COMBINING ABILITY AND GENETIC ARCHITECTURE OF OIL CONTENT, SEED YIELD AND COMPONENTAL TRAITS IN SESAME (*Sesamum indicum* L.)

तिल (सीसेमम् इन्डीकम एल.) में तेल की मात्रा, दानो की उपज एवं घटकीय लक्षणों की संयोजी क्षमता एवं आनुवंशिकीय स्थापत्य

A
THESIS
PRESENTED TO
RAJASTHAN AGRICULTURAL UNIVERSITY
BIKANER

IN PARTIAL FULFILMENT OF
THE REQUIREMENTS FOR THE DEGREE OF
Doctor of Philosophy in Agriculture
(Plant Breeding and Genetics)

By
C. A. MANSURIA

May, 1992

RAJASTHAN AGRICULTURAL UNIVERSITY, BIKANER

CAMPUS – UDAIPUR

DATED : MAY 3o , 1992

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THIS IS TO CERTIFY THAT Mr. C.A. MANSURIA HAS SUCCESSFULLY COMPLETED THE PRELIMINARY EXAMINATION HELD ON 26th DECEMBER, 1991 AS REQUIRED UNDER THE REGULATIONS FOR DOCTOR OF PHILOSOPHY IN AGRICULTURE.

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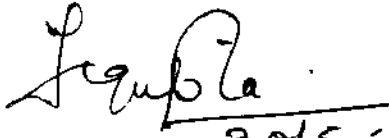
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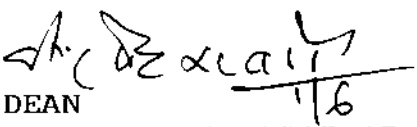RAJASTHAN AGRICULTURAL UNIVERSITY, BIKANER

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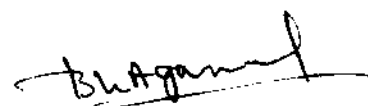RAJASTHAN AGRICULTURAL UNIVERSITY, BIKANER

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UDAIPUR

Dated the May 30 , 1992

(C.A. MANSURIA)

सारांश

राजस्थान कृषि महाविद्यालय, उदयपुर के अनुसंधान फार्म पर ।99। के खरीफ मौसम में एक प्रयोग यादृच्छिक खण्ड अभिकल्पना में तीन पुनरावृतियों में लिया गया । इसका उद्देश्य तिल (सिसेमम इण्डीकम एल.) के दस जनकों में व्यत्यासन विश्लेषण (व्युत्क्रम को छोड़ते हुए) द्वारा संकर ओज, अन्तः प्रजनन अवसाद, संयोजिता एवं उपज तथा उसके सहायक घटकों के वंशागति में प्रयुक्त जीन प्रक्रिया का अध्ययन करना था ।

प्रसरण के विश्लेषण ने जनकों, एफ$_1$ एवं एफ$_2$ में अध्ययनरत अधिकतर लक्षणों में उच्च स्तर की सार्थक परिवर्तिता दर्शायी, जिसने कि परीक्षण में प्रयुक्त संसाधनों में उपयोगी विभिन्नता सिद्ध की ।

उपज एवं उसके सहयोगी घटकों जैसे कि प्रति पौधा संपुटकों की संख्या, जननीय तने की लम्बाई, परिपक्वावस्था में पौधे की उंचाई, प्रति पौधा शुष्क भार, शस्य सूचकांक और प्रति पौधा तेल की मात्रा में उच्च परिमाण का संकर ओज प्रभाव था । इन घटकों ने एफ$_2$ पीढ़ी में उच्च अन्तःप्रजनन अवसाद बताया ।

सुसंयोजिता प्रभाव एवं स्वतः प्रदर्शन पर आधारित क्रम विन्यास ने लक्षणों जैसे कि, प्रति पौधा संपुटकों की संख्या, परिपक्वावस्था में पौधे की उंचाई, जननीय तने की उंचाई एवं प्रति पौधा शाखाओं को उपज में सीधे सहयोगी बताया । जनक बीएयूटी-।, आरटी-।25, गुजरात तिल-। एवं मृग-। सुसंयोजक थे इन जनकों को वांछित नस्ल विकास के लिये संकरण प्रक्रिया में तथा विघटन युक्त पीढ़ी में अच्छे जनक को प्रथक करने में प्रयोग लाया जा सकता है ।

संकरों के स्वतः प्रदर्शन एवं विशिष्ट संयोजिता प्रभावों में निकट संबंध था, जिससे की यह पता चलता है कि इसे प्रभाव पूर्ण संकर ओज प्राप्त करने हेतु कसौटी के रूप में लिया जा सकता है । उपज एवं उसके सहायक घटकों हेतु सुसंयोजिता प्रसरण की तुलना में विशिष्ट संयोजिता प्रसरण अधिक मात्रा में पाया गया ।

'डी' एवं 'एच' घटकों के कारण प्रसरण के आंकलन ने यह प्रदर्शित किया कि अध्ययन में प्रयुक्त अधिकतर लक्षणों की वंशागति में संयोजी एवं प्रभावी जीन प्रक्रिया सम्मिलित थी । जिसमें कि असंयोजी जीन प्रक्रिया का अधिक योगदान पाया गया । ये परिणाम अधिकांश लक्षणों के आलेखी विश्लेषण से भी संतुष्ट हुए हैं ।

वर्तमान शोध के परिणाम यह सुझाव देते हैं कि पारस्परिक प्रत्यावर्ती चयन प्रक्रिया द्वारा संयोजी जीन प्रभाव की वृद्धि की जा सकती हैं, साथ ही यह प्रक्रिया असंयोजी जीन प्रभावों का क्षय भी नहीं होने देगी । विघटन युक्त पीढ़ियों में अवांछित सम्बन्धों को तोड़ने के लिए द्विजनकीय संगम को प्रयोग में लिया जा सकता हैं ।

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ABSTRACT

An experiment was conducted in randomized block design thrice replicated at Research Farm, Rajasthan College of Agriculture, Udaipur in Kharif-1991 with a view to estimate heterosis, inbreeding depression, combining ability and nature of gene action involved in the inheritance of grain yield and its componental traits in sesame (<u>Sesamum indicum</u> L.) using diallel analysis (excluding reciprocals) involving ten genotypes.

The analysis of varaince revealed highly significant difference among parents, F_1 and F_2 for most of the traits studied, indicating considerable amount of genetic variability in the material tested.

High magnitude of heterotic effect was detected for grain yield and its components <u>viz</u>., number of capsule per plant, length of reproductive stem, plant height to maturity, dry weight per plant, harvest index and oil yield per plant. These characters expressed high inbreeding depression in F_2 generation.

Based upon the overall ranking for GCA effects and <u>per se</u> performance the characters <u>viz</u>., number of capsules per plant, plant height to maturity, length of reproductive stem and number of branches per plant were direct yield contributers. Parent BAUT-1, RT-125, Gujarat Til-1 and Mrug-1

were good combiners and can be used in crossing programme for development of desired variety and to isolate superior genotypes in segregating generation.

A close relation existed between _per se_ performance of hybrids and SCA effects, suggesting that it can be taken as a criterion for effective heterosis. Higher magnitude of SCA variance was recorded than GCA variance for grain yield and its attributes.

Estimation of variance due to D and H components revealed that additive as well as dominance gene actions were involved in the inheritance in most of the traits under study, with predominance role of non-additive gene action. These findings were also confirmed by graphical analysis for most of the traits.

The results of present investigation suggested that reciprocal recurrent selection procedure will mop up the additive gene effect and will also not allow to dissipate non-additive effect. Biparental mating may used in segregating generations to break undesirable linkage.

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Sesame (_Sesamum indicum_ L., Syn. _Sesamum orientale_ L.), a self pollinated crop is among the oldest cultivated oil seed crops of India (Watt, 1893), belonging to the order Tubiflorae and family Pedaliaceae. Several historical records indicated that sesame probably originated in Ethiopia (Africa) and from there, it was introduced into India, China and became a popular food in South Europe, North – East Africa and Southern Asia is early as 2000 B.C. Although originated in Africa, it spread early into West Asia and then to India, China and Japan which themselves became secondary distribution centres (Nayar and Mehra, 1970).

The sesame seed is the only economical part due to its oil (40 to 60 per cent) and protein (20 to 27 per cent) content. In India, its seed are mainly used for extraction of edible oil which is also utilised in manufacturing hydrogenated oils, detergents and surface active agents. Due to its synergistic action, its use in insecticides and pesticides is becoming popular unlike other oils. The sesame oil has high stability and therefore flavour and vitamins do not rancid easily. The sesame cake is rich in protein, calcium, phosphorus and vitamin E and forms a valuable cattle feed for farm and dairy animals.

Sesame grows well in the tropical and subtropical regions in the plains as well as upto an altitude of 1250 meters, though it is sensitive to low temperature conditions. Important sesame growing countries are China, India, Burma, Sudan, Pakistan and Mexico. However, it is also cultivated in Korea, Japan, Thailand, Sri Lanka, Turkey, Greece and South America.

The total area in the world under sesame during 1987 was 6677 thousand hectares with the production of 2206 thousand metric tonnes and an average yield of 330 kilogrammes per hectare. In Asian continent, it occupied 4341 thousand hectares with a production of 1406 metric tonnes (Anonymous, 1987).

India occupies fifth position in the world both in area (20.97 lakh hectares) and production (5.62 lakh tonnes). Major sesame growing states are Uttar Pradesh, Rajasthan, Madhya Pradesh, Tamil Nadu, Maharashtra, Andhra Pradesh, Karnataka and Gujarat, of which Rajasthan is the second largest sesame growing state after Uttar Pradesh. However, among the different oil seed crops in Rajasthan, sesame occupies nearly 40 – 50 per cent of the total hectares (about 3.41 lakh hectares) with a production of about 0.70 lakh tonnes. The important districts in Rajasthan state cultivating the sesame are Pali, Nagaur, Jodhpur, Jalore, Bhilwara, Sirohi and Alwar (Anonymous, 1989). However, sesame yields are the lowest of all the major oil seeds, not only in Rajasthan or in India but also world wide (Joshi, 1985).

The probably constraints that limit the yield are many and varied. The major ones appear to be poor plant type, poor cultivation techniques and lack of organised and concentrated research efforts of the magnitude compared with improvement programme of crops especially wheat and rice. Breeders have pertinently and consistently been resorting to improve the plant type through breeding, but success achieved is very limited despite availability of immense variability for quantitative traits.

Since the future of this crop lies mainly as a short duration cash crop in the multiple cropping system as an inter crop, the breeding programme requires the development of short duration, thermo and photo-insensitive varieties, having synchronised flowering and maturity responding to high management practices, resistant to insect pests and diseases, drought and stress conditions having high oil and protein content, so they can be grown under wide range of agro-climatic conditions.

Being self pollinated crop, most of the genetical improvement in sesame has been achieved through classical breeding methods, including handling of variability generated simple and complex crosses through pedigree, bulk pedigree and back crosses techniques. However, not much headway has been made so far. Thus, there is a need to study yield and its various components more systematically so that sound breeding methodology may be developed.

Now a days breeders are much concerned about the choice of parents for hybridization as per se performance of a line or a variety may be deceptive, hence the use of biometrical approaches to study the parents in advance so as to know their "breeding value" is getting more importance. A perusal of literature indicated that combining ability studies are more reliable than other methods of evaluation. The technique, diallel analysis elaborated by Hayman (1954b, 1958a) and Griffing (1956a) is systematic and analytically it effects an overall genetic evaluation of the materials under investigation that would permit the identification of crosses of best potential in early generation.

The present study in sesame (Sesamum indicum L.) was therefore, undertaken using 10x10 diallel set to study combining ability and genetic architecture of oil content, seed yield and componental traits, using following statistics :

    i. To estimate the amount of heterosis for identification of promising hybrids for commercial utilization.

    ii. To test the general and specific combining ability effects for the selection of potential parents and crosses, and

    iii. To estimate the nature of gene action and genetic components of variation of important agronomic traits for sesamum improvement.

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The efforts in India to improve seed yield of sesame were initiated as back as 1925 at Imperial Agricultural Research Institute, Pusa - Bihar, with the collection and evaluation of distinct types from different parts of India and Burma (Kashi Ram, 1930). The colected material was classified based on certain morphological features like stem and leaf characters, flower colour, pod number per axil, locules per pod, seed colour, maturity period etc. After this, the work on inheritance studies and relationship between yield and certain morphological characters was initiated (Patel, 1936; Langham, 1947; Sikka and Gupta, 1947 and Culp, 1959). As a result of this few distinct types such as TMV-1, TMV-2, Niphad-6, No.128, NP 3 and NP 7 etc. were released by pure line selection method.

The literature relating to different aspects worked out in the present study has been reviewed under following heads :

1. Heterosis and inbreeding depression

2. Combining ability

3. Gene action and genetic components.

2.1   HETEROSIS AND INBREEDING DEPRESSION :

Heterosis or hybrid vigour indicated the superiority of the hybrid over its parents. It was first reported in plants by Koelreuter (1766). He noted that vigour in crosses increased with the increase in dissimilarity of parents, Shull and East (1908) explained the cause of heterosis independently. Later on, Shull (1952) proposed the term of heterosis. Fonseca and Patterson (1968) coined a new term **'heterobeltiosis'** to describe improvement of heterozygotes in relation to better parent. According to Mather and Jinks (1982), heterosis means the amount by which average of an F_1 family exceeds its better parents. Heterosis being a complex phenomenon, no conclusive or clear cut explaination is available to account for its manifestation. However, several theories viz., dominance (Davenport, 1908; Keeble and Pellew, 1910; Bruce, 1910 and Jones, 1917), overdominance (East, 1908 and Shull, 1909), stimulation due to heterozygosity (East and Hays, 1912 and East, 1936), accumulation of favourable dominant genes from each parent in the heterozygotes (Jones, 1917 and Collins, 1921), allelic interactions (East, 1936) and non-allelic interactions (Jones, 1945; Castle, 1946; Jinks, 1955; Hayman, 1957; Bauman, 1959; Sprague et al. 1962; Gamble, 1962 and Sprague and Thomas, 1967) and mitochondrial (Hanson et al., 1960; McDaniel, 1972, 1974 and Shrivastava, 1972) have been advanced to explain heterosis.

There is now sufficient evidence that heterosis can be exploited in plants, animals and micro-organisms for various

economically important characters. In plants, the phenomenon is common both in cross as well as self pollinated crops (Sinha and Khanna, 1975).

Kinman and Martin (1954) observed heterosis large enough for seed yield in F_1s of the crosses of 36 strains of sesame.

Ricceli and Mazzani (1964) studied heterosis for development of earliness and grain yield in a diallel cross of 32 cultivars and reported that the F_1 hybrid manifested large heterosis for seed yield. They also observed that many hybrids flowered earlier than parents.

Srivastava and Singh (1968) studied hybrid vigour in F_1 hybrids of three crosses and reported that the cross Meghna x Local showed heterobeltiosis for all the traits studied except 1000-seed weight. The cross Meghna x Wild exhibited high degree of heterosis for yield, length and breadth of capsule and length of radicle. In another cross Local x Wild, length and breadth of capsule and 1000-seed weight were found to be superior to the best parent.

During heterosis study in seven hybrids of six sesamum varieties for 13 characters, Sarathe and Dabral (1969) observed high heterosis effects for leaf area, number of flowers, capsules per plant and yield.

Delgado (1972) found that 16 F_1 hybrids made between shattering and non-shattering types yielded on the average

twice as much as their parents and six of these hybrids outyielded their best parents by 200-275 per cent.

Murty (1975) studied six agronomic and two chemical characters in a 10x10 diallel of sesame and found that seed yield had maximum heterosis followed by number of capsules per plant whereas, protein had significant negative heterosis and oil content had the lowest. Heterosis was higher in Indian x Exotic crosses than Indian x Indian or Exotic x Exotic hybrids. He was of the opinion that characters like earliness, number of secondary branches, seed yield and protein content can be improved by hybridization, involving Exotic lines as the one of the parents.

High heterotic response for seed yield was also reported by Salazar and Onaro (1975) in 3 sesame crosses studied by them. While, Amirshahi and Sarafi (1976) observed heterosis in F_1 of a cross between two varieties.

Dixit (1976b) recorded high heterosis along with high inbreeding depression in six F_1 hybrids for days to flower, number of branches, number of capsules per plant and seed yield. F_1 hybrids were found to have 77 per cent more yield than parents. The depression in F_2 ranged from -4.71 to 22.07 per cent for seed yield and 20.48 to 32.01 per cent for capsules per plant. Number of branches had -10.09 to 29.94 per cent depression.

Sarafi (1976) studied six different F_1 hybrids

developed from crosses between four Iranian and Exotic sesame varieties. He recorded that four hybrids exhibited positive heterosis for plant height and seed yield per plant, while one showed negative heterosis for days to maturity.

Heterobeltiosis for seed yield per plant, number of capsule per plant, capsule length, number of branches per plant and 1000-seed weight and heterosis for number of days to first flowering and length of flowering period was noticed by Shrivastava and Prakash (1977).

Trehan (1977) recorded high range of heterosis over better parent and inbreeding depression in all the 45 crosses for all the characters.

The study of Uzo (1977) with 75 hybrids based on 21 diverse parents of sesame revealed high heterosis for yield and yield components.

Fatteh (1978) found highest heterotic effect for capsule per plant followed by seed yield per plant, number of effective branches, plant height, oil content, 1000-seed weight, capsule length to breadth ratio, days to maturity and flowering. The maximum heterosis for yield was observed in cross combinations involving high x high parents. The magnitude of heterosis for seed yield and other characters was dependent on the environmental requirement of the parents involved. The more heterotic effects were observed in crosses of Kharif x Kharif whereas, it was not so in Kharif x Semirabi or Semirabi x Semirabi crosses.

Heterosis over better parent for seed yield, plant height, capsule number and capsule length have been reported by Kotecha and Yermanos (1978) in their 8x8 diallel studies. The yield in some of the hybrids was as high as 238 per cent.

Yermanos and Kotecha (1978) studied 28 F_1 hybrids of 8x8 diallel and reported that the magnitude of heterobeltiosis for the characters viz., time of flowering, time of flowering to maturity, time of maturity and height of the first capsule ranged from -2.2 to 34.0 per cent, -4.0 to 39.4 per cent, -1.7 to 28.1 per cent and -41.5 to 10.4 per cent, respectively.

Chaudhary et al. (1979) reported heterotic effects for all the characters except length and breadth of capsule. Maximum heterosis for yield was observed in cross D7-11-1 x Dhanera-1.

Kotecha and Yermanos (1979) noted heterosis for all the characters studied by them, except for breadth of capsule in 15 F_1 sesame hybrids, however, it was highest for seed yield.

Murty (1979) reported significant heterotic effects for seed yield, number of capsules and seed weight in three of six hybrids. Heterosis in general was found to be higher in Indian x Exotic than Indian x Indian or Exotic x Exotic varieties of sesame.

Gupta (1980) observed significant heterosis for yield per plant, capsules per plant, number of branches and plant height in six parent diallel cross.

A 6x6 diallel set was studied by Nafie (1980) and observed heterosis for number of capsule per plant, capsule length, number of seeds per capsule, seed weight per capsule and yield per plant.

High heterosis for seed yield was also reported by Mazzani et al. (1981) in 510 F_1 hybrids studied by them. The mean yield of F_1 hybrids was 66 per cent higher than that of parents. Some of the hybrids even supressed their respective better parents. A high inbreeding depression for yield in F_2 and F_3 generations was noted.

In a 10x10 diallel set of sesame Shrivas and Singh (1981) reported significant heterosis over mid and better parent for yield per plant, plant height, height to first capsule, number of branches and number of capsules per plant. Number of branches and number of capsules per plant were observed to be the main contributors towards yield. In general, the magnitude of negative heterosis was higher than positive heterosis. Similarly, the number of crosses performing below the lower parents were more than the number of crosses performing above the better parents.

Fifteen sesame lines of Indian and Exotic origin were crossed with four testers and evaluated for their heterotic effect by Tyagi and Singh (1981). They found pronounced heterotic effects for number of branches, plant height, number of capsule per plant and seed yield per plant. The heterosis for oil content, test weight and number of seeds per capsule

were low. In many cases negative hybrid vigour was observed for days to flowering and maturity.

Chavan et al. (1982) observed significant positive heterosis and inbreeding depression for capsules per plant, days to maturity and yield per plant in six intervarietal crosses involving eight parents of sesame.

Paramasivan et al. (1982) observed heterosis for plant height, number of capsules per plant and seed yield per plant in 13 cross combinations.

Satani (1982) developed 21 hybrids by crossing seven parents in a diallel set of sesame. He observed high heterotic effects for number of effective branches, number of capsules and grain yield per plant The effects were small for days to flowering, length of capsule, days to maturity, test weight and oil content.

Godawat and Gupta (1983) reported heterosis and inbreeding depression for yield and four yield related traits in nine crosses involving eight parents. The cross RSE-1 x JT-7 exhibited the highest percentage of heterosis for yield which was due to simultaneous heterosis for a number of yield components.

Sharma and Chauhan (1983) observed heterosis over mid and better parents through 10x10 diallel analysis of sesame. The mid parent and better parent heterosis for seed yield ranged from 16.76 to 105.70 and 34.99 to 60.27 per cent,

respectively. The heterosis for seed yield appeared to be due to high manifestation of heterosis for number of capsules per plant. Since majority of hybrids showed inbreeding depression in F_2, it suggested that the heterosis should be exploited in the F_1 itself.

In a diallel study involving eight promising strains of sesame, Chaudhari et al. (1984b) noticed high heterosis for yield, number of effective branches and capsules per plant. The positive heterosis was observed to be high than negative heterosis.

While studying heterosis in sesame, Desai et al. (1984) observed high heterosis for yield per plant due to increase in number of branches, height and 1000-seed weight.

The 36 hybrids derived by crossing 12 female and three male parents were studied for heterosis by Krishnaswami and Appadurai (1984). The extent of heterosis was found to be high for number of capsule and seed yield.

Djigma (1984) studied five characters in a diallel cross of five varieties from different countries and found no heterobeltiosis for any character. However, five F_1s had higher seed yield per plant than the mid-parental value. Seed yield was positively correlated with the height of the main stem, number of capsules and 1000-seed weight.

Thanki (1984) carried out line x tester analysis involving 10 female lines and four testers in sesame. He

indicated greater magnitude of heterosis for seed yield, number of effective branches and number of capsules per plant, medium for 1000-seed weight, seeds per capsule and plant height. In respect of length of capsule, oil content, days to flowering and days to maturity. The degree of heterosis was relatively low.

Godawat and Gupta (1985) studied heterosis for seed yield per plant and three yield related characters in five crosses of sesame. They noticed heterosis for seed yield, plant height and number of capsules per plant. Heterosis was followed by inbreeding depression in all the five crosses.

Hybrids of sesame were derived by Dora and Kamala (1986) using 4x4 diallel. They indicated heterosis over mid parent values for branches per plant, capsules per plant, seeds per capsule and seed yield per plant. The heterosis over mid parent was found to be positive and significant for primary branches per plant and capsule length.

while studying ten quantitative traits in five crosses Shivaprakash (1986) observed heterosis for plant height in JE x Local, capsule length and number of primary branches in RE x Local and height to the first capsule in JE x E8. He noticed inbreeding depression for all the traits.

Singh et al. (1986) studied heterosis in F_1 and inbreeding in F_2 with respect to 13 traits in 30 crosses of sesame. They observed high heterotic values for primary

branches per plant, secondary branches per plant, capsule per plant, harvest index, yield per plant and protein and oil content. Almost all traits exhibited inbreeding depression.

Ding et al. (1987) showed heterosis for number of capsules per plant, test weight and number of seeds per capsule in a study of seven characters in 50 crosses.

Goyal and Sudhir Kumar (1988) studied 28 hybrids for seven characters in sesame. They found high heterosis for yield and yield contributing characters viz., number of branches, number of capsule, seeds per capsule and seed yield per plant.

While studying 76 hybrids of sesame involving 23 varieties of diverse origin, Jadon and Mehrotra (1988) observed that heterosis over mid and better parents for seed yield ranged from 38.99 to 130.68 per cent and 48.38 to 118.77 per cent, respectively. Thirtysix hybrids showed significant positive heterosis over better parent for seed yield. Heterosis for capsules per plant, branches per plant, seeds per capsule, 1000-seed weight, plant height and days to flowering was also found to be significant.

Tu et al. (1988) evaluated 77 F_1 hybrids and their parents and observed that heterobeltiosis varied greatly among the crosses ranging from -24.8 to 141.1 per cent and economic heterosis from -37.1 to 67.6 per cent for seed yield. Further, they stated that in geographically distant hybridization, it is preferable to cross an introduced high yielding variety not

adapted to local conditions with a low yielding local one to achieve maximum heterosis.

Sasikumar and Sardana (1990) showed high significant and positive heterosis for yield and its important attributes to six out of 17 F_1 of sesame, involving eight diverse parents. Their study revealed good scope for commercial exploitation of heterosis as well as isolation of pure lines among the progenies of other heterotic F_1.

In a diallel study involving 10 genotypes of sesame Sodani and Bhatnagar (1990) recorded heterosis for seed yield per plant, which was also highly correlated with heterosis for its component characters. In general, crosses with significant heterosis also showed significant inbreeding depression in the F_2 generation.

Girase $\underline{et}$ $\underline{al}$. (1991) observed heterosis and heterobeltiosis for number of branches per plant, number of capsules per plant, 1000-seed weight and yield per plant. He further indicated that inbreeding depression was for all the traits studies of which the highest amount of inbreeding depression was recorded for number of capsules per plant and yield per plant and lowest for number of seeds per capsule, length of capsule, 1000-seed weight and oil per cent.

2.2 COMBINING ABILITY :

Use of diallel cross design in plant breeding to evaluate general combining ability (GCA) and specific

combining ability (SCA) has been commonly used. Sprague and Tatum (1942) were first to estimate components of variance for both GCA and SCA. They found that lines tested and selected for yield potential had marked variance due to SCA than GCA for grain yield, showing presence of dominance and epistasis. Rojas and Sprague (1952) analysed diallel crosses in corn which were tested over number of locations and years. They reported that in superior crosses, variance due to specific combining ability was consistently more than general combining ability.

Stephns and Quinby (1952) suggested that hybrids among two unrelated inbreds (or variety) were likely to exhibit more vigour than their parents. However, very few lines producing such hybrids were economically valuable. Lines yielding superior hybrids were eventually more valuable in breeding. Hence line selection should be based on combining ability than their per se performance for producing superior hybrids.

Griffing (1956a,b) elaborated the hypothesis of Sprague and Tatum (1942) and developed technique for working out GCA and SCA effects along with their variances. These were :-

    I.   Parents, one set of F_1s and their reciprocals,

    II.   Parents and one set of F_1s without reciprocals,

    III.   One set of F_1s and their reciprocals only and

    IV. One set of F_1s only.

He further pointed out that the materials showing high degree of inbreeding depression, Method I and II be used to

all the characters studied. Further, the parents with good general combining ability were also found to have good specific combining ability effects.

Dixit (1978) studied ten hybrids in a diallel set of 5x5 lines. He found that Kanpur local was the best general combiner for protein content and test weight, while others were good combiner for test weight.

Combining ability analysis in sesame made by Fatteh (1978) revealed that general combining ability variances were higher for days to flower, plant height, number of capsules per plant, days to maturity, test weight and yield per plant. Mrug-1 and Gujarat Til-1 were found best general combiner for all the characters and specific combination involved either both or one as parent in cross combinations.

Kotecha and Yermanos (1978) observed significant general as well as specific combining ability effects for seed yield, plant height, capsule number and capsule length. However, the GCA was of prime importance in the inheritance of these characters.

Yermanos and Kotecha (1978) found an appreciable amount of variance due to general combining ability effects and relatively small amount of variances for specific combining ability and maternal effects in the characters like days to flowering, days to maturity, time taken from flowering to maturity and height of first capsule from ground.

Kotecha and Yermanos (1979) studied combining ability for seed yield per capsule in sesame. They noticed the pronounced role of specific combining ability variance, indicating importance of non-additive gene action.

While working with diallel set involving six indehiscent strains of sesame, Nafie (1980) observed that general combining ability variances were higher than those of specific combining ability variances for number of capsules, capsule length, number of seeds per capsule, seed weight per capsule and yield per plant.

Gupta (1981) conducted combining ability analysis for plant height, number of branches, capsules per plant and seed yield through 6x6 diallel set in sesame. He found that general and specific combining ability variances were highly significant for all the characters. However, the GCA variances were higher in respect of plant height, number of branches, number of capsules per plant and grain yield as compared to SCA variances.

A diallel analysis conducted by Shrivas and Singh (1981) revealed that general combining ability variances were predominant for plant height, number of branches per plant, number of capsules per plant; whereas specific combining ability variance was preponderant in respect of seed yield.

Fatteh et al. (1982) studied a diallel set among six promising strains and observed significant general and specific combining ability effects for days to flower, plant

height, number of effective branches, number of capsules per plant, ratio of capsule length to breadth, days to maturity, yield per plant, test weight and oil percentage. The ratio of GCA/SCA revealed that the variances due to GCA were higher for all the characters except oil percentage and number of effective branches suggesting thereby the predominance of additive type of genetic variation. The non-additive type of genetic variation appears to have been involved for number of effective branches and oil percentage.

While studying the heterosis and combining ability in a 7x7 diallel set Satani (1982) observed greater magnitude of general combining ability variances for days to flower, height of plant, days to maturity, test weight and yield per plant. Specific combining ability variances were significant for all the characters. The GCA/SCA variance ratio suggested the predominant role of additive genetic variance in the expression of all the characters except number of capsule per plant.

Rathnaswamy and Jagathesan (1983) reported that GCA variance were greater than SCA variances for seed yield and yield related characters. Also the GCA x environmental variance was greater than GCA x environmental variance. The parental performance appeared to be a good indicator for GCA effects.

Singh et al. (1983) in a study of 12 parents partial diallel reported the significant GCA variances for days to

flowering,number of primary branches, plant height and yield per plant in both F_1 and F_2 generations for harvest index and 1000-seed weight only in F_1 generation and for number of secondary branches, number of capsules per plant, number of seeds per capsule and oil content only in F_2 generation. The variances of SCA were significant for number of primary branches in F_1 generation and for days to flowering, number of primary branches, number of secondary branches, days to maturity and oil content in F_2 generation. The estimates of components of variance σ^2 GCA in the F_1 and σ^2 SCA in the F_2 were responsible for the expression of days to flowering, days to maturity, number of secondary branches, days to reproductive phase and harvest index for plant height and number of capsules per plant, additive genetic variance was predominant in F_1 and F_2 generations though a substantial amount of non-additive gene effect was also observed. Seed yield and primary branches were reported to be controlled by non-additive gene effects in the F_1 and additive gene effects in the F_2. For number of seeds per capsule, 1000-seed weight, oil content and protein content, non-additive gene effects were predominant in both F_1 and F_2 generations. Gujarat Til-1 and BL were good general combiners for seed yield, oil content and protein.

In a diallel analysis of six strains of sesame, Chaudhri et al. (1984a) found significant general combining ability variances for yield per plant, height of plant, number of branches per plant and number of capsules per plant. They

also observed significant specific combining ability variances for yield per plant, length of capsule and number of nodes per plant. Both additive and non-additive gene action were involved in the expression of yield and its components.

Chaudhari et al. (1984b) reported significant GCA and SCA variances in a diallel set of 8 promising strains for days to flowering, days to maturity, plant height, effective branches per plant, capsules per plant seeds per capsule, seed yield per plant, 1000-seed weight and oil content indicating the importance of both the additive and non-additive genetic variation. The GCA/SCA ratio indicated non-additive genetic variation to be predominant for all the characters except days to flowering and maturity.

Reddy et al. (1984) in a study of diallel set involving ten diverse and homozygous lines reported significant differences for GCA effects among parents as well as SCA effects among hybrids for days to flower, plant height, effective stem length, number of branches, capsules on the main stem, total number of capsules per plant, seed yield per plant, oil content and oil yield per plant. The parental performance and GCA effects were positively and significantly correlated for all the characters except for capsules on the main stem. Further, they suggested that capsule number per plant should have more pronounced effect on seed yield than other yield components. Selection for positive GCA of flowering time (lateness) significantly decreases the oil

content and enhances the effective stem length and number of branches. Therefore, selection for better combining parents for earliness (negative GCA) will be an advantage over late maturing ones to select for better combining ability for oil content.

Sharma and Chauhan (1985) evaluated 90 hybrids from a 10x10 diallel cross and reported the significant differences for GCA, SCA as well as reciprocal variances for days to flower, number of primary branches, number of secondary branches, plant height, number of capsules per plant, days to maturity, 1000-seed weight, seed yield and oil percentage. However, the estimates for GCA variances were higher in magnitude than the corresponding estimates of SCA. The per se performance and GCA effects of the parents revealed that these two parameters, in general, were directly related to each other. Further, they suggested the biparental mating in F_2 to obtain high yield coupled with high oil content.

The relative estimates of variances due to SCA were higher than GCA indicating the predominant nature of non-additive genetic variation for yield, thus indicating the high scope for exploitation of heterosis in sesame (Anand Kumar and Rangaswamy, 1987).

Bakheit and Mahdy (1987) in a diallel cross of 6 local and introduced lines reported that GCA effects were significant for all the traits. SCA effects were also

significant for all traits except days to maturity in F_1 and branch number in F_1 and F_2 generation.

Chandraprakash (1987) observed the greater GCA variance than SCA variance for all the characters. SCA variance was highly significant for all the characters except capsule length.

Dora and Kamala (1987) studied full diallel set of four varieties of sesame and observed that GCA variance was lower than SCA variance for all the 16 traits indicating the influence of all the characters.

Krishnadoss et al. (1987) studied line x tester analysis involving 20 lines and five testers and found that the combining ability variances due to lines and testers were significant for days to 50 per cent flowering, days to maturity, plant height, branches per plant and seed yield per plant indicating the importance of additive genetic variation. The combining ability variances due to line x tester interactions were significant for days to 50 per cent flowering, days to maturity and plant height indicating the importance of non-additive genetic variation. The ratio of GCA/SCA variances showed that SCA variances were greater than GCA variances indicating the predominance of non-additive genetic variation for all the characters.

Chandramony and Nayar (1988) in a study of diallel cross of six varieties reported that the GCA variances were higher in magnitude than SCA variances for plant height,

number of primary productive branches per plant, number of effective nodes on main axis, number of productive pods on main axis, total number of pods per plant, 1000-seed weight, seed yield per plant and number of days to first flowering in F_1 and in F_2 also, the GCA variances were higher in magnitude than SCA variances for all above traits in addition to oil content but in case of seed yield per plant, SCA variance was higher and for 1000-seed weight, both GCA and SCA variances were equal in mangitude.

Goyal and Sudhir Kumar (1988) observed a good relationship between GCA effects and per se performance of the parents. The mean performance of the hybrids was associated with SCA effects which were also significantly correlated with each other and therefore, they suggested that mean performance of hybrids could be considered as a criterion of high SCA effects in sesame.

Khorgade et al. (1988) in a line x tester analysis study of eight lines and three testers observed that the estimates of variances for general combining ability and specific combining ability were important for days to maturity, capsule length, number of branches per plant, number of capsules per plant and 100-seed weight indicating the importance of both additive as well as non-additive gene effects for these characters. However, the magnitude of SCA variances were higher than the GCA variances for days to maturity, capsule width, plant height, number of branches per

plant, number of capsules per plant, number of seeds per capsule, seed yield per plant and 100-seed weight.

Khorgade et al. (1989) further studied combining ability for yield and nine yield components of eight genotype and their F_1 crosses. They observed SP-125-283 parent was best general combiner for plant height, capsule length, branches per plant and seeds per capsule. N 128 was the best general combiner for seed yield per plant and oil content. TMV 1 x N 128 cross had the best specific combining ability for seed yield per plant, capsules per plant and branches per plant and JLT 7 x TC 25 had high seed oil content.

Powar (1990) recorded general combining ability effects among parental lines. A.C.No.1 and A.C.No.8 demonstrated the best GCA effects for earliness while parent A.C.No.5, A.C.No.9 and A.C.No.12 showed high GCA effects for plant height, number of seeds per capsule, 1000-seed weight, oil content and yield. About 12 cross combinations showed high SCA effects for yield and eight of 17 F_1 crosses were also significant SCA effects for other related traits.

Narkhede and Sudhir Kumar (1991a) studied ten quantitative character in a half diallel cross over two environments. The variances due to GCA and SCA were significant for all the characters suggesting that both additive and non-additive gene effects were involved in the expression of various characters. The variances due to environment, genotypes and parents v/s hybrids were highly

significant. The GCA/SCA ratio was more than unity for all characters except capsules per plant and yield per plant indicating preponderance of additive gene effects for these characters. The magnitude of variance due to GCA x environment was smaller than the variance due to SCA x environment suggesting that the parental performance appears to be more stable than the hybrid performance over environment.

The comprehensive review of combining ability in sesame revealed that there is a significant variation due to both general and specific combining ability. However, their relative magnitudes and importance of GCA and SCA depends on the type of parental material used and environmental variation.

2.3   GENE ACTION AND GENETIC COMPONENTS :

Inheritance of quantitative traits was reported as early as 1909 independently by Johannsen (1909), Nilsson-Ehle (1909) and East (1915). Since then large number of biometrical techniques have been developed by various workers for the estimation of different types of gene interactions involved in the inheritance of quantitative traits. Some of them are as follows :-

(a)   Estimation based on segregating generations from cross of two pure lines (Mather, 1949).

(b)   Covariance of half-sibs and full-sibs (Comstock and

Robinson, 1948, 1952; Anderson and Kempthrone, 1954 and Kempthrone, 1957).

(c)   Power partitioning method (Powers et al., 1950; Power, 1951, 1955 and 1963).

(d)   Triallel and quardriallel analysis (Rawlings and Cockerham, 1962a, 1962b; Hinkelman, 1965; Ponnuswamy, 1972; Wright et al. 1971).

(e)   Triple test cross (Kearsey and Jinks, 1968; Jinks et al., 1969; Virk and Jinks, 1972; Jinks and Virks, 1977; Virk and Virk, 1985a, 1985b).

(f)   Partial diallel analysis (Kempthorne and Curnow, 1961, Dhillon and Singh, 1979).

(g)   Diallel analysis (Jinks and Hayman, 1953; Hayman, 1954a, 1954b, 1957, 1958a, 1960; Griffing, 1956a; Gardner and Eberhart, 1966).

(h)   Inferences about gene action from combining abilities (Sprague and Tatum, 1942; Rojas and Sprague, 1952; Griffing, 1956b).

The general approach and application of diallel analysis was summarised by Jinks and Hayman (1953). Hayman (1954a) proposed analysis of variance for diallel table and suggested testing of significance of additive and dominance effects. Hayman (1954b) applied a genetic algebra to the theory of the diallel cross and re-established the formulae of

Jinks and Hayman (1953). Griffing (1956a) applied diallel analysis method to homozygous individuals obtained from a random mating population and presented the genetic parameters in term of additive and dominance effects for an arbitrary number of loci with arbitrary allels. Dickenson and Jinks (1956) developed a model on random mating to remove effects of epistasis and the presence of only two alleles per locus.

Hayman (1957) suggested a test and measure of epistasis in F_2 generation and the relationship between heterosis and epistasis in maize. <u>Nicotiana</u> <u>rustica</u> and cotton. Discussing the validity of $(H_1/D)^{\frac{1}{2}}$ values as a measure of degree of dominance, he concluded that multiple allelism and gene correlation did not seriously disturb $(H_1/D)^{\frac{1}{2}}$ and it was the most suitable measure for average degree of dominance.

Earlier method proposed by Jinks and Hayman (1953) for analysis of a fixed set of inbred lines was applied successfully by Hayman (1960) to sampled inbred lines to indicate the relationship between components of additive and dominance variation (D, H_1, H_2, F and h^2) with combining ability components (both general and specific).

Johnson and Aksel (1959) suggested the utilization of correlation between parental order of dominance (Wr+Vr) and parental measurements (Yr) for getting an idea about relative frequency of positive and negative dominant genes in the parental population as well as in the individual parent. Mather (1967) pointed out that when the Wr. Vr graph is

concave upwards it indicates presence of complementary gene action and when it is concave down wards it indicates presence of duplicate gene interaction. Further, he also suggested that clustering of points at the right or upper end on the line indicates presence of complementary interaction and clustering of points at the left or lower end of the line indicates presence of the duplicate interaction. Coughtrey and Mather (1970) suggested that the effect of associated and dispersed type of gene distribution are similar to duplicate and complementary epistasis respectively. Mather and Jinks (1982) suggested that the curve stemming from duplicate interaction depart by a lesser degree from the straight line than do those stemming from complementary interactions. But with non-independent gene distribution the opposite is true.

Culp (1959) while studying F_1, F_2 and F_3 and back cross generations noted that germ percentage, protein and oil content were controlled by few number of genes having heritability of 70, 60 and 50 per cent, respectively. It was therefore, possible to have rapid progress by selection for these characters in sesame.

Culp (1960) further studied inheritance of plant height and capsule number in four crosses of sesame. He reported that plant height was governed by 3-10 pairs of genes, whereas, capsule number by one pair and non linkage or interaction existed between them. The plant height had 40-50 per cent heritability.

Weiss (1971) noted that 2-3 genes govern plant height and 2-5 genes the capsule length. The heritability was 40-50 per cent and 50-70 per cent, respectively. Dominance as well as partial dominance gene action were important for both the traits.

Murty and Hashim (1973) studied the inheritance of oil and protein content in a diallel set of sesame involving 10 lines of diverse ecogeographical origin and found that oil and protein both were under additive as well as dominance gene actions, especially the latter. Epistasis of complementary nature was detected for both the characters. Oil was found to have 23 per cent heritability and protein 30 per cent.

In an another study, Murty and Hashim (1974) observed a significant maternal effect for days to flower, plant height, number of primary branches and capsule number. Additive and dominance variance conditioned all characters except secondary branches whereas, partial dominance occured for days to flower and plant height. Overdominance was important for primary and secondary branches, capsule number and seed yield. A non-allelic interaction for all the characters studied was observed by them. All traits except days to flower, primary branches and plant height had low heritability. For improvement of yield of sesame crossing of F_2 segregates by selfing was the method suggested by them.

While evaluating six varieties and their F_1, F_2 and back crosses, Dixit (1976a) reported dominant gene action for

number of branches and capsules per plant. But additive and dominant gene effects for days to flower, length of fruiting branches and yield per plant.

Selim and El-Ahmar (1976) studied genetic behaviour of oil content in F_1 and F_2 generations of one cross Sceitara x Sharika 225 and found that it was controlled by one pair of major gene with modifiers. The narrow sense heritability observed by them was 48.26 per cent.

In the combining ability analysis of 10x10 diallel set, Trehan (1977) observed preponderance of additive gene effects for all the characters he studied. The yield was found to have 0.0151 gene groups and capsules on secondary branches 37.25. Mean degree of dominance was almost equal to unity in character like capsules per plant, reproductive nodes, length and girth of capsules and seeds per capsule, $H_2 4 H_1$ was almost equal to 0.25 for primary branches, length of capsule, secondary branches, seeds per capsule and reproductive nodes.

Dixit (1978) studied a diallel set of 5x5 lines for the inheritance of test weight and protein content in sesame. Additive as well as non-additive gene actions were responsible for the inheritance of protein content, whereas for test weight, it was additive only.

Yermanos and Kotecha (1978) found a degree of dominance to a range of -3.0 to 3.9, -25.4 to 0.7, -8.9 to -1.5 snf -19.2 to 14.4 for the characters days to flowering, days to

maturity, time taken from flowering to maturity, respectively in the study of 7x7 diallel set for four traits in sesame.

Badr et al. (1979) studied segregation ratio in the F_2 from the cross Ascietera x Ismailia 296 (high x low protein content). They indicated that seed protein content was controlled by one major gene and some modifiers. Heritability values ranged from 59.29 to 83.04 per cent with broad sense mean of 72.55 per cent and narrow sense mean of 20.49 per cent.

The average and mean degree of dominance observed by Kotecha and Yermanos (1979) indicated overdominance for seed yield. The reciprocal differences denoting maternal effects for yield and yield traits were also detected.

Sen Gupta (1980) reported an additive gene action for yield per plant and non-additive for number of branches, capsule numbers and plant height in study of combining ability in half diallel set of sesame.

Chavan et al. (1981) reported the importance of additive as well as dominance gene actions for plant height, capsule on main shoot, seeds per capsule and yield per plant, however, dominance was more important for all the traits except plant height. The contribution of seeds per capsule to yield was very high. Among epistatic effects, additive x additive component was observed more important for these traits.

While Gupta (1981) studied combining ability for plant height, number of branches, capsules per plant and grain yield in F_1 diallel crosses involving 6 diverse parents of sesame. The estimates of heritability revealed that non-additive type of gene action was more important for branches, capsules per plant and grain yield. Heritability estimates observed for the traits were very high for plant height (97.9%), grain yield (97.0%) and branches (82.1%).

Uzo and Ojiake (1981) studied genetic analysis of two crosses for seed yield in sesame from the P_1, P_2, F_1, F_2, BC_1 and BC_2 generations. The cross A 59 x Lucidi had highly significant effects for dominance and additive x dominance. The dominance and dominance x dominance effects were highly significant in the cross of Aceiltera x Buse.

Mojidis (1982) studied parental F_1, F_2 and back cross generations of sesame hybrid 360 x LB for inheritance of oil content and fatty acid composition. Predominance of additive gene action for oil content and fatty acid amount was noticed. Three to seven genes were found responsible for oil content and 3 to 4 for fatty acid. A narrow sense heritability of 87.85 per cent was noticed for oil content.

Narkhede (1982) studied in a diallel cross with eight cultivars reported the relative importance of additive and non-additive gene actions.

Studying the genetic analysis through 6x6 diallel set John and Nair (1983) reported that multicapsuled character was

controlled by two independent recessive genes, designated P_1 and P_2, respectively.

Sharma and Chauhan (1984) in a 10 parent diallel study reported the significant additive component for days to flower, primary branches, plant height, days to maturity, seed yield and oil content in F_1, while in addition to all above characters it was also significant for 1000-seed weight in the F_2. The dominant components (H_1 and H_2) were significant for days to flowering and maturity, primary and secondary branches, plant height, capsules per plant, 1000-seed weight, seed yield and oil content in the F_1. In F_2, both components were also significant for all the characters except H_1 component for seed yield and H_2 component for primary branches, capsules per plant and seed yield. Dominant components were higher than additive components for all the traits except days to flowering, suggesting that dominance component were more important than additive component. The H_2 components were smaller than H_1 components for most of the characters indicating that positive and negative alleles at the loci governing these characters were not equal in proportion in the parents. The component F_1 which is a measure of covariance between additive and dominance effect was significant and positive for days to flower and oil content in both generations, while for primary branches and days to maturity only in the F_2. It was, however, non significant for the rest of the characters.

