International Invention of Scientific Journal

Available Online at http://www.iisj.in

eISSN: 2457-0958

Volume 05 | Issue 08 | August, 2021 |

Review Paper- Agriculture

A review on a role of biotechnology for cotton improvement

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Article Received 25 June 2021**, Accepted** 25 july 2021**, Publication** 01 August 2021

Abstract

This review paper has been reviewed in 2020 on different journal article, case study's, note, and short communication reports which are available at online source all over the world. The aim of this review paper is to over view the major cotton traits improved through biotechnology and methods of gene transformations. Cotton is multipurpose crop primarily grown for lint production which is the biggest source of natural fibers in the world. In addition, the seed used as a raw material for edible oil and the dry meal is utilized for animal feed. So far, the biotic and a biotic stress such as fungi, viruses, bacteria, nematodes, insects and pests is encounter problems for cotton production in the nation. Now a day biotechnology has been played a great role in cotton improvement programs. The major traits were improved such as insect and disease resistance, herbicide tolerance, stacked with herbicide tolerance and insect's resistance gens and fiber traits. To do this improvement, there are different direct and indirect transformation methods such as particle bombardment, electro proration, floral dip, Agro bacterium mediated, and T-DNA binary vector system. Among those methods, Agro bacterium mediated transfer of DNA and particle gun bombardment were most widely used in cotton improvements.

Key words: Agro-Biotechnology, Cotton, Gene, Transformation, Transgenic

How to Cite:
Endeshaw, molla. (2021). A review on a role of biotechnology for cotton improvement. *International Invention of Scientific Journal*, *5*(08), Page: 1-13. Retrieved from https://iisj.in/index.php/iisj/article/view/340

1. Introduction

Cotton is divided into 45 diploid genome groups with 2n =2x = 26 chromosomes and five tetraploid species (2n =4x = 52) [52]. The A genome diverged from genomes B, E and F, four to nine million years ago in Africa-Arabia and the two important A genome species with spinnable fibers, G. arboreum and G. herbaceum appeared over one million years ago [53]. The tetraploid species appeared in Mexico-Guatemala, one to two million years ago from a chance hybridization and chromosome doubling between A and D genome ancestors of G. arboreum and G. raimondii, respectively [54], and subsequently radiated into the five tetraploid

species, G. hirsutum, G. barbadense, G. mustelinum, G. darwinii and G. tomentosum of which only the first two are used in agriculture. Cotton is grown mainly for lint, which can be spun and woven to make cloth. The seeds also yield edible oil used in a variety of foodstuffs and industrial products. When the oil is removed, the dry meal is utilized to deliver animal feed.

Genetically modified crops is produced by up to 18 million farmers in 26 countries on 191.1 million hectares of land in 2018 [22, 21]. The top ten countries which grew over 1 million ha are USA 75 million ha which grew 39.3% of global total, Brazil 51.3 million ha (27%), Argentina 23.9 (12.5%), Canada12.7 (6.7%), India 11.6 (6.1%), Paraguay 3.8 (2%), China 2.9 (1.5%), Pakistan 2.8 (1.5%), South Africa 2.7 (1.4%) and Uruguay 1.3 (0.7%) million hectares [21].

Genetically modified (GMO) cotton has been produced globally for more than two decades. In USA, Biotech cotton was planted since 1996 and 28 events with insect resistance, herbicide tolerance, and stacked IR/HT have been approved for food, feed, and cultivation [23]. However, up to the present time only four African countries have grown Biotech cotton on a commercial basis South Africa in 1997, Burkina Faso in 2008, Sudan in 2012, and Eswatini 2018 (is newest addition to the list of countries planting biotech cotton) ([18,21]. Most of Africa's cotton is produced by smallholder farmers for whom the cotton sector is a vital source of employment and income [18]. Biotech cotton was planted in 15 nations led by India (11.6), USA (5.06), China (2.93), Pakistan (2.8), Brazil (1.0) million hectares, Argentina (370,000), Myanmar (310,000), Australia (290,000) hectares, and little areas in Sudan, Mexico, South Africa, Paraguay, Colombia, Costa Rica, and Eswatini [21].

