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Genetics of oil and yield related traits in cotton

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Abstract
Genetics of oil content, plant height, lint index, ginning out turn and lint weight showed that these traits were controlled by dominant genes and dominance x dominance interactions. The traits *viz*., monopodial branches, seed cotton yield, boll weight, sympodial branches per plant and number of bolls per plant were controlled by dominance gene effects and additive ×additive gene interactions. For seed index, additive gene interaction was prominent.

Keywords: Genetics, cotton, oil, dominance, hirsutum,

Introduction
Cotton has a proud place among the cash crops from the earliest times. It finds mention in the Rigveda the oldest scripture of the Hindus. Manu, the law giver also referred to it in his Dharma Shastra. It was the excellence of Indian cotton fibres famed as webs of woven wind which compelled European countries to seek new trade routes with India.

Since the discovery of the Mohen-jodaro relics the history of cotton and cotton manufacture came to be treated as beginning from times of the ancient Indus valley civilization, which flourished in India about 5000 years ago. Despite the advent of a multitude of other fibres, cotton, white gold rules the world of textile. Even today, it is unchallenged as a natural textile fibre. It is an important fibre and food crop of nearly 100 countries with China, India, United States, Pakistan and Brazil being five of the largest producers of cotton.

Gossypium hirsutum, *G. barbadense*, *G. arboreum* and *G. herbaceum* are grown in varied agro-climate in northern, central and southern Indiafrom 9^0 N latitude to 31^0 N latitude. *G. hirsutum* is the principal cultivated cotton and accounts for about 90 per cent of the world cotton production. *G. barbadense* accounts for about eight per cent of the world cotton production. The estimated area under cotton during 2008 to 2009 in India was 93.73 lakh ha with production and productivity of 290 lakh bales and 526 kg lint per ha, respectively (Sharma *et al*., 2009) [67]. In the year of 2008 in Karnataka, cotton was grown over an area of 3.5 lakh ha with 8.9 lakh bales production. India has 20 per cent of total cotton growing area of the world and contributes over 12 per cent to total production.

Cotton plays a key role in the national economy interms of generation of direct and indirect employment of about 60 million people in the agricultural and industrial sectors of cotton production and processing, textile and related exports which accounts for nearly 33 per cent (76,000 crores) of total foreign exchange earnings of our country. Cotton though mainly grown for fibre is also ranked as major oilseed crop in the international market. Out of the four major products *i.e*., meal, hull, oil and lint, oil is most important. Besides commercial importance in the leather industry and as a lubricant, cotton seed oil can also be used for edible purpose after refining. Cotton seed oil is premium quality oil and there are several reasons for this. India produces about 3.6 million tonnes of cotton seed annually, from which 0.545 MT of oil can be obtained by proper processing of seeds. Cotton harbours about 14 to 26 per cent oil. However, hardly 5 per cent of the cotton seed is processed scientifically resulting in losses of cotton byproducts worth Rs. 2500 crores annually.

Recently, India imported 17 per cent of palm oil and 6 per cent of soybean oil. Nearly half of our vegetable oil requirement is met through import.

Genetic research in cotton in India began at the dawn of the last century founded by the provincial governments of the states growing cotton. Later the Indian Central Committee, the Indian Council of Agricultural Research and State Agricultural Universities sponsored genetic research in cotton.

The improvement in seed, oil and seed cotton yield related traits requires the presence of genetic variability. The range of variability in cultivated *Gossypium* species is very wide for cotton seed oil. Kohel *et al*. (1985) [27] reported the existence of germplasm lines with as high as 32 per cent protein and 30 per cent of oil. Murthi and Appu Rao (1963) [41] have given an account of genetic variability for fuzz, kernel and hull percentage. Now research efforts for yield and quality improvement of oil, seed and yield related traits are in progress in India, USA, Pakistan, China and Egypt.

Cotton seed oil is one of the healthy domestic vegetable oils that is grown and processed in India and other countries of the world. Cotton seed oil has taste and flavour. It is also blended and doesn't mask the flavour of food cooked in it.

Little is known about the nature of gene action for oil content, yield and its related traits in *G. hirsutum* despite an early awareness of the good qualities of cotton seed oil. Systematic investigation on the inheritance was initiated by Kohel (1980) [26] and Khan *et al.* (1992) [23]. However, these studies are essential in knowing genetic trend, which would allow the development of more efficient selection method and genetic populations. The present investigation aims to obtain such information with reference to oil and its related traits and yield and its related traits.