The measure of degree of dominance showed over dominance for all the characters except days to flower in the F_1. $H_2/4H_1$ suggested asymmetrical distribution of positive and negative alleles among the parents for all the characters except secondary branches and capsules per plant in F_1 and F_2. KD/KR showed that for every recessive allele there was more than one dominant allele involved in the inheritance of days to flower, plant height and oil content in both generations. The number of alleles or allelic groups showing dominance (h^2/H_2) was more than one for most of the character in F_1 except for 1000-seed weight and oil percentage. Heritability was moderate for primary branches, days to maturity, seed yield and oil content while it was high for days to flower in F_1 and F_2.

Godawat and Gupta (1985) in a study of parents, F_1, F_2, BC_1 and BC_2 of five crosses grown at four locations observed the preponderance of dominance effects for days to flowering, plant height, number of capsules per plant and grain yield per plant. However, additive effects though were also significant in the crosses over the locations for these characters. The contribution of dominance x dominance was greater than additive x additive and additive x dominance components for grain yield per plant, plant height and number of capsules per plant. Duplicate type of epistasis was usually present in most of the crosses for these traits.

Hu (1985) studied a diallel cross of five lines and reported that additive effects were more important than

dominance only for capsule length. Seed number per capsule, capsule length and branches number were partially dominant while overdominance was observed for other characters. The number of dominant and recessive alleles were approximately equal for capsule number and yield. The total number of dominant alleles were three times greater than that of recessive alleles for seed number per capsule and the total number of recessive alleles were greater than that of dominant alleles for other characters. Non-allelic interaction was detected for plant height and node number. It was calculated that atleast one gene group affected capsule number and branch number. Heritability values were generally low with the exception of these two characters.

Narkhede (1986) analysed 8x8 diallel cross for the four traits with respect to the components of genetic variance, degree of dominance and heritability. He observed regression Wr on Vr. Allelic frequencies of all loci controlling the traits were asymmetric. About seven gene groups controlled seed density and one gene group controlled iodine number.

Shivaprakash (1986) in a study on generation mean analysis involving five crosses, reported that both additive and dominance gene actions were important though epistasis could not be ignored for most of the traits.

Bakheit and Madhy (1987) evaluated F_1 and F_2 of diallel cross of six local and introduced lines and detected mainly additive genetic variance for branch number, while dominance

effects predominated for other traits. The estimates of narrow sense heritability were high for branch number and days to maturity in the F_2.

Chandraprakash (1987) carried out 8x8 diallel, which revealed overdominance and complementary gene actions operating for several characters in eight parents. The proportion of $(H_1/D)^{\frac{1}{2}}$ indicated over dominance for most of the traits. The correlation coefficient between the parental performance and the order of dominance (Wr+Vr) was positive and significant for seeds per capsule, oil percentage and test weight indicating the increased effect of recessive genes for these traits. The role of dominant genes for all the traits except number of capsules on main stem. Seed yield and test weight evident from the proportion of KD/KR. The heritability values were low for test weight, capsule length, number of capsule on main stem, seed yield and height to first capsule but was high for harvest index and number of capsules on primary branches.

Yadav and Gupta (1987) studied a diallel cross involving 10 parents for oil and protein content and reported that additive (D) and dominance (H_1) components were highly significant for both the traits. The H_2 components of both the characters were significant and were different in magnitude. The estimates of F were positive and significant indicating an excess of dominant alleles in parents for oil and protein content. The h^2 indicating thereby that the mean direction of dominance was positive for both the characters. The ratio

$(H_1/D)^{\frac{1}{2}}$ was more than unity. KD/KR ratio suggested that for every recessive gene, there were atleast two dominant genes on gene groups. The number of gene groups (h^2/H_2) controlling a character were small. The narrow sense heritability estimates were low for oil and protein.

Narkhede and Sudhir Kumar (1991b) conducted 8x8 diallel excluding reciprocals over two environment in sesame. They observed dominant gene action for primary branches per plant, capsules per plant, length of capsule, seeds per capsule and yield per plant. Heritability in narrow sense was low for these characters indicating non-additive genetic variation due to large effect of heterozygosity while the length of productive main stem was under the control of additive gene action. Whereas both dominant as well as additive gene actions were operative for test weight.

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The present investigation on combining ability and genetic architecture of oil content, seed yield and componental traits in sesame (Sesamum indicum L.) was conducted during kharif, 1991-92 at the experimental Farm, Rajasthan College of Agriculture, Udaipur, situated at an elevation of 579.5 meters above mean sea level on Latitude of 24°35' N and Longitude of 70°40' E. The meteorological data are given in Appendix - I.

3.1 EXPERIMENTAL MATERIAL :

The present experiment was undertaken with a view to study the heterotic effect of F_1 over mid parent, better parent as well as check parent, inbreeding depression in F_2, nature of gene actions, genetic component and to estimate the general combining ability of parents and specific combining ability of crosses in sesame. The material consisted of ten homozygous parents of sesame (Table 1) with F_1 (excluding reciprocals) and their F_2s.

Table 1. Parents and their origin used in diallel crossing programme

S.No.	Code No.	Name	Origin
1	P_1	Tapi	Maharashtra (Jalgaon)
2	P_2	Mrug-1	Gujarat (Junagadh)
3	P_3	AT-17	Gujarat (Amreli)
4	P_4	Gujarat Til-1	Gujarat (Junagadh)
5	P_5	AHT-55	Gujarat (Amreli)
6	P_6	PY-57	Maharashtra (Jalgaon)
7	P_7	RT-125	Rajasthan (Mandore)
8	P_8	BAUT-1	Bihar (Ranchi)
9	P_9	TKG-9-86	Madhya Pradesh (Tikamgarh)
10	P_{10}	OMT-10	Orissa (Bhuvneshwar)

3.2 CROSSING PROGRAMME :

The crosses were made in diallel fashion excluding reciprocals during kharif, 1990 at Plant Breeding Farm, Rajasthan College of Agriculture, Udaipur. F_2 generation was generated from the F_1 seeds.

3.3 EXPERIMENTAL DESIGN AND CROP HUSBANDRY :

100 entries comprising of 10 parents, 45 F_1s and 45 F_2s were studied in Randomized Block Design with three replications during kharif, 1991. Plant to plant and row to row distances were 15 and 45 cm, respectively. The parents and F_1s were raised in single row plot while, F_2s were raised in

two rows plot of the five meter length. Each replication was randomized using three digit random number table to avoid soil variation. Two rows of sesame variety of Pratap were sown around the experimentation to avoid border effects. The normal agronomical and plant protection practices were adopted to raise good crop.

3.4   PROCEDURE OF RECORDING THE OBSERVATIONS :

The observations were recorded on ten randomly selected competitive plants for parents and F_1s, whereas 20 plants in F_2 in each replication. The characters studied and observational procedure used were as follows :-

3.4.1 Days to first flowering :

The number of days from the date of sowing to the date of appearance of first flower was recorded.

3.4.2 Height of plant to first flowering (cm) :

The plant height was measured in centimeters from the ground level to the tip of main shoot at the time of first flower appearing in a plot.

3.4.3 Days to 50 per cent flowering :

It was noted as the number of days from sowing to appearance of flowers in 50 per cent plants in a plot.

3.4.4 Days to maturity :

Number of days from the date of sowing to the ripening of about 75 per cent capsules on the plant were recorded.

3.4.5 Length of reproductive stem (cm) :

The capsule bearing length measured in centimeters on main stem.

3.4.6 Plant height at maturity (cm) :

The plant height was recorded in centimeters from the base of the plant to the tip of the main stem at the time of harvesting.

3.4.7 Number of branches per plant :

The total number of branches bearing capsules were counted at the time of maturity.

3.4.8 Number of capsules per plant :

The total number of seed bearing capsules per plant recorded at the time of maturity.

3.4.9 Length of capsule (cm) :

Three capsules one from lower, middle and upper portion of the main branch of the selected plants were taken and their length in centimeters was measured and mean length was derived.

3.4.10 Number of grains per capsule :

The capsules used for recording length. threshed and their seed were counted and mean seeds per capsule was computed.

3.4.11 Dry weight per plant (g) :

Dry weight per plant was obtained by substracting the seed yield of each plant from their respective total dry matter (Biological yield).

3.4.12 Grain yield per plant (g) :

The seeds from all the capsules of each selected plant was weighed separately and recorded.

3.4.13 Test weight (g) :

Random sample of 1000-seeds was taken from each of the selected plant. Each samples was weighed separately on electric balance and the weight was recorded in grams.

3.4.14 Husk seed ratio :

The husk seed ratio was calculated using the formula :

$$\text{Husk seed ratio} = \frac{\text{Total dry weight of husk (capsules without seeds)}}{\text{Economic yield (Seed yield)}}$$

3.4.15 Harvest index (%) :

The harvest index was computed from the following formula and was expressed in percentage :

$$\text{Harvest index (\%)} = \frac{\text{Economic yield per plant}}{\text{Biological yield per plant}}$$

Where, Economic yield means seed yield and biological yield means total yield.

3.4.16 **Oil content (%)** :

The oil content was estimated from a random sample of seeds obtained from each observational plant per genotype by using nuclear magnetic resonance (NMR) technique.

3.4.17 **Oil yield per plant (g)** :

The oil yield per plant was calculated by using the following expression :

$$\text{Oil yield per plant} = \frac{\text{Oil content of the seed (\%) x Seed yield per plant}}{100}$$

3.4.18 **Protein content (%)** :

The nitrogen content was estimated by micro-kjeldahl procedure (A.O.A.C. 1970) and percentage of protein was calculated using the factor 6.25.

3.5   **STATISTICAL ANALYSIS** :

The data were subjected to following statistical and biometrical analysis by using the mean of ten plant for parents and F_1s and 20 plants in F_2s.

3.5.1   **Analysis of variance for experimental design** :

The analysis of variance was performed to test the significance of differences between the genotypes for all the characters with fixed effect model. The statistical model for randomized complete block design is :

$$Y_{ij} = m + B_i + T_j + E_{ij}$$

Where, m = General mean,

B_i = Block effect,

T_j = Treatment effect and

E_{ij} = Error component.

Analysis of variance and expectations of mean squared values

Source	d.f.	SS	MSS	Expectations of mean square
Blocks	(b-1)	Sb	Mb	$V_e + PV_b$
Progenies	(p-1)	Sp	Mp	$V_e + bV_g$
Error	(b-1)(p-1)	Se	Me	V_e

3.5.2 **Heterosis, heterobeltiosis, economic heterosis and inbreeding depression :**

Heterosis, expressed as percentage increase or decrease of F_1 over mid parent (Briggle, 1963) was calculated by using following formula :

$$\text{Heterosis} = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

Where, $\overline{F}_1$ = Mean performance of F_1,

$\overline{P}_1$ = Mean performance of parent number 1,

$\overline{P}_2$ = Mean performance of parent number 2,

$\overline{MP} = \dfrac{\overline{P}_1 + \overline{P}_2}{2}$,

Me = Error mean square and

b = Number of replications.

Standard error of difference for heterotic effects was calculated by formula :

$$S.E. (Diff.) = \sqrt{\frac{3Me}{2b}}$$

The critical difference was computed by multiplying the standard error with the respective 't' value for error degrees of freedom at 5 and 1 per cent level of significance.

Heterobeltiosis :

Heterobeltiosis was calculated as the deviation of F_1 from the better parent (Fonseca and Patterson, 1968) and was expressed in percentage by the following formula :

$$\text{Heterobeltiosis} = \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

Where, $\overline{F}_1$ = Mean performance of F_1

$\overline{BP}$ = Mean performance of the better parent of the respective cross

Standard error of difference for heterobeltiosis was calculated as follows :

$$S.E. (Diff.) = \sqrt{\frac{2Me}{b}}$$

The critical difference was computed as given above for error degree of freedom at 5 and 1 per cent level of significance.

Economic heterosis :

Economic heterosis was calculated as the deviation of F_1 from check variety (RT-125) for all the characters and was expressed as percentage increase over it.

$$\text{Economic heterosis} = \frac{\overline{F}_1 - \overline{\text{Check}}}{\overline{\text{Check}}} \times 100$$

Where,

$\overline{F}_1$ = Mean performance of F_1

$\overline{\text{Check}}$ = Mean performance of check variety.

The standard error of difference for comparing the value of economic heterosis was calculated as follows :

$$\text{S.E. (Diff.)} = \sqrt{\frac{2Me}{b}}$$

The critical difference was computed as given above for error degrees of freedom at 5 and 1 per cent level of significance.

Inbreeding depression :

Inbreeding depression (ID) expressed as percentage reduction in value in F_2 over F_1 generation was calculated by the formula :

$$\text{Inbreeding depression} = \frac{\overline{F}_1 - \overline{F}_2}{\overline{F}_1} \times 100$$

Where, $\overline{F}_1$ = Mean performance of F_1

$\overline{F}_2$ = Mean performance of F_2.

The standard error of difference for comparing the value of inbreeding depression was calculated as follows :

$$S.E.\ (Diff.) = \sqrt{\frac{2Me}{b}}$$

Where, Me = Error mean square for the parents, $F_1's$ and $F_2's$ joint analysis.

Diallel analysis :

3.5.3 Combining ability analysis :

The combining ability analysis was carried out according to Model-1 (fixed effect), Method-2 (Parents and one set of F_1s and F_2s without reciprocals) of Griffing (1956a). In this model, experimental material was regarded as population about which inference was to be drawn and combining ability effects of parents could be compared when parents themselves are used as tester to identify good combiner. In Model-1, it was assumed that variety and block effects were constant but error (environmental and other uncontrolable components) was variable and normally and independently distributed mean zero and variance σ_e^2. The following was the statistical model for the combining ability in Model-1.

$$X_{ij} = M + g_i + g_j + s_{ij} + \frac{1}{b}\sum_k e_{ijk}$$

i, j = 1, --------- P (Number of parents)

k   = 1, --------- b (Number of replications)

Where, μ = Population mean,

g_i = General combining ability (GCA) effect i^{th} parent,

g_j = General combining ability effect of jth parent,

S_{ij} = Specific combining (SCA) of ij^{th} cross,

e_{ijk} = Environment component pertaining to ijk^{th} observation,

i and j = Male and female parents responsible for producing ij^{th} hybrid and

b   = Number of replications.

The restrictions imposed to this model are :

$$\sum_i g_i = 0$$

$$\sum_j S_{ij} + S_{ij} = 0 \text{ (for each i)}$$

Sum of squares for GCA and SCA were calculated as follows :

$$S_g = \frac{1}{P+2} \left[\sum_i (x_i + x_{ii})^2 - \frac{4}{P} x_{..}^2 \right]$$

The sum of squares for specific combining (Ss) was calculated as :

$$Ss = \sum_i \sum_j x_{ij}^2 - \frac{1}{P+2} \sum_i (x_i + x_{ii}) + \frac{2}{(P+1)(P+2)} x_{..}^2$$

Where, P   = Number of parents,

S_g = Sum of squares due to GCA,

Ss = Sum of squares due to SCA,

x_{ij} = Value of the cross between i^{th} and j^{th} parent,

x_i = Total of ith (row) array in diallel table (summed over j),

x.. = Grand total of 'P' parents/lines and $\frac{P(P-1)}{2}$ progenies of diallel table and

x_{ii} = Parental value of the ith parent.

Analysis of variance table for combining ability was set as follows (for Model-1, Method-2) :

Sources	d.f.	S.S.	M.S.	Expectation of M.S.
General combining ability (GCA)	(p-1)	S_g	M_g	$\sigma_e^2 + (P+2) \frac{1}{(P-1)} \sum_i g_i^2$
Specific combining ability (SCA)	$\frac{P(P-1)}{2}$	Ss	Ms	$\sigma_e^2 + \frac{2}{P(P-1)} \sum_i \sum_j s_{ij}^2$
Error	(r-1)(p-1)	Se	Mé	σ_e^2

The mean square of GCA and SCA were calculated by dividing respective sum of squares with the corresponding degrees of freedom, error mean squares for combining ability analysis was obtained as under :-

$$M\acute{e} = \frac{Me}{b}$$

Where, Me = Error mean square in the analysis of the experimental design (R.B.D.) and

b = Number of replications.

Mé was used for calculation of variance ratio (F) as a test of GCA and SCA mean squares. In F_2 also Mé was used to calculate variance ratio (F).

3.5.4 Estimation of general and specific combining ability effects :

General and specific combining ability effects were calculated as follows :

$$\hat{g}_i = \frac{1}{P+2} \left(x_i + x_{ii} - \frac{2}{P} x_{..} \right) \text{ and}$$

$$\hat{S}_{ij} = x_{ij} - \frac{1}{P+2}(x_i + x_{ii} + x_{j.} + x_{jj}) + \frac{2}{(P+1)\,(P+2)} x_{..}$$

Where, $\hat{g}_i$ = Estimation of general combining ability (GCA) effect of ith parent and

$\hat{S}_{ij}$ = Estimation of specific combining ability (SCA) effect of the hybrid between i^{th} and j^{th} parent.

Other notations were the same as explained earlier.

3.5.5 Standard errors of the estimate :

Standard errors to test the significance of GCA and SCA estimates and differences between the two estimates were calculated as the underroot of the variances of the estimates. The variance of the various estimates were computed as follows :

Variance $(\hat{g}_i)$ = $\dfrac{(P-1)}{P(P+2)}$ Mé

Variance $(\hat{S}_{ij})$ = $\dfrac{P^2 + P + 2}{(P+1)\,(P+2)}$ Mé (i $\neq$ j),

Variance $(\hat{g}_i - \hat{g}_j)$ = $\dfrac{2}{P+2}$ Mé for comparing two general combining ability estimates (i $\neq$ j),

Variance $(\hat{S}_{ij} - \hat{S}_{ik}) = \dfrac{2(P+1)}{P+2}$ Mé for specific combining ability estimates in one array $(i \neq j,k; \; j \neq k)$

and

Varaince $(\hat{S}_{ij} - \hat{S}_{kl}) = \dfrac{2p}{P+2}$ Mé for any two specific combining ability estimates $(i \neq j,k,l; \; j \neq k,l; \; k \neq l)$.

Standard error was calculated by taking the square root of the variance. Each GCA and SCA estimate was subjected to 't' test to determine the difference.

$$\text{'t' test for GCA} = t = \frac{g_i - 0}{S.E.(g_i)} \quad \text{and}$$

$$\text{'t' test for SCA} = t = \frac{S_{ij} - 0}{S.E.(S_{ij})}$$

The 't' value obtained was tested against the table 't' value at 5% and 1% probability level at error degrees of freedom.

For testing significance of difference between two effects, the critical difference was calculated by multiplying the respective standard error of difference with 't' value at error degree of freedom.

Griffing (1956b) and Gardner (1963) suggested technique for the estimation of second degree heredity parameters. Variance due to GCA effects and SCA effects were made free from environmental variation. This was calculated using the following equations.

(i)   <u>Estimated variance due to GCA</u> :

$$\sum g_i^2 = (Mg - M\acute{e}) \times \frac{P-1}{P+2}$$

(ii)   <u>Estimated variance due to SCA</u> :

$$\sum \sum_{i\,j} s_{ij}^2 = (Ms - M\acute{e}) \times \frac{P(p-1)}{2}$$

The ratio of additive to non-additive variance was estimated as follows :

$$GCA/SCA = \frac{1}{d.f.GCA} \sum g_i^2 \ \Big/ \ \frac{1}{d.f.SCA} \sum \sum_{i\,j} s_{ij}^2$$

3.5.6 **Estimation of genetic components of variation and related genetic parameters** :

Components of genetic variation and related genetic parameters were calculated according to Hayman (1954b), Jinks (1954, 1956) as described in details by Mather and Jinks (1982) and Singh and Chaudhary (1985). This biometrical analysis is based upon following assumptions :

(i)   Diploid segregation,

(ii)   No differences in reciprocal crosses,

(iii)   Independent action of non-allelic genes in diallel cross,

(iv)   Homozygous parents,

(v)   No multiple allelism,

(vi)   Genes independently distributed among parents and

(vii)   No genotype x environment interaction with location and year.

Testing of hypothesis :

Failure of any of the assumptions invalidates to some degree the inference derived by means of diallel analysis. To test failure of either of the assumptions of diallel analysis, following test was applied as suggested by Hayman (1954 a).

t^2 test :

$$t^2 = \frac{n-2}{4} + \left[\frac{(Var.\ Vr - Var.\ Wr)^2}{(Var.Vr \times Var.\ Wr) - Cov.\ (Vr,\ Wr)} \right]$$

With n-2 degree of freedom, where n is number of parents. Non-significant value of t^2 indicates probable fulfilment of the assumptions.

3.5.7 **Graphical analysis :**

For each character, Vr, Wr graphs were prepared, Vr is the variance of all the offsprings of each array and Wr is the covariance of each array with non-recurrent parents. Vr, Wr and Vp (variance of parents) were calculated with the formula given below :

(i) Variance (Vr) of the offsprings of each parental array :

$$\text{Array variance (Vr)} = \frac{\text{(Sum of square of observations in an array)}}{\text{Degree of freedom}} - C.F.$$

$$C.F. = \frac{(\text{Grand total})^2}{n}$$

Where,   n = Number of observations.

(ii) <u>Covariance (Wr) offsprings of each array with non-recurrent</u>

<u>parents</u> :

$$\text{Covariance (Wr)} = \frac{\text{Sum of products of the offsprings in any array with non-recurring parents}}{\text{Degree of freedom}} - \text{C.F.}$$

(iii) <u>Variance of the parents (vp)</u> :

$$\begin{array}{c}\text{Variance of} \\ \text{parents (Vp)}\end{array} = \frac{\text{Sum of squares of parental value}}{\text{Degree of freedom}} - \text{C.F.}$$

<u>Regression of Wr on Vr</u> :

From the Wr and Vr values, for each of the arrays the regression of Wr on Vr was calculated by using the following formulae :

$$\text{Variance of Vr values} = \frac{\sum V^2_{ri} - (\sum V_{ri})^{2/n}}{n-1}$$

$$\text{Covariance of Wr,Vr} = \frac{\sum W_{ri} V_{ri} - (\sum W_{ri} \times V_{ri})/N}{n-1}$$

Where, n = Number of Vr, Wr values (Number of arrays)

$$\text{Regression coefficient (b)} = \frac{\text{Covariance of Wr,Vr}}{\text{Variance of Vr}}$$

The significance of the difference of 'b' from zero as well as from unity was tested by using 't' test :

$$t = \frac{(b-0)}{SE(b)} \quad \text{and} \quad t = \frac{(1-b)}{SE(b)} \text{ with } n-2$$

Degree of freedom, where, n is the number of observations (Number of arrays).

Coordinates of the limiting parabola :

The Wr co-ordinates of the limiting parabola within which the array points are expected to lie were computed by equalling the inequality W_r^2 = VrVp. In this relationship, Vr is the variable factor, while Vp is a constant factor. Thus by substituting the observed values of Vr for each array seperately and Vp values in the formula Wr = $\sqrt{Vr\ Vp}$, the Wr ordinates for the limiting parabola were calculated for each of the Vr values.

Coordinates for the regression line :

The co-ordinates for the best fitting regression line were obtained by using the equation of a straight line, _viz._, Y = a+bx.

Where, b is the slope of line

      x and Y are the two co-ordinates and 'a' is the point

      of interception of the regression line with the Y axis.

The value of 'a' and expected values of Wr (Wre) were computed as under :-

(i) The 'a' value was computed by putting Y = Wr; x = Vr and b = regression of Wr on Vr in the equation as given below :

      Y = a + bx

      Wr = a + b$\overline{V}$r

      Therefore a = $\overline{W}$r - b$\overline{V}$r

Where, $\overline{Wr}$ = Mean of Wr values

$\overline{Vr}$ = Mean of Vr values.

(ii) For each value of Vr, the expected value of Wre for the best fitting line was computed by putting the values of 'a', 'b' and Vr for each array in the equation.

$$Y = a + bx$$

Where, Y = Wre

x = Vr

Thus, values of 'a' and 'b' are constant for a generation, while Vr changes with array, thus giving the expected value of Wr for the regression line for each value of Vr.

The standard error (S.E.) of regression coefficient (b) was calculated from the formulae :

$$S.E.(b) = \sqrt{\frac{(Y-\overline{Y})^2 - b\sum(x-\overline{x})(y-\overline{y})}{(n-2) \qquad \sum(x-\overrightarrow{x})^2}}$$

Where, x = Vr and Y = Wr

$\overline{x}$ = $\overline{Vr}$ and $\overline{Y}$ = $\overline{Wr}$

n = Number of arrays.

With the help of the above statistics, graphical analysis of the Vr, Wr graphs were done for different characters by plotting Vr values against Wr values, taking the former as the abscissa and the latter as the ordinate.

The limiting parabola of such a graph was constructed with the help of Wr^2 and the regression line was drawn by Wrc values fitting best to the points in the graph.

Estimation of standard deviation of Yr and Wr + Vr :

Standard parent $Y_n = \dfrac{x - \bar{x}}{s}$

Where, x = Value of individual parent,

$\bar{x}$ = Mean of the parent, and

S = Standard deviation of the parents

$S_1 = \sqrt{\text{Variance of parents}}$

Standard Wr + Vr = $\dfrac{X_1 - \bar{X}_1}{S_1}$

Where, x_1 = Value of Wr + Vr

$\bar{x}_1$ = Mean of Wr + Vr, and

S = Standard deviation of Wr + Vr

$S_1 = \sqrt{\text{Var. Wr + Vr}}$

(iii)   Estimation of variance and covariances :

Estimation of variances and covariances were carried out by using following formulae :

1. Parental mean = $\dfrac{\sum\limits_{1=i}^{P} x_{ii}}{P}$

2. Variance of parents :

$$VoLo = \frac{1}{p-1}\left[\sum\limits_{1=i}^{P} \frac{(x_{ii})^2}{r} - \frac{1}{P}(\sum\limits_{1=i}^{P} x_{ii})^2 \right]$$

3. Variance of rth array - Vr :

$$Vr = \frac{1}{}\left[\sum\limits_{1=i} \frac{(x_{ri})^2}{b} - \frac{1}{P} \frac{(x_{ri})^2}{b} \right]$$

4. Mean variance of array =

$$V_1L_1 = \frac{1}{P} \sum Vr$$

5. The covariance between the non-recurring parent and their progeny in the rth array =

$$Wr = \frac{1}{\quad} \left[\sum_i^P \sum_j^P \frac{x_{ri} \, x_{ri}}{b^2} - \frac{1}{P} \left(\sum_i^P \frac{x_{ii}}{b} \sum_r^P \frac{x_r}{b} \right) \right]$$

6. Mean covariance between parents on the arrays :

$$V_0L_0 = \frac{1}{P} \sum Wr$$

7. Variance of mean of array =

$$V_0L_1 = \frac{1}{P-1} \left[\sum_1^b \frac{(x_i)^2}{P} \frac{1}{P} \left(\sum_i^P \frac{(x_i)^2}{P} \right) \right]$$

8. The differences between the mean of parents and the mean of their p^2 progeny =

$$(ML_1 - ML_0)^2 = \left[\frac{1}{P} \left(\frac{1}{P} \sum_1 x_i - \sum_1 x_{ii} \right) \right]^2$$

Where, i = 1,2 --------- P,

x_{ii} = Parental mean of ith parent,

x_{ri} = r^{th} array involving i^{th} and j^{th} parent,

P = Number of parent,

b = Number of blocks in design,

ML_1 = Grand total,

ML_0 = Sum of parental mean as sum of diagonal values and

r = 1,2 -----------i x j.

Components of variation :

D   = Additive effects of genes,

H_1 = Dominance effects of genes,

H_2 = Proportion of dominance variation caused by positive and negative effects of genes.

F   = Mean of Fr values over array showing proportion of dominant and recessive genes in parents and

h^2 = Dominance effect as algebric sum of all the loci

Estimates of these components of genetic variance (in F_1) were determined by using following formulae :

$\hat{D}$ = VoLo − $\hat{E}$

$\hat{H}_1$ = VoLo − 4WoLo + 4V_cLr − (3n−2) $\hat{E}$/n

$\hat{H}_2$ = 4V_1L_1 − 4VoL1 − 2$\hat{E}$

$\hat{F}$ = 2 VoLo − 4WoLo1 − 2(n−2) $\hat{E}$/n

$\hat{h}^2$ = 4 (ML$_1$ − ML$_0$)^2 − 4 (n−1) $\hat{E}$/n^2

$\hat{Fr}$ = 2(VoLo − WoLo1 + V_1L_1 − Wr − Vr) −2(n−2) $\hat{E}$/n

The statistics in the above formulae have following meaning :

Vr   = Variance of the rth array,

Wr   = Covariance between parents and their offsprings in the rth array,

VoLo = Variance of the parents, i.e. Vp,

V_1L_1 = Mean variance of array, i.e. Vr,

$WoLo_L$ = Mean covariance between parents and their array i.e. Wr,

VoL_L = Variance of the means of the array i.e. Vr,

$(ML_1-ML_0)^2$ = Difference between the mean of the parents and the mean of their n^2 progeny and

E = Expected environmental components of non heritable variation which is obtained from the analysis of variance for the design of experiment, i.e. $\hat{E}$ = Me/b.

Estimation of standard error for the components of variance was calculated using mean square, $S^2 = \frac{1}{2}$ Var. (Wr-Vr) and diagonal of the covariance matrix given by Hayman (1954 a) as corresponding multiplier).

$$SE(D) = \sqrt{\frac{S^2 (n^5 + n^4)}{b^5}}$$

$$SE(H_1) = \sqrt{\frac{S^2 (n^5 + 41n^4 - 12n^3 + 4n^2)}{n^5}}$$

$$SE(H_2) = \sqrt{\frac{S^2 (36n^4)}{n^5}}$$

$$SE(F) = \sqrt{S^2 (4n^5 + 20n^4 + 16n^3 + 16n^2}$$

$$SE(h)^2 = \sqrt{\frac{S^2 (16n^4 + 16n^2 - 32n + 16)}{n^5}}$$

$$SE(E_2) = \sqrt{\frac{S^2 (n^4)}{n^5}}$$

Where, n = Number of parents.

After testing the significance of each component with corresponding standard error, following interpretations were draw from the ratios of those components of variances as given Hayman (1954a).

(1)   Mean degree of dominance : $(H_1/D)^{\frac{1}{2}}$

(2)   The proportion of genes with positive and negative effects in parents : $(H_2/4H_1)$

(3)   The proportion of total number of dominant and recessive genes in the parents :

$$\frac{KD}{KR} = [(4DH_1)^{\frac{1}{2}} + F] \ / \ [(4DH_1)^{\frac{1}{2}} - F)]$$

(4)   Number of group of genes controling the characters and exhibiting dominance : h^2 / H_2

(5)   Heritability in narrow sense (h^2) in F_1 using the formulae of Crumpeker and Allard (1962) :

$$\tfrac{1}{4} D \ / \ (\tfrac{1}{4}D + \tfrac{1}{2}H_1 - \tfrac{1}{4}F + E).$$

Estimation of components of variation in F_2 :

Components of variation of F_2 were estimated by the formulae of Jinks (1956). Expected statistics for F_2 generation were the same as those of F_1 except that contribution of 'h' was reduced to half because of one generation of inbreeding. Thus coefficients H_1 and H_2 were one

fourth of F_1 statistics while coefficient of F_1 was reduced to half being second and third degree statistics respectively (Jinks, 1956; Hayman, 1958a and Mather and Jinks, 1982).

Composition of F_2 variances and covariances :

$$\overline{Vr} = V_1L_2 = \tfrac{1}{2}\hat{D} + \tfrac{1}{16}\hat{H}_1 - 1/8\ \hat{F} + \hat{E}_2$$

$$\overline{Wr} = WoLo = \tfrac{1}{2}\hat{D} - 1/8\ \hat{F} + \hat{E}_2/n$$

$$Vm = VoL_9 = \tfrac{1}{2}\hat{D} + 1/16\hat{H}_1 - 1/16\hat{H}_2 - 1/8\ \hat{F} + \hat{E}_2/n$$

$$Vp = VoL_2 = \hat{D} + \hat{E}$$

Where, $E_2 = VE/r$, VE is the error variance of F_2 in design of experiment, and

n   = Number of parents.

Estimations of D, H_1, H_2, h^2 and F in F_2 were calculated by following formulae :

$$D = VoLo - E$$

$$H_1 = 16V_1L_2 - 16WoLo_2 + 4VoLo - \frac{4(5n-4)}{n}\ E_2$$

$$H_2 = 16V_1L_2 - 16VoL_2 - \frac{16(n-1)}{n}\ E_2$$

$$h^2 = 4(ML_2 - ML_0) - \frac{16(n-1)}{n}\ E_2$$

$$F = 4VoLo - 8WoLo_2 - \frac{4(n-2)}{n}\ E_2$$

Standard errors, to test the significance of components listed above, were calculated as follows :

$$SE(D) = \left[\frac{S^2\,(n^5 + n^4)}{n^5} \right]^{\frac{1}{2}}$$

$$SE(H_1) = \left[\frac{S^2\,(16n^5 - 65n^4 - 192n^3 + 64n^2)}{n^5} \right]^{\frac{1}{2}}$$

$$SE(H_2) = \left[\frac{S^2\,(576n^4)}{n^5} \right]^{\frac{1}{2}}$$

$$SE(F) = \left[\frac{S^2\,(16n^5 + 80n^4 - 64n^3 + 6n^2)}{n^5} \right]^{\frac{1}{2}}$$

$$SE(h^2) = \left[\frac{S^2\,(256n^4 + 256n^2 - 512n + 256)}{n^5} \right]^{\frac{1}{2}}$$

$$SE(E_2) = \left[\frac{S^2\,n^4}{n^5} \right]^{\frac{1}{2}}$$

Where, n = Number of parents and $S^2 = \frac{1}{2}$ Var. (Wr-Vr).

Significance of various statistics was tested by 't' test at n-2 degree of freedom as :

$$t = \frac{Parameter}{S.E.\ of\ parameter}$$

Following proportion of genetic components were calculated from the above components :

(1)   Degree of dominance : $\frac{1}{2}(H_1/D)^{\frac{1}{2}}$

(2)   Proportion of genes with positive effects : $(H_2/4H_1)$

(3)   Proportion of dominant and recessive genes in parents :

$$\frac{KD}{KR} = \frac{\frac{1}{2}(4DH_1)^{\frac{1}{2}} + (\frac{1}{2})\,F}{\frac{1}{2}(4DH_1)^{\frac{1}{2}} - (\frac{1}{2})\,F}$$

(4) Number of groups of genes controlling the character and exhibiting dominance : h^2 / H_2

(5) Narrow sense heritability in the F_2 was calculated by using the formulae given by Verhanlen and Murray (1969).

$$\frac{\frac{1}{4}D}{\frac{1}{4}D + \frac{1}{16} H - \frac{1}{8} F + E}$$

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The results obtained from the present investigation are presented under following headings :

1. Analysis of variance for experimental design and mean performance of the parent and hybrids,

2. Heterosis, heterobeltiosis, economic heterosis and inbreeding depression,

3. General and specific combining ability effects, and

4. Nature of gene action and genetic components of variation through diallel analysis.

4.1   ANALYSIS OF VARIANCE FOR EXPERIMENTAL DESIGN (Table-2) :

The analysis of variance for experimental design was carried out for yield and its componental traits. The mean sum of squares due to genotypes were highly significant for all the traits. High significance was also recorded in variance due to parent for the traits under study, thus indicating substantial amount of genetic variability among the parents. Mean sum of squares to hybrids (F_1) were highly significant for yield and its componental traits, along with quality traits, however, number of branches per plant, number of capsules per plant and test weight were significant only at 5

Table 2. Analysis of variance of the experimental design for different characters in sesame

Source	d.f.	Plant height to first flowering (cm)	Days to first flowering	Days to 50 per cent flowering	Days to maturity	Length of reproductive stem (cm)	Plant height at maturity (cm)	Number of branches per plant	Number of capsules per plant	Length of capsule (cm)
1	2	3	4	5	6	7	8	9	10	11
Replications	2	120.375**	1.603	6.303**	0.520	25.239**	42.390**	0.135	1.684**	0.001
Treatments	99	22.662**	18.023**	14.643**	24.740**	56.192**	267.744**	0.716**	53.420**	0.043**
Parents	9	224.547**	22.997**	23.633**	39.484**	69.757**	313.365**	0.681**	43.470**	0.040**
F_1's	44	34.896**	16.631**	14.206**	24.170**	63.058**	255.477**	0.652*	63.320**	0.029**
F_2's	44	11.915**	16.305**	11.858**	23.145**	42.599**	193.270**	0.318	26.770**	0.048**
Parents vs crosses	1	1.688	15.578**	22.938**	6.000**	144.531**	66.125**	2.075**	364.766**	0.204**
F_1's vs F_2's	1	2.789	112.515**	67.198**	3.393**	115.385**	875.420**	19.995**	568.806**	0.270**
Error	198	1.789	1.482	0.731	0.251	2.853	7.388	0.159	0.145	0.001

Contd. Table 2.

Source	d.f.	Number of grains per capsule	Dry weight per plant (g)	Grain yield per plant (g)	Test weight (g)	Husk seed ratio	Harvest Index (%)	Oil content (%)	Oil yield per plant (g)	Protein content (%)
		12	13	14	15	16	17	18	19	20
Replications	2	0.011	0.009	0.051**	0.000	0.001	0.157	0.002	0.013	0.000
Treatments	99	23.898**	4.441**	0.864**	0.006**	0.074**	22.160**	2.755**	0.202**	0.709**
Parents	9	27.600**	3.606**	0.620**	0.009**	0.056**	9.530**	5.132**	0.149**	1.717**
F_1's	44	23.685**	4.317**	0.770**	0.005**	0.089**	20.690**	2.956**	0.178**	0.604**
F_2's	44	22.406**	2.377**	0.346**	0.006**	0.065**	26.602**	2.666**	0.078**	0.629**
Parents vs crosses	1	1.688**	29.206**	5.803**	0.001*	0.005**	0.352*	0.469**	1.419**	0.008**
F_1's vs F_2's	1	87.85**	83.536**	25.333**	0.003**	0.026**	185.336**	0.058	11.616**	0.410**
Error	198	0.006	0.032	0.007	0.000	0.001	0.381	0.028	0.001	0.001

* Significant at 5 per cent level
** Significant at 1 per cent level

per cent level, revealing the existence of real variability in the parental material used in present programme. The variation due to F_2s were also highly significant for all the characters, except number of branches per plant. The parent Vs F_1s comparison indicated significance for all the traits, except plant height to first flowering, this indicated substantial amount of heterosis in hybrids. The F_1s differed significantly from their F_2s for all the characters, except plant height to first flowering and oil content, suggesting considerable amount of inbreeding depression in F_2.

The mean values for all the characters studied are presented in Appendix-II. Characterwise results of mean performance of parents and their hybrids are as under :

Plant height to first flowering (cm) :

Over all mean for parents and hybrids was 42.78 cm and 42.56 cm respectively. Parent Mrug-1 (48.73 cm) had highest mean value, while parent AHT-55 (38.83 cm) showed lowest mean value. Variability in hybrids ranged from 37.03 cm (AHT-55 x TKG-9-86) to 52.33 cm (BAUT-1 x TKG-9-86) for the trait.

Days to first flowering :

An overall mean for parents was 38.70 days and of hybrids was 39.35 days. The parental mean varied from 34.00 days (RT-125) to 42.00 days (PY-57), whereas, mean for hybrids varied from 34.00 days (RT-125 x BAUT-1) to 44.00 days (Mrug-1 x G.Til-1).

Days to 50 per cent flowering :

The parent RT-125 was earliest to flower (37.67 days), while parent PY-57 took maximum number of days to flower (47.00 days). Cross RT-125 x BAUT-1 (38.33 days) was early, whereas, cross Mrug-1 X G.Til-1 (47.33 days) was late flowering. Overall mean for parents was 42.68 days and for hybrids it was 43.56 days.

Days to maturity :

Over all mean performance was found to be almost equal in magnitude both in parents (84.43 days) and hybrids (84.03 days) for the trait. The parent RT-125 (77.33 days) was earliest, while parent PY-57 matured in maximum number of days (90.33). Mean values of hybrids varied from 75.33 days (RT-125 x BAUT-1) to 88.00 days (G.Til-1 x PY-57).

Length of reproductive stem (cm) :

Range for parent was observed from 37.47 cm (TKG-9-86) to 55.13 cm (BAUT-1) and the mean values of hybrids differed from 36.67 cm (AHT-55 x TKG-9-860) to 61.80 cm (Tapi x BAUT-1). Over all mean for parents was 44.97 cm and for hybrids it was 46.96 cm.

Plant height to maturity (cm) :

Over all mean of hybrids (98.00 cm) was more than the parents (96.60 cm). The parent PY-57 (115.93 cm) was tallest and parent AHT-55 (84.60 cm) was shortest. Mean performance

for hybrids varied from 81.93 cm (AT-17 x OMT-10) to 126.83 cm (PY-57 x BAUT-1).

Number of branches per plant :

Over all means for parents and hybrids were 1.95 and 2.19 for number of branches per plant. Mean performance of parents ranged from 1.10 (AHT-55) to 2.50 (PY-57), whereas for hybrids, it ranged from 1.00 (G.Til-1 x AHT-55) to 3.17 (Mrug-1 x OMT-10).

Number of capsules per plant :

General mean of hybrids and parents was 21.95 and 18.82 respectively for number of capsules per plant. Parent BAUT-1 (24.82) had highest mean while parent PY-57 (14.12) expressed lowest number of capsules. The range in the hybrids was from 36.2 (AT-17 x TKG-9-86) to 16.59 (AHT-55 x OMT-10).

Length of capsule (cm) :

Parental mean ranged from 2.44 cm (OMT-10) to 2.88 cm (PY-57) with over all mean of 2.65 cm, whereas hybrid mean ranged from 2.51 cm (Mrug-1 x OMT-10) to 2.92 cm (PY-57 x BAUT-1) with overall mean of 2.73 cm for the trait.

Number of grains per capsule :

Overall mean of parents and hybrids was almost equal (63.53 and 63.34). Parent OMT-10 (58.38) had minimum value whereas parent AHT-55 (68.43) had maximum. Maximum and minimum number of grains per capsule were recorded in the cross Mrug-1

x G.Til-1 (69.20) and TKG-9-86 x OMT-10 (57.32), respectively.

Dry weight per plant (g) :

Mean parental value for dry weight per plant varied from 4.31 g (AT-17) to 7.11 g (BAUT-1), whereas, hybrids ranged from 4.41 g (TKG-9-86 x OMT-10) to 10.24 g (Tapi x BAUT-1). General mean for parents was 5.23 g and for hybrid, it was 6.13 g.

Grain yield per plant (g) :

Overall mean of hybrids was more (2.82 g) than their parental mean (2.42 g). The mean yield of parents differed from 2.65 g (TKG-9-86) to 3.12 g (BAUT-1). Hybrids ranged from 1.86 g (TKG-9-86 x OMT-10) to 4.14 g (BAUT-1 x TKG-9-86) for the trait.

Test weight (g) :

Overall mean for parents and hybrids were almost equal (1.34 g and 1.35 g). Parent BAUT-1 (1.47 g) recorded maximum yield OMT-10 (1.24 g) yielded minimum. The mean of crosses varied from 1.11 g (PY-57 x TKG-9-86) to 1.47 g (Mrug-1 x PY-57).

Husk seed ratio :

Parent OMT-10 (0.78) had lowest ratio, whereas highest ratio was expressed by parent BAUT-1 (1.47). The crosses Tapi x BAUT-1 (0.75) and Mrug-1 x RT-125 (1.38) had lowest and highest ratios, respectively. Overall mean performance was 1.05 and 1.03 for parents and hybrids, respectively.

Harvest index :

Overall mean performance was observed to be almost equal in magnitude both in parents (24.02) as well as hybrids (23.92) for the trait. The parent PY-57 (21.26) had lowest, whereas parents Mrug-1 and RT-125 (26.33) had highest index. The cross G.Til-1 x PY-57 (28.61) indicated highest harvest index and the lowest was recorded by cross PY-57 x BAUT-1 (17.57).

Oil content (%):

Range for parental mean was observed from 46.00 per cent (OMT-10) to 48.33 per cent (G.Til-1). The hybrids differed from 44.18 per cent (Tapi x OMT-10) to 48.74 per cent (AT-17 x PY-57). Overall mean for parents and hybrids was 47.41 per cent and 47.53 per cent, respectively.

Oil yield per plant (g) :

Overall mean of hybrids (1.34 g) was more than their parents (1.14 g). Mean performance of parent BAUT-1 (1.47 g) was highest and twice the lowest parent TKG-9-86 (0.74 g). Mean for hybrids varied from 0.88 g (Tapi x RT-125) to 2.00 g (BAUT-1 x TKG-9-86).

Protein content (%) :

The parent BAUT-1 (26.66%) was highest in protein while, parent RT-125 was lowest with 24.16 per cent. Cross RT-125 x OMT-10 (24.69%) was lowest and cross G.Til-1 x BAUT-1

(26.57%) was highest in protein content. General mean for parents and hybrids was 25.58 per cent and 25.93 per cent, respectively.

