

A SEMINAR PAPER ON

**COTTON YIELD COMPONENTS AND NEW APPROACHES OF
BREEDING**

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SUBMITTED TO

- 1. Dr. A. K. M. Aminul Islam
Professor**
- 2. Dr. Md. Mizanur Rahman
Professor**
- 3. Dr. Md Rafiqul Islam
Professor**
- 4. Dr. Dinesh Chandra shaha
Assistant Professor**

SUBMITTED BY

Sarnaly Goon Sarna

Ms Student

Reg. No.: 17-05-4488

Department of Genetics and Plant Breeding

**BANGABANDHU SHEIKH MUJIBUR RAHMAN AGRICULTURAL UNIVERSITY
SALNA, GAZIPUR 1706**

Cotton Yield Components and New Approaches of Breeding

Sarnaly Goon Sarna

ABSTRACT

This paper had been prepared on cotton yield components and new approaches of breeding to know the quantitative characters and new approaches of cotton breeding. All data and information were collected and used from secondary sources. In cotton production, yield increases had come from increased boll/m² and selection for high lint percentage that has increased lint per seed. In addition to, there are highest maternal effect for yield and yield contributing components which is responsible for the phenotypic expression of the reciprocals. Bract trichome density have fewer adverse relationships with yield components and quality parameters in compared to leaf and stem pubescence. Moreover, genetically modified cotton, wide hybridization, tissue culture or somaclonal breeding, and mutation breeding of cotton as a new approach of breeding significantly increase cotton yield as well as cotton production.

Key words: Yield components, transgenes, somaclonal variation, hybridization.

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CHAPTER I

INTRODUCTION

Cotton is a great source of textile fiber, food for animal and food grade vegetable oil (Wakelynet et al., 2010). More than 90% of the world's cotton production is attained from *Gossypium hirsutum* L., which is known as upland cotton for its high yield and generally good fiber quality (Zhang et al., 2008). The remaining cotton supply resulting from the closely related *G. barbadense* L., *G. arboretum* L., and *G. herbaceum* L. species.

In addition to yield, traits which are often deliberated at the time of evaluating and breeding cotton lines include aspects of quality of seed, insect and disease resistance, temperature, tolerance, different morphological traits, maturity, plant conformation, characteristics related to harvest and ginning efficiency, yield component and fiber quality. Moreover, there have recently been added several transgenic traits. By maintaining positive expression, constant attention and effort are required for these traits in a breeding program.

Gossypium spp. known as Cotton is a highly economic fiber crop, being cultivated and engaging 18 crores of people of near about 100 countries around the world. Necessity of cotton yielding is gradually uprising as the population explosion has emphasizing it's importance. Though cotton producers and researchers are working together with a motto of cultivating cotton in an epidemic rate, it remains difficult with various reasons. Primarily, the ability of giving up vegetable growth, lost fruit and variation in plant density, cotton plant can attain a bumper production in several ways. Hence, the plant has adaptability in wide range of environments. Secondly, gene complexes can take control over it's achievement in cultivation of different places. More over the inheritance pattern for cultivation is complex. Thirdly, within a generic environment cultivation might vary. Because of a different production rate of a genotype perspective of environment results a hinder in direct selection of cultivation.

Transgenic cotton plants carrying modified genes from *Bacillus thuringiensis* Berliner variety Kurstaki (BTK genes) that code for the delta endotoxins (insecticidal protein) Cry I A (b) from strain HD-1 and Cry I A (c) from strain HD- 73 have already been evaluated in the field for

resistance against the devastating cotton bollworms. Initial BTK gene insertions into the cotton genome resulted in tissue expression of these insecticidal proteins that was too low to provide a useful level of insect control. Recently, genetic engineers have increased the expression of these insecticidal genes in cotton plant tissues by altering the coding sequence. Modification of key regions of the structural gene without changing the amino acid sequence resulted in the most dramatic increases in levels of protein synthesis in the plant cells. Immunological analysis indicate that the altered BTK genes of *cry I A (b)* and *cry I A (c)* expressed the insecticidal protein at 0.05 - 0.1 % of total soluble leaf protein. Moreover, the level of plant protection against bollworms were much higher and had the potential for reducing larval injury to cotton in commercial production.

To meet the increasing demand of superior quality cotton, there is an enhanced interest in the quantitative and qualitative improvement of cotton cultivars. In vitro techniques supplies advantages over conventional breeding in the field in terms of the application of biochemical selection pressure and the recovery of specific metabolic mutants. Haploidization, protoplast fusion, gene transfer and exploitation of somaclonal variation are examples of techniques offering potential for crop improvement.

Objectives:

1. To assess the quantitative characters of cotton for better production.
2. To evaluate the new approaches of cotton breeding in successful crop production.

CHAPTER II

MATERIALS AND METHODS

This seminar paper is exclusively a review paper. So, no specific methods of studies are followed to prepare this paper. All data and information were collected and used from secondary sources. This paper has been compiled through reading of different books, journals, booklets, proceeding, newsletter, souvenir, consultancy report that are available in the libraries of Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU). Maximum necessary supports were taken from internet searching. After collecting all the available information, it has been presented as per the objectives of this paper.

