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Current genetic research in cotton in India

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Abstract

Genetic research on cotton in India in recent times is reviewed. Establishment of a gene bank with global accessions of the four cultivated species, as well as wild relatives, has facilitated genetic improvement of cotton in India. Genetic control of the economic traits has been studied by biometrical approaches, particularly the line × tester analysis, diallel cross and generation mean analysis. Both additive and non-additive gene actions have been reported for most of the traits. Heritability estimates are low to high. Studies on G × E interaction and stability parameters indicate availability of lines which are stable in their performance over locations and seasons. Genetic improvement of yield, fibre properties, lint percent, seed oil, earliness and resistance to key pests and diseases has been targeted and considerable success has been achieved. Single cross, three-way cross, multiple cross, back cross, biparental mating, mutation breeding and heterosis breeding are the main procedures employed for improvement of yield. Heterosis breeding has, however, made the most significant contributions in improvement of both yield and fibre quality in recent times. While resistant genotypes have been developed for most of the pests and diseases, resistance against cotton bollworms has not been achieved. Genetic engineering to incorporate the *Bt* gene in cotton to impart resistance to bollworms is in progress. Keeping in view the increased requirements of cotton in the future, thrust areas in genetic research have been indicated.

Introduction

Cotton is an important industrial crop of India, providing 80% of the raw material for the textile industry of the country. All the four cultivated species, *Gossypium hirsutum*, *G. barbadense*, *G. arboreum* and *G. herbaceum*, are grown. They are grown in varied agroclimates in northern, central and south India from 9°N latitude to 31°N latitude. While cotton in the north is almost entirely irrigated, cotton in central and south India is predominantly rainfed.

Genetic research in cotton in India began at the dawn of the present century funded by the provincial governments of the states growing cotton. Later, the Indian Central Cotton Committee and, with its dissolution, the Indial Council of Agricultural Research and State Agricultural Universities, sponsored genetic research in cotton.

The earlier genetic research has been comprehensively reviewed by Sikka and Joshi (1960) in the monograph 'Cotton in India'. Basu (1983a) and Singh and Raut (1983) have also reviewed genetic research in cotton in India up to the late seventies. In the current review, therefore, an attempt has been made to give greater coverage to the work done in recent times.

Genetic resources

Genetic improvement of cotton in India has been facilitated recently by establishment of a gene bank at Central Institute for Cotton Research, Nagpur. The gene bank has global accessions of 4005 (*G. hirsutum*), 390 (*G. barbadense*), 1701 (*G. arboreum*), 400 (*G. herbaceum*), 24 (wild species) and about 400 involving perennials and sterile hybrids of various species. These genetic stocks are maintained, evaluated, documented and distributed to all who are engaged in cotton improvement. Standard descriptors brought out by the International Bureau of Plant Genetic Resources, Rome, were used in developing germplasm evaluation index cards. Evaluation was done for major morphological, economic and fibre properties for most of the accessions (Anonymous, 1989b). The germplasm shows a wealth of variability for various economic traits (Table 1); these are being used for genetic improvement of cotton in India.

Genetic research on cotton

Genetic research in four cultivated species of cotton in India in recent times has been aimed at the genetics of characters to aid breeding for improvement of yield through increase in boll number and boll weight, improvement of ginning outturn, improvement of fibre quality to suit current spinning processes, early maturity and resistance to major pests and diseases. Genetics of cotton seed oil has also been extensively studied.

Early maturity

The genetics of five characters related to earliness in cotton, days to first flowering, position of first sympodia and Bartlett's earliness index, were studied by Kenchangender, Salimath and Khadi (1994). They found a preponderance of additive variation in all the characters except days to first flowering, where both additive and non-additive variations were equally important. Chinnadorai, Rangaswamy and Menon (1973) and Kadapa (1975) also reported additive gene action for Bertrett's earliness index. Many other researchers, including Gupta and Singh (1970), Peter *et al.* (1973), and Patil and Chopde (1983a) reported additive gene action for inheritance of days to 50% boll opening and days to first boll bursting. Higher heritability estimates were recorded. Estimates of heritability and expected genetic advance were reported high for days to first flowering in *G. barbadense* cotton by Vadne and Thombre (1982).

It has therefore been concluded by the authors that breeding methods like pedigree or progeny testing would be required to improve this trait. However, Singh, Mor and Paroda (1987) found both additive and non-additive components of variance to be important for all the indices of earliness and suggested reciprocal recurrent selection for exploiting both types of genetic variances.

Genetic improvement for earliness has been achieved in all four cultivated species of cotton. This has helped in double and multiple cropping of cotton with other crops in irrigated areas, enabling the cotton to escape later drought in rainfed areas and late season pests like pink bollworm both in irrigated and rainfed areas.