4.2 HETEROSIS, HETEROBELTIOSIS, ECONOMIC HETEROSIS AND INBREEDING DEPRESSION :

The extent of heterosis expressed as per cent of increase or decrease in hybrids, was obtained over mid parent as well as better parent and magnitude of economic heterosis in comparison to check parent (RT-125) in all the traits. Inbreeding depression was obtained as per cent decrease in F_2 over F_1 separately for each of the characters studied. Character-wise results are presented as follows :

Plant height to first flowering (Table-3) :

Out of 36 significant heterotic crosses, 15 and 21 crosses showed positive and negative heterosis, respectively. Cross BAUT-1 x TKG-9-86 (29.22%) ranked first followed by AT-17 x AHT-55 (16.64%) and G-Til-1 x TKG-9-86 (15.12%) with a minimum heterosis of 2.34 per cent in cross PY-57 x BAUT-1. Eight hybrids had significant positive heterobeltiosis which varied from 1.91 per cent (PY-57 x BAUT-1) to 24.80 per cent (BAUT-1 x TKG-9-86). Other comparative crosses with higher heterobeltiosis were AT-17 x AHT-55 (11.81%) and G.Til-1 x TKG-9-86 (7.18%). Sixteen hybrids revealed significant economic heterosis, with a range from -13.47 per cent to 22.46 per cent. The maximum economic heterosis was observed in the

Table 3. Heterosis over mid parent, better parent, check parent (economic) and inbreeding depression in per cent for plant height to first flowering and days to first flowering

Crosses	Plant height to first flowering				Days to first flowering			
	Heterosis			Inbreeding depression	Heterosis			Inbreeding depression
	Mid parent	Better parent	Economic		Mid parent	Better parent	Economic	
1	2	3	4	5	6	7	8	9
$P_1 \times P_2$	4.90**	-1.85	11.93**	14.28**	0.00	0.00	20.59**	7.32**
$P_1 \times P_3$	-10.30**	-10.44**	-11.00**	-0.10	12.39**	23.31**	24.50**	9.45**
$P_1 \times P_4$	0.27	-3.08**	3.21**	10.72**	2.13*	7.14**	17.65**	8.33**
$P_1 \times P_5$	3.73**	-0.71	-1.31	4.13**	-6.56**	-5.78**	11.76**	4.39**
$P_1 \times P_6$	-3.03**	-3.30**	-3.88**	-1.78	-2.01*	-0.81	19.62**	0.83
$P_1 \times P_7$	-9.78**	-10.06**	-10.06**	-13.90**	4.89**	15.69**	15.68**	5.08**
$P_1 \times P_8$	0.00	-0.63	-1.24	-0.17	-5.49**	9.82**	9.79**	-21.43**
$P_1 \times P_9$	3.52**	-0.63	-1.24	2.06	-3.31**	-1.68	14.71**	-5.38**
$P_1 \times P_{10}$	0.62	-1.06	1.73	8.05**	-0.42	1.70	17.65**	0.00
$P_2 \times P_3$	-2.27**	-8.69**	4.14**	4.28**	7.97**	18.45**	19.62**	0.00
$P_2 \times P_4$	-14.04**	-16.90**	-5.22**	-5.11**	12.34**	17.86**	29.41**	5.30**
$P_2 \times P_5$	-14.43**	-23.12**	-12.31**	-18.23**	0.82	0.00	20.59**	-3.24**
$P_2 \times P_6$	-14.18**	-19.90**	-8.66**	-12.73**	-5.22**	-4.88**	15.68**	0.00
$P_2 \times P_7$	-8.31**	-13.95**	-1.87*	-2.79*	-4.89**	4.91**	4.91**	-7.46**
$P_2 \times P_8$	-3.24**	-9.99**	2.67**	2.83**	2.95**	7.02**	19.62**	-2.46*
$P_2 \times P_9$	12.91**	1.71*	16.01**	16.02**	4.96**	6.78**	24.50**	11.01**
$P_2 \times P_{10}$	-4.53**	-9.23**	3.51**	12.50**	0.42	2.54**	18.62**	9.08**
$P_3 \times P_4$	-6.87**	-10.11**	-4.28**	1.96	6.98**	11.65**	12.74**	-1.75
$P_3 \times P_5$	16.64**	11.81**	10.76**	15.42**	3.57**	12.62**	13.74**	-0.85
$P_3 \times P_6$	-1.93*	-2.05*	-2.95**	-3.13**	2.18*	13.36**	14.70**	0.85
$P_3 \times P_7$	-3.53**	-3.98**	-3.98**	-3.75**	10.24**	9.71**	10.79**	5.31**
$P_3 \times P_8$	5.93**	5.43**	4.45**	0.36	4.15**	9.71**	10.79**	-4.41**
$P_3 \times P_9$	0.57	-3.31**	-4.21**	-5.96**	6.31**	14.56**	15.68**	2.54*
$P_3 \times P_{10}$	4.02**	2.12*	5.01**	10.85**	13.12**	21.36**	22.56**	11.21**
$P_4 \times P_5$	-1.66*	-8.86**	-2.95**	-14.30**	-3.00**	0.89	10.79**	0.00
$P_4 \times P_6$	-3.57**	-7.03**	-1.09	0.70	5.04**	11.61**	22.56**	0.82
$P_4 \times P_7$	-1.58	-18.32**	-13.01**	-7.16**	2.80**	7.84**	7.85**	2.73**
$P_4 \times P_8$	-3.09**	-6.89**	-0.85	2.83**	1.77*	2.68**	12.74**	-6.97**

Contd.

Contd. Table 3.

1	2	3	4	5	6	7	8	9
$P_4 \times P_9$	15.12**	7.18**	14.13**	13.61**	6.49**	9.92**	17.65**	4.07**
$P_4 \times P_{10}$	-1.45	-3.15**	3.13**	4.02**	-4.35**	-1.78	7.85**	5.45**
$P_5 \times P_6$	11.51**	7.02**	5.78**	11.66**	-0.41	1.65	20.58**	2.53**
$P_5 \times P_7$	-1.10	-5.62**	-5.62**	-2.33*	-4.04**	4.91**	4.91**	0.95
$P_5 \times P_8$	4.99**	1.11	-0.77	2.83**	-0.43	2.63**	14.71**	7.69**
$P_5 \times P_9$	-4.92**	-5.21**	-13.34**	-9.45**	4.17**	5.04**	22.56**	5.62**
$P_5 \times P_{10}$	-5.44**	-10.93**	-8.42**	-4.09**	-3.77**	-2.54**	12.73**	-1.75
$P_6 \times P_7$	-0.59	-1.17	-1.17	4.26**	9.45**	22.55**	22.56**	4.94**
$P_6 \times P_8$	2.34**	1.97*	-0.79	2.72*	2.50**	7.89**	20.58**	-3.24**
$P_6 \times P_9$	8.49**	4.42**	3.21**	14.90**	6.12**	9.24**	27.44**	9.99**
$P_6 \times P_{10}$	6.31**	4.25**	7.18**	4.30**	3.18**	6.78**	23.53**	4.76**
$P_7 \times P_8$	-0.32	-1.25	-1.24	3.15**	-5.56**	0.00	0.00	-1.97*
$P_7 \times P_9$	-9.62**	-13.50**	-13.47**	-1.70	-6.79**	0.98	0.97	-11.65**
$P_7 \times P_{10}$	-1.85*	-3.19**	-0.47	2.26*	3.64**	11.76**	11.76**	7.03**
$P_8 \times P_9$	29.22**	24.80**	22.46**	18.75**	-5.58**	-5.26**	7.85**	-6.35**
$P_8 \times P_{10}$	4.19**	1.82	4.68**	-0.83	9.48**	11.40**	24.50**	0.78
$P_9 \times P_{10}$	-10.36**	-15.33**	-12.94**	-7.53**	7.17**	7.12**	24.50**	2.36*
S.Em	0.65	0.65	0.65	0.77	0.66	0.66	0.66	0.70
CD at 5%	1.62	1.85	1.85	2.14	1.61	1.85	1.85	1.95
CD at 1%	2.14	2.46	2.46	2.81	2.13	2.45	2.45	2.56

* Significant at 5 per cent level

** Significant at 1 per cent level

P_1 = Tapi, P_2 = Mrug-1, P_3 = AT-17, P_4 = Gujarat Til-1, P_5 = AHT-55, P_6 = PY-57, P_7 = RT-125, P_8 = BAUT-1, P_9 = TKG-9-86, P_{10} = OMT-10.

cross BAUT-1 x TKG-9-86 followed by Mrug-1 x TKG-9-86 (16.00%) and G.Til-1 x TKG-9-86 (14.13%).

In F_2, 21 and 24 segregates exhibited significant positive and negative inbreeding depression, respectively. The significant positive depression ranged from 2.26 per cent to 18.75 per cent, while negative from -2.79 per cent to -18.23 per cent. The highest inbreeding depression was exhibited by the cross BAUT-1 x TKG-9-86 followed by Mrug-1 x TKG-9-86 (16.02%) and AT-17 x AHT-55 (15.42%).

Days to first flowering (Table-3) :

Out of 45 crosses, 13 had significant negative heterosis, whereas 26 crosses had significant positive heterosis. Highest heterosis in desired (negative) direction was expressed by RT-125 x TKG-9-86 (-6.79%) followed by Tapi x AHT-55 (-6.56%) and Mrug-1 x PY-57 (-3.62%). Thirty six hybrids manifested significant heterobeltiosis, out of which 32 hybrids showed significant positive and only four had significant negative values, viz., Tapi x AHT-55 (-5.78%), RT-125 x BAUT-1 (-5.56%), Mrug-1 x PY-57 (-4.88%) and G.Til-1 x OMT-10 (-4.35%). All hybrids showed significant positive economic heterosis, except viz., BAUT-1 x RT-123 (0.00%) and RT-125 x TKG-9-86 (0.97%).

In F_2, 13 and 20 crosses had significant negative and positive inbreeding depression, respectively. Considering early flowering in favourable direction highest inbreeding depression was observed in cross Tapi x BAUT-1 (-21.43%)

followed by RT-125 x TKG-9-86 (-11.65%) and Mrug-1 x RT-125 (-7.46%).

Days to 50 per cent flowering (Table-4) :

Out of 45 crosses, 13 crosses had significant heterosis (negative) for early flowering of which highest heterotic value was expressed by Tapi x AHT-55 (-6.37%) followed by AHT-55 x RT-125 (-4.88%) and Mrug-1 x PY-57 (-3.62%). Thirty nine crosses manifested significant heterobeltiosis which ranged from -6.01 per cent (Tapi x AHT-55) to 21.24 per cent (PY-57 x RT-125). Above mentioned three higher heterotic crosses for early flowering also depicted higher heterobeltiosis. Significant positive economic heterosis was observed in all hybrids ranging from 1.75 per cent (RT-125 x BAUT-1) to 25.64 per cent (Mrug-1 x G.Til-1), while none of the hybrid had favourable effects.

Inbreeding depression in positive and negative direction was in 28 and 14 crosses, respectively. Maximum inbreeding depression in positive direction was recorded by the cross Tapi x BAUT-1 (13.09%), while the cross AT-17 x OMT-10 (-7.74%) revealed maximum in negative direction followed by Mrug-1 x TKG-9-86 (-7.71%) and Tapi x AT-17 (-6.98%).

Days to maturity (Table-4) :

Considering early maturity as desired direction, 18 crosses had significant negative effects of which cross RT-125 x BAUT-1 (-6.80%) expressed highest favourable effect followed

Table 4. Heterosis over mid parent, better parent, check parent (economic) and inbreeding depression in per cent for days to 50 per cent flowering and days to maturity

Crosses	Days to 50 per cent flowering				Days to maturity			
	Heterosis			Inbreeding depression	Heterosis			Inbreeding depression
	Mid parent	Better parent	Economic		Mid parent	Better parent	Economic	
1	2	3	4	5	6	7	8	9
$P_1 \times P_2$	0.37	0.75	19.45**	-2.27**	-0.76	0.39	12.08**	3.85**
$P_1 \times P_2$	8.66*	15.00**	22.11**	-6.98**	2.72**	6.02**	13.80**	4.55**
$P_1 \times P_4$	2.75**	8.27**	15.93**	-1.56*	-1.92**	0.00	9.92**	-1.18**
$P_1 \times P_5$	-6.37**	-6.01**	10.62**	-0.79	-2.51**	0.00	8.62**	-1.19**
$P_1 \times P_6$	-1.82**	0.75	19.46**	-2.61**	-2.61**	-1.51**	12.50**	0.00
$P_1 \times P_7$	8.50**	18.58**	18.58**	-1.52*	-2.61**	9.91**	9.92**	-4.32**
$P_1 \times P_8$	-2.70**	0.80	11.49**	13.09**	-0.38	1.98**	11.21**	-3.10**
$P_1 \times P_9$	-0.38	0.76	16.80**	5.03**	-2.89**	-0.79*	8.63**	-3.96**
$P_1 \times P_{10}$	0.00	1.54*	16.80**	5.72**	-1.57**	2.88**	7.76**	-2.40**
$P_2 \times P_3$	3.53**	10.00**	16.80**	2.22**	-0.39	2.41**	9.92**	1.56**
$P_2 \times P_4$	10.94**	17.36**	25.64**	-1.41*	-0.00	0.78*	10.78**	0.40
$P_2 \times P_5$	-1.49*	-0.75	16.80**	6.38**	-0.19	1.19**	9.92**	2.74**
$P_2 \times P_6$	-3.62**	-1.48*	17.68**	1.49*	-1.51**	0.77*	12.50**	-1.53**
$P_2 \times P_7$	-1.61*	7.96**	7.96**	8.95**	-0.20	5.60**	5.61**	1.64**
$P_2 \times P_8$	3.85**	8.00**	19.46**	4.25**	-0.78	0.39	9.49**	-1.96**
$P_2 \times P_9$	5.26**	6.87**	23.89**	-7.71**	1.36**	2.36**	12.08**	4.61**
$P_2 \times P_{10}$	2.64**	4.61**	20.33**	-3.02**	-0.79*	2.47**	7.33**	-2.01**
$P_3 \times P_4$	6.22**	6.67**	13.27**	3.74**	0.00	1.21**	8.62**	-0.80
$P_3 \times P_5$	1.98**	7.50**	14.15**	2.27**	-0.60	0.00	7.33**	-0.81*
$P_3 \times P_6$	1.15	10.00**	14.16**	2.22**	0.00	4.42**	12.08**	0.39
$P_3 \times P_7$	9.01**	12.39**	16.80**	-0.79	-1.45**	2.16**	2.16**	-2.53**
$P_3 \times P_8$	4.49**	6.67**	12.37**	2.29**	0.00	0.80*	8.20**	-1.20**
$P_3 \times P_9$	4.38**	9.17**	13.27**	2.24**	0.59	1.61**	8.62**	-0.80
$P_3 \times P_{10}$	11.20**	15.83**	22.99**	-7.74**	1.22**	2.47**	7.33**	-0.81*
$P_4 \times P_5$	-1.58*	3.31**	10.62**	10.71**	-4.93**	-4.37**	3.89**	-7.06**
$P_4 \times P_6$	4.58**	13.22**	21.24**	0.72	0.38	3.53**	13.80**	1.90**
$P_4 \times P_7$	5.13**	8.85**	8.84**	0.80	-1.03**	3.88**	3.88**	2.07**
$P_4 \times P_8$	4.88**	2.64**	14.15**	5.14**	0.39	0.79*	9.92**	-0.39

Contd. Table 4.

1	2	3	4	5	6	7	8	9
$P_4 \times P_9$	8.73**	13.22**	21.23**	-2.24**	0.19	0.39	9.92**	0.79
$P_4 \times P_{10}$	-1.20	2.48**	9.72**	-1.62*	-1.60**	0.82*	5.61**	0.00
$P_5 \times P_6$	-1.46*	1.50*	19.45**	1.46*	-1.34**	2.38**	11.21**	-0.78
$P_5 \times P_7$	-4.88**	-4.41**	3.53**	4.71**	-0.41	3.88**	3.88**	1.24**
$P_5 \times P_8$	3.87**	7.20**	18.58**	-2.29**	-0.20	0.00	8.63**	0.80
$P_5 \times P_9$	0.76	1.53*	17.69**	2.93**	1.98**	2.38**	11.21**	1.55**
$P_5 \times P_{10}$	-2.66**	1.53*	13.27**	3.02**	1.82**	3.70**	8.63**	0.80
$P_6 \times P_7$	7.87**	21.24**	21.24**	-2.24**	-2.19**	6.03**	6.04**	-0.82**
$P_6 \times P_8$	-0.75	5.60**	16.80**	8.96**	-0.38	3.95**	13.37**	-1.14**
$P_6 \times P_9$	4.41**	8.40**	25.64**	-1.66*	-2.86**	0.39	9.92**	0.79
$P_6 \times P_{10}$	2.58**	6.92**	22.99**	-0.72	1.85**	7.82**	12.93**	1.52**
$P_7 \times P_8$	-3.36**	1.71*	1.75*	3.38**	-6.80**	-2.57**	-2.59**	-3.11**
$P_7 \times P_9$	-3.28**	4.42**	4.41**	5.62**	-4.53**	0.00	0.00	1.29**
$P_7 \times P_{10}$	2.88**	10.62**	10.62**	6.00**	-1.05**	1.29**	1.29**	-1.28**
$P_8 \times P_9$	-3.13**	-0.81	9.72**	10.15**	-0.18	0.00	9.05**	-2.37**
$P_8 \times P_{10}$	9.02**	11.20**	22.99**	0.73	2.42**	0.11	9.49**	1.58**
$P_9 \times P_{10}$	4.98**	5.39**	21.24**	0.72	0.60	2.88**	7.76**	-2.40**
S.Em	0.52	0.52	0.52	0.50	0.24	0.24	0.24	0.29
CD at 5%	1.27	1.47	1.47	1.38	0.60	0.69	0.69	0.80
CD at 1%	1.68	1.94	1.94	1.81	0.79	0.91	0.91	1.05

* Significant at 5 per cent level
** Significant at 1 per cent level

P_1 = Tapi, P_2 = Mrug-1, P_3 = AT-17, P_4 = Gujarat Til-1, P_5 = AHT-55, P_6 = PY-57, P_7 = RT-125,

P_8 = BAUT-1, P_9 = TKG-9-86, P_{10} = OMT-10.

by G.Til-1 x AHT-55 (-4.93%) and RT-125 x TKG-9-86 (-4.53%). With regards to heterobeltiosis, 35 hybrids showed significant values ranging from -4.37 per cent (G.Til-1 x AHT-55) to 9.91 per cent (Tapi x RT-125). Out of 45 hybrids, four hybrids exhibited significant favourable heterobeltiosis viz., G.Til-1 x AHT-55 (-4.93%), RT-125 x BAUT-1 (-2.19%), Tapi x PY-57 (-1.51%) and Tapi x OMT-10 (-0.79%) for the trait. Considering economic heterosis, all F_1 crosses showed significant positive values, except cross RT-125 x BAUT-1 (-2.59%).

In F_2, 20 crosses expressed significant negative inbreeding depression, considering early maturity. Highest inbreeding depression was observed in cross G.Til-1 x AHT-55 (-7.06%) followed by Tapi x RT-125 (-4.32%) and Tapi x TKG-9-86 (-3.96%). The lowest inbreeding was expressed by the cross Mrug-1 x TKG-9-86 (4.61%).

Length of reproductive stem (Table-5) :

Out of 45 hybrids, 39 differed significantly from their mid parental values, along with 26 hybrids with positive and 13 with negative effects. The positive values varied from 1.41 per cent (G.Til-1 x RT-125) to 26.25 per cent (Tapi x BAUT-1). The maximum cross was followed by Tapi x AHT-55 (20.48%) and Mrug-1 x RT-125 (19.88%). Significant positive heterobeltiosis was observed in 16 crosses of which highest positive heterosis was indicated by cross Tapi x AT-17 (18.66%) followed by Tapi x AHT-55 (17.37%) and Mrug-1 x RT-125 (15.69%). Twenty nine crosses recorded significant economic heterosis of which 15

Table 5. Heterosis over mid parent, better parent, check parent (economic) and inbreeding depression in per cent for length of reproductive stem and plant height to maturity.

Crosses	Length of reproductive stem				Plant height to maturity			
	Heterosis			Inbreeding depression	Heterosis			Inbreeding depression
	Mid parent	Better parent	Economic		Mid parent	Better parent	Economic	
1	2	3	4	5	6	7	8	9
$P_1 \times P_2$	16.43**	15.49**	7.42**	10.96**	15.56**	10.88**	26.17**	18.97**
$P_1 \times P_3$	18.80**	18.66**	8.85**	19.85**	4.96	3.09	7.82**	12.79**
$P_1 \times P_4$	9.06**	5.79**	2.30	12.80**	8.42**	6.51**	15.44**	8.79**
$P_1 \times P_5$	20.48**	17.37**	13.27**	19.57**	20.50**	12.87**	18.03**	18.78
$P_1 \times P_6$	10.26**	2.76	8.86**	11.28**	3.63	-4.89*	19.04**	1.90
$P_1 \times P_7$	-1.97	-6.13**	-6.12**	-8.21**	1.04	-1.17	3.35	-14.10**
$P_1 \times P_8$	26.25**	12.09**	32.25**	11.61**	9.39**	5.00*	19.40**	2.87
$P_1 \times P_9$	9.01**	2.26	-6.42**	6.41**	2.57	-2.55	1.91	5.01*
$P_1 \times P_{10}$	5.75**	3.82*	-4.99**	16.73**	3.87*	-2.61	1.84	12.30**
$P_2 \times P_3$	-3.47*	-4.14**	-10.85**	-1.99	-6.82**	-12.11**	0.00	-7.82**
$P_2 \times P_4$	11.72**	9.23**	6.36**	22.68**	-4.18*	-6.45**	6.44**	10.07**
$P_2 \times P_5$	1.77	-0.07	-3.56*	10.81**	4.39*	-5.91**	7.06**	9.25**
$P_2 \times P_6$	2.40	-3.84*	1.86	19.05**	-11.20**	-15.24**	6.09**	-1.28
$P_2 \times P_7$	19.88**	15.69**	15.71**	17.09**	-4.96*	-10.72**	1.59	-2.34
$P_2 \times P_8$	-5.34**	-15.36**	-0.13	7.37**	-7.40**	-7.43**	5.33*	1.61
$P_2 \times P_9$	14.33**	6.44**	-0.98	15.99**	9.10**	-0.32	13.43**	13.08**
$P_2 \times P_{10}$	16.53**	13.49**	5.56**	9.79**	13.41**	2.31	16.41**	13.82**
$P_3 \times P_4$	13.09**	9.82**	6.93**	18.35**	-12.09**	-15.14**	-8.01**	6.26**
$P_3 \times P_5$	4.28**	1.70	-1.84	16.72**	-2.79	-7.38**	-6.59**	11.82**
$P_3 \times P_6$	9.42**	2.09	8.13**	9.30**	2.02	-7.88**	15.30**	3.53
$P_3 \times P_7$	-3.12*	-7.13**	-7.13**	8.82**	-3.30	-3.71	-2.87	7.11**
$P_3 \times P_8$	-8.77**	-18.92**	-4.34**	-1.79	-2.94	-8.42**	4.15	2.70
$P_3 \times P_9$	13.77**	6.61**	-2.20	5.54**	8.51**	4.89*	5.79*	0.13
$P_3 \times P_{10}$	12.69**	10.50**	1.37	12.81**	-8.04**	-12.31**	-11.55**	-12.05**
$P_4 \times P_5$	-3.38*	-3.81*	-6.33**	1.23	-4.65*	-12.15**	-4.78*	-10.09**
$P_4 \times P_6$	-9.75**	-13.40**	-8.26**	-13.66**	-16.98**	-22.54**	-3.06	-19.02**
$P_4 \times P_7$	1.41	0.07	0.09	6.51**	0.22	-3.65	4.43	9.34**
$P_4 \times P_8$	-6.32**	-14.51**	0.86	10.61**	-2.93	-5.22*	7.78**	1.86

Contd.

Contd. Table 5.

1	2	3	4	5	6	7	8	9
$P_4 \times P_9$	4 14**	-5.05**	-7 62**	17.07**	16.31**	8.67**	18.68**	21.33
$P_4 \times P_{10}$	16.65**	11.13**	8.22**	22.86**	-0.70	-8.43**	-0.76	9.90**
$P_5 \times P_6$	-4.23**	-8.48**	-3.06	4.86**	-1.43	-14.75**	6.69**	4.65*
$P_5 \times P_7$	3.08*	1.28	1.28	11.05**	7.81**	3.13	-7.66**	6.83**
$P_5 \times P_8$	-5.55**	-14.15**	1.28	6.34**	-1.76	-11.42**	0.72	1.01
$P_5 \times P_9$	-11.18**	-18.69**	-21.53**	-4.99**	-0.58	-2.06	-7.81**	-2.89
$P_5 \times P_{10}$	-0.81	-5.10**	-8.41**	14.56**	-0.14	-0.24	-8.70**	-3.23
$P_6 \times P_7$	-3.43*	-6.13**	-0.56	13.99**	4.78*	-5.75**	17.96**	13.49**
$P_6 \times P_8$	11.56**	5.86**	24.91**	26.90**	14.65**	9.40**	36.92**	22.31**
$P_6 \times P_9$	4.41**	-8.28**	-2.85	10.86**	2.99	-9.78**	12.92**	15.33**
$P_6 \times P_{10}$	-3.27*	-11.38**	-6.12**	-3.33*	-0.91	-14.23**	7.34**	-11.62**
$P_7 \times P_8$	-4.19**	-11.49**	4.43**	-10.96**	-4.23*	-10.00**	2.34	1.97
$P_7 \times P_9$	16.86**	5.28**	5.29	16.00**	6.17**	3.06	3.07	13.87**
$P_7 \times P_{10}$	9.09**	2.64	2.65	15.15**	4.70*	0.25	0.26	-1.79
$P_8 \times P_9$	14.47**	-3.87**	13.42**	11.64**	6.86**	-2.34	11.05**	5.61*
$P_8 \times P_{10}$	10.17**	-3.75**	13.56**	5.28**	7.77**	-2.75	10.58**	3.85
$P_9 \times P_{10}$	-2.29	-6.72**	-17.76**	-8.07**	-0.99	-2.37	-8.09**	-12.62**
S.Em	1.09	1.09	1.09	0.98	1.57	1.57	1.57	1.58
CD at 5%	2.66	3.08	3.08	2.72	3.83	4.43	4.43	4.38
CD at 1%	3.52	4.06	4.06	3.58	5.06	5.84	5.84	5.76

 * Significant at 5 per cent level
** Significant at 1 per cent level

P_1 = Tapi, P_2 = Mrug-1. P_3 = AT-17 P_4 = Gujarat Til-1, P_5 = AHT-55, P_6 = PY-57, P_7 = RT-125,

P_8 = BAUT-1, P_9 = TKG-9-86, P_{10} = OMT-10.

crosses had positive values. Highest significant economic cross was Tapi x BAUT-1 (32.25%) followed by PY-57 x BAUT-1 (24.91%) and Mrug-1 x RT-125 (15.71%).

Significant inbreeding depression was recorded in 42 F_2's of which highest value was observed in cross PY-57 x BAUT-1 (26.90%) followed by G.Til-1 x OMT-10 (22.86%) and Mrug-1 x G.Til-1 (22.68%), whereas lowest inbreeding depression was observed in cross G.Til-1 x PY-57 (-13.66%).

Plant height to maturity (Table-5) :

Eighteen hybrids had significant positive heterosis, whereas ten hybrids expressed negative heterosis, of which lowest values was for the cross G.Til-1 x PY-57 (-16.98%) and highest heterotic cross was Tapi x AHT-55 (20.50%) followed by G.Til-1 x TKG-9-86 (16.31%) and Tapi x Mrug-1 (15.56%). Twenty nine hybrids manifested significant heterobeltiotic effect of which only six had positive values. The top cross for heterobeltiosis was Tapi x AHT-55 (12.87%) followed by Tapi x Mrug-1 (10.88%) and PY-57 x BAUT-1 (9.41%) for tallness. Significant economic heterosis was observed in 31 F_1 combinations, of which eight crosses were negative and 23 had positive values. Cross PY-57 x BAUT-1 (36.92%) was best for useful economic heterosis followed by Tapi x Mrug-1 (26.17%) and Tapi x PY-57 (19.04%).

In F_2, 23 crosses showed significant positive inbreeding depression of which highest depression was 22.31 per cent (PY-57 x BAUT-1) followed by G.Til-1 x TKG-9-86

(21.33%) and Tapi x Mrug-1 (18.97%), whereas lowest was in cross G.Til-1 x PY-57 with -19.02 per cent.

Number of branches per plant (Table-6) :

A perusal of data revealed that 33 crosses recorded significant positive heterosis. The maximum heterosis was recorded in the cross AHT-55 x TKG-9-86 (71.65%) followed by AT-17 x AHT-55 (67.94%) and AT-17 x TKG-9-86 (67.47%). Twenty and 24 crosses exhibited significant positive and negative heterobeltiosis, respectively. The cross AHT-55 x TKG-9-86 (60.53%) had highest value followed by AT-17 x TKG-9-86 (50.00%) and AT-17 x AHT-55 (41.67%), whereas cross G.Til-1 x PY-57 (-60.00%) had lowest value. Fourty four $F_1's$ had significant economic heterosis, among these 22 crosses manifested significant positive values. Cross Mrug-1 x OMT-10 (37.67%) had highest economic heterosis followed by PY-57 x BAUT-1 (33.48%) and Mrug-1 x RT-125 (31.74%).

All the $F_2's$ significantly deviated from their respective $F_1's$, except cross AT-17 x BAUT-1 of which 39 crosses had significant positive and only five had significant negative inbreeding depression. Highest depression was recorded in cross AHT-55 x BAUT-1 (55.91%) followed by PY-57 x BAUT-1 (52.12%) and AT-17 x AHT-55 (51.54%) for the trait.

Number of capsules per plant (Table-6) :

Significant heterosis was recorded in all the crosses for the trait. Out of the 39 positive crosses, the cross AT-17

Table 6. Heterosis over **mid** parent, better parent, check parent (economic) and **inbreeding** depression in per cent for number of branches per plant and number of capsules per plant

Crosses	Number of branches per plant				Number of capsules per plant			
	Heterosis			Inbreeding	Heterosis			Inbreeding
	Mid parent	Better parent	Economic	depression	Mid parent	Better parent	Economic	depression
1	2	3	4	5	6	7	8	9
$P_1 \times P_2$	27.69**	18.57**	20.43**	42.24**	7.28**	5.27**	-21.85**	23.69**
$P_1 \times P_3$	11.11**	0.00	-17.74**	10.48**	11.73**	10.04**	-21.39**	13.71**
$P_1 \times P_4$	7.56**	6.67**	-7.39**	40.38**	16.95**	14.87**	-16.15**	35.63**
$P_1 \times P_5$	50.54**	16.67**	1.30**	32.62**	9.70**	1.73**	-27.34**	10.77**
$P_1 \times P_6$	-31.85**	-38.67**	-33.48**	9.15**	17.53**	7.10**	-23.47**	22.68**
$P_1 \times P_7$	-13.18**	-18.84**	-18.69**	-6.95**	-13.57**	-25.90**	-25.93**	-9.27**
$P_1 \times P_8$	30.65**	26.56**	17.39**	48.15**	31.41**	11.14**	14.40**	33.82**
$P_1 \times P_9$	-6.12**	-23.33**	-33.48**	19.61**	7.74**	5.16**	-21.10**	8.54**
$P_1 \times P_{10}$	5.43**	-1.45**	-1.30**	14.98**	11.08**	-3.09**	-7.03**	13.97**
$P_2 \times P_3$	35.59**	14.28**	16.09**	25.09**	7.28**	3.70**	-23.01**	6.97**
$P_2 \times P_4$	24.03**	14.28**	16.09**	50.18**	15.25**	15.14**	-14.52**	28.37**
$P_2 \times P_5$	33.98**	-1.43**	0.00	46.52**	33.69**	21.82**	-9.57**	19.83**
$P_2 \times P_6$	7.59**	4.00**	13.04**	37.31**	25.73**	12.63**	-16.40**	17.77**
$P_2 \times P_7$	30.74**	30.00**	31.74**	25.08**	26.86**	10.53**	10.53**	14.72**
$P_2 \times P_8$	17.91**	12.86**	14.35**	32.70**	-13.28**	-25.48**	-23.01**	16.86**
$P_2 \times P_9$	-3.70**	-25.71**	24.78**	4.05*	12.88**	12.27**	-15.73**	17.73**
$P_2 \times P_{10}$	36.69**	35.71**	37.87**	46.37**	9.78**	-2.63**	-6.62**	26.20**
$P_3 \times P_4$	-15.89**	-23.73**	-34.78**	-2.00**	30.71**	26.47**	-6.28**	22.34**
$P_3 \times P_5$	67.90**	41.67**	-1.30**	51.54**	61.35**	51.77**	5.16**	37.00**
$P_3 \times P_6$	5.69**	-13.33**	-5.65**	15.67**	89.02**	74.68**	21.02**	37.58**
$P_3 \times P_7$	-2.56**	-17.39**	-17.39**	26.32**	5.34**	-10.83**	-10.86**	19.42**
$P_3 \times P_8$	-3.57**	-15.63**	-21.74**	0.00	12.64**	-5.91**	-2.79**	5.57**
$P_3 \times P_9$	67.44**	50.00**	4.35**	12.50**	110.61**	102.53**	51.98**	41.43**
$P_3 \times P_{10}$	23.08**	4.35**	4.35**	20.83**	-1.55**	-15.23**	-18.68**	0.87**
$P_4 \times P_5$	34.78**	5.08**	17.39**	45.56**	86.57**	70.17**	26.05**	35.46**
$P_4 \times P_6$	-55.22**	-60.00**	-56.52**	-75.10**	32.88**	19.13**	-11.74**	9.81**
$P_4 \times P_7$	1.56**	-5.79**	-5.65**	3.23**	15.26**	0.33	0.33	2.61**
$P_4 \times P_8$	15.45**	10.94**	3.04**	36.71**	38.06**	18.53**	22.43**	40.48**

Contd.

8

Contd. Table 6.

1	2	3	4	5	6	7	8	9
$P_4 \times P_9$	15.46**	-5.09**	-18.70**	25.13**	10.11**	9.41**	-17.94**	18.20**
$P_4 \times P_{10}$	-4.69**	-11.59**	-11.74**	26.11**	20.34**	6.64**	2.29**	8.67**
$P_5 \times P_6$	14.81**	-17.33**	-10.00**	3.38**	34.90**	32.37**	-19.78**	11.78**
$P_5 \times P_7$	39.22**	2.90**	3.04**	32.49**	35.49**	9.12**	9.11**	14.99**
$P_5 \times P_8$	36.08**	3.13**	-4.35**	55.91**	21.38**	-3.43**	-0.25	15.98**
$P_5 \times P_9$	71.83**	60.53**	-11.74**	42.36**	4.89**	-4.88**	-28.63**	14.46**
$P_5 \times P_{10}$	-23.53**	-43.48**	-43.48**	-46.15**	-12.02**	-28.46**	-30.96**	0.84**
$P_6 \times P_7$	0.00	-4.00**	4.35**	44.58**	17.43**	16.63**	-6.78**	29.51**
$P_6 \times P_8$	32.37**	22.67**	33.48**	52.12**	-3.67**	-24.47**	-21.93**	5.86**
$P_6 \times P_9$	27.43**	-4.00**	4.35**	34.58**	22.55**	9.27**	-18.02**	1.07**
$P_6 \times P_{10}$	-12.50**	-16.00**	-8.70**	4.76**	38.58**	11.74**	7.20**	20.46**
$P_7 \times P_8$	6.77**	2.90**	3.04**	10.13**	9.11**	7.63**	10.90**	4.20**
$P_7 \times P_9$	30.84**	1.45**	1.30**	39.91**	15.99**	1.53**	1.50**	24.43**
$P_7 \times P_{10}$	27.54**	27.54**	27.39**	22.53**	34.08**	31.54**	31.34**	16.35**
$P_8 \times P_9$	49.02**	18.75**	10.00**	43.48**	51.28**	30.59**	34.91**	49.44**
$P_8 \times P_{10}$	29.32**	24.64**	24.78**	29.27**	-10.03**	-13.29**	-10.36**	14.02**
$P_9 \times P_{10}$	12.15**	-13.04**	-13.04**	8.50**	-15.07**	-24.32**	-27.38**	12.66**
S.Em	0.07	0.07	0.07	0.08	0.26	0.26	0.26	0.22
CD at 5%	0.17	0.19	0.19	0.22	0.64	0.73	0.73	0.61
CD at 1%	0.22	0.25	0.25	0.29	0.84	0.97	0.97	0.81

* Significant at 5% level
** Significant at 1% level

P_1 = Tapi, P_2 = Mrug-1, P_3 = AT-17, P_4 = Gujarat Til-1, P_5 = AHT-55, P_6 = PY-57, P_7 = RT-125,

P_8 = BAUT-1, P_9 = TKG-9-86, P_{10} = OMT-10.

x TKG-9-86 (110.61%) recorded highest value followed by AT-17 x PY-57 (89.02%) and G.Til-1 x AHT-55 (86.57%). The above higher heterotic crosses also exhibited higher effects of heterobeltiosis.

Fourty three crosses recorded significant economic heterosis, of which 15 crosses had positive values. Lowest economic heterosis was observed in cross AHT-55 x OMT-10 (-30.96%). The cross AT-17 x TKG-9-86 (51.89%) ranked first followed by BAUT-1 x TKG-9-86 (34.91%) and RT-125 x OMT-10 (31.34%).

In F_2, all the crosses expressed significant positive inbreeding depression except cross Tapi x RT-125 (-9.27%), of which cross BAUT-1 x TKG-9-86 (49.44%) recorded highest values followed by AT-17 x TKG-9-86 (41.43%) and G.Til-1 x BAUT-1 (40.48%) for the number of capsules per plant.

Length of capsule (Table-7) :

Thirty seven crosses recorded positive significant heterosis. Highest cross was AHT-55 x OMT-10 (9.85%) followed by RT-125 x OMT-10 (9.13%) and Tapi x Mrug-1 (8.36%) and lowest value was of -3.72 per cent in the cross G.Til-1 x TKG-9-86. Significant heterobeltiosis was observed in all the F_1 crosses, which ranged from -5.25 per cent (G.Til-1 x TKG-9-86) to 7.32 per cent (AT-17 x RT-125). The maximum cross was followed by Mrug-1 x RT-125 (7.19%) and Tapi x Mrug-1 (6.77%). Among all the significant economic heterosis crosses the cross PY-57 x BAUT-1 (10.61%) recorded highest values

Table 7. Heterosis over mid parent, better parent, check parent (economic) and inbreeding depression in per cent for length of capsule and number of grains per capsule

Crosses	Length of capsule				Number of grains per capsule			
	Heterosis			Inbreeding depression	Heterosis			Inbreeding depression
	Mid parent	Better parent	Economic		Mid parent	Better parent	Economic	
$P_1 \times P_2$	8.36**	6.77**	5.68**	7.53**	9.43**	8.46**	5.16**	5.72**
$P_1 \times P_3$	7.66**	4.59**	6.44**	3.20**	-2.15**	-3.06**	-4.22**	-1.22**
$P_1 \times P_4$	7.16**	3.29**	6.82**	7.80**	1.15**	-1.99**	1.32**	-0.83**
$P_1 \times P_5$	7.01**	4.65**	4.92**	3.61**	2.61**	-2.06**	4.48**	10.53**
$P_1 \times P_6$	3.08**	-3.13**	5.68**	2.15**	-5.16**	-6.71**	-6.50**	5.20**
$P_1 \times P_7$	0.39**	-1.64**	-1.52**	-4.23**	-1.26**	-2.76**	-2.77**	-2.35**
$P_1 \times P_8$	3.07**	0.37**	1.52**	8.58**	10.77**	9.04**	5.72**	8.87**
$P_1 \times P_9$	2.77**	0.61**	0.76**	1.13**	-1.84**	-4.18**	-2.46**	6.45**
$P_1 \times P_{10}$	1.41**	-0.53**	-4.55**	6.35**	1.07**	-2.17**	-5.14**	4.41**
$P_2 \times P_3$	5.73**	4.22**	6.06**	6.07**	5.54**	3.63**	2.33**	3.80**
$P_2 \times P_4$	2.99**	0.73**	4.17**	7.27**	8.31**	4.05**	7.55**	10.39**
$P_2 \times P_5$	0.89**	0.13**	0.38**	-4.15**	3.68**	-1.88**	4.66**	0.36**
$P_2 \times P_6$	4.80**	-0.11**	9.09**	7.99**	-1.02**	-3.49**	-3.26**	0.00
$P_2 \times P_7$	7.81**	7.19**	7.20**	6.01**	8.92**	6.33**	6.33**	2.98**
$P_2 \times P_8$	1.83**	0.62**	1.89**	1.86**	10.81**	10.05**	4.80**	5.87**
$P_2 \times P_9$	1.90**	1.26**	1.52**	4.85**	1.68**	-1.60**	0.31**	-4.42**
$P_2 \times P_{10}$	-0.26**	-3.58**	-4.92**	-2.39**	6.61**	4.10**	-0.87**	3.57**
$P_3 \times P_4$	-1.05**	-1.83**	1.52**	1.87**	-3.81**	-5.93**	-2.77**	1.81**
$P_3 \times P_5$	1.19**	0.49**	2.27**	1.86**	-3.56**	-7.12**	0.92**	5.04**
$P_3 \times P_6$	2.64**	-0.81**	8.33**	3.15**	-2.39**	-3.09**	-2.86**	1.63**
$P_3 \times P_7$	8.26**	7.32**	9.09**	9.72**	-5.85**	-6.41**	-6.42**	0.08
$P_3 \times P_8$	1.71**	1.49**	3.41**	1.47**	-2.99**	-5.38**	-6.51**	-0.08
$P_3 \times P_9$	-1.31**	-2.11**	-0.38**	-2.66**	0.73**	-0.75**	1.04**	-4.17**
$P_3 \times P_{10}$	7.22**	2.23**	0.04**	4.73**	5.13**	0.84**	-0.37**	-0.86**
$P_4 \times P_5$	5.08**	3.54**	7.20**	0.00	-7.67**	-9.10**	-3.05**	-2.36**
$P_4 \times P_6$	3.03**	0.35**	9.47**	-1.04**	-6.45**	-7.87**	-4.77**	-2.22**
$P_4 \times P_7$	5.03**	3.30**	6.82**	-3.90**	-2.89**	-4.47**	-1.26**	-1.90**
$P_4 \times P_8$	1.91**	0.86**	4.17**	-1.09**	4.83**	0.05	3.42**	2.09**

Contd. Table 7.

1	2	3	4	5	6	7	8	9
$P_4 \times P_9$	-3.72**	-5.25**	-1.89**	-1.16**	-6.63**	-7.33**	-4.21**	0.05
$P_4 \times P_{10}$	7.23**	1.47**	4.92**	6.50**	-2.35**	-8.31**	-5.22**	-2.13**
$P_5 \times P_6$	2.11**	-1.97**	6.82**	2.84**	-4.48**	-7.56**	-1.18**	0.17**
$P_5 \times P_7$	5.48**	5.28**	5.68**	9.32**	-5.35**	-8.31**	-2.19**	4.40*
$P_5 \times P_8$	4.82**	4.36**	5.68**	5.73*	0.06	-5.91**	0.36**	-2.23**
$P_5 \times P_9$	-0.38**	-0.50**	0.00	-0.38*	-6.89**	-9.02**	-2.95**	8.01**
$P_5 \times P_{10}$	9.83**	5.41**	5.68**	8.60**	-3.19**	-10.42**	-4.45**	-1.44**
$P_6 \times P_7$	0.60**	-3.59**	5.30**	-3.60**	-9.37**	-9.48**	-9.26**	0.86**
$P_6 \times P_8$	5.28**	1.51**	10.61**	11.99**	-4.89**	-7.88**	-7.66**	0.89**
$P_6 \times P_9$	-0.30**	-4.39**	4.17**	3.27**	-4.50**	-5.24**	-3.53**	9.07**
$P_6 \times P_{10}$	6.33**	-1.85**	7.20**	4.24**	-2.51**	-7.13**	-6.92**	-1.97**
$P_7 \times P_8$	3.89**	3.24**	4.55**	2.17**	-0.13	-3.16**	-3.16**	1.93**
$P_7 \times P_9$	-0.57**	-0.63**	-0.38**	4.56**	-7.28**	-8.10**	-6.45**	6.11**
$P_7 \times P_{10}$	9.13**	4.92**	4.92**	9.39**	2.18**	-2.54**	-2.55**	-1.12**
$P_8 \times P_9$	-0.31**	-0.87**	0.38**	3.77**	3.40**	-0.59**	1.20**	2.38**
$P_8 \times P_{10}$	4.50**	-0.13**	1.14**	-0.75**	11.42**	9.52**	2.88**	6.92**
$P_9 \times P_{10}$	1.71**	-2.27**	-2.27**	1.55**	-7.46**	-12.49**	-10.91**	-9.12**
S.Em	0.010	0.010	0.010	0.011	0.05	0.05	0.05	0.05
CD at 5%	0.014	0.016	0.016	0.030	0.13	0.15	0.15	0.13
CD at 1%	0.019	0.022	0.022	0.040	0.17	0.19	0.19	0.17

* Significant at 5 per cent level
** Significant at 1 per cent level

P_1 = Tapi, P_2 = Mrug-1, P_3 = AT-17, P_4 = Gujarat Til-1, P_5 = AHT-57, P_6 = PY-57, P_7 = RT-125,

P_8 = BAUT-1, P_9 = TKG-9-86, P_{10} = OMT-10.

followed by RT-17 x RT-125 (9.09%) and Mrug-1 x PY-57 (9.09%), whereas lowest cross was Mrug-1 x OMT-10 (-4.92%).

In F_2 segregating generation, 33 and 11 crosses observed significant positive and negative inbreeding depression, respectively. Maximum inbreeding depression was in the cross PY-57 x BAUT-1 (11.99%) followed by AT-17 x RT-125 (9.72%) and RT-125 x OMT-10 (9.39%) for the trait.

Number of grains per capsule (Table-7) :

Fourty three hybrids showed significant heterosis, of which 25 and 18 had negative and positive values, respectively, ranging from -9.37 per cent (PY-57 x RT-125) to 11.42 per cent (BAUT-1 x OMT-10). Other hybrids with higher values were Mrug-1 x BAUT-1 (10.81%) and Tapi x BAUT-1 (10.77%). As regards heterobeltiosis, 10 hybrids revealed significant positive and 34 hybrids had significant negative values which differed from -12.49 per cent (TKG-9-86 x OMT-10) to 10.05 per cent (Mrug-1 x BAUT-1). Twenty nine crosses had positive and 16 crosses expressed significant negative economic heterosis, of which crosses with lowest and highest values were TKG-9-86 x OMT-10 (-10.91%) and Mrug-1 x G.Til-1 (7.55%), respectively. The crosses Mrug-1 x RT-125 (6.33%) and Tapi x BAUT-1 (5.72%) also had higher values for the trait.

Significant inbreeding depression was noted in 42 F_2s of which 15 segregates had negative and 27 had positive effects. The range of the crosses was from -9.12 per cent

(TKG-9-86 x OMT-10) to 10.52 per cent (Tapi x AHT-55). High inbreeding depression cross was followed by crosses Mrug-1 x G.Til-1 (10.39%) and PY-57 x TKG-9-86 (9.07%).