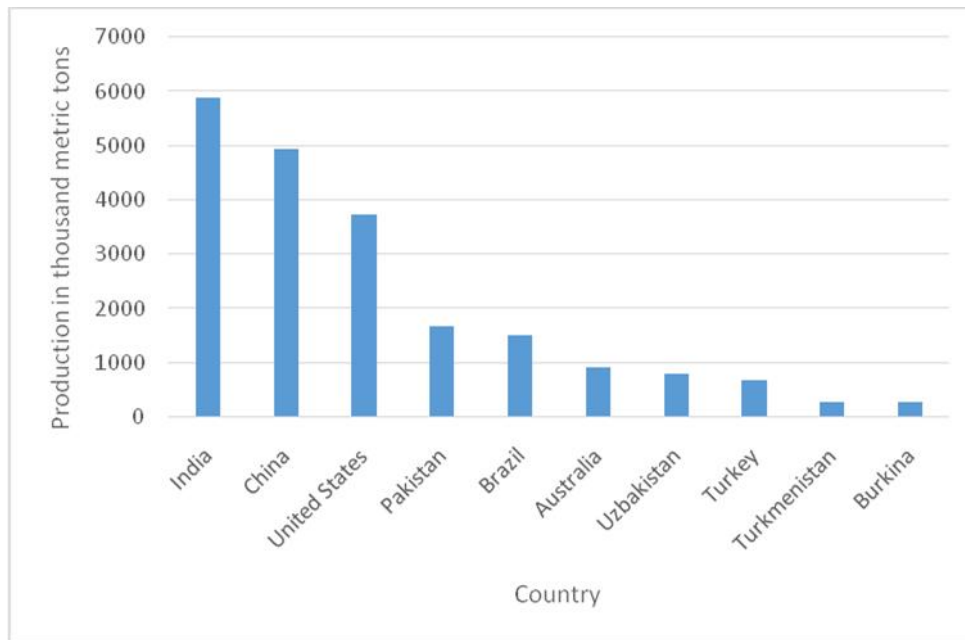
CHAPTER III

REVIEW OF FINDINGS

Cotton production through the world

The upper most cotton producing countries are China, India and the United States respectively. The Southern states of the United States traditionally harvest the maximum quantities of cotton and this region was known as the ‘Cotton Belt’.

Figure 1 showing the world’s leading cotton producing countries in 2016-2017. In that year, cotton production in India amounted 5.88 million metric tons followed by China and United States respectively.



Source: Statista 2018

Figure 1: Area and Production of Cotton in the World in 2016-2017.

Defining basic yield components

Tempering the principal components of cotton cultivation may open some space for selection of improved yield selection. “Number of seed per area” times the “Weight per seed”, that is the deterministic definition of most basic crop models cultivation. “Weight of fiber per seed” is also considered in cotton yield. “Number of seed produced per area” multiplied by the “weight of fiber per seed” is a simplified model of cotton yield by Lewis et al. (2000). High yields requires a high number of seed per area. But reliance on increased seed production to improve yield leads to less stable yields because 1) seed production requires more weight- seed makes up about 60% of seed-cotton by weight- than fiber production, 2) Oil associated with the seed requires more energy than cellulose associated with fiber and 3) number of seed per area is more greatly affected by environmental factors than is weight of fiber per seed. A little bit of changes in the partitioning can result in noteworthy lint yield increases. An increase of only 5 mg of fiber per seed produces about 75 lb per acre (84 kg per ha) in lint yield. Lint index, which is equal to weight of fibers per 100 seed, was commonly reported by cotton researchers in early 1900’s, but was consequently replaced by use of lint percentage. In addition to the ginning and fiber quality measurements normally available in cotton testing, the only other parameter needed to calculate index and seed per area is seed index (weight of 100 fuzzy seed). Selection for high lint index results in lines with higher lint weight per seed, but also larger seed. On the contrary, selection for high lint percentage will result in lines with higher gin produce, but also smaller seed. The need to reduce seed size of cotton genotypes in the early 1900’s was one reason that cotton breeders preferred lint percentage over lint index.

Yield components of high yielding cotton cultivars

Cotton yield consists of the components that make up total lint yield, which are bolls/m² (fruiting sites and boll retention) and lint/boll (seeds/boll and lint/seed). Australia produces 680 million kg of cotton lint per year and more than 95% is exported. There are complex relationships among cotton lint yield and their components. Genetic and environmental variation and the interaction between these two greatly influence the yield components. The primary yield components which contribute to cotton lint yield are bolls per unit area, seeds per boll and lint per seed (Kerr 1966; Manning 1956; Wilson et al. 1994; Worley et al. 1974).

Table 1: Area and yield of cotton in the world

Rank	Country	Yield (Kg/Ha)	Rank	Country	Yield (Kg/Ha)
1	Australia	2,202.00	41	Philippines	435.00
2	Turkey	1,853.00	42	Thailand	435.00
3	China	1,761.00	43	Benin	423.00
4	Israel	1,742.00	44	Côte D'ivoire	421.00
5	Mexico	1,597.00	45	Paraguay	416.00
6	Brazil	1,555.00	46	Senegal	413.00
7	Venezuela	1,234.00	47	Mali	403.00
8	Tunisia	1,089.00	48	Afghanistan	401.00
9	Bulgaria	1,089.00	49	Niger	392.00
10	Colombia	1,089.00	50	Ghana	381.00
11	Greece	1,080.00	51	Uganda	363.00
12	South Africa	1,030.00	52	Zambia	352.00
13	United States	1,008.00	53	Yemen	339.00
14	Syrian Arab Republic	995.00	54	Burkina Faso	333.00
15	Peru	990.00	55	Iraq	327.00
16	Spain	964.00	56	Guatemala	327.00
17	Azerbaijan	740.00	57	Togo	327.00
18	Egypt	718.00	58	Indonesia	327.00
19	Uzbekistan	671.00	59	Malawi	280.00
20	Viet Nam	653.00	60	Guinea	254.00
21	Kyrgyzstan	653.00	61	Zimbabwe	245.00
22	Ecuador	653.00	62	Costa Rica	218.00
23	Pakistan	638.00	63	Cuba	218.00
24	Ethiopia	635.00	64	Albania	218.00
25	Myanmar	634.00	65	Central African Republic	218.00
26	Bangladesh	633.00	66	Sri Lanka	218.00
27	Korea	630.00	67	Morocco	218.00
28	Tajikistan	622.00	68	El Salvador	218.00
29	Iran	610.00	69	Chad	218.00
30	Turkmenistan	569.00	70	Kenya	196.00
31	Nicaragua	544.00	71	Nigeria	190.00
32	Angola	544.00	72	Mozambique	176.00
33	Sudan	529.00	73	Dominican Republic	163.00
34	Argentina	506.00	74	Haiti	156.00
35	Kazakhstan	505.00	75	Tanzania,	156.00
36	India	504.00	76	Somalia	127.00
37	Cameroon	484.00	77	Congo	109.00