The cultivation of *Gossypium barbadense* has not been possible in north India so far, due to susceptibility to pink bollworm, which is a consequence of late maturity. Development of short duration, short statured *G. barbadense* cottons by selection from exotic germplasm of the species in recent times at the Indian Agricultural Research Institute, New Delhi, brings hope of its cultivation in north India (Singh *et al.*, 1991, Singh, Singh & Lal, 1993).

Disease and insect pest resistance

Cotton is extremely vulnerable to a large number of insect pests and diseases, accounting for considerable loss in yield. The important insect pests and diseases are jassids (*Amrasca bigutulla bigutulla*), aphids (*Aphis gossypii*), whitefly (*Bemisia tabaci*), spotted bollworm (*Earias vitella* and *E. insulana*), American bollworm (*Helicoverpa armigera*), pink bollworm (*Pectinophora gossypiella*), and bacterial blight (*Xanthomonas malvacearum*), grey mildew (*Ramularia areoli*), wilt (*Fusarium oxysporum*) and root rot (*Rhizoctonia bataticola* and *Macrophomina phaseoli*) respectively. Farmers rely mainly on pesticides for management of the above mentioned insect pests and diseases. Cotton, occupying only 5% of the cultivated area in India, consumes 53% of the pesticides used in agriculture in India (Basu, 1994a). One of the reasons for this is, while resistant/tolerant genotypes have been developed against sucking pests for many cotton growing regions, resistance against bollworms and several diseases has not been achieved to the desired extent.

The genetics of jassid resistance has been studied by workers in India and elsewhere and has been reviewed by Sikka and Joshi (1960). Breeding for resistance to jassids using the genetic sources for resistance has produced jassid resistant varieties in several cotton growing states of India. Derivatives of a three-way cross

Table 1. Number of promising accessions for various economic characters.

Elite character types	*G. hirsutum*	*G. barbadense*	*G. arboreum*	*G. herbaceum*	Wild & perennial
Stable yield potential	360	11	300	31	–
Boll weight	135	5	150	20	–
Boll number potential	110	3	60	45	2
Seed index	330	10	40	20	–
Lint index	249	12	30	12	–
Ginners	120	15	150	40	–
Fineness mv 3–4	190	30	2	30	4
Span length	200	60	50	40	–
Fibre strength	145	50	180	55	5
Compact to medium plant	42	5	10	3	–
Sympodial branching	275	12	40	20	2
Seed oil content	65	10	60	25	–
Early maturity	30	3	75	10	–
Biomass potential	400	10	120	45	12
Harvest index	120	1	15	10	–
Seed number/boll	230	2	20	30	–
Long pedicel	35	–	–	–	2
Markers	185	10	30	2	–
Morphological resistance to pest, disease and nematode	250	10	Many	Many	50
Male sterile and restorer sources	22	–	2	–	3
Aerial rooted	1	–	–	–	–
Coarse absorbent types	15	–	100	10	–
Drought resistance potential	50	–	300	150	15
Naked seeded types	5	–	1	–	3
Delayed morphogenesis of gossypol	–	–	–	–	3
Chromosomal variants	–	–	–	–	77
Less gossypol gland types	60	–	10	5	–
Fuzzy types	100	–	200	50	4
Working collections	325	–	120	50	–

(Source: Narayanan *et al.*, 1990).

between wild *Gossypium tomentosum* having the *H2* hairy gene, CO2 and Indore 2 (*Gossypium hirsutum*), which deserve particular mention in this context, led to the breeding of jassid-resistant varieties Badnawar-1, Khandwa-2, SRT-1, B1007 and DHY 286 grown in central India. Some widely grown intra-*hirsutum* hybrids, AHH468, NHH-44 and JKHY-1, are resistant to jassids as one or both the parents of these hybrids have resistance to the pest. Resistance breeding against whitefly has commenced with the resurgence of this pest in several cotton growing areas recently. One of the reasons for this resurgence is the cultivation of hairy genotypes in those areas which are conducive to increased oviposition of whitefly. The glabrous leaved genotypes confer resistance to whitefly (Butter & Vir, 1989). Lines with narrow lobed (okra) thin glabrous leaves and early maturity overcome whitefly attack (Patel, 1987). Accordingly, several lines have been identified. Two of these LPS, 141 (Kanchana) and LK 861, have been released for commercial cultivation (Anonymous, 1989a). However, glabrous leaves of these two genotypes attract jassids, and since white-fly is no more a problem in the areas of cultivation of these two varieties, they are no more popular with the farmers. Biochemical factors responsible for both jassid and whitefly resistance have to be identified to circumvent this problem.

