



## **CURRENT STATUS OF TRANSGENIC COTTON-UTILITY OF GENOTYPE INDEPENDENT *IN PLANTA* APPROACHES FOR THE GENERATION OF TRANSGENICS**

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### **ABSTRACT**

Cotton (*Gossypium spp.*), is a mercantile crop plant is grown for its fluffy fiber and cotton seed oil in around 70 countries worldwide. Cotton is an economically important crop, shows erratic productivity under rain feed conditions; it is bogged down with many biotic and abiotic stresses. Due to lack of resistant germplasm, crop improvement through conventional breeding practices has been lagging. Genetic engineering offers numerous protocols to engineer plants to overcome stress. Biotechnological intervention for cotton improvement has begun three decades ago. The recalcitrance of cotton to tissue culture has been the major constraint for *in vitro* regeneration. Alternate methods that evade tissue culture regeneration steps have thus been envisaged. Till date there are very few standardized protocols that can be employed to develop transgenics in a genotype independent manner. Thus, genotype independent *in planta* transformation strategies have gained momentum in the present days, but reproducibility of reported protocols remains an amigma in many cases. *In planta* transformations holds prominence due to viability and ease in generation of transgenic cotton plants with in less time. This review focuses on grouping efforts made by different research groups in this senior. Several reports and standardizations have been focused that reports development of transgenic cotton.

**Keywords:** Transgenic cotton, *invitro* regeneration, genotype independent, *in planta* transformation, genetic engineering.

### **INTRODUCTION**

The prosperity of Indian economy depends on positive strides in agricultural and industrial sectors. Sustainable agriculture is the need of the hour in the context of global and liberalization trends. Crop production encounters various biotic and abiotic stresses particularly in the arid and semiarid regions (Mohapatra and Saha, 2019). Cotton is a major fibre crop of global importance and has high commercial value. Cotton is grown in about 80 countries across the world and is planted in an average area of 329.49 lakh hectares. India holds 1<sup>st</sup> rank in cotton production and contributes to 33.23 % of total world produce followed by China contributing 16.02 %. The countries of USA, Pakistan, Uzbekistan and Brazil rank the next positions respectively (Directorate of Cotton Development

Government of India, 2017), where climatic conditions suit the natural growth requirements for cotton. Cotton is the most important fibre crop and is the basic input to the textile industry. India has the largest cotton growing area in the world with about 9.6 million hectares under cultivation accounting for one-fourth of the global cotton area. Cotton cultivation surpasses periods of hot and dry weather and adequate moisture obtained through irrigation. Cotton is harvested as 'seed cotton' which is then 'ginned' to separate the seed and lint. The long 'lint' fibres are further processed by spinning to produce yarn which is knitted or woven into fabrics.

Rainfed cotton production has significant contribution towards erratic cotton productivity. It is obvious that growth and development of cotton has to face one or other stress

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entities under rainfed situation. Cotton physiology portrays unique indeterminate growth habits with longer crop duration which make cotton vulnerable to abiotic stress influences from emergence to senescence. The adverse effects on the ongoing physiological processes may affect yield projection trends leading to production lapses. The various abiotic stress factors affect cotton growth, development and yield; their occurrence may be erratic or specific and their intensity may be varying in adversity.

DNA sequence data suggests that *Gossypium* genus arose about 1020 million years ago (Wendel & Albert, 1992; Seelanan et al., 1997). However evidences do not confirm the place of its origin exactly. West-central and southern Mexican regions with 18 species, North-east Africa and Arabia with 14 species and Australia with 17 species are known to be the primary centres of diversity. Cotton species, *Gossypium arboreum* and *Gossypium herbaceum* are diploid, indigenous to Asia and Africa and are confined to the "old world cotton". American cotton *Gossypium hirsutum* and Egyptian cotton *Gossypium barbadense* are amphidiploids (tetraploid,  $2n=52$ ), with centres of variability in Mexico, Central America and South America, belong to "new world cotton". *G.hirsutum* and *G.barbadense* are the two species most commonly cultivated on commercial scale. *G.hirsutum* is also known as upland cotton comprising of 90% of world plantings, it was introduced into India during the 18<sup>th</sup> century A.D. (Hutchinson, 1959).