The cotton seed oil is transfree, has neutral flavour, is highly stable, with low flavour reversion, strong shelf life, low fryer turnover, extremely versatile, heart healthy in moderation, according to the American heart Association. It is a good source of essential fatty acids (70% unsaturated, 26% saturated and good source of vitamin E). Cotton oil has a fatty acid profile that makes it acceptable as healthful oil. This profile gives it characteristics that make it very useful as cooking and frying oil (Boghara *et al*., 1985) [7]. It is one of the healthful domestic vegetable oil that is grown and processed in India. It is blended oil and does not mask the flavour of food cooked in it. Evaluation of different cotton genotypes is mainly focused on cotton yield, fibre yield, fibre quality and resistance to various pest and diseases. The byproducts were being ignored until recently; since many other oil seed like mustard, soybean, groundnut and palm oil dominate the oil seed scenario. In particular a number of genotypes having high oleic acid have been identified in cotton in order to provide high stability cooking oils. These oils provide the opportunity to replace the current wide spread use of saturated fats and hydrogenated oil that contribute significantly to increased risk of cardiovascular diseases due to the effect of saturated and trans fatty acids on elevating LDL cholesterol in the blood stream. Similarly, oil with increased stearic acid content are being developed to enable the production of solid fats without the need for hydrogenation (Sharma *et al*., 2009) [67].

Yields were low compared to world average partly because of heavy losses from insect pests particularly cotton bollworm complex. Yield losses due to insect pests are estimated to be around 10 to 14 per cent every year.

India is addressing the need for increased cotton Bt cultivars. These insect protected cotton varieties contain a naturally occurring substance, *Bacillus thuringiensis* (Bt) protein which has been used as an ingredient in safe and effective biological sprays for more than 50 years. Bt trait has been successfully transferred into several Indian lines. Extensive and fully replicated field traits of Bt cotton were conducted from 1998 to 2001 cropping seasons, meeting the government requirements for commercialization. Three Bt cotton cultivars have been approved for planting in India in 2002-03. Since, the introduction of Bt cotton hybrid around 44,500 ha were planted with three hybrids of Bt cotton in central and southern zones in 2002-03 season. This increased to some 1, 00, 000 ha in 2003-04. In 2004-05 around four Bt cotton hybrids were planted over 5, 00, 000 ha by three lakh resource poor farmers. With approval of 16 new hybrids of half a dozen companies including six Bt cotton hybrids for northern region, Bt cotton planting for 2005-06 season has experienced the highest yearly percentage growth rate increasing its area by 160 per cent (13 lakh ha). Around 10 lakh farmers elected to plant Bt cotton hybrids in northern, central and southern cotton growing zones of India as compared to 3 lakh farmers in the previous year (Anon., 2006) [6].

In India, cotton is cultivated in diverse situations ranging from irrigated situation characterized by intensive management to assured rainfed situation where moisture is not a constraint to dry rainfed situation characterized by low rainfall (less than 500 mm) accompanied by high temperature and high intensity. To achieve the target of increasing cotton production at national level, it is essential that productivity of cotton increases in all these situations. In this regard the adaptability of genotypes in different environment is very important. Thereby the present investigation to identify Bt and non Bt hybrids in South and Central India was taken up.

In a landmark decision, the Genetic Engineering Approval Committee (GEAC) of the Ministry of Environment and Forest (MOEF) has approved 43 new hybrids of Bt cotton varieties to be sold in 2006 season in addition to the 20 Bt cotton hybrids approved for sale in 2005. This brings the total of Bt cotton hybrids to 59 (63 approvals) giving farmers of India's three cotton growing zones more choices about which varieties to cultivate in 2006. This includes 14 hybrids containing three events to be sold by thirteen companies in Southern Zone of India.

Of the total available Bt cotton hybrids in 2006, four different events containing Cry1Ac gene (MON 531 event) by Mahyco sourced from Monsanto, stacked Cry X (Cry1Ac and Cry2Ab) gene event (MON 15985) developed by Mahyco sourced from Monsanto, Cry1Ac gene (Event 1) by JK-seeds sourced from IIT Kharagpur and fusion gene Cry1Ab and Cry1Ac (GF Mervent) by Nath seeds sourced from China have received commercial approval for sale in Northern, Central and Southern cotton growing zones. Till now there is not much information regarding expression of Bt gene in different genotypes at different stages of crop life and different parts of the plant.