38	Bolivia	435.00			
39	Honduras	435.00			
40	Madagascar	435.00			

Source: United States Department of Agriculture (2017)

Table 2: The average result of some quantitative yield components of cotton

Variety	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of boll plant ⁻¹	Lint yield plant ⁻¹ (g)	Seed cotton yield (g/plant)
Suvin	147.21	4.79	17.37	25.74	32.31	97.18
BCS 23-8-7	118.06	1.72	16.17	37.17	29.46	116.90
F1 Mean	126.97	3.69	15.61	39.72	53.31	158.04
F2 Mean	126.54	2.47	11.82	28.57	37.42	111.83
CV	14.16	26.09	21.99	14.19	22.61	20.51

Source: Modified from Kumar et al., 2017

Table 2 representing mean of some quantitative yield components of two parents (Suvin and BCS 23-8-7), F1 generation, F2 generation and coefficient of variance. Here F1 possesses highest seed cotton yield (158 g), lint yield (53.31 g). From this results, it can be said that the genetic variation can be created through hybridization between diverse parents.

Table 3: The average result of some qualitative yield components

CULTIVARS	Ginning percentage	Fiber length	Micronaire	Fiber strength
Sayar314	38.15de	28.08f	4.92abcd	32.50fg
Stoneville 453	37.78de	29.22cd	4.75bcde	32.87efg
Condor	39.32bc	28.43ef	5.12ab	33.68def
Lachata	38.43cd	28.60def	4.62de	29.93h
Nata	38.26d	29.38c	4.77bcde	34.70cde
Dpl 5690	40.48a	28.93cde	4.68cde	34.58de
Dpl 5409	40.30ab	28.72cdef	4.70bcde	34.35de
Dpl 90	40.34a	29.28cd	5.22a	36.92b
Giza 75	34.05g	34.17a	4.10f	38.30b
Delcerro	35.43f	33.22b	4.15f	42.08a
Ofn 7	37.21e	29.38c	4.45e	36.53bc
Luisa	40.32ab	29.13cde	4.50def	34.93cd
N 727	39.7ab	28.10f	4.37ef	33.62def
Brown color line	33.54g	24.20g	5.08abc	26.93i
Mc namara	24.99h	23.98g	4.70bcde	31.35gh
LSD	1.00	0.72	0.42	1.85
CV	1.61	1.48	5.36	3.23

Source: Modified from Copur, 2006

*: Mean shown with the same letter(s) in the same column are not significantly different at p= 0.05 probability level

From the Table 3, highest number of boll per plant was found from Stoneville 453. Highest ginning percentage as obtained from DPL 5690 followed by DPL 90, DPL 5409 and Luisa. Moreover, Giza 75 and Delcerro had the longest fibers and Delcerro variety also had the highest fiber strength. As Giza 75 and Delcerro could be grown due to their higher fiber qualities and to compensate yield vs. quality, economical analysis should be done.

Table 4: Correlation of yield components over genotypes

	Boll Size	Seed Wt./Boll	Lint Wt./Boll	Seeds/Boll	Lint Wt./Seed	Fibers/Seed	Lint %	Upper-Half Mean	Mic	Bolls/ Ha
Seed Wt./Boll	0.94*									
Lint Wt./Boll	0.92*	0.76*								
Seeds/Boll	0.79*	0.92*	0.51*							
Lint Wt./Seed	0.35	0.07	0.67*	-0.28						
Fibers/Seed	0.42*	0.22	0.71*	-0.15	0.93*					
Lint %	-0.25	-0.47*	0.16	-0.73*	0.79*	0.70*				
Upper-Half Mean	0.60*	0.76*	0.34	0.84*	-0.34	-0.15	-0.67*			
Micronaire	-0.52*	-0.71*	-0.33	-0.71*	0.24	-0.06	0.51*	-0.89*		
Bolls/ Ha	-0.64*	-0.60*	-0.55*	-0.46*	-0.21	-0.29	0.26	-0.14	0.21	
Lint Yield	0.05	-0.03	0.21	-0.07	0.3	0.25	0.40*	0.17	-0.06	0.69*

Source: Cole et al. (2016)

*: Significantly different at 0.05 level of probability

Number of fibers/seed was highly correlated with lint weight/seed, lint percentage, boll weight, and lint weight/boll (Table 4). As seed size increased, the number of fibers increased. These correlations did not result in an increase in lint yield. There was no correlation between lint yield and any within-boll component associated with fiber or seed yield. The number of bolls/hectare was negatively correlated with boll size, seed weight/boll, lint weight/boll, seed index, and seeds/boll, and positively correlated with lint yield. This was the only yield component that was positively correlated with overall yield and can help explain the similar observations between the two traits for several measured statistics. Micronaire was negatively

correlated with UHM but positively correlated with lint percentage and weight/fiber (Table 4). Upper-half mean was negatively correlated with lint percentage and weight/fiber. Lint percentage was positively correlated with lint yield, whereas no other lint characteristic showed an association.

These correlations revealed a different trend than the mean results. Correlations indicated that fiber characteristics and lint yield were not improved concomitantly, whereas the mean data indicated simultaneous increases in classically negatively correlated traits. Mean data also suggested a simultaneous increase in boll weight and bolls/hectare; however, the number of bolls/hectare was negatively correlated with boll weight and all the components that compose it. These are indications that increases observed in the heterozygous populations for many components of lint yield occurred independently and could be a byproduct of increased numbers of bolls/hectare.

