

**GENETICS OF RESISTANCE TO RENIFORM NEMATODE
(Rotylenchulus reniformis), YIELD AND YIELD
COMPONENTS IN CASTOR (Ricinus Communis L.)**

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FOR THE AWARD OF THE DEGREE**

OF

Master of Science

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IN

PLANT BREEDING AND GENETICS

BY

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1996



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MY
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PARENTS

ABSTRACT

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GENETICS OF RESISTANCE TO RENIFORM NEMATODE
(*Rotylenchulus reniformis*), YIELD AND YIELD
COMPONENTS IN CASTOR (*Ricinus communis* L.)

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The study was conducted at Departments of Plant Breeding and Nematology, B.A. College of Agriculture, Gujarat Agricultural University, Anand Campus, Anand during kharif, 1995-96 involving eleven crosses viz., SPS 43-3 x 48-1, 48-1 x ARUNA, 48-1 x TMV 5, SPS 43-3 x SKI 49, VP 1 x ARUNA, VP 1 x TMV 5, ARUNA x SKI 49, TMV 5 x SKI 12, SKI 12 x SKI 49, ARUNA x TMV 5 and ARUNA x SKI 12, each having six generations (P₁, P₂, F₁, F₂, B₁ and B₂) in a compact family block design replicated thrice for the estimation of genetic parameters (Gene action, Heterosis, Inbreeding depression, Heritability and Genetic advance) for resistance to reniform nematode, seed yield and yield components in castor (*Ricinus communis* L.).

Scaling test (Hayman and Mather, 1955) was done to check the adequacy of the additive and dominance components.

Gene effects were estimated using six parameter model suggested by Hayman (1958) and three parameter model suggested by Jinks and Jones (1958). The analysis of variance revealed significant variation among different generations for all the characters except oil content in almost all crosses studied indicating considerable variability in the material tested.

Higher magnitude of additive and non-additive gene effects in the expression of resistance to reniform nematode in hybrid combination SPS 43-3 x 48-1, and higher mean and significant heterosis (-41.42 %) and heterobeltiosis (-40.98 %) in desirable negative direction suggested that the isolation of homozygous recombinants having desirable level of resistance to reniform nematode from advance segregating generations would be feasible.

For seed yield and its components (viz., length of main raceme, number of capsules on main raceme, number of total and effective branches/plant and 100 seed weight) two hybrids viz., ARUNA x SKI 12 and VP 1 x ARUNA expressed significant positive heterosis and heterobeltiosis. The cross, ARUNA x SKI 12 showed highest relative heterosis (58.96 %) and heterobeltiosis (53.20 %) with the maximum seed yield (269.44 g) per plant followed by hybrid VP 1 x ARUNA with 45.54 % relative heterosis, 21.94 %

heterobeltiosis and 208.76 g seed yield/plant. Additive and non-additive gene effects largely involved in the expression of seed yield and its component characters suggested the feasibility of the exploitation of hybrid vigour on commercial scale or alternatively to follow cyclic method of breeding involving selection of superior recombinants and their *inter se* crossing for evolving desirable genotypes of castor.

In general, the crosses showing significant heterosis and heterobeltiosis also exhibited significant inbreeding depression.

Low magnitude of narrow sense heritability observed for resistance to reniform nematode, seed yield and yield components in almost all crosses studied revealed the importance of non-additive gene action in the expression of these traits. Moderate to high heritability coupled with moderate genetic advance as per cent of mean for seed yield and its components in various crosses suggested that seed yield and its components can be improved upon by following selection in succeeding generations. Low narrow sense heritability coupled with low genetic advance observed for oil content suggested slow improvement in this quality trait through selection.

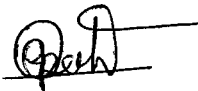
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CERTIFICATE

This is to certify that the thesis entitled "GENETICS OF RESISTANCE TO RENIFORM NEMATODE (*Rotylenchulus reniformis*), YIELD AND YIELD COMPONENTS IN CASTOR (*Ricinus communis* L.)" submitted by Shri D. J. Bhand in partial fulfilment of the requirements for the degree of "Master of Science (Agriculture) in Plant Breeding and Genetics" of the Gujarat Agricultural University is a record of bonafide research work carried out by him under my personal guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma or other similar title.

Place : ANAND

Date : October 28, 1996


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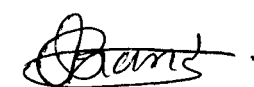
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Place : Anand
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(D. J. Bhand)

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- Appendix III Analysis of variance of six generations for various characters in six crosses of castor

INTRODUCTION

CHAPTER I

INTRODUCTION

Castor, *Ricinus communis* L., an important non edible oilseed crop of arid and semi-arid regions of India belongs to the genus *Ricinus* of Euphorbiaceae family with chromosome number $2n=20$ and amount of cross pollination to the extent of 50 %.