Genetics of oil, seed cotton yield and its related traits

Generation mean

Little is known about the nature of gene action for oil content and protein percentage in *G. hirsutum* L, despite an early awareness of the good qualities of cotton seed oil, systematic investigations on the inheritance were initiated by Kohel [1980] [26], and in isolated instances Boghara *et al.* [1985] [7] and Khan *et al.* [1992] [23]. However, these studies are essential in knowing genetic trends, which would allow the development of more efficient selection methods and genetic populations. The present investigation aims to obtain such information with reference to oil content and protein percentage, which may ultimately make a sound basis for further improvement work in upland cotton in India.

Oil percentage

Dominance components (H_1) was generally higher than the additive (D) component. Kohel (1978) [25] worked out the possibility of breeding for higher yield of oil per hactare through the combination of high yeild of seed and oil per cent. In view of range of variability in the cultivars and genetic resources, the scope for selection for high oil content in future was found to be quite high. Kohel (1980) [27] reported that the oil content in cotton seeds may be under the control of additive genes. He found a heritability of 0.35 based on F_2/F_3 standard unit regression analysis. Detected epistasis of additive and to a lesser extent that of non-additive type heritability estimates for oil content which ranged between 0.42 and 0.53. He concluded that analysis of gene effects by generation means is relatively more effective in providing genetic information for seed oil content.

Wang and Li (1991) [66] observed frequencies and directions of dominant and recessive effects and closely approached complete dominance. The frequencies and direction of dominance and recessive genes, the ratio of positive and negative genes and the narrow sense heritability of oil content trait differed within studied parents. They also studied inheritance of upland cotton parents grown in Xinjiang indicated additive dominance inheritance without epistasis inheritance. Pundhan Singh and Narayanan (1991) [50] studied pedigree selection which was carried out on G 67 × American nectariless and Khandwa-2 × Reba B-50 MB during 1982-88. Reddy and Satyanarayan (2005) [52] reported that low heritability for oil content. Naveed Murtaz *et al.* (2002) [42] reported that oil content was controlled by both additive and non-additive gene effects.

Seed index (g)

Al-Raqi and Kohel (1969) [2] The investigation of showed that seed indexwas controlled by partial dominance and polygenically inherited dominance or epistatsis or both.

Chahal and Singh (1974) [9] reported seed index influenced by epistatic gene action. Mathapati *et al.* (1978) [34] made six intra*barbadense* crosses. Their studies revealed that seed index was controlled by non-additive gene action. Similar results were observed by Waldia *et al.* (1980) [64], Ahmad *et al.* (2003) [2], Reddy and Satyanarayan (2005) [52], and Rokaya *et al.* (2005) [54].

Singh and Sandhu (1979) [59] observed both additive and non-additive gene action for seed index and they observed additive x additive type of interaction. Same type of gene action was observed by Reddy *et al.* (1999) [53].

Silva and Alves (1983) [58], their studies revealed that seed index was cotrolled by additive gene action observed. Similar results were observed by Abo-El-Zahab (1986) [1], Pavasia *et al.* (1999) [48], Iyanar *et al.* (2005) [18] and Subramanian *et al.* (2005) [62].

Reddy *et al.* (1999) [53] reported additive and additive x additive type of gene action were greater importance for seed index Wang and Li (1991) [66] observed frequencies and directions of dominant and recessive effects revealed closely approached complete dominance. They suggested that to determine the genetic conditioning of yield per plant and additive dominance and epistatic effect involved in inheritance of seed index.

Mohamed *et al.* (2001) [37] showed dominance × dominance gene interaction for seed index.

Mohammad *et al.* (2003) [38] observed non-additive gene action *i.e*., dominance or epistasis for seed index.

Seed cotton yield

Patel *et al.* (1996) [46]. Found additive type of gene action for yield.

Gad *et al.* (1974) [15] conducted on experiment on interspecific hybrids of *G. hirsutum* × *G. barbadense*. They observed dominance × dominance gene effect for seed cotton yield. Jain (1980) [20] found dominance gene effect for yield.