Conventional cotton breeding takes advantage of desirable alleles that exist in the cultivated germplasm of the same or a different *Gossypium* species. Natural variations existing within the genus of any plant species affords for continuous genetic improvement. Although improvement of lint yield remains the top priority in cotton breeding, weed control in cotton is more difficult. Cotton yield losses due to pests, including insects, are severe. Genetic traits within cotton can provide little insect resistance, but not satisfactory for controlling them. Thus the lack of dominant gene pool in cultivated germ plasma. This has stipulated for novel traits that can be introduced from other species to cotton for effective pest control through genetic engineering.

#### **Biotechnological invasions for cotton improvement**

Transgenic crops are an illustration of trait improvement. Transgenic technology has emerged as an awful tool for crop improvement with an assortment of techniques and strategies being used for gene delivery in crop plants as well as in cotton for its improvement (Birch 1997). Genetic engineering offers the feasibility to selectively introduce

one or more genes that would escort the development of transgenic cotton to overcome both biotic and abiotic stresses (Oerke 2006). The most profound and major bottlenecks for deployment of genes through transgenesis has been the amenability of the commercially important or target crops to regeneration protocols. Not all economically important crop plants are regeneration-friendly to regeneration protocols. Since the reproducibility of reported regeneration protocol becomes an amigma in the same species, the search of alternative transformation approaches have become vague. These recalcitrant plants have been labelled as "difficult to regenerate" plants. Several techniques and strategies are being employed to accommodate foreign genes delivery into plant genome; using the only natural biological plant transformation agent *Agrobacterium tumefaciens* which can aid in gene transfer. Most conventional plant transformation protocols use, *Agrobacterium* to engineer the plant genome with either tissue culture approaches or *in planta* approaches. For many plant species that are amenable to transformation and regeneration by *A. tumefaciens*, T-DNA-directed gene transfer remains the method of choice because of its ease, efficient transgene delivery and integration into the host genome. Compared to direct DNA transfer methods, *Agrobacterium*-mediated transformations are most sophisticated and established method of transformation for most of the higher plants. In addition, this method does not demand specialized equipment or associated consumables for transformation.

#### **Embryogenesis and Somatic embryogenesis in cotton**

The first report of development of cotton transgenics was reported in 1987. Somatic embryogenesis (SE) and embryogenesis was used for the development of cotton by regeneration based approaches. Transgenics in cotton cultivar Coker 210 (Firoozabady et al. 1987) and Coker 312 (Umbeck et al. 1987) are the initial reports of transgenics in cotton. The genotype plays a major role in regeneration of cotton. Screening of about 38 cultivars belonging to different cotton races (*G. hirsutum*, *G. barbadensis* and *G. Arborium*) with different hormonal regimes showed that only Coker 312 showed highest frequency of embryogenesis in all combinations, followed by Coker 304, Coker 315, T 25 and Coker 310 (Trolinder and Xhixian 1989). Thus Cooker 312 has become the most preferable genotype, followed by Zhongmiansuo-35 and YZ-1 for the production of transgenics through regeneration based approaches. Several research groups have proposed various media compositions and used different explants for cotton for transgenic development. Some studies have been listed below.

