysis is mentioned to as quantitative trait loci mapping (Paterson *et al*., 1996). The quantitative trait loci analysis supports on the principal of identification a linkage between genotype and phenotype of markers. The QTLs identification in *G.hirsutum L* using different marker engineering is listed in table-3. They identified the QTLs are the new approach to boost up the cotton betterment through marker assisted option.

Marker assisted selection (MAS)

The Marker Assisted Selection is a technique through which a phenotype is selected on the behalf of genotype of a molecular marker (Collard et al., 2005). Once the markers associated to the genes had been discovered, cotton breeders use specific DNA molecular markers to identify the plants carried out the genes (Young et al., 1996). The potency and the cost of molecular marker assisted selection are determined by the marker method; thus, it must be selecting cautiously (Young *et al*., 1996). During the previous two decades, Restriction Amplified polymorphism DNA method had been used for Marker assisted selection for acquiring the glandless seeds and glanded plants. That was exposed that DNA markers associated to the major quantitative trait loci (QTLFSI) for the fiber strength could be used in marker assisted selection to growth fiber strength of commercial genotypes in segregating population (Zhang *et al*., 2003). SSR markers namely CIR 316 closely connects to root knot nematode (RKN) resistant region on chromosome 11 and BNL 3661 marker closely linked to RKN resistant region on chromosome 14. Jenkins *et al*., (2012) by used these SSR markers selected 11 homozygous plants for chromosome 11 and 14 from f2 population derived from RKN resistant genotype M 240 RNR x Susceptible cultivars FM 966 alternatively of waiting up to F6-F8 through conventional breeding methods. That selects the plant confirmed resistance against the RKN. Upland cotton it is necessary to recognized specific genes for specific traits such as strength fineness, fiber length. Etc, to compound those genes from different genotypes through marker assisted selection.

Table 2. An overview of genetic diversity survey in upland cotton by using molecular markers.

S. No.	Country	Population type	Markers used	References
1	USA	24 lines of cotton	270 SNP loci and 92 Indel	Van *et al.,* 2009
2	India	24 lines of G. hirsutum L	6 AFLP primers	Rana *et al.,* 2005
3	Pakistan	31 Gossypium species 3 subspecies and 1 interspecific hybrid	45 RAPD primers	Khan *et al.,* 2000
4	USA	24 cultivars of G. hirsutum	88 SSR primers	Zhang *et al.,* 2005

Table 2a. An Overview of published genetic linkage maps in upland cotton *G.hirsutum* L.

S. No.	Cross parents	Mapping population		Markers	No. of mapped loci	Map Length (cM)	No.of LGs	Reference
Interspecific crosses		Type	Size					
1	Gh(palmeri) × Gb (K101)	F2	57	RFLP	705	4675	41	Reinisch *et al.,* 1994
2	Gh (CAMD-E) × Gb	F2	271	RFLP	261	3767	27	Jiang *et al.,* 1998

	(Sea Island Seaberry)							
3	Gh(Deltapine 61) × Gb (Sea IslandSeaberry)	F2	180	RFLP	-	3664	26	Jiang *et al.,* 2000
4	Gh(TM1) × Gb (3-79)	F2	171	RFLP,RAPDand dSSR	-	4766	50	Kohel *et al.,* 2001
5	Gh(Siv'on) × Gb (F-177)	F2	430	RFLP	253	-	-	Saranga *et al.,* 2001
6	Gh(Siv'on) × Gb (F-177)	F3	208	RFLP	-	-	-	Paterson *et al.,* 2003
7	(Gh(TM 1) × Gb (Hai7124)) × TM1	BC1F1	140	EST-SSR	624	5644.3	34	Han *et al.,* 2004;2006
8	Gh (Acala 44) × Gb (Pima S7)	F2	94	AFLP,SSR,and RFLP	392	3287	42	Mei *et al.,* 2004
9	Gh(Palmeri) × Gb (K101)	F2	57	RFLP	2584	4447.9	26	Rong *et al.,* 2004
10	(Gh(Tamcot 2111) × Gb (Pima S6))×Tamcot 2111	BC3F2	3662	RFLP	-	-	-	Chee *et al.,* 2005
11	(Gh(Guazuncho 2) × Gb (VH8)) × Guazuncho 2	BC1 and BC2	200	SSR and RFLP	1306	5597	26	Lacape *et al.,* 2003; Lacape *et al.,* 2005
12	Gh(Handan208) × Gb (Pima90)	F2 and F2:3	69	SSR,SRAP,RAPD, and REMAPs	1029	5472.3	26	Lin *et al.,* 2005; He *et al.,* 2007
13	Gh(TM1) × Gb (Pima 3-79)	RILs	183	EST-SSR	193	1277	19+11LG	Park *et al.,* 2005
14	Gh(7235) × Gb(TM-1)	F2 and F2:3	163	SSR	86	666.7	21	Shen *et al.,* 2005
15	Gh(TM1) × Gb (3-79)	RILs	183	SSR	433	2126.3	46	Frelichowski *et al.,* 2006
16	Gh(CRI36) × Gb (Hai7124)	F2	186	SSR, TRAP, SRAP, and AFLP	1097	4536.7	35	Yu *et al.,* 2007
17	Gh(Handan 208) × Gb (Pima 90)	RILs	121	SSR	-	5472.3	26	He *et al.,* 2008
18	Gh(Guazuncho 2) × Gb (VH8-4602)	RILs	140	SSR and AFLP	800	2044	26	Lacape *et al.,* 2009
19	(Gh(KC3) × Gb (Suvin)) × KC3	BC1F1	62	SSR	57	911.6	19	Santoshkumarr *et al.,* 2010
20	Gh(TM1) × Gb (3-79)	RILs	186	SSR and SNP	2072	3380	26	Yu *et al.,* 2012
21	Gh(SG 747) × Gb (Giza 75)	BILs	146	SSR	392	2,895	26	Yu *et al.,* 2013
22	Gh(TM-1) × Gb (NM24016)	RILs	98	SSR and SNP	841	2061	26	Michael *et al.,* 2014
23	Gb.doubled haploid line 3-79 x G. hirsutumcv. Texas Marker- 1	F2	118	SNP	19,198	4,439.6	0.23	Hulse-Kemp *et al.,* 2015
24	Giza 45 (G. barbadense) xTamcot Luxor (G. hirsutum)	F2	60	AFLP,SSR, EST-SSR	210	3503.80	26	Samer *et al.,* 2015
25	Gh(TMS22) × G.tomentosum(WT936)	F2	82	SSR	589	4259.4	52	Westengen *et al.,* 2005