Crop maturity, morphological characters and biochemical factors have been reported to contribute to resistance to bollworms in cotton (Basu, 1988a). Early genotypes, such as B.N., H777, Ganganager Ageti, F414 and F286, have less incidence of pink bollworms compared to long duration varieties such as 320F, LSS and Pramukh, due to an escape mechanism. Similarly early maturing hybrids H6, NHH44, AHH468 and

G.Cot.Hyb 8 have less bollworm incidence compared to long the duration hybrid, Hybrid 4 (Basu, 1988a).

Bhat and Basu (1984), in their studies on the role of morphological characters on bollworm incidence in cotton in the $F_2 \rightarrow F_2$ population of a cross between two lines with contrasting characters, found red stem, frego bract and nectariless leaves to impart tolerance to bollworms. Frego bract and okra leaf was found to be tolerant to bollworms by Thombre (1980). A combination of characters, however, is more useful for resistance to bollworms (Kadapa, 1980). Cultures JK 276-4, JK 260, JK 344 and JK 345 having green, less hairy leaves, small bract, and thick boll rind with early maturity are less susceptible to bollworms. JK 276-4 has since been released as a cultivar 'Abadhita' for commercial cultivation.

The genetics of many of these morphological characters have been studied. While okra leaf and frego bract are controlled by single recessive genes, nectariless is controlled by duplicate recessive genes (Basu & Bhat 1984; Basu, Duhoon & Singh, 1974). While Ramachandran, Nagarajan and Peter (1961) and other researchers found red plant body to be controlled by a single dominant gene, Basu and Bhat (1984) found the interplay of two dominant genes to be controlling the character.

Phenolic compounds, tannin, gossypol, and heliocide present in the cotton plant are found to give tolerance to bollworms (Kadapa, 1980; Chakravarty, Basu & Sahni, 1981; Sharma, Agarwal & Singh, 1982; Singh, 1987). Singh, Joshi and Agarwal (1976), in their studies on the genetics of bollworm resistance using susceptible and resistant genotypes of *G. arboreum*, found gene action to be mainly additive, indicating easy fixation of the resistant character in a breeding programme.

However, in the absence of any reliable source of resistance to bollworms in the cultivated species or its wild relatives, genetic engineering for incorporation of gene/genes from *Bacillus thuringienesis* with resistance to lepidopteran pests (bollworms) seems to be a potential tool in resistance breeding in cotton. While this has been already achieved in the Coker 312 variety of cotton with a high level of field resistance to tobacco budworm, pink bollworm and leaf perforator (Jenkins, 1994), in India work has been initiated to develop such transgenic cottons at several centres. At the Central Institute for Cotton Research, Nagpur, endotoxin genes from Btk HD-1 have been characterized. Attempts to regenerate cotton plants from cell cultures have shown that two genotypes, Coker 310 and PKV081, are amenable to regeneration with production of high embryogenic callus (Dongre *et al.*, 1994).

Table 2. Change in species composition of cotton in India.

Species	Area (million hectares)		
	1947–48	1965–66	1993–94
G. hirsutum	0.14	3.21	2.68
	(3)	(41)	(35.5)
G. barbadense	Nil	0.08	0.01
G. arboreum	2.79	2.84	1.29
	(65)	(36)	(17.0)
G. herbaceum	1.39	1.78	0.88
	(32)	(23)	(11.5)
Hybrid cotton	Nil	Nil	2.70
			(36.0)

Figures in parenthesis represent percentage.

Change in species composition with more and more area coming under more susceptible tetraploid cultivars, increased area under irrigation, indiscriminate use of pesticides and probable change in virulence of pathogens, have made disease management more difficult. Breeding for resistance to major diseases has been an important objective in management of diseases in India. As a prelude to this, inheritance of key diseases has been studied. Singh, Mor and Paroda (1987) suggested additive and additive × additive type gene action for resistance to bacterial blight, which is at variance with other studies conducted in India, and also the study of Knight, which indicates dominance for resistance to bacterial blight (Sheoraj, 1992). Srinivasan, Krishnamurthy and Kannan (1976) observed that a single dominant gene with modifiers controls *Verticillium* wilt resistance in *G. barbadense* and the *mexicanum* strain of *G. hirsutum.* Resistance to fusarium wilt in diploid cottons is governed by dominant genes (Sheoraj, 1992). However, both dominance and recessive inheritance has been reported to be involved, depending on genotypes (Temburnikar, 1994).

Varieties and hybrids resistant to bacterial blight, fusarium wilt and *Verticillium* wilt have been developed. MCU.10, Supriya, Sujata (*bacterial blight*), Eknath, G.Cot.11, G.Cot.13, AKA8401, G.Cot.DH.7, G.Cot.DH.9, DDH-2, MDCH 201 (*Fusarium wilt*) and MCU-5VT (*Verticillium* wilt) are examples.

