Chapter 1

An Introduction to Global Production Trends and Uses, History and Evolution, and Genetic and Biotechnological Improvements in Cotton

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1.1 INTRODUCTION

Cotton is the most important fiber crop in the world and belongs to the family Malvaceae and the genus *Gossypium*, and this genus has nearly 50 species. Four cultivated species of cotton are *Gossypium hirsutum* L., *Gossypium barbedense* L. (Egyptian cotton), *Gossypium herbaceum* L. (Asiatic cotton), and *Gossypium arboreum* L. (Asiatic cotton), out of these, upland cotton (*G. hirsutum*) is the most cultivated (on >90% area of total worldwide cotton cultivation) species all across the world, which is mainly due to its high yields. The oldest remains of the cotton fiber belonging to the sixth millennium BCE have been found in the Neolithic burial that is in Kachi Plains of the Mehrgarh region (near Indus River) of Pakistan (Moulherat et al. 2002).

Globally, cotton is grown in 75 countries of the world (USDA 2018b), and significantly improves the economies of many countries through the provision of fiber, oil, and several other products. The most important products of cotton may include garments, gloves, mufflers, bags, socks, jackets, beds, vegetable oil, curtains, bed sheets, and others.

Cultivated cotton is grown as an annual plant; however, the species originally possessed a perennial growth habit. Morphology and physiology of cotton have been explained in

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detail in Chapter 2 of this book. The crop is sensitive to biotic and abiotic stresses, most important of which are insect pests, drought and salt stress, diseases, weeds, viruses, and heat stress (Dogan et al. 2014; Constable and Bange 2015; Jabran 2016). Poor seed germination in cotton is another issue that is noted in many important cotton growing countries of the world. Development of genetically modified cotton cultivars has been among the important innovations that helped to control insect pests and weeds in the cotton fields. Cotton has contributed to improving the lives of people in many unprivileged areas of the world such as West Africa (Hussein et al. 2005).

This chapter discusses the global production trends of cotton, cultural, economic importance and uses of cotton, history and evolution of cotton, and the role of biotechnology in improving cotton production.

1.2 GLOBAL PRODUCTION TRENDS OF COTTON

Cotton is mainly grown in the Asia continent (~70%) followed by the Americas, which has nearly 20% of the global cotton cultivation (FAO 2018; Figure 1). Africa grows nearly 6% of the total world cotton cultivation while Europe grows less than 2% of it.

The cotton cultivation area has ranged between 30 and 35 million hectare (m ha) during the last 60 years (FAO 2018; Table 1). In the year 2016, the global cotton cultivation area was 30.2 m ha, out of which 19.5 m ha was contributed by Asia, 3.8 m ha by the North America, 1.6 m ha by the South America, 4.5 m ha by Africa, 0.28 m ha by Australia, and 0.4 m ha by the Europe (Table 1). During the last 50 years, the cotton cultivation area has been increased in the Asia (~15 to ~20 m ha), Australia (~0.02 to ~0.28 m ha), and Africa (~4.0 to ~4.5 m ha) while it has been decreased in North America (~6.3 to ~3.8 m ha), the South America (~3.0 to ~1.6) and the Europe (~3.0 to ~0.4 m ha) (Table 1). Global seed cotton production has increased from 27.5 million tons (m tons) in 1961 to 65.4 m tons in

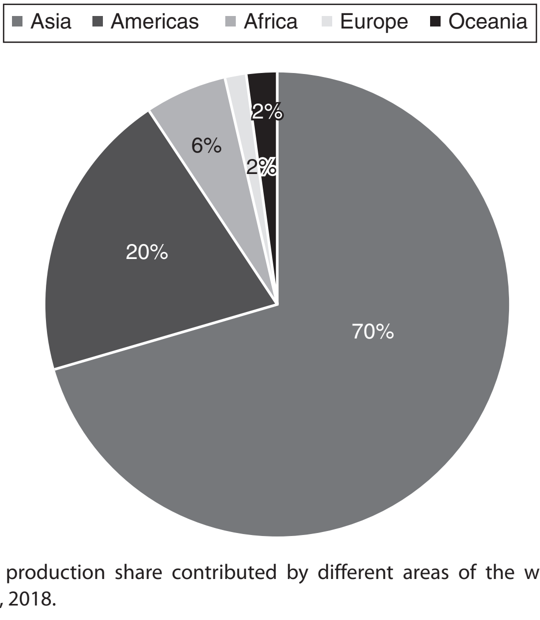

Figure 1 Seed cotton production share contributed by different areas of the world; data is average of 2007–2016 . Source: FAO, 2018.

Table 1 Seed cotton area (m ha), yield (t/ha) and production (m tons) in the world, Asia, North America, South America, Africa, Australia, and Europe (FAO 2018).