Dry weight per plant (Table-8) :

Significant positive values were recorded in 39 crosses, whereas five crosses had significant negative values, ranging from -22.99 per cent (G.Til-1 x PY-57) to 79.63 per cent (AT-17 x TKG-9-86). Maximum heterotic cross was followed by Tapi x BAUT-1 (78.95%) and Tapi x TKG-9-86 (58.95%). These crosses also indicated high heterobeltiosis for the trait. All the hybrids had significant heterotic effects, however, only three of these expressed negative values.

In F_2, 39 segregates showed significant positive inbreeding depression, whereas, only five had significant negative values. Highest inbreeding depression was in the cross Tapi x G.Til-1 (53.32%) followed by Tapi x AT-17 (47.39%) and Mrug-1 x G.Til-1 (43.63%).

Grain yield per plant (Table-8) :

Data in the Table-8 revealed 1that 42 hybrids expressed significant positive heterosis, of which cross AT-17 x TKG-9-86 (83.24%) had highest value followed by BAUT-1 x TKG-9-86 (52.98%) and PY-57 x RT-125 (48.92%). Only three hybrids showed significant negative heterosis viz., Tapi x RT-125 (-28.35%), RT-125 x BAUT-1 and TKG-9-86 x OMT-10 (-2.87%). With regard to heterobeltiosis, 32 hybrids had

Table 8. Heterosis over mid parent, better parent, check parent (economic) and inbreeding depression in per cent for dry weight per plant and grain yield per plant

Crosses	Dry weight per plant (g)				Grain yield per plant (g)			
	Heterosis			Inbreeding depression	Heterosis			Inbreeding depression
	Mid parent	Better parent	Economic		Mid parent	Better parent	Economic	
1	2	3	4	5	6	7	8	9
$P_1 \times P_2$	48.77**	27.48**	64.34**	37.87**	6.17**	1.84**	15.23**	23.73**
$P_1 \times P_3$	44.91**	44.08**	32.70**	47.79**	12.65**	-0.25**	3.52**	36.98**
$P_1 \times P_4$	46.86**	27.98**	58.65**	53.32**	33.78**	31.13**	41.80**	34.99**
$P_1 \times P_5$	12.94**	12.38**	3.38**	31.22**	2.54**	-8.88**	-5.08**	16.46**
$P_1 \times P_6$	14.44**	-5.35**	33.12**	11.25**	1.02**	-6.88**	-3.13**	33.87**
$P_1 \times P_7$	21.32**	16.54**	16.46**	5.62**	-28.35**	-29.79**	-26.95**	-24.60**
$P_1 \times P_8$	78.39**	43.91**	116.03**	27.44**	23.45**	19.88**	46.09**	36.36**
$P_1 \times P_9$	58.95**	57.07**	44.51**	37.52**	52.98**	23.78**	28.52**	28.89**
$P_1 \times P_{10}$	57.30**	53.30**	48.73**	29.36**	20.47**	9.76**	14.06**	20.22**
$P_2 \times P_3$	35.04**	15.16**	48.52**	37.07**	19.78**	2.30**	16.02**	22.22**
$P_2 \times P_4$	26.92**	24.43**	60.54**	43.63**	11.39**	8.97**	23.43**	37.34**
$P_2 \times P_5$	8.56**	-7.36**	19.41**	18.37**	16.57**	-0.12	13.28**	20.00**
$P_2 \times P_6$	11.55**	6.89**	50.42**	17.11**	2.02**	-9.31**	14.45**	11.79**
$P_2 \times P_7$	35.30**	20.06**	54.85**	33.51**	9.22**	2.76**	16.41**	11.41**
$P_2 \times P_8$	12.55**	4.64**	56.96**	40.99**	4.09**	0.43**	22.27**	19.17**
$P_2 \times P_9$	29.63**	9.98**	41.77**	29.76**	24.49**	-2.41**	10.55**	31.80**
$P_2 \times P_{10}$	38.87**	21.65**	56.96**	41.94**	29.79**	13.91**	28.91**	27.88**
$P_3 \times P_4$	3.27**	-10.44**	10.97**	18.63**	10.49**	-3.85**	4.30**	16.48**
$P_3 \times P_5$	27.03**	26.93**	15.61**	17.88**	20.94**	20.45**	-2.73**	26.10**
$P_3 \times P_6$	30.62**	7.55**	51.26**	13.25**	35.81**	29.97**	14.06**	32.88**
$P_3 \times P_7$	19.93**	14.57**	14.56**	29.47**	10.05**	-0.78**	0.78**	27.56**
$P_3 \times P_8$	5.89**	-14.95**	27.64**	-8.76**	14.05**	-5.45**	15.23**	2.71**
$P_3 \times P_9$	79.63**	48.68**	35.23**	15.29**	83.24**	65.09**	32.42**	22.42**
$P_3 \times P_{10}$	-2.13**	-5.15**	-8.02**	-4.36**	22.39**	18.57**	1.56**	11.15**
$P_4 \times P_5$	12.56**	-2.33**	21.10**	17.60**	33.24**	16.35**	26.17**	30.34**
$P_4 \times P_6$	-22.99**	-27.58**	1.90**	-8.07**	17.66**	6.49**	15.23**	21.02**
$P_4 \times P_7$	-4.37**	-13.62**	6.96**	6.31**	11.70**	7.33**	16.41**	5.03**
$P_4 \times P_8$	0.26	-8.48**	37.34**	13.82**	9.62**	3.53**	26.17**	26.62**

Contd. Table 8.

1	2	3	4	5	6	7	8	9
$P_4 \times P_9$	34.15**	15.72**	43.46**	38.23**	26.24**	0.60**	8.98**	33.33**
$P_4 \times P_{10}$	5.82**	-5.68**	16.88**	-10.11**	30.42**	16.71**	26.56**	28.46**
$P_5 \times P_6$	-15.74**	-30.58**	-2.32**	-37.80**	11.35**	6.97**	-6.25**	23.33**
$P_5 \times P_7$	7.84**	3.09**	2.95**	1.64**	25.07**	13.17**	12.89**	21.45**
$P_5 \times P_8$	3.85**	-16.54**	25.31**	29.12**	23.31**	2.56**	25.00**	15.00**
$P_5 \times P_9$	26.73**	25.85**	14.76**	18.01**	13.00**	1.45**	-17.98**	7.62**
$P_5 \times P_{10}$	15.81**	12.33**	8.86**	0.19	3.60**	0.76**	-13.67**	7.69**
$P_6 \times P_7$	25.95**	7.69**	51.48**	28.41**	48.92**	39,89**	39.84**	45.25**
$P_6 \times P_8$	19.61**	15.88**	73.83**	31.43**	-10.06**	-22.65**	-5.86**	6.22**
$P_6 \times P_9$	3.87**	-14.89**	19.83**	-1.06**	5.14**	-8.90**	-19.92**	-16.09**
$P_6 \times P_{10}$	34.56**	13.64**	59.91**	16.36**	28.78**	27.15**	11.72**	19.93**
$P_7 \times P_8$	-11.78**	-26.52**	10.34**	2.68**	16.62**	6.09**	29.30**	3.62**
$P_7 \times P_9$	26.56**	20.19**	20.04**	16.87**	27.36**	4.69**	4.69**	38.81**
$P_7 \times P_{10}$	39.14**	37.09**	36.92**	13.41**	47.05**	36.51**	36.33**	28.94**
$P_8 \times P_9$	17.94**	-5.18**	41.56**	12.22**	73.85**	32.79**	61.72**	44.68**
$P_8 \times P_{10}$	35.61**	11.62**	67.51**	10.83**	44.51**	22.97**	50.00**	38.28**
$P_9 \times P_{10}$	-0.49**	-4.13**	-6.96**	1.13**	-2.87**	-14.91**	-27.31**	-4.30**
S.Em	0.13	0.13	0.13	0.11	0.05	0.05	0.05	0.05
CD at 5%	0.31	0.36	0.36	0.30	0.13	0.15	0.15	0.14
CD at 1%	0.41	0.48	0.48	0.39	0.17	0.19	0.19	0.18

* Significant at 5 per cent level
** Significant at 1 per cent level

P_1 = Tapi, P_2 = Mrug-1, P_3 = AT-17, P_4 = Gujarat Til-1, P_5 = AHT-55, P_6 = PY-57 P_7 = RT-125

P_8 = BAUT-1, P_9 = TKG-9-86, P_{10} = OMT-10

significant positive and 12 crosses negative heterobeltiosis. The range of heterobeltiosis varied from -29.79 per cent (Tapi x RT-125) to 65.09 per cent (AT-17 x TKG-9-86). The cross with maximum value was followed by PY-57 x RT-125 (39.89%) and RT-125 x OMT-10 (36.51%). Range for economic heterosis was from -27.34 per cent (TKG-9-86 x OMT-10) to 61.72 per cent (BAUT-1 x TKG-9-86). Other two crosses with higher economic heterosis were BAUT-1 x OMT-10 (50.00%) and Tapi x BAUT-1 (46.09%).

All the segregates revealed significant positive inbreeding depression except crosses Tapi x RT-125 (-24.60%) and PY-57 x TKG-9-86 (-16.09%). Highest inbreeding depression was expressed in cross PY-57 x RT-125 (45.25%) followed by BAUT-1 x TKG-9-86 (44.68%) and RT-125 x TKG-9-86 (38.81%) to the trait.

Test weight (Table-9) :

Fifty five crosses indicated significant heterosis. The range was from -2.54 per cent (Mrug-1 x AHT-55) to 5.32 per cent (G.Til-1 x TKG-9-86). Only six hybrids exhibited significant heterobeltiosis, of which three higher heterotic crosses were G.Til-1 x TKG-9-86 (2.12%), AT-17 x PY-57 (0.75%) and AT-17 x BAUT-1 (0.56%). Significant economic heterosis was observed in all the crosses ranging from -3.08 per cent (AT-17 x AHT-55) to 10.77 per cent (G.Til-1 x TKG-9-86). Maximum cross was followed by AT-17 x BAUT-1 (10.00%) and Mrug-1 x G.Til-1 (8.46%).

Table 9. Heterosis over mid parent, better parent, check parent (economic) and inbreeding depression in per cent for test weight and husk seed ratio.

Crosses	Test weight				Husk seed ratio			
	Heterosis			Inbreeding depression	Heterosis			Inbreeding depression
	Mid parent	Better parent	Economic		Mid parent	Better parnet	Economic	
1	2	3	4	5	6	7	8	9
$P_1 \times P_2$	-0.34**	-0.48**	5.38**	0.00	39.00**	42.26**	15.46**	8.93**
$P_1 \times P_3$	0.15**	-1.52**	4.62**	-2.21**	10.61**	28.79**	9.28**	0.94**
$P_1 \times P_4$	-1.90**	-2.65**	5.38**	1.46**	-3.83**	11.77**	-5.15**	7.61**
$P_1 \times P_5$	0.15**	-3.01**	3.08**	1.49**	8.88**	35.59**	11.34**	12.96**
$P_1 \times P_6$	2.26**	0.19**	6.15**	-0.72**	14.49**	27.94**	8.25**	-19.05**
$P_1 \times P_7$	-0.68**	-3.45**	2.31**	-2.25**	43.39**	55.89**	31.96**	14.84**
$P_1 \times P_8$	-0.38**	-1.96**	7.69**	-0.71**	-15.63**	-9.23**	-22.68**	-60.00**
$P_1 \times P_9$	0.96**	-1.28**	4.62**	2.21**	-20.95**	-6.07**	-20.62**	-15.58**
$P_1 \times P_{10}$	1.93**	-3.21**	3.08**	0.00	-11.75**	-6.56**	-9.28**	-1.14**
$P_2 \times P_3$	-0.34**	-1.86**	3.85**	0.00	4.44**	20.07**	1.03**	2.04**
$P_2 \times P_4$	1.31**	0.38**	8.46**	0.70**	-0.36**	14.36**	-4.12**	-1.07**
$P_2 \times P_5$	-2.54**	-5.49**	0.00	-0.77**	15.89**	4.73**	16.49**	4.42**
$P_2 \times P_6$	1.06**	-0.85**	5.38**	1.46**	19.63**	31.86**	11.34**	-20.37**
$P_2 \times P_7$	1.63**	-1.06**	4.62**	-1.47**	57.33**	68.31**	42.27**	25.36**
$P_2 \times P_8$	-0.48**	-2.20**	6.92**	-1.44**	-0.19**	5.86**	-11.34**	12.79**
$P_2 \times P_9$	1.01**	-1.09**	2.31**	-1.50**	18.96**	4.85**	17.53**	25.44**
$P_2 \times P_{10}$	5.06**	-0.12**	6.15**	-2.17**	13.70**	36.51**	14.43**	6.31**
$P_3 \times P_4$	-0.38**	-2.78**	6.92**	0.00	7.48**	7.61**	20.62**	0.00
$P_3 \times P_5$	0.30**	-1.25**	-3.08**	-8.73**	-7.97**	-4.85**	7.22**	0.96**
$P_3 \times P_6$	1.13**	0.75**	3.85**	2.96**	8.06**	12.09**	17.53**	-15.26**
$P_3 \times P_7$	-0.72**	-1.87**	0.77**	3.82**	12.30**	0.26*	19.58**	-7.76**
$P_3 \times P_8$	3.88**	0.56**	10.00**	0.70**	-6.86**	0.32**	-2.06**	0.00
$P_3 \times P_9$	-0.28**	-0.85**	1.53**	0.00	-17.96**	-16.47**	-6.18**	-15.38**
$P_3 \times P_{10}$	-0.34**	-3.82**	-1.53**	-1.56**	-29.10**	-26.81**	-17.53**	-48.75**
$P_4 \times P_5$	2.61**	-1.38**	6.15**	4.35**	6.35**	10.09**	23.71**	9.17**
$P_4 \times P_6$	-1.16**	-3.89**	5.38**	0.74**	-18.35**	-15.44**	-11.34**	-13.95**
$P_4 \times P_7$	-2.34**	-5.77**	1.53**	0.00	-3.73**	2.38**	2.06**	-26.26**
$P_4 \times P_8$	-2.23**	-3.04**	6.15**	-0.72**	-19.80**	-13.73**	-15.96**	-14.63**

Contd.

Contd. Table 9.

1	2	3	4	5	6	7	8	9
$P_4 \times P_9$	5.32**	2.21**	10.77**	13.89**	-33.13**	-31.83**	-23.71**	-75.67**
$P_4 \times P_{10}$	1.57**	-4.25**	3.08**	1.49**	6.51**	10.09**	23.71**	16.67**
$P_5 \times P_6$	-0.33**	-1.51**	0.77**	-4.58**	-10.23**	-1.67**	1.03**	-26.53**
$P_5 \times P_7$	-1.35**	-1.74**	-1.54**	-2.34**	-1.56**	8.58**	8.25**	3.81**
$P_5 \times P_8$	-1.00**	-5.60**	3.85**	0.00	-7.26**	3.48**	1.30**	-10.20**
$P_5 \times P_9$	-0.56**	-1.54**	0.00	2.31**	30.15**	32.21**	54.64**	36.66**
$P_5 \times P_{10}$	1.71**	-0.33**	-0.77**	0.00	12.16**	12.38**	35.05**	-6.11**
$P_6 \times P_7$	0.34**	-0.45**	1.54**	3.30**	-18.66**	-16.54**	-16.49**	-50.62**
$P_6 \times P_8$	0.17**	-3.39**	6.15**	-0.73**	30.05**	34.84**	31.96**	29.69**
$P_6 \times P_9$	-0.23**	-0.43**	1.54**	0.75**	18.45**	25.52**	30.93**	17.32**
$P_6 \times P_{10}$	-1.84**	-4.93**	-3.08**	-2.38**	-2.14**	4.92**	11.31**	11.21**
$P_7 \times P_8$	1.70**	-2.66**	6.92**	7.19**	5.92**	6.91**	4.12**	11.88**
$P_7 \times P_9$	1.00**	0.40**	1.54**	0.76**	-12.38**	-4.86**	-5.15**	10.97**
$P_7 \times P_{10}$	1.40**	-1.02**	-0.77**	0.73**	-5.16**	4.45**	4.12**	-10.89**
$P_8 \times P_9$	2.16**	-1.66**	7.69**	-0.71**	-3.21**	6.34**	4.12**	-10.89**
$P_8 \times P_{10}$	3.22**	-3.46**	6.15**	0.72**	-13.74**	-3.91**	-6.19**	-4.39**
$P_9 \times P_{10}$	-1.22**	-4.14**	-2.31**	-4.72**	-23.36**	-22.33**	-9.28**	-4.54**
S.Em	0.002	0.002	0.002	0.005	0.02	0.02	0.02	0.02
CD at 5%	0.004	0.005	0.005	0.013	0.05	0.06	0.06	0.06
CD at 1%	0.006	0.007	0.006	0.017	0.06	0.08	0.08	0.08

* Significant at 5 per cent level
** Significant at 1 per cent level

P_1 = Tapi, P_2 = Mrug-1, P_3 = AT-17, P_4 = Gujarat Til-1, P_5 = AHT-55, P_6 = PY-57, P_7 = RT-125

P_8 = BAUT-1, P_9 = TKG-9-86, P_{10} = OMT-10

In F_2, minimum inbreeding depression was recorded in cross AT-17 x AHT-55 (-8.73%), whereas cross G.Til-1 x TKG-9-86 (13.89%) had maximum value followed by RT-125 x BAUT-1 (7.19%) and G.Til-1 x AHT-55 (4.35%).

Husk seed ratio (Table-9) :

Out of 45 crosses, 24 crosses had heterosis (negative) for low husk seed ratio of which highest desirable heterotic value was expressed by G.Til-1 x TKG-9-86 (-33.13%) followed by AT-17 x OMT-10 (-29.11%) and (-20.95%). Range for heterobeltiosis was from -31.83 per cent (G.Til-1 x TKG-9-86) to 68.31 per cent (Mrug-1 x RT-125). Maximum favourable heterobeltiosis was followed by AT-17 x OMT-10 (-26.81%) and AT-17 x TKG-9-86 (-16.47%) for this character. Significant economic heterosis was observed in all the crosses of which 16 and 29 hybrids showed significant negative and positive effects, respectively, ranging from -23.71 per cent (G.Til-1 x TKG-9-86) to 54.64 per cent (AHT-55 x TKG-9-86). Highest negative cross was followed by Tapi x BAUT-1 (-22.68%) and Tapi x TKG-9-86 (-20.62%) for economic heterosis.

Significant inbreeding depression was observed in all the crosses of which maximum in positive direction was for AHT-55 x TKG-9-86 (35.05%). The cross G.Til-1 x TKG-9-86 (-75.67%) had maximum value in negative direction followed by Tapi x BAUT-1 (-60.00%) and PY-57 x RT-125 (-50.62%).

Harvest index (%) (Table-10) :

The significant heterosis was in 25 and 21 hybrids for negative and positive direction, respectively. Minimum heterosis was observed in cross Tapi x RT-125 (-26.95%), whereas maximum was for cross G.Til-1 x PY-57 (26.15%) followed by BAUT-1 x TKG-9-86 (22.47%) and G.Til-1 x OMT-10 (22.11%). Significant heterobeltiosis was recorded in 42 crosses, which varied from -27.39 per cent (Tapi x RT-125) to 20.26 per cent (AT-17 x OMT-10). Best cross was followed by other crosses G.Til-1 x PY 57 (18.97%) and BAUT-1 x TKG-9-86 (16.39%) for harvest index. Only seven hybrids revealed significant economic heterosis. The highest cross was AT-17 x OMT-10 (10.36%) followed by G.Til-1 x PY 57 (8.66%) and BAUT-1 x OMT-10 (8.50%).

Minimum inbreeding depression was -31.13 per cent in cross PY-57 x BAUT-1 while, maximum was 31.14 per cent in cross AHT 55 x PY 57 followed by G.Til x PY-57 (20.51%) and BAUT-1 x TKG-9-86 (20.40%).

Oil content (%) (Table-10) :

In respect to oil content, 26 hybrids had significant positive heterosis, whereas 16 hybrids expressed negative heterosis of which lowest value was for the cross Tapi x OMT-10 (4.19%) and highest heterotic cross was AHT-53 x RT-125 (3.38%) followed by BAUT-1 x TKG 9-86 (2.95%) and Tapi x TKG-9-86 (2.70%). Significant heterobeltiosis was observed in 44 crosses. The cross with maximum value for

Table 10. Heterosis over mid parent, better parent, check parent (economic) and inbreeding depression in per cent for harvest index and oil content

Crosses	Harvest index				Oil content			
	Heterosis			Inbreeding depression	Heterosis			Inbreeding depression
	Mid parent	Better parent	Economic		Mid parent	Better parent	Economic	
1	2	3	4	5	6	7	8	9
$P_1 \times P_2$	-19.70**	-20.21**	-20.24**	-13.57**	0.49**	-1.02**	1.14**	-1.27**
$P_1 \times P_3$	-9.96**	-13.13**	-14.24**	10.63**	0.00	-2.57**	1.80**	-0.57**
$P_1 \times P_4$	0.13**	-3.51**	-4.74**	-20.01**	0.47**	-2.19**	2.38**	0.46**
$P_1 \times P_5$	-1.61**	-6.27**	-7.48**	-16.58**	1.64**	0.34**	2.06**	-0.55**
$P_1 \times P_6$	-8.14**	-16.50**	-17.58**	20.28**	-0.29**	-2.82**	1.44**	-0.04**
$P_1 \times P_7$	-26.93**	-27.39**	-27.42**	-20.83**	1.09**	0.64**	0.64**	-1.53**
$P_1 \times P_8$	-10.60**	-14.54**	-15.65**	15.26**	2.41**	1.68**	2.38**	-0.34**
$P_1 \times P_9$	9.69**	-0.10	-1.37**	-3.12**	2.70**	1.92**	2.55**	-0.96**
$P_1 \times P_{10}$	-5.56**	-10.20**	-11.36**	-4.93**	-4.19**	-4.43**	-5.29**	-0.05**
$P_2 \times P_3$	-9.11**	-12.85**	-12.83**	-12.90**	-2.20**	-3.28**	1.05**	-0.42**
$P_2 \times P_4$	-8.73**	-12.59**	-12.61**	-5.91**	-1.11**	-2.300**	2.27**	0.50**
$P_2 \times P_5$	-1.79**	-7.01**	-7.03**	-2.04**	1.94**	1.70**	3.92**	2.64**
$P_2 \times P_6$	-12.19**	-20.64**	-20.66**	13.55**	0.18**	-0.87**	3.47**	0.25**
$P_2 \times P_7$	-21.71**	-21.72**	-21.72**	-25.18**	1.58**	0.50**	2.68**	2.56**
$P_2 \times P_8$	-5.66**	-10.36**	-10.37**	-23.18**	-0.56**	-1.28**	0.86**	-0.66**
$P_2 \times P_9$	-7.11**	-15.90**	-15.91**	-4.61**	-0.23**	-0.99**	1.16**	-0.02
$P_2 \times P_{10}$	-7.19**	-12.30**	-12.31**	-12.43**	0.56**	-2.30**	-0.17**	0.25**
$P_3 \times P_4$	-0.13**	-0.26	-8.47**	-1.49**	-3.18**	-3.27**	1.24**	-1.91**
$P_3 \times P_5$	-1.02**	-2.31**	-10.37**	4.79**	1.34**	0.00	4.48**	3.14**
$P_3 \times P_6$	-4.27**	-10.02**	-17.43**	14.39**	-1.37**	-1.42**	3.00**	0.37**
$P_3 \times P_7$	-7.78**	-11.76**	-12.34**	0.78	-1.95**	-4.06**	0.24**	-1.37**
$P_3 \times P_8$	4.38**	3.39**	-5.13**	5.60**	1.73**	-0.11**	4.37**	1.35**
$P_3 \times P_9$	15.67**	8.93**	-0.04	7.67**	1.47**	-0.40**	4.07**	1.95**
$P_3 \times P_{10}$	22.11**	20.26**	10.36**	19.54**	-4.16**	-6.85**	-2.68**	-1.04**
$P_4 \times P_5$	4.94**	3.70**	-5.09**	8.72**	1.19**	-0.23**	4.42**	-0.52**
$P_4 \times P_6$	26.13**	18.70**	8.66**	20.51**	-0.56**	-0.69**	3.94**	0.02
$P_4 \times P_7$	10.65**	5.97**	5.96**	8.10**	1.79**	-0.47**	4.18**	-2.40**
$P_4 \times P_8$	9.14**	8.24**	-0.09	10.96**	1.46**	-0.46**	4.18**	-1.29**

Contd.

Contd. Table 10.

1	2	3	4	5	6	7	8	9
$P_4 \times P_9$	5.15**	-0.84**	-9.22**	8.45**	0.02	-1.91**	2.68**	-1.59**
$P_4 \times P_{10}$	7.55**	6.05**	-2.92**	16.90**	-2.60**	-5.42**	-1.01**	0.41**
$P_5 \times P_6$	14.24**	8.72**	-2.81**	31.34**	0.92**	-0.37*	3.99**	-1.29**
$P_5 \times P_7$	7.27**	1.58**	1.56**	9.23**	3.38**	2.51**	4.26**	-0.47**
$P_5 \times P_8$	10.42**	10.02**	-0.95*	6.94**	2.05**	1.54**	3.28**	-0.25**
$P_5 \times P_9$	-13.13**	-17.16**	-25.98**	-18.83**	-1.24**	-1.76**	-0.09**	0.97**
$P_5 \times P_{10}$	-8.49**	-8.69**	-18.38**	5.26**	-0.01	-1.53**	-0.13	-2.14**
$P_6 \times P_7$	10.18**	-0.41	-0.42	20.32**	2.09**	-0.04**	4.33**	0.02
$P_6 \times P_8$	-4.84**	-25.87**	-33.27**	-31.13**	1.51**	-0.28**	4.09**	2.44**
$P_6 \times P_9$	-6.95**	-7.15**	-24.72**	-14.08**	-0.93**	-2.72**	-1.54**	1.91**
$P_6 \times P_{10}$	-5.24**	-9.63**	-19.60**	0.00	-3.21**	-5.89**	-1.76**	1.55**
$P_7 \times P_8$	11.28**	5.73**	5.73**	-2.76**	1.72**	1.57**	2.27**	1.89**
$P_7 \times P_9$	3.61**	-6.17**	-6.19**	13.87**	2.17**	1.86**	2.49**	-1.57**
$P_7 \times P_{10}$	1.30**	-4.26**	-4.29**	9.60**	2.25**	1.54**	1.54**	-4.96**
$P_8 \times P_9$	22.47**	16.39**	4.78**	20.40**	2.93**	2.89**	-3.60**	1.77**
$P_8 \times P_{10}$	2.20**	2.61**	8.50**	15.82**	-1.01**	-2.03**	-1.35**	-0.02
$P_9 \times P_{10}$	10.07**	5.19**	-6.38**	2.39**	1.79**	0.77**	1.39**	-0.71**
S.Em	0.30	0.30	0.30	0.36	0.010	0.010	0.010	0.010
CD at 5%	0.72	0.84	0.84	0.99	0.024	0.028	0.028	0.027
CD at 1%	0.96	1.11	1.11	1.30	0.032	0.037	0.037	0.036

* Significant at 5 per cent level
** Significant at 1 per cent level

P_1 = Tapi, P_2 = Mrug-1, P_3 = AT-17, P_4 = Gujarat Til-1, P_5 = AHT-55, P_6 = PY-57, P_7 = RT-125

P_8 = BAUT-1, P_9 = TKG-9-86, P_{10} = OMT-10

heterobeltiosis was BAUT-1 x TKG-9 86 (2.89%) followed by AHT-55 x RT-125 (2.51%) and Tapi x TKG-9-86 (1.92%) for the trait. Range of economic heterosis varied from -5.29 per cent (Tapi x OMT-10) to 4.42 per cent (G.Til-1 x AHT-55). Highest economic heterotic cross was followed by Tapi x Mrug-1 (26.19%) and Tapi x PY-57 (19.04%).

In second filial generation, 24 crosses expressed significant inbreeding depression, of which highest inbreeding depression was observed in cross AT-17 x AHT-55 (3.14%) followed by Mrug-1 x AHT-55 (2.64%) and Mrug-1 x RT-125 (2.56%), whereas lowest cross was Tapi x OMT-10 with -5.29 per cent. The per cent of inbreeding depression was low in most of the crosses, which was confirmed from non-significant differences on F_1 vs F_2 in analysis of variance.

Oil yield per plant (Table-11) :

A perusal of data revealed that all the hybrids expressed significant positive heterosis except hybrids Tapi x RT-125 (-27.64%) and PY-57 x BAUT-1 (-8.45%). Highest heterotic cross AT-17 x TKG-9-86 (89.63%) was followed by BAUT-1 x TKG-9-86 (81.57%) and PY-57 x RT-125 (52.25%). Out of 45 crosses, 13 and 32 crosses depicted negative and positive significant heterobeltiosis, respectively ranging from -0.33 per cent (PY-57 x TKG-9-86) to 65.21 per cent (AT-17 x TKG-9-86). Maximum heterobeltiotic cross was followed by PY-57 x RT-125 (46.08%) and RT-125 x OMT-10 (38.54%). Significant positive economic heterosis was observed in 38 crosses, of

Table 11. Heterosis over mid parent, better parent, check parent (economic) and inbreeding depression in per cent for oil yield per plant and protein content

| Crosses | Oil yield per plant (g) | | | | Protein content (%) | | | |
| | Heterosis | | Economic | Inbreeding depression | Heterosis | | Economic | Inbreeding depression |
	Mid parent	Better parent			Mid parent	Better parent		
1	2	3	4	5	6	7	8	9
$P_1 \times P_2$	6.63**	0.72**	16.81**	22.73**	-1.66**	-3.16**	5.26**	0.39**
$P_1 \times P_3$	13.47**	2.71**	9.24**	36.41**	0.26**	-1.31**	7.35**	0.18**
$P_1 \times P_4$	34.19**	28.07**	46.22**	35.57**	-0.20**	-2.02**	7.16**	0.15**
$P_1 \times P_5$	4.51**	-5.96**	-1.68**	16.14**	0.07**	-1.05**	6.66**	0.05
$P_1 \times P_6$	1.14**	-4.33**	2.52**	33.99**	-0.14**	-1.01**	6.17**	0.00
$P_1 \times P_7$	-27.64**	-28.72**	-27.73**	-26.23**	0.95**	-1.62**	3.67**	-0.04
$P_1 \times P_8$	32.50**	21.81**	51.20**	36.01**	0.52**	-1.73**	8.41**	0.03
$P_1 \times P_9$	60.06**	28.18**	35.29**	23.56**	0.77**	-1.07**	8.21**	0.17**
$P_1 \times P_{10}$	15.35**	4.87**	5.88**	21.19**	-0.21**	-0.76**	4.58**	-0.53**
$P_2 \times P_3$	17.64**	1.20**	18.49**	21.90**	-0.06	-0.10**	8.66**	-0.03
$P_2 \times P_4$	10.11**	8.91**	30.25**	37.38**	-0.36**	-0.67**	8.64**	0.14**
$P_2 \times P_5$	18.59**	1.44**	19.33**	22.09**	0.21**	-0.20**	8.47**	0.69**
$P_2 \times P_6$	2.41**	-8.19**	10.08**	30.45**	-0.14**	-0.80**	7.82**	-0.03
$P_2 \times P_7$	10.73**	3.13**	26.89**	13.55**	1.14**	-2.91**	5.53**	-0.07**
$P_2 \times P_8$	3.39**	0.45**	16.96**	18.55**	-0.39**	-1.13**	9.08**	0.05
$P_2 \times P_9$	25.90**	-3.37**	13.45**	32.17**	-0.48**	-0.80**	8.51**	0.20**
$P_2 \times P_{10}$	28.87**	11.32**	33.61**	28.57**	-0.07**	-2.12**	6.39**	0.04
$P_3 \times P_4$	7.23**	-6.89**	1.68**	14.81**	-0.01	-0.28**	9.06**	0.01
$P_3 \times P_5$	22.55**	21.73**	0.84**	28.57**	-0.03	-0.48**	8.25**	0.04
$P_3 \times P_6$	33.12**	27.05**	18.49**	32.77**	-0.17**	-0.88**	7.82**	0.04
$P_3 \times P_7$	8.37**	-0.55**	2.52**	26.12**	0.29**	-3.75**	4.69**	0.40**
$P_3 \times P_8$	16.64**	-2.04**	16.81**	3.94**	-0.24**	-0.94**	9.28**	0.31**
$P_3 \times P_9$	89.63**	65.21**	38.65**	23.28**	-0.48**	-0.76**	8.55**	0.27**
$P_3 \times P_{10}$	17.80**	17.21**	1.68**	10.16**	-0.48**	-2.56**	5.99**	0.27**
$P_4 \times P_5$	34.37**	16.01**	31.93**	30.57**	0.34**	-0.38**	8.95**	0.19**
$P_4 \times P_6$	17.00**	5.91**	20.58**	21.16**	-0.55**	-1.51**	7.71**	-0.14**
$P_4 \times P_7$	14.92**	8.12**	23.53**	8.42**	3.89**	-0.56**	8.76**	0.38**
$P_4 \times P_8$	11.34**	7.04**	31.93**	27.60**	0.12**	-0.31**	9.97**	0.20**

Contd.

Contd. Table 11.

1	2	3	4	5	6	7	8	9
$P_4 \times P_9$	28.02**	-0.98**	12.18**	34.33**	-0.18**	-0.19**	10.00**	0.11**
$P_4 \times P_{10}$	26.55**	10.34**	25.67**	27.90**	0.03	-2.32**	6.83**	0.16**
$P_5 \times P_6$	12.17**	6.38**	-1.68**	24.57**	-0.76**	-1.01**	6.70**	0.32**
$P_5 \times P_7$	29.55**	18.15**	18.91**	21.51**	0.25**	-3.38**	4.15**	-0.46**
$P_5 \times P_8$	25.98**	5.22**	29.41**	15.33**	0.19**	-0.95**	9.27**	0.15**
$P_5 \times P_9$	13.73**	-0.33**	-19.33**	6.80**	-0.36**	-1.08**	8.19**	0.24**
$P_5 \times P_{10}$	3.51**	2.31**	9.24**	9.38**	0.37**	-1.29**	6.40**	0.41**
$P_6 \times P_7$	52.25**	46.08**	46.64**	44.35**	2.54**	-0.93**	6.25**	1.03**
$P_6 \times P_8$	-8.45**	-20.00**	-1.68**	8.80**	2.15**	0.73**	11.12**	1.18**
$P_6 \times P_9$	5.62**	-11.55**	-18.07**	-18.21**	0.36**	-0.62**	8.70**	0.90**
$P_6 \times P_{10}$	24.56**	19.45**	10.92**	18.93**	2.40**	0.97**	8.28**	0.87**
$P_7 \times P_8$	18.54**	7.50**	32.35**	1.69**	0.29**	-4.41**	5.46**	1.73**
$P_7 \times P_9$	32.41**	7.26**	7.98**	39.84**	0.24**	-4.06**	4.93**	0.03
$P_7 \times P_{10}$	50.30**	38.54**	39.07**	32.25**	0.08**	-1.95**	2.19**	0.65**
$P_8 \times P_9$	81.57**	36.59**	69.75**	45.75**	-0.16**	-0.59**	9.97**	0.11**
$P_8 \times P_{10}$	42.85**	20.45**	49.16**	38.30**	0.30**	-2.48**	7.59**	2.67**
$P_9 \times P_{10}$	7.63**	-6.62**	-20.01**	3.55**	0.23**	-2.13**	7.05**	0.43**
S.Em	0.023	0.023	0.023	0.022	0.013	0.013	0.013	0.018
CD at 5%	0.063	0.073	0.073	0.062	0.045	0.052	0.052	0.051
CD at 1%	0.085	0.096	0.096	0.082	0.060	0.068	0.068	0.067

* Significant at 5 per cent level
** Significant at 1 per cent level

P_1 = Tapi, P_2 = Mrug-1, P_3 = AT-17, P_4 = Gujarat Til-1, P_5 = AHT-55, P_6 = PY-57, P_7 = RT-125

P_8 = BAUT-1, P_9 = TKG-9-86, P_{10} = OMT-10

which cross BAUT-1 x TKG-9-86 (69.75%) had highest value followed by Tapi x BAUT-1 (51.20%) and BAUT-1 x OMT-10 (49.16%).

In F$_2$, all the crosses expressed positive and significant inbreeding depression, except crosses Tapi x RT-125 (-26.23%) and PY-57 x TKG-9-86 (-18.21%). Highest inbreeding depression was revealed by BAUT-1 x TKG-9-86 (45.75%) followed by PY-57 x RT-125 (44.35%) and RT-125 x TKG-9-86 (39.84%).

Protein content (Table-11) :

Significant heterosis was recorded in 42 crosses for the trait, out of this 23 and 19 crosses had positive and negative values, respectively. The cross G.Til-1 x RT-125 (3.89%) expressed highest value followed by PY-57 x RT-125 (2.54%) and PY-57 x OMT-10 (2.40%). All the crosses observed significant negative heterobeltiosis except crosses PY-57 x OMT-10 (0.97%) and PY-57 x BAUT-1 (0.73%). Whereas, Out of 45 significant economic heterotic crosses, cross PY-57 x BAUT-1 (11.12%) had highest value followed by G.Til-1 x TKG-9-86 (10.00%) and BAUT-1 x TKG-9-86 (9.97%) for protein content.

Significant inbreeding depression was noted in 33 F$_2$ segregates, of which 28 and 5 had in positive and negative direction, ranging from -0.46 per cent (AHT-55 x RT-125) to 2.67 per cent (BAUT-1 x OMT-10). Highest inbreeding depression cross followed by RT-125 x BAUT-1 (1.73%) and PY-57 x BUT-1 (1.18%) for this trait.

Combining ability effects :

The method-II, model-I given by Griffing (1956a) was followed for estimation of combining ability effects for different characters in each generation of sesame.

Analysis of variance for combining ability (Table-12) :

In both the generations, the analysis of variance revealed high significance for general and specific combining ability in all the traits, except for GCA which was non-significant for harvest index in F_1, number of grains per capsule in F_2, plant height to first flowering and husk seed ratio in both F_1 and F_2. The magnitude of specific combining ability variances was higher than general combining ability variances for most of the traits in both the generations. Thus, indicated that non-additive effects were more pronounced than additive effects.

4.3   GENERAL AND SPECIFIC COMBINING ABILITY EFFECTS :

Plant height to first flowering (Table 13, 14) :

The estimate of GCA effects revealed that parent AT-17 and PY-57 in both the generations, Tapi in F_1 and OMT-10 in F_2 revealed non-significance, while other parents showed significant GCA effects. It ranged from -1.65 (RT-125) to 1.51 (Mrug-1) and -0.56 (Tapi) to 1.51 (Mrug-1) in F_1 and F_2, respectively. Parent Mrug-1 recorded significant and maximum GCA effects followed by BAUT-1 and G.Til-1 in F_1, while in F_2

Table 12. Analysis of variance for combining ability of sesame

Effect	Generation	d.f.	Plant height to first flowering	Days to first flowering	Days to 50 per cent flowering	Days to maturity	Length of reproductive stem	Plant height to maturity	Number of branches per plant	Number capsules per plant	Length of capsule
							Characters				
1	2	3	4	5	6	7	8	9	10	11	12
GCA	F_1	9	12.039	18.373**	17.766**	41.407**	53.782**	289.333**	0.522**	31.517**	0.035**
	F_2	9	6.935	15.343**	14.447**	36.065**	48.150**	214.982**	0.338**	29.944**	0.039**
SCA	F_1	45	10.643**	3.394**	2.823**	2.278**	15.712**	46.780**	0.169**	19.934**	0.007**
	F_2	45	4.417**	3.785**	3.143**	2.897**	9.964**	42.832**	0.096**	5.711**	0.011**
Error	F_1	108	0.429	0.436	0.271	0.060	1.183	2.451	0.005	0.067	0.000
	F_2	108	0.604	0.538	0.225	0.100	0.731	2.310	0.005	0.050	0.000
σ^2_g	F_1	-	0.341	1.117	3.116	1.806	1.781	4.496	0.172	0.982	0.048
	F_2	-	0.456	0.981	0.971	1.663	1.784	3.788	0.142	1.421	0.046
σ^2_s	F_1	-	3.196	1.720	1.547	1.489	3.812	6.658	0.405	4.457	0.084
	F_2	-	1.951	1.802	1.708	1.672	3.039	6.366	0.302	2.379	0.105
σ^2_g/σ^2_s	F_1	-	0.107	0.649	0.699	1.213	0.467	0.675	0.423	0.220	0.578
	F_2	-	0.513	0.545	0.568	0.995	0.587	0.595	0.470	0.597	0.460

Contd.

Contd. Table 12.

Effect	Generation	d.f.	Characters								
			Number of grains per capsule	Dry weight per plant	Grain yield per plant	Test weight	Husk seed ratio	Harvest index	Oil content	Oil yield per plant	Protein content
			13	14	15	16	17	18	19	20	21
GCA	F_1	9	16.718**	4.049**	0.552**	0.009**	0.031	7.447	3.435**	0.126**	1.340**
	F_2	9	7.884	2.456**	0.355**	0.008**	0.030	15.610**	3.576**	0.081**	1.372**
SCA	F_1	45	6.231**	1.054**	0.225**	0.001**	0.027**	5.867**	0.500**	0.053**	0.044**
	F_2	45	7.875**	0.529**	0.089**	0.001**	0.019**	6.276**	0.502**	0.021**	0.045**
Error	F_1	108	0.003	0.016	0.003	0.000	0.000	0.089	0.000	0.001	0.000
	F_2	108	0.002	0.006	0.004	0.000	0.000	0.175	0.000	0.000	0.000
σ^2_g	F_1	-	0.935	0.499	0.165	0.026	0.015	0.363	0.495	0.078	0.328
	F_2	-	0.027	0.401	0.149	0.024	0.030	0.882	0.506	0.071	0.333
σ^2_s	F_1	-	2.496	1.019	0.471	0.320	0.164	2.404	0.707	0.228	0.240
	F_2	-	2.806	0.723	0.292	0.032	0.138	2.470	0.709	0.145	0.213
σ^2_g/σ^2_s	F_1	-	0.375	0.490	0.361	0.893	0.096	0.151	0.701	0.342	1.566
	F_2	-	0.010	0.562	0.510	0.864	0.217	0.356	0.714	0.488	1.568

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 13. Estimation of general combining ability (GCA) effects of parents for plant height to first flowering, days to first flowering, days to 50 per cent flowering, days to maturity, length of reproductive stem and plant height to maturity in sesame

Parents	Plant height to first flowering		Days to first flowering		Days to 50 per cent flowering		Days to maturity		Length of reproductive stem		Plant height to maturity	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Tapi	-0.31	-0.56**	0.56**	0.67**	0.51**	0.47**	1.77**	2.03**	1.31**	0.13	4.50**	1.94**
Mrug-1	1.51**	1.51**	1.17**	0.92**	1.10**	0.83**	1.13**	0.45**	0.07	-0.86**	3.57**	2.02**
AT-17	0.01	-0.10	-0.73**	-1.06**	-0.37**	-1.00**	-0.13	-0.22	-0.89**	-0.80**	-4.47**	-3.54**
Gujarat Til-1	0.37*	0.67**	-0.32	-0.47*	-0.53**	-1.61**	0.05	-0.08	-0.28	-0.66**	-0.90*	-0.88*
AHT-55	-1.49**	-0.53*	-0.10	-0.14	-0.37**	0.11	-0.30**	-0.08	-1.60**	-1.25**	-5.66**	-5.31**
PY-57	0.04	-0.10	1.73**	1.44**	1.85**	0.61**	2.75**	2.45**	-1.14**	1.31**	8.16**	8.29**
RT-125	-1.65**	-0.28	-2.65**	-2.42**	-2.59**	-2.36**	-4.19**	-3.91**	0.39	1.19**	-2.35**	-1.71**
BAUT-1	1.12**	0.58**	-0.82**	0.83**	-0.70**	0.44**	-0.02	0.45**	4.54**	4.66**	4.78**	4.78**
TKG-9-86	-0.07	-1.19**	0.53**	0.44*	0.51**	0.39**	0.08	-0.02	-3.33**	-2.55**	-1.96**	-3.76**
OMT-10	0.47**	0.02	0.62**	-0.22	0.60**	0.11	-1.13**	-1.08**	1.36**	-1.18**	-5.66**	-1.74**
SE (g_i)±	0.180	0.213	0.181	0.201	0.140	0.130	0.070	0.089	0.300	0.234	0.431	0.426
SE (g_i-g_j)±	0.270	0.317	0.270	0.300	0.210	0.194	0.101	0.130	0.441	0.355	0.640	0.620

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 14. Estimation of specific combining ability (SCA) effects of hybrids for plant height to first flowering, days to 50 per cent flowering, days to first flowering, days to first flowering, days to maturity, length of reproductive stem and plant height to maturity in sesame

Crosses	Plant height to first flowering		Days to first flowering		Days to 50 per cent flowering		Days to maturity		Length of reproductive stem		Plant height to maturity	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
1	2	3	4	5	6	7	8	9	10	11	12	13
$P_1 \times P_2$	4.06**	-1.74**	-0.09	-2.43**	-0.17	-1.55**	-0.28	-3.48**	1.84	2.42**	10.78**	-3.43*
$P_1 \times P_3$	-4.23**	-3.06**	3.15**	-0.13	2.29**	-0.72	2.33**	-2.14**	3.48**	-1.56*	1.83	-5.47**
$P_1 \times P_4$	1.48*	-2.53**	0.40	-2.38**	0.13	-1.10*	0.86**	-0.28	0.14	-0.51	5.33**	2.31
$P_1 \times P_5$	1.41*	-0.27	-1.81**	-3.04**	-2.03**	-2.83**	1.50**	-1.28**	6.26**	-0.31	12.48**	-2.00
$P_1 \times P_6$	-1.22*	0.67	-0.98	-0.63	-0.924*	-0.66	-1.55**	-1.81**	1.44	0.69	-0.40	3.78**
$P_1 \times P_7$	-2.15**	2.82**	2.07**	0.24	-3.18**	1.65**	3.38**	6.21**	-4.80**	3.14**	-4.41**	14.84**
$P_1 \times P_8$	-1.17	0.46	-1.76**	4.99**	-1.36**	3.17**	0.22	1.86**	8.97**	1.75*	3.31*	6.54**
$P_1 \times P_9$	0.03	1.30	-1.45	1.04	-0.59	1.23**	-1.89**	0.80**	-1.20	0.36	-6.14**	-2.68
$P_1 \times P_{10}$	0.74	-1.28	-0.54	0.71	-0.67	1.84**	-1.33**	0.05	-2.51*	-4.99**	-2.50	-11.53**
$P_2 \times P_3$	0.40	-0.61	0.87	1.96**	-0.28	0.92	-0.03	1.77**	-4.47**	1.16	-4.46**	7.22**
$P_2 \times P_4$	-3.95**	-1.42**	3.79**	2.37**	3.21**	2.20**	0.44*	-1.03**	2.94**	-3.06**	-2.07	-6.64**
$P_2 \times P_5$	-5.11**	1.51*	0.57	2.71**	-0.28	1.81**	0.13	1.98**	-0.36	-0.70	3.25*	-0.88
$P_2 \times P_6$	-5.09**	0.78	-2.92**	-1.88**	-2.17**	-1.69**	-0.91**	1.11**	-0.56	-4.93**	-11.47**	-4.94**
$P_2 \times P_7$	-0.49	0.07	-2.20**	0.99	-1.39**	1.95**	0.69**	-0.53*	6.63**	1.50	-5.12**	1.83
$P_2 \times P_8$	-1.33*	-1.26	0.96	1.07	1.04*	1.48**	-0.47*	1.11**	-4.92**	-3.57**	-8.78**	-4.97**
$P_2 \times P_9$	5.56**	-0.49	1.26*	-2.54**	1.49**	-2.13**	1.41**	-2.09**	-2.56*	-0.73	5.45**	-1.10
$P_2 \times P_{10}$	-0.32	-4.64**	-0.81	-2.88**	0.07	-1.19**	-1.03**	0.97**	3.65**	3.53**	11.92**	-1.41
$P_3 \times P_4$	-2.04**	-2.27**	0.04	1.68*	0.02	1.70**	0.05	0.63*	4.19**	-0.74	-7.41**	-9.88**
$P_3 \times P_5$	6.25**	-1.14	0.15	1.35*	0.18	0.65	0.58*	-0.37	1.41	-2.75**	-1.32	-9.03**
$P_3 \times P_6$	-1.15	1.17	-1.34*	-0.57	-1.03*	0.15	0.02	-0.23	3.32**	2.32**	5.11**	4.12**
$P_3 \times P_7$	0.11	1.15	1.71**	0.29	1.74**	1.12*	-0.69**	0.80**	-3.06**	-3.82**	-1.20	-5.35**
$P_3 \times P_8$	0.93	2.19**	-0.12	0.71	0.18	-0.02	0.19	0.11	-5.91**	-1.35	-1.63	-1.55
$P_3 \times P_9$	-1.56*	2.82**	0.18	0.10	-0.03	1.03*	0.35	0.58*	2.97**	3.52**	6.44**	10.99**

Contd.

