GENETIC VARIABILITY AND GENETICS OF TRAITS DETERMINING PLANT TYPE IN TETRAPLOID COTTON

BY

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This is to certify that the thesis entitled **"Genetic variability and genetics of traits determining plant type in Tetraploid Cotton"** submitted to the Faculty of Post-Graduate School, Indian Agricultural Research Institute, New Delhi, in partial fulfilment of the requirements, for the degree of **Doctor of Philosophy in Genetics** is a faithful record of bona fide research work carried out by **Mr. Mohammed Ariz Ahammed,** under my guidance and supervision and that no part of the thesis has been submitted for any other degree or diploma.

The assistance and help received during the course of these investigations have been duly acknowledged by him.

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The English word 'Cotton' comes from the Arabic word qutun or kutun. The scientific term Gossypium is derived from the Arabic, Persian and Afghan words goz, gozah and gozeh respectively (Muller, 1958). The time when cotton fiber was first utilised by man is not known. The oldest archaeological record of cotton textiles, which dates back to about 3000 B.C., was found in the valley of the Indus river (Gulati and Turner, 1929). The first reference in literature to cotton, so far as is known at present, is to be found in a Rig Veda hymn (Scherer, 1916).

INTRODUCTION

Cotton is the 'King of apparel fibers'. It is a unique crop species that has been a participant in many epics of history. It is one of only a few species that were domesticated in both the old and new worlds. Cotton was central to the success of the industrial revolution and also has participated in the development of several technologies like Saw gin, wash and wear fabric, Integrated pest management and also in plant research especially cytogenetics and resistance breeding. Besides food and housing, clothing is one of the primary needs of human beings. To fulfil this need cotton has provided the most versatile fiber. With a history going back to unrecorded antiquity, the fiber has maintained its pristine purity and importance to this day.

In India, cotton has had the pride of place among the cash crops from the earliest times. It was the excellence of Indian cotton fabrics famed as 'Webs of woven wind', which impelled European countries to seek new trade routes with India. Cotton plays a vital role and has woven itself inextricably into fabrics of India's agricultural and industrial economy. It is one of the most remunerative cash crops, source of employment and income for millions of people engaged in its cultivation, ginning, textile mills, manufacturing garments and an important foreign exchange earner. Cotton constitutes 85 per cent of the raw material of our textile industry. Though man made fibers may make further inroads, the pre-eminent position of cotton is likely to remain unchallenged in the years to come for its obvious advantages.

Despite the loss of vast cotton growing area during partition, India has secured a place of pride at the global level in cotton due to several distinct features such as the largest cotton growing area, cultivation of four cultivated species, larger area under tetraploid cotton, one of the largest producer of extra long staple cotton, possibly the only country to grow hybrid cotton, native home of old world cottons and wide diversity in agroclimates under which cotton is grown. However, paradoxically in the cotton production, India(with 11.6 m.b. in 1992-93) is trailing behind China and USA. This is chiefly due to very low average lint yield 261 kg/ha against world average 560 kg/ha and 1588 kg/ha of Australia.

The cotton required by 2001 AD has been placed at 14 million bales (which may go upto 20 m.b.) taking into account both the increase in the domestic market and the increase in export potential of raw cotton, cotton yarn and other value added products. Since there are constraints in the expansion of area under cotton because of severe competiton from other shorter duration oilseed or pulse crops the higher production has to be achieved solely through high productivity. This is particularly important if India wants to avoid recurrence of '94 cotton scandal due to decrease in production and to make its presence really felt in post-GATT cotton world in the coming years.

In India, present total area under cotton cultivation is 7.5 million hectares. Species wise till 1950 the major cotton area was under diploid desi cottons (90%) and the American (tetraploid) cottons were being grown on a very little area. With the intensification of research work and increased emphasis on high yielding and better quality cotton there has been replacement of desi types by improved American cotton varieties and hybrids. At present, tetraploids especially American cotton is grown in about 70% of cotton area and a few thousand hectares under Egyptian cotton. So increasing the productivity of American (tetraploid) cotton is very important to improve overall productivity and finally production in India.

Staplewise the appropriate ratio of short, medium and long staple cotton for 2000 AD would be 10:65:25. India is self sufficient in short and extralong staple cotton but has fallen short of medium staple cotton since 1981. This emphasizes the need to step up production of medium and superior medium staple cotton. It again implies need to increase the productivity of American (tetraploid) cotton.

The major reason for low productivity of tetraploid cotton in India is the cultivation of inherently low yielding varieties with low harvest index (Singh et al., 1992). The indeterminate growth and fruiting habit of our current cultivars put the cotton plant in complete disharmony with the environment and only 20-25 per cent of the total biomass of such plants gets converted into economic produce i.e., seed cotton yield (Mor et l., 1994). The success of H-1156 and LH-900, a short statured and compact plant type with high harvest index of 45-50 per cent indicates the significance of plant type improvement in cotton. Therefore, breeding for plant type with high harvest index and high yield is a timely and promising proposition to mark greater strides in the present cotton scenario. It is truely the need of the hour.

To initiate a breeding programme for a suitable plant type, it is essential to study the genetics of traits determining plant type particularly those traits having direct contribution for the characters under consideration together with high harvest index. Moreover, it is also a basic factor for deciding the appropriate breeding approach to be followed.

Though India is self sufficient in extra long staple cotton, these continue to receive attention in view of their export potential, their suitability as blends with man made fibers and the expected increase in demand for finer cottons with improvement in the standard of living of people and scope for lucrative foreign exchange.

At present, cultivation of extra long staple G. barbadense cottons is restricted to southern parts of the country because of unfavourable day length and temperature in North Indian cotton belt.

Review of the work done in the past reveals that unsuccessful attempts to cultivate G. barbadense in the northern parts was mainly due to utilisation of limited genetic variability. It is well known that crop varieties which are relatively insensitive to photoperiodic and thermal conditions can be evolved if large enough genetic variability is utilised in course of breeding programme. Efforts in the direction of developing suitable barbadense cotton variety suitable for cultivation in North zone started when a large number of genetic stocks of G. barbadense cottons with diverse origin were evaluated at Indian Agricultural Research Institute (IARI), New Delhi. Later on, intensive intervarietal crossing programme was taken up (Singh et al., 1973).

Further, since cotton is predominantly a self pollinated crop its mating system restricts the chance of new recombinants to occur after F_2 generation. This suggests the need for modifications in the conventional breeding procedures.

Keeping in view the above considerations, the present investigations were, therefore, taken up to gather information that could form the basis of constituting suitable plant types in the two species of cotton. These included

In G. hirsutum

i) Study of the nature and magnitude of gene effects and interactions for yield and its components and other morphological traits in a cross of hirsutum cotton.

ii) Estimation of heritability of above traits and the expected genetic gain as a result of exercising selection pressure.

iii) Estimating the extent of heterosis in F_1 and inbreeding depression in F_2.

iv) Estimation of the magnitude of variability in F_3 population and its nature through study of character associations.

In _G. barbadense_

i) Evaluation of magnitude of genetic variability in the segregating F_4 population of a cross advanced from F_3 following three different mating systems viz., selective intermating, random intermating (open pollination) and self pollination.

ii) Characterisation of this variability through the study of character associations.

iii) Comparison of three mating systems in terms of the recovery of transgressive segregants.

REVIEW OF LITERATURE

Cotton, a malvaceous plant belongs to the genus *Gossypium*, which is moderately large (39 species) and very diverse (Fryxell, 1984). There are four cultivated species of cotton. Two are *Gossypium arboreum* L. and *G. herbaceum* L. both diploids (2n=26), indigenous to Asia, Africa and Australia, so are commonly known as Asiatic or old world cottons. The other two are tetraploids viz., *G. hirsutum* known as American or upland cotton and *G. barbadense* known as Egyptian or Sea Island cotton. The latter two are indigenous to New World.

The origin of new world cottons has been attributed to allopolyploidy derived from progenitor genomes similar to the genomes extant in *G. herbaceum* (an old world cotton with A-genome) and *G. raimondii* (an American wild species with D-genome) (Kohel and Lewis, 1984). *G. barbadense* is supposed to be the older of the two having its centre of origin in Peru. *G. hirsutum* appears to be a later differentiation from *G. barbadense* itself, the centre of origin being the high lands of Gautemala (Sikka and Joshi, 1960).

Gossypium hirsutum was first introduced into India in latter half of the 18th century through two different routes viz., one US upland types by a western route and the Cambodian types from Mexico via Philippines and Cambodia through South eastern side (Sikka and Joshi, 1960). The present day Indian hirsutum are represented by different types viz., Panjab American cotton, Buri types, CTI types, Indo-American types and

Madras Cambodia Uganda (MCU) types. Thus Indian hirsutum types have wide genetic divergence because of their diversified parentage and geographical distribution (Singh and Raut, 1983).

Gossypium barbadense (2n=52) Sea Island or Egyptian cotton was introduced into India in the thirties of this century. Until recently, the efforts made to acclimatise the barbadense group of cotton in various parts of India ended in total failure. Only recently it has been claimed to have been successfully grown though on a small scale as an unirrigated pure crop in the southern states and the variety Andrews has been adapted for cultivation in this area (Sikka and Joshi, 1960). Latter in 1967, a variety Sujata, a selection from Egyptian variety 'Karnak' and the first Indian variety of hybrid origin Suvin in 1971 were evolved in Regional Research Station (IARI), Coimbatore. Sujata and Suvin are the best quality cottons of the country. Suvin is capable of spinning upto 120 counts, as comparable to the best varieties of world (Singh and Raut, 1983).

Cotton breeding procedures have been reviewed by Richmond (1951), Sikka and Joshi (1960) Poehlman and Borthakur (1969), Niles and Feaster (1984) and Singh (1989). With the exploitation of hybrid vigour the concepts in cotton breeding have considerably changed during the last two decades.

The scope for biometrical analysis to plan for improvement in yield and quality has been brought out by Allard (1956, 1960), Miller and Rawlings (1967), Mather and Jinks (1971), Bains (1971), Meredith (1984) and several others in recent past.

In the present review of literature, an attempt has been made to present chronologically as to what has been done so far in the understanding of morphological architecture in *G. hirsutum* and *G. barbadense* cottons, the extent of genetic variability and mating procedures to generate it and in understanding of genetic architecture through the study of generation means and nature of interrelationships between various characters, under following heads:

A. *Gossypium hirsutum*

1. Plant type and morphological architecture in cotton
2. Nature and extent of genetic variability in *G. hirsutum*
3. Genetic architecture using generation means in *G. hirsutum*
4. Heritability and genetic gain
5. Heterosis and inbreeding depression
6. Correlations

B. *Gossypium barbadense*

1. Variability in *Gossypium barbadense*
2. Character associations in *Gossypium barbadense*
3. Changes in magnitude of genetic variability and nature of character associations under different mating systems

A. GOSSYPIUM HIRSUTUM

Plant type and morphological architecture in cotton

Most plant breeding is based on defect elimination or selection for yield. A valuable additional approach available is through the breeding of crop ideotypes-plants with model characteristics known to influence photosynthesis, growth and (in cereals) grain production (Donald, 1968). Ideotype is a conceptual frame of a plant which does not exist but achievement of such a plant is the objective of plant breeding programme. However, ideotype is often taken synonymous to plant type. In fact, a plant which already exists and is described morphologically as distinct type is a plant type. In some cases, a plant type may approach the ideotype. A productive ideotype should be determined for each crop depending upon the factor limiting yield under a given environment and quantitative aspects of the processes must constitute an important component of plant ideotype (Sinha, 1988).

Presently, ideotype is conceived as physiologically efficient biological model which is expected to perform in a predictable manner in a given set of external conditions. Thus plant type concept or ideotype approach in plant breeding furnishes an useful criterion of selection and logical basis towards attaining new levels of yield (Sharma, 1994).

While breeding for ideotypes, the plant breeder confronts first with the problem of defining a suitable or ideal plant type and then with that of creating varieties which can correspond as much to the postulated ideal type as possible. The first object with respect to redesigning the plant canopy can be fulfilled by two approaches (i) by striking a balance between all the physiological components with the help of their correlations with yield and (ii) with greater rapidity and precision, by computer simulation of growth, as had been done in case of sugarbeet at the University of California, Davis, USA (Sharma, 1994).

In general, the trend in cotton breeding is towards a diminution of plant size. The degree to which this modification is acceptable is influenced both by yield potential and harvest methods. In the Pima series, plant type has been modified appreciably in recent years. Since 1951, each succeeding cultivar release of the Pima series has been shorter and more compact and they begin fruiting at a lower node on the main stem (Niles and Feaster, 1984).

Singh _et al_. (1991) suggested the combination of small leaves, big boll size, more bolls per plant, high ginning out-turn, high harvest index and acceptable quality to maximise yields in cotton. Singh _et al_. (1992) reported that for the North Indian irrigated cotton belt, medium tall plant type of sympodial habit with higher boll weight, same of higher bolls/m^2 and higher harvest index than the present day plant type will be ideal for achieving high productivity in cotton. It is suggested that the choice of parents with high fruiting coefficients, the introduction of shorter fruiting branches or short multinoded sympodia in hybridization work are some of the means to limit the vegetative growth, reduce the excess dry matter and accelerate greater fruitfulness so that yields of seed cotton can be realised. The work done at Delhi also proposed that the plant type suited to North Indian agroclimatic conditions should have fewer sympodia and less leaf area, high leaf per boll ratio, greater boll set, adaptability to low light and high fruiting coefficient and relative fruitfulness (Bhat, 1992). Joshi (1994) emphasized on the breeding objectives of combining larger boll number per plant with higher boll weight and breeding cotton varieties having higher yield and fiber properties compared to hybrids and produce superior barbadense cottons.

The indeterminate growth and fruiting habit of our current commercial varieties put the cotton plant in complete disharmony with the environment and only 20 to 25% of the total biomass of such plants was converted into economic produce i.e., seed cotton. The success of H 1156 and LH 900, a short statured and compact plant type with a harvest index of 40-45% indicate that the efficient plant type for North zone should consist of short stature, short fruiting branching with reduced bearing internodes giving a compact pyremidal plant, with determinate growth habit, with rigid balance between vegetative and reproductive phases so that plant type does not change even under extreme environmental fluctuations (Mor *et al*., 1994).

Nature and extent of genetic variability in hirsutum cottons

For genetic improvement of field crop varieties, it is axiomatic to a plant breeder that germplasm collection representing the widest possible spectrum of genetic variation be built up and properly assessed. The genetic variability present in the available germplasm may be utilised either for direct selection or for hybridization programme which involves a choice of potential parents that can produce an offspring population outyielding the parents in a set of desirable characters viz., characters related to yield. Therefore, assessment of available variability in a population is very important in a breeding programme. The review on variability, in cotton is given below chronologically.

Bains (1967) reported that varieties of upland cotton differed significantly and exhibited maximum genotypic coefficient of variation (GCV) for seed index and lint index against minimum values for ginning percentage. Bains (1971) observed better mean performance for all the characters studied in a biparental intermated population.

Patil and Mathapati (1976) tested 18 varieties of *G. hirsutum* for 9 quantitative traits. Mean sum of squares for varieties were significant for all the traits except for bolls per plant, and ginning percentage showed high genotypic variance.

In jassid tolerant *G. hirsutum* varieties, Basu and Bhat (1987) observed that harvest index ranged from 22.8 to 34.6%, selection 29 having the highest value. H-777 was best for seed cotton yield and harvest index.

Singh *et al*. (1987) observed comparatively high coefficients of phenotypic and genotypic variability for yield per plant and number of bolls per plant and low for rest of the characters.

High phenotypic and genotypic coefficients of variations were observed for lint yield per plant and for lint index (Nadarajan and Rangasamy, 1990). Mohan *et al*. (1992) reported significant differences among genotypes for seed cotton yield, total biomass per plant and harvest index in both *G. arboreum* and *G. hirsutum* cottons.

Variability among 49 *G. hirsutum* genotypes indicated wide variation for different traits. The range for plant height was 54.3-145 cms. Six genotypes were sympodial whereas 10 were monopodial. Bolls per plant were 9-21 and boll weight 3.0-5.7 g/boll. The biological yield was 1.1-10.2 t/ha, seed cotton yield, 0.47-2.66 t/ha and harvest index 14.7-46.0. Also genetic variability from intraspecific crosses was generated for plant height, biological yield, seed cotton yield and harvest index (Singh *et al.*, 1992).

Genetic architecture using generation means

Success in breeding for quantitative traits depends upon the gene actions involved for the traits concerned. In a crop like cotton where there are increasing evidences for polygenic action in determining economic characters, breeding methodologies must be based on refined biometrical techniques.

The exploitation of genetically diverse breeding material for improving the plant type traits depends upon the estimates of the nature and magnitude of the gene effects governing the inheritance of quantitative characters. In 1932, Fisher *et al.* developed a method for determining the contribution of each gene to the additive (fixable) and dominance effects (non-fixable) following the crossing of two true breeding strains.

The methods currently used for the determination of genetic architecture of quantitative characters can be broadly classified into two groups viz., those using variances, covariances and other using first order statistics such as generation means to detect and estimate epistasis. Hayman and Mather (1955) suggested the use of two parameters: [d], the phenotypic difference between two homozygotes and [h], the increment to mid parent in F_1 in order to find out the effect of single gene pair in heterozygotes.

Hayman (1958) and Jinks and Jones (1958) independently developed methods of estimating additive, dominance and epistasis parameters viz., [i] additive x additive, [j] additive x dominance and [l] dominance x dominance type of interactions from generation means. Such partitions of first degree statistics affords less biased estimates of the genetic parameters. As Gilbert (1958) point out, this not only means that the methods employed are desirable from statistical point of view, but they in fact do not require all the assumptions usually involved in polygenic analysis using second degree statistics. This was further elaborated by Mather and Jinks (1971, 1977), Besford et al. (1979). Mather (1949) and Cavalli (1952) gave individual sealing tests and joint scaling tests respectively to detect epistasis. The available information in literature on gene effects and interactions through generation mean analysis is given below:

Dhillon and Singh (1980) noted that dominance, additive x additive and dominance x dominance components were antagonistic to each other in an intrahirsutum cross and the interactions observed were of duplicate type i.e. [h] and [l] had opposite signs. Comparison of generation means showed a significant decrease in F_2 over F_1 for yield, boll weight and seed index.

Bains et al. (1982) estimated that additive effects were significant for all characters. The dominance effects were also important except for yield. Singh and Raut (1983) summarised the type of gene actions for various polygenic traits in cotton. They reported additive, dominance and epistatic gene action for yield, plant height, sympodia, boll number, and ginning out-turn. Only dominance and epistatic gene action for monopodia, additive and epistasis for boll weight and additive and dominance effects for seed weight.

The plant height character was found to be controlled by additive, dominance effects and additive x additive interaction (Srivastava and Kalsy, 1990).

Silva and Alves (1983) noted that the number of nodes on the first fruiting branches and the number of non-fruiting branches were significantly affected by epistasis. For the number of fruiting branches, additive gene action predominated. Raghbir Singh and Chhabra (1991) reported that additive gene effects were significant for first fruiting node number.

For boll number, Silva and Alves (1983) reported predominance of additive gene action besides the dominance effects. Singh _et_ _al_. (1983b) observed that none of the main effects or interactions were significant for this trait. Srivastava and Kalsy (1990) noted significant additive and dominance gene effects and [i] and negative [j] interactions for the trait. Raghbir Singh and Chhabra (1991) reported the significance of additive gene effects for this trait. Jagtap (1993) revealed that dominance [h] and additive [d] effects and [l], [i], [j] epistasis were controlling boll number but main effects [i] and [h] had major role than epistasis.

For economic yield, Singh _et_ _al_. (1983b) observed that none of the main effects and interactions were significant. for the same trait, Kalsy and Garg (1988) observed the significance of dominance, additive gene actions and all three interactions. Srivastava and Kalsy (1990) observed presence of additive genetic component and all the three types of nonallelic interactions. Nadarajan and Sree Rangasamy (1991) noticed additive and epistatic gene action, and Raghbir Singh and Chhabra (1991) reported significance of additive gene effects. Jagtap (1993) revealed that the main effects [h] and [d] had the major contribution over epistasis for this trait.

Raghbir Singh and Chhabra (1991) reported that the additive gene effects were highly significant for seed index, ginning percentage and lint index.

Heritability and genetic gain

Heritability and genetic gain are the important selection parameters. The concept of heritability,which gives an idea of transmissibility of characters from parents to their offspring is important both for plant breeders and geneticists as it determines whether phenotypic differences observed among individuals are due to genetic changes or due to the effect of environmental factors. According to Lush (1940), heritability in broadsense is ratio of total genetic variance to the phenotypic variance. In narrow sense, it is the ratio of additive genetic variance to the total phenotypic variance. Genetic gain refers to the improvement in the mean genotypic value of selected individuals over the parental population. The available recent literature on two parameters in cotton is presented below characterwise.

Plant height: Singh and Singh (1991) observed high heritability coupled with intermediate genetic gain for plant height. Al-Rawi et al. (1986) recorded high values of heritability for the same trait. Singh et al. (1987) noticed low heritability and low genetic advance for this trait.

First fruiting node number, monopodia and sympodia: Singh and singh (1981) observed high heritability estimates for first fruiting node number. Both Singh and Singh (1981) and Seth et al. (1984) reported high heritability estimates coupled with high genetic advance for monopodia. Singh and Singh (1981) also observed high heritability and intermediate genetic advance for sympodia.

Boll number: Heritability estimates for boll number were found to be high with maximum genetic advance (Singh and Singh, 1981; Khorgade and Ekbote, 1981; Seth et al., 1984), moderate to high (Thombre et al., 1982) and high (Al-Rawi et al., 1986). But Singh et al. (1987) observed low heritability with intermediate genetic advance for this trait.

Boll weight: Singh and Singh (1981) observed high heritability with low genetic advance for this trait. Atta et al. (1982) reported low heritability (in F_3) for the same trait. Thombre et al. (1982) recorded low to moderate heritability and genetic advance. Singh et al. (1987) noted high heritability with intermediate genetic advance.

Economic yield: Thombre et al. (1982) reported moderate to high heritability and genetic advance for this trait. High heritability coupled with high genetic advance was observed by Seth et al. (1984), Singh et al. (1987) and Nadarajan and Rangasamy (1990).

Murray and Verhalen (1969) reported broadsense heritabilities of spaced plants of 75% and 0% for lint yield and 55% and 0% for earliness in two successive years. Meredith (1984) observed that heritability of yield is generally lower than that for yield components and fiber properties. Selection progress for many characters has been achieved as evidenced by the steady genetic selection progress for the most important characteristic, yield of about 0.7% per year, for at least in the past 20 years.

Seed index: For seed index, heritability estimates were found to be low in F_3 generation (Atta et al., 1982), high with low genetic advance (Singh et al., 1987), high (Al-Rawi et al., 1986) and high with moderate genetic advance (Nadarajan and Rangasamy, 1990).

Ginning percentage: High heritability estimate for ginning percentage was recorded by Bala Kotaiah and Butany (1971) but Singh et al. (1987) noted moderate heritability with low genetic advance for this trait.

Lint index: Heritability estimates were reported to be low (Atta et al., 1982), moderate with intermediate genetic advance (Singh et al., 1987) and high coupled with high genetic advance (Nadarajan and Rangasamy, 1990).

Heterosis and Inbreeding depression

The term heterosis was first coined by Shull (1914). He interpreted heterosis as increase in vigour, size, fruitfulness, speed of development, resistance to diseases and pests which is manifested by cross bred organism as compared with corresponding inbred as the specific results of unlikeness in the constitution of uniting gametes.

Heterosis in F_1 hybrids arises mainly from an accumulation of maximal number of dominant favourable alleles (for growth and vigour), contributed or nicely complemented by either of the constituent parents (Davenport, 1908). Jones (1917) suggested that a large number of favourable loci involved in heterotic expression, are randomly distributed on different chromosomes. Thus they may be linked with some unfavourable alleles also on a particular chromosome. Shull and East around 1910 proposed that vigour in F_1 hybrids is conditioned mainly by heterozygosity at individual loci.

Williams (1959) suggested that heterosis could be explained by dominance or partial dominance of alleles for the favourable expression of the component characters. Ramanujam _et al_. (1974) analysed the yield heterosis observed by them in a number of mungbean crosses and concluded that complimentation at the component level as suggested by Williams could largely explain the occurrance of heterosis in the crosses studied.

Jinks (1955) proposed that non-allelic interactions might be the cause of heterosis, rather than special relation between genes at the same locus. Mather (1955) considered heterosis as an expression of genetic balance which might vary with breeding behaviour of species. Jinks and Jones (1958) stated that heterosis is a complex genetic phenomenon depending upon the balance of additive action, dominance action, and interaction of homozygous x homozygous and homozygous x heterozygous component as well as on the distribution of genes in the parent lines.

Hays and Foster (1976) suggested that the heterosis may result from one or more of the following genetic interactions.

i) The accumulated action of favourable dominant or semi-dominant genes dispersed among the two parents i.e., dominance

ii) complementary interaction of additive, dominant or recessive genes at different loci, i.e., non-allelic interactions or epistasis.

iii) favourable interaction between two alleles at the same locus i.e., intra-locus or intra-allelic interaction referred to as overdominance.

If heterosis is due to overdominance, it is impossible to fix such heterosis in the homozygous condition in subsequent segregating generations. Only by the production of F_1 hybrids or by the duplication of the relevant chromosome segments, heterozygosity can be maintained.

According to Falconer (1960), the amount of heterosis expressed as the difference between F_1 and the mid-parental value is directly proportional to Σdy^2 where [d] is the dominance comoponent of gene action and y is the difference between the gene frequencies and the parents. Furthermore, he stated that-

a) Loci without dominance (d=0) cause neither heterosis nor inbreeding depression.

b) The amount of heterosis following a cross between two particular lines or populations depends upon the square of the difference of gene frequencies (y^2) between the parents.

c) If some loci are dominant in one direction, some in the other, the effect will tend to cancel out no heterosis may be observed, in spite of dominance at the individual loci, meaning thereby that the occurrence of heterosis depends on directional dominance.

In cotton, it was Mell in 1894 who first observed an increase in fiber length and agronomic characters in the F_1 hybrid of *G. hirsutum* with *G. barbadense*, as compared to parents. Cook (1909) was the first to suggest the possibility of economic exploitation of this hybrid. Since then hybrid vigour has been reported at intraspecific and interspecific levels both in diploid and tetraploid cotton. The first step in this direction was the release of first commercial intra-hirsutum hybrid H_4 (Patel, 1971). The work on heterosis was reviewed by Loden and Richmond (1951), Davis (1978), Singh (1983), Singh (1987) and Singh and Narayanan (1992).

Marani (1963) reported many aspects on heterosis in cotton viz., boll number and boll weight in intraspecific hybrids and boll number in interspecific hybrids were major components of yield heterosis in cotton. The extent of heterosis was higher in interspecific crosses than in intraspecific crosses. Heterosis for boll weight was usually observed G. hirsutum crosses. In intraspecific crosses, bolls are usually larger than the mid parent sometime even over better parent. Heterosis for boll size is associated with heterosis for lint index and seed index. The performance of intraspecific crosses was usually related to performance of parental varieties.

Tetraploid cottons exhibited lower heterosis than diploids, which was partially due to gene duplication in tetraploids. Thus inbreeding depression was less in G. hirsutum. Any heterosis found in good hybrid will probably persist for several generations and will be of importance in synthetic variety production (Young and Murray, 1966).

In upland cotton, a close relationship was observed between the genetic diversity of parental varieties and performance of their hybrids for lint yield (Hawkins et al., 1965). Heterosis was also related to genetic divergence of sympodia and bolls per plant (Siddiqui et al., 1976).

Brown (1942) studied the effect of inbreeding carried over a 10 year period in Upland cotton and observed that while flowering rate, boll size and seed cotton production were reduced, respectively by 6.2, 9.3 and 9.3 per cent; seed germination, vegetative growth, earliness, staple length, ginning outturn and seed weight were not appreciably affected. Extent of natural crossing considerably influences the degree of inbreeding depression (Simpson, 1948). Simpson and Duncan (1953) reported reduced yields by about 15 per cent upon prolonged selfing. Richmond (1951) suggested several factors as contributory or related to reduction of productivity following inbreeding: (i) degree of heterogeneity of the original parent stock; (ii) improbability of accumulating and holding all or most of the favourable yield genes in one homozygous line; (iii) mechanical mixtures and cross pollinations with inferior varieties; and (iv) selection for one or few characters without regard to other important characters in the genetic complex.

Al-Rawi and Kohel (1969) observed that both heterosis and inbreeding depression effects were small but significantly different from zero for plant height, and number of nodes. Singh et al. (1983a) observed negative heterosis for first fruiting node number.

Heterotic effects for boll number were found to be small (Al-Rawi and Kohel, 1969) significant (Thombre et al., 1982), low in magnitude (Singh et al., 1983b), positive (Singh et al., 1983a) and 17.04% (Singh et al, 1990) and small and moderate Inbreeding effects were reported for the same trait by Al-Rawi and Kohel (1969) and Singh et al. (1990) respectively.

Singh et al. (1983b) observed low magnitude of heterosis for boll weight while Wang (1988) observed boll size and lint percentage played more important part in yield increase in hybrids than in varieties. Singh et al. (1990) observed a heterosis and inbreeding depression of 1.96 and 2.75 respectively for this trait.

Singh et al. (1983b) observed low magnitude of heterosis for seed index and lint index.

Marani (1963) reported that mid parent heterosis for lint yield averaged from 20 to 25% in intraspecific crosses of *G. hirsutum*. Al-Rawi and Kohel (1969) observed that both heterosis and inbreeding depression effects were small but significantly different from zero for yield. Significant heterosis for seed cotton yield was reported by Thombre et al. (1982). Positive heterosis was recorded by Singh et al. (1983a; 1990).

Singh and Narayanan (1992) in their review, observed that heterosis was high for seed cotton yield, moderate to low for boll size and low for ginning percentage and technological characters. Various morphological traits viz., growth habit, plant type, length of sympodia, type of leaf and staple length as well as some genetical traits of parental lines viz., geographical and genetic diversity, agronomic performance adaptability and genetic base were found to play an important role in the manifestation of heterosis in cotton.

Correlations

Correlation coefficients indicate the magnitude of association between pairs of characters and form the basis of selection thereby aiding the plant breeder in developing superior progenies as they provide information that the selection for one character will result in a progress for all positively correlated characters. An attempt must be made to improve correlated characters in desirable direction and in negative direction for characters with undesirable associations.