The crop has wide adaptability and is grown in tropical, subtropical and temperate regions of the world. It is cultivated in about 30 different countries on commercial scale. Among these, Brazil, India, China, Russia, Thailand and Philippines are the principal castor growing countries accounting for 88 % of total world production (Fatteh, 1986).

India, being the largest castor producer in the world, occupied about 8.7 lakh tonnes with about 70 % of the world production, surpassing 6.4 lakh tonnes crop in 1995-96 with an impressive rise of 35 %. Similarly, India has outclassed all other exporting countries by exporting as much as 1.7 lakhs tonnes, worth Rs. 330 crores representing a predominant share (i.e. 85 %) in the world export trade of about 2 lakhs tonnes of castor oil (Anon., 1995). Overseas producers of speciality chemicals, lubricants and certain other products opt for castor oil, among other things as it is environment-friendly.

Gujarat, Andhra Pradesh, Karnataka, Orissa and Tamil Nadu are the major castor growing states of the country. Gujarat occupies 49 % of total area producing 81 % of the country's total production (Anon., 1996) and ranks first in area, production and productivity where it is cultivated in 3.06 lakhs hectares of land with 4.96 lakh tonnes of production and 1622 kg/ha of productivity (Desai and Patel, 1996). This has been attributed mainly to the speedy adoption of hybrids and ample availability of other inputs and water.

Castor seed contains 48 to 56 % oil of tremendous industrial value and is mainly used in the production of plastics, nylone, all purpose greases, hydraulic fluids, artificial leather, rubber, printing ink, soaps, fast drying oils, paints, varnishes, recinolyl alcohol and medicine. The refined oil also has a good domestic market. The oil differs from other vegetable oils in the sense that it does not freeze even under adverse temperature of -12° to -18°C. It is, therefore, considered as best lubricating agent particularly for both high speed engines and aeroplanes. The stalk is used as source of pulp for paper industry, card boards, news prints and as a fuel in villages. In India, the castor plants are also grown for rearing 'Eri' silk worm for the production of 'Eri' silk. The castor press cake is a valuable source of nitrogen (5.5 %) applied in seed beds to promote early growth of the plant and even shows some

nematicidal effect (Omran, 1991) and controls termite. However, it is poisonous for cattle because of the presence of a protein ricin (blood coagulating factor) and a toxic alkaloid "ricinine".

Developing high yielding hybrid or variety with multiple resistance to biotic and abiotic stresses is the ultimate aim of all the crop improvement programmes. Even after the exploitation of biotechnology in crop improvement, hybridization has its own advantage and still is frequently used in breeding programme aimed to improve yield and resistance to important stresses.

In India, most of the castor cultivars had been developed by hybridization followed by selection till seventies. Since last two decades, hybrid vigour is being exploited on commercial scale and hybrids viz., GCH 3, GAUCH 1, GCH 2 and GCH 4 have been released for cultivation. The hybrids are well accepted by the farmers because of their high production potentiality over other varieties and this has led to an increase in area, production and productivity of the crop in Gujarat.

Such an important oilseed crop is attacked by several biotic and abiotic factors affecting successful and profitable cultivation of castor crop. Plant parasitic nematodes are one of them. Besides two important fungal diseases viz., wilt incited by *Fusarium oxysporum* and root

rot by *Macrophomina phaseolina*, several plant parasitic nematodes such as *Meloidogyne arenaria* (Martin, 1958), *M. arenaria thamesi* (Linde et al., 1959), *M. hapla* (Gaskin and Crittenden, 1956), *M. incognita* (Minz, 1956), *M. incognita acrita* (Linde, 1956), *M. javanica* (Tarjan, 1953), *Pratylenchus vulnus* (Jensen, 1953), *P. zae* (McBridge et al., 1961), *Radopholus similis* (Birchfield, 1956) and *Rotylenchulus reniformis* (Seshadri and Sivakumar, 1963) have been reported to be parasitic to castor crop.