Maternal Effects on Reciprocals of Some Yield and Yield Components of Cotton

Cotton research in genetics is very vital to increase the yielding ability of locally developed cotton varieties that will make them attractive and profitable to farmers so as to stimulate interest in cotton production. Maternal effects show normal reciprocal cross differences which have been evaluated genetically and analysed in animals and plants (Jinks et al. 1972; Mather and Jinks, 1982; Falconer, 1989). Maternal inheritance arises when mother makes contribution to her progeny's phenotype above that which results from the genes she contributes to the zygote. Maternal inheritance results to produce difference between reciprocal crosses that are shared between the offspring of both sexes in all generations where they occur. Maternal effects also lead to a reflection of the progeny to the maternal parent.

Table 5 representing the maternal effects. From this table, Samcot 11 is the maternal parent that had highest maternal effects on the phenotypic expression of the reciprocal and the effects are positive for six characters namely; days to boll opening, boll size (cm), number of boll per plant, lint percentage, seed yield (g), lint yield (g). Samcot 12 and EX-Benin are in second position as they had positive maternal effects on five characters followed by Samcot 13 that had positive

effects on four characters. Samcot 9 and Samcot 8 had positive effects on two characters followed by Samcot 10 and Tamcotcamd-E which had only one positive effects.

Table 5: Estimates of maternal effects for yield and yield components of parents, combined across locations

Maternal parent	Paternal lines	Days to boll opening	Boll size (cm)	No of bolls/plant	Lint %	Seed Yield (g)	Lint Yield (g)	Days to maturity
MAT 1	Samcot 8	-6.031	-1.170	-4.996	-0.621	-5.501	0.482	12.062
MAT 2	Samcot 9	-9.026	0.037	-1.884	-0.402	-8.921	-0.578	7.584
MAT 3	Samcot 10	-10.605	-0.642	-1.199	-0.216	-4.509	-0.248	1.226
MAT 4	Tamcotcamd-E	-5.219	-0.158	-0.682	0.247	-3.073	-0.596	-4.627
MAT 5	Samcot 13	3.225	-0.120	3.144	0.169	2.982	-0.226	-3.419
MAT 6	EX-Benin	8.468	-0.341	2.198	0.229	5.275	0.235	-5.468
MAT 7	Samcot 11	11.925	2.204	3.239	0.232	5.783	0.701	-5.720
MAT 8	Samcot 12	7.263	-0.809	0.181	0.361	7.965	1.232	-1.635
	SE	2.01	0.41	0.75	0.03	2.46	0.34	5.12

Source: Simon et al. (2014)

Relationships of Plant Trichomes to Yield Components of Cotton:

Trichomes are hair-like protrusions that may occur on abaxial and adaxial surfaces of leaves, bracts, as well as on stems and seed of cotton (*Gossypium hirsutum* L.) plants. On seed, the epidermal trichomes are known as cotton fibers. Extensive breeding efforts have been made to reduce trichomes on leaves, and some attention has been made to reduce trichomes on stems and bracts. There is concern that these efforts might have unwitting negative effects on number of fibers produced on the seed and on other agronomic parameters. Reducing trichomes on cotton leaves, stems and bracts can reduce trash in ginned cotton lint, but might negatively impact fibers on seed and other parameters. Reduced leaf pubescence (i.e. lower trichome density) has been associated with enhanced cleaning efficiency of seed cotton and improved grades of ginned cotton (Anthony and Rayburn, 1989; Novick et al., 1991; Boykin et al., 2013). Yield stability could be enhanced by placing a greater reliance on weight of fiber seed⁻¹ rather than number of seed area⁻¹. Weight of fiber seed⁻¹ is a function of number of fibers seed⁻¹ times the average weight fiber⁻¹.

Table 6 showing linear mixed model regression analyses, leaf pubescence was more frequently associated with the dependent variables rather than the other independent variables. Stem pubescence was the second most frequently used independent variable and bract trichome density was the least frequently used independent variable. Leaf pubescence positively influenced seed ha⁻¹. The only other variable that leaf pubescence influenced in both Strain and Variety Tests was lint index, but the direction of the influence differed between the two sets of tests.

Table 6: Relation of trichome and pubescence measurements on yield-components

Dependent variable	Intercept (SE)		Leaf pubes. rating (SE)		Stem pubes. rating (SE)		Bract trichome density (SE)	
	A	B	A	B	A	B	A	B
Seed ha ⁻¹	14.877 (1.425)	14.669 (1.981)	0.136 (0.047)**	0.247 (0.052)	-	-	-	0.042 (0.052)
Lint index 1	7.118 (0.118)	6.925 (0.121)	0.033 (0.015)*	-0.025 (0.015)+	-	-	-	-
Lint index 2	-	7.014 (0.146)	-	-	-	-0.030 (0.016)	-	-
Lint percentage	38.675 (0.302)	40.446 (0.389)	-	-	0.105 (0.036)**	0.039 (0.040)ns	-	-
Seed index 1	11.042 (0.202)	10.044 (0.199)	-	-	-0.027 (0.021)ns	-0.055 (0.022)	-	-
Seed index 2	-	9.896 (0.160)	-	-0.048 (0.020)*	-	-	-	-
Seed index 3	-	10.113 (0.190)	-	-0.038 (0.020)+	-	-0.045 (0.020)*	-	-
Fibers seed ⁻¹	14884 (313)	16426 (455)	129 (35)***	-	-	-124 (49)*	-	-
Fiber density	134.74 (3.60)	161.26 (4.60)	129 (35)***	-	-	-0.62 (0.48)ns	-	-

+, *, **, *** Significant at the 0.10, 0.05, 0.01, and 0.001 probability levels, respectively.

z Data taken from 2 replications of tests (800 observations over 10 years).

y None of the trichome measurements had significant effects on plant height, seed index, or fiber micronaire. A dash (“-”) indicates that the respective independent variable was not chosen to explain variation in the dependent variable.

A= In the 2006 through 2015 Advanced and New Cotton Strain Tests at Keiser, AR.

B= In the 2006 through 2015 Arkansas Cotton Variety Test at Keiser.