	World			Asia			North America			South America			Africa			Australia			Europe		
Year	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]
1961	31.9	862	27.5	14.7	526	7.7	6.3	1349	8.5	3.0	768	2.3	3.8	577	2.2	0.02	473	0.01	3.0	1737	5.2
1962	32.2	914	29.4	14.6	577	8.4	6.3	1396	8.8	3.3	811	2.7	3.8	731	2.8	0.01	513	0.01	3.1	1598	5.0
1963	33.0	984	32.5	15.9	646	10.3	5.8	1556	8.9	3.3	794	2.6	3.8	713	2.7	0.02	320	0.00	3.1	1912	5.9
1964	33.7	1004	33.8	16.6	694	11.5	5.7	1574	9.0	3.4	752	2.5	4.0	702	2.8	0.02	442	0.01	2.9	2012	5.8
1965	33.7	1063	35.8	16.4	785	12.9	5.5	1593	8.8	3.4	726	2.5	4.3	707	3.0	0.02	1693	0.03	2.9	2170	6.2
1966	31.5	1071	33.8	16.2	845	13.7	3.9	1468	5.7	3.2	832	2.6	4.4	694	3.0	0.02	2383	0.05	2.9	2265	6.6
1967	32.7	1012	33.1	16.8	856	14.4	3.2	1401	4.5	4.5	571	2.6	4.3	704	3.1	0.02	2163	0.05	2.8	2326	6.5
1968	33.1	1083	35.8	16.2	895	14.5	4.1	1602	6.6	4.7	632	2.9	4.3	712	3.0	0.03	2775	0.09	2.8	2301	6.5
1969	34.0	1014	34.5	16.0	841	13.5	4.5	1312	5.9	5.1	624	3.2	4.6	838	3.8	0.03	2735	0.09	2.9	2148	6.3
1970	34.1	1042	35.6	15.8	871	13.8	4.5	1309	5.9	5.3	596	3.1	4.8	800	3.8	0.03	2303	0.07	3.1	2431	7.4
1971	34.9	1067	37.2	16.3	918	15.0	4.6	1320	6.1	5.3	585	3.1	4.8	771	3.7	0.04	1362	0.05	3.1	2495	7.7
1972	35.5	1097	39.0	16.4	885	14.5	5.3	1499	7.9	5.1	586	3.0	4.8	774	3.7	0.04	2716	0.11	3.1	2559	7.9
1973	35.0	1165	40.7	16.0	1012	16.2	4.8	1523	7.4	5.4	658	3.6	4.8	723	3.5	0.04	1814	0.08	3.1	2689	8.2
1974	34.9	1188	41.5	16.5	999	16.5	5.1	1301	6.6	4.8	701	3.3	4.3	824	3.5	0.04	1875	0.08	3.2	2804	9.0
1975	32.5	1113	36.2	15.9	942	15.0	3.6	1328	4.7	5.1	641	3.2	4.1	789	3.3	0.04	2252	0.09	3.2	2650	8.5
1976	31.8	1106	35.2	15.2	888	13.5	4.4	1368	6.0	4.4	567	2.5	4.0	736	2.9	0.03	2198	0.07	3.2	2724	8.8
1977	35.4	1159	41.0	16.3	903	14.7	5.4	1516	8.1	5.4	634	3.4	4.1	757	3.1	0.04	2113	0.07	3.3	2822	9.3
1978	35.4	1099	38.9	16.4	899	14.8	5.0	1243	6.2	5.4	600	3.2	4.4	756	3.3	0.04	2796	0.12	3.3	2751	9.0
1979	34.3	1227	42.1	16.1	956	15.4	5.2	1623	8.4	5.0	612	3.1	3.7	857	3.2	0.05	2643	0.13	3.3	2914	9.7
1980	34.3	1206	41.4	16.3	1032	16.8	5.3	1211	6.5	5.0	628	3.1	3.6	903	3.3	0.08	2920	0.22	3.4	2855	9.7
1981	34.5	1319	45.5	17.1	1053	18.0	5.6	1644	9.2	4.5	688	3.1	3.3	940	3.1	0.08	3114	0.26	3.4	3013	10.3
1982	33.2	1338	44.4	17.5	1144	20.0	3.9	1754	6.9	4.5	692	3.1	3.3	955	3.1	0.10	3417	0.35	3.4	2871	9.8
1983	31.7	1361	43.1	17.5	1235	21.7	3.0	1508	4.5	3.7	685	2.6	3.4	922	3.2	0.10	2645	0.26	3.4	2843	9.8
1984	34.5	1586	54.7	18.2	1607	29.3	4.2	1785	7.5	4.2	876	3.6	3.6	931	3.4	0.14	2413	0.33	3.6	2541	9.3
1985	33.4	1523	50.9	16.6	1418	23.6	4.1	1863	7.7	4.8	949	4.6	3.5	1059	3.7	0.18	3600	0.66	3.7	2601	9.5
1986	30.9	1445	44.6	15.2	1380	21.0	3.4	1625	5.6	4.3	884	3.8	3.6	1023	3.6	0.18	3668	0.65	3.8	2401	9.2
1987	30.1	1615	48.7	15.2	1522	23.2	4.1	2081	8.4	2.9	979	2.8	3.6	1021	3.7	0.16	3536	0.55	3.9	2322	9.0
1988	34.0	1568	53.3	17.0	1438	24.5	4.8	1831	8.9	3.9	1200	4.7	3.8	1009	3.8	0.24	2878	0.70	3.8	2561	9.7
1989	32.3	1554	50.2	17.0	1452	24.8	3.9	1787	6.9	3.5	1094	3.8	3.6	1009	3.7	0.19	3670	0.71	3.8	2562	9.6
1990	33.1	1639	54.2	17.1	1567	26.8	4.7	1851	8.8	3.4	1225	4.2	3.8	983	3.7	0.24	3329	0.80	3.5	2618	9.3
1991	34.8	1731	60.3	18.3	1726	31.6	5.2	1929	10.1	3.3	1301	4.2	4.0	929	3.8	0.28	4061	1.13	3.3	2597	8.7

(*continued*)

Table 1 (*Continued*)