Kumar *et al.* (1974) [28] reported non-additive type of gene action for seed cotton yield. Similar results were observed by Mathapati *et al.* (1978) [34] in *G. barbadense*, Waldia *et al.* (1980) [64].

Desai *et al.* (1980) [10] reported both additive and non-additive gene action in control of seed cotton yield. Similar results observed by Lertprasertrat *et al.* (1987) [35] and Jagtap and Kohel (1987) [19], who made graphical analysis applied to 5 × 5 crosses of *Gossypium hirsutum* indicated over dominance for seed cotton yield, Reddy *et al.* (1999) [53], Kumaresan *et al.* (1999) [29], Subramanian *et al.* (2005) [62], observed additive type of gene action in kapas weight. Kashif –Nadeem and Azhar (2004) [21] realized that additive type with partially dominance type of gene action for seed cotton yield.

Milan *et al.* (1989) [36] took six *G. hirsutum* strains used in their experiment and based on generation mean analysis, seed cotton yield controlled by dominant gene effects.

Sambamurthy and Ranganadhacharyalu (1999) [56] conducted experiment on *G. hirsutum* strains. Their studies exhibited seed cotton yield controlled by epistasis type of gene action.

Boll weight

Gad *et al.*(1974) [15] studied gene effects for boll weight in the cross *G. barabadense* × *G. hirsutum*. Their study revealed additive × additive epistasis as being significant for boll weight.

Singh *et al.* (1976) [60] conducted on experiment involving J34 and H14 which were crossed as female parents with 20 other varieties. Based on their study, they noticed that additive gene action was important for boll weight. Similar results were observed by Pathak and Kumar (1975) [47], Iyanar *et al.* (2005) [18].

Waldia *et al.* (1980) [64] reported that non-additive gene action was predominant for boll weight. Same effects were observed by Aba-El-Zahab (1986) [1], Waldia *et al.* (1984) [65], Valarmathi and Jehangir (1998) [63], Subramanian *et al.* (2005) [62] and Saeed Rou *et al.* (2005) [55]. Desai *et al.* (1980) [10] observed both additive and non-additive gene action for boll weight. Milan *et al.* (1989) [36], Silva and Alves (1983) [58], Reddy *et al.* (1999) [53], Kumaresan *et al.*(1999) [29], Nimbalkar *et al.* (2004) [44], Rokaya *et al.* (2005) [54] also reported similar gene effects.

Jagtap and Kohel (1987) [19] applied graphical analysis to 5 × 5 cross of *Gossypium hirsutum* indicated that over dominance for boll weight. Khan *et al.* (1999) [24] and Naveed-Murtaza (2002) [42] also observed the same results.

Iftkhar-Ahmad *et al.* (2001) [75] showed that the gene action controlling the inheritance of boll weight studied a 4 × 4 diallel cross experiment in cotton. Additive type of gene action with partial dominance was observed for boll weight. Ahmad and Mehra (2003) [2] studied generation means analysis of data from the intra *hirsutum* cross Pusa 45-3-6 × Pusa 19-27 which indicated the presence of dominance and epistatic interactions in the genetic control of boll weight. Kashif Nadeem and Azhar (2004) [21] found that additive type of gene action with partial dominance.

Mohamed *et al.* (2001) [37] found additive × additive type of gene interaction for boll weight. Similar results were observed by Reddy *et al.* (1999) [53].

Number of bolls per plant

Aguado *et al.* (2008) [4] reported that number of bolls per plant

were controlled by both additive and dominance type of gene action.
Do Thi Ha An *et al.* (2008) [12] observed non-additive (Dominant) gene action for number of bolls per plant.
Neelima and Reddy (2008) [43] noticed that number of bolls per plant was controlled by both additive and non-additive gene action in *G. hirsutum*. Similar results were observed by Pale *et al.* (2008) [45], Zhang Yong Shan (2008) [74] observed additive type of gene action for number of bolls per plant in *Gossypium hirsutum* L. Similar results observed by Elangaimannan *et al.*(2007) [13] and Mei-Yong Jan *et al.* (2006) [35].

Fruiting node
Soliman *et al.* (2007) [61] conducted on experiment on biparental mating system. They found fruiting node was controlled by additive type of gene action. Similar results were observed by Zhang-Young Shan *et al.* (2008) [74]. They found both additive and dominance gene effects.