Source: Modified from Bourland et al. (2017)

Variables influenced by leaf pubescence in only one set of tests included seed index (negatively in Variety Tests), fibers seed⁻¹ (positively in Strain Tests), and fiber density (positively in Strain Tests). Consistent relationships over the both Strain and Variety Tests suggest more important effects. Positive influences of increased leaf pubescence on seed ha⁻¹ may be related to pest or environment tolerance associated with increased trichomes on the plant (Jenkins and Wilson, 1996). Leaf pubescence did not influence lint percentage in either the Strain or Variety Tests. Leaf pubescence positively influenced both fibers seed⁻¹ and fiber density in the Strain Tests, but not in the Variety Tests (Tables 6). This suggests that trichomes on leaves and on seed may be related. Stem pubescence did not influence seed ha⁻¹ in either the Strain or Variety Tests. Bract trichome density had a positive influence on seed ha⁻¹ in the Variety Tests. The lack of influence on lint index, lint percentage, fibers seed⁻¹, fiber density suggest that trichomes on bracts are independent of seed trichomes, and may be reduced without negatively affecting these yield component and fiber quality parameters. The only parameter influenced by both bract trichome density and leaf pubescence rating was seed ha⁻¹ in the Variety Tests. These relationships suggest that trichomes on leaves and bracts may influence seed and fiber production, and causes concern if breeders seek to lower hairiness of leaves and bracts.

New approaches of breeding

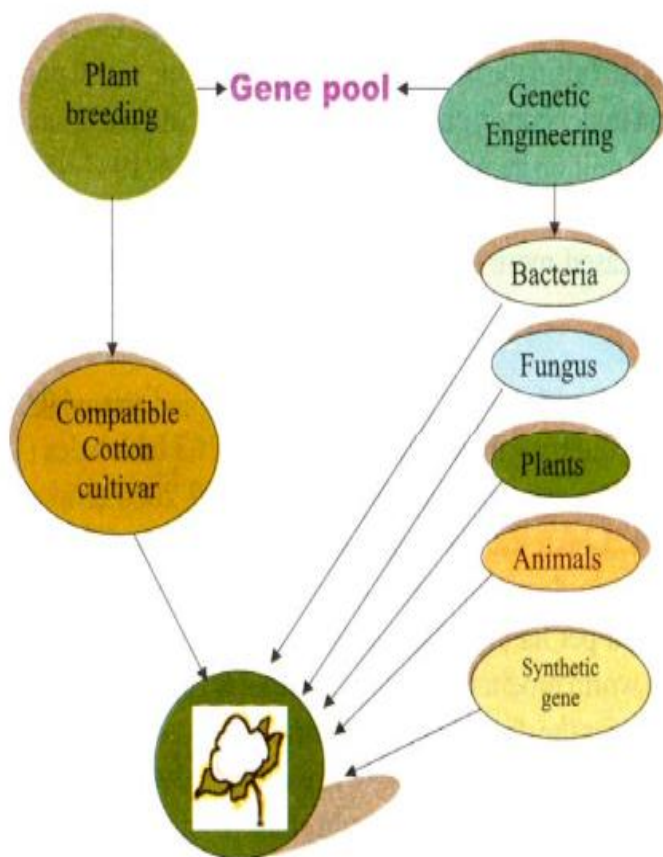
Transgenic Breeding

Transferring genes other species into cotton was well thought-out as science fiction earlier. But transgenic cotton is orthodox today and grown extensively in many countries. Transgenic technology has made it a reality to obtain qualities that were otherwise not available through escalating the gene pool to other species. Limitations on the use of transgenic technology have provided seed companies an additional means to protect and regulate seed sales. Transgenic cottons has very positive effects on cotton production and promise to continue to provide positive impacts. The major two transgenic types used today are the different forms of Bt genes for worm control and herbicide-resistance genes to assist with weed control. In the mid 1990's cottons processing Bt genes were introduced. These cottons instantly influenced insect control

and concurrently led to increased yields and reduced insect control costs. In the mid 1990's Glyphosate-resistant cottons, also introduced, have profoundly affected cotton production systems in the U.S. Use of glyphosate for over-the-top weed control has simplified weed control and decreased the time and effort need to control weeds. Concurrently, growers have been able to increase their farm size, while reducing their per unit production costs. Reducing the use of tillage and incorporated herbicides have allowed cotton plants to develop better root systems and incur less injury from tillage and incorporated herbicides.

Genetic engineering for cotton improvement

Genetic engineering provides an alternate and powerful method for gene transfer from any organisms into cotton, whereas cross breeding is restricted to compatible cotton cultivars. The transferred foreign gene(s) integrates efficiently in to the plant chromosome. There is potential to improve cotton insect pest resistance traits (which is unique and extremely desirable at the present time), herbicide tolerance, fiber characteristics, oil content, tolerance to environmental extremes and even more fundamental physiological processes such as water and nutrient balance.



Source: www.google.com

Figure 2: Relationship between plant breeding and genetic engineering to produce transgenes.

Bt cotton as a new approach of breeding

Bt cotton is genetically altered by the insertion of genes from a common soil bacterium, *Bacillus thuringiensis*, to produce certain proteins that are toxic to specific insects. Currently available Bt cotton varieties produce either or both crystal (Cry) and vegetative insecticidal proteins (Vip) that target specific caterpillar pests such as beet armyworm, cotton bollworm, and tobacco budworm.

Bt traits that are available

Since its introduction in 1996 into US agriculture, Bt technology has developed from a single gene trait to multi-gene trait packages. The first-generation Bt cotton (Bollgard) had a single Bt gene that expressed (produced) Cry1Ac. The second-generation Bt technologies, such as Bollgard

2, TwinLink, and WideStrike, produce two Bt toxins, and the most recent third-generation Bt technologies (WideStrike 3, Bollgard 3, and TwinLinkPlus) are three-gene trait products.