	World			Asia			North America			South America			Africa			Australia			Europe		
Year	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]	Area	Yield	Prod.[a]
1992	33.8	1556	52.7	21.4	1575	33.8	4.5	2036	9.2	3.3	1075	3.5	3.8	950	3.6	0.31	4178	1.30	0.4	2515	1.0
1993	30.3	1578	47.8	19.2	1590	30.6	5.2	1791	9.3	1.9	1273	2.4	3.3	1042	3.5	0.29	3276	0.94	0.4	2837	1.1
1994	32.1	1652	53.0	20.1	1647	33.1	5.4	2074	11.2	2.3	1253	2.9	3.4	960	3.3	0.29	2833	0.83	0.4	3280	1.4
1995	35.5	1598	56.8	21.9	1673	36.7	6.5	1561	10.1	2.5	1403	3.5	3.6	980	3.6	0.25	3450	0.85	0.5	3115	1.4
1996	34.4	1613	55.4	21.3	1575	33.6	5.1	2069	10.6	2.4	1356	3.2	4.4	1053	4.6	0.30	3343	1.02	0.5	3085	1.6
1997	34.0	1612	54.8	20.6	1621	33.5	5.4	1914	10.4	1.9	1257	2.4	4.9	973	4.7	0.40	3712	1.47	0.5	3217	1.7
1998	33.4	1571	52.4	21.2	1586	33.5	4.3	1827	7.9	2.1	1262	2.7	4.5	931	4.2	0.44	3667	1.61	0.5	3277	1.7
1999	32.6	1631	53.2	19.7	1673	32.9	5.4	1741	9.5	1.7	1553	2.6	4.5	937	4.2	0.57	3079	1.74	0.5	3137	1.7
2000	31.6	1675	53.0	19.7	1675	33.0	5.3	1814	9.6	1.6	1899	3.0	4.0	937	3.8	0.46	3848	1.79	0.5	3166	1.6
2001	34.6	1739	60.2	21.1	1723	36.4	5.6	1998	11.2	1.8	2119	3.8	5.0	980	4.9	0.53	3715	1.96	0.5	3324	1.7
2002	30.8	1752	53.9	18.6	1806	33.6	5.0	1862	9.4	1.3	2166	2.8	4.9	939	4.6	0.41	4295	1.76	0.5	3409	1.6
2003	31.0	1796	55.7	19.5	1825	35.6	4.9	2063	10.0	1.3	2317	2.9	4.6	998	4.6	0.22	4156	0.93	0.5	2947	1.4
2004	35.0	2020	70.7	21.7	2080	45.2	5.3	2373	12.5	2.0	2488	5.0	5.3	1001	5.3	0.20	4254	0.84	0.5	3424	1.6
2005	34.7	2004	69.6	20.9	2077	43.4	5.6	2305	12.9	2.2	2219	4.8	5.2	965	5.0	0.32	4853	1.56	0.5	3505	1.6
2006	34.4	2070	71.3	22.0	2178	48.0	5.2	2262	11.7	1.7	2286	3.9	4.6	1003	4.6	0.34	4296	1.44	0.4	2708	1.2
2007	33.5	2197	73.6	22.3	2323	51.9	4.2	2393	10.2	1.9	2747	5.2	4.3	943	4.1	0.14	4799	0.69	0.4	2719	1.2
2008	31.0	2136	66.3	21.7	2262	49.0	3.1	2185	6.7	1.7	2941	4.9	4.2	964	4.0	0.06	5113	0.32	0.3	3140	1.0
2009	30.2	2046	61.8	21.7	2147	46.6	3.0	2106	6.4	1.3	2666	3.6	3.6	904	3.3	0.16	4848	0.80	0.3	3133	0.9
2010	31.8	2177	69.2	22.1	2274	50.2	4.3	2188	9.5	1.5	2677	4.0	3.3	1024	3.3	0.21	4508	0.94	0.3	2630	0.8
2011	34.5	2305	79.5	23.6	2344	55.3	3.8	2545	9.7	2.3	2828	6.5	3.6	1110	4.0	0.59	3731	2.20	0.4	2711	1.0
2012	34.7	2285	79.3	22.9	2351	53.9	3.8	2725	10.3	2.2	2753	6.0	4.7	953	4.5	0.60	4957	2.96	0.4	2725	1.0
2013	32.2	2267	73.1	22.1	2388	52.7	3.1	2498	7.6	1.5	2784	4.3	4.6	940	4.4	0.44	5532	2.46	0.3	3031	1.0
2014	34.7	2209	76.7	23.5	2232	52.5	3.8	2589	9.8	1.9	2998	5.6	4.6	1027	4.7	0.39	5478	2.14	0.4	2946	1.0
2015	31.9	2094	66.8	21.7	2111	45.8	3.3	2565	8.4	1.7	3003	5.1	4.5	911	4.1	0.20	6468	1.27	0.3	4287	1.5
2016	30.2	2165	65.4	19.5	2220	43.3	3.8	2612	10.0	1.6	2800	4.4	4.5	912	4.1	0.28	5416	1.52	0.4	3932	1.5

[a] Prod. = Production.

2016, and lint production has increased from 9.5 m tons in 1961 to 26.2 m tons in 2014 (FAO 2018). Historically, 2011 and 2012 were the years with the highest seed cotton production that was more than 79 m tons (FAO 2018). Total seed cotton production mainly comes from the Asia (~45 m tons) followed by the North America (~10 m tons), the South America (~5 m tons), Africa (~4 m tons), Australia (~1.52 m tons) and the Europe (1.5 m tons) (Table 1). Globally, the highest seed cotton yields come from the Australian continent (5416 kg/ha) followed by Europe (3932 kg/ha) while the lowest average seed cotton yield has been recorded from Africa (912 kg/ha). The global average seed cotton yield is around 2000 kg/ha, and the Asian continent has also a similar level of the average seed cotton yield.

The top 10 cotton producers in the world are China, India, the US, Pakistan, Brazil, Uzbekistan, Turkey, Australia, Greece, and Turkmenistan (FAO 2018). Cotton cultivation area in China has decreased from ~6 m ha in 2007 to 3.4 m ha in 2016, and total seed cotton production has been decreased from ~23 to 16 m tons during the same time period (Table 2). However, average seed cotton yield has been increased in China from 3860 kg/ha (2007) to 4748 kg/ha in 2016. During the last decade, the cultivation area, seed cotton production and average yield faced only slight variations in India, the United States and Pakistan. Among these, the highest seed cotton yield has been noted in the United States (~2500 kg/ha) followed by Pakistan (~2000 kg/ha) and the India (1400 kg/ha) (Table 2).

1.3 USES AND PRODUCTS OF COTTON

Seed cotton is delinted in the gins to obtain lint, cottonseed, and trash. Complete details of the cotton ginning process have been provided in Chapter 8 of this book. The fiber obtained from cotton is a raw material for the textile industry. The seed can be extracted to get oil (nearly 20% of seed is oil); this oil can be used to produce vegetable oil, margarine, and soaps, etc. (Proto et al. 2000).

Textile is one of the biggest industries of the world that turn cotton fiber into a variety of products. A few examples may include garments, underwear, towels, carpets, or sheets, socks, t-shirts, fishnets, coffee filters, book binding, and archival paper.

Several by-products of seed cotton are obtained along with the major cotton product (fiber). Post ginning byproducts of seed cotton (e.g. cottonseed cake) could be used as animal feed and for the production of biofuel (Holt et al. 2000; Rogers et al. 2002; Plácido et al. 2013). Production of biofuel from cotton may cause some environmental problems (Lima et al. 2017).