It is felt that understanding of the molecular basis of pathogenicity of various races of *Xanthomonas mal-*

vacearum will help in the control of bacterial blight, the most important disease of cotton in India. Study of plasmids of the bacteria shows their reproducible and conserved nature, which is suggestive of their epidemiological importance and use in race differentiation (Chakravarty & Sheoraj, 1994).

Ginning outturn

Genetic studies carried out for inheritance of ginning outturn indicate a preponderance of non-additive genetic variation in *G. arboreum* (Sandhu, Gill & Singh, 1993), and additive (Gururajan & Basu, 1992) and dominant (Julka, Gadewadikar & Shroff, 1979) gene actions in *G. hirsutum*. Heritability estimates were low in many instances.

Ginning outturn or lint percent has, however, improved through appropriate breeding methods in *G. hirsutum*, *G. arboreum* and *G. herbaceum*. Most of the *G. hirsutum* varieties released recently have lint percent of 36 to 38, as compared to 33 to 35% in older varieties. AKH081, Anjali (LRK 516), Abadhita, JK119, NA 920, Sharada, MCU 10, the varieties of the eighties, have 36 to 38% lint. There has been remarkable improvement in lint percent of *G. arboreum* in all the three cotton growing zones of India. However, improvement in lint percent is higher in varieties of northern and central zones as compared to southern zone (Singh & Narayanan, 1991). Most of the currently cultivated *G. arboreum* varieties of northern and central zones have lint percent of 39 or more. DS1 (39%), RG 8 (39%), LD327 (41%), AKA5 (39%), Eknath (39%), Rohini (39%) are examples. Races of *cernuum* and *bengalense* are good sources of high lint percent (Singh & Raut, 1983) and they have been used for genetic improvement of lint percent of the species.

In *G. herbaceum* a few varieties developed in the late seventies and early eighties (G.Cot.11, G.Cot.13) from Gujarat Agricultural University, Surat, have a high lint percent of 39

There is, however, potential for further improvement of lint percent of all the four species based on variability available in genetic resources.

Yield of seed cotton

Yield in cotton is a complex character and is mostly controlled by additive, dominant and epistatic gene action (Singh & Raut, 1983). Bhandari (1978), Kalsy *et al.* (1981), Bhandari, Bhardwaj and Kumar (1981), Amalraj and Gawande (1985), Gupta (1993), and Patel and Badaya (1993) among others, from their studies with line × tester, diallel or generation mean analysis, found both additive and non-additive gene effects to be important in the inheritance of seed cotton yield and its components, number of bolls and boll weight in upland cotton (*G. hirsutum*). Rao, Rajsekharan and Basu (1989) evaluated elite varieties of upland cotton of different cotton growing zones of India for their adaptability across the zones and found varieties Suman, LRA 5166, F414, DS56 and DS 59 having maximum yield and score with minimum standard deviation values and thus more stable under different agroclimatic conditions. Stability parameters indicated that varieties H 777, F414, LRA 5166 and MCU 7 were more stable in their performance over locations and seasons.

Both additive and non-additive gene actions were found important for seed cotton yield, number of bolls and boll weight in *G. barbadense* cotton as reviewed by Basu, Singh and Narayanan (1993). Estimates for heritability and genetic advance in a narrow sense are medium for seed cotton yield, while they are high for number of bolls and boll weight (Patel *et al.*, 1991). Combining ability studies conducted by Hapase, Arther and Thombre (1987) and Sandhu, Gill and Singh (1993) in *G. arboreum* cottons have found non-additive gene action to be preponderant for yield and yield components. Lines which are good general combiners have also been identified for utilisation in breeding programmes. Overdominance was, however, found preponderant for these characters by Duhoon, Vijairaghavan and Rao (1983). Studies on genotype × environment interaction and stability parameters in *G. arboreum* showed G × E interaction to be highly significant for yield and its components, indicating that different varieties behave differently (Kalsy & Singh, 1974; Srinivasan & Rao, 1976; Singh & Kalsy, 1980)

Number of bolls per plant and boll weight are the two major yield components. However, they are negatively correlated, making improvement in yield through improvement of both the components a difficult task. Biparental mating has helped in breaking the negative association of boll number and boll weight, and a few genotypes have been developed by this method (Singh *et al.*, 1989). Disruptive selection has also proved to be efficient in breaking linkage of boll number and boll weight (Narayanan *et al.*, 1987). Single, double cross, three way cross, mutation breeding and heterosis breeding procedures have also been employed for improvement of yields in the four cultivated species of cotton in recent times. Genetic improvement of yield through methods other than heterosis breeding will be dealt with first, to be followed by heterosis breeding separately. In the northern cotton region, which is predominantly *G. hirsutum* cotton growing tract, the latest varieties F505, F846, LH886, LF1054, LH1134, H974, HS6 and RST9 are earlier in maturity and higher in seed cotton yield than the older varieties.