Table 7: Bt technologies with protein expressed

Bt Technologies	Protein Expressed	Bt Technologies	Protein Expressed
Second Generation		Third Generation	
Bollgard 2	Cry1Ac+Cry2Ab	WideStrike 3	Cry1F+ Cry1Ac+Vip3A
WideStrike	Cry1Ac+Cry1F	Bollgard 3	Cry1Ac+Cry2Ab+Vip3A
TwinLink	Cry1Ab+Cry2Ae	TwinLinkPlus	Cry1Ab+Cry2Ae+Vip3Aa19

Source: Vyavhare S. (2017)

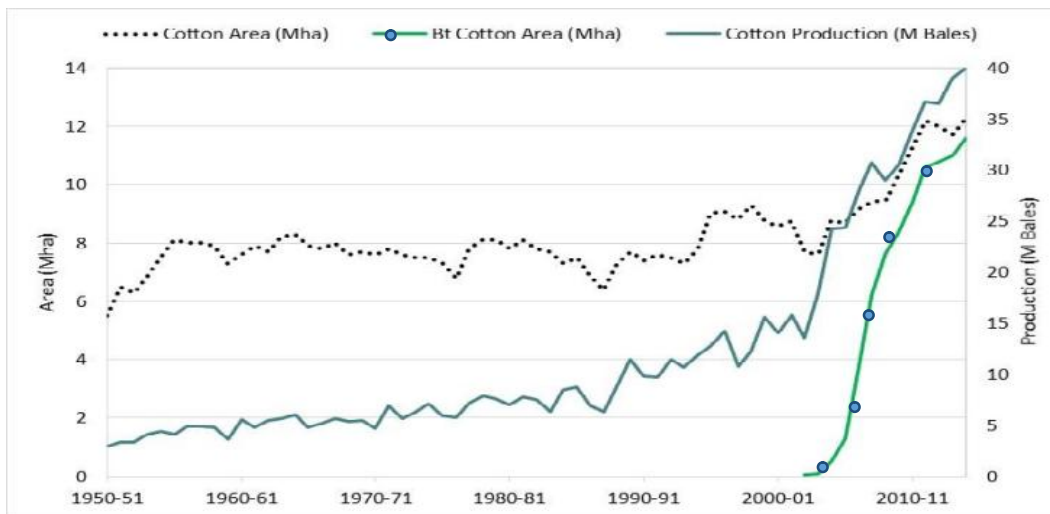
Table 8 represents the effectiveness of Bt genes against caterpillar pests. From the table, Bt traits have complete control on tobacco bollworm, pink bollworm, and soybean looper from 1996 to 2017. Recently, the third generation Bt technologies having three genes are expected to be more effective for controlling worms. Biotic (living organism) and abiotic (physical factors) stress negatively affect plant growth and protein expression in Bt crops.

Table 8: Relative Efficacy of Bt Traits against Caterpillar pest

Pest	Bollgard (Cry1Ac)	Bollgard II (Cry1Ac + Cry2Ab)	Widestrike (Cry1Ac + Cry1F)	TwinLink (Cry1Ab + Cry2Ae)	Widestrike 3 (Cry1Ac + Cry1F + Vip3A)	Bollgard 3 (Cry1Ac + Cry2Ab + Vip3A)	TwinLink Plus (Cry1Ab + Cry2Ae + Vip3Aa19)
	1996	2003	2005	2013	2014	2017	2017
Bollworm	4	2.5	4	2.75	2.5	2*	2*
Tobacco budworm	1	1	1	1	1	1	1
Pink bollworm	1	1	1	1	1	1	1
Beet armyworm	2	2	2	2	1-2*	1-2*	1-2*
Fall armyworm	2.5	2	1	2	1	1-2*	1-2*
Soybean looper	1	1	1	1	1	1	1

1 = Complete control
2 = Rarely requires oversprays
3 = Sometimes requires oversprays
4 = Frequently requires oversprays
*Incomplete data

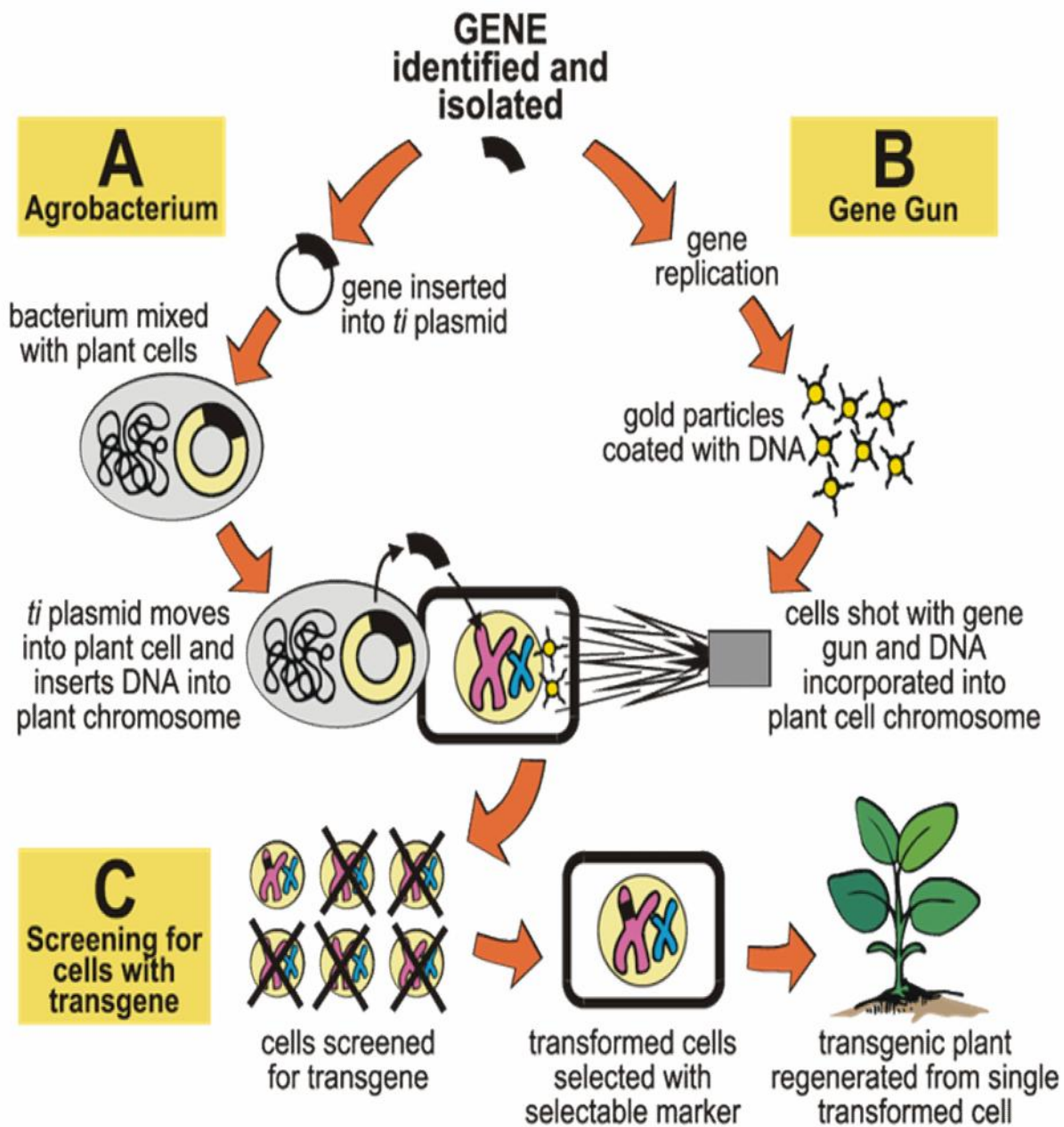
Source: Vyavhare S. (2017)