1.4 HISTORY AND EVOLUTION OF COTTON

Cultivated cotton belongs to the genus *Gossypium* that has 54 species which usually grow in the arid and semi-arid regions of tropical climate. Out of 54 *Gossypium* species, only four are cultivated, i.e. *G. hirsutum, G. barbadense, G. herbaceum,* and *G. arboreum*. The former two are tetraploid whereas the latter two are diploid. The evolutionary history of cotton is very interesting and includes trans-oceanic mating of parental species as diploid progenitors of tetraploid cotton belongs to different continents. Tetraploid species contain AADD genome and were discovered from the new world (America) in which the A genome originated from Africa and Asia, and the D genome has new world origin. Here

Table 2 Area (m ha), seed cotton production (m tons), and seed cotton yield (kg/ha) in the major cotton producing countries of the world (FAO 2018).

	China			India			United States			Pakistan		
Year	Area	Seed cotton production	Seed cotton yield	Area	Seed cotton production	Seed cotton yield	Area	Seed cotton production	Seed cotton yield	Area	Seed cotton production	Seed cotton yield
2007	5.9	22.9	3860	9.4	13.8	1461	4.2	10.2	2393	3.1	5.7	1859
2008	5.8	22.5	3906	9.4	11.8	1258	3.1	6.7	2185	2.8	5.8	2046
2009	5.0	19.1	3863	10.3	12.8	1238	3.0	6.4	2106	3.1	6.3	2040
2010	4.8	17.9	3694	11.1	17.8	1594	4.3	9.5	2188	2.7	5.6	2088
2011	5.0	19.8	3924	12.2	19.2	1575	3.8	9.7	2545	2.8	6.6	2330
2012	4.7	20.5	4377	12.0	18.2	1517	3.8	10.3	2725	2.9	6.4	2211
2013	4.3	18.9	4356	11.7	18.9	1618	3.1	7.6	2498	2.7	6.2	2272
2014	4.2	18.5	4390	13.1	18.5	1413	3.8	9.8	2589	3.0	6.8	2302
2015	3.8	16.8	4468	11.9	16.0	1349	3.3	8.4	2565	2.9	4.9	1679
2016	3.4	16.0	4748	10.5	14.4	1373	3.8	10.0	2612	2.5	4.9	1986

the question arises that how two genomes belonging to two different continents joined together to form a tetraploid cotton even before the discovery of the new world. There are different theories about hybridization of the genome of two continents but most authentic theory is that the progenitor genome of tetraploid cotton, i.e. A and D genome diverged at between 5 and 10 million years ago and about 1–2 million years ago trans-oceanic dispersal of maternal A genome, which is very much similar *to G. herbaceum* and D genome which resembles to *Gossypium raimondii* followed by hybridization and chromosome doubling give rise to tetraploid *Gossypium* species with spinnable fiber evolved from A genome (Senchina et al. 2003; Paterson et al. 2012). The newly developed AADD genome diverged into at least seven species (seven known tetraploid species of *Gossypium*, i.e. *G. hirsutum, G. barbadense, Gossypium darwinii, Gossypium mustelinum, Gossypium lanceolatum, Gossypium caicoense* and *Gossypium tomentosum*). Interspecific hybridization followed by genome doubling has led to the molecular genetic interactions and deletion, duplication, and translocations in the genome with a change in gene expression which makes possible the evolution of new world tetraploid cotton.

This theory of AADD cotton development is further strengthened by the gene sequence data of tetraploid cotton. It is revealed from gene sequence data that allotetraploid species of cotton originated during mid-Pleistocene, at the time when continents were not completely isolated geographically (Wendel et al. 1989; Flagel et al. 2012). Characterization of mitochondrial and plastid DNA revealed that during hybridization of two genomes, "A" genome served as the maternal parent (Wendel et al. 1989; Xu et al. 2012; Li et al. 2014). Then by some biological phenomenon or by chance, hybridization of two genome occurs and hybrid might be sterile due to the incompatibility of two genomes to pair up. This may lead to polyploidization of newly developed hybrid and first form of modern tetraploid cotton. After polyploidization, diversification of polyploids took place rapidly (Wendel and Grover 2015). Due to diversification and adaptation to different climates, changes in gnome occurred, which led to speciation.

Gossypium species spread all over the world but it has maximum diversity in Kimberley region in NW Australia, Horn of Africa, southern Arabian Peninsula and central and western Mexico. Although only four species have been domesticated, all wild species have parallel evolution and genetic diversity. This genetic diversity in wild species has been often used by plant breeders to develop new cotton genotypes (Liang et al. 1978; Adams and Wendel 2005; Iqbal et al. 2017). Four species of *Gossypium* (two tetraploids, i.e. *G. hirsutum* and *G. barbadense* and two diploids *G. herbaceum* and *G. arboreum*) domesticated independently and parallel, i.e. two in America and two in Africa and Asia for single cell trichrome (Brubaker and Wendel 1994; Liu and Wendel 2002). Wild relatives of all four cultivated species are a perennial shrub and were traditionally grown as summer crops, but with time they were domesticated as an annual crop. Unique properties of fiber (spin-able fiber) were discovered by Aboriginal people, which make it a valuable crop from ancient times (Wendel and Cronn 2003).

Archeological records showed that the earliest species of cotton to be domesticated was *G. arboreum* in the Indus valley (Pakistan) by Harappan civilization. Similarly, the archeological record showed that a major trade of the Mohenjo Daro civilization was based on cotton fiber (Moulherat et al. 2002). Due to the tropical and subtropical climate nature of the crop, it could not spread outside of the Indian subcontinents until thousands of years after its domestication (Brite and Marston 2013). Domestication of *G. herbaceum* has not been traced out by archeological records, but the distribution of its wild relatives suggests that it was domesticated in north and eastern Africa.

It is evident from archeological records that *G. hirsutum* was first domesticated in the Tehuacan Valley of Mexico dated between 3400 and 2300 BCE. Recent genetic studies showed that it was originally domesticated in the Yucatán Peninsula of Mexico in the same period. Parallel to this *G. barbadense* is believed to be domesticated in Ancón-Chillón area of the central coast of Peru (d'Eeckenbrugge and Lacape 2014). In different Mesoamerican cultures, cotton was a precious exchange item and Mayan and Aztec kings used to present cotton products to Noble guests and army leads. With the period of time, selection, and genetic improvements have changed many aspects of the crop including yield and fiber traits.