Among *G. arboreum* (race *bengalense*) cottons which occupy about 10 to 15% of the area in the region, LD133, LD230, DS1, LD327 and RG8 are high yielding varieties developed during the eighties. LD327, a product of a three-way cross, G57 × (G27 × LD124) and RG8, a product of a single cross (G1 × *cernuum*) (Singh & Narayanan, 1991) with yield potential of more than 25 q/ha developed by Punjab Agricultural University and Rajasthan Agricultural University, respectively, now occupy more than 95% of the area under the diploid species. LD327 has brought about a significant breakthrough in *arboreum* yields in Punjab (Sandhu, 1989).

The most spectacular achievement in genetic improvement in yield in the central and southern cotton regions of the country is the development and release of LRA5166 in 1982 by Central Institute for Cotton Research, Regional station, Coimbatore. This variety developed from a three-way cross (AC122 × Reba B.50) × Laxmi is tolerant to abiotic stress, which makes it eminently suitable for cultivation in rainfed situations. Other high yielding *G. hirsutum* varieties developed recently are MCU 9, G.Cot.14, Anjali (LRK 516), CNH 36 and Abadhita.

Suvin (*G. barbadense*), developed by hybridization of Sujata (a reselection of Karnak) and St. Vincent and released for commercial cultivation in 1974, is endowed with a yield potential of 30 quintals per hectare and spinning potential of 120 s counts. It is comparable to Egyptian cotton Giza 45 and is a landmark in the history of cotton breeding in India (Krishnamurthy *et al.*, 1975). It is the only *G. barbadense* cotton variety grown currently in India. No further improvement in yield or quality has been achieved. Recently released high yielding *G. arboreum* varieties AKH4 and AKA 5 from Punjabrao Agricultural University, Akola (Maharashtra), Eknath and Rohini from Marathwada Agricultural University Parbhani (Maharashtra) and an old high yielding variety Y1 occupy most of the *arboreum* area of central India. Recently, AKA8401, a variety derived from an interspecific cross (*G. arboreum* × *G. anomalum*) has been released for cultivation in Maharashtra. Genetic improvement of yield in *G. herbaceum*, which occupies about 13% of the total area under cotton in India in the states of Gujarat and Karnataka under rainfed situation, has been limited due to lack of enough variability in yield components. DB3-12, a spontaneous mutant of variety W1 characterised by early maturity and high yield, was released for cultivation in Karnataka to replace the old variety Jayadhar but did not succeed. G.Cot.11, a high yielding variety released in Gujarat in 1979, did succeed in establishing itself. It is a derivative of a three-way cross (320 × P2) F10 (Singh, Narayanan & Singh, 1993). G.Cot.13, a high yielding, open boll culture, has been released to replace closed boll wagad cotton in the Wagad tract of Gujarat (Basu, 1988b).

Fibre quality

Fibre length, strength, fineness and maturity, which contribute to fibre quality, are governed genetically and also by agroclimatic conditions and cultural practices. Genetic studies, however, are mostly related to fibre length. Both additive and non-additive genetic variances were found to be significant for this trait (Bhandari, 1978; Patil & Chopde 1983a,b; Singh, Mor & Paroda, 1983; Duhoon, Vijairaghavan & Rao 1983). Moderately high to high heritability was observed by Patil and Chopde (1983), Duhoon, Vijairaghavan and Rao (1983) and Jain, Mor and Nehra (1984) for fibre length in tetraploid and diploid cottons, respectively.

Heterosis and inbreeding depression were found to be low in fibre length by Singh, Mor and Paroda (1983). Study of genetics of fibre fineness and fibre bundle strength in *G. barbadense* cotton (Patel *et al.*, 1991) showed high heritability along with moderate predicted genetic advance, suggesting the role of additive gene effects in their character expression.

Fibre quality of cotton in India has improved by two ways, firstly by shifting from diploid to tetraploid species mainly *Gossypium hirsutum*, and secondly by breeding better quality cottons within the species. *G. hirsutum*, which occupied only 3% of the area under cotton during 1947–48, now occupies almost 36% of the total area. In association with tetraploid hybrids, they cover almost 70% of the area. Extra long staple cotton *G. barbadense* has about 10,000 ha under its cultivation in the Salem tract of Tamilnadu in south India.

Though breeding for improvement of fibre quality was initiated for all the four cultivated species, *G. hirsutum* received priority under the All India Coordinated Cotton Improvement Project of the Indian Council of Agricultural Research launched in 1967. Medium and superior medium stapled cottons were developed and released for commercial cultivation in the different cotton growing regions of the country. F414, H777, SH131, GA, F505, Vikas, LRA5166, SRT 1, Khandwa 2, G.Cot.14, Bhagya, NA920, AKHO81, CNH36, CICR HH1, AHH468 and G.Cot.hyb.8 are some of them. Among the long stapled *hirsutum* cottons DHY 286, LRK 516, JK119, Abadhita and JKHy 1 deserve mention. Some of them are early and resistant to one pest or another.