As in the case of many important crops, the biotic stress of cotton caused by pests and diseases causes a global annual loss of 10% to 30% [42]. The most important diseases affecting cotton are those caused by bacteria such as bacterial blight [25], Pathogenic fungi such as Fusarium wilt [7], Anthracnose [45] gray branch mold [46], root rot [36], leaf blight [5], [44] and leaf spot [16]. Viruses such as cotton leaf curl and mosaic disease [37], and blue and yellow cotton disease [47]. In the cotton system around the world, more than 1,300 pests have been found that feed on plants, including insects and mites. The most destructive pests include cotton worm, pink worm, armyworm, leaf worm, boll weevil and aphid, Trips, dusky cotton bug, spider mites, tarnished plant bug, and cotton flea hopper [3].

So far, the control of pests and diseases relies heavily on conventional pesticides, which is the most widely used method of crop protection. However, its wide application has caused serious ecological problems, including harm to human and animal health, development of resistance to target pests and pathogens, and environmental pollution. Therefore, there is an urgent need to develop creative and environmentally friendly strategies to effectively control these cotton pests and pathogens in order to achieve agricultural sustainability [2]. In this case, agricultural biotechnology solution helps to maintain the sustainable development of the cotton industry and reduce the use of chemical compounds in producing countries. Therefore, the main objective of this review paper is to over view the major cotton traits improved through biotechnology and methods of gene transformation.

2. Major Cotton traits improved

In 1995, transgenic cotton production was null globally. Two decades later, it is estimated that 67.57% of the world's 37 million hectares of cotton production is planted to varieties carrying one or more biotech traits [24]. Similarly, the adoption of transgenic cotton increased at about 5% yearly. The cotton growers went from null percent of planted transgenic cotton to 85% in USA, 65% China in four years and 90% India in eight years.

Another evidence of distribution of transgenic cotton (Figure 1), in which events with both herbicide tolerance and insect resistance comprised more than 25% of the events approved, while events with more than one trait made up at least 43% (herbicides tolerance (HT) + pollination control (PC), insect resistance (IR) + disease resistance (DR), and HT + product (PQ)) of the approved events.