Currently, more than 98% of the world's cotton fiber is produced from new world tetraploid species, but before the nineteenth century other species like *G. herbaceum* and *G. arboreum* also had a major share.

1.5 GENETIC IMPROVEMENT IN COTTON

As it is well known that wild relatives and progenitors of cotton are bushy plants with a perennial growth habit but in recent times cotton is grown as an annual crop. Since its known history, a lot of genetic improvement has been made in cotton germplasm regarding its growth habit, yield, fiber quality, and tolerance to biotic and abiotic diseases which are briefly discussed here.

Cotton is a perennial crop with an indeterminate growth habit, which means that reproductive and vegetative growth progress side by side. This makes it difficult to harvest and manage. A lot of plant growth regulators have been developed that slow down the vegetative growth and promote reproductive growth for better yields. The use of plant growth regulators can promote early reproductive growth and early harvesting, thus shifting growth habit to annual (Pettigrew and Johnson 2005; Cothren and Oosterhuis 2010).

Seed cotton yield has been improved dramatically in the last 100 years. In 1920–1921 average seed cotton yield of the world was only 219.4 kg/ha which crossed 300 kg/ha in 1960 and in 1991 it was about 600 kg/ha and in the next 20 years it improved up to 760 kg/ha. Historically, the highest seed cotton yield was recorded in 2013–2014 where it touched 1800 kg/ha (USDA 2018a). Low yields have been recorded in developing countries and the highest yields have been recorded in the Australian region (ICAC 2017). There was a huge difference between the lowest and the highest yields, i.e. in Australia and New Zealand yield was recorded as 2300 kg/ha and in eastern Africa, it was 250 kg/ha (ICAC 2017). There are various factors involved in the improvement of seed cotton yield which include improvement in genetic potential, the introduction of new world genotypes into the old world, insect pest resistance, development of *Bt* cultivars, and development of genotypes with more response to fertilizer and irrigation. Genetic improvement in cotton has been made in various ways which are discussed here.

1.5.1 Genetic Improvement for Yield and Fiber Traits

Genetic improvement in seed cotton yield has been mainly brought through selection and hybridization of the available germplasm. As more than 98% cultivated cotton belongs to tetraploid cotton, therefore, it will be our main focus of discussion.

Seed cotton yield is a complex trait and depends on many morphological and physiological traits which contribute to the yield. Zhang et al. (2005) reported that seed cotton yield and lint yield of Acala cotton in the USA improved steadily since 1930. They analyzed experimental data of the last 30 years in China and reported that yield and yield-related traits were improved through the years, i.e. improvement of yield traits in new varieties compared to the previous one was 24.3% in lint yield, 3.49% in bolls per plant, and 2.80% in the lint percentage. Genetic variability in the germplasm plays a vital role improvement in any crop, because crossing of diverse genotypes gives a chance to a combination of required traits in one genotype. Green and Culp (1990) reported simultaneous improvement in yield and fiber traits through inter-mating of several diverse genotypes. They further suggested testing the general combining ability of genotypes before being used in a breeding program.

Cotton is mainly grown for fiber, which is a function of the seed epidermal cells. Manipulations of different hormones in the cell have an effect on fiber yield and quality. It was reported that fiber yield and quality can be enhanced by manipulating the auxin biosynthesis in epidermal cells. In a four-year field experiment, transgenic plants having more capability of auxin biosynthesis in epidermal cells produced 15% more fiber yield with notably improved fiber quality (Zhang et al. 2011a). Involvement of gibberellins in fiber development has also been reported. Transgenic plants with more capability to produce gibberellins in epidermal cells produced significantly more fiber with better quality than control (Xiao et al. 2010). Various other hormones synthesized in epidermal cells has been reported to have a share in fiber development (Luo et al. 2007; Lee et al. 2010). Overexpression of the genes responsible for these hormones improved fiber yield and quality. Looking at the world's cotton demands, research is needed for commercialization of such genotypes with more fiber yield and quality.

Along with conventional breeding, modern techniques in plant breeding like marker-assisted selection (MAS) have made it easy to select genotypes with high yield and better quality. Various markers and quantitative trait loci (QTLs) have been identified closely linked with the yield and fiber quality that made selection possible at the early stages of plant development, which save time and money. Shen et al. (2007) developed a genetic linkage map by using a series of recombinant inbred lines (RILs) of upland cotton and identified 25 major QTLs linked with fiber yield, seed cotton yield and fiber quality out of which four QTLs had a major effect on fiber quality and seven QTLs had a major effect on seed cotton yield, whereas all other QTLs had more or less equal contribution both on fiber yield and quality. Paterson et al. (2003) constructed a genetic linkage map of cotton under water stress and full water conditions. He reported 14 QTLs for water stress conditions which were responsible for fiber yield and quality and only two QTLs under well-watered conditions. Presence of more QTLs under water stress conditions depicts complicated genetic control of fiber yield and quality traits under water stress conditions than in well-watered conditions. Identification of QTLs facilitates MAS selection, as genotypes are selected on the basis of markers linked to QTLs without field evaluation. Lacape et al. (2005) analyzed various QTLs for fiber yield and quality and identified 19 QTL-rich chromosomal regions on 15 chromosomes which may be used as target regions for MAS.

1.5.2 Genetic Improvement for Biotic and Abiotic Stress Tolerance

Insect pest, disease, and harsh environment are major reasons for low yield of high genetic potential genotypes. Various management strategies have been devised to diminish the effect of these stresses which ranged from agronomic amendments to exogenous application of hormones and pesticides. But the most sustainable and economic strategy is to develop genotypes tolerant to the stresses. Normally only a few types of stresses may prevail in one region so for producing tolerant genotypes for a specific region may not be too difficult a job.

Insect pests, especially boll worms remained the biggest threat to cotton production throughout the world until the commercialization of *Bt* cotton cultivars in the late 1990s and early 2000s (Pray et al. 2002). With the passage of time, insect pests (most importantly *Helicoverpa armigera*) have developed some tolerance against *Bt* toxin (Tabashnik et al. 2013). To overcome these, double-gene genotypes have been developed (Cui et al. 2011) which has improved resistance to cotton boll worms.