North India, which grows medium stapled cotton, has two long stapled cottons, Pusa 31 and LH1134, bred by IARI and PAU respectively.

Among the extra long staple *hirsutum* cottons MCU 5, a derivative of a multi-cross hybrid, is most important. The variety released for cultivation in 1968 is still popular and widely grown in both central and south India. It has a mean fibre length of 29 mm and spins 60 s counts. It is a classic example of introgression of genes from *G. barbadense* and is considered to be the most outstanding genetic improvement in fibre quality of Indian cotton (Singh & Raut, 1983). MCU 5 VT, a *verticillium* wilt tolerant version of MCU 5, has similar fibre properties and yielding ability to MCU 5 and is recommended for wilt prone tracts of south India. Recently, an intrahirsutum hybrid with fibre properties of MCU 5, but with higher yield, has been released for cultivation in the south. MCU 9, a derivative of the cross MCU 5 × MCU 8, was developed, which has the fibre quality of MCU 5 but with better lint percent and yield. The intrahirsutum hybrids H4, Savita and H6, and interspecific (*hirsutum* × *barbadense*) hybrids Varalaxmi, DCH 32, TCHB213 and HB224 also belong to extra long staple cottons.

Suvin, a derivative of cross between Sujata and St. Vincent, having a fibre length of 35 mm, micronaire of 3.4, fibre strength of 40, maturity value of 0.89 and spinning potential of 120 s counts, represents a landmark in the history of evolution of quality cottons in India. Suvin and Giza 45 of Egypt are the finest cottons in the world today (Santhanam, 1993).

While *G. arboreum* race *bengalense* cottons grown in north India are short stapled cottons, used as blends with finer cottons and wool, the *G. arboreum* cottons grown in central and south India are medium and long stapled cottons. Gaorani cottons of central India, which have very little area under them, belong to the long and extra long staple categories. Karungani cottons of the south K9 and K10, which also occupy very little area, belong to long staple cottons. A diploid interspecific hybrid (*G. arboreum* × *G. herbaceum*) G.Cot. hyb.9, with Gaorani as the *arboreum* parent, has fibre length of 28 mm, with spinning value of 50 s counts (Basu, 1994b).

Change in species composition and genetic improvement of fibre quality is reflected in the increase in quantum of quality cottons in India over periods (Fig. 1).

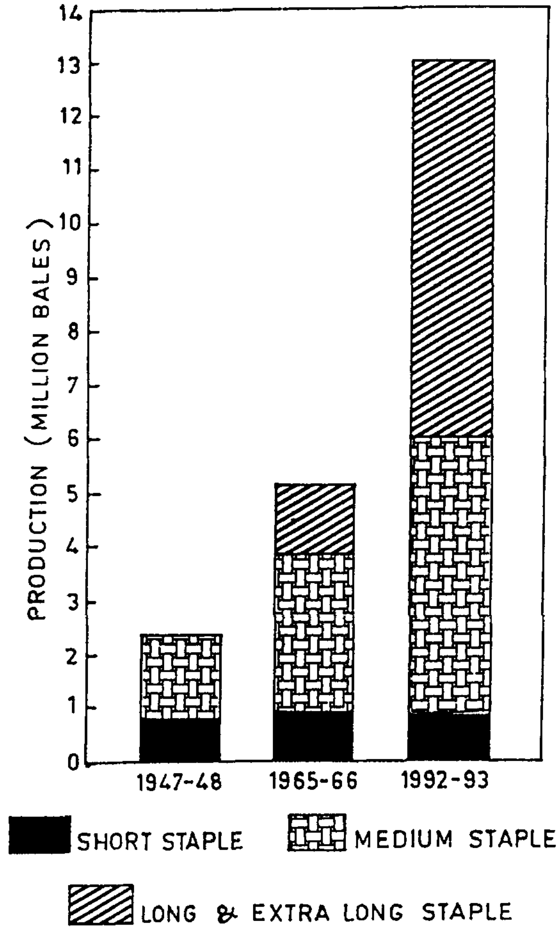

Fig. 1. Production and quality improvement in Indian cotton.

Heterosis

Considerable work on heterosis, including heterobeltiosis and useful heterosis in both tetraploid and diploid cottons, has been carried out at different research centres in India and has been reviewed by Singh *et al.* (1980), Basu (1988b), Singh and Narayanan (1991, 1992) and Basu, Singh and Narayanan (1993).