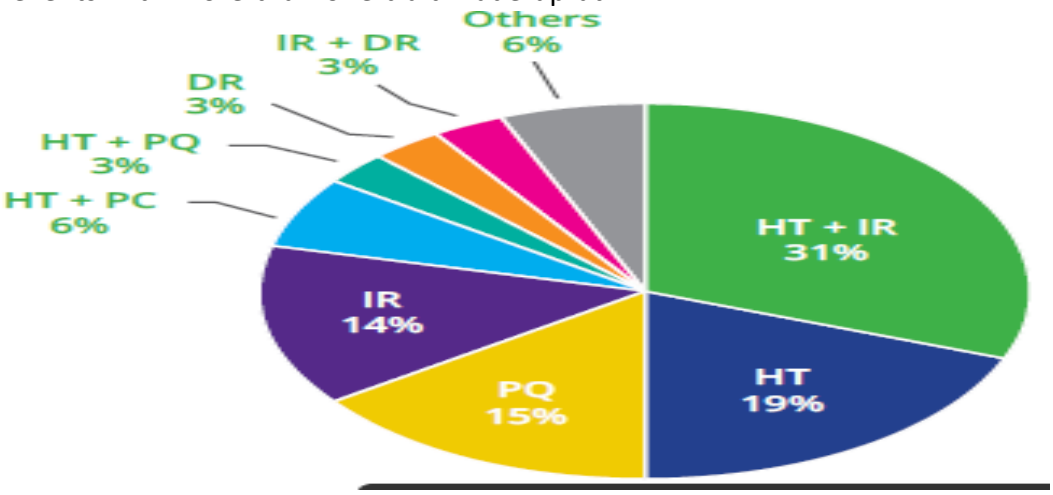

Figure: 1. Trait distribution in approved events, 1992–2016

Source: ISAAA, 2016

2.1. Insect resistance

The use of biotechnology in cotton has made significant contribution in radical reduction in insecticides applied to global cotton crops. The adoption of biotechnology has lower chemical pesticide uses in 37% globally [30], 8% in United States [14], 20% in China from 1996 (before widespread cultivation of Bt cotton) to 1999 (2 years after widespread cultivation of Bt cotton) [34], and 89% of Australia over last 10 years [6]. A genotype or individual which is developed by the techniques of genetic engineering is referred to as transgenic [31]. When resistance genes are not found in a particular species or even in its wild relatives and land races, resistance cannot be introduced through conventional hybridization. In this situation, genes of resistance are introduced from unrelated species through recombinant DNA technology to overcome the genetic barriers. Foreign genes are transferred to crop plants using different transformation tools like gene gun or particle bombardment, electro proration, floral dip (direct transformation methods), and Agro bacterium mediated transformation (indirect transformation methods [4]. There are two transformation methods most widely in cotton, involve Agro bacterium mediated transfer of DNA and bombardment of cells with DNA coated particles through particle acceleration gene delivery system [31].

One of the most important traits that have been improved through the transgenic approach is insect resistance. Transfer of insecticidal protein coding genes present in Bacillus thuringiensis (a gram positive, naturally occurring soil-borne bacterium) to crop plants has conferred resistance against chewing type insects. Crops transformed with Bacillus thuringiensis-based genes are termed Bt crops and Bt cotton, maize, and eggplant are the

most noteworthy examples of such transgenic crops. These transgenic plants produce toxic proteins that damage the insect gut region, resulting in insect death. This also lowers the cost of production of crops as no sprays of pesticides/insecticides to kill chewing Lepidoptera insects are required [4].

Bt-cotton transformed with the cry1Ac gene was grownup during a field for years and still even soil didn't show traces of Bt toxins, showing their environmentally friendly nature [19]. Bacillus thuringiensis synthesized crystalline proteins known as 'end toxins' are extremely harmful to certain insects. They kill the insect by engaged on the epithelial tissue tissues of middle gut of caterpillars. These proteins typically seem microscopically as clearly formed crystals and represent regarding 20-30% of dry weight of sporulated cultures [31]. Five major categories of Bt (cry) genes are cry1, cry2, cry3, cry4, and cyt1 [4]. These proteins are characterized by their insecticidal activity and are so sorted into four categories i.e., Lepidoptera specific (Cry I), Lepidoptera and Diptera-specific (Cry II), order Coleoptera (beetles)-specific (Cry III) and Diptera (mosquitoes and black flies)-specific (Cry IV) [31,4]. Completely different strains of Bt produce over twenty-five different however connected insecticidal crystal proteins (ICPs). These are toxic to larvae of various insects as well as disease vectors and plenty of agricultural pests. Cotton bollworms belong to the Lepidoptera and so are sensitive to Bt Cry I and Cry II proteins that are specific to them [31].

Most of the poisonous substances have a core portion regarding half the toxin size that digests the middle gut of the insect, leading to insect death needed [4]. The CrylAc gene has been transferred into cotton to form it tolerant to the tobacco budworm [11], cryIA provided resistance against chew insects once cotton was transformed with this gene [61]. Bt cotton is ready to ward off insects and pests while not extra pesticides. Reducing the requirement for pesticides minimizes environmental injury whereas increasing agricultural yields [10].

2.2. Disease resistance

Transgenic cotton transformed with the AtNPR1 gene has been developed that have resistance to Fusarium oxysporum f.sp. Vasinfectum and nematodes [39]. Genes used so far for Disease resistance, Chitinases, glucanases and glucose oxidases which act on the cell wall of invading fungi make the pathogen more susceptible to natural plant defenses, Use of viral coat protein genes or replicase genes is another approach for generating disease resistant transgenics, Magainin I and II, from frogs and antibacterial cecropins from silk moth and other insects are under investigation for disease resistance [31], and Recently, an antisense DNA of CLCuV DNA-A borne ACI gene along with the antisense DNA of the AC2 and AC3 gene was used for the vector construction and transgenic cotton resistant to the CLCuV cited in Kranthis et al. [31].