Besides boll worm, epidemic conditions of various diseases have destroyed millions of acres of cotton, which have been overcome by the development of resistant cultivars. Cotton leaf curl virus disease (CLCuD) has been known as one of the most important diseases of cotton and was first noted in Pakistan in the 1960s. But it was not epidemic until 1992 when it caused huge losses to cotton production in the country and losses to Pakistan economy were around US$ 5 billion (Briddon and Markham 2000). In a few years of research in conventional plant breeding, scientists had developed genotypes which were tolerant to this disease (Briddon 2003). Among fungal diseases, fusarium wilt and verticillium wilt are the two most important diseases for cotton. These two diseases caused huge losses to cotton yield and later also destroyed the quality of the fiber (Paul 2002). Black root rot and bacterial blight are other important diseases which caused significant losses to the cotton-based economy of the world (Bell and Stipanovic 1978). By genetic manipulation and breeding of existing germplasm and introgression from wild relatives, these diseases have been controlled and even with favorable conditions of the disease, cotton varieties survived.

With climate change, abiotic stresses are a main concern to the cotton production. Crop yield reductions due to climate change factors like drought and heat and salinity, etc. are not easy to manage and have become a threat to cotton production. These abiotic stresses can be managed agronomically or genetically. Agronomic management needs extra resources at the farm level, whereas genetic management requires extra resources only at the research level, as once a tolerant genotype has been produced, it can perform equally both in stress and non-stress condition without any extra management.

Cotton is an often cross-pollinated crop due to abundant insect population which makes it a relatively heterozygous crop. Due to its heterozygous nature, there is a potential for hybrid development for this crop. Soomro (2000) reported 32–38% heterosis against commercial genotypes and proposed hybrid development in cotton. China is a pioneer in the hybrid development for this crop. Dong et al. (2004) developed a hybrid between a *Bt* and a non-*Bt* cotton lines and reported 20% enhanced yield of hybrid in northern China. Hybrid cotton not only improves yield but also improves resistance against insects. A long-term study (Wan et al. 2017) reported that a hybrid of *Bt* and non-*Bt* cotton can resist the attack of pink boll worm which is the most divesting to the cotton crop. Thus, hybrid development in cotton can be exploited not only for yield, but also for resistance to biotic and abiotic stresses and fiber traits. A list of varieties and hybrids developed resistant to different biotic and abiotic stress and for high yield in different countries has been given in Table 3.

Table 3 List of cotton cultivars/hybrids developed in different regions of the world to combat various biotic and abiotic stresses.

Sr. No	Variety	Country	Resistant/tolerant against	Reference
1	Bollgard cotton	USA	Bollworms	Perlak et al. (2001)
2	GK-12	China	Bollworms	Pray et al. (2002)
3	CCRI 29	China	Bollworms	Dong et al. (2004)
4	NuCOTN 33B	Australia	Bollworms	Knox et al. (2006)
5	HSP1	Pakistan	CLCuD	Akhtar et al. (2015)
6	Auriga-213	Pakistan	CLCuD	Akhtar et al. (2015)
7	Z-33	Pakistan	Bacterial blight	Sajid et al., (2017)
8	SG1	China	*Verticillium* wilt	Wang et al. (2016)
9	SG4	China	*Verticillium* wilt	Wang et al. (2016)
10	UK 08	Tanzania	*Fusarium* wilt, jassid, bacterial blight	Faustine et al. (2016)
11	BRS Cedro	Brazil	Cotton blue disease, *Ramularia areola*, bacterial blight	Faustine et al. (2016)
12	FH-118	Pakistan	Drought and heat stresses	Iqbal et al. (2017)
13	IUB-QM-65	Pakistan	Drought and heat stresses	Iqbal et al. (2017)
14	IUB-63	Pakistan	Heat stress	Iqbal et al. (2017)
15	Deltapine 61	USA	Drought stress	Penna et al. (1998)
16	Coker 348	USA	Drought stress	Penna et al. (1998)
17	DAK-66/3	Turkey	Drought stress	Sezener et al. (2015)
18	CZ91	China	Salinity stress	Wang et al. (2017)
19	Zhong 07	China	Salinity stress	Guo et al. (2015)
20	TX2285	USA	Heat	Wu et al. (2014)
23	RCHB 708 (Hybrids)	India	Sub-optimal conditions	Sankaranarayanan and Nalayini (2015)

1.6 ROLE OF BIOTECHNOLOGY AND GENETIC ENGINEERING IN IMPROVING COTTON

Genetic engineering is an application to alter the inbuilt information of DNA by adding, changing, or excising genes in it. The modification of this information results in the amount or type of proteins naturally produced in organisms. Genetic engineering has widespread applications varying from drug development, enhanced agriculture productivity, food processing, and friendly environment to the chemical and pharmaceutical industries and human gene therapy (Gasser and Fraley 1989).

Biotech crops are produced either by direct transformation or by in direct transformation methods. Micro projectile bombardment and protoplast transformation are among the most applied direct transformation methods. On the other hand, indirect transformation is dependent on the use of the binary vector for inserting a gene into a plant cell. Most common vector is *Agrobacterium tumefaciens*, while agrobacterium rhizogenes can also be used (Dai et al. 2001). In addition electroporation of cells and tissues, infiltration, liposome-mediated transformation, microinjection, silicon carbide fiber-mediated transformation and transformation via the pollen-tube pathway are also among transformation techniques (Zhu et al. 1993; Vasil 1994; Songstad et al. 1995; Newell 2000; Rao et al. 2009).

Cotton is one of the most important crops being cultivated for feed (livestock), food, fiber, oil, and cotton cake (Keshamma et al. 2008). Cotton breeders always look for better cotton varieties and they keep on using conventional breeding methods for this purpose (Agrawal et al. 1997). The cotton crop is exposed to many issues including biotic (pests, insects, weeds, viruses) and abiotic stresses (drought and salinity) (Poehlman 1987; Bakhsh et al. 2015).