Contd. Table 14.

1	2	3	4	5	6	7	8	9	10	11	12	13
$P_3 \times P_{10}$	1.81**	-1.72*	2.43**	-0.57	2.54**	-0.35	0.24	0.63*	2.66**	0.28	-5.92**	3.01*
$P_4 \times P_5$	0.03	5.46**	-1.26*	-0.57	-0.98*	2.92**	-3.44**	1.83**	-1.29	2.14**	-3.23*	9.12**
$P_4 \times P_6$	-0.67	-0.37	0.90	1.51*	0.79	0.76	1.16**	-0.37	-4.94**	5.07**	-15.45**	5.36**
$P_4 \times P_7$	-4.10**	-2.36**	0.29	-0.29	0.57	0.06	0.44*	-1.67**	-0.30	0.20	1.99	-3.87**
$P_4 \times P_8$	-1.69**	-1.89**	0.12	1.79**	0.68	1.26**	0.94**	0.63*	-4.08**	-4.87**	-2.04	0.10
$P_4 \times P_9$	-5.91**	0.85	1.43*	0.51	2.13**	0.65	0.83**	0.11	-0.13	-3.99**	13.96**	-3.69**
$P_4 \times P_{10}$	0.65	-0.19	-2.98**	-3.49**	-2.28**	-3.08*	-1.28**	-1.51**	5.25**	-1.87*	0.50	-8.61**
$P_5 \times P_6$	4.09**	-1.24	-0.01	-0.15	-0.03	-0.30	-0.47*	-0.03	-1.19	0.04	-1.67	-2.91*
$P_5 \times P_7$	0.92	0.27	-0.92	-0.96	-1.59**	-1.33**	0.80**	-1.01**	1.58	-0.84	5.55**	1.85
$P_5 \times P_8$	0.21	-0.66	0.57	-3.54**	2.18**	-1.13*	0.30	-1.37**	-2.56**	-2.07*	-3.82*	-1.28
$P_5 \times P_9$	-3.95**	0.45	1.87**	0.18	0.63	0.92	2.19**	0.44	-5.35**	-0.70	-4.97**	2.76*
$P_5 \times P_{10}$	-2.40**	-0.56	-1.54*	0.51	-1.11*	-0.47	1.41**	0.16	1.19	-4.01**	-2.10	0.28
$P_6 \times P_7$	1.28*	-0.99	3.23**	1.79**	2.85**	1.17**	-0.58*	-0.20	-2.03*	-5.54**	5.45**	-6.21**
$P_6 \times P_8$	-0.66	-0.39	0.73	1.21	-0.70	2.04**	0.91**	1.44**	5.71**	-6.30**	15.88**	-8.70**
$P_6 \times P_9$	1.57*	-2.98**	1.71**	-1.74*	-1.40**	-0.58	1.86**	-2.42**	0.63	-1.30	0.40	-10.13**
$P_6 \times P_{10}$	2.71**	2.11**	0.29	-0.07	-0.32	0.04	1.69**	0.30	-2.87**	2.20**	-1.06	9.25**
$P_7 \times P_8$	0.17	-1.24	-1.87**	-2.59**	-1.92**	-2.66**	-4.47**	-3.20**	-3.10**	5.26**	-5.62**	-4.31**
$P_7 \times P_9$	-3.85**	-2.73**	-2.90**	1.46*	-2.14**	-0.60	-2.58**	-2.06**	5.17**	-0.30	1.78	-6.46**
$P_7 \times P_{10}$	-.15	0.03	0.68	-0.88	0.10	2.34**	-0.36	-0.01	1.97*	-2.31**	2.88*	-3.92**
$P_8 \times P_9$	3.72**	2.14**	-2.40**	-1.13	-2.03**	0.92	0.24	1.58**	4.82**	1.73	2.04	1.91
$P_8 \times P_{10}$	1.57	2.70**	3.18**	2.54**	2.88**	1.87**	1.80**	-0.37	2.92**	3.79**	5.31**	9.26**
$P_9 \times P_{10}$	-6.75**	-0.63	1.82**	2.26**	0.99*	1.26**	0.35	2.11**	-3.92**	2.26**	-5.23**	7.30**
SE $(S_{ij})\pm$	0.60	0.710	0.60	0.669	0.47	0.433	0.22	0.288	0.99	0.781	1.43	1.387
SE $(S_{ij}-S_{ik})\pm$	0.89	1.053	0.89	0.993	0.70	0.642	0.33	0.427	1.47	1.158	2.12	2.058
SE $(S_{ij}-S_{lk})\pm$	0.85	1.004	0.85	0.947	0.67	0.612	0.32	0.407	1.40	1.104	2.02	1.961

* Significant at 5 per cent level
** Significant at 1 per cent level

highest GCA effects were expressed by Mrug-1 followed by G.Til-1 and BAUT-1 suggesting stability for combining ability for plant height to first flowering.

Estimates of SCA effects showed that 27 in F_1 and 19 crosses in F_2 expressed significant SCA effects. Ten and eight hybrids were with positive values and 17 and 11 hybrids were with negative values in F_1 and F_2, respectively. The corresponding ranges were -5.91 (G.Til-1 x TKG-9-86) to 8.72 (BAUT-1 x TKG-9-86) for F_1 and -3.06 (Tapi x AT-17) to 5.46 (G.Til-1 x AHT-17) for F_2. The crosses PY-57 x OMT-10 and BAUT-1 x TKG-9-86 showed positive significant and constant SCA effects over the generations.

Days to first flowering (Table - 13, 14) :

GCA effects varied from -2.65 (RT-125) to 1.73 (PY-57) and -2.42 (RT-125) to 1.44 (PY-57) for F_1 and F_2, respectively. Estimates of GCA effects in both the generations indicated that parent RT-125 and AT-17 had negative values, suggesting their potentiality toward earliness, while Tapi, Mrug-1, PY-57 and TKG-9-86 had positive significant values indicating their ability to impart lateness in hybrids. It was suggested that these parents would be stable and better donor for imparting earliness and lateness.

Estimates of SCA effects revealed that in F_1 generation, the values ranged from -2.89 (G.Til 1 x OMT-10) to 3.79 (Mrug-1 x G.Til-1). Out of 45 crosses, 10 and 13 hybrids

showed significant negative and positive SCA effects. In F_2, 23 hybrids showed significant SCA effects, of these 10 segregates were with negative and 13 with positive values. A range of 3.49 (G.Til-1 x OMT-10) to 3.21 (Mrug-1 x G.Til-1) was recorded in hybrids.

On the basis of two sets of data it was observed that crosses Tapi x AHT-55, Mrug-1 x PY-57, G.Til-1 x OMT-10 and RT-125 x BAUT-1 showed constant significant negative and crosses Mrug-1 x G.Til-1, PY-57 x RT-125 and BAUT-1 x OMT-10 expressed constant significant positive SCA effects. It was also interesting to reveal that 11 crosses showed SCA effects in desired direction.

Days to 50 per cent flowering (Table 13, 14) :

This character is considered to be important for earliness or lateness in sesame. Plants having lesser days to 50 per cent flowering generally mature early. Data revealed that GCA estimates varied from -2.59 (RT-125) to 1.85 (PY-57) and -2.36 (RT-125) to 0.83 (Mrug-1) in F_1 and F_2, respectively. Estimates of GCA effects in both the generations indicated that parents RT-125, G.Til-1 and AT-17 had significantly lower GCA effects and found to be good general combiners for earliness. On the other hand, parent Tapi, Mrug-1, PY-57 and TKG-9-86 exhibited significant positive effects and hence, were good general combiners for lateness.

On the basis of two sets of data, it was clear that parents RT-125, G.Til-1 and AT-17 had constant significant negative effects. Results suggested that these parents would be stable and better donor for imparting earliness.

Estimates of SCA effects revealed that in F_1 and F_2 generations, 26 and 28 crosses exhibited significant SCA effects, respectively. Fifteen and eleven had negative and positive significant effects respectively in F_1, while 10 and 18 had negative and positive significant effects, respectively in F_2. The range was from -3.18 (Tapi x RT-125) to 2.88 (BAUT-1 x OMT-10) and -3.08 (G.Til-1 x OMT-10) to 3.17 (Tapi x BAUT-1) in respective generations.

Two sets of data, revealed that crosses Tapi x AHT-55, Mrug-1 x PY-57, G.Til-1 x OMT-10, AHT-55 x RT-125 and RT-125 x BAUT-1 had negative SCA effects, while Mrug-1 x G.Til-1, Mrug-1 x BAUT-1, AT-17 x RT-125, PY-57 x RT-125, BAUT-1 x OMT-10 and TKG-9-86 x OMT-10 showed constant significant positive SCA effects. The results indicated possibilities for development of early hybrid for light soils and suitable for dry land agriculture. It was also interesting to note that more of hybrids showed negative effects in F_1, however, it was reverse in F_2.

Days to maturity (Table 13, 14) :

EStimates of GCA effects indicated that ten parents under study showed significant GCA effects in both the

generations. Variations in the values were in the range from -4.19 (RT-125) to 2.75 (PY-57) and -3.91 (RT-125) to 2.45 (PY-57) in F_1 and F_2 generations, respectively. Effects of GCA in both the generations indicated that parent RT-125 (-4.19 in F_1 and -3.91 in F_2) showed significant maximum favourable effects followed by OMT-10 (-1.33 in F_1 and -1.08 in F_2), hence, these parents were good general combiners for this trait. On the other hand PY-57 (2.75 in F_1 and 2.45 in F_2) had significant maximum effect toward positive direction followed by Tapi and Mrug-1.

Out of 45 cross sets, 32 and 31 crosses respectively differed significantly in F_1 and F_2. During F_1, highest negative and positive SCA effects were observed in the cross RT-125 x BAUT-1 (-4.47) and Tapi x RT-125 (3.38). However, in F_2, the highest negative SCA effect was recorded in cross Tapi x Mrug-1 (-3.48) and the highest positive SCA effect in Tapi x RT-125 (6.21).

On the basis of two generations data it was observed that the crosses Tapi x PY-57, G.Til-1 x OMT-10, RT-125 x BAUT-1 and RT-125 x TKG-9-86 expressed constant significant negative SCA effects while crosses Tapi x RT-125, G.Til-1 x BAUT-1 and PY-57 x BAUT-1 exhibited constant significant positive SCA effects over the generations. In general more number of hybrids were with positive effects than negative.

Length of reproductive stem (Table 13, 14) :

The estimates of GCA effects revealed that all the

parents were with significant GCA effects in both the generations except Mrug-1 in F_1 and Tapi in F_2. Values of GCA effects varied from -3.33 (TKG-9-86) to 4.54 (BAUT-1) and -2.55 (TKG-9-86) to 4.66 (BAUT-1) in F_1 and F_2 generations, respectively. Constant positive GCA effects over the generations were recorded by the parents PY-57 and BAUT-1, thereby indicating them as good general combiners for increasing length of reproductive part on main stem.

The results on SCA effects indicated that 31 and 27 crosses differed significantly for SCA effects during F_1 and F_2. The magnitudes of SCA varied from -5.91 (AT-17 x BAUT-1) to 8.97 (Tapi x BAUT-1) and -6.30 (PY-57 x BAUT-1) to 5.26 (RT-125 x BAUT-1) during F_1 and F_2 generations, respectively. Reviewing the two generation data, it was noticed that the crosses, Tapi x BAUT-1, Mrug-1 x OMT-10, AT-17 x PY-57, AT-17 x TKG-9-86 and BAUT-1 x OMT-10 recorded significant positive SCA effects in both the generations.

Plant height to maturity (Table 13, 14) :

Significant GCA effects were observed for all parents in both the generations. It ranged from -5.66 (AHT-55) to 8.16 (PY-57) and -5.31 (AHT-55) to 8.29 (PY-57) for F_1 and F_2, respectively. In both the generations, PY-57 recorded positive and maximum GCA effects followed by BAUT-1, Tapi and Mrug-1, while parent AHT-55 showed maximum negative GCA effects followed by OMT-10, AT-17 and TKG-9-86.

SCA effects revealed that 29 and 32 cross combinations differed significantly in F_1 and F_2, respectively. Thus corresponding ranges were -15.45 (G.Til-1 x PY-57) to 15.58 (PY-57 x BAUT-1) and -11.53 (Tapi x OMT-10) to 14.84 (Tapi x RT-125). On the basis of two generations, crosses Tapi x BAUT-1, AT-17 x PY-57, AT-17 x TKG-9-86 and BAUT-1 x OMT-10 showed constant significant positive effects, while Mrug-1 x PY-57, Mrug-1 x BAUT-1, AT-17 x G.Til-1 and RT-125 x BAUT-1 expressed constant negative effects.

Number of branches per plant (Table 15, 16) :

The estimate of GCA effects indicated that of the ten parent under study, nine and seven showed significant GCA effects in F_1 and F_2, respectively. The range was from -0.24 (AHT-55) to 0.34 (Mrug-1) for F_1 and -0.31 (AHT-55) to 0.23 (OMT-10) for F_2. A critical examination of the two sets of data indicated that parents, Mrug-1, RT-125 and OMT-10 expressed constantly positive GCA effects and were best combiner for more number of branches per plant.

A perusal of the Table 16 revealed that SCA effects were significant in 33 and 28 combinations in F_1 and F_2, respectively. The corresponding ranges of SCA effects were -1.01 (G.Til-1 x PY-57) to 0.62 (PY-57 x BAUT-1) and -0.69 (PY-57 x RT-125) to 0.59 (AT-17 x TKG-9-86). Out of 45 crosses, 21 and 12 crosses only recorded significant positive SCA effects in both the generations. The crosses Tapi x AHT-55, Mrug-1 x RT-125, AT-17 x TKG-9-86, G.Til-1 x AHT-55

Table 15. Estimation of general combining ability (GCA) effects of parents for number of branches per plant, number of capsules per plant, length of capsule, number of grains per capsule, dry weight per plant and grain yield per plant in sesame

Parents	Number of branches per plant		Number of capsules per plant		Length of capsule		Number of grains per capsule		Dry weight per plant		Grain yield per plant	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Tap1	-0.07**	0.02	-2.22**	-1.60**	-0.03**	-0.05**	0.35*	-0.35**	0.31**	-0.28**	0.02	0.01
Mrug-1	0.34**	0.09**	-1.55**	-1.14**	-0.01**	-0.02**	1.85**	1.03**	0.74**	-0.13**	0.13**	0.08**
AT-17	-0.14**	-0.01	0.55**	-0.35**	0.02**	0.01**	-0.31	0.14	-0.44**	-0.24**	-0.14**	-0.10**
Gujarat T11-1	-0.19**	-0.08**	0.56**	-0.23**	0.03**	0.05**	0.79**	1.26**	-0.06	-0.14**	0.21**	0.09**
AHT-55	-0.24**	-0.31**	-1.18**	-1.07**	0.01**	0.01**	1.35**	0.91**	-0.91**	-0.44**	-0.25**	-0.14**
PY-57	0.02	0.12**	1.55**	-1.19**	0.11**	0.12**	-1.52**	-0.88**	0.39**	0.79**	-0.18**	-0.17**
RT-125	0.15**	0.18**	2.28**	3.21**	0.01**	0.01**	0.57**	-0.27*	-0.42**	-0.22	0.03	0.13**
BAUT-1	0.22**	-0.01	2.51**	1.64**	0.00	-0.02**	0.32*	-0.41**	-0.92**	0.84**	0.43**	0.35**
TKG-9-36	-0.22**	-0.20**	0.07	-0.78**	-0.07**	-0.03**	-0.39**	-0.37**	-0.34**	-0.32**	-0.21**	-0.23**
OMT-10	0.13**	0.23**	0.51**	1.51**	-0.07**	-0.09**	-1.87**	-1.06**	-0.18	-0.13**	-0.02	-0.02*
SE (g_i)±	0.019	0.019	0.071	0.061	0.003	0.003	0.013	0.012	0.034	0.020	0.014	0.017
SE (g_i-g_j)±	0.028	0.029	0.112	0.091	0.004	0.005	0.020	0.018	0.052	0.030	0.021	0.025

* Significant at 5 per cent level
** Significant at 1 per cent level

Table 16. Estimation of specific combining ability (SCA) effects of hybrids for number of branches per plant, number of capsules per plant, length of capsule, number of grains per capsule, dry weight per plant and grain yield per plant in sesame

Crosses	Number of branches per plant		Number of capsules per plant		Length of capsule		Number of grains per capsule		Dry weight per plant		Grain yield per plant	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
1	2	3	4	5	6	7	8	9	10	11	12	13
$P_1 \times P_2$	0.30**	-0.19**	0.58*	-1.22**	0.11**	-0.02	2.11**	0.62**	0.60**	0.14*	-0.02	-0.10
$P_1 \times P_3$	0.03	0.30*1	-1.41**	-0.04	0.10**	0.10**	-1.75**	0.08	0.28*	0.27**	-0.04	-0.50**
$P_1 \times P_4$	0.21**	-0.35**	0.13	-3.49**	0.10**	-0.06**	0.69**	2.33**	1.13**	-1.17**	0.59**	-0.01
$P_1 \times P_5$	0.46**	0.18**	-1.09**	-0.04	0.07**	0.06**	2.17**	-2.91**	-0.62**	1.02**	-0.16**	-0.11
$P_1 \times P_6$	-0.59**	-0.15*	0.19	-1.28**	0.00	0.12**	-2.01**	2.03**	-0.52**	-0.01	-0.17**	-0.46**
$P_1 \times P_7$	-0.40**	0.12	-4.23**	-0.45	-0.10**	0.10**	-0.56**	2.17**	-0.49**	0.60**	-1.00**	0.26**
$P_1 \times P_8$	0.36**	-0.29**	5.33**	-0.06	0.00	0.14**	4.00**	0.27**	2.86**	1.77**	0.46**	-0.24**
$P_1 \times P_9$	-0.35**	-0.26**	-0.86**	1.42**	0.04**	0.05**	-0.53**	-3.05**	0.75**	-0.23**	0.66**	0.30**
$P_1 \times P_{10}$	0.02	-0.01	2.07**	1.02**	0.09**	-0.16**	-0.78**	-2.74**	0.75**	0.03	0.11*	0.06
$P_2 \times P_3$	0.27**	0.19**	-2.47**	0.41	0.06**	-0.03**	1.00**	-0.31**	0.60**	-0.31**	0.15**	0.06
$P_2 \times P_4$	0.32**	-0.39**	-0.44	-2.21**	0.00	-0.15**	3.21**	-2.77**	0.75**	-0.55**	0.00	-0.46**
$P_2 \times P_5$	0.00	-0.27**	2.49**	1.35**	-0.06**	0.11**	0.80**	2.68**	-0.31*	0.08	0.19**	0.10
$P_2 \times P_6$	0.04	-0.30**	1.22**	0.56*	0.05**	-0.12**	-1.42**	-0.39**	-0.13	0.15**	-0.13**	-0.36**
$P_2 \times P_7$	0.34**	0.27**	3.84**	2.63**	0.10**	0.02	3.78**	3.13**	0.89**	0.12	-0.01	0.16**
$P_2 \times P_8$	-0.13*	-0.03	-4.43**	-3.40**	-0.02	0.02	1.91**	0.36**	-0.56**	-1.43**	-0.25**	-0.17**
$P_2 \times P_9$	-0.57**	0.19**	-0.25	-0.29	0.03**	0.19**	-0.34**	4.16**	0.19	0.06	0.09	-0.19**
$P_2 \times P_{10}$	0.49**	-0.34**	1.50**	2.09**	-0.12**	0.01	0.47**	-0.95**	0.74**	-0.79**	0.37**	0.10
$P_3 \times P_4$	-0.34**	-0.10	-0.57*	-0.21	-0.09**	-0.09**	-0.25**	-2.45**	-0.36**	-0.45**	0.20**	-0.03
$P_3 \times P_5$	0.47**	-0.31**	3.92**	-0.95**	-0.05**	0.02	-0.62**	-2.99**	0.70**	0.07	-0.07	-0.19**
$P_3 \times P_6$	0.10	-0.01	8.10**	1.40**	0.00	-0.02	0.99**	-0.27**	1.09**	0.57**	0.43**	-0.04
$P_3 \times P_7$	-0.29**	-0.50**	-3.39**	-3.88**	0.12**	-0.08**	-2.23**	-2.19**	0.76	-0.82**	-0.17**	-0.46**
$P_3 \times P_8$	-0.46**	0.10	-1.68**	2.50**	0.02*	-0.03**	-3.19**	-2.01**	-0.58**	0.88**	-0.15**	0.35**
$P_3 \times P_9$	0.58**	0.59**	13.91**	4.24**	-0.04**	0.06**	2.38**	5.47**	1.07**	0.88**	0.93**	0.69**

Contd.

Contd. Table 16.

1	2	3	4	5	6	7	8	9	10	11	12	13
$P_3 \times P_{10}$	0.22**	-0.05**	-3.50**	-1.60**	0.07**	0.03**	2.95**	3.09**	-1.14	-0.45**	-0.05	0.15*
$P_4 \times P_5$	0.31**	0.14*	8.94**	2.24**	0.05**	0.11**	-3.10**	-0.81**	0.58**	0.21**	0.45**	0.02
$P_4 \times P_6$	-1.01**	0.11	0.22	2.26**	0.02*	0.08**	-1.34**	-0.23**	-1.62**	-0.52**	0.12*	0.13*
$P_4 \times P_7$	0.01	0.28**	-0.71**	2.22**	0.04**	0.22**	-0.03	1.27**	-0.56**	0.01	-0.07	0.33**
$P_4 \times P_8$	0.14*	-0.12*	4.37**	-2.51**	0.00	0.09**	2.08**	1.81**	-0.47**	-0.19**	-0.22**	-0.34**
$P_4 \times P_9$	0.09	-0.03	-2.88**	-1.14**	-0.09**	-0.07**	-2.11**	-1.77**	1.08**	-0.44**	-0.01	-0.27**
$P_4 \times P_{10}$	-0.09	-0.37**	1.52**	2.89**	0.08**	-0.04**	-1.28**	-0.40**	-0.33**	1.01**	0.24**	-0.02
$P_5 \times P_6$	0.10	0.47**	0.19	1.20**	-0.02*	-0.05**	0.41	0.86**	-0.97**	0.93**	0.02	-0.13*
$P_5 \times P_7$	0.26**	0.01	3.14**	1.87**	0.04**	-0.14**	-1.19*	-2.96**	0.09	0.36**	0.29**	-0.01
$P_5 \times P_8$	0.02	-0.43**	0.67**	1.29**	0.05**	-0.02	-0.44	3.03**	-0.20	-1.29**	0.21**	0.23**
$P_5 \times P_9$	0.31**	-0.04	-3.71**	-1.76**	-0.02*	-0.01	-1.85**	5.58**	0.56**	0.11	-0.25**	0.03
$P_5 \times P_{10}$	-0.77**	0.26**	-4.70**	-2.27**	0.13**	-0.03**	-1.33**	0.04	0.13	0.35**	-0.34**	-0.08
$P_6 \times P_7$	0.03	-0.69**	-0.30	4.52**	-0.07**	0.09**	-2.87**	-2.45**	1.08**	-0.53**	-0.91**	-0.28**
$P_6 \times P_8$	0.62**	-0.36**	-4.17**	-1.08**	0.08**	-0.20	-2.73**	-2.80**	0.79**	-1.07**	-0.65**	-0.20**
$P_6 \times P_9$	0.41**	-0.07	-0.79**	3.17**	0.00	-0.10**	0.64**	-4.79**	-0.49**	0.17*	-0.37**	0.51**
$P_6 \times P_{10}$	-0.24**	-0.07	4.82**	1.87**	0.06**	0.25**	-0.05	0.53**	1.24**	0.32**	0.25**	0.20**
$P_7 \times P_8$	-0.20**	0.24**	-0.12	2.40**	0.01	0.05**	-0.78**	-0.69**	-1.40**	-0.63**	0.02	0.43**
$P_7 \times P_9$	0.21**	-0.30**	0.05	-2.29**	-0.04**	-0.13**	-2.18**	-5.33**	0.33**	0.16*	0.03	-0.53**
$P_7 \times P_{10}$	0.45**	0.14*	6.78**	3.29**	0.10**	-0.07**	-1.80**	2.25**	0.97**	0.60**	0.66**	0.09
$P_8 \times P_9$	0.34**	-0.07	7.85**	-2.75**	0.00	-0.07**	1.84**	1.86**	0.00	0.27**	1.10**	-0.11
$P_8 \times P_{10}$	0.31**	0.10	-3.46**	-2.91**	0.01	0.14**	4.40**	0.61**	1.07**	1.01**	0.61**	-0.24**
$P_9 \times P_{10}$	-0.09	0.09	-5.12**	-3.78**	0.00	-0.01	-3.75**	1.51**	-1.18**	-1.56**	-0.71**	-0.09
SE (S_{ij})	0.060	0.065	0.240	0.233	0.009	0.010	0.046	0.040	0.116	0.068	0.048	0.057
SE $(S_{ij}-S_{ik})$	0.090	0.097	0.350	0.302	0.013	0.016	0.068	0.059	0.173	0.101	0.070	0.084
SE $(S_{ij}-S_{lk})$	0.090	0.092	0.340	0.288	0.013	0.015	0.065	0.057	0.165	0.096	0.067	0.080

* Significant at 5 per cent level

** Significant at 1 per cent level

and RT-125 x OMT-10 showed constantly positive effects in both generations, whereas cross Tapi x PY-57 and AT-17 x RT-125 had constant negative SCA effects. A critical examination further revealed that more number of hybrids had constant significant positive effect than negative.

Number of capsulesper plant (Table 15, 16) :

The GCA estimates revealed significant effects in all the parents except TKG-9-86 in F_1. The range of effects was from -2.22 (Tapi) to 2.51 (BAUT-1) and -1.60 (Tapi) to 3.21 (RT-125) in F_1 x F_2 generations, respectively. Parent RT-125 recorded significant positive and maximum GCA effects followed by BAUT-1 and OMT-10 in F_1 and F_2 generations suggesting stability for combining ability for this trait.

Estimates of SCA effects showed that 36 and 38 crosses displayed significant SCA effects in F_1 and F_2, respectively. Eighteen crosses showed positive SCA effects in each generation, however 18 hybrids in F_1 and 20 hybrids in F_2 were with negative effects. The corresponding ranges were -5.12 (TKG-9-86 x OMT-10) to 13.91 (AT-17 x TKG-9-86) and -4.52 (PY-57 x RT-125) to 4.24 (AT-17 x TKG-9-86) for this trait. Twelve crosses expressed significant positive and constant SCA effects over the generations. In both the generations maximum SCA effects were recorded by AT-17 x TKG-9-86 followed by G.Til-1 x AHT-55 and AT-17 x PY-57.

Length of capsule (Table 15, 16) :

Significant GCA effects were recorded for all the parents in both generations, except BAUT-1 in F_1. Values of GCA effects varied from -0.07 (TKG-9-86 and OMT-10) to 0.11 (PY-57) and -0.09 (OMT-10) to 0.12 (PY-57) in F_1 and F_2, respectively. An examination of two sets of the data indicated that parents PY-57, G.Til-1, AT-17, AHT-55 and RT-125 recorded constant and significant positive GCA effects and were best combiners for branches per plant. However, positive effects were more in both the generations.

It was revealed that 35 crosses expressed significant SCA effects during both the generations. The ranges for F_1 and F_2 of SCA effects were -0.12 (Mrug-1 x OMT-10) to (AHT-55 x OMT-10) and -0.20 (PY-57 x BAUT-1) to 0.25 (PY-57 x OMT-10), respectively. Among the above crosses 23 and 18 recorded significant positive SCA effects in F_1 and F_2, respectively. The ten crosses revealed constantly positive effects over the generations, of which cross PY-57 x OMT-10 was highest followed by G.Til-1 x RT-125, Mrug-1 x TKG-9-86, Tapi x AT-17 and AT-17 x OMT-10.

Number of grains per capsule (Table 15, 16) :

A perusal of data for GCA effects revealed that all parents had significant effects, except AT-17 in both the generations. General combining ability varied from -1.87 (OMT-10) to 1.85 (Mrug-1) and -1.06 (OMT-10) to 1.26 (G.Til-1)

in F_1 and F_2, respectively. Constant positive GCA effects over the generations were recorded with parents Mrug-1, G.Til-1 and AHT-55, hence these parents were good combiner for increasing number of grains per capsule.

Forty one and 44 crosses significantly differed in F_1 and F_2, respectively. In first filial generation, 24 crosses expressed significant negative values, whereas 17 combinations exhibited significant positive SCA effects with a range of -3.75 (TKG-9-86 x OMT-10) to 4.40 (BAUT-1 x TKG-9-86). In F_2 generation, 22 crosses expressed significant positive values. Lowest cross was RT-125 x TKG-9-86 (-5.33) and highest was AHT-55 x TKG-9-86 (5.58). A critical examination of two sets of data revealed that 11 combinations had constant significant positive values, however of these promising crosses were Tapi x BAUT-1, Mrug-1 x RT-125, G.Til-1 x BAUT-1 and BAUT-1 x OMT-10.

Dry weight per plant (Table 15, 16) :

General combining ability data revealed that except G.Til-1 and OMT-10 in F_1, all other parents showed significant GCA effects with a range from -0.92 (BAUT-1) to 0.72 (Mrug-1) and from -0.44 (AHT-55) to 0.84 (BAUT-1) in F_1 and F_2 generations, respectively. Significant and negative GCA effects were observed for the parents AT-17, AHT-55 and TKG-9-86, whereas only one parent PY-57 showed significant negative GCA effect in both the generations.

Estimates of SCA effects showed that 37 crosses were

significant in each generation. The variation of values was from -1.62 (G.Til-1 x AHT-55) to 2.86 (Tapi x BAUT-1) and -1.56 (TKG-9-86 x OMT-10) to 1.77 (Tapi x BAUT-1) in F_1 and F_2, respectively. Eleven combinations expressed constant SCA effects for high dry weight per plant. Out of these crosses Tapi x BAUT-1 ranked first followed by BAUT-1 x OMT-10, AT-17 x TKG-9-86 and PY-57 x TKG-9-86.

Grain yield per plant (Table 15, 16) :

An examination of the data pertaining to GCA effects revealed that parents Mrug-1, G.Til-1, RT-125 and BAUT-1 showed positive and significant GCA effects in both the sets and emerged as good general combiners for grain yield. However, on the basis of two generations data parent BAUT-1 was recorded the best general combiner as it had given maximum GCA effects.

An estimate of SCA effects indicated that 33 and 28 crosses had significant effects in F_1 and F_2, respectively. Out of these 19 and 12 crosses recorded positive effects during respective generations. The crosses Tapi x G.Til-1, Tapi x TKG-9-86, AT-17 x TKG-9-86, RT-125 x TKG-9-86 and BAUT-1 x TKG-9-86 in F_1 and AT-17 x BAUT-1, AT-17 x TKG-9-86 and PY-57 x TKG-9-86 in F_2 expected the high and significant positive effect. Crosses Tapi x TKG-9-86, AT-17 x TKG-9-86, G.Til-1 x PY-57, AHT-55 x BAUT-1 and PY-57 x TKG-9-86 showed positive, significant and constant SCA effects over the generations.

Table 17. Estimation of general combining ability (GCA) effect of parents for test weight, husk seed ratio, harvest index, oil content, oil yield per plant and protein content in sesame

Parents	Test weight		Husk seed ratio		Harvest index		Oil content		Oil yield per plant		Protein content	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Tapi	0.02**	0.02**	-0.06**	-0.05**	-0.46**	0.63**	-0.52**	-0.16**	-0.01	-0.02**	0.02**	-0.20**
Mrug-1	0.02**	0.03**	-0.01*	-0.08**	-0.71**	1.37**	-0.01**	0.03**	0.06**	0.04**	0.03**	0.14**
AT-17	0.00	0.00	0.01*	0.05**	0.33**	-0.28*	0.23**	0.35**	-0.07**	-0.04**	-0.00	0.16**
Gujarat Til-1	0.03**	0.02**	-0.03**	0.02**	0.21*	0.61**	0.50**	0.49**	0.11**	0.06**	0.02**	0.32**
AHT-55	-0.03**	-0.02**	0.10**	0.05**	0.08	0.11	0.35**	0.16**	-0.11**	-0.06**	-0.02**	0.06**
PY-57	0.01	-0.01	0.02**	0.06**	0.43**	-2.74**	0.47**	0.62**	-0.08**	-0.06**	-0.01**	0.06**
RT-125	-0.02**	-0.03**	0.02**	0.01	0.74**	0.82**	0.08**	-0.03**	0.02**	0.05**	-0.03**	-0.22**
BAUT-1	0.05**	0.05**	-0.07**	-0.07**	0.38**	0.51**	0.17***	0.17**	0.21**	0.17**	0.05**	0.32**
TKG-9-86	-0.06**	-0.02**	0.01*	-0.02**	-0.47**	-0.46**	0.01**	-0.31**	-0.10**	-0.11**	-0.022**	0.24**
OMT-10	-0.04**	-0.03**	0.01*	0.05**	0.13	-0.57**	-0.27**	-1.32**	-0.05**	-0.04**	-0.03**	-0.39**
SE (g_i)±	0.001	0.001	0.005	0.006	0.081	0.115	0.003	0.006	0.006	0.005	0.002	0.004
SE (g_i-g_j)±	0.002	0.002	0.007	0.009	0.121	0.171	0.004	0.009	0.009	0.008	0.003	0.005

* Significant at 5 per cent level

** Significant at 1 per cent level

Table 18. Estimation of specific combining ability (SCA) effects of hybrids for test weight, husk seed ratio, harvest index, oil content, oil yield per plant and protein content in sesame

Crosses	Test weight		Husk seed ratio		Harvest index		Oil content		Oil yield per plant		Protein content	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
1	2	3	4	5	6	7	8	9	10	11	12	13
$P_1 \times P_2$	-0.01**	-0.02**	0.15**	0.14**	-1.72**	-1.55**	0.17**	0.57**	-0.01	-0.02	-0.36**	-0.46**
$P_1 \times P_3$	0.00	-0.04**	0.09**	0.01	-1.19**	-3.58**	0.25**	0.22**	-0.01	-0.21**	0.12**	0.06**
$P_1 \times P_4$	-0.03**	-0.03**	-0.02	-0.17**	0.43	5.46**	0.25**	-0.14**	0.29**	0.01	-0.08**	-0.14**
$P_1 \times P_5$	-0.01**	-0.02**	0.01	-0.10**	0.85*	4.25**	0.25**	0.52**	-0.07**	-0.03	0.05**	0.02
$P_1 \times P_6$	0.03**	0.03**	0.07	0.21**	-0.31	-3.99**	-0.15**	-0.47**	-0.08**	-0.22**	-0.12**	-0.08**
$P_1 \times P_7$	0.01**	0.03**	0.30**	0.09**	-5.26**	-1.76**	-0.13**	0.52**	-0.48**	-0.01	0.07**	0.11**
$P_1 \times P_8$	0.01**	-0.01	-0.15**	0.27**	-1.60**	-5.73**	0.59**	0.57**	0.24**	-0.09**	0.11**	0.20**
$P_1 \times P_9$	0.01*	-0.01	-0.19**	-0.08**	3.00**	3.20**	0.84**	1.46**	0.34**	0.18**	0.24**	0.19**
$P_1 \times P_{10}$	0.02**	0.01	-0.10**	-0.12**	-0.23	1.02**	-1.56**	-1.66**	-0.01	-0.01	-0.08**	0.12**
$P_2 \times P_3$	0.01**	-0.01	-0.05**	-0.05*	-0.58*	-1.41**	-0.62**	-0.39**	0.06**	0.02	0.09**	0.09**
$P_2 \times P_4$	0.01**	0.02**	-0.07**	-0.04*	-1.39**	-1.01*	-0.32**	-0.39**	-0.01	-0.23**	-0.08**	-0.12**
$P_2 \times P_5$	-0.04**	-0.04**	-0.01	0.01	1.21**	0.11	0.59**	-0.34**	0.11**	0.04*	0.13**	-0.05**
$P_2 \times P_6$	0.01**	-0.01	-0.03	0.28**	-0.88**	-3.97**	0.27**	0.39**	-0.06**	-0.17**	-0.08**	-0.01
$P_2 \times P_7$	0.02**	0.01	0.33**	0.05*	-3.53**	0.21	0.30*	-0.68**	0.01	0.07**	0.17**	0.23**
$P_2 \times P_8$	-0.02**	-0.01	-0.09**	-0.14**	0.03	3.80**	-0.64**	-0.19**	-0.14**	-0.09**	-0.08**	0.01
$P_2 \times P_9$	0.01**	0.01	0.10**	-0.09**	-0.58*	-1.15**	-0.34**	0.13**	0.03	-0.09**	-0.04**	0.02
$P_2 \times P_{10}$	0.05**	0.08**	0.07**	0.05*	-0.24	1.76**	0.31**	0.39**	0.18**	0.02	0.01	0.07**
$P_3 \times P_4$	-0.01**	0.01	0.16**	0.06**	-1.34**	0.73	-1.02**	-0.06**	-0.13**	-9.02	0.00	0.00
$P_3 \times P_5$	0.01**	-0.01	0.10**	-0.11**	-0.71*	-0.76*	0.63**	-0.65**	0.05*	-0.11**	0.05**	0.05**
$P_3 \times P_6$	0.01**	-0.02**	0.08**	0.06**	-1.07**	-1.78*	-0.18**	-0.45**	0.19**	-0.04	-0.10**	-0.04**
$P_3 \times P_7$	-0.01**	-0.05**	0.10**	0.15**	-1.94**	1.04**	-1.07**	-0.27**	-0.11**	-0.21**	-0.07**	-0.11**
$P_3 \times P_8$	0.06**	0.04**	-0.01	-0.08**	0.37	-0.06	0.76**	0.17**	-0.05*	0.17**	-0.06**	-0.02
$P_3 \times P_9$	-0.01**	-0.01	-0.13**	-0.02	2.56**	-1.63**	0.79**	0.58**	0.47**	0.34**	-0.06**	-0.11**

Contd.

1	2	3	4	5	6	7	8	9	10	11	12	13
$P_3 \times P_{10}$	-0.02**	-0.01	-0.25**	0.07**	4.69**	0.82*	-1.08**	-0.57**	-0.05*	0.06**	-0.12**	-0.10**
$P_4 \times P_5$	0.04**	0.03**	0.09**	-0.02	-0.20	-1.30**	0.33**	0.46**	0.23**	0.02	0.06**	0.02
$P_4 \times P_6$	0.02**	-0.02**	-0.16**	-0.14**	4.92**	1.48**	-0.01	0.03	0.06**	0.06**	-0.29**	-0.19**
$P_4 \times P_7$	-0.03**	-0.01	-0.03	0.17**	1.85**	0.81*	0.49**	-0.34**	-0.01	0.15**	0.76**	0.71**
$P_4 \times P_8$	-0.04**	-0.01	-0.11**	0.05*	0.60*	-1.29**	0.40**	-0.03	-0.09**	-0.17**	-0.05**	0.01
$P_4 \times P_9$	0.06**	-0.06**	-0.27**	0.26**	-0.74**	-1.67**	-0.13**	-0.38**	-0.01	-0.14**	-0.07**	-0.08**
$P_4 \times P_{10}$	0.01**	-0.01	0.18**	0.09**	0.32	-2.20**	-0.58**	0.15**	0.09**	-0.02	-0.07**	-0.03**
$P_5 \times P_6$	-.01**	0.06**	-0.17**	0.09**	3.03**	-3.20**	0.16**	-0.25**	0.01	-0.07**	-0.28**	-0.29**
$P_5 \times P_7$	-0.01**	0.02**	-0.10**	-0.10**	1.82**	-0.06	0.68**	0.94**	0.16**	0.04*	-0.11**	0.07**
$P_5 \times P_8$	-0.02**	-0.01	-0.08**	0.05*	1.72**	3.57**	0.12**	0.39**	0.10**	0.12**	0.03*	0.11**
$P_5 \times P_9$	-0.01**	-0.03**	0.35**	-0.12**	-4.02**	0.12	-1.27**	-0.13**	-0.15**	0.01	-0.06**	-0.10**
$P_5 \times P_{10}$	0.02**	-0.01	0.16**	0.27**	-2.63**	-2.58**	0.10**	-0.46**	-0.16**	-0.05**	0.07**	0.06**
$P_6 \times P_7$	0.01**	-0.02**	-0.26**	0.11**	2.80**	-0.60	0.60**	0.74**	0.46**	-0.10**	0.35**	0.20**
$P_6 \times P_8$	-0.01**	-0.01	0.30**	-0.13**	-5.28**	1.87**	0.39**	-0.73**	-0.30**	-0.10**	0.43**	0.29**
$P_6 \times P_9$	-0.01**	-0.01	0.22**	-0.03	-2.18**	2.41**	-0.62**	0.63**	-0.19**	0.25**	0.02	-0.14**
$P_6 \times P_{10}$	-0.03**	-0.02**	0.01	-0.17**	-1.44**	1.08**	-0.90**	-0.10**	0.09**	0.09**	0.48**	0.40**
$P_7 \times P_8$	0.02**	-0.06**	0.03	-0.10**	2.62**	3.88**	-0.06**	1.15**	0.01	0.25**	-0.15**	-0.43**
$P_7 \times P_9$	0.01**	0.02**	-0.13**	-0.22**	0.33**	-2.48**	-0.21**	0.07**	0.02	-0.25**	-0.10**	-0.04**
$P_7 \times P_{10}$	0.01**	0.01	-0.05**	0.04*	0.23	-0.87*	1.04**	-0.86**	0.34**	0.03	-0.20**	-0.23**
$P_8 \times P_9$	0.02**	0.04**	0.04*	0.16**	3.78**	-1.49**	0.64**	0.28**	0.55**	-0.05*	-0.06**	0.04**
$P_8 \times P_{10}$	0.03**	0.01	0.06**	-0.05*	-0.32	-3.06**	-0.41**	-0.19**	0.26**	-0.12**	0.00	-0.50**
$P_9 \times P_{10}$	0.03**	0.02**	-0.17**	-0.13**	1.08**	1.69**	1.05**	0.95**	-0.26**	-0.02	0.05**	0.07**
SE (S_{1j})	0.002	0.005	0.017	0.019	0.271	0.382	0.009	0.020	0.021	0.018	0.012	0.011
SE $(S_{1j}-S_{1k})$	0.003	0.008	0.025	0.029	0.402	0.567	0.013	0.030	0.031	0.027	0.018	0.016
SE $(S_{1j}-S_{1k})$	0.002	0.007	0.024	0.028	0.384	0.540	0.013	0.028	0.029	0.026	0.017	0.015

* Significant at 5 per cent level
** Significant at 1 per cent level

Test weight (Table 17, 18) :

Significant GCA effects were found in all the parents, except AT-17 and PY-57 in both the generations. Five parents viz., BAUT-1, G.Til-1, Tapi, Mrug-1 and PY-57 had significant positive values for F_1 and F_2 and appeared as good general combiners.

Forty four F_1 and 14 cross set F_2 recorded significant SCA effects, out of these 18 and 13 crosses were with positive values in the respective generations. On the basis of two sets of data, it was observed that 11 hybrids had constant significant positive and seven crosses had constant negative effects. Out of these four high value crosses were Tapi x PY-57, Mrug-1 x OMT-10, G.Til-1 x AHT-55 and BAUT-1 x TKG-9-86.

Husk seed ratio (Table 17, 18) :

Out of ten, nine parents were found significant for GCA effects in both the generations. The values ranged from -0.04 (BAUT-1) to 0.01 (AHT-55) and -0.07 (BAUT-1) to 0.06 (PY-57) in F_1 and F_2, respectively. Estimation of GCA effects during F_1 and F_2 generations indicated that parent BAUT-1 showed significant and maximum GCA effects in desired (negative) direction, whereas Tapi and Mrug-1 were also observed to be good general combiner for husk seed ratio.