Al-Rawi *et al*. (1986) and Arshad *et al*. (1993) in commercial cotton varieties reported positive and significant correlation of plant height with seed cotton yield. Singh *et al*. (1992) observed positive correlation of this trait with seed cotton yield. Chimanshette *et al*. (1993) in *G. hirsutum* hybrids and Arshad *et al*. (1993) in *G. hirsutum* varieties observed positive correlation between sympodia and yield.

The relationship between boll number and seed cotton yield was found to be positive and significant in 9 different strains (Javali, 1984). Muhammed Aminkhan *et al*. (1985) also observed positive association between boll number and seed cotton yield. Similar relationship was observed by Zhou (1986), Singh *et al*. (1987), Alam and Islam (1991) and Arshad *et al*. (1993).

A positive and significant association has been generally observed between boll weight and yield (Singh *et al*., 1987; Alam and Islam, 1991; Singh *et al*., 1993).

Singh (1988) reported that biomass was highly associated with seed cotton yield, shoot weight and root weight all of which are thought to be capable of improvement by selection.

Basu and Bhat (1987) observed that harvest index was highly and positively correlated with seed cotton yield, sympodial branches per plant and bolls per plant but independent of plant height and monopodia. Singh *et al*. (1992) observed a negative correlation between harvest index and plant height.

Muhammed Amin Khan *et al*. (1985) in F_4 generation and

Al-Rawi *et al*. (1986), observed that seed index was highly correlated with seed cotton yield whereas Chimanshette *et al*. (1990) observed a nonsignificant association in cotton hybrids for the same trait with seed cotton yield.

A very low and nonsignificant association between lint index and seed cotton yield was observed by Singh *et al*. (1987). Tyagi (1987) observed significant but negative correlation of yield with ginning percentage and lint index in F_3 generation.

High yielding strains were selected by exercising selection pressure for medium plant height, higher boll number, boll weight and harvest index in hirsutum cottons by Singh *et al*. (1992).

B. GOSSYPIUM BARBADENSE

Gossypium barbadense is restricted in its cultivation in India to small pockets in the southern parts of the country. It has been believed that conditions of day length and temperature in the northern and penninsular parts of country are not favourable for its cultivation.

Dastur (1949) reported that varieties of *G. barbadense* are sensitive to day length and night temperatures and susceptible to diseases and pests, all of which restrict its distribution.

Based on a review of all the work done in this country, Singh *et al*. (1973) concluded that there is no compelling evidence at present to suggest that attempts to cultivate *G. barbadense* in the northern part of the country are likely to fail because past attempts were based on a limited genetic variability. Suitable crop varieties which are relatively insensitive to photoperiodic and thermal conditions can be evolved, if large enough genetic variability is utilised in breeding programmes. An intervarietal crossing programme in *G. barbadense* was initiated at IARI with a view to generate suitable variability for north Indian conditions and some promising F_2 plants were selected.

Singh *et al.* (1978) reported very poor yields in introduced strains of *G. barbadense* under Punjab conditions.

Mathapati *et al.* (1978) in their study involving 10 varieties of *G. barbadense* of diverse origin observed that yield of seed cotton and boll number exhibited the highest genetic variance. Yield of seed cotton also exhibited high phenotypic and genotypic coefficients of variation.

Chavan (1980) and Sharma and Govila (1981) reported promising selections for different traits viz., earliness, habit, height and yield in *G. barbadense* via intervarietal crosses. For the first time in the history of cotton development in North India, suitable breeding material in *G. barbadense* comparable to that of Southern and Central Zones has been developed as a result of intervarietal crossing programme and wide variability was observed for boll weight and ginning percentage (Govila *et al.*, 1985).

Singh *et al.* (1993) noted mean, range and coefficient of variation in F_3 generation of *G. barbadense* intraspecific crosses. In a promising cross Pima S2 x 18-2-3, mean, range and C.V. were 1189 kg/ha, 783-1830 kg/ha and 28.5% respectively for yield.

Character associations in *Gossypium barbadense*

Berdymuradov (1976) observed a negative correlation between fiber yield and 1000-seed weight in barbadense cotton. Mathapati *et al.* (1978) reported that yield of seed cotton was highly and positively correlated with number of bolls per plant in Egyptian cotton.

Govila *et al.* (1985) recorded highly significant positive correlations between yield and boll number, yield and boll weight, ginning percentage and lint index and seed index and lint index.

Lertprasertrat *et al.* (1987) reported positive correlations for seed cotton yield with number of bolls per plant and boll size.

Yakubov and Shermukhamedov (1987) in their study on relationship between economic yield and biological yield of several varieties and hybrids observed that harvest index was positively correlated with economic yield. Singh *et al.* (1993) observed positive and significant correlation between yield and boll weight in F_3 generation of a *G. barbadense* cross.

Changes in magnitude of variability and character associations

Cotton is predominantly a self pollinated crop, there is little chance of new recombinants to occur after the F_2 generation (Meredith, 1984). Basing the theoretical calculations of linkage associations between parents of diverse genetic backgrounds, Hanson (1959) recommended to include at least one and preferably 3 or 4 generations of selective intermating preceeding to selfing generations, if possible, in the breeding program to ensure a degree of breakup of the linkage groups and to increase the genetic recombinations within linkage group.

Miller and Rawlings (1967) and later Meredith and Bridge (1971) reported independent intercrossing studies which produced similar results. Miller and Rawlings (1967) observed decrease in genotypic variances for six traits for which coupling phase linkages would be expected to predominate and increase for one trait for which repulsion linkages might have been more important. Genotypic correlations between traits tended to shift toward values observed in populations assumed to be more nearly at linkage equilibrium. These observed changes conform with expectations that intermating dissipates initial linkage disequilibrium.

Mean comparisions between the two generations of random mating and selfed populations after reaching F_3 showed small but significant differences for traits, indicating that selection in the intermated population may have taken place or that linked epistasis was involved. Genotypic variances were approximately the same for both populations. The negative genetic correlation between lint yield and fiber strength was decreased by intermating. Genetic correlations between other traits were generally reduced by intermating. These results imply that some modifications of conventional method of cotton breeding are necessary to improve yield and fiber strength. Modifications discussed are the use of random intermating, diallel selective mating, use of selection indexes,backcrossing and bulk breeding (Meredith and Bridge, 1971).

Breeding successes indicate that several generations in intercrossing reduce deleterious genetic associations in cotton germplasm of great diversity (Meredith, 1984).

Bains _et_ _al_. (1982) observed that in NCD, biparental mating populations showed significant increase over F_2 mean for boll weight but increase was limited and inconsistent in case of yield per plant and boll number. By taking composite values into consideration he concluded that intercrosses were, in general, better than F_2 and corresponding F_3 and reached the level of F_1 in some cases. Therefore, there was substantial variation among the segregants which can be exploited by intermating. Secondly, the inbreeding depression did not appear to be large. Therefore, there is a likelihood of considerable additive genetic variation becoming available provided intermating is practised to release the variability.

Tyagi (1986, 1987, 1994) reported the alteration in character associations among yield and quality traits (e.g. for yield and halo length associations changed from negative significant to positive nonsignificant) in biparental intermating populations compared to F_3 population in upland cotton.

Significant improvements in yield components were observed in selective and random crossing compared to the values obtained in the F_3 from selfing of the F_2. Generally selective crossing gave better results than random crossing (Govila _et_ _al_., 1988). In contrast, Lu _et_ _al_. (1990) observed the decrease in phenotypic variance due to selfing in _G. hirsutum_.

Singh (1991) observed the change in correlation from negative side to positive side for number of bolls and boll weight by approach of selective intermating.

The mean yield of six selected lines exceeded that of the F_1 by 5.5%. Each of the six lines was higher in lint yield and lint percentage than the higher parent of the original cross, which indicated that transgressive segregation for these traits had occurred (El-Adl and Miller, 1971). Chavan (1980) also noted the transgressants in the progeny of *G. barbadense* intervarietal crosses.

MATERIALS AND METHODS

The material for the present investigation consisted of F_1, F_2, BC_1, BC_2 and F_3 generations of <u>Gossypium</u> <u>hirsutum</u> cross involving parents Pusa 45-3-6 (P_1) and Pusa 19-27 (P_2) and F_3 and F_4 generations of <u>Gossypium</u> <u>barbadense</u> cross 10-98-P_1 x 11-181-P_2.

The parental material for hirsutum cross was chosen from the existing variability of American cotton. A tall type Pusa 45-3-6 with spreading habit, high biological yield due to high boll number and boll weight and high harvest index was crossed with dwarf genotype Pusa 19-27 which was characterised with low biological yield and moderately high harvest index during Kharif 1990 at Indian Agricultural Research Institute (IARI), New Delhi.

The parents and F_1s were grown in winter season nursery at Coimbatore during 1990-91. The backcrosses to either parents were attempted at Coimbatore. During Kharif season of 1991 intra-hirsutum cross, Pusa 45-3-6 x Pusa 19-27 was grown at New Delhi, in a set comprising of parents, F_1s, F_2s, BC_1s and BC_2s in a compact family block design with two replications. In 1992, Kharif the plants with high harvest index in F_2 were selected keeping a selection pressure of 0.10 and the progenies of the selected plants were grown in a replicated progeny row trial with three replications in RBD at New Delhi.

In <u>Gossypium</u> <u>barbadense</u>, F_3 single plants of a cross involving dwarf and low yielder parent 10-98-P_1 and tall moderate yielder parent (11-181-P_2), were selected. The selected plants were subjected to three different mating systems viz., selective intermating, open (random) pollination and self pollination. In selective intermating selected plants were mated and their crossed produce advanced to next generation (F_4). In open (random) pollination, the selected plants were crossed with pollen from other random plants. In self pollination, plants were selfed with their own pollen. In rainy season of 1993, the progenies from the three mating systems were grown in a progeny row trial. Data for the plant type characters were recorded. The characters under study were:

i) Plant height: The measurement was taken from cotyledonary node to the tip of the main stem at the time of maturity in centimetres.

ii) First fruiting node number: Total number of nodes from the base to the node bearing first fruiting branch on the main stem were counted and recorded.

iii) Monopodia: Number of vegetative branches emerging directly from the main shoot were recorded at the time of maturity.

iv) Sympodia: The number of fruiting branches were recorded at the time of maturity.

v) Boll number: The total number of opened bolls picked from each plant.

vi) Boll weight (g): Seed cotton of three bolls picked from each plant at second picking was weighed.

vii) Economic yield (g): Total produce of all the pickings of each plant was collected and weighed in grams.

viii) Biological yield (g): Individual plants were cut back at the ground level and were dried in oven and weighed + (vii).

ix) Harvest index: It is the ratio of economic yield to biological yield expressed in percentage.

x) Seed index (%): Weight of 100 well developed healthy seeds from each plant, was recorded in grams.

xi) Ginning percentage: It is the proportion of lint to seed cotton expressed in percentage.

xii) Lint index: It is the weight of lint obtained from hundred seeds usually calculated by

$$\text{LI} = \frac{\text{Seed index x Ginning percentage}}{100 - \text{Ginning percentage}}$$

Statistical Methods

The data recorded on different characters were subjected to the following statistical analyses.

Gossypium hirsutum

Generation mean analysis: The estimates of gene effects and interactions were obtained from the generation mean analysis following Jinks and Jones (1958) and Mather and Jinks (1971).

i) Generation means were calculated from individual plant data as $\overline{X}$ = sum total of observations/number of observations.

ii) Variances of generation means $V\overline{X}$ were obtained dividing the variance within *generation* (VX) by the total number of individuals in that generation.

$$\text{Variance} \quad VX = \frac{\Sigma X^2 - (\Sigma X)^2/n}{n-1} \quad ; \quad V\overline{X} = \frac{VX}{n}$$

where $V\overline{X}$ = variance of generation mean

VX = variance among the individuals within generation

n = number of individuals within generation.

The values of mean($\overline{X}$) and variances of generation means ($V\overline{X}$) were finally used for further analysis.

iii) Scaling tests: The individual scaling tests A, B, C and D of Mather (1949) and Hayman and Mather (1955) were estimated and their standard errors were estimated for calculating 't' values associated with the values of A, B, C and D as under.

$$A = 2\overline{B}_1 - \overline{P}_1 - \overline{F}_1$$

$$VA = 4V\overline{B}_1 + V\overline{P}_1 + V\overline{F}_1$$

$$B = 2\overline{B}_2 - \overline{P}_2 - \overline{F}_1$$

$$VB = 4\ V\overline{B}_2 + V\overline{P}_2 + V\overline{F}_1$$

$$C = 4\overline{F}_2 - 2\overline{F}_1 - \overline{P}_1 - \overline{P}_2$$

$$VC = 16\ V\overline{F}_2 + 4V\overline{F}_1 + 4V\overline{P}_1 + V\overline{P}_2$$

$$D = 2\ \overline{F}_2 - \overline{B}_1 - \overline{B}_2$$

$$VD = 4\ V\overline{F}_2 + V\overline{B}_1 + V\overline{B}_2$$

The standard errors (SE) of A, B, C and D have been computed from variances,

e.g. for A, $t = A/SE(A)$. The significance of 't' was seen from t-table using appropriate degrees of freedom, e.g. $dfA = dfVB_1 + dfVP_1 + dfVF_1$.

iv) Estimation of gene effects and interactions

a) Six-parameter model: The components of generation means were analysed for digenic interaction in *G. hirsutum* cross where the additive-dominance model was found inadequate. The estimates of various gene effects and non-allelic interactions were computed according to Jinks and Jones (1958).

m = mean $= \frac{1}{2}\,\overline{P}_1 + \frac{1}{2}\,\overline{P}_2 + 4\,\overline{F}_2 - 2\,\overline{B}_1 - 2\,\overline{B}_2$

$[d]$ = Additive effect $= \frac{1}{2}\,\overline{P}_1 - \frac{1}{2}\,\overline{P}_2$

$[h]$ = Dominance effect $= 6\,\overline{B}_1 + 6\overline{B}_2 - 8\,\overline{F}_2 - \overline{F}_1 - \frac{3}{2}\,\overline{P}_1 - \frac{3}{2}\,\overline{P}_2$

$[i]$ = Additive x additive gene interaction $= 2\,\overline{B}_1 + 2\,\overline{B}_2 - 4\overline{F}_2$

$[j]$ = Additive x dominance gene interaction $= 2\overline{B}_1 - \overline{P}_1 - 2\overline{B}_2 + \overline{P}_2$

$[l]$ = Dominance x dominance gene interaction $= \overline{P}_1 + \overline{P}_2 + 2\overline{F}_1 + 4\overline{F}_2 - 4\overline{B}_1 - 4\overline{B}_2$

Where,

$\overline{P}_1, \overline{P}_2$ = means of the parents of a cross

$\overline{F}_1, \overline{F}_2$ = means of the first and second generation of a cross

$\overline{B}_1, \overline{B}_2$ = means of the backcross (F_1 x P_1) and (F_1 x P_2) progenies.

Variances of gene effects and corresponding degrees of freedom (df) were computed using the formula given as-

$$V_m = \frac{1}{4} V\bar{P}_1 + \frac{1}{4} V\bar{P}_2 + 16\ V\bar{F}_2 + 4V\bar{B}_1 + 4V\bar{B}_2$$

$$df_m = df\ VP_1 + df\ VP_2 + df\ VF_2 + dfVB_1 + dfVB_2$$

$$V_d = \frac{1}{4} V\bar{P}_1 + \frac{1}{4} V\bar{P}_2$$

$$df_d = dfVP_1 + dfVP_2$$

$$V_h = 36\ V\bar{B}_1 + 36\ V\bar{B}_2 + 64\ V\bar{F}_2 + V\bar{F}_1 + \frac{9}{4} V\bar{P}_1 + \frac{9}{4} V\bar{P}_2$$

$$df_h = dfV\bar{B}_1 + dfV\bar{B}_2 + dfV\bar{F}_2 + dfV\bar{F}_1 + dfV\bar{P}_1 + dfV\bar{P}_2$$

$$V_i = 4\ V\bar{B}_1 + 4\ V\bar{B}_2 + 16\ V\bar{F}_2$$

$$df_i = dfVB_1 + dfVB_2 + dfVF_2$$

$$V_j = 4\ V\bar{B}_1 + V\bar{P}_1 + 4\ V\bar{B}_2 + V\bar{P}_2$$

$$df_j = dfVB_1 + dfVP_1 + dfVB_2 + dfVP_2$$

$$V_l = V\bar{P}_1 + V\bar{P}_2 + 4V\bar{F}_1 + 16\ V\bar{F}_2 + 16V\bar{B}_1 + 16V\bar{B}_2$$

$$df_l = dfVP_1 + dfVP_2 + dfVF_1 + dfVF_2 + dfVB_1 + dfVB_2$$

Standard errors of all the six estimates of gene effects were determined by taking square of variances.

b) Three parameter model: Three parameter model given by Jinks and Jones (1958) was utilised for characters with no epistatic interaction.

$m = \frac{1}{2}\,\overline{P}_1 + \frac{1}{2}\,\overline{P}_2 + 4\,\overline{F}_2 - 2\overline{B}_1 - 2\overline{B}_2$

$d = \frac{1}{2}\,\overline{P}_1 - \frac{1}{2}\,\overline{P}_2$

$h = 6\overline{B}_1 + 6\overline{B}_2 - 8\,\overline{F}_2 - \overline{F}_1 - \frac{3}{2}\,\overline{P}_1 - \frac{3}{2}\,\overline{P}_2$

The variances of these estimates are calculated as follows:

$V_m = \frac{1}{4}\,V\overline{P}_1 + \frac{1}{4}\,V\overline{P}_2 + 16\,V\overline{F}_2 + 4\,V\overline{B}_1 + 4\,V\overline{B}_2$

$V_d = \frac{1}{4}\,VP_1 + \frac{1}{4}\,VP_2$

$V_h = 36\,V\overline{B}_1 + 36\,V\overline{B}_2 + 64\,V\overline{F}_2 + V\overline{F}_1 + \frac{9}{4}\,V\overline{P}_1 + \frac{9}{4}\,V\overline{P}_2$

The test of significance of gene effects and interactions were carried out by 't' test. The calculated 't' was compared with tabulated value for 't' at 0.05 probability levels of significance against appropriate degrees of freedom, e.g. $df_d = dfVP_1 + dfVP_2$

$t = (X)/SE(X)$

where (X) = is any one of the six or three estimates of gene effects.

Heritability, expected genetic gain, heterosis and inbreeding depression: These were calculated using the following formulae:

i) <u>Heritability</u> (broadsense) $h^2_b = \frac{VF_2 - VE}{VF_2}$ or $h^2_b = \sigma^2 g / \sigma^2 p$

where $VE = \frac{VP_1 + VP_2 + VF_1}{3}$; h^2_n = regression of F_3 progeny mean on F_2 parents.

$\sigma^2 g$ = estimate of genotypic variance

$\sigma^2 p$ = estimate of phenotypic variance (Allard, 1960)

ii) Expected genetic gain = $i \times h_b^2 \times \sigma p$

i = Intensity of selection (e.g. 1.76 for 10% selection pressure)

σp= phenotypic standard deviation of F_2

expected genetic gain was expressed in per cent of the population (F_2) mean (Allard, 1960).

Heterosis over mid parent, over better parent and from estimates of genetic parameters were expressed in percentage and were estimated as below:

iii) Heterosis over mid parent = $\frac{F_1 - \overline{MP}}{\overline{MP}} \times 100$

iv) Heterosis over better parent = $\frac{F_1 - \overline{BP}}{\overline{BP}} \times 100$

where, F_1 = mean value of hybrid for a character under study

$\overline{MP}$ = mean value of mid parent for a character under study

$\overline{BP}$ = mean value of better parent of a cross.

v) Heterosis from genetic parameters (Mather and Jinks, 1971)

For positive heterosis = $\overline{F}_1 - \overline{P}_1 = [h + l] - [d + i]$

For negative heterosis = $\overline{F}_1 - \overline{P}_2 = [h + l] - [-d + i]$

For characters, first fruiting node number and monopodia in cotton, parent with lower value was considered as better parent.

vi) Inbreeding depression (ID): It was measured as the decrease of F_2 in its mean performance over F_1 and is expressed in percentage.

$$ID = \frac{\overline{F}_1 - \overline{F}_2}{\overline{F}_1} \times 100$$

$\overline{F}_1$, $\overline{F}_2$ are means of F_1 and F_2 population respectively. The standard error (SE) for heterosis and inbreeding depression were calculated from sampling variance of generation means ($V\overline{X}$) used in the estimation.

$$\text{SE for heterosis over mid parent} = \sqrt{V\overline{F}_1 + V\overline{MP}}$$

$$\text{SE for heterosis over better parent} = \sqrt{V\overline{F}_1 + V\overline{BP}}$$

$$\text{SE for inbreeding depression} = \sqrt{V\overline{F}_1 + V\overline{F}_2}$$

The differences, $\overline{F}_1 - \overline{BP}$, $\overline{F}_1 - \overline{MP}$ and $\overline{F}_1 - \overline{F}_2$ were tested against their standard errors 't' test with appropriate degrees of freedom.

Analysis of variance of F_3 progenies (families)

Differences between and within families for different characters were statistically analysed using analysis of variance technique following Snedecor and Cochran (1967). The significance was tested by referring F-table values at appropriate degrees of freedom.

Estimation of mean, range and other parameters of variability

(i) The mean value for each character was calculated by dividing the grand total with the corresponding number of observations.

(ii) Range : It is the difference between the lowest and the highest values present in the observations included in the sample.

(iii)Variance $= \dfrac{[\Sigma X^2 - \dfrac{(\Sigma X)^2}{n}]}{(n-1)}$

where Σ , X, X^2 and n are summation, an observation, square of an observation and number of observations respectively.

(iv) Coefficient of variation: The coefficients of variation were calculated using the formulae adopted by Burton (1952).

(a) Genotypic coefficient of variation (GCV)= $\dfrac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$

(b) Phenotypic coefficient of variation (PCV)= $\dfrac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$

where $\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

$\bar{X}$ = general mean of the character.

(v) Transgression : Frequency of transgression in F_4 generation advanced from F_3 by three different mating systems was estimated by 95 per cent confidential limits for the two parents. Any progeny value falling beyond these limits was considered transgressant.

vi) Frequency distribution: Line graphs and curves were prepared by first grouping the observations into classes with class values as twice the standard deviation estimated from parental variances. The frequencies were plotted against the class values using Harvard graphics.

Character association

Phenotypic correlation coefficients were obtained using formula suggested by Pearson et al. (1921).

$$r_{xy} = \frac{\text{Cov }(X,Y)}{\sqrt{V_{(X)}\ V_{(Y)}}}$$

where r_{xy} = Phenotypic correlation between X and Y

Cov (X,Y) = Covariance between X and Y

$V_{(X)}$ = Variance of X

$V_{(Y)}$ = Variance of Y

The correlation coefficients were compared with the Table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5 per cent level, where 'n' denotes the number of paired observations used in the calculation.

Comparison of means and variances

Means of different samples were tested by 't' test using the following formulae.

$$t = \frac{\bar{X}_1 - \bar{X}_2}{\sqrt{\sigma^2 \left(\frac{1}{n_1} + \frac{1}{n_2} \right)}}$$

σ^2 = Pooled estimates of population variance

$$= \frac{(n_1 - 1)S_1^2 + (n_2 - 1)S_2^2}{(n_1 - 1) + (n_2 - 1)}$$

where S_1^2 and S_2^2 are the estimated variances from two samples, n_1, n_2 are the number of observations in the two samples.

Significance was tested from t-table at $(n_1 + n_2 - 2)$ degrees of freedom. 'F' test was used to test the significance of ratio of two variances, by comparing calculated and Table 'F' values.

$F = \frac{S_2^2}{S_1^2}$ at n_1-1 and n_2-1 degrees of freedom, and S_2^2 is greater of the two variances.

EXPERIMENTAL RESULTS

In the present study, observations were recorded on various plant type characters in segregating populations of tetraploid cottons viz., <u>Gossypium hirsutum</u> and <u>G. barbadense</u>.

In <u>G. hirsutum</u> the observations from parents, F_1, F_2 and backcross generations of a cross Pusa 45-3-6 x Pusa 19-27 were utilised in estimating gene effects and interactions through generation mean analysis. The F_2 population was further characterised by estimating the parameter of heritability and calculating the expected genetic gain. The inbreeding depression observed in F_2 was studied in relation to heterosis observed in F_1 generation for yield and other characters. The magnitude of variability was studied in F_3 population by estimating the parameters of range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and expected genetic gain. The nature of variability in F_3 was examined through character associations.

In <u>G. barbadense</u> the F_4 populations advanced from F_3 following three different mating systems viz., selective intermating, open (random) pollination and self-pollination were studied to compare the efficiency of mating systems in releasing the bound genetic variability through recombinations by dissipating initial linkage disequilibrium and subsequent formation of new recombinants resulting in release of transgressive segregants. The nature of variability was examined through analysis of character associations.

GOSSYPIUM HIRSUTUM

The results of the genetic analysis of G. hirsutum cross are discussed under the heads of (a) generation means, (b) scaling tests and estimates of gene effects and interactions, (c) heritability and genetic gain, (d) heterosis and inbreeding depression, (e) familywise estimates of parameters of variability, and (f) nature of associations in different character pairs in F_3 generation.

a) Analysis of generation means

The mean values along with their standard errors for the characters studied in different generations have been given in Table 1. The wide range in mean values of different generations indicated the existence of substantial genetic variability in the material for different characters studied.

Plant height: The average plant height of the parents ranged from 65.21 cm (Pusa 19-27) to 119.08 cm (Pusa 45-3-6). F_1 was found to be taller than the tall parent Pusa 45-3-6. The F_2 generation had a mean height less than the F_1 showing inbreeding depression. BC_2 mean was higher than P_2 mean and the mean of BC_1 was lower than the mean of P_1.

First fruiting node number: The P_2 (Pusa 19-27) mean was lower than P_1 mean. F_1 exhibited a high mean value leaning towards P_1.

Monopodia: The mean number of monopodia for P_1 was 0.17 while for P_2, it was 0.39. The F_1, BC_1 and BC_2 generations showed a higher mean number of monopodia than either of the parents.

Table 1: Mean performance of six generations of cross Pusa 45-3-6 (P_1) X Pusa 19-27 (P_2) for different characters in Gossypium hirsutum

Character	generation					
	P_1	P_2	F_1	BC_1	BC_2	F_2
Plant height (cm)	119.08 ± 2.84	65.21 ± 2.37	125.88 ± 2.12	103.58 ± 4.85	93.71 ± 1.98	95.38 ± 1.08
First fruiting node number	10.60 ± 0.46	7.95 ± 0.16	10.01 ± 0.38	10.29 ± 0.59	9.74 ± 0.24	9.48 ± 0.12
Monopodia	0.17 ± 0.40	0.39 ± 0.14	0.76 ± 0.17	0.88 ± 0.27	0.71 ± 0.10	0.92 ± 0.73
Sympodia	14.25 ± 2.21	12.26 ± 0.67	14.21 ± 0.55	14.70 ± 0.57	13.74 ± 0.40	15.04 ± 0.21
Boll number	16.33 ± 2.41	8.84 ± 0.85	23.47 ± 2.14	16.41 ± 1.89	16.27 ± 0.92	20.00 ± 0.72
Boll weight@(g)	12.15 ± 0.76	9.06 ± 0.52	11.30 ± 0.34	11.38 ± 0.41	11.39 ± 0.17	10.55 ± 0.14
Economic yield (g)	68.48 ±10.60	23.88 ± 2.26	89.04 ± 7.08	59.58 ± 7.66	60.81 ± 3.93	65.86 ± 2.41
Biological yield (g)	137.35 ±17.12	58.67 ± 4.67	196.98 ± 14.57	140.26 ± 15.78	143.77 ± 7.88	148.68 ± 4.94
Harvest index (%)	48.80 ± 2.71	40.42 ± 1.68	45.73 ± 1.80	42.87 ± 2.75	43.73 ± 0.88	43.98 ± 0.51

@ Three bolls weight.

The F_2 mean was more than F_1 mean.

Sympodia: The mean sympodia number for P_1 was 14.25 and for P_2 was 12.26. The mean number of sympodia in F_1 was at par with $\overline{P}_1$. Backcross progenies followed similar trend with respect to their recurrent parents. There was an increase in mean number of sympodia in F_2 as compared to F_1.

Boll number per plant: The parent Pusa 45-3-6 recorded high number of bolls per plant (16.33) while P_2 recorded lowest mean (8.84). The mean boll number per plant in F_1 generation was higher than that in the better parent (P_1). The mean number of bolls per plant in $\overline{BC}_1$ was at par with $\overline{P}_1$ while BC_2 showed better performance than its recurrent parent P_2. The F_2 mean was lower than F_1 mean.

Boll weight: The three bolls weight mean was maximum in the parent Pusa 45-3-6 (12.15 g) and minimum in Pusa 19-27 (9.06 g). In F_1 the three bolls weight was slightly lower than that in the better parent Pusa 45-3-6. BC_2 showed better mean boll weight performance as compared to its recurrent parent P_2. Mean boll weight of F_2 showed a reduction in comparison to F_1 mean boll weight.

Economic yield per plant: The parents showed wide difference in mean economic yield from 23.88 g in Pusa 19-27 to 68.48 g in Pusa 45-3-6. The F_1 surpassed the better parent. The backcross progeny showed opposite trend with BC_2 exhibiting superior performance over its recurrent parent P_2 while BC_1 showed slightly lower mean yield than P_1. The F_2 mean was lower than that of F_1.

Biological yield: The parents differed widely in biological yield. A high mean value was recorded in Pusa 45-3-6 (P_1) while Pusa 19-27 (P_2) recorded the least. Biological yield in F_1 with mean 196.98 g showed an increase over the biological yield of the better parent. BC_1 and BC_2 also surpassed the mean performance of their respective recurrent parents. The F_2 mean value was lower than F_1.

Harvest index: Among parents, a higher harvest index (48.8%) was recorded by Pusa 45-3-6 as compared to Pusa 19-27 (40.4%). F_1 performance was closer to mid parental value. The backcross progenies showed opposite trend with respect to their parents. There was a decline in mean performance in F_2 over F_1.