2.3. Herbicide tolerance and resistance

Herbicide resistant transgenic cotton crops have been under commercial cultivation in the US since 1997. 'BXN cotton', resistant to bromoxynil and 'Roundup Ready cotton' resistant to glyphosate. Recently stacked gene varieties 'Bt+ Roundup Ready' and 'Bt + BXN' cotton expressing combined resistance to herbicides and bollworms were released for commercial cultivation in 1998 cited on [31]. Cotton plants impervious to sulfonylurea herbicides made by detaching a cotton quality for acetohydroxyacid synthase (AHAS), presenting point transformations at specific serine (653) or tryptophan (574) codons, and afterward once again introducing these equivalent changed AHAS qualities back into cotton to make cotton plants resistance to certain sulfonylurea and imidazolinone herbicides referred to in Anderson and Rajasekaran [9].

Since this first successful introduction, biotech cotton has been adopted by many cotton-growing

countries and new biotech cotton varieties have been developed, such as herbicide-tolerant (HT) cotton or biotech hybrid cotton that produces two or more Bt toxins with different action modes or combined with herbicide tolerance [24]. United states of America acres planted to glyphosate-tolerant cotton reached 65 % in 2006 and 93 % in 2009, and at present, approximately 98 % of cotton acres are glyphosate tolerant (Roundup-Ready Flex and Glytol from Bayer Crop Sciences) [9]. In 2018 Biotic cotton productions, 9.6% of USA and 16.9% of Brazil are herbicide tolerant and 87%, 73.6% are stacked with HT/IR respectively [21].

GM insect-resistant traits used in cotton have accounted for 99.3% of additional cotton production. Positive yield impacts from the use of this technology have occurred in all user countries (except for genetically modified insect resistant cotton in Australia where the levels of Heliothis sp. (boll and bud worm pests) control previously obtained with intensive insecticide use were very good; the main benefit and reason for adoption of this technology in Australia has emerged from tremendous expense reserve funds and the related ecological increases from decreased insect spray use when contrasted and normal yields got from crops utilizing regular innovation, (for example, utilization of insect sprays and seed treatment) [6].

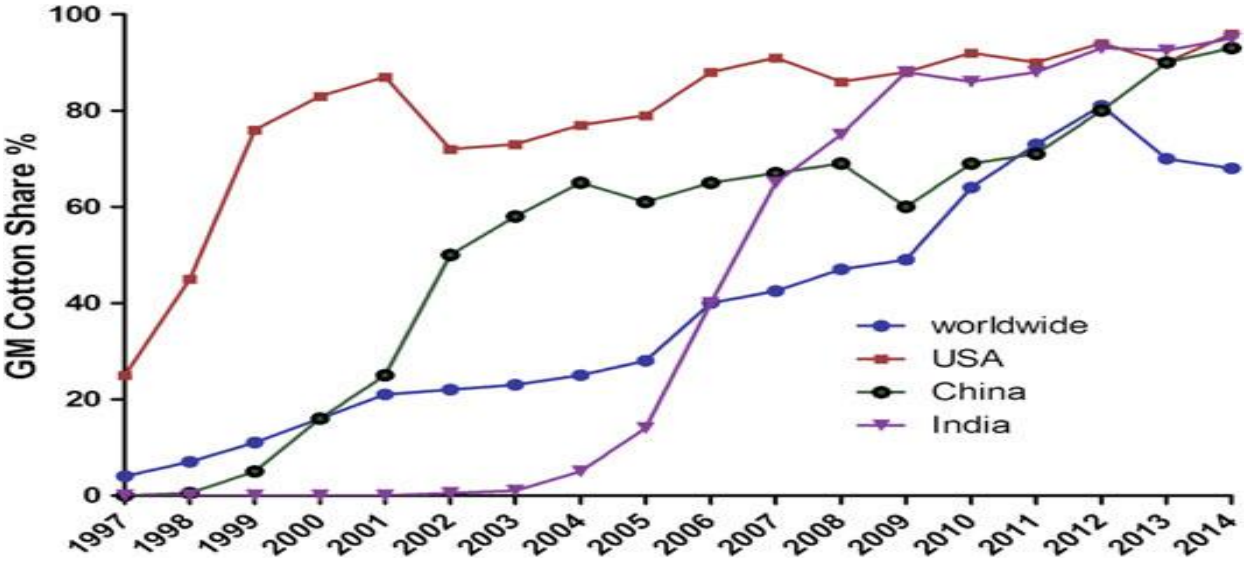

Figure:2. Transgenic cotton share (%) in the total global cotton acreage and in three selected Countries Cited in Anderson and Rajasekaran [9].