Source: CAB, 2014; Blaise et al., 2014; Analyzed by ISAAA, 2014

Figure 3: The Adoption and Impact of Bt Cotton on the Cotton Production in India, 1950 to 2014.

Gene transfer into an organism



Source: www.google.com

Figure 4: Process of gene transfer into cotton plant.

Herbicide Resistance in Cotton

Genes that give plants tolerance to herbicides have been isolated and incorporated into cotton plants. For a number of technical and practical reasons, resistance to herbicides was among the first traits to which these new genetic approaches were applied. First, a specific target of herbicide action had been identified through physiological and biochemical studies. Secondly, genetic studies had shown that resistance to herbicides was a dominant trait exhibiting the simple Mendelian inheritance pattern of a mutation in a single nuclear gene. Dominance makes genetic selection of herbicide resistance mutants or transformants easier. The potential utility of herbicide resistance genes as dominant selectable genetic marker for research in plants (as antibiotic resistance genes in bacteria).

A part from insect resistance herbicide resistant cotton is also under cultivation. Monsanto Company, USA (Roundup ready cotton) has already developed the non-selective herbicide glyphosate tolerant cotton (GTCOT). Glyphosate [*N*-(phosphonomethyl) glycine] is a herbicide that provides cheap control options for annual, perennial, and biennial herbaceous species of grasses, sedges, and broad leaf weeds, as well as woody brush and tree species, and has been used for over several decades. The mode of action of glyphosate lies in the inhibition of the enzyme 5-enolpyruvylshikimate-3-phosphate (EPSP) synthase, which is key catalyst in the production of aromatic amino acids. Since animals do not synthesize aromatic amino acids glyphosate has low toxicity to humans but broad toxicity to plants. Two different routes have accomplished resistant to glyphosate. In the first, a strong constitutive promoter was placed in front of a natural EPSP synthase gene so that, the enzyme was overproduced in the transformed plants. In the second, a mutated bacterial EPSP synthase gene that changed one amino acid in the enzyme protein resulted in the enzyme being insensitive to the herbicide. With an appropriate promoter, plants transformed with this gene were resistant to glyphosate. The principal motivation in developing glyphosate resistance in cotton is related to the broad spectrum of activity of the herbicide and its relatively low level of environmental contamination. Since the activity of the herbicide is directed against an enzyme in the chloroplast most plants are susceptible to it.

Wide Hybridization

Wide hybridization refers to the interspecific and intergeneric hybridization which is the first step to introduce alien variation and to transfer desirable genes from wild species into cultivated species.

Table 9: Main characters of two parents and interspecific hybrid of cotton

Organ	<i>G. herbaceum</i>	<i>G. herbaceum</i> × <i>G. raimondii</i>	<i>G. raimondii</i>
Stigma	Light yellow; 3–5 mm length	Light yellow; 4–7 mm length	Light yellow; 3–5 cm length
Androecium	Light yellow staminal column and filaments; yellow anther cases	Deep red staminal column and filaments; yellow anther cases	Deep red staminal column and filaments; red anther cases
Capsule	3 locules; 1–6 seeds per locule	No boll setting	3 locules; 2–3 seeds per locule

Source: Wu et al. 2017

The changes in the morphology characteristics of the new interspecific hybrids are consistent with the above reports (Table 9). Most of the morphological characteristics of the hybrids were found to be intermediate between *G. herbaceum* and *G. raimondii*. It has been reported that the newly formed hybrids may be non-viable or sterile. Various abnormal meiotic behaviors in PMC and abnormal pollen grains may be existed in the hybrids which may involve in the sterilization of the hybrids.

Tissue culture and somaclonal variation

Development of tissue culture protocols to incite efficient proliferation in a genotype independent manner is desirable for genetic transformation of cotton. Cotton plants are strictly limited in their regeneration *in vitro* from callus, protoplast or leaf tissues. This widespread problem now a days restricts improvement of the few potential commercial genotypes through genetic engineering (Gould *et al.*, 1991, McCabe & Martinell, 1993). Somaclonal variation in commercial species generated by *in vitro* crop has been widely reported in the literature as well as their use to plant breeding, as a way of generating variability (Miguel and Marum, 2011; Yang et al., 2013; Springer, 2013).