(b) Scaling tests and estimates of gene effects and interactions

To test the adequacy of 3-parameter model individual scaling tests (A,B,C and D) were applied. The results are presented in Table 2. The scaling tests A and C were significant for plant height, the test B was significant in first fruiting node number, test C was significant in both monopodia and sympodia while the test D was significant in boll number. The tests B and D were significant in boll weight, while for economic yield, test A was significant. Thus for all the above traits either one or the other scaling test was found significant. All the scaling tests were found to be nonsignificant for biological yield and harvest index indicating adequacy of 3-parameter model for these two traits.

With the presence of epistasis, evident by the significance of scaling tests, various genetic components viz., 6-parameters m, $\hat{d}$, $\hat{h}$, $\hat{i}$, $\hat{j}$ and $\hat{l}$ were estimated for plant height,

Table 2: Scaling tests of generation means for cross Pusa 45-3-6 X Pusa 19-27 for different characters in Gossypium hirsutum

Character	Scaling test			
	A	B	C	D
Plant height (cm)	37.80* ± 10.31	-3.67 ± 5.08	-54.43* ± 7.09	-6.53 ± 5.65
First fruiting node number	-0.03 ± 1.33	1.52* ± 0.63	-0.65 ± 1.01	-1.07 ± 0.68
Monopodia	0.83 ± 0.69	0.34 ± 0.30	1.67* ± 0.62	0.25 ± 0.32
Sympodia	0.94 ± 2.30	1.01 ± 1.18	5.27* ± 2.68	1.66 ± 0.61
Boll number	-6.98 ± 4.98	0.23 ± 2.95	7.89 ± 5.76	7.32* ± 2.55
Boll weight$^@$(g)	-0.69 ± 1.17	2.42* ± 0.71	-1.61 ± 1.27	1.67* ± 0.52
Economic yield (g)	-38.36* ± 19.74	8.70 ±10.82	-7.0 ±20.27	11.33 ± 9.78
Biological yield (g)	53.81 ± 38.71	31.89 ±21.96	4.74 ±39.42	13.33 ±20.20
Harvest index (%)	-8.79 ± 6.39	1.31 ± 3.04	-4.76 ± 5.23	1.36 ± 3.07

@ Three bolls weight. * Significant at P = 0.05

Table 3: Estimates of components of generation means based on six parameter model for cross Pusa 45-3-6 x Pusa 19-27 in *Gossypium hirsutum*

Character	Components					
	m	[d]	[h]	[i]	[j]	[l]
Plant height (cm)	79.09* ± 11.46	26.94* ± 1.85	18.39 ± 33.08	13.06 ± 11.31	-34.13* ± 11.09	28.41 ± 22.09
First fruiting node number	7.14* ± 1.38	1.32* ± 0.25	6.51 ± 4.03	2.14 ± 1.36	-1.55 ± 1.37	-3.63 ± 2.75
Monopodia	0.75 ± 0.68	-0.08 ± 0.22	0.69 ± 1.94	-0.50 ± 0.64	0.49 ± 1.00	-0.67 ± 1.31
Sympodia	16.28* ± 1.67	0.99 ± 1.15	-3.74 ± 4.68	-3.32* ± 1.21	-0.07 ± 2.47	1.37 ± 3.21
Boll number	27.23* ± 5.25	3.75* ± 1.28	-25.15 ± 14.55	-14.64* ± 5.09	-7.49 ± 4.93	21.39* ± 10.21
Boll weight@ (g)	7.27* ± 1.14	1.55* ± 0.46	9.11* ± 3.22	3.34* ± 1.05	-3.11* ± 1.28	-5.07* ± 2.18
Economic yield (g)	68.84* ± 20.20	22.30* ± 5.41	-32.12 ± 57.30	-22.66 ± 19.56	-47.06* ± 20.16	52.32 ± 39.45
Biological yield# (g)	124.68* ± 41.36	39.34* ±11.05	23.74* ± 0.20			
Harvest index# (%)	47.33* ± 6.34	4.19* ± 1.60	-11.80* ± 18.54			

* : Significant at P [illegible] 0.05; @ Three bols weight; # Three parameter model

first fruiting node number, monopodia, sympodia, boll number, boll weight and economic yield, whereas with the non-significance of any of the scaling tests for biological yield and harvest index only three genetic parameters viz., m, d and h were estiamted, for these two traits. The estimates of gene effects and gene interactions are presented in Table 3.

Plant height: Scaling tests A and C gave significant values for plant height, indicating the presence of epistasis. Based on the estimates of 6 parameter model it was observed that [d] (additive effect) and [j] (additive x dominance gene interaction) were significant. The additive gene effect [d] was positive whereas additive x dominance interaction[g] was found to be negative.

First fruiting node number: Additive effect [d] was found to be significant for first fruiting node number while the estimates of dominance effect [h] and all the three interactions were higher in magnitude than their respective standard errors.

Monopodia: The significance of scaling test C showed the inadequacy of 3-parameter model for monopodia but none of the estimates of the gene effects and gene interactions were found to be significant. The [h] and [j] were positive while [i] and [l] were negative.

Sympodia: Only the additive x additive gene interaction [i] was found to be significant for sympodia.

Boll number: The individual sacling test D exhibited significant value for boll number. The 6-parameter model also showed significance of [d] (additive effect), [i] (additive x additive gene interaction) besides [l] (dominance x dominance gene interaction). But the magnitude of [l] was much more than [d]. Moreover, [i] component was negative.

Three bolls weight: Boll weight exhibited the presence of epistasis. For this trait all gene effects and interactions were found to be significant. The component [d] (additive effect), [i] (additive x additive gene interaction) and [h] (dominance effects) were positive while [j] and [l] were found to be negative. The magnitude of dominance effect was maximum. The estimates of components [d] and [j] as also the estimates of [h] and [l] were opposite in sign.

Economic yield: Presence of epistasis in the expression of economic yield was indicated by the scaling test A. Both [d] (additive effect) and [j] (additive x dominance) were significant but opposite in sign.

Biological yield and harvest index: The non-significant individual scaling tests indicated the absence of epistasis and adequacy of 3-parameter model for biological yield and harvest index. The trait biological yield was found to be governed by additive as well as dominance gene effects. However, the magnitude of additive component [d] was higher than dominance component [h]. The additive gene effect [d] was significantly responsible in the expression of harvest index.

(c) Heritability and expected genetic gain

The data obtained from six generations viz., P_1, P_2, F_1, F_2, BC_1 and BC_2 of the cross Pusa 45-3-6 x Pusa 19-27 were utilized to estimate heritability and expected genetic gain

Table 4: Estimates of broadsense heritability (h^2_b), expected genetic gain (EGG), heterosis and inbreeding depression in *Gossypium hirsutum* cross Pusa 45-3-6 x Pusa 19-27

Character	h^2_b (%)	EGG (% of mean)	Heterosis (%)			Inbreeding depression (%)
			Over mid-parent (%)	Over better parent (%)	from estimates of genetic parameters	
Plant height	64.0	21.5	36.07* ±2.81	5.70 ±3.45	-	24.00* ±2.37
First fruiting node number	35.0	12.9	7.86 ±0.45	25.90* ±0.41	-	5.29 ±0.39
Monopodia	25.0	58.7	204.00* ±0.27	347.00* ±0.44	-	21.00 ±0.37
Sympodia	-	-	7.16 ±17.27	-0.28 ±2.26	-	-5.90 ±0.58
Boll number	45.0	47.8	86.41* ±2.50	43.72* ±3.22	32.7	14.78 ±2.26
Boll weight@ (g)	1.0	0.3	6.50 ±0.57	-7.00 ±0.83	5.8	7.00* ±0.36
Economic yield (g)	37.0	40.0	92.80* ±8.91	30.02* ±12.78	-	35.19* ±7.48
Biological yield (g)	47.0	46.4	100.97* ±17.05	30.27 ±22.47	-	24.52* ±15.38
Harvest index (%)	-	-	2.50 ±2.41	-6.20 ±6.50	-	3.83 ±1.87

*: Significant at P=0.05; -: non-significant estimates of relevant genetic parameters

@ : Three bolls weight.

expressed as per cent of the mean. The results of this analysis are presented in Table 4.

Among various traits, plant height showed the highest heritability (64.0) with an estimated moderate genetic gain. The heritability and genetic gain estimates were high and moderate respectively in first fruiting node number, moderate and high respectively for monopodia, high for boll number, economic yield and biological yield, and very low for boll weight. The traits sympodia and harvest index exhibited predominance of environmental influence with Zero estimates of heritability.

(d) Heterosis and inbreeding depression

Heterosis over mid and better parents and the expected heterosis from the estimates of genetic parameters and the inbreeding depression of F_2 mean over F_1 mean for various characters were computed and are presented in Table 4.

Plant height exhibited significant heterosis over mid parent and significant inbreeding depression. However, heterosis over better parent and heterosis estimated from the estimates of genetic parameters was found to be non-significant.

First fruiting node number showed high heterosis over parent with lower fruiting node number (better parent).

Monopodia exhibited very high heterosis over both mid parent and better parent values. However, the inbreeding depression was found to be non-significant.

The trait sympodia exhibited non-significant heterosis and non-significant inbreeding depression.

The heterosis over mid and better parents was positive and significant for boll number. Heterosis from genetic estimates was found to be 32.7. A positive but non-significant inbreeding depression in F_2 was observed for the same trait.

Boll weight exhibited positive but non-significant heterosis over mid parent only but heterosis over better parent was not observed. The theroetical heterosis from estimates of genetic parameters was 5.8. The inbreeding depression was positive and significant.

Economic yield showed positive and significant heterosis over both mid and better parents. This trait also showed positive and significant inbreeding depression.

The heterotic effects in biological yield were positive and significant over mid parent and positive but non-significant over better parent. The harvest index exhibited non-significant heterosis and inbreeding depression.

(e) Familywise analysis of variability in F_3 generation

Analysis of variance for between and within families for twelve quantitative traits in F_3 generation of *G. hirsutum* cross Pusa 45-3-6 x Pusa 19-27 has been presented in Table 5. The between family mean squares for all characters, except monopodia and harvest index, were found to be significant.

Mean, range, genetic parameters of heritability and expected genetic gain in F_3 generation of *G. hirsutum* are presented in Table 6.

Table 5: **Analysis of variance for Between and Within families for twelve quantitative traits in F_3 generation of Gossypium hirsutum cross 45-3-6 x Pusa 19-27**

Source of Variation	d.f.	Quantitative traits											
		Plant height	First fruiting node number	Monopodia	Sympodia	Boll number	Boll @ weight	Economic yield	Biological yield	Harvest index	Seed index	Ginning percentage	Lint index
Between families	29	688.86*	3.18*	0.30^{ns}	12.00*	61.86*	4.40*	1003.90^{+}	3617.14*	62.30^{ns}	1.45^{+}	23.36*	0.94*
Within families	60	134.43	1.82	0.25	6.64	31.90	2.62	655.44	2206.10	66.61	1.01	10.19	0.44

* : Significant at P= 0.05; + : Significant at P = 0.10; @ Three bolls weight.

ns: non-significant.

Table 6: Estimates of parameters of variability for F_3 *generation of* Gossypium hirsutum *cross Pusa 45-3-6 X Pusa 19-27*

Character	mean	range	Variance	Coefficient of variation		Broadsense heritability (%)	Expected genetic gain (% of mean)
				Genotypic (%)	Phenotypic (%)		
Plant height	93.17	53.00-135.00	293.45	14.77	19.28	58.8	23.33
First fruiting node number	10.51	7.00- 15.00	3.06	6.29	14.51	18.8	5.62
Monopodia	0.37	0.00- 3.00	0.38	34.11	125.03	7.4	19.51
Sympodia	19.81	11.00- 28.00	11.44	7.03	14.53	23.4	7.00
Boll number	18.08	6.00- 40.00	53.95	17.54	35.41	24.5	17.92
Boll weight@ (g)	13.10	6.80- 18.80	4.49	6.53	13.10	24.9	6.70
Economic yield (g)	70.18	15.20-191.50	1019.68	15.76	39.10	16.3	13.08
Biological yield (g)	141.19	42.60-367.70	3875.57	15.60	36.59	18.2	13.69
Harvest index (%)	50.35	18.00- 74.00	73.17	0.06	16.15	0.0	0.00
Seed index	9.64	5.80- 12.88	1.27	3.87	11.17	12.0	2.78
Ginning percentage	31.46	18.83- 49.49	20.55	7.26	11.32	41.2	9.61
Lint index	4.45	2.11- 8.24	0.87	9.80	16.58	34.9	12.00

@ Three bolls weight.

The F_3 means were higher than their parents for most of the characters except in case of plant height and first fruiting node number. The mean yield in F_3 (70.18 g) was higher as compared to that of the better parent Pusa 45-3-6 (68.48 g). Plant height mean for F_3 families exhibited medium stature (93.17 cm). Mean harvest index (50.35%) in F_3 was more than that in the better parent (48.80%). However, first fruiting node mean number remained similar to that in the undesirable parent (P_1).

Range recorded for F_3 family means was highest for biological yield (42.60-367.70 g) followed by economic yield, plant height, harvest index, boll number and ginning percentage. Narrow range was recorded for monopodia, lint index, seed index, first fruiting node number, boll weight and sympodia.

The magnitude of pooled F_3 families variances were significantly higher than that of their parents. Highest phenotypic coefficient of variation was recorded for monopodia (125.03) followed by economic yield (39.10) and biological yield (36.6). Lower values for both genotypic and phenotypic coefficient of variation were observed in first fruiting node number, sympodia boll weight, harvest index, seed index, ginning percentage and lint index. Moderate values of genotypic coefficient of variation were recorded for boll number, economic yield, biological yield and plant height.

The broadsense heritability estimates showed that plant height, ginning percentage and lint index were highly heritable whereas the harvest index and monopodia were least heritable.

Moderate heritability estimates were observed for rest of the characters. The estimates of expected genetic gain expressed as per cent of the mean, were relatively highest for plant height (23.33%) followed by monopodia, boll number, biological yield, economic yield and lint index.

Frequency distributions for the twelve characters were illustrated in Fig. 1 to 7. The plant height, first fruiting node number, sympodia, boll weight, seed index, ginning percentage and lint index showed more or less normal curves whereas curves for monopodia, economic and biological yield were highly skewed. The frequency curve for boll number and harvest index was slightly anormal.

Familywise analysis

The familywise mean, range and variance for 12 characters in 30 families of G. hirsutum cross Pusa 45-3-6 x Pusa 19-27 are given in Table 7.

Significantly higher mean plant height as compared to pooled mean was observed in 16 families. Medium plant height (80-100 cm) was observed in 13 families. Out of these, 4 families namely, 1,19,21 and 22 showed low to moderate range and variance while the rest 9 families viz., 2,3,9,14,16,17,18, 28 and 29 exhibited high range and variance.

For first fruiting node number lower values (compared to pooled mean) were noted in thirteen families. Out of these high range and variance values were observed in four families viz., 11, 13, 16 and 21. Lower mean with low range and