2.4. Fiber trait improvement

Genetic engineering of cotton to provide a bigger kind of colored fibers has received some attention in recent decades with a primary specialize in the two main colors used for mass made blue and black denim [15]. Genes to blame for animal pigment and indigo production were inserted into cotton leading to some color formation within the fibers [49]. whereas the color intensity wasn't comfortable for business use, these tries counsel that there's potential for manufacturing novel fibers through genetic modification [15].

The artificial textile business has made several innovative fiber products, as well as bi-component fibers that contain a core chemical compound encircled by recombinant DNA technology of cotton to provide a bigger kind of colored fibers has received some attention in recent decades with a primary specialize in the two main colors used for mass made blue and black denim [15]. Associate in nursing attempt tries at replicating this innovation

in cotton fiber have enclosed the introduction of microorganism genes for the assembly of an acyclic polyester compound, poly chemical group butyrate (PHB), a natural perishable thermoplastic with physical and chemical properties like plastic. The fibers of the transgenic plants showed slower rates of warmth uptake and cooling compared with fibers from wild-type plants, and though the results were little, offer some promise for this approach. The fibers from the transgenic plants were reported to own improved strength and thermal properties and were hour longer than the wild-type controls. However, this gramme trait has not appeared in gm use, presumptively as a result of its reported distinctive properties GM inherited [15].

Kranthis et al. [31] discuses improved cotton fiber quality by: 1. The assembly of polyhydroxy butyrate (biopolymers were not square measure polyester like compounds made by certain bacteria) by transgenic cotton fibers has already been incontestable within the US. 2. Blue cotton through sequence manipulation by synthesis of pigments like indigo in fibers. 3. Fiber specific expression of bioremediation enzymes, melanin's and variety of enzymes and peptides to reinforce fiber quality and strength, superior dye binding, permeability and thermal properties square measure are parameters being treated through recombinant DNA technology.

Genetic engineering of cotton to produce a greater variety of colored fibers has received some attention in recent decades with a primary focus on the two main colors used for mass produced blue and black denim [15]. Genes responsible for melanin and indigo production were inserted into cotton resulting in some color formation in the fibers [49]. While the color intensity was not sufficient for commercial use, these attempts suggest that there is potential for producing novel fibers through genetic modification [15].

The synthetic textile industry has produced many innovative fiber products, including bi-component fibers that contain a core polymer surrounded by a sheath polymer that combines the properties of the two polymers in one fiber. Attempts at replicating this innovation in cotton fiber have included the introduction of bacterial genes for the production of an aliphatic polyester compound, poly hydroxyl butyrate (PHB) [27], a natural biodegradable thermoplastic with physical and chemical properties similar to polypropylene. The fibers of the transgenic plants showed slower rates of heat uptake and cooling compared with fibers from wild-type plants, and although the effects were small, provide some promise for this approach. The fibers from the transgenic plants were reported to have improved strength and thermal properties and were 60% longer than the wild-type controls. However, this GM trait has not appeared in commercial use, presumably because it's reported unique properties were not inherited [15].

2.4.1. Genes involved in fiber development

The recent advances in functional genomics, genetic and analytical tools, especially comprehensive gene expression profiling of cotton fiber cells, together with the availability of a sequenced genome, have provided new opportunities to improve cotton fiber traits through genetic modification. Many fiber-specific genes involved in fiber cell initiation, fiber elongation or cell wall biogenesis have been identified as candidates for genetic manipulation to improve fiber yield and/or quality [15]. For example, two MYB genes, GhMYB25 and GhMYB25-like, which are related to a petal epidermal cell patterning MIXTA-MYB from Antirrhinum majus, and a homeodomain transcription factor (GhHD-1) were identified from microarray comparisons between fiber less mutants and wild-type cotton [55. Silencing these genes in tetraploid cotton affects either the initiation or timing of expansion of fiber initials and their over-expression under a constitutive or seed coat-specific promoter results in an increased number of fiber initials on the surface of the ovule

[51]. Whether this increased fiber initiation translates into an increase in lint percentage or yield remains to be tested in the field.