Table 2b. An overview of published genetic linkage maps in upland cotton.

	Interspecific 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	F2 and F3	96	RFLP	120	865	31	Shappley *et al.,* 1998
2	Gh× Gh	F2:3	569	RFLP	284	1502.6	47	Ulloa *et al.,* 2002
3	Gh(TM 1) × G.anomalum(7235)	F2 and F3	186	SSR and RAPD	-	-	-	Zhang *et al.,* 2003
4	Gh (Handan208) × Gh(Pima90)	F2	129	SRAP	237	3030.7	39	Lin *et al.,* 2005
5	Gh (Acala 44) × Gb(Pima S7)	F2	94	AFLP, SSR, and RFLP	392	3287	42	Mei *et al.,* 2004
6	G.trilobum(Skovsted)× G. raimondii(Ulbr)	F2	62	RFLP	763	1493.3	13	Rong *et al.,* 2004
7	Gh(Yumian 1) × Gh(T586)	F2 and F2:3	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)	F2	251	SSR	73	650.8	17	Guo *et al.,* 2008
14	Gh× Gh	4WC	273	SSR, ESTSSR	286	2113.3	56	Qin *et al.,* 2008
15	Gh(DH962) × Gh(Jimian5)	F2	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)	F2	124	SSR, ESTSSR, 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)	F2	94	AFLP	240	2068.5	27	Cuming *et al.,* 2015

Table 3. List of QTLs recognized in upland cotton.

S. No	Traits	Descriptor	Population	Marker (number and Type)		QTLs No.	Reference
			Type	Size	216 RFLP, 139 RAPDs		Kohel *et al.,* 2001
1	Fiber quality	FS, FL, FF	F2	171	217 SSRs, 800 RAPDs UBC and 1040 OPERON	13	Zhang *et al.,* 2003
		FS	F2	186	144 AFLPs, RFLPs and 150	2	Mei *et al.,* 2004