FREQUENCY DISTRIBUTION FOR F3 POPULATION
OF GOSSYPIUM HIRSUTUM CROSS
PUSA 45-3-6 X PUSA 19-27

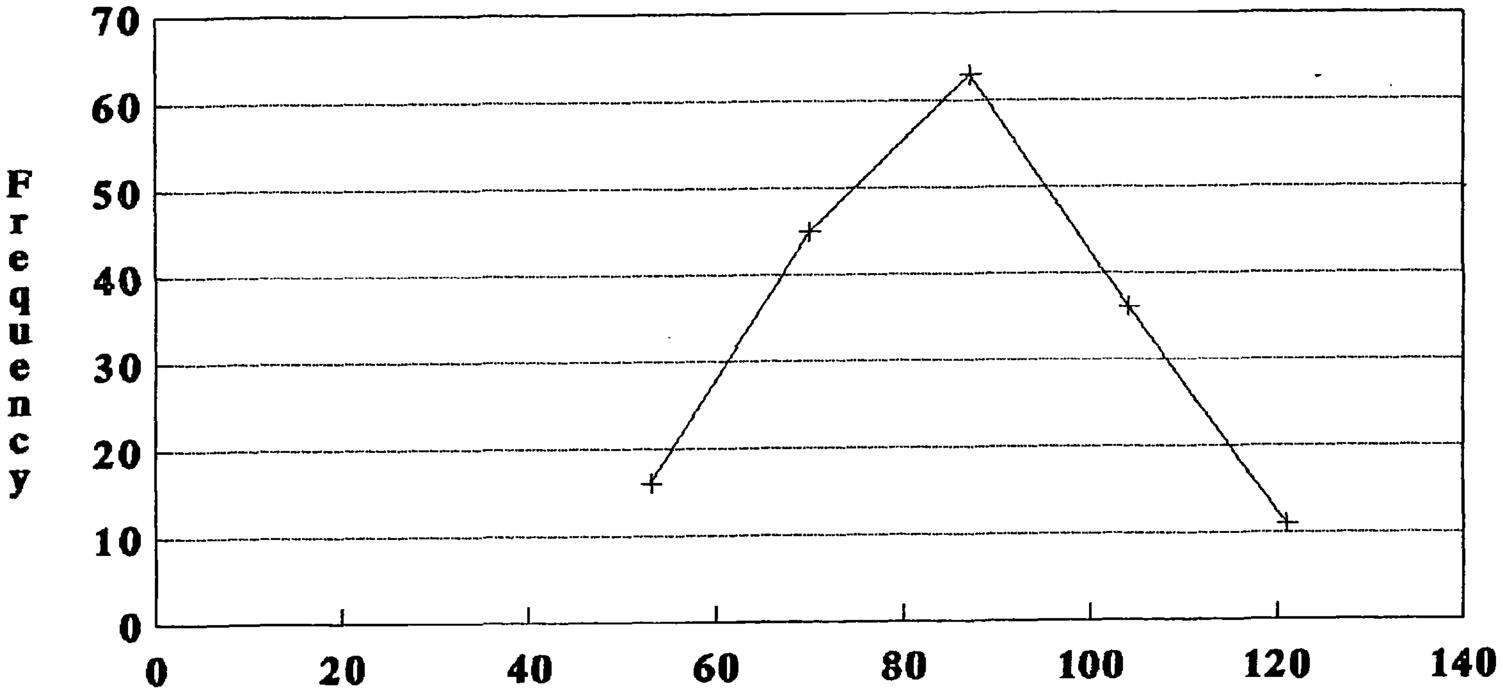

Fig.1

FREQUENCY DISTRIBUTION FOR F3 POPULATION OF GOSSYPIUM HIRSUTUM CROSS
PUSA 45-3-6 X PUSA 19-27

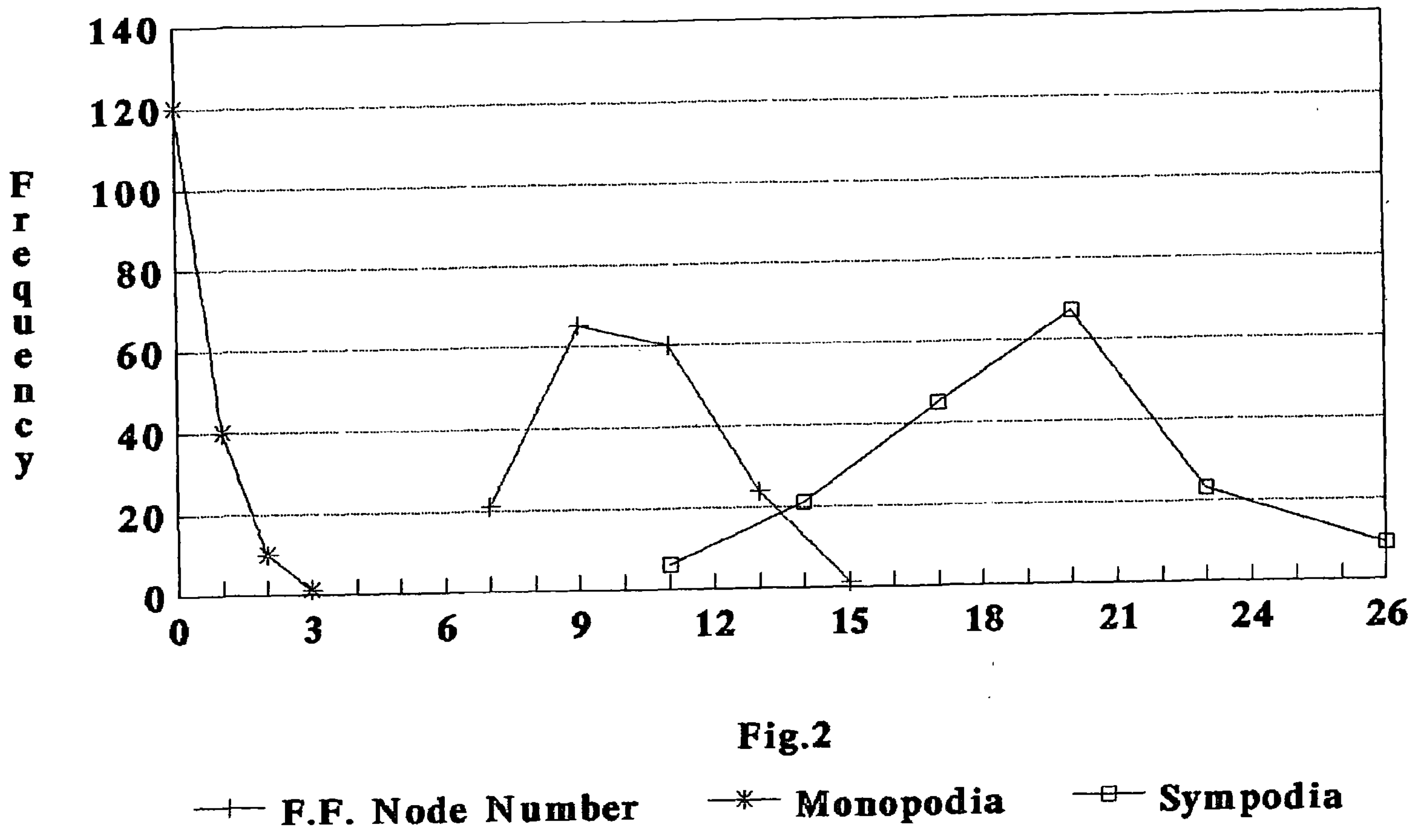

Fig.2

FREQUENCY DISTRIBUTION FOR F3 POPULATION
OF GOSSYPIUM HIRSUTUM CROSS
PUSA 45-3-6 X PUSA 19-27

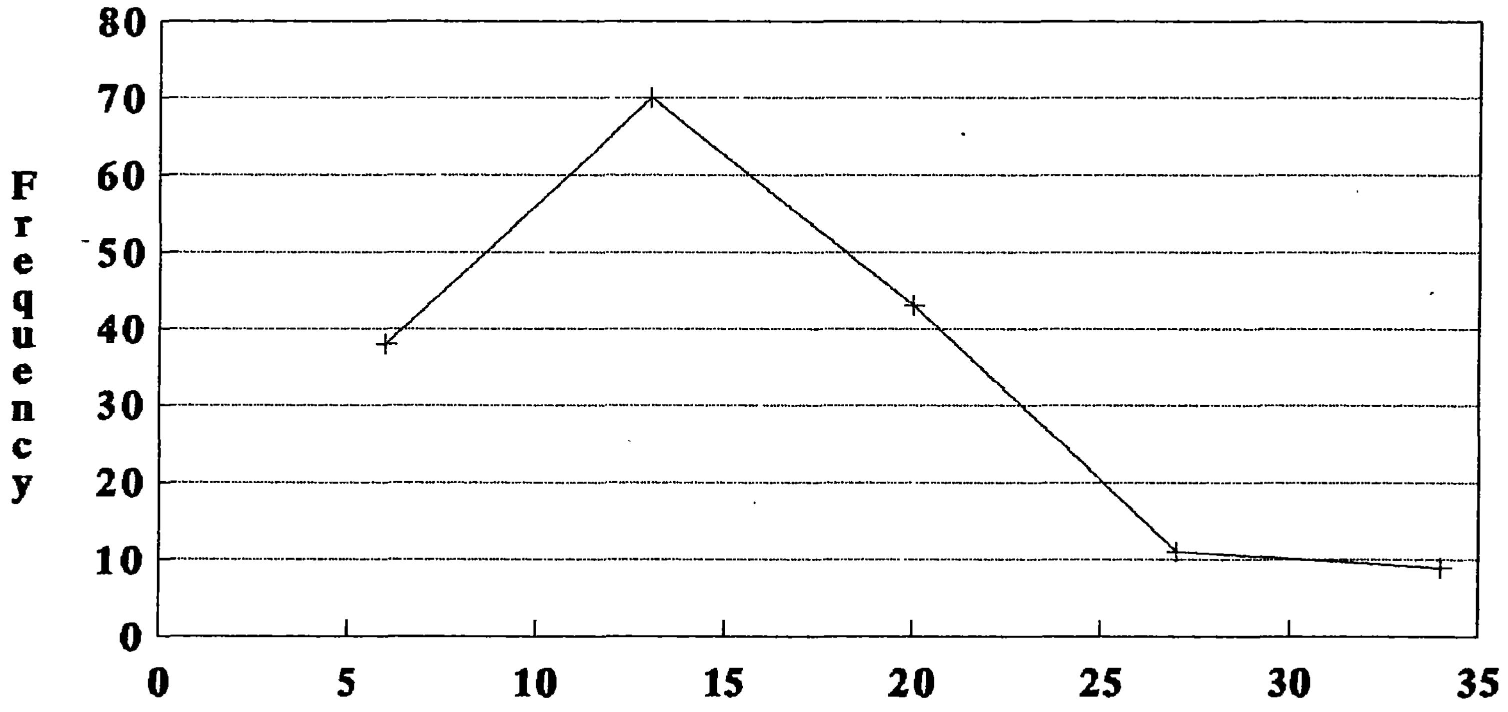

Fig.3

FREQUENCY DISTRIBUTION FOR F3 POPULATION
OF GOSSYPIUM HIRSUTUM CROSS
PUSA 45-3-6 X PUSA 19-27

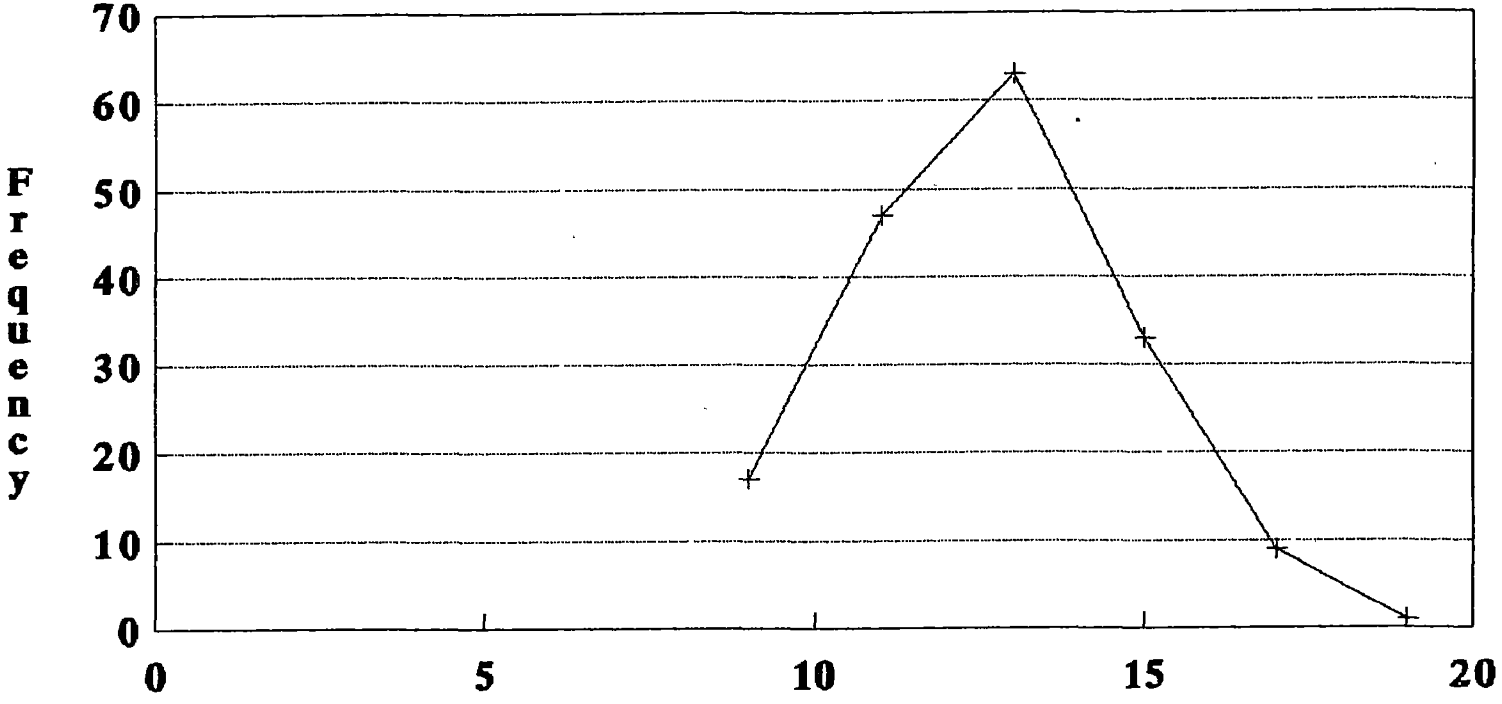

Fig.4

FREQUENCY DISTRIBUTION FOR F3 POPULATION
OF GOSSYPIUM HIRSUTUM CROSS
PUSA 45-3-6 X PUSA 19-27

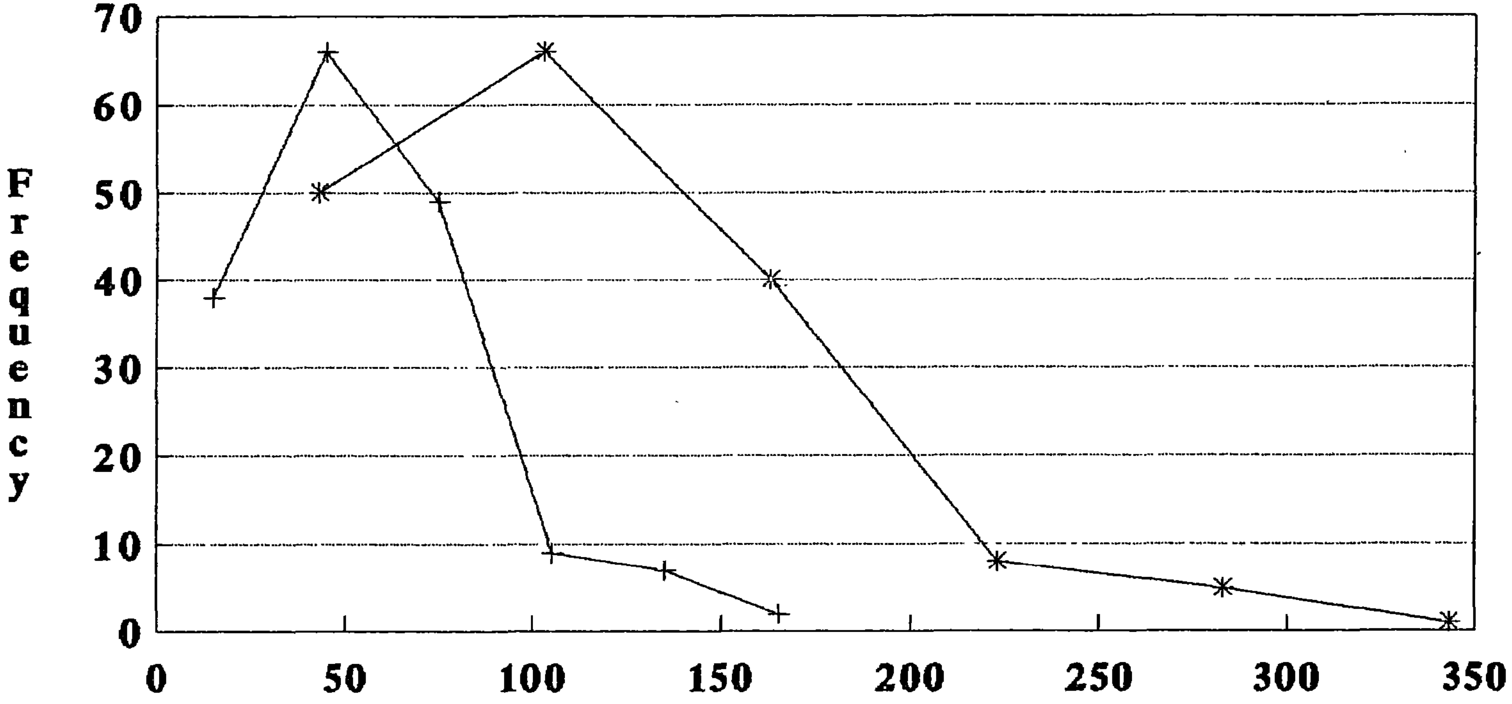

Fig.5

FREQUENCY DISTRIBUTION FOR F3 POPULATION OF GOSSYPIUM HIRSUTUM CROSS PUSA 45-3-6 X PUSA 19-27

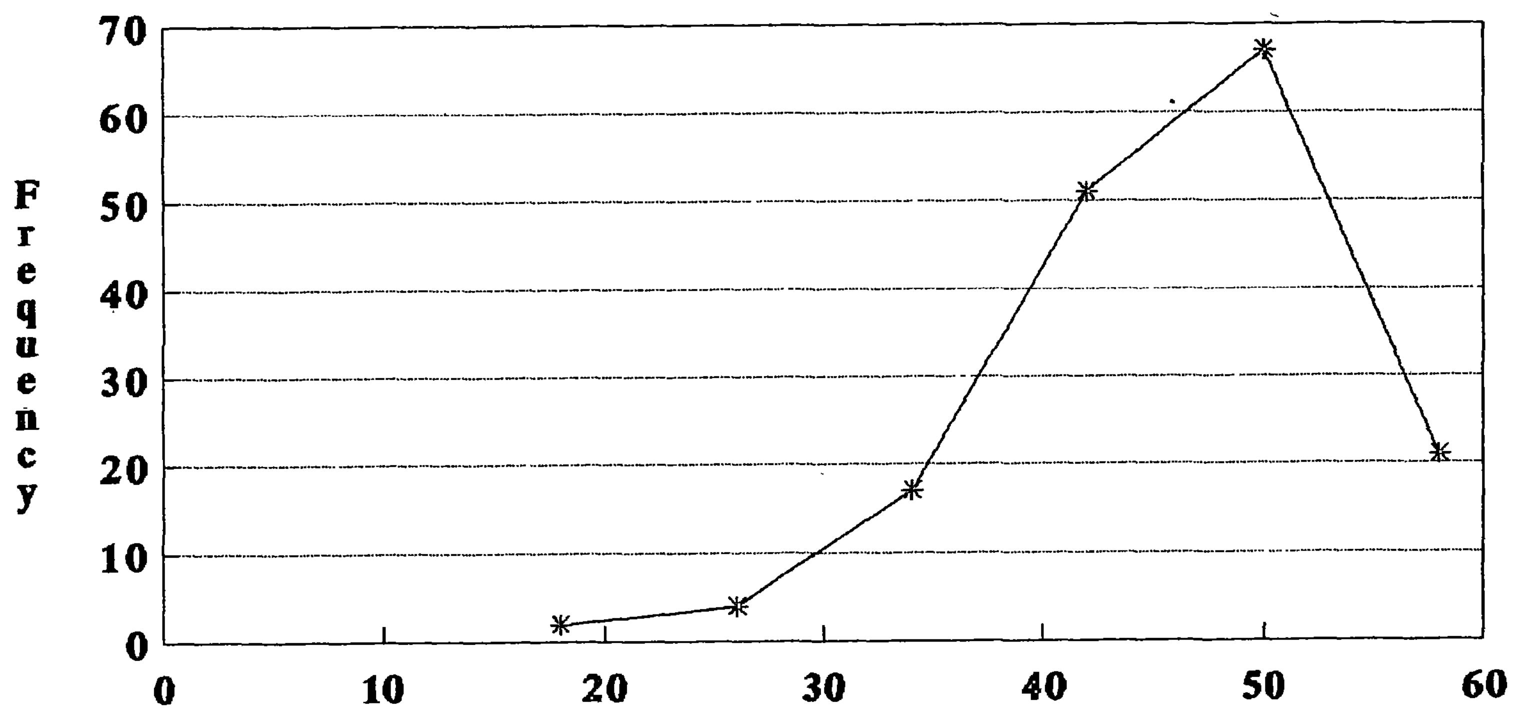

Fig.6

FREQUENCY DISTRIBUTION FOR F3 POPULATION OF GOSSYPIUM HIRSUTUM CROSS PUSA 45-3-6 X PUSA 19-27

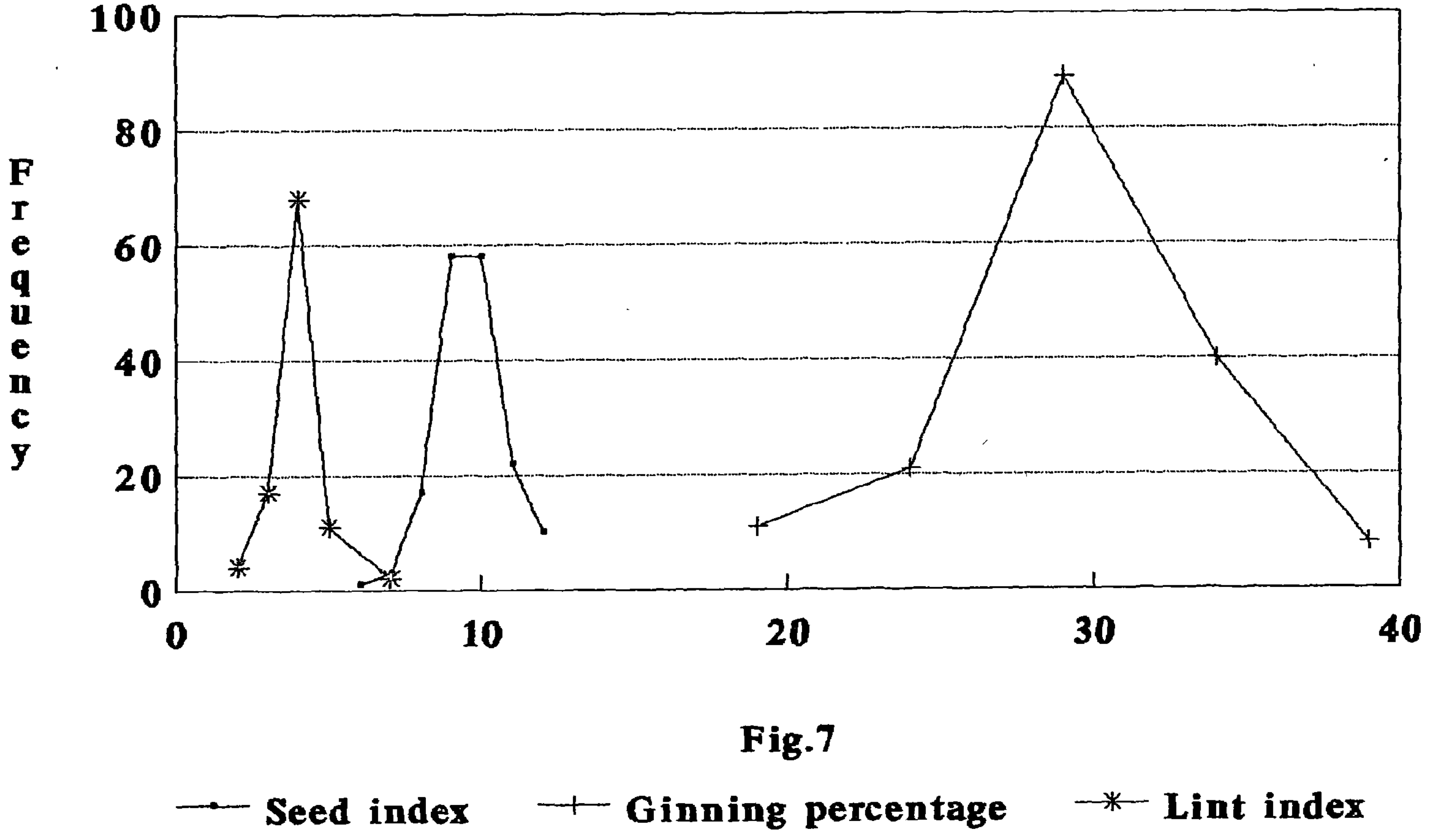

Fig.7

Table 7: Estimates of mean, range and variance for 12 characters in 30 families of F_3 generation of <u>Gossypium</u> <u>hirsutum</u> cross Pusa 45-3-6 X Pusa 19-27

7.1 :Plant height

Family	mean (cm)	range (cm)	variance (cm^2)
1*	83.00 ± 2.95	75.00 - 92.00	43.50
2*	91.71 ± 2.81	81.00 -103.00	55.23
3*	97.00 ± 4.83	83.00 -105.00	93.33
4.	112.63 ± 4.58	101.00 -135.00	167.98
5.	106.86 ± 5.62	81.00 -122.00	220.81
6.	104.17 ± 6.31	75.00 -117.00	238.97
7.	108.20 ± 6.81	91.00 -126.00	231.70
8.	106.38 ± 2.77	95.00 -121.00	61.70
9*	98.75 ± 2.98	90.00 -115.00	70.79
10.	110.60 ± 6.52	96.00 -130.00	212.80
11.	107.29 ± 4.85	83.00 -125.00	164.90
12.	115.75 ± 4.46	105.00 -126.00	79.58
13.	79.00 ± 4.97	65.00 - 94.00	148.40
14*	82.14 ± 3.96	69.00 -100.00	109.81
15.	106.14 ± 2.23	100.00 -118.00	34.81
16*	90.00 ± 5.20	77.00 -101.00	108.00
17*	84.00 - 8.04	74.00 -108.00	258.67
18*	91.57 ± 2.75	78.00 -102.00	52.95
19*	84.83 ± 2.63	78.00 - 94.00	84.83
20.	66.57 ± 2.74	58.00 - 76.00	52.62
21*	85.17 ± 3.38	77.00 - 95.00	68.57
22*	95.40 ± 2.89	88.00 -102.00	41.80
23.	72.80 ± 4.29	59.00 - 81.00	92.20
24.	75.00 ± 2.04	68.00 - 80.00	20.70
25.	69.80 ± 2.35	64.00 - 78.00	27.70
26.	61.33 ± 4.17	53.00 - 66.00	52.33
27.	77.25 ± 2.72	70.00 - 83.00	29.58
28*	93.43 ± 3.87	75.00 -102.00	93.43
29*	100.00 ± 3.30	88.00 -113.00	65.20
30.	112.00 ±13.50	85.00 -135.00	547.00
Pooled	93.17 ± 1.31	53.00 -135.00	293.45

* Families with medium plant height (80-100 cm).

Contd..

7.2 : First fruiting node number

Family	mean	range	variance
1.*	10.54 ± 0.68	9.00-12.00	0.68
2.*	10.29 ± 0.47	8.00-12.00	1.57
3.	11.75 ± 1.03	10.00-14.00	4.25
4.	11.50 ± 0.68	9.00-15.00	3.71
5.	10.00 ± 0.76	7.00-13.00	4.00
6.	11.00 ± 0.52	9.00-13.00	1.60
7.	10.60 ± 0.40	10.00-12.00	0.80
8.	10.88 ± 0.79	7.00-14.00	4.98
9.	10.88 ± 0.61	8.00-13.00	2.98
10.	11.80 ± 0.37	11.00-13.00	0.70
11.*	9.28 ± 0.61	7.00-12.00	2.57
12.	11.00 ± 0.91	9.00-13.00	3.33
13.*	10.00 ± 0.73	8.00-13.00	3.20
14.	11.29 ± 0.89	9.00-14.00	5.57
15.	11.57 ± 0.84	8.00-14.00	4.95
16.*	9.25 ± 1.10	7.00-12.00	4.92
17.	11.00 ± 0.82	9.00-13.00	2.67
18.	11.00 ± 0.65	9.00-13.00	3.00
19.	10.67 ± 0.49	9.00-12.00	1.47
20.*	9.14 ± 0.51	7.00-11.00	1.81
21.*	9.33 ± 0.76	7.00-12.00	3.47
22.	10.80 ± 0.80	8.00-13.00	3.20
23.*	9.80 ± 0.37	9.00-11.00	0.70
24.*	9.20 ± 0.37	8.00-10.00	0.70
25.*	10.40 ± 0.68	8.00-12.00	2.30
26.*	8.00 ± 0.57	7.00- 9.00	1.00
27.*	9.50 ± 0.65	8.00-11.00	1.67
28.	11.86 ± 0.40	10.00-13.00	1.14
29.	11.33 ± 0.42	10.00-13.00	1.07
30.*	9.00 ± 0.00	9.00- 9.00	0.00
Pooled	10.51 ± 0.13	7.00-15.00	3.063

* Families with low first fruiting node number (compared to pooled mean)

Contd...

7.3: Monopodia number

Family	mean	range	variance
1.	0.60 ± 0.25	0.00-1.00	0.30
2.*	0.29 ± 0.18	0.00-1.00	0.24
3.*	0.00 ± 0.00	0.00-0.00	0.00
4.*	0.25 ± 0.16	0.00-1.00	3.71
5.*	0.29 ± 0.18	0.00-1.00	0.24
6.*	0.33 ± 0.21	0.00-1.00	0.27
7.	0.60 ± 0.40	0.00-2.00	0.80
8.	1.00 ± 0.37	0.00-3.00	1.14
9.	0.75 ± 0.25	0.00-2.00	0.50
10.	0.80 ± 0.37	0.00-2.00	0.70
11.*	0.29 ± 0.18	0.00-1.00	0.29
12.	0.75 ± 0.25	0.00-1.00	0.25
13.*	0.17 ± 0.17	0.00-1.00	0.17
14.*	0.29 ± 0.29	0.00-2.00	0.57
15.*	0.00 ± 0.00	0.00-0.00	0.00
16.*	0.00 ± 0.00	0.00-0.00	0.00
17.*	0.00 ± 0.00	0.00-0.00	0.00
18.*	0.00 ± 0.00	0.00-0.00	0.00
19.	0.67 ± 0.42	0.00-2.00	1.07
20.*	0.14 ± 0.14	0.00-1.00	0.14
21.*	0.00 ± 0.00	0.00-0.00	0.00
22.	0.40 ± 0.40	0.00-2.00	0.80
23.*	0.20 ± 0.20	0.00-1.00	0.20
24.	0.40 ± 0.40	0.00-2.00	0.80
25.	0.40 ± 0.25	0.00-1.00	0.30
26.	1.00 ± 0.58	0.00-2.00	1.00
27.*	0.25 ± 0.25	0.00-1.00	0.25
28.	0.57 ± 0.20	0.00-1.00	0.29
29.*	0.17 ± 0.17	0.00-1.00	0.17
30.	0.67 ± 0.33	0.00-1.00	0.33
Pooled	0.37 ± 0.05	0.00-3.00	0.39

* Families with less mean monopodia (compared to pooled mean)

Contd...

7.4 :Sympodia number

Family	mean	range	variance
1.	17.80 ± 0.37	17.00-19.00	0.70
2.	19.00 ± 1.73	14.00-26.00	21.00
3.*	22.25 ± 0.95	21.00-25.00	3.58
4.	18.50 ± 1.17	14.00-25.00	10.86
5.*	20.43 ± 1.50	14.00-26.00	15.62
6.	19.17 ± 0.70	17.00-21.00	2.97
7.	19.00 ± 1.38	14.00-21.00	9.50
8.*	20.50 ± 0.82	17.00-23.00	5.43
9.*	20.50 ± 1.46	14.00-28.00	17.14
10.*	22.40 ± 1.16	20.00-26.00	6.80
11.*	22.71 ± 0.97	20.00-27.00	6.57
12.*	20.25 ± 0.75	19.00-22.00	2.25
13.	19.50 ± 1.69	13.00-26.00	17.10
14.	17.29 ± 0.99	13.00-21.00	6.91
15.*	21.86 ± 0.63	19.00-24.00	2.81
16.*	21.00 ± 1.47	17.00-24.00	8.67
17.	18.75 ± 1.03	16.00-21.00	4.25
18.	17.86 ± 1.88	11.00-26.00	24.81
19.	19.33 ± 0.99	16.00-22.00	5.87
20.	16.71 ± 1.21	11.00-20.00	10.24
21.*	19.83 ± 1.01	16.00-23.00	6.17
22.	19.80 ± 0.97	16.00-21.00	4.70
23.	18.60 ± 1.60	14.00-23.00	12.80
24.	18.80 ± 1.74	12.00-22.00	15.20
25.	17.80 ± 1.59	14.00-23.00	12.70
26.	16.00 ± 1.73	13.00-19.00	9.00
27.*	21.75 ± 1.70	17.00-25.00	11.58
28.*	21.71 ± 1.27	17.00-26.00	11.24
29.*	22.50 ± 0.96	21.00-27.00	5.50
30.*	24.00 ± 1.00	22.00-25.00	3.00
Pooled	19.81 ± 0.26	11.00-28.00	11.45

* Families with high mean sympodia

Contd..

7.5 : Boll number

Family	mean	range	variance
1.	14.20 ± 2.13	9.00-18.00	22.70
2.	16.43 ± 1.48	13.00-24.00	15.29
3.	12.25 ± 3.35	7.00-22.00	44.92
4.*	18.88 ± 1.64	13.00-29.00	21.55
5.*	21.43 ± 3.61	9.00-40.00	91.29
6.	15.33 ± 2.51	7.00-21.00	37.87
7.*	20.20 ± 3.20	10.00-30.00	51.20
8.*	20.88 ± 1.75	13.00-29.00	24.41
9.*	21.50 ± 3.63	10.00-38.00	105.43
10.*	27.00 ± 2.22	22.00-24.00	24.80
11.*	19.57 ± 2.45	11.00-31.00	41.95
12.*	19.25 ± 3.71	9.00-26.00	54.92
13.	15.50 ± 1.84	8.00-21.00	20.30
14.	12.86 ± 1.84	7.00-19.00	23.81
15.*	18.29 ± 3.44	7.00-34.00	82.57
16.	12.75 ± 1.32	9.00-15.00	6.92
17.	17.50 ± 2.60	11.00-23.00	27.00
18.	11.57 ± 1.33	8.00-17.00	12.29
19.	13.33 ± 3.92	6.00-31.00	92.27
20.	12.57 ± 0.78	9.00-15.00	4.29
21.*	19.33 ± 2.42	12.00-27.00	35.07
22.*	20.00 ± 2.03	13.00-24.00	20.50
23.	15.00 ± 3.16	9.00-27.00	50.00
24.	14.20 ± 1.46	9.00-17.00	10.70
25.	14.60 ± 2.46	9.00-21.00	14.60
26.*	19.33 ± 3.83	13.00-24.00	32.33
27.*	23.25 ± 2.49	19.10-30.00	24.92
28.*	25.00 ± 3.17	14.00-36.00	70.33
29.*	24.50 ± 3.34	16.00-35.00	67.10
30.*	27.67 ± 6.49	18.00-40.00	126.33
Pooled	18.08 ± 0.56	6.00-40.00	53.95

* Families with high mean boll number

Contd...

7.6: Boll weight@ (g)

Family	mean	range	variance
1.*	14.18 ± 0.56	13.1-15.9	1.56
2.*	14.09 ± 0.70	11.9-16.8	3.40
3.	11.88 ± 0.66	10.5-13.5	1.72
4.	12.43 ± 0.74	9.3-15.0	4.35
5.*	13.17 ± 0.46	10.8-14.2	1.49
6.	11.35 ± 0.57	9.6-12.8	1.92
7.	12.60 ± 1.15	9.4-14.7	6.65
8.*	13.38 ± 0.76	11.2-17.8	4.66
9.*	14.28 ± 0.45	13.0-16.3	1.63
10.*	13.48 ± 0.97	11.4-17.1	4.66
11.	12.79 ± 0.67	10.5-15.3	3.18
12.	12.76 ± 0.58	11.3-13.7	1.34
13.	11.69 ± 0.56	10.0-13.5	1.89
14.*	13.71 ± 0.96	10.1-16.9	6.41
15.*	14.37 ± 0.81	10.8-17.8	4.63
16.*	14.00 ± 1.62	9.9-17.5	10.55
17.*	14.50 ± 0.80	12.7-16.3	2.58
18.	12.97 ± 0.93	8.9-15.2	6.06
19.*	16.35 ± 0.89	13.5-18.8	4.78
20.	10.84 ± 0.53	9.5-13.4	1.98
21.*	13.62 ± 0.74	11.4-15.7	3.31
22.	12.10 ± 0.49	10.3-13.2	1.19
23.	12.70 ± 0.52	11.5-14.1	1.33
24.	12.98 ± 0.80	11.2-15.6	3.20
25.	12.64 ± 0.96	9.2-14.8	4.63
26.	13.07 ± 1.75	10.5-16.4	9.14
27.	11.30 ± 0.61	9.9-12.6	1.50
28.	12.44 ± 1.13	6.8-15.8	9.033
29.*	13.37 ± 0.56	11.7-15.5	1.88
30.*	13.60 ± 1.87	9.9-16.0	40.80
Pooled	13.10 ± 0.16	6.8-18.8	4.49

@ Three bolls weight; * Families with high mean boll weight.

Contd..

7.7: Economic yield (g)

Family	mean	range	variance
1.	60.60 ± 8.82	37.70 - 83.22	389.02
2.	68.74 ± 8.15	45.50 -104.60	464.57
3.	46.68 ±13.85	24.80 - 87.80	768.16
4.*	74.11 ±10.05	39.20 -138.30	808.85
5.*	78.04 ±13.35	33.40 -131.00	1248.15
6.	54.75 ±10.61	21.50 - 80.40	676.17
7.*	82.90 ±12.43	34.20 -103.30	772.63
8.*	91.06 ±11.19	60.40 -142.00	1001.95
9.*	95.26 ±19.32	45.90 -188.00	2985.17
10.*	105.62 ±10.69	85.70 -144.30	571.49
11.	65.53 ± 9.37	26.50 -100.60	614.59
12.	69.03 ±14.34	33.00 -101.70	822.09
13.	54.25 ± 6.14	33.10 - 71.20	226.46
14.	52.34 ± 8.73	31.00 - 85.20	533.99
15.*	77.08 ±15.83	24.90 -142.70	1754.25
16.	46.28 ±10.88	15.20 - 66.00	473.65
17.	63.15 ± 8.96	41.90 - 83.10	320.97
18.	53.44 ± 9.24	20.90 - 83.00	597.23
19.	61.75 ±16.53	31.00 -141.60	1639.72
20.	42.76 ± 4.18	23.60 - 57.10	122.48
21.*	82.35 ± 6.30	63.40 -101.10	238.24
22.*	75.18 ± 8.12	48.20 - 97.70	329.58
23.	50.52 ±11.59	33.10 - 96.20	671.03
24.	55.38 ± 6.99	36.20 - 73.10	246.89
25.	62.14 ±11.25	36.40 - 97.60	632.60
26.*	78.00 ±16.04	48.60 -103.80	771.48
27.*	73.50 ± 7.89	51.70 - 88.20	249.24
28.*	83.69 ±14.53	47.90 -162.50	1477.53
29.*	84.78 ±11.67	58.20 -123.20	816.40
30.*	116.53 ±38.25	65.90 -191.50	4388.167
Pooled	70.19 ± 2.44	15.20 -191.50	1019.69

* Families with high mean economic yield.
(elite families)

Contd...

7.8 : Biological yield (g)

Family	mean	range	variance
1.	116.04 ± 16.89	68.40-155.50	1427.90
2.*	142.17 ± 12.74	109.80-195.40	1136.06
3.	114.50 ± 33.60	62.00-211.30	4516.26
4.*	150.23 ± 24.41	95.50-304.80	4766.27
5.*	162.59 ± 23.55	69.50-255.50	3883.85
6.	126.10 ± 26.38	42.60-219.10	4176.36
7.*	174.88 ± 30.63	75.10-262.60	4690.65
8.*	185.25 ± 21.83	107.50-284.20	3813.40
9.*	203.01 ± 38.36	88.00-367.70	11770.82
10.*	214.52 ± 25.39	137.40-293.40	3225.07
11.	136.70 ± 17.23	61.40-191.80	2078.02
12.*	156.53 ± 31.19	70.20-202.70	3890.11
13.	99.42 ± 12.33	48.90-129.30	912.04
14.	106.31 ± 21.58	49.20-187.90	3259.95
15.*	156.10 ± 21.73	98.40-237.50	3305.32
16.	88.53 ± 10.03	76.00-118.30	402.63
17.	126.45 ± 14.20	104.40-167.30	806.69
18.	103.37 ± 17.43	48.00-167.60	2127.07
19.	131.37 ± 30.60	77.60-280.20	5619.41
20.	76.77 ± 7.52	50.60- 97.60	395.32
21.*	144.87 ± 9.45	124.40-179.30	535.71
22.*	151.28 ± 17.89	94.60-204.60	1600.42
23.	95.26 ± 19.00	63.40-168.50	1805.67
24.	114.98 ± 13.46	78.70-155.70	905.25
25.	125.24 ± 20.18	76.70-196.80	2036.55
26.	136.50 ± 36.79	82.10-206.60	4059.93
27.	140.73 ± 15.73	117.90-185.40	945.82
28.	176.42 ± 30.51	86.10-335.95	6516.43
29.*	155.40 ± 19.69	92.00-216.60	2325.94
30.*	197.30 ± 43.53	121.90-272.70	5685.19
Pooled	141.19 ± 4.76	42.60-367.70	3875.57

* Families with high mean biological yield.

Contd..

7.9: Harvest index (%)

Family	mean	range	variance
1.*	52.20 ± 1.02	49-55	5.20
2.	48.29 ± 3.71	38-66	96.57
3.	41.50 ± 4.52	31-53	81.67
4.*	50.63 ± 2.88	41-65	66.55
5.	47.57 ± 2.61	36-54	47.62
6.	44.33 ± 3.44	33-55	71.07
7.	48.20 ± 3.70	39-60	68.70
8.	49.25 ± 1.71	44-56	23.36
9.	47.63 ± 2.54	33-55	51.41
10.	50.00 ± 3.48	44-63	60.50
11.	45.57 ± 2.96	35-59	61.29
12.*	52.25 ± 7.69	38-74	236.25
13.*	55.83 ± 3.45	45-67	71.37
14.*	52.00 ± 3.43	39-63	82.33
15.	46.71 ± 4.29	25-60	128.91
16.*	52.50 ± 11.85	18-69	561.67
17.	50.00 ± 4.32	38-58	74.67
18.*	51.71 ± 2.08	41-59	30.24
19.	46.17 ± 3.75	37-62	84.57
20.*	56.14 ± 2.57	47-67	46.47
21.*	56.83 ± 1.78	51-62	18.97
22.	50.00 ± 1.30	46-53	8.50
23.*	52.40 ± 1.44	49-57	10.30
24.	47.80 ± 1.66	43-52	13.70
25.	49.80 ± 4.34	33-56	94.20
26.*	59.00 ± 5.19	50-68	81.00
27.*	53.00 ± 4.79	42-62	92.00
28.	48.00 ± 1.87	40-56	24.33
29.*	54.67 ± 2.51	47-63	37.87
30.*	57.00 ± 6.81	47-70	139.00
Pooled	50.35 ± 0.65	18-74	73.17

* Families with high mean harvest index.

Contd...