Transcript profiling and ovule culture experiments both indicate that several phytohormones, including auxin, gibberellic acid and brass no steroids mediate cotton fiber initiation and early growth [51]. Seed-specific expression of the iaaM gene (a gene involved in auxin indole-3-acetic acid synthesis), for example, increased the number of fiber initials, mature lint fibers and cotton yield with no deleterious effects on fiber fineness, strength or maturity.

Manipulating the other hormones or hormone response pathways may offer alternate targets. During fiber elongation, cell wall extensibility is essential to allow the rapid expansion and elongation of these single fiber cells. Xyloglucan endotransglucosylases (XTHs) cleave cell wall xyloglucans and reconnect them to other xyloglucan molecules [32], allowing movement of cellulose micro fibrils relative to each other for rapid cell expansion. Over-expression of GhXTH1 in cotton resulted in longer fibers than their controls, without adversely affecting other fiber characters. Fiber elongation also relies on the cleavage of sucrose into UDP-glucose and fructose to increase osmotic pressure and to provide the substrate for cellulose synthesis during SCW formation that begins towards the end of elongation. Sucrose synthase is a key enzyme in this reaction and is abundant in fiber initials [44]. A novel cotton sucrose synthase gene, GhSusA1, was identified from G. hirsutum. Silencing of GhSusA1 reduced fiber length and yield whereas over-expression of this gene increased fiber length and strength [26]. Additionally, over-expression of a potato sucrose synthase in transgenic cotton enhanced leaf expansion and improved early seed development, thereby enhancing seed set and promoted fiber elongation [56]. Both of these studies suggest that sucrose synthase is an important regulator of sink strength in cotton that is tightly associated with productivity. It is therefore a promising candidate gene that can be developed to increase cotton fiber yield and quality – possibly by improving seed development as a whole, rather than solely focusing on manipulating fiber growth [56]. Cellulose synthesis is a key biochemical event during SCW formation and at least five cellulose 12 synthase (CesA) genes have been shown to increase in expression during this stage [17] so increasing cellulose production is an obvious target for improving fiber quality. The fibers from transgenic cotton expressing two cellulose synthase genes (acsA and acsB), from the bacterium Acetobacter xylinum, were approximately 15% longer and 17% stronger than wild type [33].

3. Method of cotton gene transfer

3.1 Cotton Tissue Culture

Plant tissue culture or the aseptic culture of cells, tissues and organs, is an important tool in both basic and applied studies. It is founded upon the research of Haberlandt, a German plant physiologist, who in 1902 introduced the concept of totipotency: that all living cells containing a normal complement of chromosomes should be capable of regenerating the entire plant. Considerable research work was undertaken in plant tissue culture in the 1950s and 1960s.

Cotton somatic embryogenesis was first observed by Price and Smith in 1979 in Gossypium koltzchianum, but no plantlet regeneration was reported. Davidonis and Hamilton [8] first described plant regeneration from two-year old callus of Gossypium hirsutum L. CV Coker 310 via somatic embryogenesis.

In vitro cultured cotton cells have been induced to undergo somatic embryogenesis in numerous laboratories using varied strategies [60]. Regenerated plants have been obtained from explants such as hypocotyls, cotyledon, root and anther, and from various cotton species [59]. In 1987, Trolinder and Goodin [63] reported cotton regeneration from suspension cultures. Eight

cotton cultivars were screened for their ability to form embryogenic callus from hypocotyls sections and Coker 312 was described as having a high embryogenic response. A system that is simple, easy to manipulate, and can provide large numbers of somatic embryos for study in a short time was described. A limitation, however, was that among the 78 flowering plants obtained; only 15.4% set seed.

Another approach to develop a cell culture system for cotton that was genotype independent was first reported [41]. This system used the isolated shoot meristem from seedlings of G. hirsutum L. cv. Paymaster 145. Isolated shoots could be cultured into rooted plants. Since this method did not involve a callus intermediate stage, it was genotype-independent and saved a considerable amount of time. Zapata et al. [62] also reported the regeneration of cotton plants from shoot meristems. This method has also been successfully used in cotton transformation when combined with particle bombardment [35].