A breakthrough in cotton research came when the first genetically modified cotton was reported by two groups working independently in 1987. They transferred phosphotransferase (*npt II*) and confirmed their results by molecular analysis (Firozabady et al. 1987; Umbeck et al. 1987). This opened the era of biotech cotton (Haq 2004). Cotton faces challenges during its reproductive growth; biotic and abiotic stresses limit the yield of crop significantly. Highly toxic pesticides are being used to combat losses from pests which are an ultimate danger for the environment and for human health (Bakhsh et al. 2012). There is a strong need to address the increasing use of hazardous insecticides, herbicides, etc. In addition, improved fiber quality became the need of time after development of the synthetic fiber industry (Li et al. 2009a, b; Bajwa et al. 2013).

1.7 BIOTECH COTTON AGAINST BIOTIC AND ABIOTIC STRESSES

1.7.1 Insect Resistant Cotton

Agricultural crops are under a continuous threat by insect pests and diseases which are responsible for an ultimate loss of 37% of worldwide agricultural production with insects alone causing 13% loss (Gatehouse et al. 1992). Utilization of genetic engineering for moving a distant gene into crop plants has enabled scientists to develop resistance against insects and pests (Lycett and Grierson 1990; Dhaliwal et al. 1998). The insecticidal protein produced by *Bacillus thuringiensis* is lethal to selected insect pests, i.e. coleopterans (Krieg et al. 1983; Herrnstadt et al. 1986), dipterans (Andrew et al. 1987), and lepidopteron (Hofte and Whitely 1989; Cohen et al. 2000). At the same time, it is not toxic for beneficial insects, animals, and humans (Yamamoto and McLaughlin 1981).

Insect resistance in cotton was introduced by researchers at Monsanto Company (United States) by introducing Bt genes (*cry1Ac*) into cotton plants (Coker-312). Field trials proved that plants showed considerable resistance against cotton bollworm (*Helicoverpa zea*) (*Pectinophora zea*) and the pink bollworm (*Pectinophora gossypiella*) (Perlak et al. 1991). Different types of cry genes have been introduced in cotton by researchers to encode resistance against target insect pests (Table 4) (Perlak et al. 1990; Majeed et al. 2000; Leelavathi et al. 2004; Wu et al. 2005; Guo et al. 2007; Hussain et al. 2007; Katageri et al. 2007; Rashid et al. 2008; Siebert et al. 2008; Tohidfar et al. 2008; Khan et al. 2011; Bakhsh et al. 2012; Kiani et al. 2013).

In addition to *cry1* gene, researchers have also introduced some other genes, for example, vegetative insecticidal protein (VIP) genes from bacillus species including VIP1, VIP2, and VIP3 genes in cotton plants. Among these genes, VIP3 showed remarkable insecticidal activity against lepidopterans of maize and cotton (Estruch et al. 1996; Fang et al. 2007).

Although cotton bollworms are among the most devastating cotton pests, some other insects including jassids, aphids, and whiteflies also ruin a major quantity of crop (Amudha et al. 2011). Bt genes could not provide resistance against these sap sucking pests. Plants naturally defend from these by synthesizing proteins, i.e. lectins and protease inhibitor

Table 4 Summary of some important insect-resistant cotton crops developed using *Bt* as well as non-*Bt* gene sources.

Sr. No.	Gene introduced	Target insect pest	Reference
1	*cry1Ac + cry1Ab*	*Helicoverpa zea and Spodoptera exigua*	Perlak et al. (1990)
2	*cry1Ab*	*Helicoverpa armigera*	Majeed et al. (2000)
3	*cry1Ia5*	*Heliothis armigera*	Leelavathi et al. (2004)
4	*cry1Ac*	*Heliothis armigera*	Wu et al. (2005)
5	*cry1Ac*	*Helicoverpa armigera*	Katageri et al. (2007)
6	*cry1Ac*	*Heliothis armigera*	Hussain et al. (2007)
7	*cry1C, cry2A, cry9C*	*Helicoverpa armigera*	Guo et al. (2007)
8	*cry1F*	*Spodoptera frugiperda*	Siebert et al. (2008)
9	*cry1Ac + cry2A*	*Heliothis armigera*	Rashid et al. (2008)
10	*cry1Ab*	*Heliothis armigera*	Tohidfar et al. (2008)
11	*cry1Ab*	*Heliothis armigera*	Khan et al. (2011)
12	*cry1Ac*	*Heliothis armigera*	Bakhsh et al. (2012)
13	*cry1Ac*	*Heliothis armigera*	Kiani et al. (2013)

Table 5 Important herbicide-tolerant cotton trait.

Herbicide Resistant Cotton	Herbicide Tolerant Gene	Commercialization Trait	Commercialization year
Glyphosate	CP4 EPSPS	MON1445/1698	1996
	Two CP4 EPSPS	MON88913	2006
	ZM-2MEPSPS	GHB614	2009
Glufosinate	PAT	A2704-12	2009

(Yarasi et al. 2008) mechanism. The inhibitory effect of protease inhibitors II genes against insect digestive enzymes has also been utilized by researchers using recombinant DNA technology to introduce resistance against insects in cotton plants (Majeed 2005). Plant lectins have been utilized as a resistance factor against various insects for crop protection. Binding of lectins with epithelial cells of mid gut seems to be a reason to mediate a toxic effect on insects. It may either act by inhibiting nutrient absorption or by disrupting mid gut cells (Czalpa and Lang 1990). Many researchers have used this phenomenon for producing insect resistant crops including cotton (Rao et al. 1998; Hussain 2002; Yao et al. 2006; Yarasi et al. 2008; Vajhala et al. 2013).

1.7.2 Herbicide Resistant Cotton

Herbicide resistant cotton has revolutionized weed management practices and has been proven to be an important tool in crop protection. Herbicide resistance in cotton has been introduced mainly by making it glyphosate tolerant, which has increased farm productivity (Chen et al. 2006; Zhao et al. 2006; Cerny et al. 2010; Tong et al. 2010; Green 2012). Glyphosate resistant crop cultivars (including those of cotton) have been developed by using the gene EPSPS that has been isolated from CP4 strain of agrobacterium (Padgette et al. 1996). In later years glufosinate resistance was also introduced in cotton (Daud et al. 2009; Table 5).