7.10: Seed Index

Family	mean	range	variance
1.*	10.28 ± 0.41	9.36 - 11.41	0.83
2.*	9.97 ± 0.38	8.20 - 11.00	1.03
3.	8.44 ± 0.73	6.25 - 9.29	2.14
4.	9.37 ± 0.23	8.13 - 10.00	0.42
5.	9.18 ± 0.36	7.83 - 10.22	0.91
6.	9.00 ± 0.31	8.17 - 10.30	0.57
7.	8.71 ± 0.85	5.80 - 10.74	3.64
8.	9.45 ± 0.28	8.30 - 11.04	0.63
9.*	10.07 ± 0.43	9.36 - 12.88	1.49
10.	8.56 ± 0.57	6.80 - 10.18	1.65
11.*	10.01 ± 0.47	8.64 - 12.29	1.56
12.*	9.82 ± 0.50	8.70 - 10.83	1.01
13.	9.32 ± 0.21	8.71 - 10.00	0.26
14.*	9.78 ± 0.20	9.11 - 10.59	0.28
15.*	9.93 ± 0.48	8.66 - 11.71	1.63
16.	9.36 ± 0.47	8.60 - 10.73	0.89
17.*	10.17 ± 0.39	9.08 - 10.80	0.63
18.*	9.82 ± 0.46	8.00 - 11.93	1.47
19.*	10.93 ± 0.41	9.62 - 11.93	0.99
20.	9.43 ± 0.41	7.44 - 10.72	1.19
21.*	9.78 ± 0.29	8.42 - 10.40	0.51
22.	8.99 ± 0.31	7.93 - 9.64	0.49
23.*	10.07 ± 0.48	8.76 - 11.15	1.13
24.*	10.15 ± 0.22	9.67 - 10.95	0.24
25.*	10.01 ± 0.34	9.30 - 11.33	0.59
26.*	11.15 ± 0.89	9.38 - 12.10	2.36
27.	9.12 ± 0.36	8.44 - 10.13	2.64
28.	9.24 ± 0.53	8.03 - 11.67	1.96
29.	8.90 ± 0.44	6.98 - 10.10	1.18
30.*	10.93 ± 0.74	9.85 - 12.35	1.65
Pooled	9.64 ± 0.09	5.80 - 12.88	1.27

* Families with high mean seed index

Contd...

7.11 : Ginning percentage

Family	mean	range	variance
1.	31.42 ± 0.59	30.25 - 33.43	1.74
2.	30.79 ± 1.95	23.64 - 40.47	26.55
3.	25.18 ± 2.34	18.83 - 28.80	22.00
4.*	31.88 ± 1.38	27.02 - 39.25	15.28
5.*	31.67 ± 1.28	26.85 - 36.62	11.51
6.*	33.94 ± 3.17	28.13 - 49.49	60.30
7.	30.68 ± 2.61	22.55 - 38.29	34.13
8.	29.99 ± 1.54	21.42 - 34.83	18.86
9.	31.38 ± 0.71	28.84 - 34.50	4.08
10.*	36.93 ± 0.75	35.08 - 38.80	2.79
11.	30.65 ± 1.44	24.11 - 37.14	14.41
12.*	34.03 ± 1.15	30.97 - 36.25	5.35
13.	26.13 ± 1.79	21.00 - 32.59	19.27
14.	26.26 ± 2.29	20.15 - 33.79	37.00
15.	29.29 ± 1.28	24.03 - 33.33	11.47
16.*	33.63 ± 0.47	32.57 - 34.84	0.89
17.*	32.89 ± 0.91	31.30 - 35.04	3.28
18.*	34.01 ± 1.60	26.96 - 41.18	17.94
19.	29.36 ± 1.84	25.13 - 37.64	20.36
20.	27.85 ± 2.03	22.11 - 35.82	28.83
21.*	34.41 ± 2.07	29.29 - 42.03	25.71
22.*	32.73 ± 1.15	30.30 - 36.89	6.58
23.	30.84 ± 1.16	26.61 - 33.04	6.75
24.	31.43 ± 1.64	26.78 - 36.43	13.35
25.*	34.45 ± 0.78	32.60 - 37.00	3.05
26.	30.55 ± 1.91	27.62 - 34.15	11.04
27.*	34.24 ± 0.81	33.30 - 36.66	2.64
28.*	33.96 ± 1.11	30.38 - 38.23	8.56
29.*	34.54 ± 1.20	31.85 - 39.34	8.65
30.	30.86 ± 1.45	29.29 - 33.75	6.29
Pooled	31.46 ± 0.35	18.83 - 49.49	20.55

* Families with high mean ginning percentage.

Contd...

7.12 : Lint Index

Family	mean	range	variance
1.*	4.68 ± 0.10	4.42 - 4.99	0.05
2.	4.37 ± 0.27	3.30 - 5.09	0.49
3.	2.83 ± 0.35	2.11 - 3.71	0.47
4.	4.26 ± 0.21	3.46 - 5.21	0.35
5.	4.27 ± 0.27	3.53 - 5.22	0.50
6.*	4.76 ± 0.70	3.76 - 8.24	2.95
7.	3.95 ± 0.29	2.97 - 4.50	0.43
8.	4.16 ± 0.33	2.67 - 5.90	0.87
9.*	4.69 ± 0.19	4.01 - 5.49	0.30
10.*	4.61 ± 0.60	2.39 - 5.84	1.88
11.	4.44 ± 0.40	3.09 - 6.48	1.13
12.*	5.04 ± 0.11	4.79 - 5.32	0.05
13.	3.32 ± 0.29	2.51 - 4.40	0.49
14.	3.58 ± 0.47	2.47 - 5.25	1.56
15.	4.28 ± 0.28	2.82 - 5.29	0.56
16.*	4.77 ± 0.25	4.32 - 5.47	0.24
17.*	4.98 ± 0.18	4.64 - 5.50	0.14
18.*	5.06 ± 0.32	3.63 - 6.39	0.70
19.*	4.72 ± 0.46	3.58 - 6.74	1.28
20.	3.73 ± 0.33	2.66 - 5.32	0.73
21.*	5.20 ± 0.43	4.28 - 7.17	1.01
22.	4.33 ± 0.15	3.96 - 4.82	0.12
23.*	4.49 ± 0.32	3.71 - 5.43	0.50
24.*	4.71 ± 0.35	3.75 - 5.54	0.59
25.*	5.27 ± 0.25	4.75 - 6.13	0.31
26.*	4.97 ± 0.79	3.55 - 6.28	1.88
27.*	4.72 ± 0.15	4.40 - 5.08	0.09
28.*	4.73 ± 0.25	3.85 - 5.78	0.45
29.*	4.68 ± 0.21	4.09 - 5.50	0.27
30.*	4.90 ± 0.39	4.12 - 5.40	0.47
Pooled	4.45 ± 0.07	2.11 - 8.24	0.87

* Families with high mean lint index.

variance were recorded in families 1,2,20,23,24,25,26,27 and 30.

Lower mean number of monopodia (Zero estimates) were observed in six families 3, 15, 16, 17, 18 and 21. The families 2, 5, 6, 11, 13, 20, 23, 27 and 29 also showed low mean compared to pooled mean) with low to moderate range and variance, whereas families 4 and 14 showed high mean coupled with high range and variance.

For sympodia high mean values (compared to pooled mean) were observed in 14 families. In these, 12 families viz., 3, 8, 10, 11, 12, 15, 16, 21, 27, 28, 29 and 30 showed low to moderate range and variance while the rest two families 5 and 9 showed high range and variance.

High mean boll number was observed in 16 families viz., 4, 8, 10, 11, 12, 21, 22, 26, 27, 5, 7, 9, 15, 28, 29 and 30. In these, the first 9 families showed low to moderate range and variance, while the latter seven exhibited high range and variance.

For boll weight high mean values were observed in 14 families. In these 8 families viz., 1, 2, 5, 9, 17, 19, 21 and 29 showed low range and variance and the other 6 families viz., 8, 10, 14, 15, 16 and 30 exhibited high range and variance.

For economic yield significantly higher mean values (more than pooled mean) were observed in 14 families. Nine of these families viz., 4,5,7,8,9,15,28,29 and 30 showed wide range and high variance estimates. Higher mean with low to moderate range and variance were observed in families 10,21,22,26 and 27.

High mean biological yields were exhibited by 13 families. In these high range and variance values were recorded in 4,5,7, 8, 9, 10, 12, 15, 22, 29 and 30. High mean with low to moderate range and variance was observed in families viz., 2 and 21.

For harvest index, high mean values (more than pooled mean) were recorded in 14 families. In these, high range and variance were observed in families 12 and 16. High means with low to moderate range and variance were recorded in families 1, 4, 13, 14, 18, 21, 23, 26, 27, 29 and 30.

High mean values for seed index were observed in 16 families. In these, maximum range and variance were recorded in 8 families viz., 2,9,11,15,18,23,26 and 30. Higher mean with low to moderate range and variance were recorded in eight families viz., 1, 12, 14, 17, 19, 21, 24 and 25.

For ginning percentage, higher mean estimates were exhibited in 14 families. In these, families viz., 5, 10, 12, 16, 17, 22, 25, 27, 28 and 29 exhibited low to moderate range and variances. The rest 4 families viz., 4, 6, 8 and 21 showed higher range and variance values.

High mean values for lint index were exhibited in 18 families. In these, higher range and variance values were observed in 7 families viz., 6, 10, 19, 21, 24, 26 and 28. Higher mean with low to moderate range and variance were observed in 1, 9, 12, 16, 17, 18, 23, 25, 27, 29 and 30.

(f) Nature of associations in different character pairs in F_3 generation

The nature of variability was examined through the analysis of associations. The phenotypic correlation coefficients among yield and other characters are presented in Table 8.

Economic yield in F_3 exhibited strong positive and significant correlation with biological yield (0.927), boll number (0.897), monopodia (0.436) and plant height (0.393). The boll weight, sympodia, harvest index, lint index and seed index were also positively and significantly associated with yield. Only two characters namely ginning percentage and first fruiting node number showed a non-significant correlation with yield.

Plant height showed positive and significant association with first fruiting node number, sympodia, boll number and biological yield and significant negative correlation with harvest index.

First fruiting node number showed positive and significant association with sympodia and negatively significant association with harvest index and seed index.

Positive and significant correlations were observed for monopodia with boll number and biological yield and negative correlations with sympodia, harvest index and ginning percentage.

Sympodia showed a positive and significant association with boll number and biological yield and a negative significant

Table 8: Phenotypic correlation coefficients among yield and other characters in F_3 generation of <u>Gossypium</u> <u>hirsutum</u> *cross Pusa 45-3-6 X Pusa 19-27*

Character	2	3	4	5	6	7	8	9	10	11	12
1. Plant height	0.273*	0.068	0.493*	0.413*	0.079	0.393*	0.517*	-0.312*	-0.110	0.138	0.018
2. First fruiting node number		-0.053	0.169*	-0.099	-0.013	-0.086	0.043	-0.343*	-0.312*	0.121	-0.126
3. Monopodia			-0.068	0.378*	0.048	0.436*	0.521*	-0.119	0.121	-0.025	0.035
4. Sympodia				0.282*	0.014	0.250*	0.331*	-0.287*	-0.105	-0.009	-0.093
5. Boll number					0.114	0.897*	0.860*	0.141*	0.063	0.199*	0.135
6. Boll weight@						0.299*	0.266*	0.083	0.543*	0.127	0.455*
7. Economic yield (g)							0.927*	0.238*	0.171*	0.140	0.205*
8. Biological yield (g)								-0.097	0.168*	0.104	0.161*
9. Harvest iodex									0.000	0.103	0.099
10. Seed index										-0.158*	0.481*
11. Ginning percentage											0.732*
12. Lint index											1.000

* Significant at P=0.05; @ Three bolls weight.

correlation with harvest index.

The trait boll number exhibited strong positive and significant correlation with biological yield, harvest index and ginning percentage.

A positive and significant correlation was observed for boll weight with biological yield, seed index and lint index.

Biological yield exhibited a strong positive and significant correlation with seed index and lint index. A negative but non-significant association was observed between biological yield and harvest index.

Seed index was positively and significantly correlated with lint index, but was negatively and significantly correlated with ginning percentage. The association of ginning percentage with lint index was positive and significant.

GOSSYPIUM BARBADENSE

Effective selection in any crop plant is dependent on the existance of sufficient genetic variability. Early unsuccessful attempts to cultivate G. barbadense in the northern part was mainly due to utilization of limited genetic variability. Cotton being a predominantly self pollinated crop, it is believed that biparental crossings particularly in early segregating generations may release variability hidden in the repulsion phase linkages. In the present study, an attempt was made to evaluate genetic variability liberated by adopting different mating systems and simultaneouslty to compare the magnitude and nature of variability in F_4 generation following three mating systems viz., selective biparental mating, open (random) pollination and self pollination. The results of this study are presented in Tables 9 to 13. Frequency distribution curves for F_4 population along with parental ranges are illustrated in Fig. 8 to 19.

Parameters of variability

For plant height, high mean was recorded in F_4 population raised from F_3 through open pollination, followed by populations raised through self pollination and selective intermating, but a higher range was observed in selective intermating system followed by open pollinated system. This was illustrated in Fig. 8. Transgressives range with respect to both the parents was found to be equidistant in open pollinated system while the population raised through selective intermating exhibited maximum frequency of transgressants towards the side of the dwarf parent (Fig. 8).

Highest population mean for first fruiting node number was recorded in F_4 population raised from self pollination followed by selective intermating. For first fruiting node number, the magnitude of variance was significantly high in populations raised through selective intermating and self pollination as compared to that through open pollination. For this trait, frequency of transgressants towards the (better) parent with lower node number was found to be more. Maximum transgression range was observed in selective intermating followed by self-pollinated and open pollinated system (Fig. 9).

Table 9: Agronomic characteristics of parents of *Gossypium barbadense* cross 10-98-P_1 x 11-181-P_2

Character	P_1: 10-98-P_1	P_2: 11-181-P_2
Plant height (cm)	72.80 ± 2.23	104.40 ± 4.6
First fruiting node number	6.80 ± 0.58	9.50 ± 0.9
Monopodia	0.40 ± 0.25	0.80 ± 0.4
Sympodia	14.20 ± 1.16	18.60 ± 1.0
Boll number	13.20 ± 0.58	21.80 ± 2.0
Boll weight (g)	2.60 ± 0.18	3.00 ± 0.2
Economic yield (g)	12.70 ± 1.18	17.10 ± 1.0

Table 10 : *Estimated parameters of variability in* Gossypium barbadense *populations advanced from* F_3 *generation of a cross* $10\text{-}98\text{-}P_1 \times 11\text{-}181\text{-}P_2$ *by three different mating systems*

Character	Selective intermating			Open pollinated			Self pollinated		
	mean $(\bar{x})$	range	variance	mean $(\bar{x})$	range	variance	mean $(\bar{x})$	range	variance
Plant height (cm)	76.78 ±1.64	42.00-112.00	235.57	80.73 ±4.92	58.00-120.00	364.92	80.18 ±3.91	57.00-108.00	245.49
First fruiting node number	6.66 ±0.21	3.00- 13.00	3.79	6.87 ±0.31	5.00- 9.00	1.41	7.94 ±0.62	5.00- 13.00	6.06
Monopodia	1.115 ±0.13	0.00- 4.00	1.36	1.33 ±0.29	0.00- 3.00	1.24	1.06 ±0.69	0.00- 3.00	1.26
Sympodia	12.92 ±0.46	6.00- 25.00	17.98	14.40 ±0.88	10.00- 19.00	11.69	12.56 1.21	7.00- 24.00	23.46
Boll number	8.17 ±0.38	3.00- 20.00	12.35	6.33 ±0.74	1.00- 13.00	8.10	9.50 ±0.89	3.00- 17.00	12.67
Boll weight@(g)	6.86 ±0.18	1.20- 13.10	2.75	6.42 ±0.34	3.50- 9.00	1.77	6.36 ±0.31	3.80- 7.80	1.49
Economic yield(g)	18.08 ±0.84	4.20- 41.30	61.92	12.93 ±1.52	3.00- 26.00	34.78	19.14 ±1.90	3.80- 31.60	63.57
Biological yield (g)	85.89 ±4.43	22.10-191.40	1705.92	79.91 ±11.83	40.20-218.10	2100.50	80.78 ±8.59	38.20-161.00	1182.40
Harvest index (%)	23.14 ±0.90	7.46- 44.35	70.01	18.80 ±2.53	4.86- 35.96	96.17	25.18 ±2.55	8.65- 47.09	103.96
Seed index	9.45 ±0.15	5.37- 12.77	1.91	9.74 ±0.38	7.05- 12.66	2.13	9.19 ±0.36	6.53- 12.00	2.03
Ginning percentage	36.55 ±0.88	13.18- 58.54	67.57	31.85 ±1.57	18.18- 41.46	37.04	33.32 ±1.30	18.92-39.06	27.17
Lint index	5.64 ±0.21	1.38- 11.47	3.93	4.62 ±0.34	2.12- 7.33	1.72	4.70 ±0.32	2.42- 6.90	1.66

@ Three bolls weight.