3.2. Agro bacterium -Mediated Cotton Transformation

The genus Agro bacterium has been divided into a number of species based on its disease symptom logy and host range. A. radiobacter is an 'a virulent' species, A. tumefaciens causes crown gall disease, A. rhizogenes causes hairy root disease and a new species, A. viis, which causes galls on grape and a few other plant species [38]. The host range of Agro bacterium is extensive. As a genus, Agro bacterium can transfer DNA to a remarkably broad group of organisms including numerous dicot and monocot angiosperm species and gymnosperms. In addition, Agro bacterium can transform fungi, including yeast, ascomycetes and basidiomycetes [48].

The most widely used specie in plant transformation is A. tumefaciens. A. tumefaciens is a naturally occurring soil borne pathogenic bacterium that causes crown gall disease. The crown gall disease has been shown to be due to the transfer of a specific fragment, the T-DNA (transfer DNA), from a large tumor-inducing (Ti) plasmid within the bacterium to the plant cell [57]. After transfer, the T-DNA becomes integrated into the plant genome and its subsequent expression leads to the crown gall phenotype. There are two bacterial genetic elements required for T-DNA transfer to plants. The first element is the T-DNA border sequences that consist of 25 bp direct repeats flanking and defining the T-DNA. The borders are the only sequences required in cis for T-DNA transfer. The second element consists of the virulence (vir) genes encoded by the Ti plasmid in a region outside of the T-DNA. The vir genes encode a set of proteins responsible for the excision, transfer and integration of the T-DNA into the plant genome [58].

Agro bacterium-mediated transformation is the most widely used method to transfer genes into plants. Transformation is typically done on a small excised portion of a plant known as explants. The small piece of transformed plant tissue is then regenerated into a mature plant through tissue culture techniques. The first reported plant transformation by Agro bacterium was in 1983 [13]. Since then, major advances have been made to increase the number of plant species that can be transformed and regenerated using Agro bacterium. In cotton, the first report of a genetically engineered plant was in 1987 [12]. In the report [50] hypocotyls explants of G. hirsutum cv. Coker 312 were transformed by Agro - bacterium tumefaciens strain LBA4404 with neomycin phospho transferase II (NPT II) and chloramphenicol acetyl transferase (CAT) genes regulated by the nopaline synthase promoter (NOS). Molecular analysis confirmed that the genes were in the primary plants, but progeny evaluation was not reported. Perlak et al. [40] were the first to insert an ergonomically important gene into cotton, cv. Coker 312 by using Agro bacterium strain A208. The gene was the cry IA (b) gene from Bacillus thuringiensis (Bt) for insect resistance

regulated by the CaMV 35S promoter. Insect feeding bioassays and immunological (Western) analysis confirmed the expression of the Bt protein in the primary transgenic plant.