The significance for GCA effects was expressed in 31 and 39 crosses in F_1 and F_2 generations, respectively. During

F_1, the highest and lowest SCA effects were observed in cross G.Til-1 x TKG-9-86 (-0.27) and AHT-55 x TKG 9-86 (0.35), respectively. However, in F_2 the lowest SCA effects were recorded by PY-57 x RT-125 (-0.22) and highest was Mrug-1 x PY-57 (0.28). The ten crosses viz., Tapi x TKG-9-86, Tapi x OMT-10, Mrug-1 x AT-17, Mrug-1 x G.Til-1, Mrug-1 x BAUT-1, AT-17 x BAUT-1, G.Til x PY-57, AHT-55 x RT-125, RT-125 x TKG-9-86 and TKG!9-86 x OMT-10 showed constant and significant SCA effects in desired direction.

Harvest index (Table 17, 18) :

All the parents showed significant GCA effects in both the generations, except AHT-55 in both and OMT-10 in F_1 generation. Its range was from -0.71 (Mrug-1) to 0.75 (RT-125) and -2.74 (PY-57) to 1.37 (Mrug-1) in F_1 and F_2, respectively. Parents RT-125, BAUT-1 and G.Til-1 showed significant positive GCA effects over the generations, suggesting that they were good combiners for high harvest index.

Significant SCA effects were observed in 34 and 38 hybrids during F_1 and F_2 generations, respectively. Of these 15 hybrids were with positive effects for both the generations. On reviewing the data of two generations, nine crosses displayed positive and significant SCA effects over the generations. It was noted that the magnitude of positive SCA effects were generally higher than the negative effects.

Oil content (Table 17, 18) :

In general all the parents had significant SCA effects for oil content in both the generations. Parents Tapi and OMT-10 had negative GCA effects, whereas AT-17, G.Til-1, AHT-55, PY-57, RT-125 and BAUT-1 had positive effect in both the generations and were good combiners for the trait.

Out of 45 crosses, 24 had significant positive effect for high oil content in F_1 and 22 crosses in F_2 generations. Nineteen in F_1 and 22 combinations in F_2 were significantly poor specific combinations. Crosses Tapi x TKG-9-86, AT-17 x BAUT-1, AT-17 x TKG-9-86 and TKG-9-86 x OMT-10 were best specific combinations both in F_1 and F_2 generations. No relevance between GCA of parents and SCA of crosses was observed.

Oil yield per plant (Table 17, 18) :

This trait was directly related to oil content and grain yield. Data revealed that GCA estimates varied from -0.11 (AHT-55) to 0.21 (BAUT-1) and -0.11 (TKG-9-86) to 0.17 (BAUT-1) for F_1 and F_2, respectively. Parents BAUT-1, G.Til-1, Mrug-1 and RT-125 indicated significant positive GCA effects both in F_1 and F_2 generations, whereas AHT-55, TKG-9-86, PY-57, OMT-10 and Tapi had negative significant effects indicating their poor combining ability for oil yield. More number of parents had negative GCA effects in both the sets.

Estimates of SCA effects revealed that in F_1 and F_2 generations 26 and 28 crosses exhibited significant SCA effects, respectively, of which 15 crosses had negative and 11 crosses had positive SCA effects in F_1, whereas 18 crosses had positive and 11 had negative SCA effects in F_2. The respective ranges varied from -0.48 (Tapi x RT-125) to 0.55 (BAUT-1 x TKG-9-86) and -0.25 (RT-125 x BAUT-1) to 0.34 (AT-17 x TKG-9-86), in F_1 and F_2. On the basis of two sets of data, it was observed that crosses Tapi x TKG-9-86, Mrug-1 x AHT-55, AT-17 x TKG-9-86, G.Til-1 x PY-57, AHT-55 x RT-125, AHT-55 x BAUT-1 and PY-57 x OMT-10 expressed constant significant positive SCA effects.

Protein content (Table 17, 18) :

In both the generations, all the parents indicated significant GCA effects, except AT-17 in F_1. General combining ability of Mrug-1, G.Til-1 and BAUT-1 was positive in both the generations. Parent BAUT-1 was best general combiner and OMT-10 was the poorest general combiner among the parents.

Forty one crosses revealed significant SCA effects in F_1 and 37 in F_2 generation. Significant positive SCA effects were recorded in 17 crosses, whereas 24 crosses showed significant negative effect in F_1, while in F_2 19 and 18 combinations possessed negative and positive SCA effects respectively. Crosses Tapi x AT-17, Tapi x TKG-9-86, Mrug-1 x RT-125, PY-57 x BAUT-1 and PY-57 x TKG-9-86 were good specific combinations for protein content.

4.4   DIALLEL ANALYSIS :

A set of 10 x 10 diallel cross each in F_1 and F_2 was analysed. The objectives were to test the validity of assumptions underlying diallel analysis, to study gene actions involved and components of genetic variance.

Validity of the assumptions :

Assumptions underlying diallel analysis are parental homozygosity, diploid segregation, absence of reciprocal effects, no multiple alleles, uncorrelated gene distributions and independent action of non-allelic genes (Hayman, 1954b). Failure of any one invalidates the inferences drawn to a certain extent. In the present study, parental homozygosity is assured as the parents are self-pollinated. Though, sesame is known to be of polyploid in origin, yet it is believed to behave in deploid manner. Absence of reciprocal effects was not tested in this investigation, but could well have been present, as reported by Murty (1975), Singh (1981), Sharma and Chauhan (1985), Dora and Kamala (1987) and Pawar and Pawar (1990). For other assumptions general tests were employed to screen the traits for such failures as it was difficult to analyse individually.

In first general test of assumption, heterozygosity of (Wr-Vr) was analysed by t^2 test of significance. The t^2 values calculated for each character in each set of experiment are presented in Table-19. The results indicated that t^2 values

Table 19. Estimates of t^2 values, regression coefficient (b) of Wr on Vr and correlation (r) between (Wr + Vr) and Yr for different characters in sesame

Characters	Genera-tion	t^2 value	'b' value	SE b	t value for b-0/ SE b	t value for 1-b/ SE b	r value
1	2	3	4	5	6	7	8
Plant height to first flowering	F_1	0.284	0.342	0.310	1.103	2.123	0.606
	F_2	1.003	0.499	0.456	1.093	1.099	0.020
Days to first flowering	F_1	0.011	0.822	0.189	4.351**	0.946	-0.583
	F_2	2.716	0.332	0.186	1.785	3.592**	-0.305
Days to 50 per cent flowering	F_1	0.145	0.758	0.179	4.232**	1.355	-0.711*
	F_2	3.367	0.850	0.164	5.312**	0.938	-0.686*
Days to maturity	F_1	0.883	0.698	0.162	4.315**	1.869	-0.439
	F_2	4.209	0.682	0.267	2.554*	1.192	0.508
Length of reprod-uctive stem	F_1	0.491	0.713	0.209	3.411**	1.376	0.015
	F_2	0.358	0.399	0.258	1.545	2.333*	0.288
Plant height to maturity	F_1	0.491	0.538	0.398	1.351	1.159	-0.035
	F_2	0.409	0.775	0.157	4.927**	1.430	-0.024
Number of branches per plant	F_1	0.523	0.198	0.268	0.738	3.016*	0.394
	F_2	0.080	0.811	0.245	3.308**	0.774	-0.078
Number of capsules per plant	F_1	10.988*	0.037	0.134	0.276	7.186**	0.198
	F_2	0.208	0.681	0.208	3.275**	1.533	0.772*
Length of capsule	F_1	0.937	0.692	0.164	3.796**	1.875	-0.523
	F_2	1.411	0.597	0.172	3.472**	2.841*	-0.497
Number of grains per capsule	F_1	0.108	-0.368	0.329	-1.120	4.162**	-0.198
	F_2	4.066	-0.458	0.151	-3.354	9.665**	0.401
Dry weight per plant	F_1	5.135	0.373	0.150	2.491	4.193**	0.015
	F_2	0.880	0.295	0.240	1.226	2.933*	-0.357
Grain yield per plant	F_1	2.978	0.443	0.168	2.632*	3.317**	-0.073*
	F_2	0.115	0.693	0.159	4.345**	1.924	0.289
Test weight	F_1	2.493	0.939	0.143	6.583**	0.425	-0.738*
	F_2	0.585	0.967	0.152	6.365**	0.214	-0.349
Husk seed ratio	F_1	0.802	0.124	0.256	0.484	2.015	0.264
	F_2	1.988	0.153	0.568	0.269	1.493	0.343
Harvest index	F_1	2.392	0.126	0.207	0.606	4.220**	-0.721*
	F_2	5.165	0.384	0.150	2.562*	4.104**	0.669*
Oil content	F_1	0.619	0.370	0.244	1.515	2.578*	0.118
	F_2	3.589	0.161	0.185	0.872	4.537**	-0.267
Oil yield per plant	F_1	2.501	0.433	0.177	2.444*	3.196**	-0.784*
	F_2	0.064	0.621	0.311	1.999	1.217	0.172
Protein content	F_1	2.876	0.713	0.239	2.982*	1.202	-0.787*
	F_2	0.520	0.814	0.134	6.063**	1.388	0.401

* Significant at 5 per cent level   ** Significant at 1 per cent level

were non significant for both the generations and suggested validity of hypothesis of diallel analysis.

The second test of assumption is an analysis of (Wr-Vr) regression. The coefficients in the tests are expected to be significantly different from zero, but not from one, if all the assumptions are correct (Jink and Hayman, 1953).

The regression presented in Table-19 indicated that regression coefficient deviated significantly from zero in days to first flowering (F_1), days to 50 per cent flowering (F_1 and F_2), days to maturity (F_1 and F_2), length of reproductive stem (F_1), plant height to maturity (F_2), number of branches per plant (F_1 and F_2), number of capsules per plant (F_2), length of capsules (F_1 and F_2), grain yield per plant (F_1 and F_2), test weight (F_1 and F_2), harvest index (F_2), oil yield per plant (F_1) and protein content (F_1 and F_2). On the other hand, regression varied significantly from unity for the characters, number of branches per plant, number of capsules per plant, grain yield per plant, oil yield per plant in F_1, while days to first flowering, length of reproductive stem, length of capsule in F_2 and number of grains per capsule, dry weight per plant, harvest index in both the generations. It indicated partial failure of assumptions and role of gene interactions and hence conclusion drawn are therefore, subjected to those limitations of the techniques.

4.4.1 Graphical analysis :

To evaluate parental lines Vr, Wr values were plotted in graph separately for each of the character in F_1 and F_2. The linear regression of Wr on Vr and the limiting parabola Wr = Vr. Wr^2 = Vp x Vr for all the characters are given in Figures 1 to 18. The slope of regression line was studied by calculating the regression coefficient (b). To test the uniformity of Wr - Vr, t^2 value and correlation between parental order of dominance (Wr + Vr) and parental measurement (Yr) was also computed. Parents Tapi, Mrug-1, AT-17, Gujarat Til-1, AHT-55, PY-57, RT-125, BAUT-1, TKG-9-86 and OMT-10 have been represented in the graphs 1 to 10, respectively.

Plant height to first flowering (Fig.1) :

Since t^2 value was significant, analysis was performed after removing the parent TKG-9-86 in F_1, then this character showed partial fulfilment of assumption. The data on two generations indicated that the regression value of Wr on Vr (b = 0.342 $\pm$ 3.10 in F_1 and 0.499 $\pm$ 0.456 in F_2) neither significantly deviated from zero nor unity in both the generations and non significant value of 't^2' showed validity of assumption in the use of diallel analysis. The interception of Wr axis by regression slope below the point of origin denoted the occurance of over-dominance in F_1 and F_2. The array points widely scattered along the regression line showed considerable genetic diversity among the parent for plant

Fig.1· Wr,Vr AND STANDARDISED DEVIATION GRAPH FOR PLANT HEIGHT TO FIRST FLOWERING

height to first flowering. The parent BAUT-1 was near the lower end of the regression line denoted excess of dominant alleles over recessive alleles, whereas parent Mrug-1 had most of recessive alleles. Above results were also confirmed by standardized deviation graphs.

The correlation between parental order of dominance (Wr + Vr) and parental measurement (Yr) was non-significant which indicated that equal proportion of dominant genes with positive and negative effect were present in the parents. The results suggested that the trait was not entirely determined by the dominant genes.

Days to first flowering (Fig.2) :

Regression co-efficient 'b' differed significantly from zero and did not differ significantly from unity for F_1 indicating the validity of additive dominance model. Non significant values of t^2 indicated that Wr-Vr was homozygous over arrays. However, 'b' value was significant from unity in F_2. The position of interception of the Wr axis by regression line showed the occurance of over dominance in F_1 and partial dominance in F_2. The scattered distribution of arrays along the regression lines indicated considerable variability among the parents. The parent PY-57 was near the point of origin indicating preponderance of dominant genes, while parent BAUT-1 had mostly recessive alleles in both the generations, whereas parent TKG-9-86 had mostly recessive alleles in F_1. Standardized deviation graphs confirmed the above results.
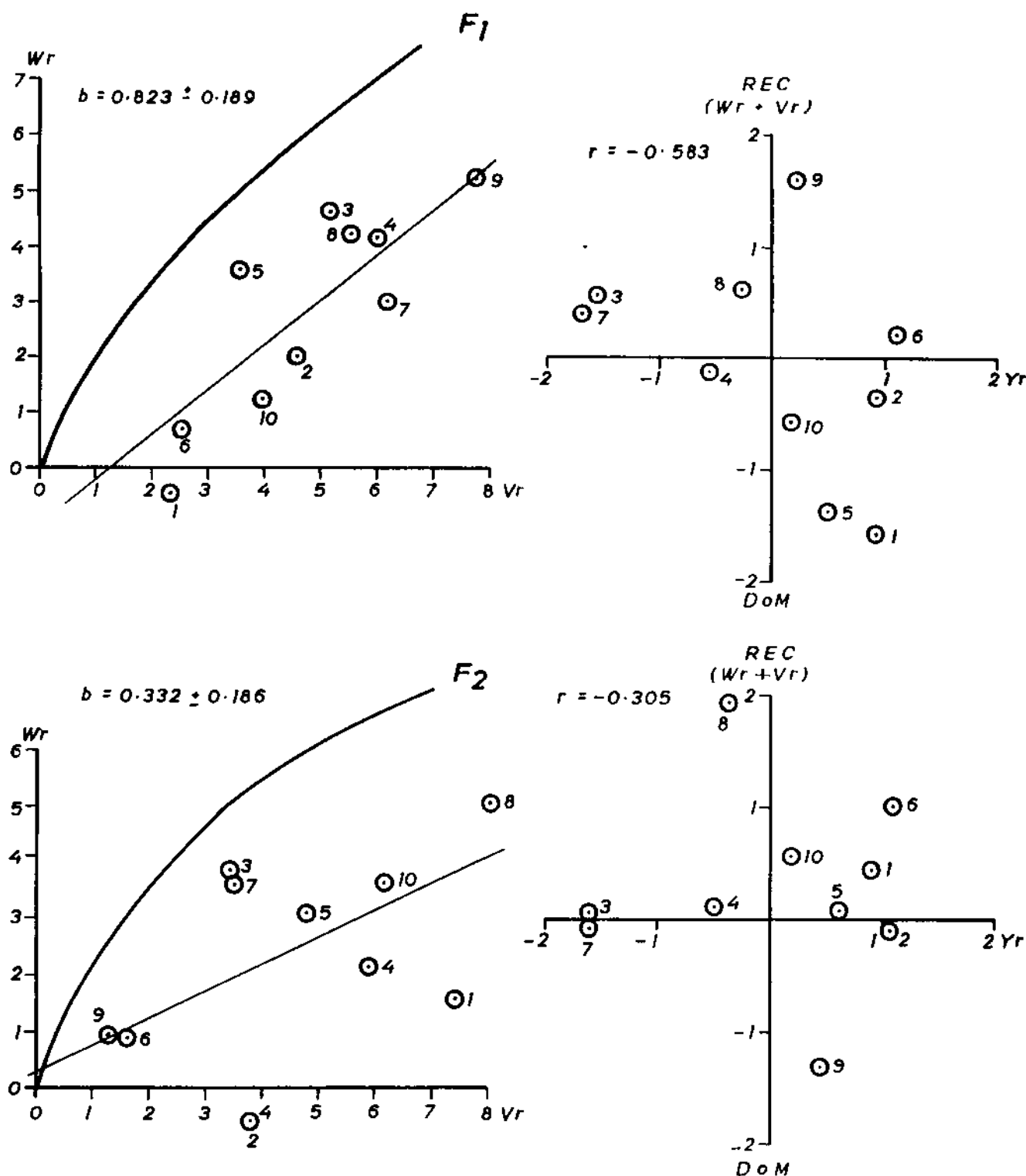
Fig.2. *Wr,Vr AND STANDARDISED DEVIATION GRAPH FOR DAYS TO FIRST FLOWERING*

The relationship between parental measurement (Yr) and parental order of dominance (Wr + Vr) was negative and non-significant in both F_1 and F_2, indicated that dominant and recessive genes were equally associated with high mean performance.

Days to 50 per cent flowering (Fig.3) :

The regression value (b = 0.758 $\pm$ 0.179 in F_1 and 0.850 $\pm$ 0.164 in F_2) differed significantly from zero and did not deviate significantly from unity, suggesting fitness of additive dominance model and 't^2' values were also non-significant in both the generations. In Wr, Vr graphs, regression lines intersected the Wr axis below the point of origin in both the generations, indicating over-dominance effect. The array points were well distributed along the regression line, implied that the parents were genetically diverse. A perusal of both the graphs, indicated that parent PY-57 had maximum dominant genes, while parents BAUT-1 RT-125 and G.Til-1 showed maximum number of recessive alleles. Parent TKG-9-86 exhibited different positions, on graphs in two generations, thus indicated presence of minor genes.

Correlation between parental order of dominance (Wr+Vr) and parental measurement (Yr) was negative and significant in both the generations, indicated tendency of dominant genes to be associated with days to 50 per cent flowering.
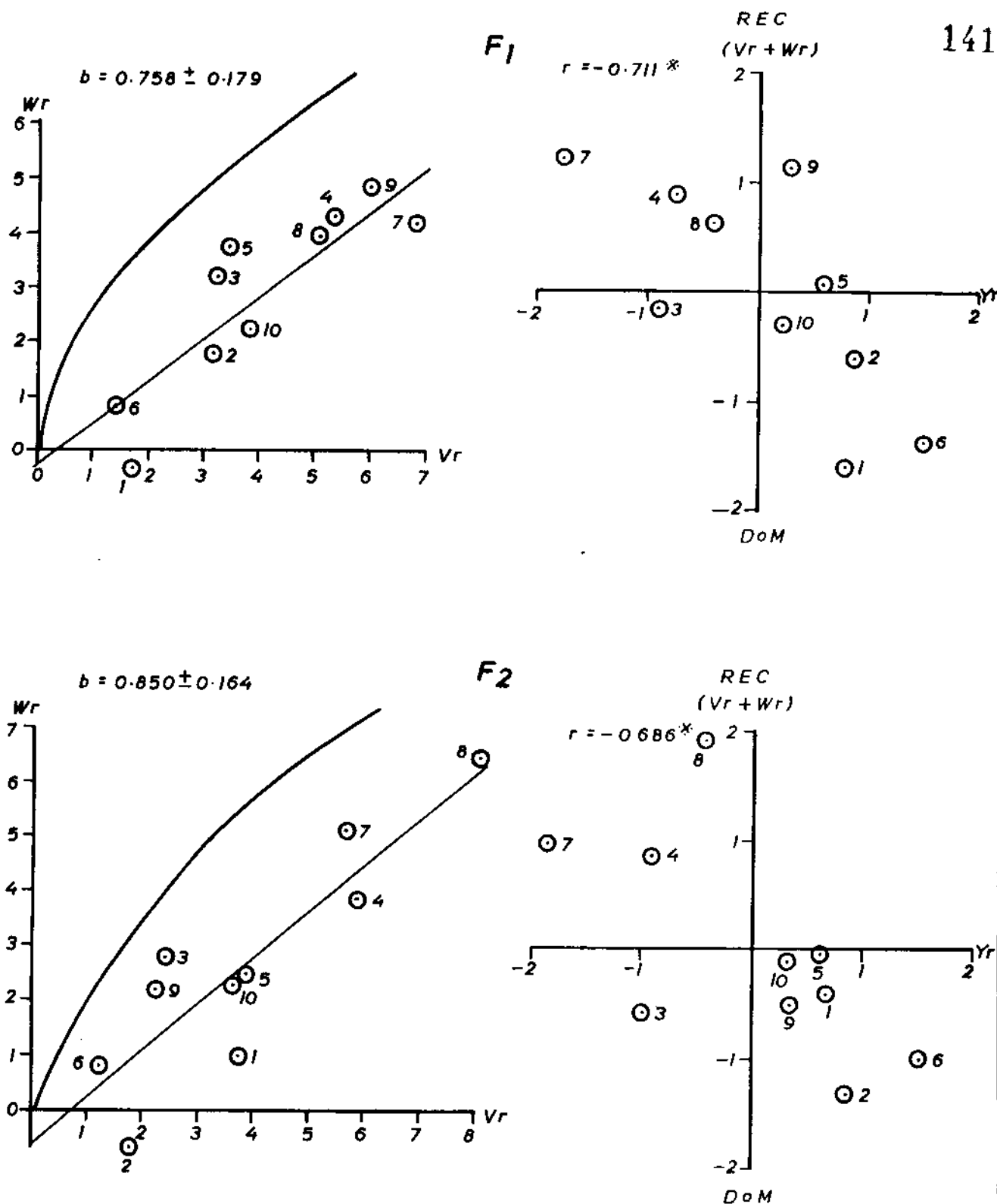
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Fig.3. Wr, Vr AND STANDARDISED DEVIATION GRAPH FOR DAYS
TO 50% FLOWERING.

Days to maturity (Fig.4) :

Additive dominance model fits well for this character as the 'b' values differed significantly from zero, but did not differ significantly from unity and non-significant values of 't^2' for both the generations. Thus both tests showed validity of the assumptions underlying diallel analysis. Regression lines intersected the Wr axis above the point of origin in both the generations, indicating partial dominance. Parents Tapi and Mrug-1 had maximum number of dominance genes, while parents BAUT-1 and RT-125 possessed most recessive genes and parent TKG-9-86 had equal number of dominant and recessive genes, being points distributed around centre position. Similar results were also revealed by standardized deviation graphs in both the generations.

Correlation between parental order of dominance (Wr+Vr) and parental measurement (Yr) was negative and non-significant in F_1 generation, while it was positive and non-significant in F_2 indicating that the trait was not entirely determined by dominant genes.

Length of reproductive stem (Fig.5) :

The 'b' values differed significantly from zero but not unity in F_1. The reverse trend was observed in F_2, which partly revealed the absence of non-allelic interactions. Non-significant values of 't^2', indicated the validity of assumption in use of diallel analysis (Table-19). Wide distribution of parents in the graphs indicated high degree of
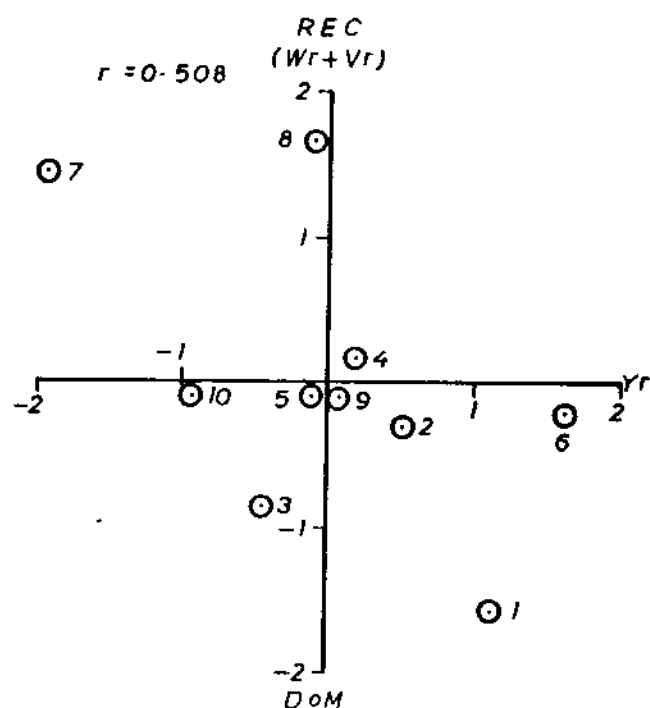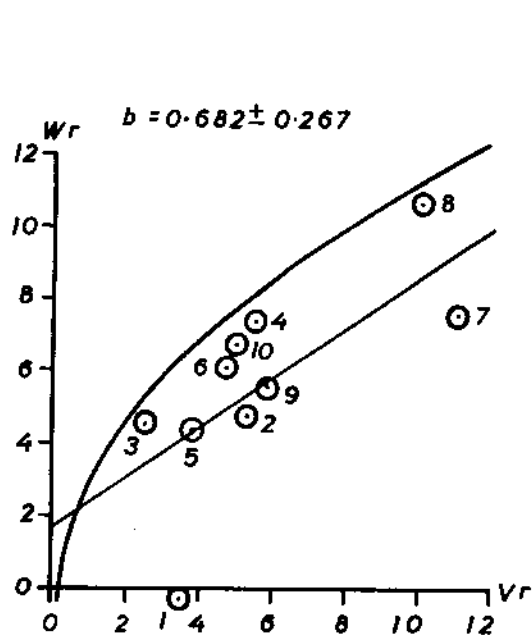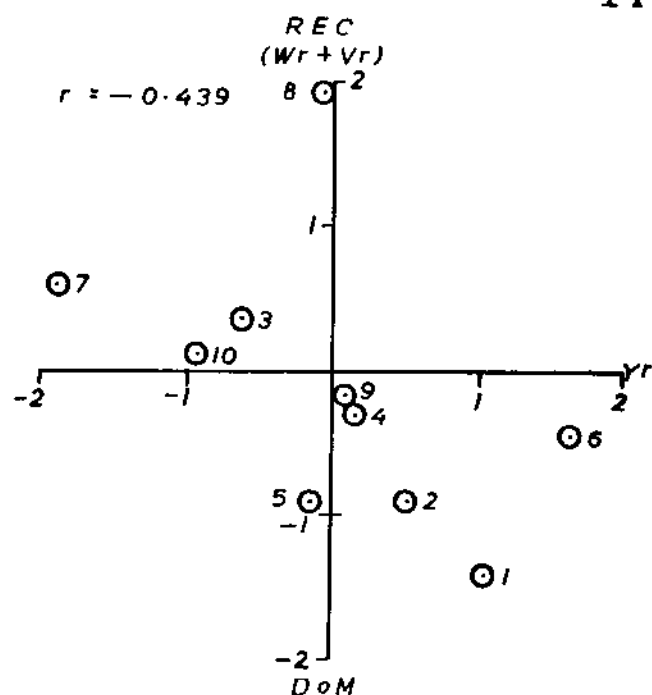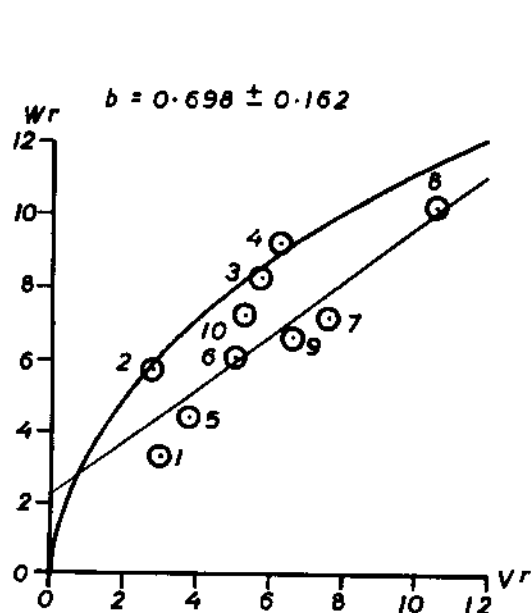
Fig.4 Wr, Vr AND STANDARDISED DEVIATION GRAPH FOR DAYS TO MATURITY.
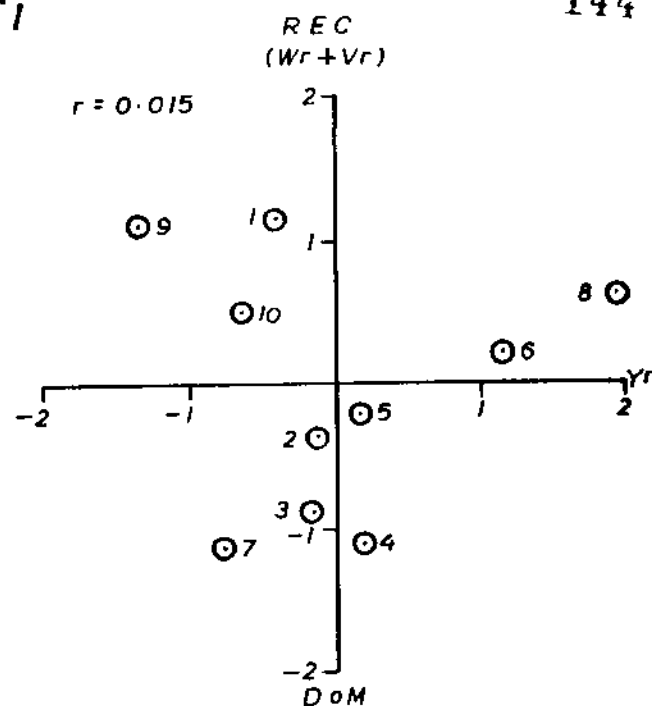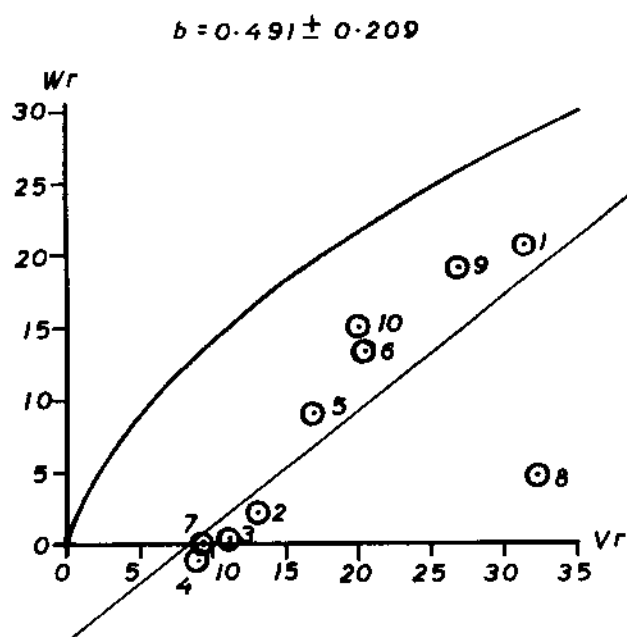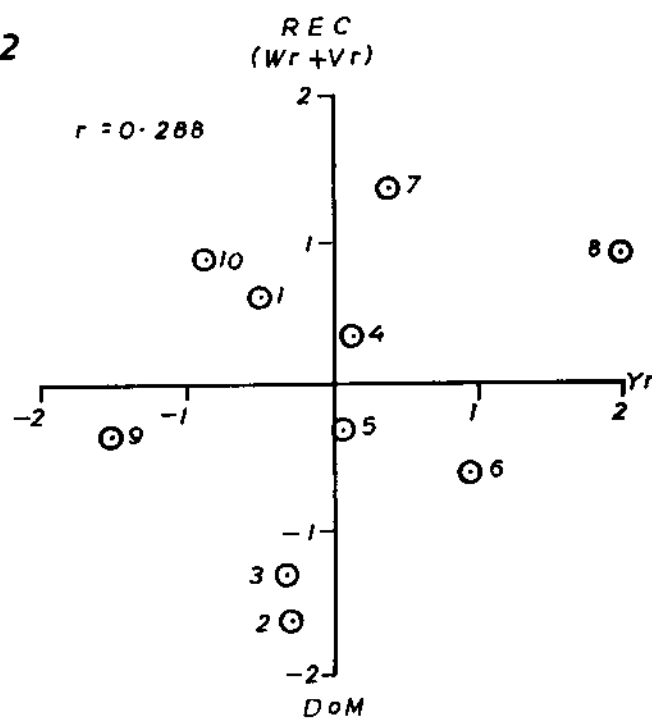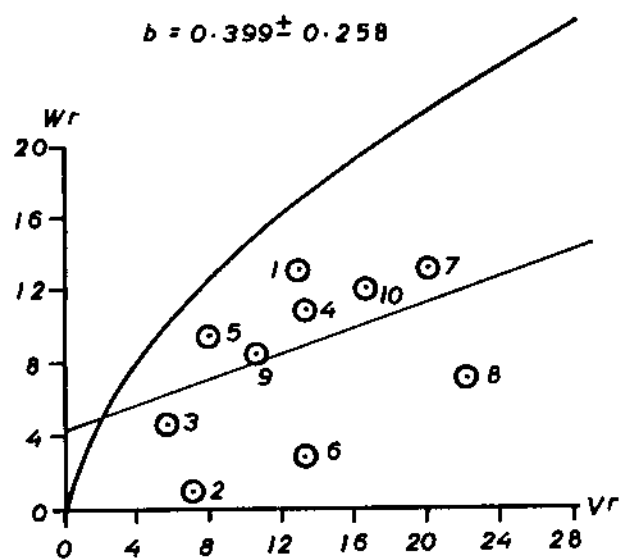
Fig. 5. Wr, Vr AND STANDARDISED DEVIATION GRAPH FOR LENGTH OF REPRODUCTIVE STEM.

genetic diversity of parents. The regression line intersected the Wr axis of Wr, Vr graphs below the point of origin in F_1 indicating over dominance while in F_2 graph showed partial dominance. Parent AT-17 and Mrug-1 had more number of dominant alleles being near the point of origin. Parent Tapi and Baut-1 possessed excess of recessive alleles and parent AHT-55 was constant in middle position indicating equal number of dominant and recessive alleles. The above results were also confirmed by standardized deviation graphs for both the generations.

Correlation between (Wr + Vr) and Yr was positive and non-significant which indicated that equal proportion of dominant genes with positive and negative effects were present in the parents and thus the trait was not entirely determined by the dominant genes.

Plant height to maturity (Fig.6) :

The 'b' value of Wr on Vr significantly deviated from zero but not unity for F_1, while regression co-efficient (b) neither significantly deviated from zero nor unity in F_1 indicated genetic interaction arising from the diversity in parental genotype. Values of 't^2' were non-significant for both F_1 and F_2 showed validity of the assumption. Regression line intersected the Wr axis above the point of origin in F_1 and just below the point of origin in F_2 indicating partial dominance and over dominance, respectively. Parent, BAUT-1 shifted its position at far end of regression in F_2 indicating
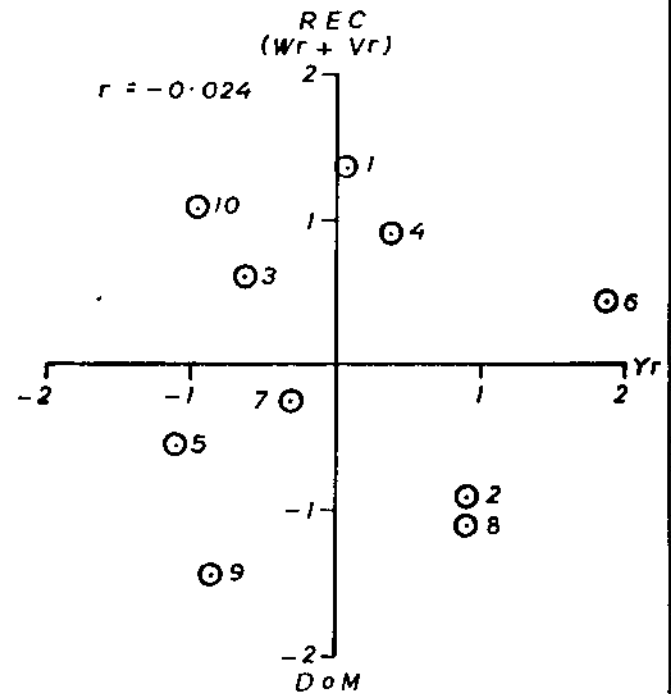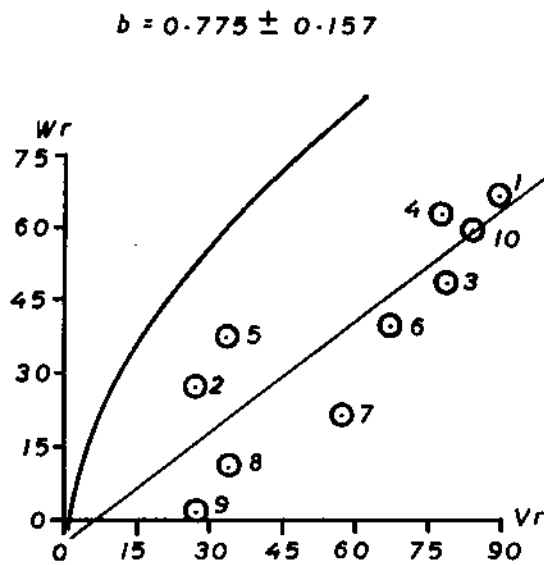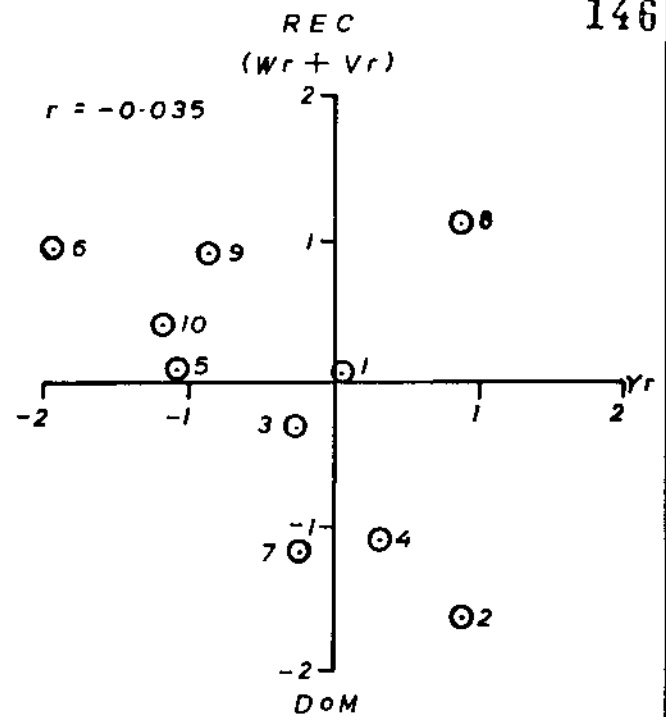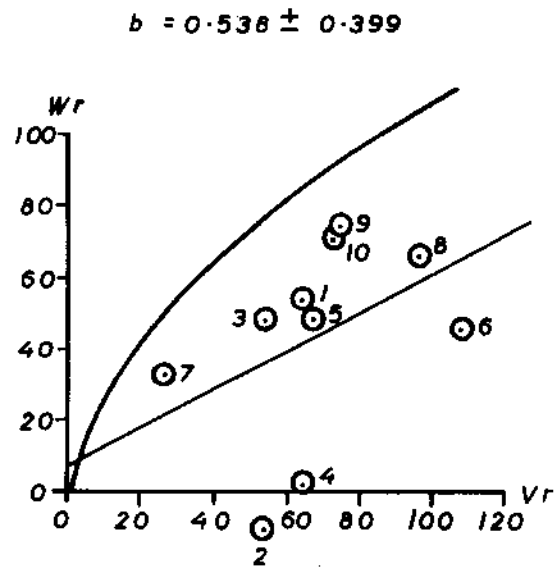
Fig. 6. Wr,Vr AND STANDARDISED DEVIATION GRAPH FOR PLANT HEIGHT TO MATURITY.

the existence of minor genes. Standardised deviation graph strongly confirmed the above results.

The negative and non-significant correlation of Yr with (Wr + Vr) explained that dominant and recessive genes were equally associated with high mean performance.

Number of branches per plant (Fig.7) :

The character showed partial fulfilment of assumptions as indicated by two tests. The regression co-efficient (b) differed significantly from unity in F_1, while in F_2, regression of Wr on Vr deviated significantly from zero but not from unity. Non-significant values of 't^2' in both the generations showed uniformity of (Wr-Vr) over arrays. Thus both the tests showed validity of the assumptions for F_2. The Wr, Vr regression lines intersected the axis above the point of origin in F_1 and below the origin in F_2 suggesting partial dominance in F_1 and over dominance in F_2, parents PY-57 and OMT-10 possessed maximum number of recessive genes for F_1. Parent OMT-10 shifted its position from upper (F_1) to lower (F_2) indicated that it might have minor genes. Similar results were also indicated by standardised deviation graphs.

The co-efficient of correlation between parental measurement and parental order of dominance was positive and non-significant in F_1, while it was not correlated in F_2 (r = 0.078) indicating little or no relation between dominance and recessiveness.

Fig.7· Wr,Vr AND STANDARDISED DEVIATION GRAPH FOR NUMBER OF BRANCHES PER PLANT·

Number of capsules per plant (Fig.8) :

In F_1 generation, 't^2' value was significant, even after removing parents AT-17 and TKG-9-86. The 'b' value significantly deviated from unity, but had non-significant deviation from zero. Thus, two sets showed complete failure of assumptions for diallel analysis. Reverse trend was observed for F_2, indicating validity of diallel assumptions. The line of unity slope intersected the regression line from the point of origin indicated complete dominance. The array points implied that parents were genetically diverse. The array point of parents RT-125, BAUT-1 and OMT-10 were situated farthest from the origin which indicated that they had maximum number of recessive genes. Whereas, parents PY-57, AT-17 and TKG-9-86 possessed maximum number of dominant alleles as the points were closure to origin. Similar results were also indicated by standardised deviation graph.

Correlation between parental order of dominance (Wr+Vr) and parental measurement Yr was positive and significant indicated that high values were associated with recessive genes.

Length of capsule (Fig.9) :

For this trait the regression values of Wr, Vr were significantly different from zero in both the sets, but not from unity in F_1 indicating presence of non-allelic interactions and the partial failure of the assumption in the diallel model. Non - significant 't^2' values in both the

Fig. 8. Wr, Vr AND STANDARDISED DEVIATION GRAPH FOR NUMBER OF CAPSULES PER PLANT.

Fig. 9· Wr, Vr AND STANDARDISED DEVIATION GRAPH FOR LENGTH OF CAPSUL·

generations showed validity of assumptions in the use of diallel analysis. The regression line intersected Wr axis just below the point of origin indicated slightly over-dominance. The array points were well distributed along the regression line implied that the parents were genetically diverse. A perusal of both the graphs indicated that the parent TKG-9-86 had maximum accumulation of dominant genes, while parent OMT-10 and Tapi showed maximum number of recessive genes. Standardised deviation graphs confirmed above results.

Correlation between (Wr + Vr) and Yr was negative and non-significant in both the generations indicated that dominant and recessive genes were equally associated with higher mean performance.

Number of grains per capsule (Fig.10) :

The deviation regression of Wr on Vr was non-significant from zero, however differed significantly from unity, suggesting failure of additive-dominance model. The non-significant values of $'t^2'$ in both the generations indicated uniformity of (Wr-Vr) over arrays. Wr axis was intersected much below the point of origin suggested over dominance. Parents PY-57, AT-17 and G.Til-1 possessed more of dominant genes, whereas TKG-9-86 and AHT-55 had recessive genes. Similar results also indicated standardised deviation graphs.

The correlation co-efficient between order of dominance (Wr + Vr) and parental measurement (Yr) was non-significant,

Fig. 10. Wr, Vr AND STANDARDISED DEVIATION GRAPH FOR NUMBER OF GRAINS PER CAPSULE.

but was negative in F_1 and positive in F_2 indicating dominance and recessive genes equally associated with this trait.

Dry weight per plant (Fig.11) :

Since 't^2' value was significant, analysis was carried after excluding parent TKG-9-86, which was interacting. Wr, Vr graphs showed that regression line intersected the Wr axis below the point of origin in F_1 and above the point of origin in F_2 denoting over dominance and partial dominance, respectively. Position of array points on graphs indicated that parents G.Til-1, AHT-55 and AT-17 in F_1 and RT-125 and PY-57 in F_2 had maximum number of dominant genes. Whereas recessive genes were more in parents Tapi and OMT-10 in both F_1 and F_2. These results were also confirmed by standardised deviation graphs.

The Correlation co-efficient between (Wr + Vr) and Yr was not significant (r = 0.015 in F_1 and r = -0.359 in F_2) suggesting tendency of equal proportion of dominance and recessiveness to be associated with dry weight per plant.

Grain yield per plant (Fig.12) :

This character showed partial fulfilment of assumptions as indicated by two tests. Regression co-efficient (b) differed significantly from zero and unity in F_1. Non-significant values of t^2 in F_1 and F_2 showed uniformity of (Wr - Vr) over arrays. The intersect of regression line on Wr axis was below the point of origin, indicating over-dominance.

Fig. 11· Wr, Vr AND STANDARISED DEVIATION GRAPH FOR DRY WEIGHT PER PLANT·

Fig. 12. Wr, Vr AND STANDARISED DEVIATION GRAPH FOR GRAIN YIELD PER PLANT.

Parents Mrug-1 and G.Til-1 were closer to the point of origin whereas parents TKG-9-86 and OMT-10 were far away to the origin suggesting more dominant and recessive genes, respectively in F_1. The parent OMT-10 had maximum dominant and RT-125 had maximum recessive gene in F_2. Similar results were also indicated by standardised deviation graphs.

The correlation coefficient was negative and significant in F_1, but non-significant and positive in F_2, indicating the tendency of dominant genes to be associated with higher grain yield.

Test weight (Fig.13) :

Assumptions underlying diallel analysis showed validity since 't^2' values were non-significant and did not differ significantly from unity in both the generations. The regression line passed through Wr axis above the point of origin in F_1, hence the partial dominance was indicated, while in F_2, it intersected just below the point of origin, showed slightly over dominance. Position of array points in Wr, Vr graphs indicated that Tapi and Mrug-1 possessed excess of dominant genes whereas, OMT-10 had more recessive genes in both the generations. Above results were also confirmed by the standardised deviation graphs.

Graphs for F_1 showed negative and significant correlation (r = -0.728), it reflected the parents with excess of dominant genes.

Fig.13. Wr, Vr AND STANDARISED DEVIATION GRAPH FOR TEST WEIGHT.