Table 10: Agronomic traits recorded individually of cotton plants via *in vitro* cropping and by seeds

Pop 1	PH	NB	WB	Oil %	Pop 2	PH	NB	WB	Oil %
R1	101	15	5.7	19.8	R1	98	12	6.2	20.3
R2	99	12	5.9	19.9	R2	98	12	5.6	19.9
R3	106	15	6.1	21.1	R3	102	11	5.9	21.1
R4	98	12	6.2	21.2	R4	99	12	6.4	21.3
R5	98	12	5.9	21.0	R5	106	15	5.7	19.8
R6	101	13	5.5	21.2	R6	104	15	6.5	19.3
R7	105	12	5.9	20.3	R7	98	13	5.9	20.3
R8	98	13	6.3	20.6	R8	103	14	6.3	20.2
R9	96	14	6.2	20.5	R9	99	15	6.1	21.0
R10	99	15	6.5	20.3	R10	99	15	5.9	21.1
R11	101	12	5.9	19.9	R11	103	13	6.0	20.9
R12	102	12	6.1	19.9	R12	104	14	6.2	20.8
R13	104	13	6.1	19.8	R13	101	12	6.5	21.2
R14	101	14	6.3	20.6	R14	105	12	5.8	21.0
R15	101	14	6.2	21.0	R15	99	14	6.0	19.9
R16	99	15	5.9	21.1	R16	100	11	6.2	21.0
R17	98	14	5.9	19.9	R17	99	11	6.1	19.9
Mean	100	13	6.0	20.5	Mean	101	13	6.1	20.5

Source: Sources et al. (2017)

PH= Plant Height

NB= No. of Bolls Plant⁻¹

WB = Weight of Bolls

Pop 1 = Plants obtained from regenerated embryos via *in vitro* cropping

Pop 2 - Plants obtained from seeds

In the table 10, the seventeen plants acquired from embryos 25 days after fertilization (Population1) were grown in the greenhouse, adopting the same management as to Population 2 (cv.BRS 8H grown by seeds). The values found individually inplants were too close, so that the means were quite similar in both populations, suggesting nooccurrence of any somaclonal variations in regenerated plants, based on the traits evaluated.

Mutation Breeding

Mutation techniques have been widely applied to enhance crop yield, quality, disease and pest resistance and produced more germplasm with novel, desired traits. somaclonal variation in crop plants narrate a new source of variability, and therefore, constitutes an additional tool for the breeder. This protocol in cotton can produce large populations through in vitro mutation breeding, which increases the probability of obtaining mutant lines with the desired traits.

Table 11: Morphological and fiber yield contributing characters of the isolated mutant line of cotton

Mutants	Plant height (cm)	No. of Bolls	Yield of Seed Cotton (g)	Ginning percent	Micronaire value	Strength (G/tex)
Control	110.2	47.0	190.2	36.5	3.5	23.8
M1	123.5	54.0	213.5	43.5	3.6	24.1
M2	125.6	60.2	228.5	41.5	4.1	23.9
M3	162.8	67.2	235.6	43.6	4.1	24.6
sM4	130.5	63.1	240.5	44.5	3.9	24.8
M5	140.6	68.3	258.3	46.3	3.7	25.3
M6	145.6	64.1	246.1	44.2	4.1	25.1
M7	138.9	69.1	258.6	46.7	4.1	20.8
M8	148.2	54.0	257.5	45.5	4.2	19.3
M9	115.7	50.1	208.9	39.6	4.2	25.2
M10	133.6	56.6	224.5	45.7	2.3	24.9
M11	134.5	58.2	228.6	44.6	4.1	24.5
M12	144.8	67.2	254.6	45.8	4.1	24.7
M13	156.3	64.3	255.6	44.8	3.8	25
M14	161.8	59.5	248.9	41.5	3.8	26.4
M15	132.6	54.2	249.3	44.6	3.9	24.8
M16	154.6	61.3	247.5	43.4	4.1	23.6
M17	158.4	64.1	238.4	45.8	4.2	24.8
M18	162.1	64.5	235.6	45.8	4.1	23.6
M19	144.8	68.4	258.3	46.5	4.2	24.8
Agdas-3	97.5	-	341.0	37.7	4.9	29.3
Agdas-6	93.5	-	387.0	37.0	4.8	28.8
Agdas-7	90.0	-	393.0	39.3	4.5	29.0
Agdas-17	98.3	-	365.0	38.6	4.8	27.0
Maras-92(STD)	97.4	-	375.5	39.0	3.6	31.0
Sayar-314(STD)	97.5	-	375.0	41.5	4.4	25.7
Stoneville-453 (STD)	-	-		41.9	3.84	28

Source: Modified from Muthusami et al., 2011

Selected mutant line revealed great variation in case of plant height (Table 11). Among these M18, M3 and M14 possess highest plant height respectively whereas Agdas-3, Agdas-6, Agdas-7, Agdas-17, Maras-92(STD), Sayar-314(STD) showed the lowest. Again the mutant line M7 showed highest number of bolls and ginning percentage also. Among all the mutant line, most lines showed higher yield and yield contributing characters over the control plant. The yield of seed cotton is highest in Agdas-7. The variation which is showed in the table in case of mutant lines, it may be due to genetic variation which is cause by radiation. Mutagenesis is important way in crop improvement. It helps to identify the novel lines or genotypes which can be used for breeding program.

CHAPTER IV

CONCLUSION

The cotton production of the top cotton producing countries is improving significantly but the yield per unit area is still lower due to some biotic and abiotic factors. Its importance in our economy is reflected in terms of generating employment, and foreign exchange earnings.

- Better management of yield components may increase the cotton fiber strength and fiber quality. By considering yield components, superior hybrids can be developed to increase cotton production.
- Through new approaches of breeding such as wide hybridization, somaclonal variation, mutation breeding, genetically modification along with conventional breeding of cotton plant will help in the better production of cotton.

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