**Table 1: List of various studies that developed transgenic cotton using different explants.**

<b>Genotype/cultivar</b>	<b>Explant</b>	<b>References</b>
<i>G. hirsutum</i>	Cotyledon	Davidonis and Hamilton. 1983
<i>G. klotzschianum</i> Anderss	Hypocotyl	Finer and Smith. 1984
<i>G. hirsutum</i> L. cv. Coker, 201, 208, 310, 315, DES 56, GSA 71, Lankart 57, Paymaster 145, Quapaw, RC10-3, Stroman 254.	Hypocotyl	Shoemaker <i>et al.</i> 1986
<i>G. hirsutum</i> L. cv. Coker 312, T 25, T 169, Paymaster 303,784.	Hypocotyl	Trolinder and Goodin. 1987
<i>G. hirsutum</i> L. cv. Coker 310	Cotyledon	Finer. 1988
<i>G. hirsutum</i> L. cv. Stoneville 215, 453, 506, Acala, Lu, Coker 5110, 313, 100s, 304, 315, 310, 312, 15, Paymaster 303, 784, 145. <i>G. arboreum</i> L. var. Jyoti	Hypocotyl	Trolinder and Xhixian. 1989
<i>G. hirsutum</i> L. cv. Coker 201, 310, 315, 4360, GSA 71,75,78,CSC 25, G 8160	Cotyledon, hypocotyl, leaf sections	Firoozabady and DeBoer. 1993
<i>G. hirsutum</i> L. cv. Coker 201, CRI 12	Cotyledon, hypocotyl	Zhang <i>et al.</i> 2000
<i>G. hirsutum</i> L. cv. Deltapine 90, GB 35, B126	Cotyledon, hypocotyl	Sakhanokho <i>et al.</i> 2001
<i>G. hirsutum</i> L. cv. Coker 312, Acala cv. Maxxa, Riata, Ultima	Hypocotyl	Mishra <i>et al.</i> 2003
<i>G. hirsutum</i> L. cv. Coker 310	Hypocotyl, cotyledon	Kumria <i>et al.</i> 2003
<i>G. hirsutum</i> L. cv. Ekang 3, 4, 6, 8, 9, 10, Emian 22, Ejing B1, B11, Coker 201	Hypocotyl	Wu <i>et al.</i> 2004
<i>G. hirsutum</i> L. cv. Nazilli M 503, Nazilli 143	Shoot apices, hypocotyl, nodes	Aydin <i>et al.</i> 2004
<i>G. hirsutum</i> L. cv. Coker 312	Hypocotyl, cotyledon	Kumar <i>et al.</i> 2004
<i>G. hirsutum</i> L. cv. SH 131, Khandwa 2.		
<i>G. arboreum</i> L. cv. Sarvottam, Jawahartapti	Hypocotyl, cotyledon	Khan <i>et al.</i> 2006
<i>G. hirsutum</i> L. cv. Coker	Hypocotyl	Aydin <i>et al.</i> 2006
<i>G. hirsutum</i> L.	Hypocotyl, immature zygotic embryos	Hussain <i>et al.</i> 2009
<i>G. hirsutum</i> L. cv. Khandwa, RS 810, Pusa 37, Pusa 26, Stoneville, F1084, CA 1193	Cotyledonary node with shoot apex	Gupta <i>et al.</i> 1997
<i>G. arboreum</i> L. cv. Shyamly, Lolnt		
<i>G. hirsutum</i> L. cv. Anjali and <i>G. hirsutum</i> L. cv. LRK 516	Cotyledonary node with shoot apex devoid of cotyledons	Agrawal <i>et al.</i> 1997
<i>G. hirsutum</i> L. cv. Stoneville 7A and Paymaster HS26	Shoot apices Secondary leaf node Cotyledonary nodes	Hemphill <i>et al.</i> 1998
NCS 3, NA 1325, NA 920, NHH 390, DCH 32, Anjali, Srisailam, PMC, LRA, MCU 5	Shoot tip	Tripathy and Reddy. 2002
<i>G. hirsutum</i> L. cv. MCU-5, DCH 32, Coker 310FR	Shoot tip	Satyavathi <i>et al.</i> 2002
<i>G. hirsutum</i> L. cv. NIAB 999	Cotyledonary node with both cotyledons	Rauf <i>et al.</i> 2005
<i>G. hirsutum</i> L. cv. Barac (67)B	Cotyledonary node devoid of cotyledons and apical meristems	Abdellatef and Khalafalla. 2007
<i>G. hirsutum</i> L. cv. Bharani, Durga, JKCH 99	Hypocotyl	Divya <i>et al.</i> 2008
<i>G. hirsutum</i> L. hybrid H8		
<i>G. hirsutum</i> L. Khandwa 2		
<i>G. arboreum</i> L. cv. BD ,1BD 6, Sarvottam	Cotyledonary node	Obembe <i>et al.</i> 2011

<i>G. hirsutum</i> L. cv. MCU 11	Cotyledonary node devoid of cotyledons	Mushke <i>et al.</i> 2012
<i>G. hirsutum</i> L. cv. NA 1325	Embryo axis	Pathi and Tuteja. 2013
<i>G. hirsutum</i> L. cv. NC 601	Cotyledonary node	Chakravarthy. 2013

**Source:** Jutur *et al.*, 2015.

### ***In planta* transformation in cotton**

Tissue culture based transformations are tedious, time consuming, lead to variations in plant morphology and poor quality of seed pool that may not be viable to carry the modified trait to the subsequent generations. Development of a large number of uniform plants in short time with less labour efforts and minimal reagent requirements is the triumph of *in planta* transformations for trait modification

in recalcitrant plant species. These tissue culture-independent *in planta* techniques were first initiated in *Arabidopsis thaliana* and has thrown new insight in the scientific community to development high throughput transformation protocols with the aid of *Agrobacterium*. *In planta* transformation methods in *Arabidopsis* such as “clip 'n' squirt” and vacuum infiltration have been successfully used by many researchers.