Commercial availability of herbicide tolerant cotton has made its adoption easy to farmers. Some of the commercially available herbicide resistant cotton varieties are mentioned in Table 5 (reviewed in Bakhsh et al. 2015).

1.7.3 Wilt-resistant Biotech Cotton

Fungal diseases are also among one of the major biotic stresses for cotton crop in addition to insect pests and weeds. Most common fungal diseases are furasium wilt (caused by *Fusarium oxysporum*) and verticillium wilt (caused by *Verticillium dahlia*) and most of the upland cotton varieties are susceptible to verticillium wilt (Klosterman et al. 2009; Ganesan et al. 2009; Miao et al. 2010).

Biotech cotton resistant to fungi has also been developed by using genetic engineering technology. Transgenic cotton showing resistance to *Verticillium dahliea* has been reported by many researchers who used different genes in their studies (Wang et al. 2004; Rajasekaran et al. 2005; Tohidfar et al. 2005; Miao et al. 2010; Munis et al. 2010; Parkhi et al. 2010a, b; Tian et al. 2010; Zhang et al. 2011b; Zhang et al. 2012a, b).

1.7.4 Virus-Resistant Biotech Cotton

In the past few decades, cotton leaf curl disease (CLCuD) has emerged as a major threat to cotton growers. It is caused by begomoviruses of the Geminivirdae family. The virus is transmitted by white flies (*Besmisi tabaci*) (Rahman et al. 2012). Management of viral disease by the development of CLCuD resistant cotton is environmentally safe (Beachy 1997). Transgenic cotton resistant to CLCuD was developed by antisense RNA expression using antisense coat protein (ACP) (Amudha et al. 2011). An RNAi-mediated approach has also been successfully implemented by researchers to target CLCuD (Chakrabarty et al. 2010; Yasmeen et al. 2016; Ahmad et al. 2017).

1.8 BIOTECH COTTON WITH ENHANCED RESISTANCE AGAINST ABIOTIC STRESS

Abiotic stresses, especially drought and salinity are expected to cause salinization of land (more than 50%) by 2050 (Ashraf 1994). Breeders have implemented conventional plant breeding methods to produce drought tolerance in cotton plants, but it is a lengthy process. Genetic engineers have tried to develop biotech crops by introducing genes encoding tolerance to chilling stresses, drought, and salinity (Lata et al. 2011; reviewed in Bakhsh 2014; Table 6).

Table 6 Biotech cotton with enhanced yield under drought stress.

Gene(s)	Gene source	Abiotic stress type	References
Beta	*Eschercia coli*	Drought	Lv et al. (2007)
TsVP	*Thellungiella halophila*	Drought	Lv et al. (2009)
Osmotin	Tobacco	Drought	Parkhi et al. (2009)
AVP1	*Arabidopsis thaliana*	Drought and salt	Pasapula et al. (2011)
SNAC1	Rice	Drought and salt	Liu et al. (2014)
AtEDT1/HDG11	*A. thaliana*	Drought and salt	Yu et al. (2015)
ScALDH21	*Syntrichia caninervis*	Drought	Yang et al. (2016)

1.8.1 Drought Resistant Biotech Cotton

Drought is the major devastating abiotic factor which affects the production and quality of crops; it has become even more important due to increasing global climate change (Boyer 1982; Araus et al. 2002; HongBo et al. 2005). Up- and downregulations of genes for protein expression is used by plants to combat multiple abiotic stresses which ultimately causes alteration of various biological functions (Deeba et al. 2012). So regulating the genes responsible for draught stress is a key factor in developing draught resistant plants (Hozain et al. 2012). Many genes have been identified which are involved in drought stress in plants (Park et al. 2004).

Scientists have used genetic engineering technology either to introduce drought-tolerant genes from different plants into cotton (Vierling 1991; Joshi and Nguyen 1996; Yue et al. 2012; Mittal et al. 2014) or by increasing or decreasing the expression of some proteins (Maqbool et al. 2010; Shamim et al. 2013). Table 6, summarizes some of these drought-tolerant cotton strategies. But all of these are lab experiments or greenhouse trials. Field studies did not give appreciable results yet and more research is needed in this regard.

1.8.2 Salt Tolerant Biotech Cotton

Salinity is among the major devastating abiotic stresses, affecting nearly 20% of the cultivated area worldwide (Zhu 2001). Although cotton is among the salt-tolerant crops, but during the time of germination its seedlings are susceptible to saline conditions (Ashraf 2002). Osmotic stress as a result of increased salinity results in the senescence of leaves (with accumulated salts) and also affects the growth of cotton plants (Munns 2002; Pic et al. 2002). Researchers have attempted to produce biotech cotton plants by delaying the senescence of leaves. It has been achieved by the introduction of isopentenyl transferase (*IPT*) gene (which is capable of delaying leave senescence and enhancing salt tolerance) by Agrobacterium mediated transformation (Liu et al. 2012).

The role of glycinebetaine is also reported to be very crucial for the management of abiotic stresses in plants (Meek and Oosterhuis 2000; Blunden et al. 2001; Farooq et al. 2008; Hussain et al. 2008, 2010). The induction of salt tolerance in cotton plants is reported by the over-expression of genes coding glycinebetaine (Lv et al. 2007) and choline oxygenase (Zhang et al. 2009).

1.9 CONCLUSIONS

Global cotton cultivation area has been nearly stagnant, while total seed cotton production has increased over time. China, India, the United States, Pakistan, and Brazil are the leading cotton-producing countries. With domestication and the development of high yielding cultivars, the genetic base of cultivated cotton become narrow, which give rise to various threats of susceptibly of biotic and abiotic stresses. Drought stress, insect pests, diseases, and weed infestation have been the major factors that cause a great decline in cotton productivity in major cotton-producing countries. These stresses can be overcome by transgenic means (development of transgenic cultivars like *Bt* cotton) or by introgression of a tolerant/resistant gene from wild relatives. Introduction of genetically modified (insect pest and herbicide resistant) cotton cultivars has significantly increased seed cotton production by providing improved control of insect pests and weeds. Genetic improvement in cotton is a continuous process for high lint yields in a changing climate.

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