					SSRs		
		LY, LP, SW, NS, UQ, SF, FL, FE, FT, FF and IF	F2	120	448 RFLP	28	Zhang *et al.,* 2011
		FS,FE, FF, FU and FL	F2	200	290 SSRs and 9 AFLPs	28	Zhang *et al.,* 2005
		FS, FE, FL, FU, LP and FF	F2	117	262 RFLPs	16	Draye *et al.,* 2005
		FF	BC3F2	3,662	262 RFLPs	41	Chee *et al.,* 2005
		FL, FLU and SFC	BC3F2	3,662	95 SSRs, 72 CSR	45	Park *et al.,* 2005
		FS, FL, FF, FE	RILs	-	1378 SSRs	13	Shen *et al.,* 2005
		FL, FS, FF and FE	F2	-	4106 SSRs, AFLPs, RAPDs and SRAPs	39	Wang *et al.,* 2006
		FS, FL, FF, FMT, FE and SFI	RIL's	180	7508 SSRs, 384 SRAPs and 740 IT-ISJs	48	Zhang *et al.,* 2009
		FS, FE, FU, FL and FF	RIL's	270	16052 SSRs	13	Zhang *et al.,* 2012
		FE, FL, FS, FF and FU	CP	172	25,313 SSRs	63	Tang *et al.,* 2015
		FE, FL, FS, FF and FU	RIL's	180	123 AFLPs	62	Cuming *et al.,* 2015
		FL, FS, FE, FU and FC	F2	94	141 SSRs	43	Wu *et al.,* 2009
2	Fiber and agronomical	SCY, LY, LP, BW, SI, FMT, PER, WF,WT, FF, FL, FE and FS	RIL's	188	50 EST, 18 EST-SSR, 36 SSRs and 64 AFLP	36	Samer *et al.,* 2015
		BW, LP, FF.ES, FU, DFF and DFN	F2	60	834 SSRs, 437 SRAPs, 107 RAPDs, 16 REMAPs	81	He *et al.,* 2008
3	Yield and fiber	SCY, LI, SI, LY, no. of seeds per boll, FS, FL and FF	F2	69	2131 SSRs	57	Shen *et al.,* 2007
		FS, FL, FF, FE, LP, SI, NB, SCY and LY	RIL's	258	834 SSRs, 437 SRAPs, 107 RAPDs and 16 REMAPs	53	He *et al.,* 2007
		LI, SI, LY, SCY, NSB and FS	F2	69	6123 SSRs and EST-SSRs	31	Qin *et al.,* 2008
		NB, BW, SI, LP, LI, SCY, LY, FL, FS, FF, FE and FU	4WCandin bred lines	280	2675 EST-SSRs	111	Liu *et al.,* 2012
		SCY, LY, NB, BW, LP, SI, LI and FBN	RIL's and IF2	180	121 SSRs	180	Zhang *et al.,* 2013
		PH, FBN, BW, LP, LI, SI, LY, FL, FS, FE, FF and FU	G.hirsutum accessions	81	2,041 SSRs	67	Yu *et al.,* 2013

BW; Boll weight, NB: number of bolls per plant, SI: seed index, LI; Lint index, LP: lint percent, SCY; Seed cotton yield per plant, SI: seed index, LY: lint yield per plant, FS; Fiber strength, FL: fiber length, FU; Fiber Uniformity, FE: fiber elongation, FY: fiber yellowness, FF: fiber fineness, PH; Plant height, FMT: fiber maturity, 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).

CONCLUSION

Molecular Marker-Assisted technology for upland cotton Improvement involve in most specific permeative application along SSR and AFLP markers. Being costly effective, simple to manage and devoid of any radioisotope demand, SNP and simple sequence repeats molecular markers are known as the most important suitable and dependable system for DNA fingerprinting. Marker assisted selected had been successful for introgression and pyramiding major-effect genes, moreover other many dispute remain to be solved before marker assisted selection can routinely sum value for breeding very complex factors. MAS for qualitative characters aspect

most successful after deoxyribonucleic acid fingerprinting whereas for quantitative characters, insect resistance genes and genes controlling quantitative trait loci for abiotic stress tolerance, that is anticipated that application of molecular markers will remain restricted in these zones till the allele-specific markers are available and the price of molecular marker analysis is decreased. Although there had been numerous quantitative trait loci mapping studies for a broad range in upland cotton crop, comparatively a little molecular markers have actually been enforced in cotton breeding programs for cotton improvement. The scope, rate, and scale, of uptake of marker assisted selection in crop breeding program have continuously slowdown behind expectations. There are many expert and logistical components that have block the speed and compass of marker assisted selection uptake. Steady advancement and advancement in DNA markers will make it more attractive for molecular crop breeding and plant genetics and finally used in upland cotton for improvement.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interests regarding the publication of this review paper.

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AUTHOR CONTRIBUTIONS

QFM conceived to wrote the review paper, LW, XW, ZHJ investigations and interpretations of this review paper, AHJ wrote this review paper, and FS finalized the review paper, all authors read and approved the final Review paper for publication.

ABBREVIATIONS

AP-PCR= Arbitrarily primed-PCR, RAPD= Random amplified polymorphic DNA, AFLP= Amplified fragment length polymorphism, RFLP= Restriction fragment length polymorphism, CAPS= Cleaved amplified polymorphic sequence, DAF= DNA amplification fingerprinting, SNP=Single nucleotide polymorphism, SSR= Simple sequence repeats, SSCP= Single Strand Confirmation Polymorphism, SCAR= Sequence characterized amplified region, TRAP= Target region amplification polymorphism, SRAP= Sequence Related Amplified Polymorphism, RAMP= Randomly amplified micro satellite polymorphisms, REMAP= Retransposon Microsatellite Amplified Polymorphism, IRAP= Inter-retrotransposon amplified polymorphism, TD= Transposable display, MITES= Miniature Inverted Repeat transposable elements, S-SAP= Sequence-Specific amplification polymorphism, IMP= Inter-MITE polymorphism, EST= Expressed Sequence Tag, ROS= Reactive oxygen species, GWAS= Genome Wide Association Studies, RIL= Recombinant inbred line, WGS= Whole genome sequence.

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