Husk seed ratio (Fig.14) :

The regression co-efficient did not deviate either from zero or from unity. Thus additive-dominance model was inadequate to explain the results precisely. Though, regression line intersected Wr axis just below the point of origin in F_1 and just above the origin in F_2, indicating moderate over dominance and slightly partial dominance, respectively. A perusal of Wr, Vr and standardised graphs indicated the parents AT-17 and PY-57 had higher number of dominant genes and parents TKG-9-86 and OMT-10 possessed more number of recessive genes.

Non-significant correlation co-efficient between parental order of dominance (Wr + Vr) and parental measurement Yr indicated equal proportion of dominant with positive and negative effects in the parents.

Harvest index (Fig.15) :

The 't^2' value showed significance, therefore analysis performed after removing the parent TKG-9-86 in F_2 generation. The 'b' value revealed significance from unity and zero. These results indicated partial failture of assumption of diallel analysis. The regression line intersected the Wr axis below the point of origin in F_1 and just above the origin in F_2. The degree of dominance was therefore from over dominance to partial dominance. The array points indicated presence of genetic diversity among the parents. Parent BAUT-1 had minor genes, while parent OMT-10 showed equal number of positive and

Fig. 14. Wr,Vr AND STANDARISED DEVIATION GRAPH FOR HUSK SEED RATIO.

Fig. 15. Wr, Vr AND STANDARISED DEVIATION GRAPH FOR HARVEST INDEX.

negative genes. Standardised deviation graphs for both the generation confirmed the above results.

The co-efficient of correlation between parental measure (Wr + Vr) and parental order of dominance (Yr) was significant in both the sets, but it was negative in F_1 showed dominant genes to be associated with high harvest index.

Oil content (Fig.16) :

This character showed partial fulfilment of assumption as indicated by two tests (Table-19). Regression line intersected the Wr axis above the points of origin in both the generations, indicating partial dominance. Tapi had maximum number of recessive genes and parent Mrug-1 possessed most of dominant genes for both the generations. Standardised deviation graphs also showed similar results.

The co-efficient of correlation between (Wr + Vr) and Yr was non-significant indicated that positive and negative genes were equally distributed among the parents.

Oil yield per plant (Fig.17) :

The regression value deviated significantly from unity in F_1 while in F_2 neither differed significance from unity nor zero, indicating non-additive gene action. The regression line intersected the Wr axis below the point of origin, showing over dominance. The array points were well distributed along the regression line implied that the parents were genetically diverse. Parents TKG-9-86 and RT-125 had maximum recessive
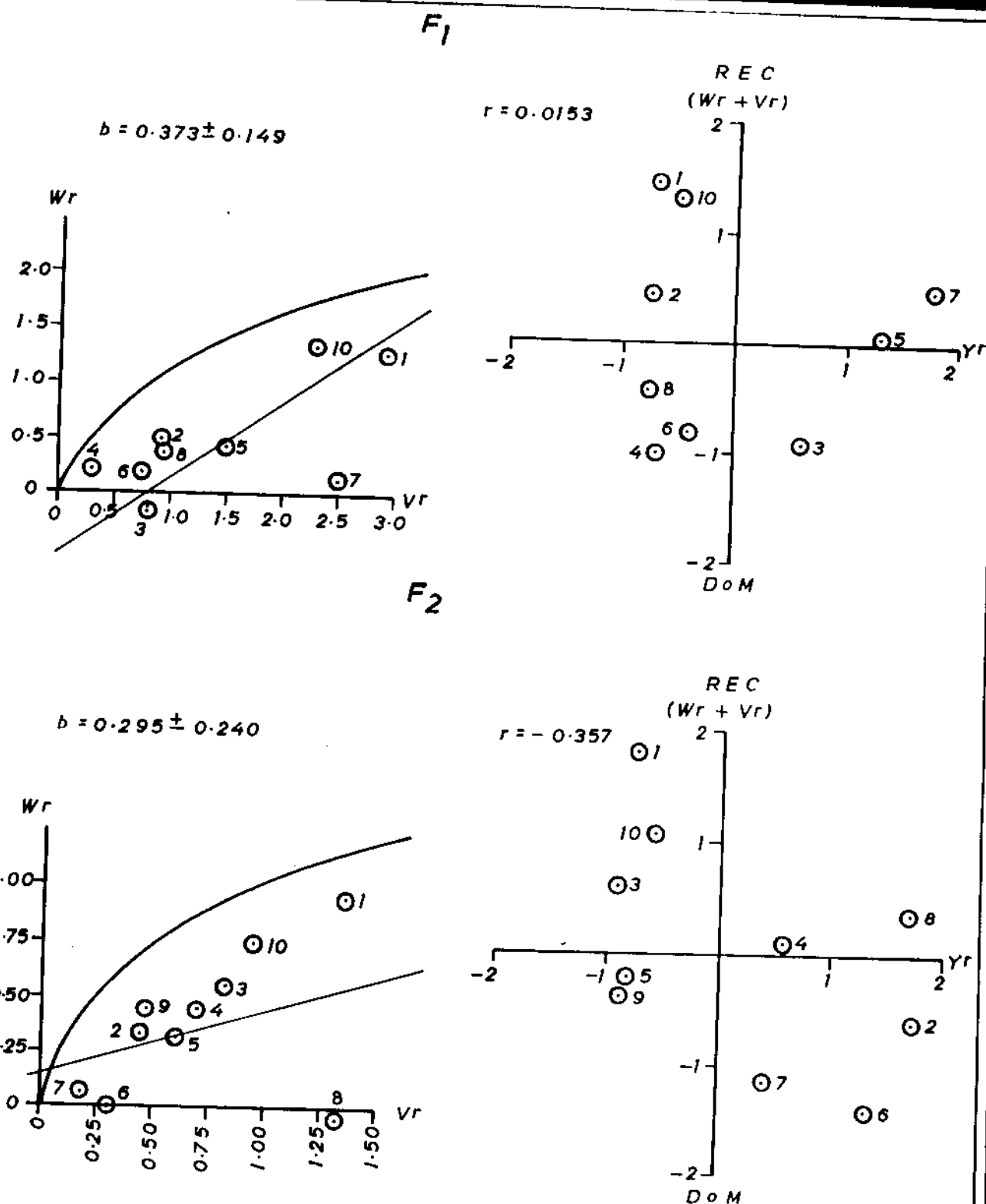
Fig. 16. Wr, Vr AND STANDARISED DEVIATION GRAPH FOR OIL CONTENT.

Fig.17. Wr, Vr AND STANDARISED DEVIATION GRAPH FOR OIL YIELD PER PLANT.

genes in F_1 and F_2 respectively. While, parent Mrug-1 and OMT-10 had maximum dominant genes in F_1 and F_2, respectively. Standardised deviation graphs also confirmed the above results.

The correlation between (Wr + Vr) and Yr was negative and significant in F_1. Thus showed that the expression of traits was associated with dominant alleles.

Protein content (Fig.18) :

In both F_1 and F_2 generations the 't^2' values were non-significant, whereas the regression co-efficient (b) differed significantly from zero and unity. Thus additive-dominance model explain the results more accurately. In both the sets regression line intersected much above the point of origin, showing partial dominance. Parent RT-125 possessed most of recessive alleles and G.Til-1 had maximum dominant genes in both the sets.

Correlation between parental order of dominance (Wr + Vr) and parental measurement(Yr)was significant and negative in F_1 indicating tendency of dominant genes to be associated with protein content in sesame.

4.4.2 Components of genetic variation through diallel analysis :

Genetic components of variances viz., D, H_1, H_2, h^2, F and E along with their standard errors and various ratios studied for F_1 and F_2 are presented characterwise as under :

Fig.18. Wr, Vr AND STANDARISED DEVIATION GRAPH FOR PROTEIN CONTENT.

Plant height to first flowering (Table-20) :

Non-additive components of genetic variances H_1 and H_2 were significant in both sets. The additive genetic component (D) was non-significant in F_1, but had significance in F_2. The magnitude of non-additive component was higher than additive component revealing dominance toward over-dominance side. The estimate h^2 was non-significant in both generations. The F value was non-significant in F_1, while in F_2 it showed significance. The value of $(H_1/D)^{\frac{1}{2}}$ was more than unity in both generations (2.402 in F_1 and 1.463 in F_2) confirmed above results. Asymmetry in distribution of positive and negative genes among parents was denoted by the ratio of $H_2/4 H_1$, which was less than 0.25.

The ratio KD/KR was 1.712 and 2.556 for F_1 and F_2, respectively, revealed presence of more dominant gene groups among parents. The gene action was not undirectional and because of internal cancellation, the values of h^2/H_2 were very low (-0.151 in F_1 and -0.105 in F_2). Heritability estimates exhibited low (24.01%) magnitude in F_1, whereas medium (44.99%) in F_2 for the trait.

Days to first flowering (Table-20) :

The additive genetic component (D) and dominance components (H_1 and H_2) were highly significant in both the generations, thus indicated the importance of both additive and non-additive components for the trait. The estimate h^2 was

Table 20. Estimation of genetic components of variance for plant height to first flowering, days to first flowering, days to 50 per cent flowering, days to maturity, length of reproductive stem and plant height to maturity.

Genetic components	Plant height to first flowering F_1	F_2	Days to first flowering F_1	F_2	Days to 50 per cent flowering F_1	F_2	Days to maturity F_1	F_2	Length of reproductive stem F_1	F_2	Plant height to maturity F_1	F_2
D	7.364+	7.389+	7.237+	7.114+	7.605+	7.617+	13.102+	12.738+	21.993+	22.412+	102.006+	105.395+
	4.747	1.650	0.793	1.699	0.639	0.780	0.933	1.646	4.514	3.813	20.726	9.546
H_1	43.176+	63.295+	13.030+	57.621+	11.099+	45.643+	9.291+	46.921+	60.199+	148.802+	194.689+	691.992+
	10.104	14.051	1.689	14.464	1.360	6.642	1.987	14.012	9.608	32.468	44.117	81.275
H_2	36.573+	49.700+	10.998+	48.926+	9.306+	40.052+	8.551+	43.625+	53.804+	133.495+	167.434+	608.423+
	8.587	11.942	1.435	12.293	1.156	5.645	1.688	11.908	8.165	27.595	37.495	69.074
h^2	-0.555-	-5.208+	1.885+	-21.339+	2.919+	19.926+	0.762+	-48.193+	18.581+	-3.257+	7.755+	-248.615+
	5.759	7.993	0.961	8.229	0.774	3.779	1.130	7.971	5.466	18.471	25.097	46.236
F	9.905+	18.655+	3.201+	8.996+	3.622+	9.275+	-0.186+	3.164+	10.713+	22.381+	30.360+	117.981+
	10.952	7.606	1.830	7.830	1.474	3.595	2.154	7.584	10.414	17.575	47.821	43.995
E	0.952+	0.927+	0.428+	0.552+	0.272+	0.261+	0.061+	0.101+	1.259+	0.840+	2.452+	2.541+
	1.431	0.498	0.239	0.512	0.193	0.235	0.281	0.496	1.361	1.149	6.249	2.878
$(H_1/D)^{\frac{1}{2}}$	2.402	1.463	1.342	1.424	1.208	1.224	0.841	0.959	1.655	1.288	1.381	1.281
$(H_2/4H_1)$	0.212	0.196	0.210	0.212	0.209	0.219	0.230	0.232	0.233	0.234	0.205	0.219
$\dfrac{(4DH_1)^{\frac{1}{2}} + F\ KD}{(4DH_1)^{\frac{1}{2}} - F\ KR}$	1.712	2.516	1.395	2.567	1.490	2.979	0.983	1.297	1.343	2.265	1.241	2.552
h^2/H_2	-0.151	-0.105	0.171	-0.436	0.314	0.497	0.089	-1.105	0.345	-0.224	0.046	-0.408
Heritability ns (%)	24.01	44.99	38.59	36.91	47.05	49.36	57.41	54.70	28.74	43.28	36.94	45.91

* Significant at 5 per cent level

** Significant at 1 per cent level

negative and significant in F_2. The ratio KD/KR suggested that 2 to 3 dominant genes were present for each recessive allele. As the F values were non-significant in both F_1 and F_2, suggested equal distribution of recessive and dominant genes in the parents.

The $(H_1/D)^{\frac{1}{2}}$ showed the presence of over-dominance in both the generations. The estimate $H_1/4H_2$ indicated asymmetrical distribution of negative and positive genes. The ratio of h^2/H_1 also showed unidirectional gene action. Narrow sense heritability estimates for the traits were medium in both F_1 (38.59%) and F_2 (36.91%).

Days to 50 per cent flowering (Table-20) :

Both additive genetic component (D) and dominance components (H_1 and H_2) of variation were highly significant in both F_1 and F_2 with higher magnitude of dominant components. Thus indicating the significance of over all dominance effect (h^2) in both the generations and also suggested unidirectional distribution of dominant gene for this trait. Positive and significant values of F indicated the presence of more dominant alleles. This finding was supported by the estimate KD/KR (1.490 in F_1 and 2.979 in F_2).

The mean degree of dominance $(H_1/D)^{\frac{1}{2}}$ revealed the presence of over dominance, while the value of $H_2/4H_1$ was 0.209 and 0.219 (F_1 and F_2) which indicated asymmetrical distribution of positive as well as negative alleles among the parents. The ratio of h^2/H_1 supported above findings. Medium

heritability was recorded in both F_1 (47.05%) and F_2 (49.36%).

Days to maturity (Table-20) :

D, H_1 and H_2 components were highly significant both for F_1 and F_2 revealing the importance of additive as well as non-additive type of gene actions in the inheritance of this trait, however, magnitude of additive component was higher in F_1. Mean degree of dominance of both the generations revealed partial dominance, since $(H_1/D)^{\frac{1}{2}}$ ratio was 0.841 in F_1 and 0.959 in F_2. Symmetry in distribution of positive and negative genes among parents was denoted by ratio $H_2/4\,H_1$, which was very close to the maximum value of 0.25.

The values for KD/KR proportion were near to unity, thereby indicating that gene distribution was more or less symmetrical. Presence of limited number of dominant genes was further indicated by negative value in F_1. Value of h^2 was significant and negative in F_2. Unidirectional gene action was evidenced by high negative value of h^2/H_2 ratio in F_2. Heritability estimates were high in both the generations (57.41% in F_1 and 54.70% in F_2), thus confirming the importance of additive gene effects.

Length of reproductive stem (Table-20) :

Additive (D) and non-additive (H_1 and H_2) components of variance were highly significant both in F_1 and F_2 generations, however magnitude of non-additive component was

higher. The degree of dominance $(H_1/D)^{\frac{1}{2}}$ revealed over-dominance in both the generations. There was almost symmetric distribution of positive and negative genes as indicated by the ratio of $H_2/4\ H_1$ (0.233 in F_1 and 0.239 in F_2). This was further confirmed by non-significant differences between H_1 and H_2 in both the sets. KD/KR ratio indicated that there were one to two positive gene groups for every one negative gene. Non-significant F indicated equal number of positive and negative genes present in both sets. Heritability for F_1 and F_2 was low (28.74%) and medium (43.28%) respectively.

Plant height to maturity (Table-20) :

Both D as well as H_1 and H_2 components of genetic variance were significant for both the sets suggesting importance of both additive and dominance components in the inheritance of plant height The estimate h^2 was significant in F_2 generation. Positive and significant value of F for F_2 suggested the presence of more number of dominant alleles. This finding was further supported by estimate KD/KR.

Mean degree of dominance $(H_1/D)^{\frac{1}{2}}$ was more than unity in both the cases, thus showed over dominance. Estimate of $H_2/4\ H_1$ was less than 0.25 indicated asymmetrical distribution of negative and positive genes. Narrow sense heritability was 36.94 per cent in F_1 and 45.91 per cent in F_2 for the trait.

Number of branches per plant (Table-21) :

The components D, H_1 and H_2 were highly significant,

Table 21. Estimation of genetic components of variance for number of branches per plant, number of capsules per plant, length of capsule, number of grains per capsule, dry weight per plant and grain yield per plant in sesame

Genetic components	Number of branches per plant		Number of capsules per plant		Length of capsule		Number of grains per capsule		Dry weight per plant		Grain yield per plant	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
D	0.222**±0.054	0.222**±0.016	14.409**±9.779	14.434**±1.839	0.013**±0.002	0.013**±0.004	9.197**±2.885	9.197**±5.292	1.237**±0.522	1.196**±0.285	0.204**±0.092	0.203**±0.036
H_1	0.712**±0.116	1.542**±0.141	55.068**±10.826	101.295**±15.664	0.026**±0.004	0.170**±0.030	34.537**±5.076	149.652**±45.055	4.961**±1.151	9.780**±2.424	0.843**±0.196	1.480**±0.307
H_2	0.584**±0.098	1.255**±0.120	49.484**±9.419	84.262**±13.313	0.022**±0.003	0.165**±0.026	20.073**±4.314	110.821**±38.292	4.182**±0.990	7.617**±2.060	0.793**±0.166	1.234**±0.261
h^2	0.272**±0.066	0.469**±0.080	37.193**±6.316	-35.166**±8.911	0.027**±0.003	0.049**±0.074	0.216*±2.888	17.117**±25.631	3.194**±0.663	-2.703**±1.379	0.765**±0.11	-0.131±0.175
F	0.166±0.126	0.386±7.619	8.343±11.128	17.831±8.479	0.006±0.005	0.003±0.016	16.537±5.502	31.957±24.389	0.532±1.217	1.813±1.312	0.067±0.212	0.304±0.166
E	0.005±0.016	0.001±0.005	0.094±1.569	0.056±0.554	0.01±0.062	0.0001±0.001	0.002±0.719	0.023±1.585	0.009±0.165	0.006±0.086	0.003±0.028	0.004±0.011
$(H_1/D)^{\frac{1}{2}}$	1.179	1.317	1.769	1.324	1.396	1.808	1.937	2.017	2.003	1.429	2.031	1.349
$(H_2/4H_1)$	0.205	0.203	0.225	0.208	0.208	0.242	0.145	0.185	0.211	0.195	0.235	0.208
$\dfrac{(4DH_1)^{\frac{1}{2}} + F}{(4DH_1)^{\frac{1}{2}} - F} = \dfrac{KD}{KR}$	1.527	4.872	1.309	2.745	1.367	1.141	2.706	2.513	1.240	3.255	1.175	3.572
h^2/H_2	0.464	0.374	0.752	-0.417	1.227	0.291	0.011	0.154	0.764	-0.354	0.964	-0.106
Heritability ns (%)	28.15	53.34	27.21	27.05	39.27	24.39	33.65	23.15	21.81	43.37	20.53	46.14

* Significant at 5 per cent level

** Significant at 1 per cent level

thus indicated importance of additive and dominant components in this trait. Further magnitude of dominant component was higher than additive, thereby indicating over dominance values of mean degree of dominance $(H_1/D)^{\frac{1}{2}}$, ratio $H_2/4\,H_1$ indicated symmetrical distribution of positive and negative genes among parents as values were very close to 0.25. It was also confirmed by non-significant values of F in both the generations.

The values of KD/KR for both the generations were 1.527 (F_1) and 4.872 (F_2) indicated two to five dominant genes for each recessive gene. Ratio h^2/H_2 indicated that gene action was unidirectional. Heritability estimate was low (28.15%) in F_1, while high in F_2 (53.34%).

Number of capsules per plant (Table-21) :

Additive (D) and non-additive (H_1 and H_2) variances were significant in both the generations, however magnitude of additive component was lower than H_1 and H_2. It indicated the major role of dominant components which was confirmed by significant value of h^2. Non-significant value of F indicated equal proportion of positive and negative genes.

The values of KD/KR for both the generations showed the presence of one to two positive genes for every one respective gene. Ratio $H_2/4\,H_1$ was less than 0.25 and value of h^2/H_2 indicated one gene was governing inheritance of this trait in both the sets. Estimated narrow sense heritability was low both in F_1 (27.21%) and F_2 (27.05%).

Length of capsule (Table 21) :

The genetic parameters D, H_1 and H_2 were highly significant, thus revealing that both additive and dominant genetic variances were playing greater role both in F_1 and F_2. Significant h^2 suggested that dominance was unidirectional. This was further confirmed by ratio KD/KR, which was more than unity. The ratio further exhibited that for every one recessive gene there were one to two dominant genes in the parents. Mean degree of dominance was more than one (1.396 in F_1 and 1.808 in F_2) indicated over dominance for length of capsule. The ratio h^2/H_2 showed that one to two gene groups were governing the inheritance of this trait in F_1 and F_2. Further gene distribution among parents was asymmetrical in F_1 and almost symmetrical in F_2 as evidenced by H_2 / 4 H_1 ratio. Heritability estimates were 39.24 per cent in F_1 and 24.39 per cent in F_2.

Number of grains per capsule (Table 21) :

Dominant (H_1 and H_2) and additive (D) components were significant in both generations, except additive in F_1. The magnitude of non-additive components was higher than additive components revealing dominance toward over dominance side. The mean degree of dominance also confirmed the same trend. Ratio $H_2/4$ H_1, exhibited asymmetry of positive and negative alleles among parents. The estimated value of KD/KR was 2.706 for F_1 and 2.513 for F_2, suggesting there were about three dominant genes or gene groups for each recessive gene

affecting this trait. Positive and significant F values confirmed that there were more number of dominant genes governing this trait, in F_1, while F was non-significant in F_2. However, in both h^2 was non-significant and h^2/H_2 ratio was low revealing unidirectional nature of gene action. Heritability estimates for F_1 and F_2 were 33.65 per cent and 23.15 per cent, respectively.

Dry weight per plant (Table 21) :

In determining the genetic control of dry weight per plant, additive (D) and non-additive (H_1 and H_2) genetic variances were observed to play a major role. The magnitude of non-additive component was higher than additive both in F_1 and F_2. The unequal proportion of positive and negative genes among parents was evidenced by low values of $H_2/4 H_1$ in both the sets. Over dominance effects of heterozygote loci (h^2) was highly significant in F_1 generation only. Component F was positive but non-significant.

High ratio of KD/KR indicated that for every one recessive gene two to four dominant genes existed in the parents. h^2/H_2 ratio indicated that at least one gene group is operating for controlling this character. Estimated heritability was low for F_1 (21.81%) and medium for F_2 (43.37%).

Grain yield per plant (Table 21) :

Additive component of variance (D) was significant only in F_1, whereas dominance components (H_1 and H_2) were

significant in both F_1 and F_2. This indicated the predominance of non-additive variation in the inheritance of this trait. The mean degree of dominance was 2.301 (F_1) and 1.349 (F_2), which suggested the over dominance was operating in this trait. The estimated values of $H_2/4 H_1$ (0.235 F_1) revealed almost symmetrical distribution of positive and negative alleles among the parents, while asymmetrical distribution was observed in F_2.

The estimated values of KD/KR were 1.175 for F_1 and 3.572 for F_2 suggesting that there were about two to four dominant genes for each recessive gene affecting this trait. The value of h^2 was significant in F_1 indicated that non-additive component was higher whereas h^2/H_2 ratio was near unity showed almost complete dominance of positive alleles. Heritability estimates for the trait were 20.53 per cent (low) and 46.14 per cent (medium) in F_1 and F_2, respectively.

Test weight (Table 22) :

Highly significant additive (D) and dominant components H_1 and H_2 indicated the influence of both, additive and dominance in controlling the expression of test weight. However in F_2, additive component (D) was more that of H_1 and H_2, indicating greater importance of additive gene action. It was also confirmed by negative and significant h^2 value.

Degree of dominance was in the range of partial dominance in F_1 and near complete dominance in F_2. In F_1 symmetry of gene distribution was borne by the fact that

Table 22. Estimation of genetic components of variance for test weight, husk seed ratio, oil content, oil yield per plant and protein content

Genetic component	Test weight F_1	Test weight F_2	Husk seed ratio F_1	Husk seed ratio F_2	Harvest index F_1	Harvest index F_2	Oil content F_1	Oil content F_2	Oil yield per plant F_1	Oil yield per plant F_2	Protein content F_1	Protein content F_2
D	0.031 ** ± 0.002	0.031 ** ± 0.0001	0.018 ± 0.009	0.018 ** ± 0.005	3.229 ± 2.112	2.849 ± 1.662	1.098 ** ± 0.205	1.710 ** ± 0.263	0.049 ± 0.023	0.049 ** ± 0.008	0.572 ** ± 0.031	0.572 ** ± 0.025
H_1	0.002 ** ± 0.0004	0.015 ** ± 0.001	0.119 ** ± 0.019	0.326 ** ± 0.050	26.643 ** ± 4.511	65.661 ** ± 14.677	2.480 ** ± 0.436	11.022 ** ± 2.241	0.201 ** ± 0.048	0.356 ** ± 0.073	0.192 ** ± 0.065	0.785 ** ± 0.219
H_2	0.002 ** ± 0.0004	0.021 ** ± 0.001	0.100 ** ± 0.016	0.279 ** ± 0.043	21.274 ** ± 3.834	57.401 ** ± 12.617	1.752 ** ± 0.371	6.481 ** ± 1.905	0.187 ** ± 0.041	0.291 ** ± 0.062	0.161 ** ± 0.055	0.699 ** ± 0.186
h^2	0.001 ** ± 0.002	0.011 ** ± 0.001	0.001 ± 0.011	0.028 ± 0.029	0.005 ± 2.566	-12.247 ± 8.453	0.061 ± 0.248	-3.371 * ± 1.275	0.187 ** ± 0.027	-0.025 ± 0.041	0.012 ± 0.037	-1.974 ** ± 0.125
F	0.001 ± 0.005	0.002 ± 0.001	0.026 ± 0.021	0.039 ± 0.027	5.361 ± 4.889	-3.021 ± 7.744	0.550 ± 0.473	3.140 * ± 1.123	0.020 ± 0.052	0.080 ± 0.039	0.175 * ± 0.071	0.314 * ± 0.118
E	0.004 ± 0.062	0.003 ± 0.004	0.001 ± 0.003	0.001 ± 0.002	0.104 ± 0.639	0.163 ± 0.527	0.0001 ± 0.062	0.001 ± 0.081	0.001 ± 0.068	0.001 ± 0.003	0.001 ± 0.009	0.001 ± 0.007
$(H_1/D)^{\frac{1}{2}}$	0.833	1.115	2.543	2.128	1.436	0.808	1.502	1.269	2.020	1.348	0.580	0.585
$(H_2/4H_1)$	0.238	0.209	0.210	0.215	0.199	0.218	0.176	0.148	0.233	0.205	0.210	0.223
$\dfrac{(4DH_1)^{\frac{1}{2}}+F}{(4DH_1)^{\frac{1}{2}}-F}=\dfrac{KD}{KR}$	1.053	1.804	1.768	3.080	1.813	0.638	1.400	6.228	1.226	4.090	1.719	2.758
h^2/H_2	0.062	-0.977	0.005	0.097	0.001	-0.318	0.035	-0.520	0.999	-0.089	0.074	-2.837
Heritability ns (%)	60.39	52.55	16.29	22.48	13.03	13.29	36.27	59.03	21.12	50.03	62.23	61.77

* Significant at 5 per cent level

** Significant at 1 per cent level

estimates of H_1 and H_2 were equal in magnitude. The estimate of $H_2/4 H_1$ (0.238) was near to 0.25 thus indicated almost asymmetry of positive and negative alleles among parents. This view was also supported by the value of F being non-significant and value of KD/KR near unity. This suggested that the parent appear to possess equal number of dominant and recessive genes. The ratio h^2/H_2 (0.062) was low suggesting that at least one group of genes control this character and would also occur when the negative and positive effects of dominant gene nullify the effects of one another. High estimate of heritability in F_1 (60.39%) and F_2 (52.55%) suggested that test weight appeared to be controlled by additive gene action.

Husk seed ratio (Table 22) :

The components of genetic variance <u>viz</u>., D, H_1 and H_2 were highly significant, hence revealing that the dominant and additive genetic components are equally responsible in determining the genetic control of this character. The components H_1 and H_2 were larger than the D. Thus indicated higher role of dominance effect. The estimate of h^2 was non-significant for both the sets showed equal distribution of recessive and dominance genes.

The measure of degree of dominance $(H_1/D)^{\frac{1}{2}}$ showed the operation of over dominance for this attribute. The frequencies of dominant alleles were not equal to that of recessive alleles (u = v = 0.5) as indicated by $H_2/4 H_1$ in

both generations. Heritability estimates for F_1 and F_2 were low i.e. 16.29 per cent and 22.48 per cent, respectively and it indicated that character was controlled mostly by dominant genes.

Harvest index (Table 22) :

Additive components were non-significant, while dominant components (H_1 and H_2) were significant for both F_1 and F_2. Higher values of dominant component indicated preponderance of dominance in the control of this trait. Over all effect of heterozygote loci (h^2) and F were non-significant for both the sets indicating equal distribution of recessive and dominant genes. However, the value of KD/KR for both F_1 and F_2 were 1.813 and 0.638, respectively.

The measure of mean degree of dominance $(H_1/D)^{\frac{1}{2}}$ showed the operation of over dominance and partial dominance in F_1 and F_2, respectively. The ratio $H_2/4 H_1$ deviated from the theoritical value of 0.25 which showed that the distribution of negative and positive alleles were not symmetrical. Heritability for this trait was low i.e. 13.03 for F_1 and 13.29 for F_2.

Oil content (Table 22) :

D, H_1 and H_2 components were highly significant both in F_1 and F_2 revealing the importance of both additive and dominance type of gene actions in the inheritance of this

trait. Further, magnitude of dominance was higher in F_2, which was also indicated by significant h^2. The mean degree of dominance was towards over dominance side since $(H_1/D)^{\frac{1}{2}}$ ratio was 1.502 and 1.269 in F_1 and F_2, respectively. The prevalence of negative and positive genes among parents were unequal in both generations as was indicated from $H_2/4\ H_1$ which was lesser than 0.25.

The values of KD/KR in F_1 and F_2 was 1.400 and 6.228 indicated that two to seven positive genes or gene pairs control this character. It was also confirmed by significant F values. Ratio of $h^2/4\ H_2$ was low revealing unidirectional gene action. Heritability estimate for F_1 was medium (36.27%) and high for F_2 (59.03%).

Oil yield per plant (Table 22) :

Non-fixable genetic components (H_1 and H_2) of variation were highly significant in both generations, while fixable genetic components (D) were significant in F_1 and non-significant in F_2 generation, indicating that non-fixable component was more important for the inheritance of the character. This finding was supported by the significant value of over all dominance (h^2) for F_1 suggesting unidirectional distribution of dominant genes. Positive and significant value of F for F_1 indicated the presence of more of dominant alleles controlling the trait. This finding was supported by the estimate of KD/KR.

The value of degree of dominance indicated that over dominance was operative both in F_1 and F_2. Asymmetrical and symmetrical distribution of dominant as well as recessive genes was recorded in F_1 and F_2, respectively. The heritability values were low for F_1 (21.12%) and high for F_2 (51.00%).

Protein content (Table 22) :

Highly significant values of additive (D) and non-additive (H_1 and H_2) genetic components revealed importance of additive and non-additive components for inheritance of the trait. The additive component was higher in magnitude than non-additive component as indicated by higher value of D. The estimate h^2 was non-significant in F_1 and significant negative in F_2. The covariance between additive and dominance effect (F) was significant in both generations suggested preponderance of dominant genes. This was in agreement with KD/KR estimates in both generations.

The mean degree of dominance indicated dominance in both the generations. The ratio $H_2/4 H_1$ deviated from the theoritical value of 0.25 which showed that distribution of negative and positive alleles in the parent was asymmetrical. Estimated heritability were high (62.23% F_1 and 61.77% F_2) for both generations, indicating high proportion of additive gene actions for the trait.

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The success of any breeding programme depends upon the selection of parents together with the information regarding nature and magnitude of gene action controlling various traits of importance. Diallel mating system extensively used for the estimation of combining ability (Griffing, 1956b) and gene action (Hayman, 1954b) is of immense value in identifying parents and crosses which are likely to yield maximum improvement for the character under consideration.

The prime importance of a plant breeding programme is to increase the yield potential of crop which is achieved by manipulating yield components. In the past, improvement in autogamous crops in general and sesame in particular was achieved through convential breeding procedure of selection in the naturally occuring or induced variability through hybridization following the traditional pedigree method of breeding. Information on the genetic architecture of different characters in sesame in limited for adopting any suitable breeding method for its further improvement.

Keeping these points in view, the present investigation was undertaken to study heterosis and inbreeding depression, combining ability, components of genetic variance and graphical analysis in the material generated through diallel

cross mating in a set of ten divergent parents. The significant points emerged from these studies are discussed below :

Analysis of variance revealed significant differences among parents, F_1, F_2, parents vs F_1 and F_1 vs F_2, except traits, number of branches in F_1, plant height to first flowering in parent vs F_1 and F_1 vs F_2 for oil content. This emphasized the need of selecting diverse parents for maximization of hybrid vigour with respect to grain yield and its componental traits. The significant differences between F_1 and F_2 indicated considerable amount of inbreeding depression in F_2 for all the traits, except oil content.

Heterosis and inbreeding depression :

The concept of heterosis, was given by Shull in the year 1914. Since then, the heterosis breeding has been successfully used for the improvement of cross pollinated crops like maize, bajra, castor etc. and to a limited extent in self-pollinated crops. In view of this, in present study apart from heterosis and heterobeltiosis the economic heterosis was also worked out using check parent (RT-125) for all the traits.

The prime objective of any breeder is to bring about improvement in crop plants, so that their yielding ability is increased. In the present study, heterosis over mid parent for grain yield was positive and significant in 42 out of 45

crosses. Highest heterotic cross was AT-17 x TKG-9-86 followed by BAUT-1 x TKG-9-86, Tapi x TKG-9-86, PY-57 x RT-125 and RT-125 x OMT-10. Likewise considerable heterosis for the characters viz., number of capsules per plant, number of branches per plant, dry weight per plant, plant height to maturity, length of reproductive stem and oil yield per plant was observed. The hybrids which showed maximum heterosis in different traits did not involve altogether superior parents. These findings are in agreement with the Joshi and Dhawan (1966) and Djigma (1983) who found the better influence of genetical and geographical diversity on magnitude of heterosis. The expression of considerable heterosis in some hybrids and little in other might be due to :

      i. Agronomic condition in the experiment particular soil type and plant spacing,

     ii. Genetic diversity in the parents and

   iii. Non-allelic interaction which either increase or decreases the expression on heterosis (Paramsivam et al., 1982).

The measure of heterosis over mid-parental value has relatively limited importance and is of more academic interest than of practical use. Therefore, the heterobeltiosis measured in terms of superiority over the better parent is more viable. The degree of heterobeltiosis varied from cross to cross for all the characters studied. Considerably high heterosis over better parent in certain hybrids and low in others revealed that nature of gene action varied with the genetic

architercture of the parents. Such nature as well as magnitude of heterosis helps in identifying superior cross combinations.

In the present study, grain yield per plant had high heterobeltiosis in 32 out of 45 croses. A comparative study of six most heterobeltiotic crosses for grain yield and its components (Table 23) revealed that cross combination AT-17 x TKG-9-86 had highest heterobeltiosis followed by PY-57 x RT-125, RT-125 x OMT-10, BAUT-1 x TKG-9-86, Tapi x Gujarat Til-1 and AT-17 x PY-57 for grain yield, of which all the crosses showed significant and positive values for number of capsules per plant and oil yield per plant. The number of branches per plant, oil content, length of reproductive stem and husk seed ratio had significant values toward desired direction in four crosses. Whitehouse _et al_. (1958) and Grafius (1959) have also suggested that there can not be any gene system for yield _per se_ and that yield was an end product of the multiplicative interactions of several yield components. A number of correlation studies conducted in sesame (Solanki and Paliwal, 1981; Ding _et al_., 1987; Khorgade _et al_., 1987; Bakheit and Maddy, 1988 and Osman, 1988) further supported and strengthen this view.

High heterotic effects for the traits viz., grain yield, capsules per plant, branches per plant and plant height have been reported by Srivastava and Singh (1968), Murty (1975), Dixit (1976b), Sarif (1976), Fatteh (1978), Chaudhry _et al_. (1979), Gupta (1980), Sharma and Chauhan (1983), Godawat and Gupta (1985), Goyal and Sudhir Kumar (1988), Jadon

Table 23. Comparison of per cent heterosis (over better parent) for yield and its components in six most heterotic crosses in sesame

Characters	Crosses					
	AT-17 x TKG-9-86	PY-57 x RT-125	RT-125 x OMT-10	BAUT-1 x TKG-9-86	Tapi x G.Til-1	AT-17 x PY-57
Grain yield per plant	65.09**	39.89**	36.51**	32.79**	31.13**	29.97**
Number of capsules per plant	102.53**	16.63**	31.54**	30.59**	14.87**	74.68**
Number of branches per plant	50.00**	-4.00**	27.54**	18.75**	6.67**	-13.33**
Oil yield per plant	65.21**	48.08**	38.54**	36.59**	28.07**	27.05**
Dry weight per plant	48.68**	7.69**	37.09**	-5.18**	27.98**	7.55**
Oil content	4.07**	-0.04**	1.54**	2.89**	-2.19**	3.00**
Length of reproductive stem	6.61**	-6.13**	2.64**	-3.87**	5.79**	2.09**
Plant height to maturity	4.89**	-5.75**	0.25*	-2.34	6.51**	-7.88**
Husk seed ratio	-16.47**	-16.54**	4.45**	6.34**	11.77**	12.09**
Harvest index	8.93**	-0.41	-4.26**	16.39**	-3.51**	-10.02**
Length of capsule	-2.11**	-3.48**	4.91**	-0.87**	3.23	-0.81**
Protein content	-0.76**	-0.93**	-1.95**	-0.59**	-2.02**	-0.88**
Test weight	-0.85**	-0.45**	-1.02**	-1.66**	-2.65**	0.75**
Number of grains per capsule	-0.75**	-9.48**	-2.54**	-0.59**	-1.99**	-3.09**
Plant height to first flowering	-3.31**	-1.17**	-3.19**	-4.80**	-3.08**	-2.05**
Days to maturity	1.61**	6.03**	1.29**	0.00	0.00	12.08**
Days to 50 per cent flowering	9.17**	21.24**	10.62**	-0.81	8.27**	10.00**
Days to first flowering	14.56**	22.55**	11.76**	-5.26**	7.14**	13.36**

* Significant at 5 per cent level
** Significant at 1 per cent level

and Mehrotra (1988), Reddy and Haripriya (1990), Zhan et al. (1990) and Girase (1991).

In the present investigation cross BAUT-1 x TKG-9-86 recorded highest economic heterosis followed by BAUT-1 x OMT-10, Tapi x BAUT-1, Tapi x Gujarat Til-1 and PY-57 x RT-125 for grain yield over the check variety (RT-125). The crosses Tapi x Gujarat Til-1 and PY-57 x RT-125 also expressed higher heterosis over better parent. These crosses showed ample scope for exploitation of hybrid vigour at commercial level.

Sesame is usually cultivated as a catch crop in many parts of India and at times intercropped with other crops. Therefore, cultivar should have early maturity with higher yield. Thus for these, the desirable crosses were RT-125 x BAUT-1, Gujarat Til-1 x RT-125 and Mrug-1 x RT-125 (Appendix II). Yermanodos and Kotecha (1978), Tyagi and Singh (1981), Jadon and Mehrotra (1988) and Girase et al. (1991) reported heterosis for early maturity in some of the crosses.

With respect to oil and protein content 26 and 23 hybrids for heterosis, 13 and 2 for heterobeltiosis and 34 and 45 for economic heterosis had significant and positive values, respectively. Highest heterobeltiotic cross for oil content was BAUT-1 x TKG-9-86 followed AHT-55 x RT-125 and Tapi x TKG-9-86 and for protein content best cross was PY-57 x OMT-10 followed by PY-57 x BAUT-1. Similar results were observed by Fatteh (1978), Tyagi and Singh (1981), Satani (1982), Desai et al. (1984) and Navadia (1990).

The magnitude of inbreeding depression, in general showed a positive trend with the extent of heterosis in grain yield per plant, number of capsules per plant, number of branches per plant, length of reproductive stem, plant height at maturity, dry weight per plant and oil yield per plant, indicating that these characters are largely influenced by non-additive type of gene action (Godawat and Gupta, 1985). In general these findings were in agreement of Sharma and Chauhan (1983), Singh et al. (1986), Sodani and Bhatnagar (1990) and Girase (1991).

However, few crosses viz., RT-125 x BAUT-1 and Gujarat Til-1 x RT-125 for grain yield per plant, Tapi x RT-125 for days to maturity, AT-17 x TKG-9-86 for plant height to maturity and number of grains per capsule, Gujarat Til-1 x AHT-55 for length of capsule, RT-125 x BAUT-1 for oil content and AT-17 x AHT-55 for test weight had significant heterosis and less inbreeding depression which may be ascribed to higher additive gene actions. In general, similar results were indicated by Dixit (1976b), Chavan et al. (1981 and 1982) and Girase (1991).

Combining ability :

The success of any breeding programme largely depends on choice of parents included and breeding procedure adopted. Combining ability analysis not only helps in identification and early assessment of breeding potential of parental lines to be included in crossing programme but also provides

specific promosing combinations to exploit heterosis or build up the favourable fixable gene. In self fertilized crops, where exploitation of heterosis at commercial level is not feasible, the breeder will primarily be interested in higher magnitude of additive genetic variance for establishing superior genotypes.

In the present study, the analysis of variance for combining ability indicated that general and specific combining ability variances were highly significant for all the traits except plant height to first flowering (F_1 and F_2), number of grains per capsule (F_2), husk seed ratio (F_1 and F_2) and harvest index (F_1). This suggested that in most of the characters both additive and non-additive gene effects were involved. The ratio of additive to non-additive genetic variance for various characters showed that non-additive gene action was predominant in all the traits, except days to maturity, test weight and protein content. The results in general are in accordance with the findings of Murty (1975), Kotecha and Yermanos (1978), Shrivas and Singh (1981), Choudhari et al. (1984a), Thanki (1984), Dora and Kamala (1984), Krishnadoss et al. (1987), Khargade et al. (1988) and Narkhede and Sudhir Kumar (1991a).

An overall appraisal of GCA effects (Table 24) for material used in the present study indicated that in general none of the parent was a good general combiner for all the traits studied. However, parent BAUT-1 was a good general combiner for most of the traits. Parents Mrug-1, Gujarat

Table 24. Summary of general combining ability effects of various characters in sesame

Characters		Tapi	Mrug-1	AT-17	G.Til-1	AHT-55	PY-57	RT-125	BAUT-1	TKG-9-86	OMT-10
Plant height to first flowering	F$_1$	A	G	A	G	P	A	P	G	A	G
	F$_2$	P	G	A	G	P	A	A	G	P	A
Days to first flowering	F$_1$	A	P	G	A	A	P	G	G	P	P
	F$_2$	P	P	G	G	A	P	G	P	P	A
Days to 50 per cent flowering	F$_1$	P	P	G	G	G	P	G	G	P	P
	F$_2$	P	P	G	G	A	P	G	P	P	A
Days to maturity	F$_1$	P	P	A	A	G	P	G	A	A	G
	F$_2$	P	P	A	A	A	P	G	P	A	G
Length of reproductive stem	F$_1$	G	A	P	A	P	P	A	G	P	G
	F$_2$	A	P	P	P	P	G	G	G	P	P
Plant height to maturity	F$_1$	G	G	P	P	P	G	P	G	P	P
	F$_2$	G	G	P	P	P	G	P	G	P	P
Number of branches per plant	F$_1$	P	G	P	P	P	A	G	G	P	G
	F$_2$	A	G	A	P	P	G	G	A	P	G
Number of capsules per plant	F$_1$	P	P	G	G	P	G	G	G	A	G
	F$_2$	P	P	P	P	P	P	G	G	P	G
Length of capsule	F$_1$	P	P	G	G	G	G	G	A	P	P
	F$_2$	P	P	G	G	G	G	G	P	P	P
Number of grains per capsule	F$_1$	G	G	A	G	G	P	G	G	P	P
	F$_2$	P	G	A	G	G	P	P	P	P	P
Dry weight per plant	F$_1$	G	G	P	A	P	G	P	P	P	A
	F$_2$	P	P	P	P	P	G	P	G	P	P

Contd. Table 24.

Characters		Tapi	Mrug-1	AT-17	G.Til-1	AHT-55	PY-57	RT-125	BAUT-1	TKG-9-86	OMT-10
Grain yield per plant	F_1	A	G	P	G	P	P	A	G	P	A
	F_2	A	G	P	G	P	P	G	G	P	P
Test weight	F_1	G	G	A	G	P	A	P	G	P	P
	F_2	G	G	A	G	P	A	P	G	P	P
Husk seed ratio	F_1	G	G	P	G	P	P	P	G	P	P
	F_2	G	G	P	P	P	P	A	G	G	P
Harvest index	F_1	P	P	G	G	A	G	G	G	P	A
	F_2	G	G	P	G	A	P	G	G	P	P
Oil content	F_1	P	P	G	G	G	G	G	G	G	P
	F_2	P	G	G	G	G	G	P	G	P	P
Oil yield per plant	F_1	A	G	P	G	P	P	G	G	P	P
	F_2	P	G	P	G	P	P	G	G	P	P
Protein content	F_1	G	G	A	G	P	P	P	G	P	P
	F_2	P	G	G	G	G	G	P	G	G	P

G = Good general combiner
A = Average general combiner
P = Poor general combiner

Til-1 and BAUT-1 were good general combiners for grain yield as well as plant height to first flowering, number of grains per capsule, test weight, oil yield per plant, oil and protein content. Native parent RT-125 was good general combiner for early maturity, number of capsules, length of capsule, oil yield per plant and harvest index, while it was poor for plant height to maturity, test weight and protein content. Though the magnitude of GCA effects in different characters varied yet the trend in F_2 was quite similar to that observed in F_1 for most of the traits studied. This suggested the feasibility of use of F_2 generation for estimating the GCA effects. Singh et al. (1983) has also advocated the use of F_2 generation for the estimation of GCA effects in sesame.

The study indicated that the parents showing high general combining ability effects also had high per se performance in almost all the traits, however their rank magnitude differed (Table 25). This suggested that selection of parents for hybridization programme in sesame is possible on per se performance also. The parent BAUT-1 was best for grain yield, test weight, oil yield per plant and protein content, while Gujarat Til-1 was good for length of capsule and oil content. Parent RT-125 was best in per se as well as in GCA for early maturity.