Among these, reniform nematode (*Rotylenchulus reniformis* Linford and Oliveira, 1940) was first reported on castor by Seshadri and Sivakumar (1963) in India and is key nematode dreadly affecting castor crop. Plants heavily infested by nematodes show dieback and stunting as secondary symptoms under field conditions. They being ubiquitous browsers and hidden enemies by hibernating in higher population cause discernable damage to the crop as it is of longer duration with deeper root system. It has been observed that castor plants once attacked by *R. reniformis* become more prone to the attack of other pathogenic organisms like fungi, especially (*Fusarium* spp. and *Macrophomina* spp.) and breaking disease resistance by the evolution of new pathotypes virulent to the hitherto resistant genes. Such damage recurrently occurs in castor growing areas of North Gujarat comprising Banaskantha, Sabarkantha and Mehsana districts. Nematode infestation

delays crop maturity and reduces castor seed size (Sivakumar and Seshadri, 1971) resulting in reduction of yield and quality of oil in terms of reduction in saponification value. Reduction in oil upto the extent of 3.4 and 6.6 % in castor seeds had been reported due to reniform nematodes infestation of 500 and 1000 females (4th instar stage) per kg of soil, respectively (Patel, 1995).

Several methods are used for the control of nematodes. Among these, cultural method is not of much use in control of reniform nematode, having wide host range and requires a long time for effective control. Physical method is not economical as well as not applicable on a large scale. Biological control requires long time and due to its own limitations, it is not practical at field level. Chemical control (nematicides) is more effective for controlling nematodes due to its quick killing action, but it is too costly, laborious to apply, phytotoxic, aggravates environmental pollution and requires skilled hand.

Because of heavy pressure on land from major food crops as well as slow but steady demand on land for non-agricultural purpose, it may not be possible to increase the area under cultivation. The only alternative is to augment the high production per unit time by improving yield potential of the existing varieties of castor through genetical improvement. Development of either resistant or

tolerant varieties to reniform nematode is the cheapest way to improve productivity of castor crop.

Though, the crop has got great commercial value, the information on genetics of resistance to reniform nematode is not available and the information on genetics of yield which is a complex quantitative character is very limited. Moreover, such informations are specific to the experimental material and the environment under which it is studied. Present investigation was, therefore, undertaken with the following objectives :

1. To study the nature of gene action governing resistance to reniform nematode and yield.
2. To estimate the magnitude of heterosis and heterobeltiosis in F_1 .
3. To estimate inbreeding depression in F_2 .
4. To study heritability expected genetic advance for resistance to reniform nematode, yield and yield components.

**REVIEW
OF
LITERATURE**

CHAPTER II

REVIEW OF LITERATURE

The available literature pertaining to gene action, heterosis, inbreeding depression, heritability and expected genetic advance with reference to resistance to reniform nematode, seed yield and yield components in castor is reviewed and presented in this chapter.

2.1 Reaction to reniform nematode

2.1.1 Screening of genotypes

2.1.2 Inheritance studies

2.2 Yield and its components

2.2.1 Gene action

2.2.2 Heterosis and inbreeding depression

2.2.3 Heritability and genetic advance

2.1 REACTION TO RENIFORM NEMATODE :

2.1.1 Screening of genotypes :

The reniform nematode, *Rotylenchulus reniformis* was first reported by Linford and Oliveira (1940) from Ohio and Hawaii (U.S.A.) on cowpea (*Vigna unguiculata* L.). In India, it was first reported by Siddiqi and Basir (1959) on coffee roots from Southern India, while in Rajasthan, it was reported for the first time by Swarup et al. (1969). Seshadri and Sivakumar (1963) were first to report the occurrence of reniform nematode on castor in India. They

reported die-back and stunting of plants as secondary symptoms in fields heavily infested with this nematode. Pathogenic behaviour of nematodes varies with types of nematodes based on their habit of parasitism. Reniform nematode being endoparasitic, feeds mainly on phloem. The infested tissues at the site of infection show hypertrophy, hyperplasia, thickening of cell walls, granular protoplasm and enlarged nuclei in castor (Sivakumar and Seshadri, 1972). Castor is a highly favoured host for *R. reniformis* showing symptoms of stunting and necrosis resulting in poor growth reduced root-development and reduction in yield (Verma and Prasad, 1969; Chandrasekharan, 1964).

Sivakumar and Seshadri (1971) reported reniform nematode (*R. reniformis*) to be pathogenic to castor exhibiting growth reduction, shedding of leaves, early flowering, malformation, seed discolourization leading to inferior quality seeds with lesser oil content.

Reniform nematode, (*R. reniformis*) was found highly pathogenic to castor affecting plant height, root and shoot weight and nutrient uptake. Histological studies of infested castor roots revealed that the nematode feeds on phloem as well as cortex tissues, killing feeder roots (Patel, 1981).

Verma and Prasad (1970) studied reaction of high resistant in cultivars of castor to reniform nematode and

concluded Bhagalpur local, HC 6 and T3 cultivars as highly resistant.

In a pot experiment, Darekar et al. (1990) screened 24 varieties of castor against *R. reniformis* and reported all 24 varieties as highly susceptible.