Heterosis in yield and number of bolls or boll weight in both intra- and interspecific diploid and tetraploid crosses were mainly due to non-additive gene action as reported by Singh and Narayanan (1992) in their review on the subject. In general, it has been reported that hybrids which showed maximum heterosis in F_1F_2 also showed maximum inbreeding depression in F_2 for yield and yield components (Gunaseelan & Krishnaswamy, 1988).

If any breeding approach has had a spectacular impact on improvement in terms of production and quality of cotton in India, it is heterosis breeding. Though heterosis was known in cotton since the end of nineteenth century, the gigantic task of hand emasculation and pollination for hybrid seed production acted as a deterrent for its commercial exploitation (Davis, 1978; Singh *et al.*, 1980). It was the vision of the late C.T. Patel which made hybrid cotton a reality. He utilised the cheap labour available in rural India for production of hybrid seeds through hand emasculation and pollination; thus Hybrid-4, a cross between G 67 (a cultivar of Gujarat) and American nectariless (an accession from the USA) was produced in 1970. This was the first commercial hybrid cotton of the world (Patel, 1971). It recorded 137% heterosis over the better parent, G 67, with spinning potential of 50 s counts, equal to that of G 67. An interspecific hybrid (*hirsutum* × *barbadense*), Varalaxmi, capable of spinning 80 s was released immediately thereafter (Katarki, 1971). Their instant popularity among the farmers of central and south India gave encouragement to hybrid cotton research in India, and as a result, more than 40 hybrids have been developed and released for commercial cultivation in central and peninsular India (Basu, 1994b). These hybrids include tetraploid intraspecific (*G. hirsutum* × *G. hirsutum*), interspecific (*G. hirsutum* × *G. barbadense*) and diploid interspecific (*G. herbaceum* × *G. arboreum*) hybrids.

JKHY 1, G.Cot.Hyb6, G.Cot.Hyb8, NHH 44, MECH 1, Ankur 15, Jagannath, Somnath, AHH 468 (tetraploid intraspecific), Varalaxmi, DCH 32 and TCHB 213 (tetraploid interspecific) are the most widely grown hybrids. Quality-wise, the hybrids have a range from short staple to extra long staple cottons spinnable from 20 s to 80 s counts.

There is no hybrid in the irrigated northern cotton zone. Recently, three intra *hirsutum* hybrids, PCHH 31, Raj 16 and HHH 81, showing useful heterosis over the best varieties of the region, have been identified for release for commercial cultivation.

It is noteworthy that the bulk of extra long staple cottons in India are from hybrids, both intraspecific and interspecific. The interspecific hybrids have special genetic implications as by this method, the yield of *G. hirsutum* and fibre quality of *G. barbadense* could be combined, which otherwise would not be possible due to the genetic breakdown in segregating generations in a varietal improvement programme (Singh & Raut, 1983). The genetic improvement of yield and quality, recorded through hybrid cottons which occupy 36% of the total area under cotton in India, is appreciable.

Studies on different aspects of heterosis in cotton indicate that: (i) improved germplasm lines, widely adapted lines, broad based or introgressed lines with G 67, SB 289E, Khandwa 2, SRT 1, AK 32, Bikaneri Nerma, or LRA 5166 as one of the parents make good hybrids; (ii) multilines of female parents as in Hybrid 4 and JKHY 1 proved to be better in adaptability compared to pure bred lines; (iii) a locally adapted cultivar as one of the parents contributed to superior hybrids; (iv) number of bolls per plant is the main component of heterosis, followed by boll weight in both diploid and tetraploid interspecific hybrids. In intraspecific (intra *hirsutum*) crosses, boll number and boll weight contributed equally to heterosis; and (v) vegetative vigour, leaf area index and photosynthetic rates are appreciably high in hybrids, with very high yield potential (Basu, Narayanan & Bhat, 1993).

Genetic and cytoplasmic-genetic male sterility

Stable genetic and cytoplasmic-genetic male sterile systems are available (Basu, 1983b). Of the eleven known sources of genetic male sterility (Mehetre, 1988), the Gregg male sterile line of Weaver, conditioned by *ms5 ms6* double recessive genes, is the most promising (Srinivasan & Gururajan, 1978). This was used to develop the first genetic male sterile hybrid Suguna in India (Srinivasan & Gururajan, 1983). The hybrid, however, did not make much impact. Subsequent GMS hybrids developed by private seed companies have become popular among farmers in south and central India.

Cytoplasmic-genetic male sterility has been developed with the transfer of the *G. hirsutum* genome into the cytoplasm of *G. harknessii*. A single dominant gene from *G. harknessii* is necessary for fertility restoration (Meyer, 1975; Weaver & Weaver, 1977). A gene for enhancing the fertility of pollen is available in *G. barbadense*. The CMS lines of Meyer and CMS lines developed in India by backcrossing the Indian agronomic bases with the *harknessii* CMS line are stable in different temperatures and day length (Shroff, 1980). Two hybrids, CAHH468 and MECH 4, with CMS background have been released for commercial cultivation. More are under multilocation trials. Preliminary investigations on the performance of CMS hybrids with regard to GMS hybrids point to the superiority of the latter over the former. Local adaptability, genetic background and genetic diversity of the parents may be reasons for superiority of GMS hybrids. Presence of a sterile cytoplasm may also be responsible for such performance of CMS hybrids (Bhale & Bhat, 1990).