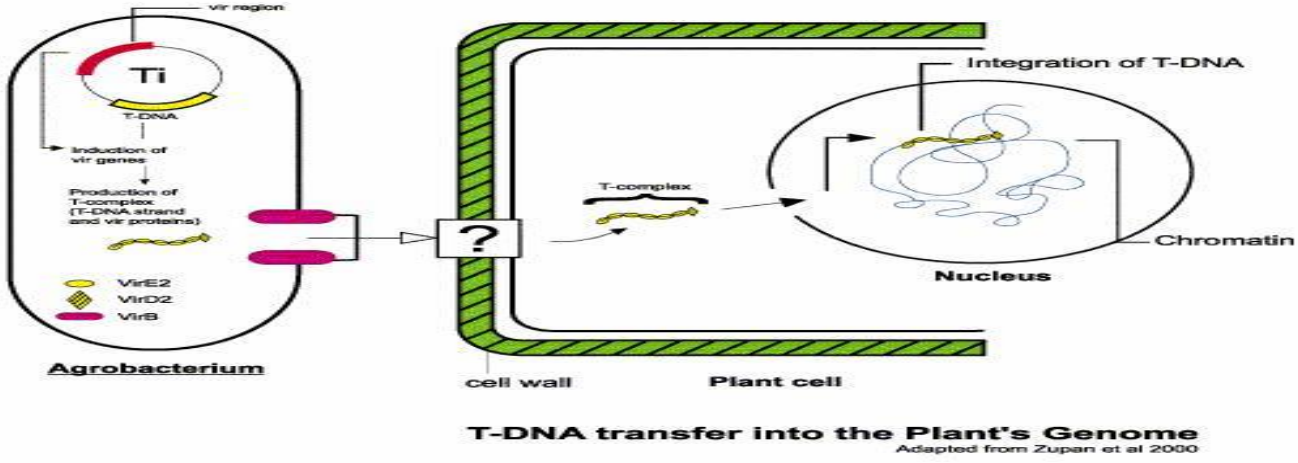

Figure 3: shows the mechanism of T-DNA transfer to a plant's genome

3.3. T-DNA Binary Vector System

The development of DNA vectors using A. tumefaciens is based on the fact that besides the border repeats, none of the T-DNA sequences is required for transfer and integration. This means that the T-DNA genes can be replaced by any other DNA of interest, which will be transferred into the plant genome. Also, the length of the T-DNA is not critical Small (a few kb or less) as well as large T-DNAs (150kb) [20] will be transferred by the A. tumefaciens into plant cell. This achievement has allowed development of a binary vector system to transfer foreign DNA into plants.

Two plasmids are used in the binary method, i.e., the Ti plasmid containing the vir genes with oncogenes eliminated, a so called 'disarmed' plasmid or 'vir helper', and a genetically engineered TDNA plasmid containing the desired genes [1]. The plasmids in T-DNA binary vectors are smaller than plasmids in Agro bacterium and easier to manipulate in both E. coli and Agro bacterium. This has allowed researchers without specialized training in microbial genetics to easily manipulate Agro bacterium to create transgenic plants.

The development of DNA vectors employing a. tumefaciens relies on the actual fact that besides the border repeats, none of the T-DNA sequences is needed for transfer and integration. this suggests that the T-DNA genes can be replaced by the other DNA of interest, which is able to be transferred into the plant genome. Additionally, the length of the T-DNA isn't essential little (a few kb or less) furthermore as giant T-DNAs (150kb) [20] are going to be transferred by the A. tumefaciens into plant cell. This achievement has allowed development of a binary vector system to transfer foreign polymer into plants.

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3.4. Particle Bombardment Method of Transformation

Biolistic transformation was initially welcomed as an alternative method for generating transgenic plant species but is not yet amenable to Agro

bacterium-mediated transformation methods. Particle bombardment utilizes high velocity metal particles to deliver biologically active DNA into plant cells. The technology was first reported by Klein et al. [29]. The first transgenic cotton plants created using the particle gun method was reported in 1990. Embryogenic suspension cultures of G. hirsutum L. cv. Coker 310 were transformed using particle bombardment. Southern hybridization confirmed the presence of the trans gene in embryonic tissue and in regenerated plants.

There are two main types of explants used in particle bombardment methods. One is the embryo meristem (shoot apex) and the other is embryogenic cell suspension cultures. The advantage of using the embryo meristem as explants is that it allows genotype independent transformation and the relatively rapid recovery of transgenic progeny [28]. The disadvantage of using embryonic meristems is that the preparation of shoot tip-meristems is an extremely tedious, labor intensive task, which involves the surgical removal of leaf primordial to expose the meristem, followed by the careful excision of meristem explants from imbibed seeds. Also, the stable transformation rate is very low (0.001 to 0.01 %).

4. Summary

Cotton is a major supply of interchange for several countries round the globe; thus, the most important focus remains the improvement of yield and quality of fiber. This challenge can be accomplished by introducing new alleles from wild species and also the use of contemporary molecular technologies serving to in increasing genetic gain of economic traits. Biotechnology is critical for the acceleration of varietal development. Though the QTL mapping for the assorted traits, that is, fiber yield and quality, drought tolerance, disease resistance, and pest's resistance.

Genetic engineering offers a directed methodology of plant breeding that by selection targets one or many traits for introduction into the crop plant. The event and business unleash of transgenic cotton plants believe completely on two basic needs. The primary one could be a methodology that may transfer a citrons or genes into the cotton genome and govern its expression within the relative. The 2nd main gene delivery systems for achieving this finish are Agrobacterium-mediated transformation and particle gun bombardment. The opposite demand is that the ability to regenerate fertile plants from transformed cells.

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