Plant height
Al-Raqi and Kohel (1969) [2] selected nine varieties, whose all possible F_1 hybrid combinations and their corresponding F_2s were investigated. This revealed that plant height was controlled by epistasis.
Silva and Alves (1983) [58] reported plant height was affected significantly by epistasis. Waldia and Yadava`s (1984) [65] data on yield and six yield related characters from a cross between 10 (Female) lines and 3 (Male) testers indicated gene action was predominantly non-additive for plant height.
Lertprasertrat *et al.* (1987) [35], generation mean analysis of revealed that plant height controlled by additive × additive interaction.
Kumaresan *et al.* (1999) [29] reported that both additive and non-additive gene effects were important for these traits. Similar observations were made by Malek and Shamsuddin (1999) [33].
The height of main stem was controlled by additive type ofgene action with parallel dominance by Khan *et al.* (1999) [24].
Ahmed and Mehra (2000) [3] conducted on experiment on generation mean analysis the data was generated from the intra-*hirsutum* cross Pusa 45-36 × Pusa 1927. The investigation indicated the presence of dominance and epistatic interactions in the genetic control of plant height.
The studies of Kashif Nadeem and Azhar (2004) [21] revealed maximum number of dominance genes for plant height.
Iyanar *et al.* (2005) [18] noticed predominance of additive gene action for plant height. Similar results were reported by Subramanian *et al.* (2005) [62], Pavasia *et al.* (1998) [49]. However, plant height was controlled by non-additive type of gene action (Waldia *et al*., 1980) [64].

Monopodial branches
Ahmed and Mehra (2000) [3] conducted on experiment on generation means analysis of intra *hirsutum* crosses. Pusa 45-3-6 × Pusa 19-27 indicated the presence of dominance and epistatic interaction for number of monopodia per plant.
Nimbalkar *et al.* (2004) [44] studied eight genetically diverse genotypes of desi cotton (*G. arboreum* and *G. herbaceum*) for genetics of monopodia, their study revealed additive type of gene effect controlled the number of monopodia per plant. Kaushik and Kapoor (2007) [22] also observed similar results.

Lint index
El-Zahab (1973) [14] studied 15 selected lines of diverse geographical origin with two commercial local varieties. There was predominantly non-additive gene action for lint index. Chahal and Singh`s (1974) [9] studies exhibited epistasis type of gene action for lint index.
Kumar *et al.* (1974) [28] observed that lint index was controlled by non-additive gene action. Similar type of results was observed by Mahammed *et al.* (2003) [40].

Number of sympodia per plant
Neelima and Reddy (2008) [43] reported additive as well as non-additive gene effects for number of sympodial branches per plant.
Punitha *et al.* (2008) [51] observed non-additive type of gene action for number of sympodial branches per plant. Similar results were observed by Muhammad *et al.* (2007) [39] and Pale *et al.* (2008) [45]. Do Thi Ha An *et al.* (2008) [12] found that number of sympodia controlled by additive gene effect. Similar gene effects were observed by Zhang Yong Shan (2008) [74].

Lint yield per plant
Lack of previous studied of lint weight for gene action.