Diversification of male sterility sources

There is a report of induction of cytoplasmic male sterility in *G. hirsutum* by using *G. aridum* cytoplasm at Punjabrao Krishi Vidyapeeth, Akola (Anonymous, 1993). There is also a report of the development of genetic male sterility in *G. arboreum* by interaction of the cytoplasm of *G. anomalum* with the genome of *G. arboreum*. The sterility has been found to be monogenic (genic symbol *arms ms*). The GMS lines can be maintained by crossing the homozygous recessive male sterile with the fertile heterozygote, carrying one dominant and one recessive allele (Anonymous, 1990). A new GMS source, a spontaneous mutant, has also been reported in the DS5 cultivar of *G. arboreum* at Haryana Agricultural University, Hisar (Singh & Lather, 1994). The GMS line is temperature sensitive and sheds pollen when temperature reaches 14°C or below. Thus, the line does not require sib mating for its maintenance.

While CMS and GMS systems reduce cost of hybrid seed by almost 50%, further reduction in cost can be achieved by pollination with insects.

Honey bees are principal pollinators. Studies conducted at Indore, Nagpur and Coimbatore showed that in general, boll setting with bee pollination is about 30 to 40% lower than hand pollination (Basu & Paroda, 1994). However, pollination with bees during summer at Coimbatore has shown considerable improvement in setting percentage (Chitra & Gunaseelan, 1994).

F2 hybrids

The possibility of commercial cultivation of F_2 hybrids of intraspecific crosses to reduce cost of seeds has been explored (Basu, Narayanan & Bhat, 1993). The prerequisites for F_2 hybrids are minimal inbreeding depression and minimal segregation for fibre quality. Preliminary results show the F_2 of hybrids like AHH 468 and NHH 44 have promise.

Inheritance of seed oil

Oil content is primarily under non-additive genetic effects (Singh, Singh & Chahal, 1985). Both additive and non-additive effects were, however, found to be significant for seed oil (Dani, 1984, 1989). Mannikar, Dani and Narayanan (1988) advocated selection following biparental mating for increasing oil content. Naked seed, which is characterised by higher seed oil, is controlled by a single dominant gene (*N1*) or a single recessive gene (Singh & Narayanan, 1990). Naked seeded genotypes have been developed. Glandless cottons (without gossypol glands) have also been developed, utilising exotic genetic sources (Anonymous, 1989a). However, they are not successful because of their vulnerability to pests.

Studies in *G. hirsutum* indicate useful heterosis for seed oil, ranging from 7 to 22%. Crosses between genetically diverse parents show greater heterosis for oil content (Dani, 1990). The absence of a major negative association between oil content, seed size, lint yield, fibre length and fibre strength (Turner, Ramey & Worley, 1976) indicates the opportunity for simultaneous improvement of seed oil and fibre.

There is a wide range of variability in seed oil content in all the four cultivated species of cotton for genetic improvement of this trait (Kohel, 1978; Singh & Singh, 1983; Dani, 1990). Seed oil content has been found to range from 15 to 33% (Kohel, 1978), whereas seed oil content of presently grown cultivars in India does not exceed 22%. There is thus a great scope for improvement of seed oil content of cotton in India. There is also a need for improvement of the present level of unsaturated fatty acids in the elite cultivars (Pandey & Thejappan, 1981).

Future thrusts

Notable strides have been made in genetic research contributing to genetic improvement in cotton in India over years. Enhancement of crop productivity further will require the crop to be tolerant to biotic and abiotic stresses. Basic genetic studies in these areas are meagre and need to be pursued for identifying ideal breeding approaches. In the absence of any reliable source for resistance to lepidopteran pests, genetic engineering to incorporate alien genes (such as the *bt* gene from *Bacillus thuringiensis*) for pest resistance will be rewarding.

Heterosis breeding has made notable contributions in enhancing productivity of rainfed and irrigated cotton in central and southern cotton growing tracts of the country. Exploitation of heterosis for the north should be a priority area of research. Cytoplasmic genetic male sterile hybrids are currently relying on *G. harknessii* as a source. Diversification of CMS sources for genetic diversification of hybrids needs emphasis.

With the innovations in fibre processing technology the fibre parameter which needs utmost attention is fibre strength; this trait should be emphasized in future studies concerning the genetic improvement of cotton.

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