The hybrids, which had maximum SCA effects in F_1 generation (Table 26) for yield and its components, were BAUT-1 x TKG-9-86 for grain yield, Tapi x BAUT-1 for length of reproductive stem, PY-57 x OMT-10 for plant height to maturity,

Table 25. Best two parents on the basis of _per se_ performance
and GCA effects

Characters	Best parent per se	Best parent for GCA	
		F_1	F_2
1	2	3	4
Plant height to first flowering	Mrug-1 G.Til-1	Mrug-1 BAUT-1	Mrug-1 G.Til-1
Days to first flowering	RT-125 AT-17	RT-125 BAUT-1	RT-125 AT-17
Days to 50 per cent flowering	RT-125 AT-17	RT-125 BAUT-1	RT-125 G.Til-1
Days to maturity	RT-125 OMT-10	RT-125 OMT-10	RT-125 OMT-10
Length of reproductive stem	BAUT-1 PY-57	BAUT-1 OMT-10	BAUT-1 PY-57
Plant height to maturity	PY-57 Mrug-1	PY-57 BAUT-1	PY-57 BAUT-1
Number of branches per plant	PY-57 Mrug-1	Mrug-1 BAUT-1	OMT-10 RT-125
Number of capsules per plant	BAUT-1 RT-125	BAUT-1 RT-125	RT-125 BAUT-1
Length of capsule	PY-57 G.Til-1	PY-57 G.Til-1	PY-57 G.Til-1
Number of grains per capsule	AHT-55 G.Til-1	Mrug-1 AHT-55	G.Til-1 Mrug-1
Dry weight per plant	BAUT-1 PY-57	Mrug-1 PY-57	BAUT-1 PY-57
Grain yield per plant	BAUT-1 G.Til-1	BAUT-1 G.Til-1	BAUT-1 RT-125
Test weight	BAUT-1 G.Til-1	BAUT-1 G.Til-1	BAUT-1 Mrug-1
Husk seed ratio	Mrug-1 Tapi	BAUT-1 Tapi	BAUT-1 Tapi
Harvest index	Mrug-1 RT-125	RT-125 PY-57	Mrug-1 RT-125

Contd.

Contd. Table 25.

1	2	3	4
Oil content	G.Til-1 AT-17	G.Til-1 PY-57	PY-57 G.Til-1
Oil yield per plant	BAUT-1 TKG-9-86	BAUT-1 G.Til-1	BAUT-1 G.Til-1
Protein content	BAUT-1 G.Til-1	BAUT-1 Mrug-1	BAUT-1 Mrug-1

Table 26. Best cross combinations per se in F$_1$ and F$_2$, Best SCA cross combinations, specific cross combinations in both per se and SCA and crosses with maximum heterobeltiosis for various characters in sesame

Characters	Best cross combination per se (Mean basis)		Best SCA cross combinations		Specific cross combinations in both per se and SCA	Crosses with maximum heterobeltiosis
	F$_1$	F$_2$	F$_1$	F$_2$		
1	2	3	4	5	6	7
Plant height to first flowering	RT-125xTKG-9-86 G.Til-1xTKG-9-86	G.Til-1xAHT-55 BAUT-1xOMT-10	BAUT-1xTKG-9-86 AT-17xAHT-55	G.Til-1xAHT-55 AT-17xTKG-9-86	G.Til-1xAHT-55	BAUT-1xTKG-9-86 AT-17xAHT-55
Days to first flowering	RT-125xBAUT-1 RT-125xTKG-9-86	RT-125xBAUT-1 G.Til-1xOMT-10	G.Til-1xOMT-10 Mrug-1xPY-57	AHT-55xBAUT-1 G.Til-1xOMT-10	G.Til-1xOMT-10	TapixAHT-55 BAUT-1xTKG-9-86
Days to 50 per cent flowering	RT-125xBAUT-1 AHT-55xRT-125	RT-125xBAUT-1 AHT-55xRT-125	Mrug-1xPY-57 TapixAHT-55	G.Til-1xOMT!10 TapixAHT-55	-	TapixAHT-55 AHT-55xRT-125
Days to maturity	RT-125xBAUT-1 RT-125xTKG-9-86	RT-125xBAUT-1 RT-125xTKG-9-86	RT-125xBAUT-1 G.Til-1xAHT-55	TapixMrug-1 RT-125xBAUT-1	RT-125xBAUT-1	G.Til-1xAHT-55 RT-125xBAUT-1
Length of reproductive stem	TapixBAUT-1 PY-57xBAUT-1	RT-125xBAUT-1 BAUT-1xOMT-10	TapixBAUT-1 Mrug-1xRT-125	RT-125xBAUT-1 G.Til-1xPY-57	TapixBAUT-1	TapixAT-17 Mrug-1xRT-125
Plant height to maturity	PY-57xBAUT-1 TapixMrug-1	PY-57xOMT-10 TapixRT-125	PY-57xOMT-10 G.Til-1xTKG-9-86	TapixRT-125 AT-17xTKG-9-86	PY-57xOMT-10 TapixRT-125	TapixAHT-55 TapixMrug-1
Number of branches per plant	Mrug-1xOMT-10 PY-57xBAUT-1	RT-125xOMT-10 RT-125xBAUT-1	AT-17xTKG-9-86 Mrug-1xOMT-10	G.Til-1xTKG-9-86 AHT-55xPY-57	Mrug-1xOMT-10	AHT-55xTKG-9-86 AT-17xTKG-9-86
Number of capsules per plant	BAUT-1xTKG-9-86 RT-125xOMT-10	RT-125xOMT-10 RT-125xBAUT-1	AT-17xTKG-9-86 G.Til-1xAHT-55	AT-17xTKG-9-86 RT-125xOMT-10	RT-125xOMT-10	AT-17xTKG-9-86 AHT-55xPY-57

Contd.

Contd. Table 26.

1	2	3	4	5	6	7
Length of capsule	PY-57xBAUT-1 G.Til-1xPY-57	G.Til-1xRT-125 G.Til-1xPY-57	AHT-55xOMT-10 TapixMrug-1	PY-57xOMT-10 G.Til-1xRT-125	G.Til-1xRT-125	Mrug-1xG.Til-1 TapixMrug-1
Number of grains per capsule	Mrug-1xG.Til-1 Mrug-1xRT-125	Mrug-1xTKG-9-86 Mrug-1xAHT-55	BAUT-1xOMT-10 TapixBAUT-1	AT-17xTKG-9-86 Mrug-1xTKG-9-86	TapixBAUT-1	Mrug-1xBAUT-1 BAUT-1xTKG-9-86
Dry weight per plant	TapixBAUT-1 PY-57xBAUT-1	BAUT-1xOMT-10 AT-17xBAUT-1	TapixBAUT-1 PY-57xOMT-10	TapixBAUT-1 BAUT-1xOMT-10	TapixBAUT-1 BAUT-1xOMT-10	TapixTKG-9-86 TapixOMT-10
Grain yield per plant	RT-125xTKG-9-86 RT-125xOMT-10	RT-125xBAUT-1 AT-17xBAUT-1	BAUT-1xTKG-9-86 AT-17xTKG-9-86	AT-17xTKG-9-86 PY-57xTKG-9-86		AT-17xTKG-9-86 PY-57xRT-125
Test weight	AT-17xBAUT-1 G.Til-1xTKG-9-86	AT-17xBAUT-1 Mrug-1xOMT-10	G.Til-1xTKG-9-86 Mrug-1xOMT-10	Mrug-1xOMT-10 AHT-55xPY-57	G.Til-1xTKG-9-86 Mrug-1xOMT-10	G.Til-1xTKG-9-86 AT-17xPY-57
Husk seed ratio	TapixBAUT-1 TapixTKG-9-86	Mrug-1xBAUT-1 RT-125xTKG-9-86	G.Til-1xTKG-9-86 PY-57xRT-125	RT-125xTKG-9-86 PY-57xOMT-10	RT-125xTKG-9-86	G.Til-1xTKG-9-86 AT-17xOMT-10
Harvest index	AT-17xOMT-10 G.Til-1xPY-57	TapixG.Til-1 Mrug-1xBAUT-1	G.Til-1xPY-57 AT-17xOMT-10	TapixG.Til-1 TapixAHT-55	AT-17xOMT-10 TapixG.Til-1	AT-17xOMT-10 G.Til-1xPY-57
Oil content	AT-17xAHT-55 G.Til-1xAHT-55	G.Til-1xPY-57 G.Til-1xAHT-55	AHT-55xRT-125 TapixTKG-9-86	TapixTKG-9-86 RT-125xBAUT-1		BAUT-1xTKG-9-86 AHT-17xRT-125
Oil yield per plant	RT-125xTKG-9-86 TapixBAUT-1	RT-125xBAUT-1 AT-17xBAUT-1	BAUT-1xTKG-9-86 AT-17xTKG-9-86	AT-17xTKG-9-86 RT-125xBAUT-1	RT-125xTKG-9-86 RT-125xBAUT-1	AT-17xTKG-9-86 PY-57xRT-125
Protein content	PY-57xBAUT-1 RT-125xTKG-9-86	PY-57xBAUT-1 G.Til-1xBAUT-1	G.Til-1xRT-125 PY-57xOMT-10	G.Til-1xRT-125 PY-57xOMT-10		PY-57xOMT-10 PY-57xBAUT-1

AT-17 x TKG-9-86 for branches per plant, AHT-55 x OMT-10 for length of capsule, BAUT-1 x OMT-10 for grains per capsules, Gujarat Til-1 x TKG-9-86 for branches per plant and husk seed ratio, AHT-55 x OMT-10 for length of capsule and Gujarat Til-1 x PY-57 for harvest index. These crosses involved poor x poor, poor x good and good x good general combiners. Specific combining ability effects did not show any specific trends for general combining ability of the parents. They involved all types of combinations. However, in majority of the crosses poor and good combination gave high SCA effect.

High per se performance crosses for yield viz., BAUT-1 x TKG-9-86, BAUT-1 x OMT-10, Tapi x BAUT-1 and AT-17 x TKG-9-86 also had high SCA effects. However, most of traits studied also showed close relation between per se performance of hybrids and SCA effects. No cross combination was constantly good for all the traits (Table 2₆). However, some of best specific combinations which were having superior mean, high SCA and maximum heterobeltiosis for different characters viz., RT-125 x BAUT-1 (early maturity), Gujarat Til-1 x TKG-9-86 (test weight), Gujarat Til-1 x PY-57 and AT-17 x OMT-10 (harvest index), whereas crosses Tapi x BAUT-1 for length of reproductive stem, RT-125 x OMT-10 for number of capsule, Tapi x BAUT-1 for dry weight and RT-125 x TKG-9-86 for oil yield per plant were good for per se performance and SCA effects. These crosses in general involved good x good and good x poor GCA effects indicating additive gene action or additive x dominance type of gene interactions. It was further

observed that poor general combiners resulted into high SCA effects in some of the traits. This may be because of the role of high magnitude of non-additive interaction. These crosses may be utilized through intermating in the segregating generation and simultaneous selection for desirable plant type for yield and its components. In general, similar results were observed by Fatteh (1978), Gupta (1981), Satani (1982), Chaudhari et al. (1984a), Thanki (1984), Reddy et al. (1984), Goyal and Sudhir Kumar (1988), Khorgade et al. (1988), Power et al. (1990) and Narkhede (1991b) in sesame.

Gene action :

The components of genetic variances and nature of gene actions for different characters were estimated by different approaches viz., graphical, numerical and combining ability.

Results of combining ability analysis indicated predominantly non-additive gene action for all the characters studied, except days to maturity, test weight and protein content which showed additive gene action. The estimates of additive (D) and dominance (H_1) from diallel analysis provided further evidence for the presence of similar gene actions in these characters.

These results are in general agreement with Murty and Hashim (1973), Murty (1975), Dixit (1976a), Delgada (1977), Kotecha and Yermanos (1979), Gupta (1981), Shrivas and Singh (1989), Uzo and Ojiake (1981), Sharma and Chauhan (1984), Dara and Kamala (1986), Bakheit and Mahdy (1987), Chandraprakash

(1987), Chandramony and Nayar (1988), Goyal and Sudhir Kumar (1988), Khorgade et al. (1988), Narkhede and Sudhir Kumar (1991b), Raut et al. (1991) and Shinde et al. (1991) in sesame.

The average degree of dominance estimated by numerical approach $(H_1/D)^{0.5}$ showed partial dominance for days to maturity, test weight and protein content, while other traits indicated over dominance gene action for both the generations. Graphical analysis and combining ability analysis (Chaudhary et al. 1977) further confirmed similar trend of average degree of dominance, except where, partial dominance was indicated in Vr, Wr graphs. This inflation in the measure of dominance might be due to particular dispersion and unidirectional dominance as suggested by Hayman (1954b) or may be done to complementary interactions (Jinks, 1955).

In the present study over-dominance for grain yield, number of capsules per plant, seed number, oil content and plant height was observed which is in agreement with that of Murty and Hashim (1974), Kotecha and Yermanos (1979), Gupta (1981), Sharma and Chauhan (1984), Chandraprakash (1987), Chandramony (1988) and Raut et al. (1991).

These results confirmed the theory advanced by Grafius (1959) that non-allelic interaction would account for over dominance effects in geometrically complex traits like yield. He described multiplicative interactions between components rather than loci as additive geometric epistasis and cited many examples where high level of dominance or over dominance

effects were observed for complex traits and lesser degree of dominance found for the components. The over dominance for length of reproductive stem, number of capsules per plant, number of grains per capsule, dry weight per plant and husk seed ratio may be upward bais in the estimations of dominance due to linkage, epistasis and genotype-environment interactions indicated by Moll and Robinson (1967) in maize, Dixit (1976a), Chauhan et al. (1981), Godawat and Gupta (1985) in sesame.

Analysis of other estimate of components of genetic variation showed assymetric distribution of positive and negative genes and unequal frequency of dominance and recessive genes for all the characters studied, except days to maturity in both generations, grain yield, test weight, oil content in F_1 and length of capsule in F_2.

Presence of two to three dominant genes for every one recessive gene was observed for most of the characters studied, whereas two to four genes were for dry weight per plant, grain yield per plant, husk seed ratio, oil yield per plant and two to seven for oil content.

Heritability estimates for days to maturity, test weight and protein content were high and medium to high for oil content while for remaining traits, it was low to medium. Similar results were observed by Culp (1959), Murty and Horsham (1973, 1974), Mojidis (1982), Sharma and Chauhan (1984), Bakheit and Mahdy (1987), Li (1988) and Narkhede and

Sudhir Kumar (1991). High estimates of heritability for plant height, seeds per capsule and grain yield have been reported by Gupta (1981) and harvest index by Chandraprakash (1987). Low heritability for oil content estimated by Yadav and Gupta (1987). The distribution of genes was unidirectional for all the traits in both the generations except plant height to maturity, number of grains per capsule, harvest index, protein content in F_1, length of reproductive stem, oil yield per plant in F_2 and for test weight as was evidenced by(h^2/H_2) values.

Correlation between parental order of dominance (Wr+Vr) and parental measurement (Yr) suggested that the traits, grain yield per plant, test weight, harvest index, oil yield per plant, protein content and days to 50 per cent flowering were controlled by dominant genes.

Breeding methodology suggested :

From the forgoing discussion of results obtained in the present study, certain suggestions can be made in respect for future sesame improvement programme based on the ten lines used.

In recent years, a major break through in breeding for yield per se performance has been brought about in self-polinated crops such as sorghum, tomato, eggplant through

heterosis. The heterotic breeding could effectively be utilized in these crops primary due to the presence of high magnitude of non-additive gene effects couped with additive effects for yield and its components. However, important bottleneck is in the production of F_1 hybrids on commercial scale. Brar (1982) isolated three genetically diverse male sterile lines which can be used for the production of hybrids on commercial scale, but more research is needed for commercial production of F_1 hybrids in sesame.

Genetic improvement of grain yield, a complex trait, dependent upon the main concern of the plant breeders. Khorgade et al. (1987) revealed that number of capsules per plant, number of branches per plant and seeds per capsule were the main direct contributing traits to grain yield per plant. Grafius (1964) indicated that all the changes in yield were accompained by changes in one or more of its components and such changes in components need not be expressed in the yield.

Parents BAUT-1, Mrug-1 and Gujarat Til-1 were found to be best general combiner for grain yield and for the most of yield contributing traits. For early flowering, early maturity and more number of capsule, parent RT-125 whereas for oil and protein content Gujarat Til-1 were best general combiners. Therefore, these parents may be involved in building up a desirable gene pool.

An efficient breeding programme takes into consideration , parents with desirable agronomical traits and

good general combining ability for grain yield and its components, which in cross combination may result in high heterosis over better parent and high specific combining ability with least depression in subsequent generations. The present study revealed that combinations BAUT-1 x TKG-9-86 and Tapi x Gujarat Til-1 were most promising combinations for grain yield on the basis of their specific combining ability effects, besides high heterotic and <u>per</u> <u>se</u> performance. These crosses involved one parent with high degree of general combining ability for yield and thus can be utilized further breeding programme.

Thus, grain yield and its components had preponderance of non-additive gene effects besides additive effects. Under such a condition, improvement in sesame for the character under study may be expected through standard selection procedures which may first exploit the additive gene effects, simultaneously care should be taken that non-additive effects were not dissipated rather concentrated. It is, therefore, suggested that reciprocal recurrent selection breeding procedure should be followed which meets the requirement of utilising both types of gene actions.

The segregating population should preferably be derived from multiple crosses which helps to bring together coadapted gene complexes. Biparental mating (Comstock and Robinson, 1948) approach will be more useful in these crosses to break the undesirable linkage groups present in repulsion phase.

This will ensure utilization of additive and additive x additive gene effects and ultimately lead to the fixation of the characters at desired level.

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The present investigation in sesame (Sesamum indicum L.) was undertaken with a view (i) to examine the manifestation of heterosis and inbreeding depression, (ii) to assess the combining ability of the parents and crosses and (iii) to evaluate the nature of gene action involved in the expression of yield and other characters in order to suggest a sound breeding methodology for production of high yielding genotypes.

The experimental material consisted of parents and their F_1's and F_2's derived by crossing ten varieties of sesame (Tapi, Mrug-1, AT-17, Gujarat Til-1, AHT-55, PY-57, RT-125, BAUT-1, TKG-9-86 and OMT-10) in diallel fashion excluding reciprocals. The experiment was laid in randomized block design with thrice replicated during the kharif, 1991 at experimental field of Rajasthan College of Agriculture, Udaipur. Distances maintained between plant to plant and row to row were 15 and 45 cm, respectively. Observations were recorded for 18 characters viz., plant height to first flowering (cm), days to first flowering, days to 50 per cent flowering, days to maturity, plant height to maturity (cm), length of reproductive stem (cm), number of branches per plant, number of capsules per plant, length of capsule (cm), number of grains per capsule, grain yield per plant (g), dry

weight per plant (g), husk seed ratio, test weight (g), oil content (%), oil yield per plant (g) and protein content (%). The data were analysed for combining ability utilizing the method-II, model-I of Griffing (1956a). The genetic components of variation were calculated following the method Hayman (1954b) and the heterosis as suggested by Hayes et al. (1955). The salient results of the investigation are summarized here under :

(1) Differences between various treatments were highly significant for all the characters.

(2) Heterosis for grain yield per plant was reflected through heterosis in number of capsules per plant, plant height to maturity, length of reproductive stem, number of branches per plant, dry weight per plant, harvest index and husk seed ratio. Exploitable heterosis for grain yield was observed in crosses viz., AT-17 x TKG-9-86, BAUT-1 x TKG-9-86, Tapi x TKG-9-86, PY-57 x RT-125 and RT-125 x OMT-10.

(3) Crosses indicating heterosis for grain yield showed varied expression of hybrid vigour in its components. Heterosis in general was low for test weight, days to maturity, protein content, oil content and number of grains per capsule.

(4) Crosses which showed heterosis in grain yield also expressed economic heterosis for this trait. Highest

economic heterosis for grain yield was observed in cross BAUT-1 x TKG-9-86.

(5) Hybrids with high heterotic effects for yield and its important attributes also showed high inbreeding depression, suggesting that heterosis was mainly due non-additive gene action.

(6) Estimates of GCA/SCA variances ratio indicated high magnitude of non-additive gene for all the traits except days to maturity, test weight and protein content.

(7) Estimates of GCA indicated that parent BAUT-1 was best general combines for yield and other attributes viz., early flowering, length of reproductive stem, plant height, number of capsules per plant, number of branches per plant, test weight, husk seed ratio, oil yield per plant and protein content. Native parent RT-125 was good for early flowering, early maturity, harvest index and more capsules per plant whereas, Gujarat Til-1 was good for length of capsule, oil content and oil yield per plant.

(8) The per se performance appears to be a good indication of GCA and SCA effects for the parent and crosses, respectively in the traits, hence can be utilized while selecting the parents and crosses for breeding programme.

(9)   Parents with high GCA effects in F_1 also showed similar trend in F_2, suggesting the feasibility of using F_2 generation for estimating of GCA.

(10)   Cross AT-17 x TKG-9-86 was best specific combiners for yield in both the generations and also for plant height to maturity, number of branches per plant, number of capsules per plant, grains per capsule and oil yield per plant.

(11)   Crosses with high SCA effects in general had combination of parents with good x good or good x average GCA effects.

(12)   The graphical analysis showed over-dominance for grain yield, length of reproductive stem, number of capsules per plant and oil yield per plant, whereas days to lmaturity, test weight, oil and protein content had partial dominance, whereas different trend was observed for the traits in F_1 and F_2, generations.

(13)   Asymetrical distribution of positive and negative genes and unequal frequency of dominant and recessive gene was recorded for all the traits except days to maturity (F_1 and F_2), length of capsule (F_2), grain yield (F_1), test weight (F_1), and oil yield per plant (F_1), which showed symetrical distribution.

(14)   Most of the characters were preferred by two to three gene groups, but grain yield, husk seed ratio two to

four and oil content were under the control of two to seven gene groups.

(15)   Heritability estimates, in general were high for days to maturity, test weight and protein content, whereas it was low in grain yield, number of branches per plant, number of capsules per plant, husk seed ratio and harvest index. Other traits, days to first flowering, days to 50 per cent flowering, plant height at maturity, length of capsule and oil content exhibited medium kind of heritability.

(16)   Correlation between parental order of dominance (Wr+Vr) and parental measurement (Yr) suggested high grain yield, test weight, harvest index, oil yield per plant, protein content and days to 50 per cent flowering were governed by dominant gene.

(17)   On the basis of various studies conducted, it may be suggested the crosses BAUT-1 x TKG-9-86 and Tapi x Gujarat Til-1 may be advanced and exploited in future breeding programme for improving yield and its components.

(18)   Suggestions regarding breeding methodology for further improvement in grain yield and its components contributing towards it have been made.

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APPENDIX – I

Mean weekly meteorological data recorded during the crop growth period of 1991-92

Standard week No.	Period	Mean temperature (°C)		Relative humidity (%)		Rainfall (mm)
		Maximum	Minimum	Maximum	Minimum	
28	08 Jul. – 15 Jul.	35.6	24.3	84	61	91.2
29	16 Jul. – 22 Jul.	31.5	23.3	87	81	59.2
30	23 Jul. – 29 Jul.	27.8	23.5	93	86	122.2
31	30 Jul. – 5 Aug.	28.8	23.7	85	75	91.8
32	06 Aug. – 12 Aug.	29.6	23.8	84	70	31.2
33	13 Aug. – 19 Aug.	30.9	24.1	84	65	0.5
34	20 Aug. – 26 Aug.	28.1	23.5	89	79	68.0
35	27 Aug. – 02 Sep.	27.5	22.9	86	75	0.8
36	03 Sep. – 09 Sep.	28.6	19.0	82	67	0.0
37	10 Sep. – 16 Sep.	30.8	19.7	89	58	0.0
38	17 Sep. – 23 Sep.	31.3	20.1	83	42	0.0
39	24 Sep. – 30 Sep.	33.4	18.5	79	47	1.0
40	01 Oct. – 07 Oct.	33.1	14.0	66	21	0.0

APPENDIX - II

Mean values parents and crosses for various characters in sesame

Geno-types	Plant height to first flowering (cm)	Days to first flowering	Days to 50% flowering	Days to maturity	Length of reproductive stem (cm)	Plant height to maturity (cm)	Number of branches per plant	Number of capsule per plant	Length of capsule (cm)	Number of grains per capsule	Dry weight per plant (g)	Grain yield per plant (g)	Test weight (g)	Husk seed ratio	Harvest Index (%)	Oil content (%)	Protein content (%)	Oil yield per plant (g)
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
PARENTS																		
P_1	42.47	41.00	44.67	88.33	42.77	96.87	2.00	17.17	2.53	62.38	4.36	2.67	1.38	0.82	25.99	46.23	25.46	1.23
P_2	48.73	41.00	45.00	86.33	43.41	105.40	2.33	17.84	2.61	61.27	6.11	2.90	1.38	0.78	26.33	47.66	26.26	1.38
P_3	42.33	34.33	40.00	83.00	42.87	93.43	1.60	26.65	2.69	63.57	4.31	2.05	1.34	1.09	24.16	48.74	26.28	0.99
P_4	45.50	37.33	40.33	85.00	45.50	100.40	1.97	17.80	2.73	66.51	5.87	2.77	1.40	1.09	24.10	48.83	26.43	1.35
P_5	38.83	40.33	44.33	84.00	45.10	84.60	1.10	14.67	2.65	68.43	4.32	2.07	1.30	1.17	23.53	47.44	26.05	0.98
P_6	42.23	42.00	47.00	90.33	49.50	115.93	2.50	14.12	2.88	64.49	6.67	2.25	1.33	1.31	21.26	48.70	25.91	1.10
P_7	42.73	34.00	37.67	77.33	46.73	92.63	2.30	24.03	2.64	64.34	4.74	2.56	1.31	0.97	26.33	46.65	24.16	1.19
P_8	41.93	38.00	41.67	84.33	55.13	105.33	2.13	24.82	2.67	60.44	7.11	3.12	1.43	0.95	23.70	45.97	26.66	1.47
P_9	39.07	39.67	43.67	84.67	37.47	87.20	1.27	18.03	2.64	65.50	4.26	1.65	1.32	1.13	21.35	46.94	26.43	0.74
P_{10}	43.93	39.33	43.33	81.00	41.20	84.77	2.30	23.05	2.44	58.38	4.60	2.19	1.24	1.16	23.43	46.00	25.18	1.01

Contd. Appendix - II

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
F_1																		
$P_1 \times P_2$	47.83	41.00	45.00	86.67	50.20	116.87	2.77	18.78	2.79	67.66	7.79	2.95	1.38	1.12	21.00	47.18	25.43	1.39
$P_1 \times P_3$	38.03	42.33	46.00	88.00	50.87	99.87	2.03	18.89	2.81	61.62	6.29	2.65	1.36	1.06	22.58	47.49	25.94	1.26
$P_1 \times P_4$	44.10	40.00	43.67	85.00	48.13	106.93	2.13	20.15	2.82	65.19	7.52	3.63	1.37	0.92	25.08	47.76	25.89	1.73
$P_1 \times P_5$	42.17	38.00	41.67	84.00	52.93	109.33	2.33	17.46	2.77	67.22	4.90	2.43	1.34	1.08	24.36	47.61	25.77	1.16
$P_1 \times P_6$	41.07	40.67	45.00	87.00	50.87	110.27	1.53	18.39	2.79	60.16	6.31	2.48	1.39	1.05	21.70	47.32	25.65	1.18
$P_1 \times P_7$	38.43	39.33	44.67	85.00	43.87	95.73	1.87	17.80	2.60	62.56	5.52	1.87	1.34	1.28	19.11	46.95	25.05	0.88
$P_1 \times P_8$	42.20	37.33	42.00	86.00	61.81	110.60	2.70	27.59	2.68	68.02	10.24	3.74	1.40	0.75	22.21	47.76	26.20	1.79
$P_1 \times P_9$	42.20	39.00	44.00	84.00	43.73	94.40	1.53	18.96	2.66	62.76	6.85	3.29	1.37	0.77	25.97	47.84	26.15	1.58
$P_1 \times P_{10}$	43.47	40.00	44.00	83.33	44.40	94.33	2.27	22.34	2.52	61.03	7.05	2.92	1.34	0.88	23.34	44.18	25.27	1.29
$P_2 \times P_3$	44.50	40.67	44.00	85.00	41.67	92.63	2.67	18.50	2.80	65.84	7.04	2.97	1.35	0.98	22.95	47.14	26.26	1.40
$P_2 \times P_4$	40.50	44.00	47.33	85.67	49.70	98.60	2.67	20.54	2.75	69.20	7.61	3.16	1.41	0.93	23.01	47.71	26.25	1.51
$P_2 \times P_5$	37.47	41.00	44.00	85.00	45.07	99.17	2.30	21.73	2.65	67.34	5.66	2.90	1.30	1.13	24.48	48.48	26.21	1.40
$P_2 \times P_6$	39.03	39.33	44.33	87.00	47.60	98.27	2.60	20.09	2.88	62.24	7.13	2.63	1.37	1.08	20.89	48.27	26.05	1.27
$P_2 \times P_7$	41.93	35.67	40.67	81.67	54.07	94.10	3.03	26.56	2.83	68.41	7.34	2.98	1.36	1.38	20.61	47.90	25.50	1.43
$P_2 \times P_8$	43.87	40.67	45.00	84.67	46.67	97.57	2.63	18.50	2.69	67.43	7.44	3.13	1.40	0.86	23.60	47.05	26.36	1.47
$P_2 \times P_9$	49.57	42.33	46.67	86.67	46.27	105.07	1.73	20.25	2.68	64.45	6.72	2.83	1.36	1.14	22.14	47.19	26.22	1.34
$P_2 \times P_{10}$	44.23	40.33	45.33	83.00	49.33	107.83	3.17	22.44	2.51	63.78	7.44	3.30	1.38	1.11	23.09	46.57	25.71	1.54
$P_3 \times P_4$	40.90	38.33	42.67	84.00	49.97	85.20	1.50	22.52	2.68	62.56	5.26	2.65	1.37	1.17	24.10	47.23	26.35	1.26
$P_3 \times P_5$	47.33	38.67	43.00	83.00	45.87	86.53	2.27	25.27	2.70	63.75	5.48	2.49	1.32	1.04	23.60	48.74	26.16	1.21
$P_3 \times P_6$	41.47	39.00	44.00	86.67	50.53	106.80	2.17	29.08	2.86	62.50	7.17	2.92	1.35	1.14	21.74	48.05	26.05	1.39
$P_3 \times P_7$	41.03	37.67	42.33	79.00	43.40	89.97	1.90	21.42	2.88	60.21	5.43	2.54	1.31	1.16	23.08	46.76	25.30	1.19
$P_3 \times P_8$	44.63	37.67	42.67	83.67	44.70	96.47	1.80	23.36	2.73	60.15	6.05	2.95	1.44	0.95	24.98	48.69	26.41	1.44

III

Contd. Appendix - II

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
$P_3 \times P_9$	40.93	39.33	43.67	84.00	45.90	98.00	2.40	36.52	2.63	65.01	6.41	3.39	1.33	0.91	26.32	48.55	26.23	1.65
$P_3 \times P_{10}$	44.87	41.67	46.33	83.00	47.37	81.93	2.40	19.54	2.75	64.10	4.36	2.60	1.29	0.80	29.00	45.40	25.61	1.18
$P_4 \times P_5$	41.47	37.67	41.67	80.33	43.77	88.20	2.70	30.29	2.83	62.38	5.74	3.23	1.39	1.20	24.99	48.71	26.33	1.57
$P_4 \times P_6$	42.30	41.67	45.67	88.00	42.87	89.80	1.00	21.21	2.89	61.27	4.83	2.95	1.35	0.86	28.61	48.49	26.03	1.43
$P_4 \times P_7$	37.17	36.67	41.00	80.33	46.77	96.73	2.17	24.11	2.82	63.53	5.07	2.98	1.32	0.99	27.90	48.60	26.28	1.46
$P_4 \times P_8$	42.37	38.33	43.00	85.00	47.13	99.83	2.37	29.42	2.73	66.54	6.51	3.23	1.38	0.82	26.09	48.60	26.57	1.57
$P_4 \times P_9$	48.77	41.00	45.67	85.00	43.17	109.10	1.87	19.73	2.59	61.63	6.80	2.79	1.47	0.74	23.90	47.90	26.38	1.34
$P_4 \times P_{10}$	44.07	36.67	41.33	81.67	50.57	91.93	2.03	24.58	2.77	60.98	5.54	3.24	1.34	1.20	25.56	46.18	25.81	1.49
$P_5 \times P_6$	45.20	41.00	45.00	86.00	45.30	98.83	2.07	19.42	2.82	63.58	4.63	2.40	1.31	0.98	25.59	48.51	25.78	1.17
$P_5 \times P_7$	40.33	35.67	39.00	80.33	47.33	95.53	2.37	26.22	2.79	62.93	4.88	2.89	1.28	1.05	26.74	48.64	25.17	1.41
$P_5 \times P_8$	42.40	39.00	44.67	84.00	47.33	93.30	2.20	23.97	2.79	64.57	5.94	3.20	1.35	0.98	26.08	48.18	26.41	1.54
$P_5 \times P_9$	37.03	41.67	44.33	86.00	36.67	85.40	2.03	17.15	2.64	62.44	5.44	2.10	1.31	1.50	19.49	46.61	26.14	0.98
$P_5 \times P_{10}$	39.13	38.33	42.67	84.00	42.80	84.57	1.30	16.59	2.79	61.48	5.16	2.21	1.29	1.02	21.49	46.71	25.71	1.03
$P_6 \times P_7$	42.23	41.67	45.67	82.00	46.47	109.27	2.40	22.40	2.78	58.38	7.18	3.58	1.32	0.81	26.22	48.67	25.67	1.74
$P_6 \times P_8$	43.07	41.00	44.00	87.67	58.37	126.83	3.07	18.76	2.92	59.41	8.24	2.41	1.38	1.28	17.57	48.56	26.85	1.17
$P_6 \times P_9$	44.10	43.33	47.33	85.00	45.40	104.60	2.40	19.70	2.75	62.07	5.68	2.05	1.32	1.27	19.82	47.37	26.28	0.97
$P_6 \times P_{10}$	45.80	42.00	46.33	87.33	43.87	99.43	2.10	25.76	2.83	59.89	7.58	2.86	1.26	1.07	21.17	45.83	26.16	1.31
$P_7 \times P_8$	42.20	34.00	38.33	75.33	48.80	94.80	2.37	26.65	2.76	62.31	5.23	3.31	1.39	1.01	27.84	47.71	25.48	1.58
$P_7 \times P_9$	36.97	34.33	39.33	77.33	49.20	95.47	2.33	24.39	2.63	60.19	5.69	2.68	1.33	0.92	24.70	47.81	25.36	1.28
$P_7 \times P_{10}$	42.53	38.00	41.67	78.33	47.97	92.87	2.93	31.56	2.77	62.70	6.49	3.49	1.29	1.01	25.20	47.37	24.69	1.65
$P_8 \times P_9$	52.33	36.67	41.33	84.33	53.00	102.87	2.53	32.42	2.65	65.11	6.71	4.14	1.41	1.01	27.59	48.33	26.50	2.30
$P_8 \times P_{10}$	44.73	42.33	46.33	84.67	53.07	102.43	2.87	23.54	2.67	66.19	7.94	3.84	1.38	0.91	24.09	46.02	26.00	1.77
$P_9 \times P_{10}$	37.20	42.33	45.67	83.33	38.43	85.13	2.00	17.45	2.58	57.32	4.41	1.86	1.30	0.88	24.65	47.30	25.87	0.94

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
F_2																		
$P_1 \times P_2$	41.00	38.00	44.00	83.33	44.70	94.70	1.60	14.33	2.58	63.79	4.84	2.25	1.37	1.02	23.85	47.78	25.35	1.05
$P_1 \times P_3$	38.07	38.33	43.00	84.00	40.77	87.10	2.00	16.30	2.72	62.37	4.85	1.67	1.40	1.05	20.18	47.76	25.90	0.80
$P_1 \times P_4$	39.37	36.67	43.00	86.00	41.97	97.53	1.27	12.97	2.60	65.73	3.51	2.36	1.35	0.85	30.10	47.54	25.85	1.12
$P_1 \times P_5$	40.43	36.33	42.00	85.00	42.57	88.80	1.57	15.58	2.67	60.14	3.37	2.03	1.32	0.94	28.40	47.87	25.76	0.97
$P_1 \times P_6$	41.80	40.33	45.67	87.00	45.13	108.17	1.67	14.22	2.85	63.29	5.60	1.64	1.39	1.26	17.30	47.34	25.65	0.75
$P_1 \times P_7$	43.77	37.33	44.00	88.67	47.47	109.23	2.00	19.45	2.71	64.03	5.21	2.33	1.36	1.09	23.09	47.67	25.06	1.17
$P_1 \times P_8$	42.27	45.33	48.33	88.67	49.53	107.43	1.40	18.26	2.45	61.99	7.43	2.38	1.41	1.20	18.82	47.92	26.19	1.14
$P_1 \times P_9$	41.33	41.00	46.33	87.33	40.93	89.67	2.23	17.34	2.63	58.71	4.28	2.34	1.34	0.89	26.78	48.30	26.10	1.13
$P_1 \times P_{10}$	39.97	40.00	46.67	85.33	36.97	82.73	1.93	19.22	2.36	58.34	4.98	2.31	1.34	0.89	24.49	44.20	25.40	1.02
$P_2 \times P_3$	42.60	40.67	45.00	83.67	42.50	99.87	2.00	17.21	2.63	63.34	4.43	2.31	1.35	0.96	25.91	47.34	26.26	1.09
$P_2 \times P_4$	42.57	41.67	46.67	85.33	38.43	88.67	1.33	14.71	2.55	62.01	4.29	1.98	1.40	0.94	24.37	47.47	26.21	0.94
$P_2 \times P_5$	44.30	42.33	47.00	82.67	40.20	90.00	1.23	17.42	2.76	67.10	4.62	2.32	1.31	1.08	24.98	47.20	26.03	1.10
$P_2 \times P_6$	44.00	39.33	45.00	88.33	38.53	99.53	1.63	16.52	2.65	62.24	5.91	1.83	1.36	1.30	18.06	48.39	26.06	0.85
$P_2 \times P_7$	43.10	38.33	44.67	80.33	44.83	96.30	2.27	22.65	2.66	66.37	4.88	2.64	1.35	1.30	25.80	46.67	25.52	1.23
$P_2 \times P_8$	42.63	41.67	47.00	86.33	43.23	96.00	1.77	15.38	2.64	63.47	4.39	2.53	1.41	0.75	29.07	47.36	26.34	1.22
$P_2 \times P_9$	41.63	37.67	43.33	87.67	38.87	91.33	1.80	16.66	2.81	67.30	4.72	1.93	1.36	0.85	23.16	47.20	26.27	0.91
$P_2 \times P_{10}$	38.70	36.67	44.00	84.67	44.50	92.93	1.70	16.56	2.57	61.50	4.32	2.38	1.41	1.04	25.96	46.45	25.70	1.01
$P_3 \times P_4$	40.10	39.00	44.33	84.67	40.80	79.87	1.53	17.49	2.63	61.43	4.28	2.23	1.37	1.17	24.46	48.13	26.35	1.07
$P_3 \times P_5$	40.03	39.00	44.00	83.67	38.20	76.30	1.10	15.92	2.65	60.54	4.50	1.84	1.31	1.03	22.47	47.21	26.15	0.87
$P_3 \times P_6$	42.77	38.67	45.00	86.33	45.83	103.03	1.83	18.15	2.77	61.48	6.22	1.96	1.32	1.21	18.61	47.87	26.05	0.94
$P_3 \times P_7$	42.57	35.67	42.00	81.00	39.57	83.57	1.40	17.26	2.60	60.16	3.83	1.84	1.26	1.25	22.90	47.40	26.20	0.88
$P_3 \times P_8$	44.47	39.33	43.67	84.67	45.50	93.87	1.80	22.06	2.69	60.20	6.58	2.87	1.42	0.95	23.58	48.03	26.33	1.36
$P_3 \times P_9$	43.33	38.33	44.67	84.67	43.17	97.87	2.10	21.39	2.70	67.72	5.43	2.63	1.32	1.05	24.30	47.97	26.16	1.26

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
$P_3 \times P_{10}$	40.00	37.00	43.00	83.67	41.30	91.80	1.90	17.84	2.62	64.65	4.55	2.31	1.31	1.19	23.38	45.87	25.54	1.06
$P_4 \times P_5$	47.40	37.67	46.67	86.00	43.23	97.10	1.47	19.55	2.83	63.85	4.73	2.25	1.36	1.09	22.81	48.46	26.28	1.09
$P_4 \times P_6$	42.00	41.33	46.00	86.33	48.73	106.93	1.87	19.13	2.92	62.63	5.22	2.33	1.34	0.98	22.74	48.50	26.06	1.13
$P_4 \times P_6$	39.83	35.67	41.33	78.67	43.73	87.70	2.10	23.48	2.93	64.74	4.75	2.83	1.32	1.25	25.64	47.46	26.18	1.34
$P_4 \times P_7$	41.17	41.00	45.33	85.33	42.13	97.97	1.50	17.51	2.78	65.15	5.61	2.37	1.39	0.94	22.23	47.98	26.52	1.14
$P_4 \times P_8$	42.13	39.33	44.67	84.33	35.80	85.83	1.40	16.14	2.62	61.60	4.20	1.86	1.28	1.30	21.88	47.15	26.35	0.88
$P_4 \times P_9$	42.30	34.67	40.67	81.67	39.30	82.83	1.50	22.45	2.59	62.28	6.10	2.32	1.33	1.00	21.24	46.37	25.77	1.08
$P_4 \times P_{10}$	39.93	40.00	45.67	86.67	43.10	94.23	2.00	17.23	2.74	63.37	6.38	1.84	1.37	1.24	17.57	47.89	25.70	0.88
$P_5 \times P_6$	41.27	35.33	40.67	79.33	42.10	89.00	1.60	22.29	2.53	60.16	4.80	2.27	1.31	1.01	24.27	48.41	25.28	1.11
$P_5 \times P_7$	41.20	36.00	43.67	83.33	44.33	92.37	0.97	20.14	2.63	66.01	4.21	2.72	1.35	1.08	27.59	48.06	26.36	1.31
$P_5 \times P_8$	40.53	39.33	45.67	84.67	38.50	87.87	1.17	14.67	2.65	57.44	4.46	1.94	1.27	0.95	23.16	47.07	26.07	0.91
$P_5 \times P_9$	40.73	39.00	44.00	83.33	36.57	87.30	1.90	16.45	2.55	62.37	5.15	2.04	2.29	1.39	20.36	45.73	25.60	0.93
$P_5 \times P_{10}$	40.43	39.67	44.67	82.67	39.97	94.53	1.33	15.79	2.88	58.88	5.14	1.96	1.28	1.22	20.89	48.68	25.41	0.97
$P_6 \times P_7$	41.90	42.33	48.33	88.67	42.67	98.53	1.47	17.66	2.57	58.39	5.65	2.26	1.39	0.90	23.04	47.40	26.54	1.08
$P_6 \times P_8$	37.53	39.00	45.67	84.33	40.47	88.57	1.57	19.49	2.66	56.44	5.74	2.38	1.32	1.05	22.61	48.29	26.03	1.15
$P_6 \times P_9$	43.83	40.00	46.00	86.00	45.33	109.87	2.00	20.49	2.95	61.07	6.34	2.29	1.29	0.95	21.17	46.55	25.94	1.06
$P_6 \times P_{10}$	40.87	34.67	39.67	77.67	54.10	92.93	2.13	25.53	2.70	61.11	5.09	3.19	1.29	0.89	28.61	48.53	25.04	1.55
$P_7 \times P_8$	37.60	38.33	41.67	78.33	41.33	82.33	1.40	18.43	2.51	56.51	4.73	1.64	1.31	0.82	21.29	47.07	25.35	0.77
$P_7 \times P_9$	41.57	35.33	44.33	79.33	40.70	94.53	2.27	26.40	2.51	63.40	5.62	2.48	1.28	1.12	22.78	45.73	24.53	1.72
$P_7 \times P_{10}$	43.33	39.00	46.00	86.33	46.83	97.10	1.43	16.39	2.55	63.56	5.89	2.29	1.41	1.12	21.96	47.49	26.47	1.09
$P_8 \times P_9$	45.10	42.00	46.67	83.33	50.27	106.37	2.03	18.52	2.69	61.61	7.08	2.37	1.37	0.95	20.28	46.01	25.31	1.09
$P_8 \times P_{10}$	40.00	41.33	46.00	85.33	41.53	95.87	1.83	15.24	2.54	62.55	4.36	1.94	1.31	0.92	24.06	46.67	25.76	0.91

VI

Contd. Appendix - II

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Parent Range	38.83 to 48.73	34.00 to 42.00	37.67 to 47.00	77.33 to 90.33	37.47 to 55.13	84.60 to 115.93	1.10 to 2.50	14.12 to 24.82	2.44 to 2.88	58.38 to 68.43	4.31 to 7.11	1.65 to 3.12	1.24 to 1.47	0.78 to 1.47	21.26 to 26.33	46.00 to 48.83	24.16 to 26.86	0.74 to 1.47
F_1 Range	37.03 to 52.33	34.00 to 44.00	38.33 to 47.33	75.33 to 88.00	36.60 to 61.80	81.93 to 126.83	1.00 to 3.17	36.52 to 16.59	2.51 to 2.92	57.32 to 69.20	4.41 to 10.24	1.86 to 4.14	1.11 to 1.47	0.75 to 1.38	17.57 to 28.61	44.18 to 48.74	24.69 to 26.57	0.88 to 2.00
F_2 Range	37.53 to 47.40	34.67 to 45.33	39.67 to 48.33	77.67 to 88.67	35.80 to 54.10	76.30 to 109.37	0.97 to 2.27	12.97 to 26.40	2.36 to 2.93	56.44 to 67.72	3.37 to 7.43	1.64 to 3.19	1.26 to 1.42	0.75 to 1.30	17.30 to 29.67	45.13 to 48.68	24.53 to 26.54	0.77 to 1.55
Overall mean	42.09	39.12	44.01	84.15	44.99	96.02	1.96	20.26	2.69	62.85	5.65	2.56	1.34	1.04	23.62	47.47	25.90	1.21
S.Em	0.77	0.70	0.50	0.29	0.98	1.58	0.08	0.22	0.01	0.04	0.10	0.05	0.00	0.02	0.36	0.10	0.02	0.02
CD at 5%	2.14	1.95	1.37	0.39	2.72	4.57	0.21	0.61	0.03	0.12	0.28	0.13	0.01	0.05	0.99	0.26	0.04	0.06
CV %	3.18	3.11	1.95	0.59	3.78	2.85	6.83	1.88	0.69	.0.12	3.18	3.25	0.59	3.26	2.62	0.35	0.11	3.16