Ginning outturn (%)
Singh *et al.* (1968a) [64] in crosses involving 15 selected lines of diverse geographical origin which carried local two varieties, reported gene action for ginning outturn percentage as being predominantly non-additive.
El-Zahab (1973) [14] reported that ginning outturn percentage controlled was by additive type of gene action in *G. hirsutum*. Similar results were observed by Singh *et al.* (1976) [60], Chahal and Singh (1974) [9], Pathak and Kumar (1975) [47], Gad *et al.* (1974) [15], Deshmukh *et al.* (1980) [11], Abo-El-Zahab (1986) [1], Milan *et al.* (1989) [36], Pavasia *et al.* (1999) [48], Za-Ul-Islam *et al.* (2001) [73], Reddy and Satyanarayana (2005) [52] in *G. hirsutum*.
Singh and Sandhu (1979) [59] reported that dominance effects were more important than additive effects in the inheritance of ginning outturn. Similar results were observed by Silva and Alves (1983) [58].
However, for ginning outturn (%), non-additive type of gene action was observed by Waldia *et al.* (1980) [64], Larik *et al.* (1997) [34], Valarmathi and Jehangir (1998) [63], Subramanian *et al.* (2005) [62] and Ahmad *et al.* (2003) [2] in G, *hirsutum* gonotypes.
Nimbalkar *et al.* (2004) [44] reported both additive and non-additive gene action were important for ginning outturn percentage. Similar results were observed by Rokaya *et al.* (2005) [54].
Chanbunmee and Sriwarnat (1987) [31] found additive × additive gene interaction for ginning outturn percentage. Similar results were observed by Pathak and Kumar (1975) [47] also observed same results.
Jagtap and Kohel (1987) [19] observed over dominance gene action in *G. hirsutum* crosses for ginning outturn.
Amarturdiev (1989) [5] observed the inheritance of ginning outturn in $F_{1's}$ nine hybrids were intermediate between their parents and one showed over dominance of low outturn found
Mohamed *et al.* (2001) [37] reported that additive gene effects were significantly positive for lint percentage and also significant for additive × additive gene action.
Kashif Nadeem and Azhar (2004) [21] carried out studies in order to determine type of gene action controlling lint percentage in *G. hirsutum*. Their studies revealed additive type of gene action with partial dominance.

Experiment III

a) High oil content genotypes	Bt genotypes	Non-Bt genotypes
23-Lyy	JKCH-2245	JKCH-2245
F-1861	SBCH-302	SBCH-302
23 ES	K-5038	K-5038
CSH-7106	KDCHH-441	KDCHH-441
B58-1290	JK-Indtra	JK-Indtra
VCH (F)	RCH-2	RCH-2
3HS	JK-Ishwar	JK-Ishwar
RS-810	JKCH-1947	JKCH-1947
DHH-11 (check)	RCH-134	RCH-134
NHH-44 (check)	JKCH-22	JKCH-22
	Ankur-651	Ankur-651
	RCH-144	RCH-144
	JKCH-1050	JKCH-1050
	SBCH-311	SBCH-311
	PCH-2270	PCH-2270
	NCEN-3R	NCEN-3R
	KDCHH-9810	KDCHH-9810
	NCEN-2R	NCEN-2R
	RCH-118	RCH-118
	JKCH-266	JKCH-266
	Dhruva	Dhruva
	K-5316	K-5316
	KDCHH-9632	KDCHH-9632
	JK-Varun	JK-Varun
	PCH-2171	PCH-2171
	RCH-20	RCH-20
	JK-Durga	JK-Durga
	JKCH-99	JKCH-99
	RCH-138	RCH-138
	JKCH-1945	JKCH-1945
	JK-Gowri	JK-Gowri
	RCH-377	RCH-377
	VICH-111	VICH-111
	VICH-5	VICH-5
	VICH-9	VICH-9

Estimates of genetic variance

Genetic variance was estimated for experiment I and II.

a) Component variance

The components *viz*., phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) variances were used for estimation of phenotypic and genotypic coefficient variations as per the method suggested by Burten and Devane (1953) [8].

1) Genotypic coefficient variability

$$GCV\ (\sigma^2g) = \frac{MSS\ (Genotype) - MSS\ (Error)}{Number\ of\ replications}$$

2) Phenotypic coefficient of variability

$PCV\ (\sigma^2p) = MSS\ (Genotype) - MSS\ (Error)$

b) Heritability (broad sense)

It was estimated by formulae as suggested by Hanson *et al.* (1956) [18].

$$H = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where,

σ^2g = Genotypic variance and σ^2p = phenotypic variance

c) Genetic advance

The genetic gain was predicted using the formula given by Lush (1949) [32] and Johnson *et al.* (1955) [22] and it is as follows.

Where,

GA = Genetic advance

H = Heritability = σ^2g/σ^2p

Σp = Phenotypic standard deviation

K = Standard selection differential which is 2.06 at 0.05 level

Genetics of oil, seed cotton yield and related traits

In the present study two cultivars *viz*., B58-1290 and VCH were used to produce the F_1 and three other generations *viz*., F_2, BC_1 and BC_2. The study thus had six generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2.Quantitative analysis based on additive and non-additive gene effects using six generation means was considered appropriate to describe inheritance of characters related to seed and seed cotton yield. Significance of different parameters in scaling tests (ABC) revealed possibility of non-allelic interaction effects. Six parameters model of Hayman (1958) [16] was used to estimate gene effects (m, d, h, i, j and l) in different characters.