**Table 2:** *In planta* approach based *Agrobacterium* mediated gene transfer for transgenic cotton developed.

Genotype/cultivar	Transformed gene(s)	Method of transformation	References
Zheda B	<i>bptII</i> , <i>uidA</i> and <i>nptII</i> , <i>uidA</i>	Ovarian injection following pollination	Bibi <i>et al.</i> 2013
Sahana and BC 68-2	<i>cry1Ac</i> , <i>cry1Ia5</i> , <i>cry1Aa3</i> and <i>cry1F</i>	Stigmatic surface treatment	Mogali <i>et al.</i> 2013
Xinluzao 019	<i>susy</i> , <i>gus</i> and <i>nptII</i>	Pollen mediated transformation	Zhang <i>et al.</i> 2008
NC 71	<i>uidA</i> and <i>nptII</i>	Meristem transformation	Keshamma <i>et al.</i> 2008
Khandwa 2, Anjali and Coker 310	<i>uidA</i>	Meristem transformation	Kumar <i>et. al.</i> 2013
P8-6	<i>bptii: gfp</i>	Meristem transformation	
Meristem transformation	<i>Kesiraju et al.</i> , 2020		
P8-6	<i>nptii:CP4-EPSPS</i>		Karthik <i>et al.</i> , 2020

Several research groups have adopted diverse *in planta* transformation strategies for the generation of transgenic cotton (Rajasekaran *et al.*, 2005; Zhang *et al.* 2009; Tian *et al.*, 2010; Jin *et al.*, 2012; Bibi *et al.* 2013; Mogali *et al.*, 2013; Pathi and Tuteja., 2013; Vajhala *et al.*, 2013; Kalbande and Patil *et al.*, 2016; Guo *et al.* 2018). Though apical meristem has been the preferred target in most of these studies, the mode of infection has been different. However, the hypothesis of the standardized protocols have been the introduction of transgenes into the differentiating meristematic cells leading to concomitant transgenic expression in the shoots, ultimately resulting in their inheritance (Maher *et al.*, 2020).

### **CONCLUSIONS**

Tremendous progress has been made in the development of transgenic cotton. Both *Agrobacterium* mediated and direct gene delivery methods have been developed by many research groups across the world. Despite of such advances also, genotype dependency is still considered as

major constraint and splendors the potential of transformation approaches in transgenic development. Recent reports on cotton improvement have shown that apical meristem targeted *in planta* strategy can tackle the problem of genotype dependency (Karthik *et al.*, 2020; Kesiraju *et al.*, 2020). As this *in planta* transformation method was previously reported by Keshamma *et al.* 2008 (using GUS gene as a screenable marker) in a different cultivar, the recent report of successful deployment of the same technique was reported by Karthik *et al.*, 2020 in two different reports, where GFP was used in one study and a herbicide tolerance gene *CP4-EPSPS* was used in another study in the same genotype.

Introduction of genetic changes into meristems reported concomitant transgenic expression in the shoots which later on produced flowers and seeds, ultimately transmitting transgenes and gene edits to the next generation (Maher *et al.*, 2020). *Agrobacterium* mediated *in planta* transformation approaches using apical meristem

has been the preferred target for successful development of transgenics as reported by most of the recent studies (Maher *et al.*, 2020; Tyagi *et al.*, 2020; Zlobin *et al.*, 2020).

*In planta* transformation transformation of *A. thaliana* was made feasible by vacuum filtration which was considered as a tedious task before (Clough and Bent 1998). These *in planta* methodologies are reliable and reproducible also. Moreover this apical meristem targeted *in planta* transformation has also been proved to be genotype independent. The utility of this protocol was investigated in different crops (Kesiraju *et al.*, 2017) and its genotype independent nature was demonstrated crops like capsicum, pigeon pea, groundnut (Karthik *et al.*, 2020). Thus this protocol has the power to speed up cotton transformation programmers efficiently. Transgenic cotton for herbicide resistance and insect resistance has become a reality in achieving enormous yield gains. However, further development of insect resistant cotton with different genes and modes of actions is the need of the hour. Hope this strategy would also be useful for the demonstration and validation of RNA interference and CRISPR based genome editing strategies in cotton and aid in crop improvement.

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