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

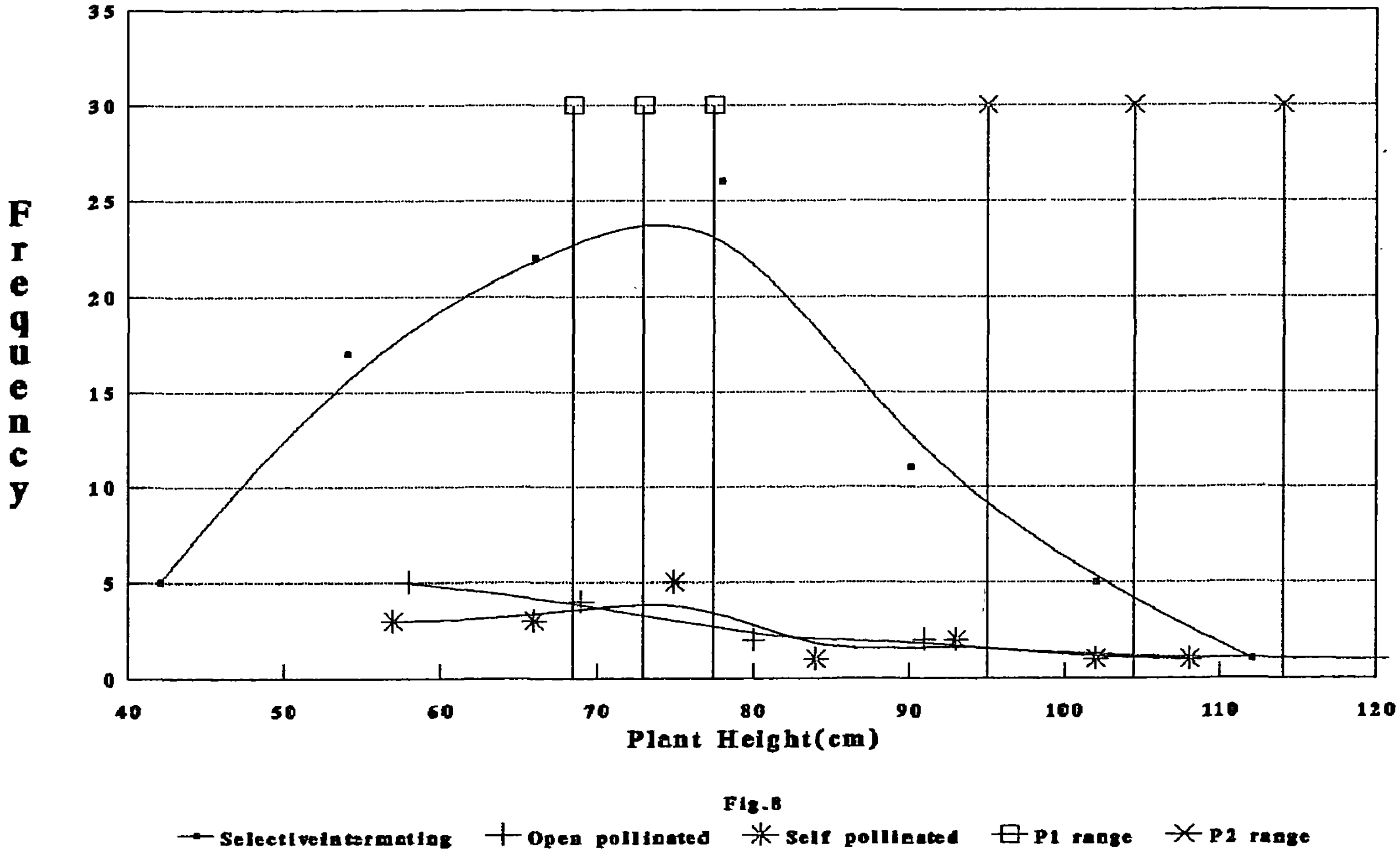

Fig.8

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

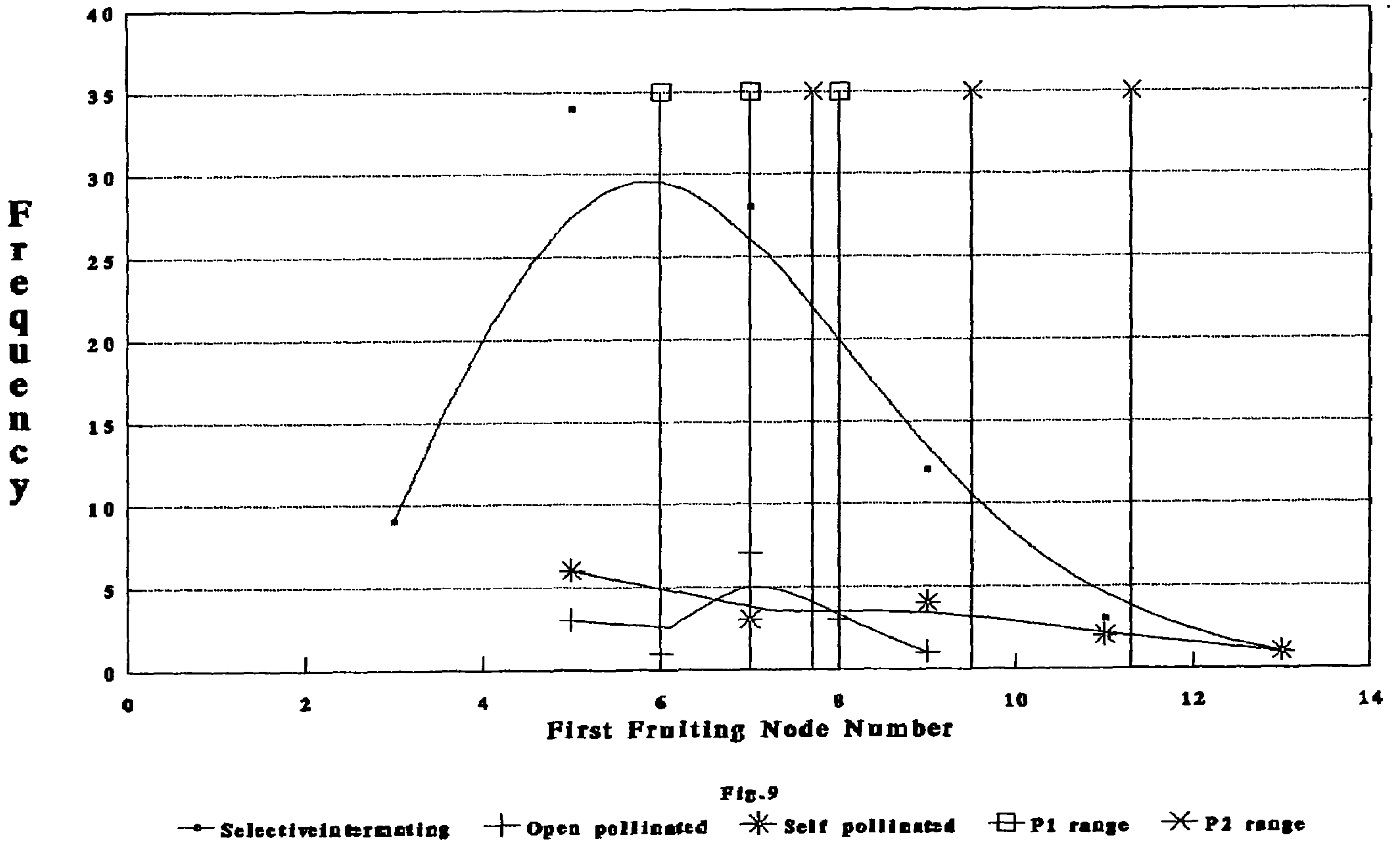

Fig.9

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

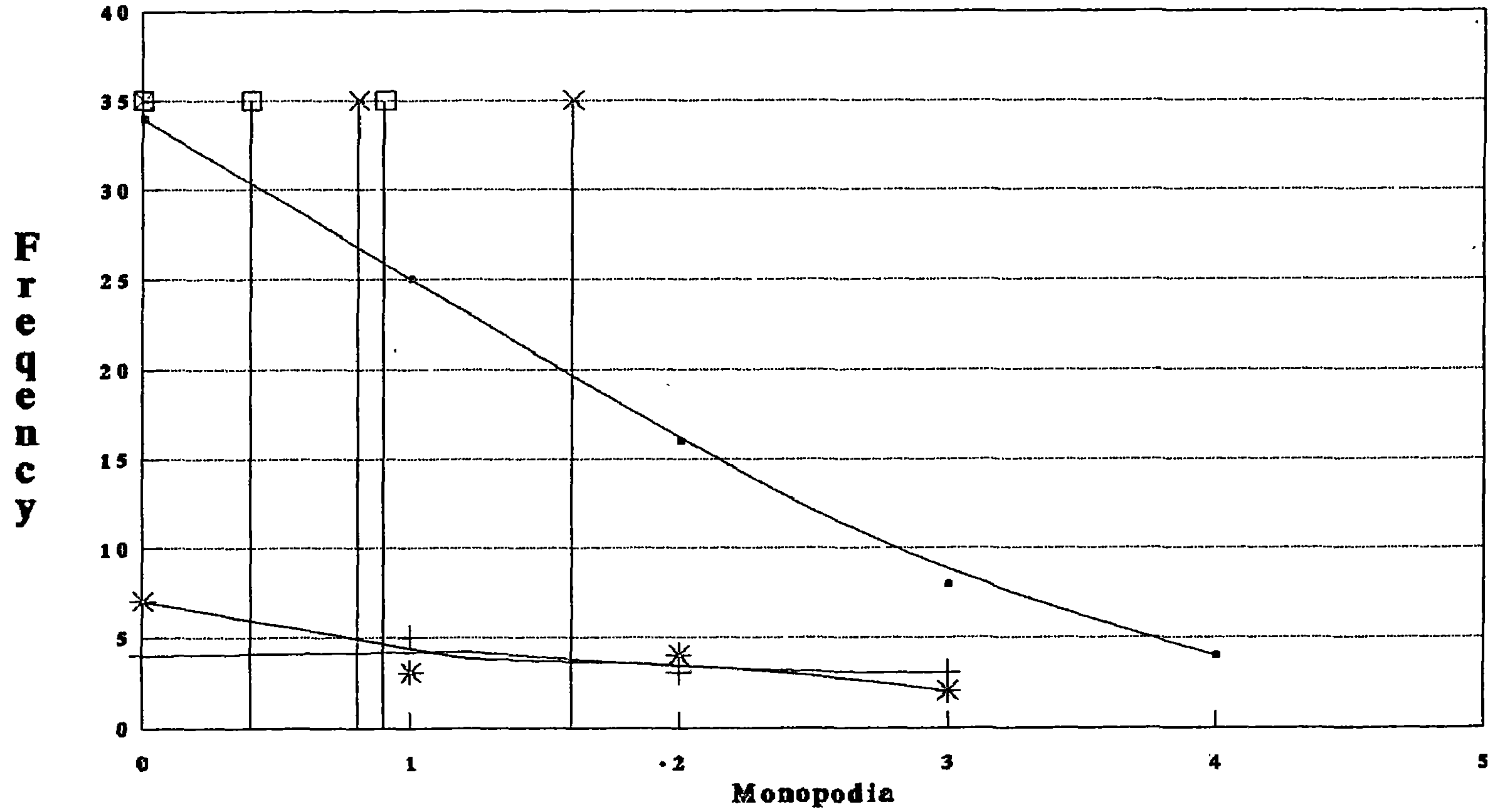

Fig.10

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

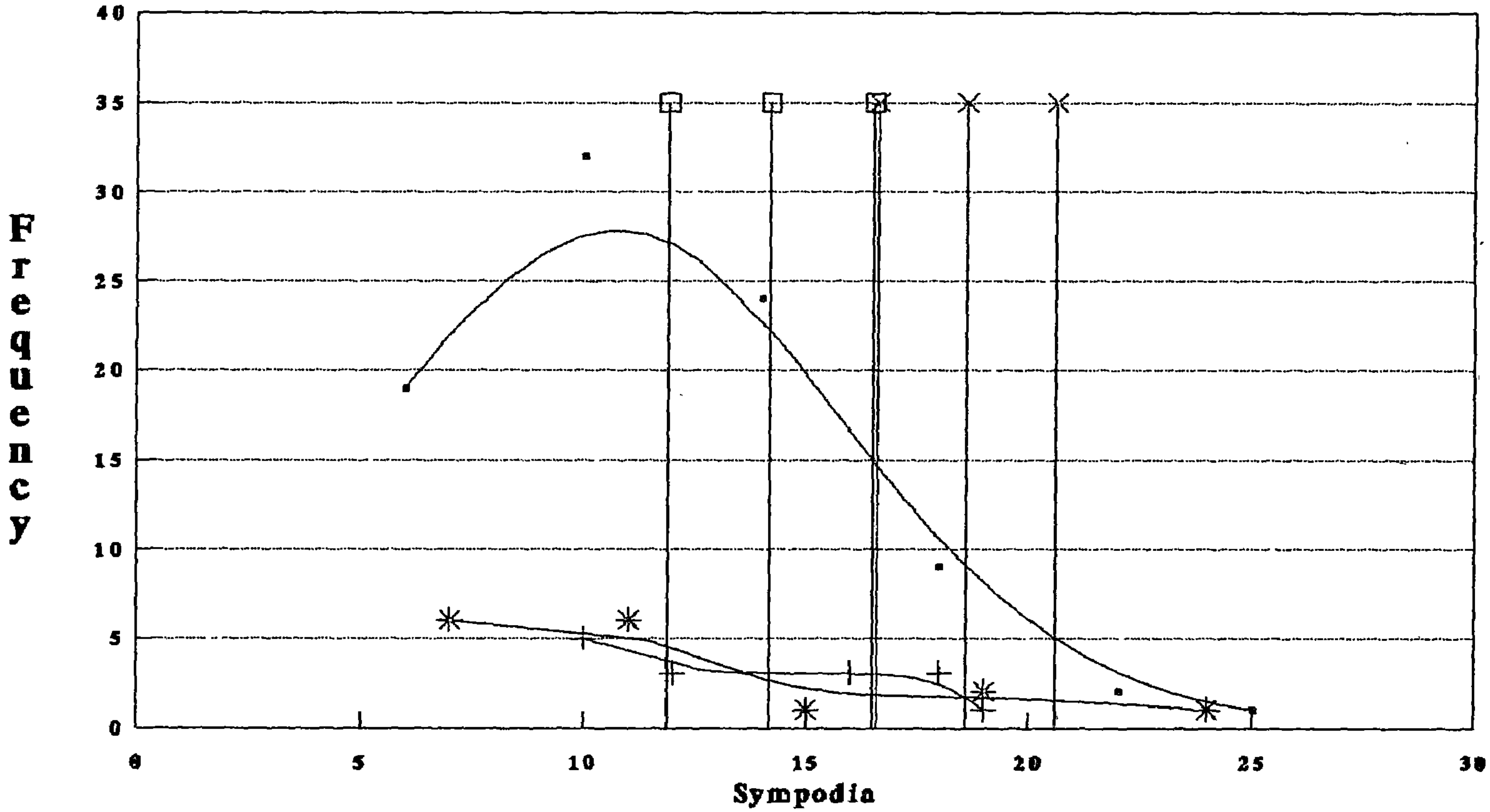

Fig.11

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

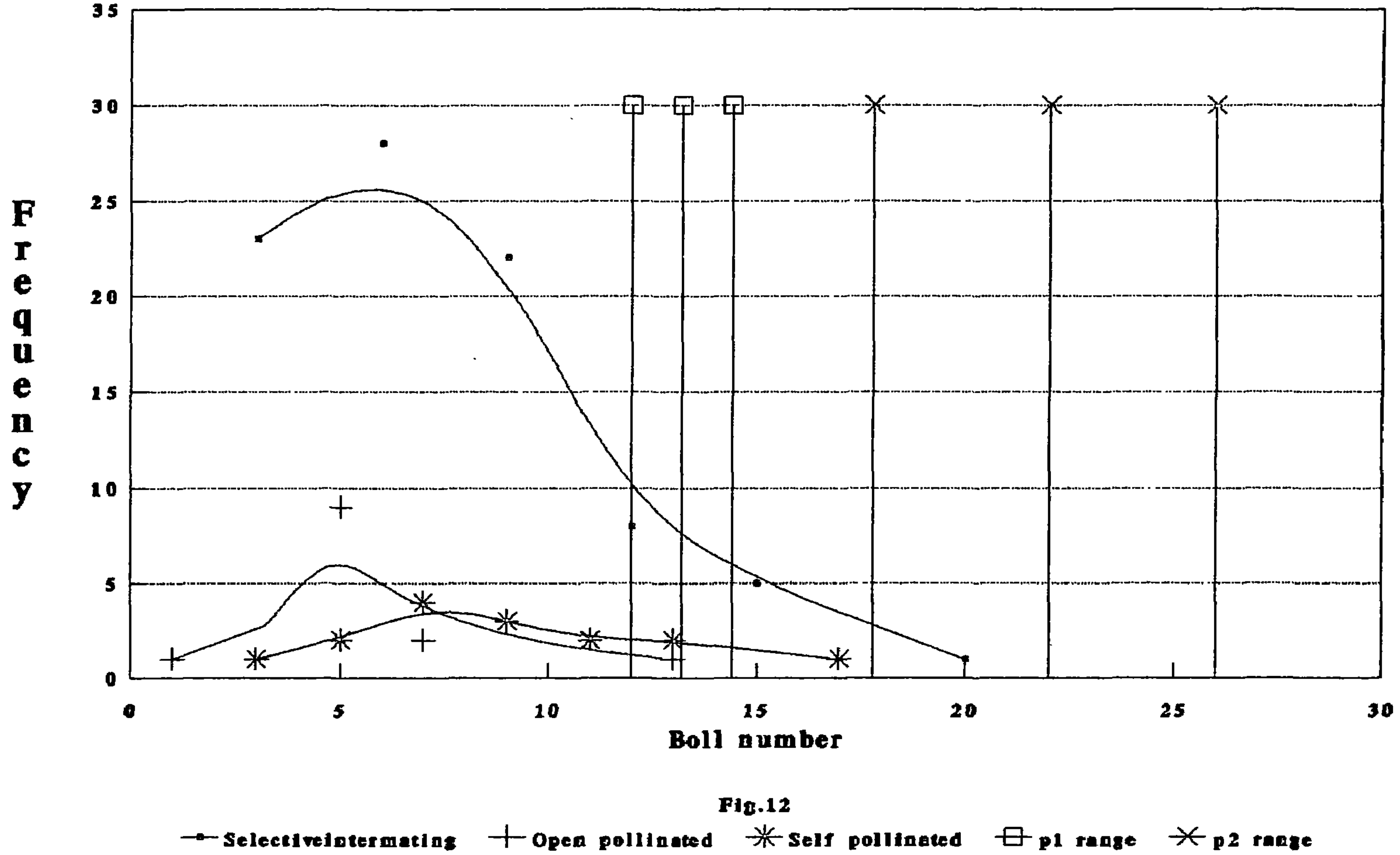

Fig.12

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

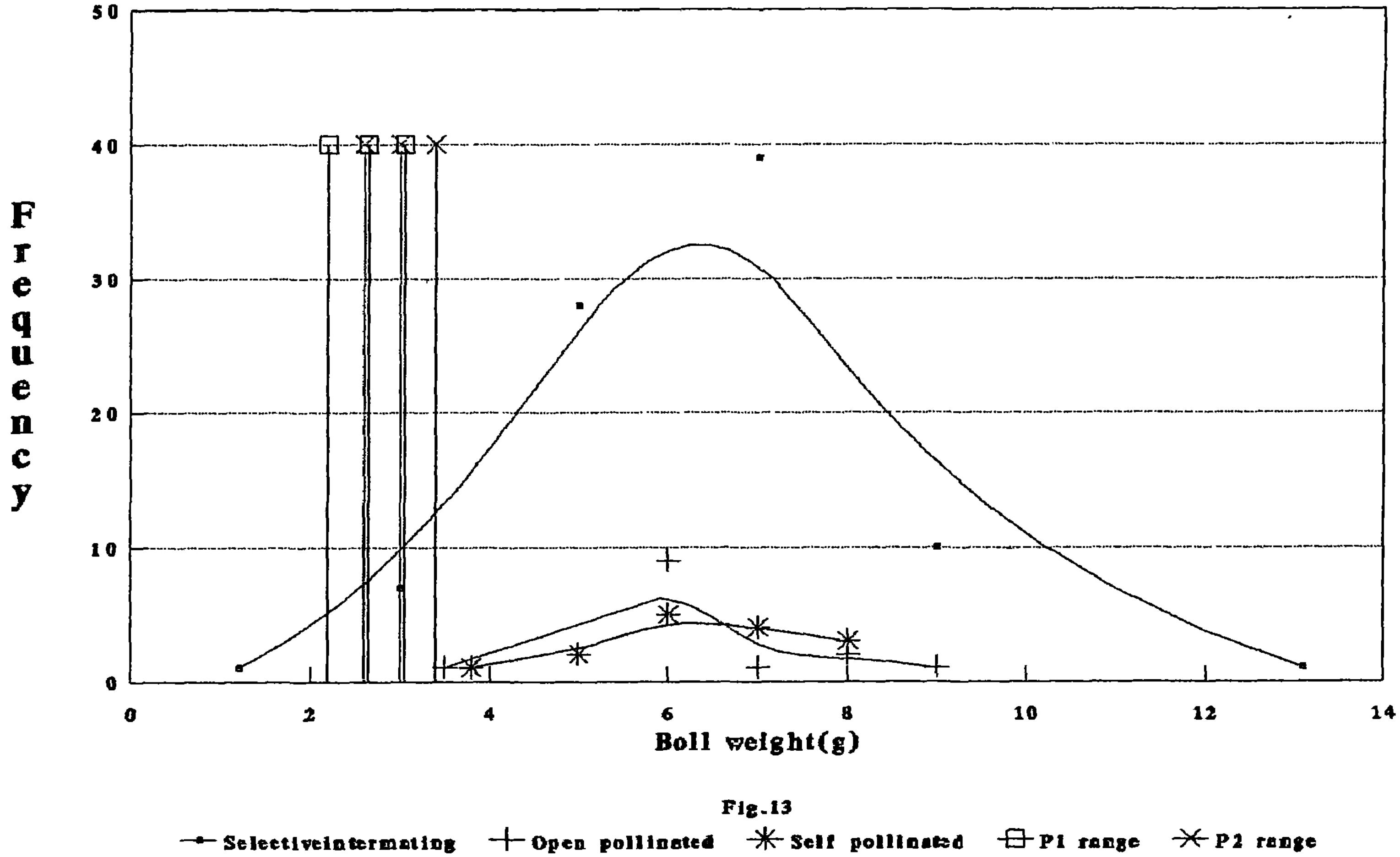

Fig.13

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

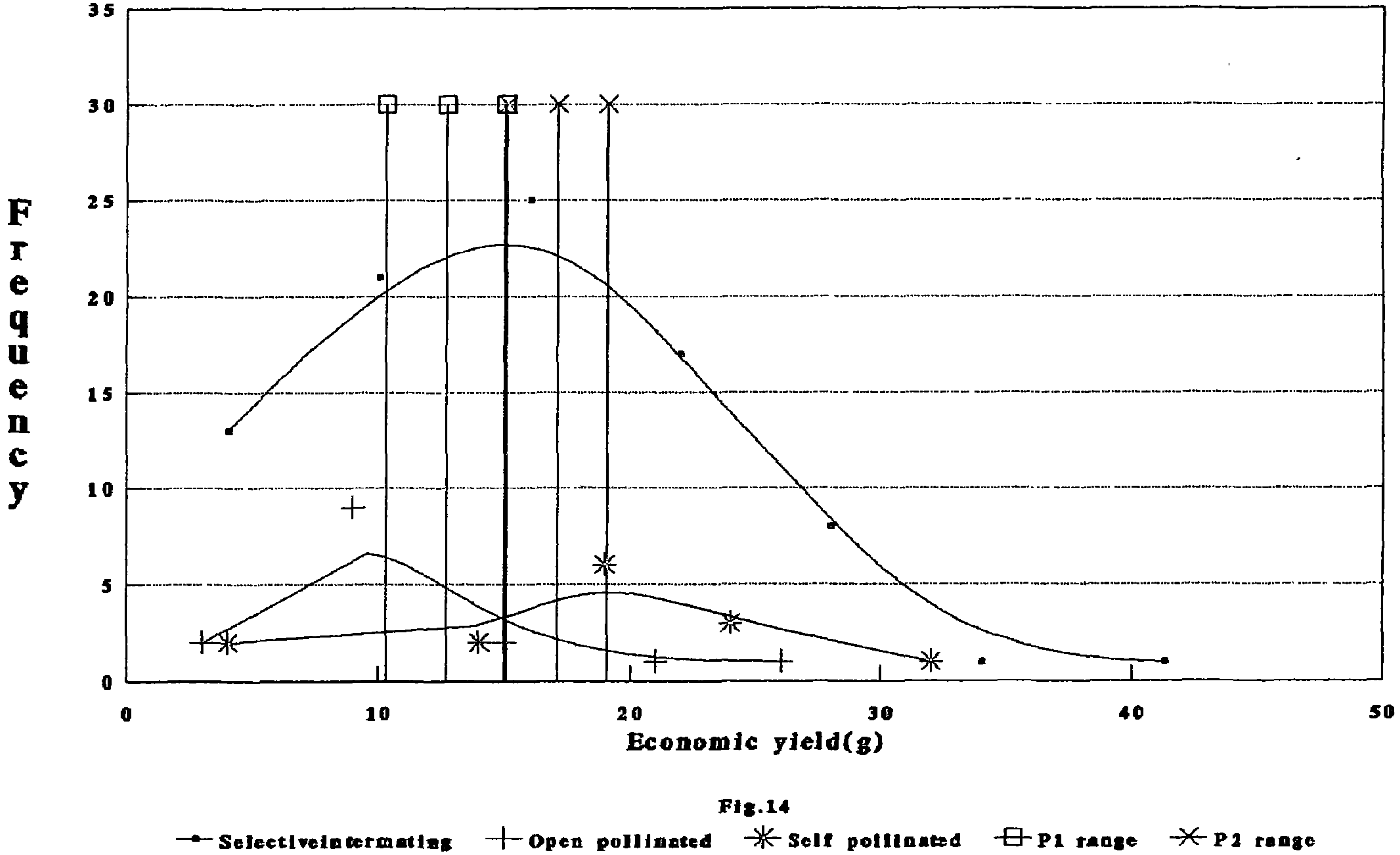

Fig.14

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

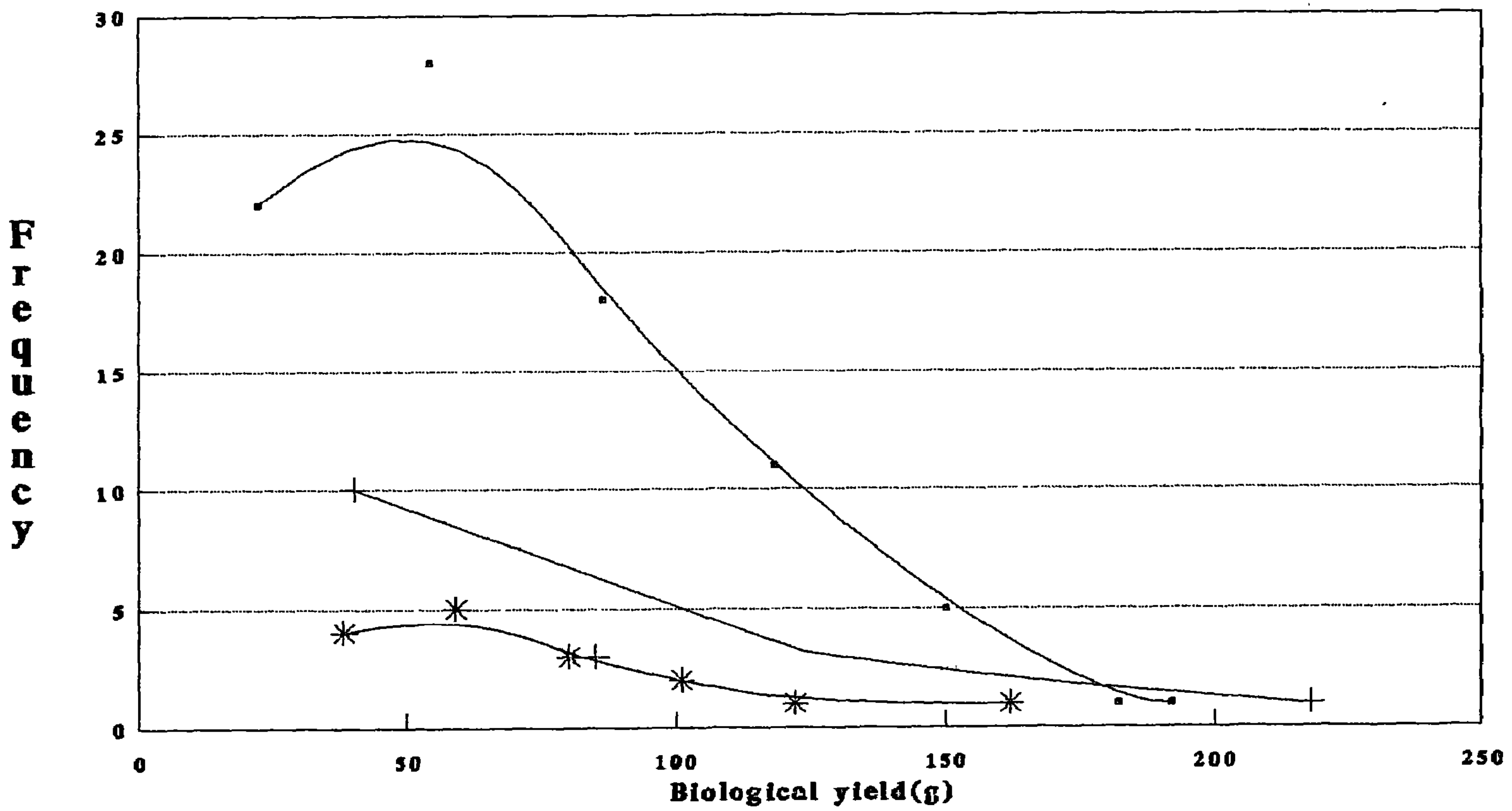

Fig.15

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

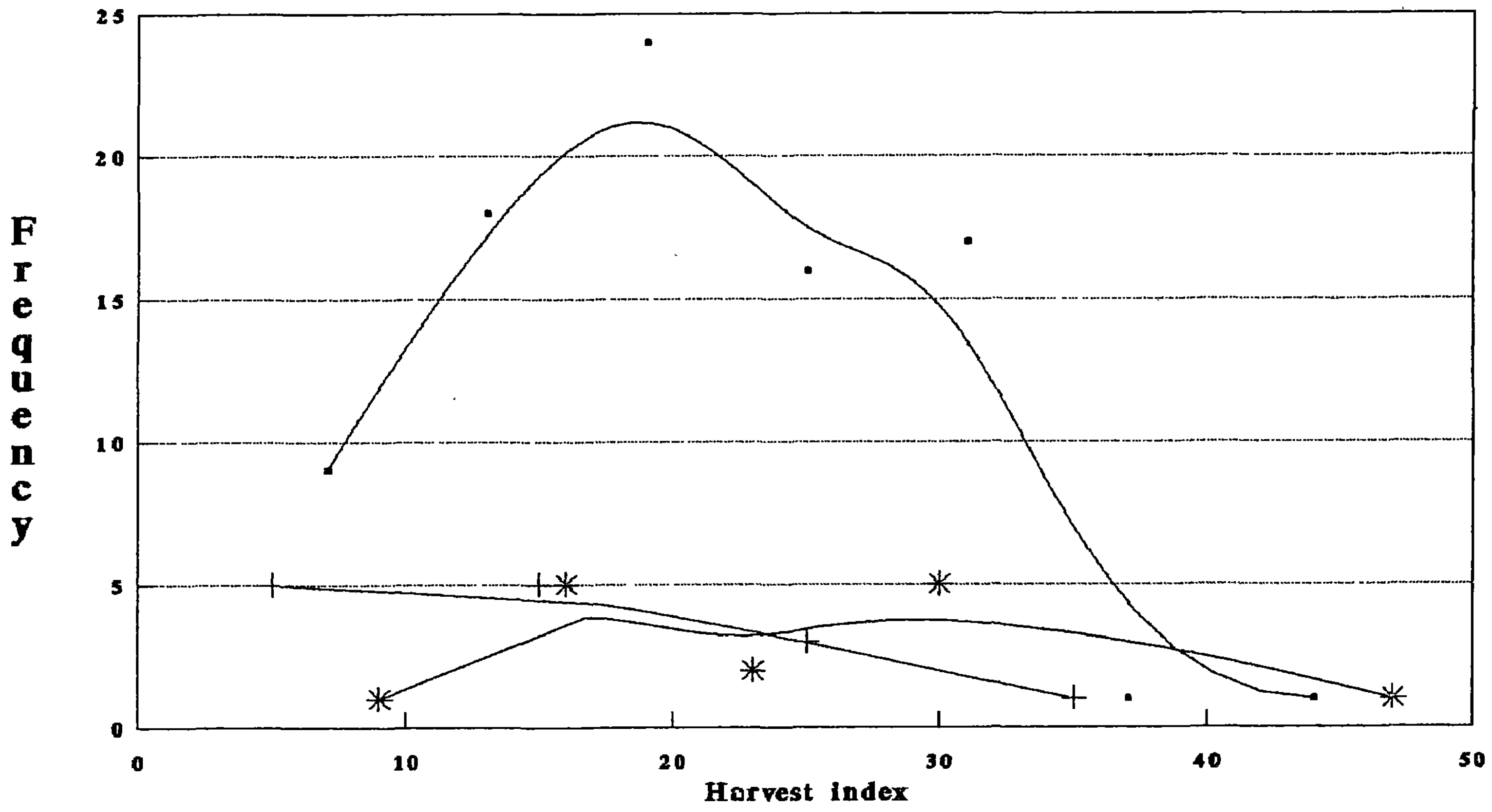

Fig.16

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

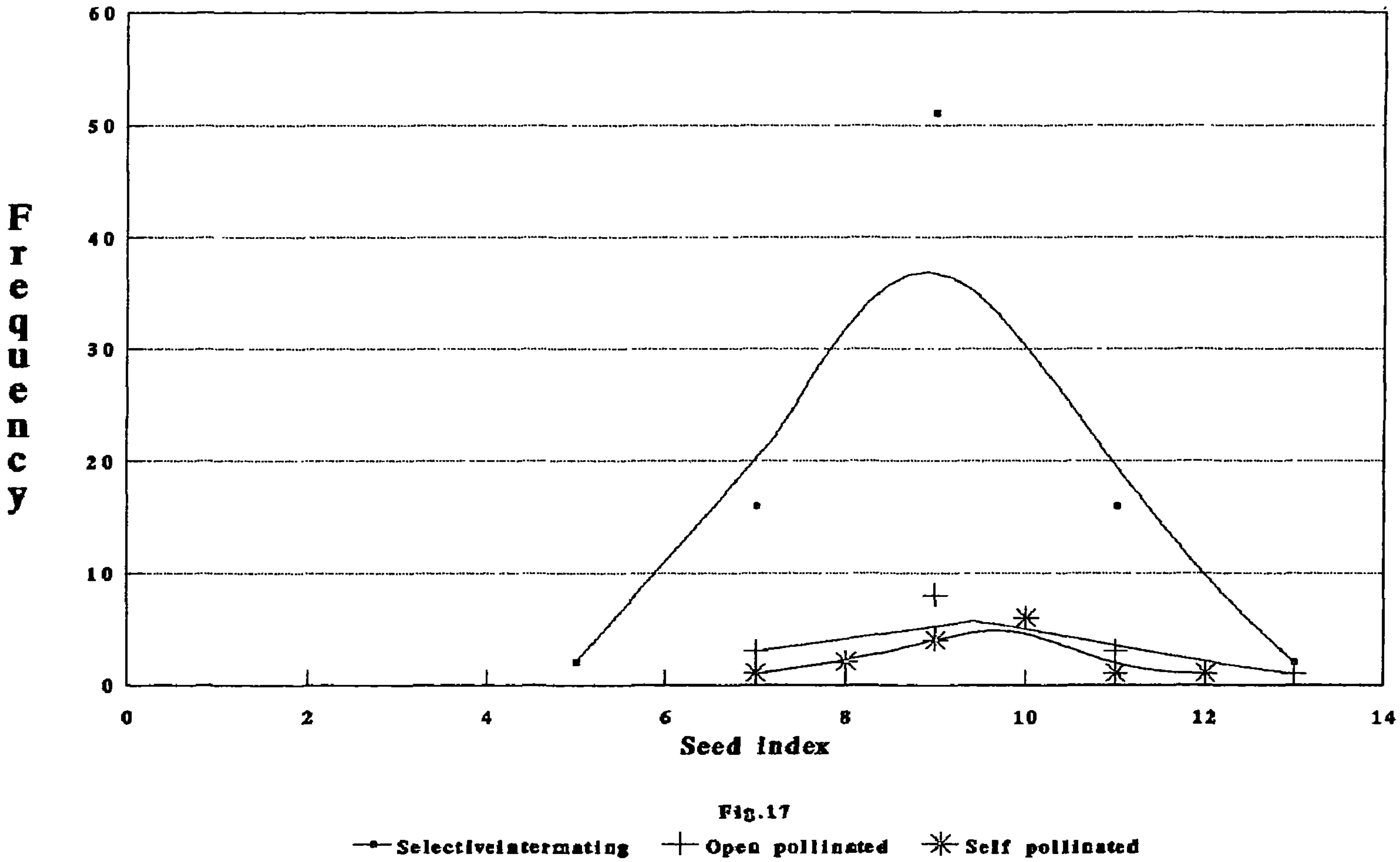

Fig.17

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

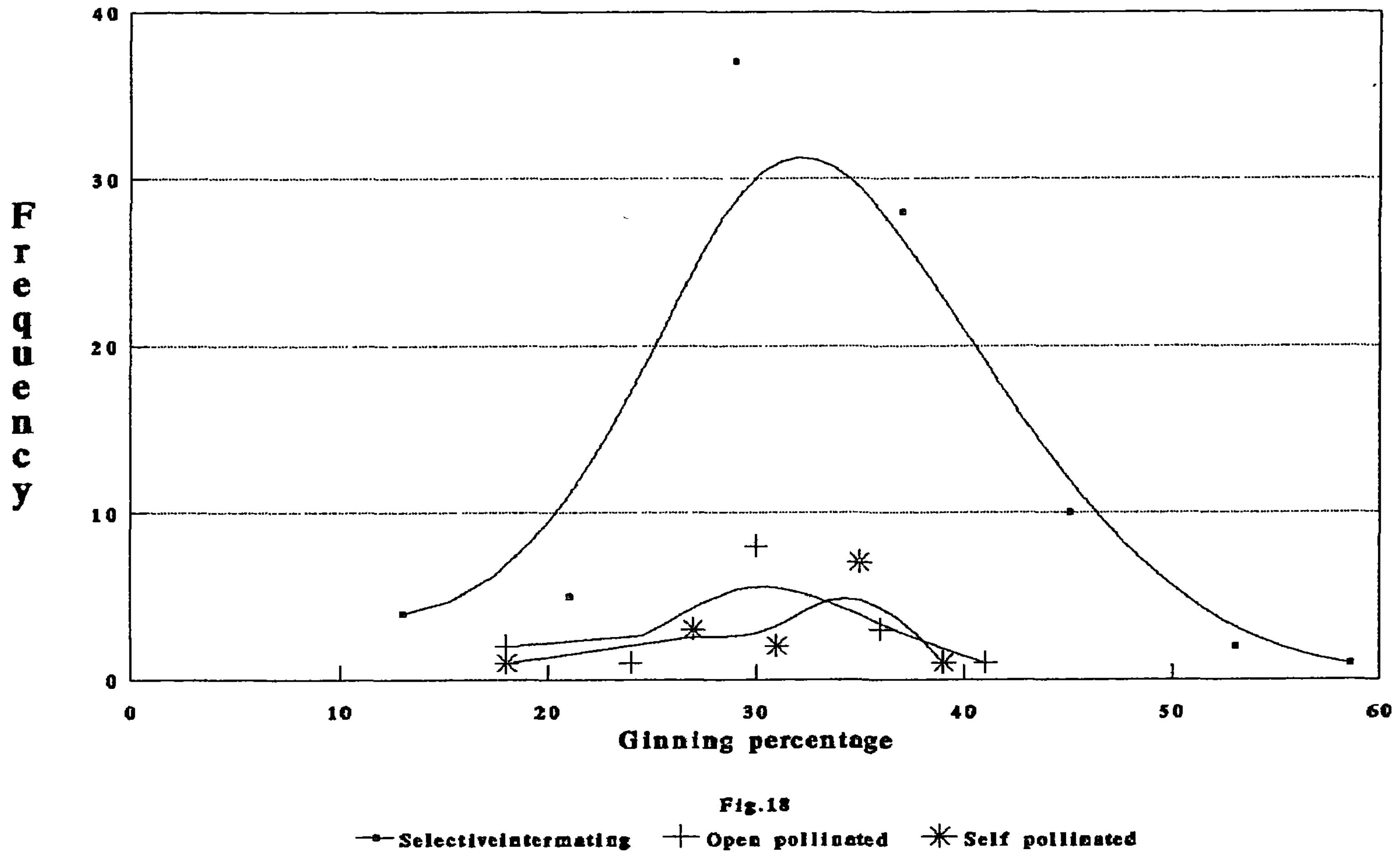

Fig.18

FREQUENCY DISTRIBUTION FOR F4 POPULATION OF GOSSYPIUM BARBADENSE ADVANCED FROM F3 BY THREE DIFFERENT MATING SYSTEMS

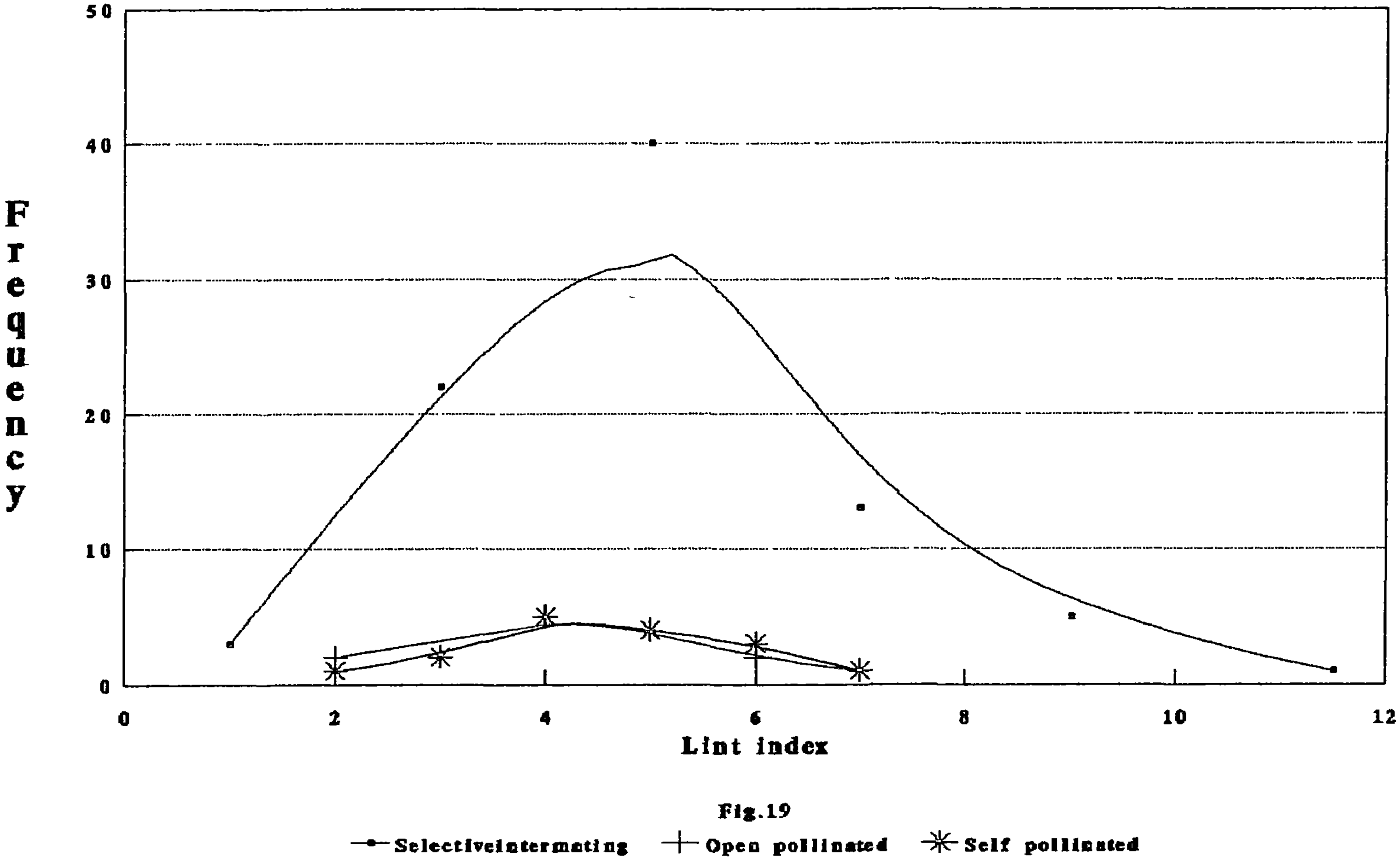

Fig.19

Lowest number of monopodia (1.12) with low range was recorded in selective intermating. However, the variance was of the same order in all the three populations. Maximum frequency of transgressants showing Zero monopodia was observed in selective intermating F_4 population (Fig. 10).