Oil content

Dominance (h) gene effect was found prominent. Among the interaction effects, dominance × dominance gene interaction played major role in the control of oil content. Significant and opposite signs were observed in (h) and (l) parameters revealing the presence of duplicate nature of epistasis. Wang and Li (1991) [66], Mohammad *et al.* (2001) [37] and Mohammad *et al.* (2003) [38] obtained similar results.

Seed index (g)

Seed index is one of the important parameters contributing to the seed cotton yield and oil percentage. All the other genetic parameters *viz*., d, i, j and l were found to be significantly important except dominance effect (h). There was higher magnitude of additive gene (d) action than the dominance (h) gene action. Similar reports of prominence of additive gene action were made by Silves and Alves (1983) [58] Abo-El-Zahab (1986) [1], Pavasia *et al.* (1999) [48], Iyanar *et al.* (2005) [18] and Subramanian *et al.* (2005) [62]. Simple selection for higher seed index is thus recommended.

Seed cotton yield (g)

Based on estimation of gene effects in the present study, dominance component (h) was found more prominent than additive component. Desai *et al.* (1980) [10], Lertprasertrate *et al.* (1987) [35], Reddy *et al.* (1999) [53], Kumaresan *et al.*(1999) [29] and Subramanian *et al.* (2005) [62] also reported the importance of dominance gene action. Based on the average value of F_1 which exceeded both parents P_1 and P_2, over- dominance is implicated. Jagtap and Kohel (1987) [19] made similar conclusions. Presence of dominance and over dominance in these hybrids produce their high heterotic performance for seed cotton yield.

Boll weight (g)

The estimation of gene effects depicted that the dominance component (h) and additive × additive gene interaction were significant in the inheritance of boll weight. Similar results were observed by Ahmed and Mehra (2000) [3]. Considering

interaction effects, additive × additive effects played a major role in the genetic control of the trait. Significance of epistatic effects for the trait was also narrated by Gad *et al.* (1974) [15], Reddy *et al.* (1999) [53] and Mohamed *et al.* (2001) [37]. Considering the complex inheritance patterns noticed in all the traits studied, it is advisable to go for development of hybrids to realize higher seed cotton yield.

Number of bolls per plant

With respect to boll number, all genetic parameters were found to be significant except additive × additive interaction (i) effect. The magnitude of dominance effect (h) with highest magnitude (7.33) was found to play a major role in the inheritance of the trait. Among interactions, dominance × dominance effect was found prominent. The opposite sign of 'h' and 'l' revealed duplicate type of epistasis for this trait. Similar results were observed by Do Thi Ha An *et al.* (2008) [12], Aguado *et al.* (2008) [4], Nilima and Reddy (2008), Pale *et al.* (2008) [45] and Zhang Yong Shan *et al.* (2008) [74].

Fruiting node

Dominance effect (h) with highest magnitude (3.66) was found to play major role in the inheritance of fruiting node. Components h and l were in similar direction, revealing complementary gene epistasis. Similar kind of results was observed by Zhang Yong Shan *et al.* (2008) [74].

Plant height (cm)

The mean of F_1 generation was higher than both the parents for this trait.

Though all the genetic parameters were significant, based on relative magnitude, dominance effect (h) and dominance × dominance gene effects (l) were found important in the genetic control of plant height. Similar results were observed by Waldia *et al.* (1980) [64], Silva and Alves (1983) [58], Waldia and Yadava (1984) [64], Ahmed and Mehra (2000) [3], Malek and Shamsuddin (1999) [33], Kashif Nadeem and Azhar (2004) [21]. But, additive and additive × additive gene control for plant height was observed by Lestprasertrat *et al.*(1987) [35], Pavasia *et al.* (1998) [49], Kumaresan *et al.* (1999) [29], Khan *et al.* (1999) [24], Iyanar *et al.* (2005) [18] and Subramanian *et al.* (2005) [62].

Monopodial branches

Perusal of gene effects revealed higher magnitude of dominance component (h) than additive component (d) revealing its prominence in the genetic control of number of monopodial branches. Among the interaction effects, additive × additive (d) and dominance × dominance effects (l) were found most important indicating duplicate epistasis in the inheritance of this trait. The reports of Ahmed and Mehra (2000) [3] supported this observation. But, Nimbalkar *et al.* (2004) [44] observed additive gene effects for this trait.