Highest mean number of sympodia (14.40) were recorded in open pollinated system but the highest range was observed in selective intermating. The maximum magnitude of variance was recorded in self pollinated system. The frequency of transgressants was higher towards the parent with lower value as compared to the parent with higher values (Fig. 11).

Highest mean boll number was recorded in population raised through self pollination system followed by selective intermating and open pollination system. Highest range for this trait was recorded in selective intermating followed by self pollinated system. The frequency of transgression by the three systems for this trait was found to be more on the side of the parent with lesser boll number (Fig. 12).

The mean boll weight for all the three populations was of the same order, however, maximum value was recorded in selective intermating followed by the populations raised through open pollinated and self pollinated systems. For boll weight, a significantly higher variance was observed in selective intermating derived population as against that through self pollination. The frequency of transgressants over the better parent was found to be more than the frequency of transgressants over the parent with lower mean boll weight (Fig. 13).

High mean estimates for economic yield were observed in self pollinated system followed by selective intermating (18.08 g) but the range was maximum in selective intermating (14.2-41.30 g). All the three mating systems were found to give transgressants on both sides of the parents with maximum in selective intermating (Fig. 14).

For biological yield, highest mean value was obtained in selective intermating (85.89 g) followed by self pollinated and open pollinated systems. The maximum range was observed in open pollinated system followed by selective intermating and self pollinated system (Fig. 15).

High mean, range and variance values for harvest index were observed for self pollinated system followed by selective intermating. The recombinants showing the highest harvest index were recovered in population raised from selective intermating and self pollinated system (Fig. 16).

For seed index, the means and variances in populations raised through the three mating systems were of the same order. The maximum range was observed in selective intermating (Fig.17).

Maximum ginning percentage was observed in population raised from selective intermating, followed by populations derived from self and open pollination. Frequency curves were represented in Fig. 18. For lint index, high mean and range were observed in selective intermating over the other systems (Fig. 19). For both ginning percentage and lint index, a significantly higher variance was observed in selective intermating over the other two systems.

Study of associations through correlation coefficients among different traits

Phenotypic correlation coefficients were calculated among yield and other characters in three populations of a Gossypium barbadense cross 10-98-P_1 x 11-181-P_2 in F_4 generation raised from F_3 by different mating systems viz., self pollination, open pollination and selective intermating and are presented in Tables 11, 12 and 13. Out of the total 66 character pairs only 9 showed significant association in population raised from self pollination, 17 character pairs showed significant association in population raised from open pollination and as many as 22 character pairs showed significant association in population raised by selective intermating.

Association among traits in F_4 population

Economic yield was positively associated with boll number and boll weight in population raised from self pollination, with boll number and lint index in population raised from open pollination and with plant height, boll number and boll weight, biological yield and harvest index in selective intermating population.

Plant height was positively correlated with sympodia and biological yield in F_4 population from self pollinated system. In case of population raised from open pollination in addition to above associations, plant height showed a significant positive association with seed index and a negative significant association with harvest index. For population raised through

Table 11: Phenotypic correlation coefficients among yield and other characters in F_4 generation of a *Gossypium barbadense* cross 10-98-P_1 x 11-181-P_2 advanced from F_3 by self pollination

Character	2	3	4	5	6	7	8	9	10	11	12
1. Plant height (cm)	0.011	0.086	0.609*	0.139	0.371	0.349	0.900*	-0.317	0.211	0.277	0.329
2. First fruiting node number		-0.480	0.121	-0.483	0.246	-0.412	-0.135	-0.227	0.140	-0.204	-0.111
3. Monopodia			-0.374	0.325	-0.120	0.186	0.173	-0.084	0.148	0.333	0.432
4. Sympodia				0.168	0.460	0.379	0.480	0.140	0.251	-0.239	-0.113
5. Boll number					0.444	0.900*	0.257	0.728*	0.523	0.358	0.538*
6. Boll weight@(g)						0.629*	0.394	0.426	0.371	0.029	0.161
7. Economic yield (g)							0.472	0.679	0.464	0.372	0.492
8. Biological yield (g)								-0.292	0.273	0.342	0.394
9. Harvest index									0.334	0.066	0.177
10.Seed index										0.061	0.585*
11.Ginning Percentage											0.831*
12.Lint index											1.000

@ : Three bolls weight; * Significant at P=0.05

Table 12: Phenotypic correlation coefficients among yield and other characters in F_4 generation of a *Gossypium barbadense* cross 10-98-P_1 x 11-181-P_2 advanced from F_3 by open pollination

Character	2	3	4	5	6	7	8	9	10	11	12
1. Plant height	0.036	0.206	0.852*	-0.201	0.238	-0.117	0.778*	-0.607*	0.522*	0.047	0.299
2. Frist fruiting node number		-0.397	0.120	0.141	-0.400	0.115	-0.068	0.044	-0.290	-0.227	-0.413
3. Monopodia			0.150	-0.015	0.265	-0.051	0.509*	-0.352	0.629*	-0.445	-0.001
4. Sympodia				-0.294	0.230	-0.189	0.612*	-0.637*	0.248	0.024	0.127
5. Boll number					-0.190	0.822*	0.044	0.598*	-0.213	-0.576*	-0.624*
6. Boll weight@						0.163	0.084	-0.071	0.471	0.347	0.589*
7. Economic yield							0.069	0.743*	-0.095	-0.386	-0.406
8. Biological yield								-0.502*	0.474	-0.301	-0.045
9. Harvest index									-0.386	-0.076	-0.276
10.Seed index										-0.096	0.509*
11.Ginning percentage											0.802*
12.Lint index											1.000

@ : Three bolls weight; * Significant at P=0.05

Table 13: Phenotypic correlation coefficients among yield and other characters in F_4 generation of a *Gossypium barbadense* cross 10-98-P_1 x 11-181-P_2 advanced from F_3 by selective intermating

Character	2	3	4	5	6	7	8	9	10	11	12
1. Plant height	-0.076	0.197	0.585*	0.099	0.231*	0.261*	0.462*	-0.335*	-0.158	0.048	-0.044
2. First fruiting node number		-0.126	0.012	-0.190	-0.084	-0.208*	-0.193	0.045	0.118	0.133	0.179
3. Monopodia			-0.083	0.117	-0.097	0.054	0.257*	-0.309*	-0.154	0.123	0.072
4. Sympodia				0.045	0.249*	0.163	0.187	-0.107	0.052	0.071	0.029
5. Boll number					0.085	0.806*	0.413*	0.336*	-0.099	0.022	-0.049
6. Boll weight@						0.339*	0.084	0.112	0.234*	0.096	0.219*
7. Economic yield							0.510*	0.326*	-0.025	0.105	0.081
8. Biological yield								-0.481*	-0.335*	0.165	-0.003
9. Harvest index									0.339*	-0.181	-0.011
10. Seed index										-0.233*	0.189
11. Ginning percentage											0.888*
12. Lint index											1.000

@ : Three bolls weight; * Significant at P=0.05

selective intermating a similar association was observed except that here a new association was also established between plant height and economic yield.

First fruiting node number showed negative and significant association with economic yield only in F_4 population from selective intermating system, but in the population raised through the other two systems, all correlations between this trait and others were found to be non-significant.

The correlation coefficients of monopodia were positive and significant with biological yield, harvest index both, in open pollinated system and selective intermating. A negative and significant association was observed with harvest index only in selective intermating. All these associations in self pollinated system were found to be non-significant.

Sympodia exhibited a positive and significant correlation with plant height in self pollinated system; with plant height and biological yield in open pollinated system and with plant height and boll weight in selective intermating. A negative and significant association was also observed with harvest index in open pollinated system.

A positive and significant correlation was observed for boll number with economic yield, harvest index and lint index in self pollinated system; with economic yield and harvest index in open pollinated system, and with economic yield, biological yield, and harvest index in selective intermating. Negative and significant correlations were recorded with ginning percentage and lint index in population raised through open pollination.

The correlation coefficients of boll weight were positive and significant with economic yield in self pollinated system; with lint index in open pollinated system and with plant height, sympodia, economic yield, seed index, lint index in selective intermating system.

Biological yield exhibited a positive and significant correlation with plant height in population from self pollinated system; with plant height, monopodia, sympodia in population from open pollinated system and with plant height monopodia, boll number, economic yield in population from selective intermating system. A negative and significant correlation was observed with harvest index in open pollinated system and with harvest index and seed index in selective intermating system.

Positive and significant correlations were observed for harvest index with boll number in self pollinated system; with boll number and economic yield in open pollinated system and with boll number, economic yield and seed index in population from selective intermating system. Negative and significant correlations were observed with plant height, monopodia and biological yield in selective intermating.

The correlation coefficients of seed index were positive and significant,with lint index in self pollinated population; with plant height, monopodia and lint index in open pollinated system, and with boll weight and harvest index in selective intermating system. Negative and significant correlations were noted with biological yield and ginning percentage in population from selective intermating system.

Ginning percentage exhibited a positive and significant correlation with lint index in all the three mating systems. A negative and significant correlation was observed with boll number in open pollinated system, and with seed index in selective intermating system.

Positive and significant correlations were observed for lint index with traits viz., boll number, seed index and ginning percentage in self pollinated system; with boll weight, seed index and ginning percentage in open pollinated system and with boll weight and ginning percentage in selective intermating. A negative and significant correlation was observed with boll number in open pollinated system.

DISCUSSION

India is one of the native centre of old world cottons but the fascination for better and long staple cotton, captivated it so much that it became one of the major tetraploid new world cotton producing countries. Historically the urge of the British Lancashire mills to be free from dependence on the American long staple produce made India to take up these new world tetraploid cottons. It soon became one of the major cotton producing countries. Despite the loss of vast cotton growing area during partition, India had made greater strides in cotton production since independence, from 2.3 million bales in 1947 to 11.6 million bales in 1992-93 which can be rightly called as white gold revolution. Though it is a significant achievement, but on global level our productivity continues to be very low (261 kg lint/ha) against world average of 560 kg lint/ha and of more than 1000 kg lint/ha in some countries. Cultivation of inherently low yielding varieties with low harvest index was one of the major reasons for low productivity in India (Singh _et al_., 1992). So breeding for a suitable plant type having high yield and high harvest index is a promising proposition.

To initiate a breeding programme for a suitable plant type, it is essential to study the genetics of traits determining plant type particularly those traits having direct contribution for the characters under consideration. Yield is a complex character and end product of the multiplicative interaction between its components. The yield components themselves are polygenically controlled in most of the cases hence detailed investigations are necessary to understand their mode of inheritance and magnitude of gene effects which serve as a basis for effective and consistent improvement.

Keeping above all into consideration, the present investigation was taken up to study the genetic architecture of traits determining plant type, besides estimating heritability, genetic gain, heterosis, inbreeding depression and genetic variability in G. hirsutum and analysis and comparison of different mating systems in the release of variability and changes in character associations in barbadense cotton.

Generation means

The mean performance of the basic generations P_1, P_2, F_1, F_2, BC_1 and BC_2 of cross Pusa 45-3-6 x Pusa 19-27 presented in Table 1 showed the existence of substantial variability in the selected material for different characters under study. Parents showed wide divergence for all the characters studied, more particularly so far economic yield, biological yield, harvest index, plant height, first fruiting node number and boll number. A wide range of variability for different traits had been reported earlier by Bains (1967), Patil and Mathapati (1976), Basu and Bhat (1987), Singh et al. (1987), Nadarajan and Rangasamy (1990) and Singh et al. (1992).

In general F_1 mean performance was better than either of the parents for boll number, economic yield and biological yield. It appears that P_1 (Pusa 45-3-6) with its large boll number, high boll weight, biological and economic yield contributed largely towards the increased boll number, boll weight, biological yield and economic yield of the F_1. Probably it carried the dominant genes for these traits. Although P_1 had more sympodia with low magnitude it did not contribute much towards better performance of these two traits in F_1. Similar was the case for first fruiting node number in P_2. However, P_2 seems to be contributing to increased monopodia in F_1.

Significant decline in performance of F_2 from F_1 was observed for economic yield, biological yield, plant height, boll number, boll weight and harvest index. This implied that dominance and its interaction contributed significantly in F_1 performance. Possibly epistatic interactions along with overdominance have contributed to the heterosis for these traits (Hays and Foster, 1976). Surprisingly, monopodia and sympodia exhibited negative inbreeding with mean values in F_2 higher than F_1. Similar situation was reported by Baker and Verhalen (1975) for micronaire value. This was possibly due to sampling error in F_2.

Genetic architecture based on components of generation means

Genetic analysis of morphological architecture of traits determining plant type and yield components was carried out through the partitioning of generation means. The knowledge of the type of gene action involved in the expression of economic traits is essential for formulating an efficient breeding methodology. The analysis of first degree statistics is simple and one can detect the different kinds of gene effects and interactions. However, it has a limitation of internal cancellation of positive and negative effects and certain genetic parameters may be under-estimated. It may be emphasised that estimates of different types of non-allelic interactions for quantitative characters from analysis of first degree statistics as compared to any other analysis are more rewarding and useful.

The presence of non-allelic interactions can be inferred from the failure to observe the relationships between generation means that are expected on an additive-dominance model by scaling tests (Mather, 1949). Each type of test is capable of detecting its own characteristic constellation of interactions. Thus D provides a test largely of the [i] type interaction. Test C depends to a greater extent on the [l] type interaction and C and D combined provide a means of assessing the relative importance of [i] and [l] interactions. The [j] type interactions have no effect on tests (C) and (D) but will affect the outcome of the backcross tests (A) and (B) (Mather and Jinks, 1971).

Hayman (1958) and Jinks and Jones (1958) outlined a methods of estimating genetic parameters [d], [h], [i], [j] and [l]denoting additive, dominance, additive x additive, additive x dominance and dominance x dominance gene effects and interactions respectively in a cross between two inbred lines in terms of means of six populations (P_1, P_2, F_1, F_2, BC_1 and BC_2) using digenic model. Hayman (1958) however suggested that a three parameter model neglecting epistasis should be fitted first and 5 or 6 parameter model should be tried only if 3-parameter model does not provide a good fit to the observed data. However, one may directly go for estimation of gene effects and interactions using 6-parameter model.

With the above background, the present experiment was conducted to gather information about nature and magnitude of different types of gene effects and interactions involved in the expression of traits determining plant type from an inter-varietal cross Pusa 45-3-6 (P_1) x Pusa 19-27 (P_2).

Individual scaling tests revealed that the genes governing the inheritance of plant type traits viz., seed cotton yield per plant, plant height, monopodia, sympodia, boll number and boll weight were not independent in their action i.e., non-allelic interactions were involved. Adequacy of the additive-dominance model for Biological yield and harvest index indicated simple inheritance of these two traits. For both these traits, additive component is important though dominance component was also significant in biological yield but in case of harvest index the dominance effect is negative and non-significant.

Gene action for yield and its components

For seed cotton yield, additive effect [d] and additive x dominance interaction [j] were found significant. However, the analysis did not detect significant dominant gene effects. The manifestation of additive effect and epistatic gene interactions for yield was also reported by Kalsy and Garg (1988),Srivastava and Kalsy (1990), Nadarajan and Sree Rangasamy (1991) and Jagtap (1993). However, yield itself being a super character, for improvement in yield, one has to look into its components. The direct components of seed cotton yield are boll number and boll weight.

Boll number showed predominance of interactions [i] and [l], besides the significant positive additive effect [d], whereas for boll weight all effects and interactions were significant. The signs of estimates [d and j] and [h and l] were opposite in sign showing duplicate epistasis. Since epistasis was involved in both these traits, selection should be delayed to much latter generations to enable sufficient number of epistatic gene interactions, get fixed. Dhillon and Singh (1980) noted that inclusion of [h] in model [m,d,h] which was not actually involved caused inflation of the χ^2 value indicating inadequacy of the model involving m, [d] and [h]. From this, they inferred that this trait was controlled by simple additive effects. Other reason for such behaviour could be the presence of higher order interactions.

For boll number, the present results contradict the reports of Silva and Alves (1983). It may however, be kept in mind that when epistasis is present, the results obtained from generation mean analysis of a particular cross are applicable to that cross alone and can't be extrapolated to other crosses (Hayman, 1958). However, this is not a great handicap with self pollination taxa where the breeder's interest lies in obtaining relevant information about that cross rather than about any extrapolated population. Jagtap (1993) noted that additive effects [d] and main effects [(d) + (h)] respectively were predominant over interactions. But with regard to boll weight, similar results were reported by Jasmel Singh et al.(1982) and Jagtap (1993).

Biological yield and harvest index are indirect but important yield components. Both additive and dominance effects for biological yield and only additive effect for harvest index were found significant. Harvest index measures the proportion of biological yield that gets converted into reproductive (economic) part but both economic yield and harvest index are artefacts and it is, therefore, important to look into genetic control and improvement of their causal components for genetic improvement of yield. The improvement of trait biological yield can be brought about by delaying the selection for 2-3 generations so that effect of dominance component is reduced (Mehra et al., 1986). In case of harvest index since only the additive component is significant, pedigree breeding method will be quite useful for selection of segregants for fixing superior genotypes.

Only additive x additive interaction [i] was significant for sympodia, that too, it was negative. Contrary to this, Silva and Alves (1983) noted predominance of additive gene effects for this trait.

Though test C showed significance, indicating the involvement of dominance x dominance interaction, none of the main effects or interactions were found significant for monopodia. Other factors, no doubt, could be operating but relatively high magnitude of standard errors of the estimates was the most probable cause for non-significance of [l] components, another disturbing factor could be higher order interactions or linkage of genes or both. Similar situation was reported by Singh *et al*. (1983) for yield and number of bolls. There is, however, no provision in the present material to test for the presence of higher degree epistasis.

When we consider the characters of plant frame, such as plant height and first fruiting node number, the additive component was important in the inheritance of these two traits. However, additive x dominance interaction [j] was significant for plant height but [d] and [j] were opposite in signs showing duplicate epistasis.

Analysis of heritability and genetic gain

The next step in the analysis is to estimate the heritability, since it provides a measure of the effectivenss with which selection can be expected to exploit the genetic variability.

Heritability (h^2) is a population parameter which gives an idea to the plant breeder that how far he may be successful in transferring the desirable characters from parents to the progenies. Phenotypic performance of an individual is based on two components viz., genotypic part and environmental influence. It is the genotypic component which is of great interest to the breeder. Larger the proportion of genotypic component to phenotypic variability, more the chance of transmission of characters from parents to the progenies.

However, the estimates of heritabilities are influenced by many factors viz., (i) h^2 is a property not only of trait but also of the population; (ii) it is greatly influenced by the development of population i.e., selection for a trait, hence the gene frequencies concerned. In particular small populations maintained under domestication are expected to show low h^2 than the large populations; (iii) The h^2 estimate cannot be generalised to a crop since it is highly specific and valid for the material involved in the experiment and for the environment of experimentation. (iv) Environmental variance (V_E) is dependent upon the conditions of culture and environment. (v) The h^2 values change with generations. (vi) Characters associated with reproductive fitness, such as yield, manifest low h^2 while those are least important, as judged on biological grounds, show high heritabilities. (vii) Heritability in a broadsense (h_b^2) indicates only whether there is sufficient genetic variation present in a population or not, which implies then, whether a population respond to selection pressure or, in other words, whether a selection can be operative. And is also influenced by linkage, sampling and method of calculation.

When a population with considerable variability (predominantly of additive nature) is subjected to selection, a change in gene frequency in the progenies is the natural consequence. This change in gene frequency is responsible for the shift in the population mean, that is reflected in the next generation, in terms of genetic advance. Its predicted value depends on heritability, selection intensity and variability.

Genetic advance, though not an independent entity, has an added advantage over heritability where a character is to be improved through a series of segregating generations. Johnson et al. (1955) stated that without genetic advance, the estimates of heritability based on phenotypic appearance would not be of practical importance. They emphasized the importance of both genetic advance and heritability estimates in selection programme. According to Hanson (1963), heritability and genetic advance are complementary to each other.

Keeping in view all the above considerations, estimates of heritability and expected genetic gain were obtained for various characters. In the present study, these estimates ranged from very low to very high values. High broadsense heritability accompanied with high genetic advance was observed in biological yield, boll number and economic yield in that order. However, estimates of narrow-sense heritability were moderately low for biological yield and boll number and low for economic yield (Table 14). The realised genetic gain is expected to be rather low for such traits unless repulsion phase linkage present which may have resulted in large non-additive variance, could be broken down through breeding manipulations such as biparental matings or diallel selective mating procedures. However, Allard (1960) reported that heritability estimates are inadequate measures of the genetic progress. This is because h^2 could be as high as 100 per cent when genotypic variance has a large value in comparison to environmental variance, whereas genetic progress would be larger with large additive genotypic variance.

Table 14 :Heritability in narrowsense and intergeneric correlations (F_2, F_3) in <u>G. hirsutum</u> cross Pusa 45-3-6 x Pusa 19-27

Character	Narrowsense heritability (%)	Intergeneration correlation
Plant height	42.1	0.540*
First fruiting node number	-	-0.102
Monopodia	-	0.066
Sympodia	-	0.034
Boll number	12.1	0.320
Boll weight	16.3	0.328
Economic yield	8.2	0.220
Biological yield	18.8	0.464*
Harvest index	7.7	0.108

- : Zero estimates

* : Significant at P = 0.05

High heritability estimates for boll number were earlier reported by Thombre *et al.* (1982), Singh and Singh (1981), Seth *et al.* (1984), Khorgade and Ekbote (1981) and for economic yield were reported by Seth *et al.* (1984), Singh *et al.* (1987) and Nadarajan and Rangasamy (1990).

A high broad and narrow sense heritability accompanied with moderate to low genetic advance was observed for plant height. The moderate to low expected genetic gain may probably be due to existence of low genetic variability in material. The high heritability observed in this trait may be due to very small contribution of environmental to the total phenotypic values of the genotypes for this trait. Selection for such traits may not be as rewarding as that in traits with high h^2 and high genetic gain. Similar results were reported by Singh and Singh (1981).

For first fruiting node number, high broadsense heritability was accompanied by low genetic variability (Table 4), therefore no gain was realisable as a result of exercising selection.

Monopodia exhibited moderate broadsense and low narrow-sense heritability (estimated from parent progeny regression Table 14) coupled with high genetic gain. The moderate broad-sense heritability is being exhibited due to low environmental effects and sufficiently large non-additive component of genetic variance. So selection may not be effective in such cases. However, Singh and Singh (1981) observed high h^2 accompanied with high genetic advance for this trait. Hanson (1963) points out that two parameters in different materials are not comparable as they are influenced by method of estimation, generation of hybrid, experimental sample employed and environment.

Boll weight exhibited low broadsense heritability accompanied with low expected genetic advance but it showed moderate narrowsense heritability. The reason for this anomaly was that the broadsense heritability in F_2 was estimated from F_2 variance corrected for environment variance (estimated from parents and F_1s). Therefore, the extremely low estimated broadsense heritability in F_2 could have resulted from inflated estimates of error variance however the narrowsense heritability has been estimated from parent progeny regression where the environmental covariances are negligible, hence better estimates of narrowsense heritability is obtained. Genetic analyses (Table 3) had revealed that dominance and its interaction were quite predominant in the genetic control of this trait. Therefore, selection would be ineffective in early generations. The present results were in conformity with the reports of Atta _et al_. (1982) and Thombre _et al_. (1982).

For sympodia and harvest index Zero heritability and nil genetic gain estimates were obtained. This indicated that these two traits lacked genetic variability and were greatly influenced by the environment.

Heterosis in F_1 and Inbreeding depression in F_2

Heterosis has been a phenomenon of great interest for plant breeders and its utilisation led to significant yield improvement in crop plants. The classic case of heterosis exploitation is of course that of maize but subsequently heterosis breeding had led to outstanding breakthroughs in the productivity of several crop plants including cotton.

The expression of heterosis is influenced by the magnitude of genetic differences (Hawkins *et al.*, 1965; Marane and Avish, 1973; Ramanujam *et al.*, 1974). According to Williams (1959) heterosis has been considered in its broadest sense to include not only hybrid vigour per se but also the related aspects of inbreeding depression and hybrid homeostasis etc. In Cotton, the first attempt in this direction was made in India at cotton Research Station, Surat and the first commercial hybrid H4 was released in 1970 (Patel, 1971).

The study of the magnitude of heterosis and inbreeding depression present in the cotton material might be helpful to the cotton breeder to decide whether he could go for development of hybrid cotton or a homozygous genotype (variety) or for both.

In the present study, seed cotton yield exhibited significant positive heterosis over both mid and better parents, with high magnitude of mid parent heterosis. This showed that parents of the cross were probably good general and specific combiners for yield. The F_1 also exhibited significant inbreeding depression for yield. Similar results were observed by Marani (1963), Thombre *et al.* (1982) and Singh *et al.* (1992). However, Al-Rawi and Kohel (1969) reported small heterosis and inbreeding depression.

Yield by itself is a super character (Grafius, 1959) and therefore it might be interesting to analyse the basis for heterosis in this character through the study of heterosis in its components. Hence, heterosis has been estimated for two major yield components, boll number and boll weight besides other direct/indirect components of yield.

Among yield components, monopodia and boll number showed significant positive heterosis over mid and better parents. In addition, boll number showed significant theoretical heterosis calculated from genetic parameters. Surprisingly all three estimates i.e., heterosis over mid parent, over better parent and theroetical heterosis were found to be high (>30%). In contrast, the inbreeding depression for these traits was non-significant indicating heterosis plausibly be due to differences in frequency of genes in the two parents. One of the major contributing factors could be the diversity between parents calculated for each trait as a ratio of high to the low mean (H/L) parental performance (Baker and Verhalen, 1975). This measure of variability was high (2.29 and 1.84 for monopodia and boll number respectively) for both traits. Similar results of significant heterosis were reported by Thombre et al. (1982) and Singh et al. (1990). However, a low magnitude heterosis was reported by Al-Rawi and Kohel (1960) and Singh et al. (1983b).

Plant height and biological yield exhibited heterosis over mid parent but failed to show significant heterosis over better parent and theoretical heterosis. In these two traits only plant height showed significant but low (compared to its heterosis) inbreeding depression . This revealed that plant height was possibly controlled by both additive and epistatic interaction. This was confirmed by the results of genetic analysis presented earlier.

The nonsignificance of inbreeding depression for biological yield indicated the predominance of additive effects. This was also confirmed through the genetic analysis of the cross using three-parameter model. In case of sympodia, both heterosis and inbreeding depression were nonsignificant. The negative inbreeding depression may be due to more buffering effects of heterogeneous population in F_2 or likelihood of some sampling error involved in it. The low heterosis was plausibly due to low H/L variability (1.16) and negative additive x additive interaction and duplicate dominance epistasis.

First fruiting node number exhibited significant heterosis over better parent but not over mid parent. This was because the parent with less number of first fruiting node was considered as better parent. Similar result was reported by Singh (1983a), but Al-Rawi and Kohel reported only small heterotic effects for this trait.

Boll weight exhibited positive but non-significant heterosis over mid parent and negative non-significant heterosis over better parent, but showed significant theoretical heterosis and inbreeding depression. This small heterosis was plausibly due to (i) relatively less diversity between parents (H/L= 1.34) and (ii) duplicate dominance epistasis. Surprisingly all the four estimates viz., heterosis over mid parent, over better parent, theoretical heterosis and inbreeding depression were more or less with same magnitude. But heterosis over better parent was negative. Singh et al. (1983b) also observed lower heterosis for this trait. Both heterosis (all the 3 estimates) and inbreeding depression were non-significant for harvest index.

On the basis of study of heterosis in yield components, the manifestation of heterosis for yield seems to be due to heterotic response of direct and indirect yield contributing traits.

Analysis of variability in F_3 generation

Plant breeders are commonly faced with the problems of handling segregating populations and selection procedures. Mean and variability are the important factors for exercising selection. Selection for the improvement of quantitative characters can be effective only when the segregating generations possess the potential variability. For characters of low heritability, family selection is preferred against individual selection. Even for characters, of moderate heritability, a combination of between and within family selection may be more desirable (Falconer, 1960).

According to Finkner et al. (1973) a cross or family with highest mean was really effective in identifying the superior segregants. Allard and Hansche (1964) observed that success in improving adaptation requires that population under selection be genetically variable. Sneep (1977) contended that yield tests with self pollinated crops should begin with F_3 progenies.

However, Knott (1979) concluded that F_3 yield tests do not justify the extra work. Byth et al. (1969) indicated that selection of soybeans in early generations for yield on a small plot basis resulted in maximum yield advance.

Manivasakam and Kamalanathan (1987) in G. barbadense observed expression of wide variability and transgressive segregation in F_3. This suggested the commencement of selection in F_3 would be ideal rather than in F_2 for the present material. Mc Ginnis and Shebeski (1968) also concluded that there is no advantage in selection of F_2 plants for high yield.

Singh et al. (1993) in their study observed that comparision of F_3 progeny mean with F_2 mean showed that average number of bolls per plant was higher in all the F_3 families in comparison to F_2s, however, increase in mean boll weight in F_3 compared to F_2 was insignificant owing to narrow variability for this trait in Egyptian cotton.