Lint index (g)

Persual of data indicated that mean value of F_1 generation exceeded the better parental mean of P_1 indicating over-dominance for lint index. Similar result was observed by Chahal and Singh (1974) [9] considering gene interaction effects all of which were noticed to be significant at 1 per cent level. For lint index, higher magnitude of interaction observed was dominance × dominance type. Chahal and Singh (1974) [9] obtained similar kind of interaction.

Sympodial branches per plant: Dominance (h) gene effect was highest, revealing dominance gene effect in the control of this trait. Among the interaction effects, additive × additive effect (i) was found prominent followed by additive × dominance (j) effect. Further, estimates of 'h' and 'l' were significant with positive and negative values, respectively. This indicated that duplicate nature of gene interaction was operating for the trait sympodial branches per plant. Punita *et al.* (2008) [55] also observed similar kind of results.

Lint yield per plant (g)

The mean of F_1 was better than both parents P_1 and P_2 revealing over dominance for lint weight.

Among the interaction effects, additive × additive type of interaction was found prominent among the interactions to indicate presence of complementary gene action was operating for this trait.

Ginning outturn (%)

The ginning outturn percentage is very important in cotton crop, because cotton is mainly grown for its fibre. Jain (1980) [20] reported over -dominance for the trait. Singh and Sandhu (1979) [59] and Silvas and Alvas (1983) [58] reported that dominance gene action was predominant to additive effects in the inheritance of ginning outturn. In the present study perusal of data indicated that ginning outturn controlled by dominance gene effects. Similar results were observed by Jagtap and Kohel (1987) [19]. Both the additive (d) and dominance (h) gene effects were significant. However, magnitude of dominance (h) was higher than additive (d) component. Thus revealing its importance in the inheritance of the trait.

The interaction effect, dominance × dominance also showed a major role in the expression of this trait. These heterosis breeding thus will help in increasing the ginning outturn.

Summary

Studies on these Bt hybrids had become important so as to find out the best hybrid suited to a situation. In addition, the oil content and its components in Bt genotypes has not been studied. With these in view a comprehensive study was initiated across two different cotton growing zones of India. The conclusions drawn from the present study has been summarized.

At Nagpur, bolls per plant, 20-boll weight, ginning outturn percentage, seed index (g), fuzz percentage, hull percentage and kernel percentage showed high genetic variability. The seed cotton yield, plant height, number of monopodial branches and number of sympodial branches per plant were noticed to have higher genetic variability at Bagalkot.

Of the three locations, higher heritability was observed for yield (92.40%), 20-boll weight (59.70%), ginning outturn (74.10%), seed index (92.50%), fuzz percentage (97.80%) and kernel percentage (43.50%) at Nagpur. The sympodial branches (39.40%) had higher heritability at Dharwad. The plant height (78.50%), monopodial branches (92.50%), number of bolls per plant (77.30%) and oil percentage (87.80%) expressed higher heritability at Bagalkot.

The higher genetic gain for yield (79.20%), bolls per plant (38.16%), 20-boll weight (23.87%), ginning outturn (15.15%), seed index (35.68%), hull percentage (14.63%) and kernel percentage (9.86%) was observed at Nagpur. The plant height (24.65%), monopodial branches (69.83%), sympodial branches (13.62%), oil percentage (20.67%) and fuzz percentage (23.15%) showed higher genetic gain at Bagalkot.

Cotton seed oil had fatty acid composition of 2:1 ratio of poly unsaturated to saturated fatty acid. Generally, 70 per cent of it

was unsaturated fatty acids including18 per cent mono-unsaturated (oleic) and 52 per cent poly unsaturated (linoleic) and 26 per cent saturated (palmitic and stearic) fatty acids.

On an average, oil content of Bt hybrids (17.43%) was on par with non-Bt hybrids (17.40%). Unsaturated fatty acid composition of Bt (59.71%) and non-Bt hybrids (59.15%) was similar. It can be safely concluded that the presence of the Cry1Ac gene did not affect the oil content or its profile in the Bt hybrids. The myristic acid of Bt hybrids (1.42%) was numerically superior over non-Bt (1.28%) hybrids which helps to increase the keeping quality of oil.

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