Except for plant height and first fruiting node number, the F_3 means were higher than their parental mean for all characters. With respect to F_2,higher mean values in desirable direction were observed for harvest index, economic yield, boll weight and sympodia; more or less similar mean values were observed for plant height and biological yield, but means for boll number and first fruiting node number moved towards undesirable direction. The significant feature was increase in mean harvest index in F_3 in response to selection pressure in F_2 generation, for this trait. Despite decrease in boll number, F_3 mean for economic yield was increased. The major component contributing to this increase was boll weight ($\overline{F}_3$ exhibited 24% increase over $\overline{F}_2$). This might be result of correlated response in boll weight as a result of selection for harvest index in F_2

The phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the traits in F_3. This indicated that the apparent variation in each trait is not only due to genotypes but also due to the influence of environment. So selection for such traits sometimes may be misleading.

High heritability accompanied with relatively high expected genetic gain for plant height indicates the importance of additive gene effects and selection may be effective for this trait.

Moderate heritability coupled with moderate expected genetic gain for boll number, biological yield and economic yield in F_3 as compared to high broadsense heritability and high expected gain in F_2 for these traits indicates either dissipation of variance due to dominance effects and interactions as a result of fixation of some of the loci in heterozygous phase, or reduction in phenotypic variance due to correlated response to selection for harvest index in F_2.

Lint index and ginning percentage exhibited high broadsense heritability accompanied with moderate to low genetic gain, indicating existence of low genetic variability in these traits in the present material. The high heritability exhibited was due to low influence of environment rather than high genotypic variability. So selection for such traits may not be rewarding. Harvest index exhibited very low genotypic coefficient of variation accompanied with Zero heritability estimates. This strongly suggested that the material lacked presence of sufficient genetic variability for this trait.

Monopodia exhibited relatively high phenotypic and high genotypic coefficient of variation and low heritability. Thus indicated that this trait was highly under the influence of environment.

Moderate values of genotypic and phenotypic coefficients of variation and moderate h^2 and expected genetic gain for boll number, economic yield and biological yield suggested possibilities of genetic improvement in yield through recombination breeding and recurrent selection.

Frequency distribution line graphs illustrated in Fig. 1 to 7 indicates the existence of skewness for some traits. The characters, viz., plant height, first fruiting node number, sympodia, boll weight, ginning percentage and lint index showed more or less normal curves. The plausible reasons for this normal distribution are polygenic nature of traits, low heritability, high environmental influence, epistasis and also recovery of new recombinants in equal frequency in both the directions of the mean. Presence of epistasis in the material was confirmed through the generation mean analysis.

Skewed curves were obtained for monopodia, boll number, economic yield, biological yield and harvest index. The reasons for skewed distribution in boll number, economic and biological yield and harvest index may be many such as, isodirectional dominance or some blurring effect produced by environmental agencies or zygotic elimination of some genotypes.

Familywise analysis

Analysis of variance indicated significant differences between F_3 families for all the characters when tested against within family variance except for monopodia and harvest index (Table 8). This suggests that selection for harvest index in F_2 proved successful without largely eroding the variability of other characters in the present material.

Results of familywise analysis presented earlier in Table 7 revealed that many F_3 families were quite promising from the point of view of exercising further selection for different traits (Table 15). The family 21 showed a higher mean than F_3 population mean for all the traits. The other promising families which showed higher mean for a large number of traits in order are 29, 30, 9, 27, , 10, 15, 4 and 23. Again, among all the families only three families viz., 21,29 and 30 showed high mean for all 5 major components viz., boll number, boll weight, economic yield, biological yield and harvest index. Other families with high mean values for boll number, boll weight and economic yield were 5,8,9,10 and 15.

Family 21 showed high mean coupled with lower range and variance for boll number, boll weight and economic yield indicating that in this family, fixation may have already taken place for most of the segregating loci and in this case further selection may be lead to elimination of residual heterozygosity or all the genotypes of the family may carry same number of positive dominant genes for the traits under consideration.

Table 15 : Distribution of elite F_3 families* for different traits in hirsutum cotton

Trait	Elite Families													
	4	5	7	8	9	10	15	21	22	26	27	28	29	30
Economic yield	#	#	#	#	#	+	#	+	+	+	+	#	#	#
Plant height					#			+	+			#	#	
First fruiting node number(FNN)								#		+	+			+
Monopodia	#	+					+	+			+		+	
Sympodia		#		+	#	+	+	+			+	+	+	+
Boll number	+	#	#	+	#	+	#	+	+	+	+	#	#	#
Boll weight		+		#	+	#	#	+					+	#
Biological yield	#	#	#	#	#	#	#	+	#				#	#
Harvest index	+							+		+	+		+	+
Seed index					#		#	+		#				#
Ginning percentage	#	+				+		#	+		+	+	+	
Lint index					+	#		#		#	+	#	+	+
Total	2+ 4#	3+ 4#	3#	2+ 3#	2+ 6#	4+ 3#	2+ 5#	9+ 3#	4+ 1#	4+ 2#	8+	2+ 4#	6+ 4#	4+ 5#

+ : high mean with low variance for a trait but in case of FNN, monopodia it refers to low mean with low variance

: high mean with high variance for a trait but in case of FNN, monopodia it refers to low mean with high variance

* : Reference Table 7.7

Character associations in F_3 generation

Correlation studies are of primary importance to know the variability of various characters for selection, because selection for a particular trait may induce desirable or undesirable changes in the associated characters. Generally, direct selection for yield may not be aimed at, as according to Grafius (1959) genes for the complex trait, yield do not exist there are only genes for component traits. As such, high genotypic and environmental interactions are likely to restrict the direct improvement.

One of the aims of correlation study is to know the suitability of various characters for indirect selection, because selection for one or more traits may result in correlated response in several other traits (Searle, 1965). Therefore, a precise knowledge of nature of genetic relationship between yield and its direct and indirect components is essential.

Almost every study that detected genetic variation in two or more traits also obtained evidence of genetic associations. The genetic mechanisms underlying such genetic correlations are pleiotropy or linkage or both. If the relationship of characters is due to manifold effect of a gene or genes (pleiotropy) it is difficult to separate by breeding, the characters so related. If the correlation is due to genetic linkage, it is possible to reverse the correlation provided the linkage is not very close. It is, also therefore, important to establish the genetic basis of correlation before launching any selection programme.

Correlations between various traits (Table 8) in F_3 generation indicated that biological yield, boll number, monopodia and plant height in that order were strongly, positively and significantly correlated with seed cotton yield. In contrast, harvest index was negatively correlated with plant height, first fruiting node number, sympodia, monopodia and biological yield. In other words, plant height was negatively correlated with harvest index but positively correlated with seed cotton yield. It indicated that improvement of harvest index in tall type was difficult because plant height was positively associated with biological yield. In other words, for improvement of harvest index reduction in plant height is important. Similar results were reported by Mehra et al. (1987) and Singh et al. (1992). Similar was the case with monopodia and biological yield.

In this material, positive and significant correlation of boll number with both economic yield and harvest index indicated that selection for more boll number will improve both harvest index and seed cotton yield, however in the present material only moderate amount of genetic gain may be realised as the genetic variability available for this trait is rather low (Table 6).

Another significant feature was that the correlation of boll number and boll weight was also positive though non-significant as against negative relationship between these two traits, reported by many authors. Therefore, selection for either of the yield components or simultaneously for both the components is likely to improve the seed cotton yield significantly. The similar results were reported by Singh *et al.* (1993).

Based on the genetic analysis of traits determining plant type and yield components in *G. hirsutum*, the following architecture of plant ideotype is suggested.

- Medium plant height (80-100 cm)
- Less number of first fruiting node number
- Low monopodia
- More sympodia (> 20)
- More boll number accompanied with same or more boll weight
- High harvest index (> 50%) along with good biological yield
- High ginning percentage (>35%)

In addition, good quality attributes.

Towards this goal, the present *G. hirsutum* material can be improved by taking up biparental selective intermating or any other suitable recurrent selection procedure to enhance desirable gene frequency and to generate substantial variability in the material especially for traits viz., boll weight, first fruiting node number, sympodia and also boll number. the selection may be delayed to later generations to reduce dominance effect and to fix epistasis.

The positive significant correlations of boll number with harvest index, biological yield and seed cotton yield; and also positive correlation with boll weight and ginning percentage suggest that selection based on boll number may possibly effect in the harmonious blend of characters.

GOSSYPIUM BARBADENSE

In India, early unsuccessful attempts to cultivate Gossypium barbadense in the Northern parts was mainly due to utilization of limited genetic variability. It is well known that crop varieties, which are relatively insensitive to photoperiodic and thermal conditions can be evolved if large enough genetic variability is utilised in course of breeding programme.

Cotton breeding methods probably are not as well defined as those of other predominantly self pollinated crops. In general, the pedigree method has been used most frequently. Selection usually starts with F_2 plants followed by progeny rows and further selections in subsequent generations. Cotton breeders selecting for higher yield and fiber quality; and high boll number and high boll weight have not been satisfied with the results of this approach. A high selection intensity in the early generations usually has resulted in very few desirable recombinants. Some modifications of the conventional system seem necessary (Meredith and Bridge, 1971).

Cotton is predominantly a self pollinated crop. This is particularly so with G. barbadense (5-10% natural cross pollination), so there is little chance of new recombinants to occur after the F_2 generation (Meredith, 1984). Basing the theoretical calculations on the linkage associations between parents of diverse genetic backgrounds, selective with Random intermating has been suggested by Hanson (1951) and by Miller and Rawlings (1967). This method would produce the most recombinants when linkage is involved, but its disadvantage is that no genetic advance is made during the several generations of intermating. The availability to breeders of large gene pools that have been produced by selective random mating procedures would greatly reduce this limitation.

Jensen (1970) has proposed a diallel selective mating (DSM) system to overcome some of the difficulties of conventional breeding system. Multiple parents are used to form a large gene pool, which through selective matings of individuals is advanced through successive generations. This procedure would breakup linkage blocks by intermating and provide a large gene pool but at the same time allow genetic advance.

A practical method would be one of selecting plants in F_2 as per classical procedure and intermate them followed by selfing to permit breakup of linkages. Depending on the amount of variability generated, breeder may decide either to go for selection and intermate again or following selfing in subsequent generation.

The major objective of the present study has been to evaluate the genetic variability generated in three populations following different mating systems viz., selective intermating, open (random) pollination and self pollination in F_3 generation and to compare the magnitude and nature of variability in F_4 generation.

Parameters of variability

The study of parameters of variability of *G. barbadense* following above procedure (Table 10) revealed that for both boll weight and seed index population means of similar magnitude were exhibited by all the three populations. This may be due to low genetic divergence between parents for these characters.

The population derived through selective intermating showed high mean values for biological yield, ginning percentage and lint index and lowest mean value for monopodia. It also showed high range for plant height, first fruiting node number, monopodia, sympodia, boll number, boll weight, economic yield, seed index, ginning percentage and lint index. This indicated that selection for monopodia, boll weight, seed index, ginning percentage and lint index would be effective in this population.

The F_4 population raised through open pollination showed higher mean values for plant height and sympodia; and it also showed higher range for sympodia and biological yield.

The population raised through self pollination exhibited high mean values for first fruiting node number, boll number, economic yield and harvest index and it also showed higher range and variance for harvest index.

The F_4 populations were compared for available variability in the three populations from different mating systems. This will permit the evaluation of the breeding procedures.

Using F-test for comparing the variance estimates, significant increase was noted in variability for first fruiting node number. The variances were in the order: open < selective intermating < self.

The variability for boll weight, ginning percentage and lint index was significant in selective intermating derived population. The order of magnitude of variances in three characters were selective > open > self.

Using t-test for comparison of means in the three populations, significantly higher means were observed for first fruiting node number and boll number in self pollinated population; for economic yield in populations derived from selective intermating and self pollination and for ginning percentage in selective intermating derived population.

Joint consideration of both F- and t-tests revealed that improvement for first fruiting node number will be effective in population raised through self pollination and for ginning percentage further selection could be effective in selective intermating derived population.

Miller and Rawlings (1967), and Meredith and Bridge (1971) attributed differences between F_3 progenies of original population and intermated population particularly for yield to selection which may have inadvertantly entered into their experiment. This possibility cannot be ruled out in the present study also. Further, Miller and Rawlings (1967) supposed that the more vigorous and higher yielding plants produced more pollen at flowering time and thus contributed more than their proportional share of gametes to the succeeding generation and changes for characters other than yield could be accounted for by correlated responses. In all cases, the changes were of the magnitude and direction were expected for changes in unselected traits due to the observed genotypic correlations between yield and these traits. However, in the present material the observed changes in means can also be attributed to: (i) differences in population size; (ii) epistasis, besides correlated response due to selection.

An F_2 population is not generally in linkage equilibrium. Hanson (1959) has shown that genetic variances may vary considerably from those expected for genetic equilibrium. Crosses with a predominant coupling phase linkages would be expected to have reduced genetic variances upon intermating. Genetic variance would be expected to increase for those crosses with a predominant repulsion phase linkage. While significant changes in genetic variances indicate the presence of linkage, non-significance does not necessarily exclude absence of such linkages.

The estimates of variances (Table 10) show little differences for most of the characters among 3 populations. Economic yield, plant height, first fruiting node number, sympodia, boll number, harvest index and seed index showed decreasing trend in intermating derived population over self pollination derived population. Under these conditions, one might expect predominant coupling phase linkages and a reduction in magnitude of genetic variances. As more selection pressure is applied, the variance is likely to further reduce in population with predominant coupling phases. This inference is on the assumption that considerable linkage disequilibrium exists in F_3 also and differences in population size do not seriously bring about changes.

Transgressive segregation

It is not infrequently noticed in the course of plant breeding work that certain segregates are obtained in the F_2 or subsequent generations of a cross, in which the magnitude of expression of certain characters trasgresses the limits covered by the parental strains. The transgressive segregants represent individuals in which several additive genes may have accumulated in the homozygous condition (Sikka and Joshi, 1960). It was stated that though all polygenically held characters can manifest transgressive segregation, flowering time and plant height are the two traits which are most frequently transgressed.

Combining distantly related parents possessing desirable traits in the required intensity but controlled by different set of genes tends to ensure release of transgressive segregants. Chance recombinations of productivity genes might be expected to enhance the yield level of such segregants. Then, it is obvious that the first objective of hybridization i.e., development of productive variety is transgressive breeding. It is also referred to "assembling productivity genes". The appearance of transgresive progenies in F_2 is the function of several favourable genetic situations associated with the parents viz., (i) the character must be polygenically controlled; (ii) parents should be completely homozygous; (iii) parents should be complementary to each other for the (+) and (-) genes conditioning the trait in point; (iv) there should be no linkage (Sharma, 1994). Considering all this in view, frequency distribution curves were drawn (Fig. 8 to 19) for different characters.

In selective intermating derived population, plant height, first fruiting node number, boll weight, harvest index, seed index, ginning percentage and lint index followed normal curves indicating the possible role of epistasis and environmental influences, whereas the curves in case of monopodia, sympodia, boll number, biological yield and economic yield were skewed which may be either due to high heritability, or isodirectional dominance or blurring effect of environment.

For economic yield, the frequency curve got skewed towards the side of the better parent in the population raised through selective intermating indicating the potential of selective intermating in obtaining superior recombinants. Among yield components only boll weight showed transgression beyond the better parent in all the three systems. Surprisingly, both self and open pollinated systems show recovery of individuals only beyond the better parental range, suggesting operation of strong gametic/zygotic selection for this trait. Contrary to this, monopodia showed transgressants beyond the limit of undesirable parent though the frequencies of recombinants was more towards desirable parent (parent with Zero monopodia). However, this is understandable, as the number of monopodia cannot be less than Zero.

For plant height, in all three systems more or less maximum frequency of transgressants were observed towards the side of lower parent. Generally medium plant height was desirable from crop improvement point of view but a ~~D~~dwarf plant types with high harvest index and seed cotton yield are much more useful. Nearly equidistant range was observed independently for selective intermating and self pollinated systems.

In the present study, the differences in population sizes arose as a result of (i) intially maximum attention was given to selective intermating because of possible low rate of successful crossing, and (ii) carrying out of random and self pollination late in the season thus resulting in maximum boll drop which was further aggravated by inclement weather.

The above study revealed that selective intermating offers good opportunity to release wider range of yield transgression (of course coupled with high frequency) over the other systems. Comparison of yield of recombinants indicated that although magnitudewise positive transgressants were more in selective intermating but per cent wise these were high in self pollinated system followed by selective intermating. All positive yield transgressants were also positive transgressants for boll weight but on the contrary all the three systems did not give rise to transgressants for boll number.

Correlations and changes in character associations in three different mating systems

Indirect selection is more effective when a trait has a low heritability and/or is not easily measurable. One of the aims of the correlation study is to know the suitability of various characters for indirect selection because selection for one or more traits results in correlated response for several other traits (Searle, 1965); and pattern of variation will also change. Therefore, a precise knowledge of the nature of genetic relationship between yield and its direct and indirect components is essential.

High yield potential is the basic requirement with which breeder is generally concerned. And grain yield is the resultant of end product of cautioned efforts of various factors complementing or counteracting which reflects for sum total of yield. The extent to which linkage blocks are broken and genetic recombination occurs is of critical interest to the plant breeder, since the success of his breeding program depends upon obtaining desirable character recombinations. Intermating in early generations like F_3 may result breakup in such linkages. The effect of the mating systems in dissipation of such linkage blocks has been examined through study of resultant changes in genetic associations.

The phenotypic correlation coefficients among yield and other characters are given in Tables 11, 12, and 13. Correlations involving seed cotton yield (Table 16) are of primary importance. The components of yield that most frequently correlated with yield has been boll number and harvest index.

The major objective of this study was to generate variability so as to combine yield with good plant type traits. This was realised to some extent. The non-significant correlation of plant height with yield was changed to significant positive association in the intermating population. Similar was the case for biological yield. Boll weight and yield showed little association in open pollinated system but in selfed and

Table 16 :The changes in associations of yield with its components in three populations advanced through three different mating systems

Population	Yield components										
	Plant height	First fruit-inf node number	Monopo-dia	Sympo-dia	Boll number	Boll weight	Biological yield	Harvest index	Seed index	Ginning percentage	Lint index
Self pollinated	+ns	-ns	+ns	+ns	+s * (0.900)	+s * (0.629)	+ns	+s * (0.679)	+ns	+ns	+ns
Open pollinated	-ns	+ns	-ns	-ns	+s * (0.822)	+ns	+ns	+s * (0.743)	-ns	-ns	-ns
Selective intermating	+s	-ns	+ns	+ns	+s * (0.806)	+s * (0.339)	+s	+s * (0.326)	-ns	+ns	+ns

s :Significant correlation at P=0.05; ns= nonsignificant at P=0.05

+ :Positive correlation ; - : negative correlation selective intermating population, this association was significant and positive. However, for monopodia selective intermating showed an establishment of positive association of yield with monopodia which is not desirable from plant type point of view. Further the negative correlation of sympodia, seed index, ginning percentage and lint index with yield was changed to positive though non-significant. Similar results for other characters were reported by Miller and Rawlings (1967), Meredith and Bridge (1971) and Tyagi (1986, 1987, 1994).

For most traits that had high genotypic associations in original (selfed or open pollinated) population, correlations were found to be lower in the intermated population. For example, in case of boll number, boll weight and harvest index (Table 13). Similar results were reported by Miller and Rawlings (1967) and Meredith and Bridge (1971).

The significant changes in associations observed in populations of <u>G. barbadense</u> cross 10-98-P_1 x 11-181-P_2 advanced to F_4 generation by three different mating systems were presented in Table 17. As many as 24 character associations, out of a possible 66 showed some changes in the populations raised through three mating systems. The change or increase in correlation coefficients can be obtained if the initial linkages in a predominant repulsion phase are broken down.

The character pairs (1,6), (1,7), (4,6), (5,8), (6,10), (7,8), (9,10), (2,7), (3,9), (8,10) and (10,11) which were non-significant in both self and open pollinated populations, showed significance in selective intermating derived population. The character pairs (3,8), (6,12), (7,9) and (1,9), (8,9) also

Table 17: Types of changes in associations observed in the populations of *Gossypium barbadense* cross 10-98-P$_1$ X 11-181-P$_2$ advanced to F$_4$ generation by three different mating systems

Character pair	Population-1 (self pollination)	Population-2 (open pollination)	Population-3 (Selective inter-mating)
1,6	ns	ns	+s
1,7	ns	ns	+s
1,9	ns	-s	-s
1,10	ns	+s	ns
2,7	ns	ns	-s
3,8	ns	+s	+s
3,9	ns	ns	-s
3,10	ns	+s	ns
4,6	ns	ns	+s
4,8	ns	+s	ns
4,9	ns	+s	ns
5,8	ns	ns	+s
5,11	ns	-s	ns
5,12	+s	-s	ns
6,7	+s	ns	+s
6,10	ns	ns	+s
6,12	ns	+s	+s
7,8	ns	ns	+s
7,9	ns	+s	+s
8,9	ns	-s	-s
8,10	ns	ns	-s
9,10	ns	ns	+s
10,11	ns	ns	-s
10,12	+s	+s	ns

+s: Positively significant; -s: negatively significant; ns: not significant showed positive and negative significance respectively only in selective intermating and open pollinated populations. The character pair boll weight and economic yield (6,7) exhibited positive and significant association in both selective intermating and self pollinated population.

The character pairs (1,10), (3,10), (4,8), (4,9) and (5,11) which are uncorrelated in selective intermating and self pollinated populations were found to be significant in open pollinated population. The association of seed index and lint index was found to be positively significant in both selective intermating and self pollinated populations. The correlation of boll number and lint index was found to be positively significant in self pollinated population but it changed to negatively significant in open pollinated population.

This study indicated that in this population linkage disequilibrium is still a contributing factor to cause difficulties in improving yield with both high boll number and boll weight.

Phenotypic correlation coefficients of three different populations showed that economic yield was positively associated with boll number and boll weight in population raised from self pollination; with boll number and lint index in population raised from open pollination and with plant height, first fruiting node number, boll number and boll weight, biological yield and harvest index in selective intermating population. This indicated that both boll number and boll weight were positively and significantly correlated with seed cotton yield in all populations except for population derived from open pollination where only boll number is positively and significantly correlated with yield. On the other hand, both boll number and boll weight were positively correlated between themselves and with harvest index, in both populations derived from self pollination and selective intermating in the same order. So yield and harvest index improvement through simultaneous selection of boll number and boll weight was possible in populations derived from self pollination and selective intermating.

Another feature that came out was that plant height was significantly and negatively correlated with harvest index in populations derived through random pollination and selective intermating while in case of self pollination derived population, this correlation was found negative but non-significant. Moreover, boll number and boll weight were positively correlated with plant height only in populations derived from self pollination and selective intermating. This indicated that simultaneous selection for high boll number, boll weight to improve high harvest index and economic yield could be effective in population derived from selfing than in the other two.

From the results, it appears that the intermated populations should provide a better source of material for selection of negatively or nonsignificantly correlated characters than the original population, perhaps due to a partial breakup of linkage blocks in the original material. Hanson (1959) on the basis of theoretical calculations suggests that at least 1 or more and preferably four intermating cycles should precede selfing generations to ensure a degree of breakup of the linkage groups and to increase the genetic recombination within linkage groups. Present data tend to support this conclusion however more cycles of intermatings are needed to derive exploitable results.

Based on the foregoing genetic variability studies and analysis of associations desirable plant type in *G. barbadense* should possess the following attributes:

- Medium dwarf stature
- Low or Zero monopodia
- More number of sympodia
- High boll number and high boll weight
- High harvest index along with high biological yield
- In addition, good quality attributes

In order to achieve this above plant type, creation of sufficient genetic variability will be required for most of the traits, along with improvement in correlations especially of boll number and boll weight; and biological yield and harvest index favourably which can be possibly achieved by giving further cycles of selective intermating or through any other recurrent selection procedure.

SUMMARY AND CONCLUSIONS

The present study was undertaken to generate basic information needed for planning a rational programme to develop a suitable plant type/ideotype in cotton. The investigations included-

1. Examination of nature of genetic architecture of seed cotton yield and its components.
2. Estimation of genetic variability for various components of yield and morphological traits in hirsutum cotton, and
3. Examination of three mating systems in the generation of genetic variability in barbadense cotton.

The material involves F_1, F_2, BC_1, BC_2 and F_3 generations of an intervarietal *G. hirsutum* cross Pusa 45-3-6 x Pusa 19-27 and F_3 and F_4 generations of a *G. barbadense* cross 10-98-P_1 x 11-181-P_2.

G. hirsutum

1. Analysis of morphological components of variability

i) The mean performances of basic generations of the cross showed the existence of substantial variability in the material for different characters under study.

ii) In general, F_1 mean performance was better than either of the parents for boll number, economic yield and biological yield.

iii) The significant decline in F_2 performance from F_1 for economic yield, biological yield, plant height, boll number, boll weight and harvest index implied presence of significant inbreeding depression.

2. Nature of genetic control for yield components and other morphological traits

i) The nature of gene effects and interactions was studied through the generation mean analysis following Mather (1949), Jinks and Jones (1958), Mather and Jinks (1971) using first degree statistics.

Individual scaling tests revealed the importance of non-allelic interaction in the expression of seed cotton yield, plant height, monopodia, sympodia, boll number, boll weight while the biological yield and harvest index were governed by simple additive-dominance model.

ii) Additive gene effects and additive x dominance gene interactions were involved in the expression of seed cotton yield. Similarly, the non-additive component was predominant for boll number and boll weight though additive effects were also significant. For biological yield, harvest index, plant height and first fruiting node number additive effects were significant in the phenotypic expression of these traits. Biological yield also showed presence of significant dominance effects. Additive x additive gene interaction was important in sympodia.

iii) As a whole fixation of superior genotypes may be successful to some extent under pedigree system of breeding since a considerable amount of additive genetic effect was noticed for a number of yield components. However, the predominance of dominance effect in case of biological yield and boll weight and predomiannce of epistasis in genetic control of many characters suggest that these characters can be improved upon by use of recurrent selection schemes or selective intermating and by postponing selection to later generations till sufficient epistatic gene interactions get fixed.

iv) Heritability and expected genetic gain study revealed predominance of non-additive genetic control in the expression of seed cotton yield, biological yield and boll number which was ealier also confirmed by generation mean analysis. Similar was the case with first fruiting node number and monopodia which exhibited moderate to high broadsense heritability and expected genetic gain but low magnitude of narrow sense heritability indicating that additive genetic variability was low for these two traits.

The harvest index and biological yield were greatly affected by the environment. Plant height with high heritability (both broadsense and narrowsense) along with moderate genetic gain indicated the possibility of selection. Boll weight showed moderate narrowsense heritability as estimated from parent progeny regression as against low estimate of broad sense heritability was probably because of inflated estimates of environmental variance.

3. Analysis of heterosis

The study of heterosis showed positive significant heterosis over mid and better parents and inbreeding depression for economic yield. In terms of yield components, this heterosis was mainly contributed by heterosis for boll number. Plant height showed significant heterosis and inbreeding depression suggesting that this trait was controlled by both additive and non-additive components. The sympodia and harvest index failed to exhibit significant heterosis or inbreeding depression. Biological yield also exhibited only mid parent heterosis.

4. Analysis of variance for "Between and Within families"in F_3

i) The ANOVA showed that all 30 families differed significantly from each other for different characters except for monopodia and harvest index.

ii) Significant feature in the study of variability was the observation of correlated response for boll weight in F_3 as a result of selection in F_2 for harvest index.

iii) The coefficient of variation studies indicated the variation in traits was caused by both genotype and environment. Low variability was exhibited for harvest index, lint index and ginning percentage.

iv) Moderate values of genotypic and phenotypic coefficients of variation and moderate heritability and genetic gain for boll number, economic yield and biological yield suggested use of recombinant breeding and use of recurrent selection procedures for genetic improvement in yield.

v) Frequency distribution for plant height, first fruiting node number, sympodia, boll weight, ginning percentage and lint index revealed normal pattern. The skewed curves of monopodia, boll number, economic yield, biological yield and harvest index indicated the existence of isodirectional dominance and/or zygotic selective elimination of genotypes in one direction.

vi) Familywise analysis revealed, three families 21, 29 and 30 were having high mean value for 5 major components, boll number, boll weight, economic yield, biological yield and harvest index. Family 21 exhibited high mean value for all traits coupled with lower range and variance for boll number, boll weight and economic yield indicating that fixation may already have taken place for most of the segregating loci for these traits. It's mean economic yield was also higher than F_3 population mean. Thus the plants in this family at all probability represent genotypes with optimum combination of characters to maximise yield.

vii) Character associations revealed that selection for boll number would simultaneously improve both economic yield and harvest index. The positive association of boll number and boll weight further offer opportunity to increase the number of bolls without reducing boll weight.

viii) Based on the above genetic analysis the suggested plant type in hirsutum cotton should have medium plant height (80-100 cm), more sympodia, more boll number with existing or more boll weight, high harvest index (> 50%) along with high biological yield, high ginning percentage in addition to good quality attributes which may be developed by selective intermating or recurrent selection and delay in selection to later generations to reduce dominance effects and to fix epistasis.

<u>G. barbadense</u>

5. Study of variability in the three populations raised by selective intermating, random intermating and self pollination

exhibited identical magnitude of population means for boll weight and seed index. For economic yield significantly higher means were observed in selective intermating and self pollination system and for first fruiting node number population raised through self pollination showed significant increase in variance over the others. The analysis also revealed that improvement is effective for first fruiting node number in self pollinated system and for ginning percentage in selective intermating.

Study of recombinants revealed that selective intermating and self pollinated system offers good opportunity for releasing yield transgressants over the open pollinated system. The positive yield transgressants were also found to be transgressants for boll weight over better parent. However, none of the systems gave rise to transgressants for boll number. For plant height, all three systems gave transgression towards the side of lower parent which are considered as agronomically potential.

Analysis of associations showed differential changes in pairwise characters correlated in the populations raised through three different mating systems. Maximum changes were observed in selective intermating population offering possibilities to improve correlations in the desirable direction especially of both boll number and boll weight by increasing the cycles of selective intermating.

The suggested plant type for G. barbadense was medium dwarf stature, low monopodia, high boll weight together with more boll number, high harvest index and high biological yield, in addition to good quality attributes.

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* Original not seen.

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