Patel (1995) conducted a study on effect of reniform nematode, (*R. reniformis*) on quantitative and qualitative losses in castor. He observed significant reduction in plant height, fresh shoot and root weights due to *R. reniformis* inoculation. Seed yield (20.08 %), test weight of castor seeds and chlorophyll content were reduced significantly at 500 and 1000 inoculum levels/kg soil. There was 3.14 and 6.60 % reduction in oil content of castor seeds due to nematode infection at 500 and 1000 nematodes/kg soil respectively.

2.1.2 Inheritance studies :

Literature scanned did not reveal any research information pertaining to inheritance studies on resistance to reniform nematode (*Rotylenchulus reniformis*) in castor. Hence, review on other crops has been cited.

Watts (1947) reported more than one gene for resistance to root-knot nematode (*Meloidogyne incognita*) in tomato.

Sasser (1954) reported two races of peanut root-knot nematode (*Meloidogyne arenaria*) capable of reproducing on soybean. However, race 2 was more aggressive and damaging than race 1.

Inheritance of resistance to root-knot nematode (*Meloidogyne incognita*) in tomato was studied by Barham and Winstead (1957). They reported that resistance to *M. incognita* in tomato was governed by an incomplete dominant gene.

Andersen (1961) reported single dominant gene responsible for resistance to cyst nematode (*Heterodera avenae*) in barley.

Resistance in cereals to nematodes especially cereal cyst nematode (*Heterodera avenae*) was restricted to barley and oats till, Danish spring wheat cv. Loros was reported as resistant governed by a single dominant gene located on chromosome 2B (Nielsen, 1966).

Andersen and Andersen (1968) studied inheritance of resistance to cyst nematode (*Heterodera avenae*) in F₂ population of barley and reported that the genes for resistance to race 1 and 2 were located on different loci.

Cotten and Hayes (1969) identified four genes, for resistance to cyst nematode (*H. avenae*) in barley.

Hartmann (1971) studied inheritance of resistance to root-knot nematode (*Meloidogyne incognita*) using Alabama No.1 (resistant) x Hawaiian Wonder (susceptible) genotypes in beans (*Phaseolus vulgaris* L.). He found more than 1/16 resistant plants in F₂ population which was insufficient to account for 2 gene hypothesis. It was assumed that the resistance is controlled by 3 pairs of genes.

Sidhu and Webster (1973a) reported that resistance to root-knot nematode (*M. incognita*) in tomato was governed by a single dominant gene. While, in a study on identification of resistance gene in tomato against *M. incognita*, Sidhu and Webster (1973b) noticed the presence of dominant or recessive genes for resistance to *M. incognita* in tomato.

Brown (1974) reported a distinct biotype of cyst nematode (*H. avenae*) in Australia responsible for differential reaction of resistant genotype at different places.

Kallow *et al* (1978) reported that inheritance of resistance to root-knot nematode (*M. incognita*) is governed by a single dominant gene.

Inheritance of resistance to cyst nematode (*H. avena*) in five cultivars of barley viz., Arthinais, CI 8147, Marocaine 079, Nile and Morocco was studied by

Obrien et al. (1979). They concluded that resistant genes were not the same in different cultivars. Resistance in Athinais, CI 8147, Marocaine 079 and Nile was governed by a single dominant gene. However, relation of this gene to genes in other cultivars could not be established indicating a possibility of involvement at least five different major genes in the expression of resistance.

Obrien et al. (1980) studied F₂ generations of 3 single crosses involving two resistant wheats, AUS 10894 and Loros and a susceptible one Halberd. The reactions of progeny suggested presence of partial dominance supporting single gene hypothesis for resistance to *H. avenae*.

Inheritance of resistance to root-knot nematode (*Meloidogyne incognita*) in cowpea was studied by Singh and Reddy (1982). They reported that two cultivars, IC 9642B and TVU 2430 P were resistant to *M. incognita*.

Singh and Reddy (1986) studied the nature of inheritance of resistance to *M. incognita* in four crosses of cowpea viz., S 228 (susceptible) x IC 9642 B (resistant), S 288 x TVU 2430 P (resistant), S 488 (susceptible) x IC 9642 B and S 488 x TVU 2430 P, and found all F₁ progenies as resistant. Segregation of progenies into 3 resistant and 1 susceptible ratio in F₂ revealed that resistance was governed by single dominant gene.

From the study of six generations involving resistant and susceptible parents in tomato, Aswathappa *et al.* (1987) revealed that resistance was governed by single dominant gene with additive and dominant effects controlling the expression of resistance.

Large scale screening of soybean germplasm for resistance to root-knot nematode (*M. incognita*) revealed two lines, PI 200538 and PI 230977 with higher level of resistance to race 2 (Luzzi *et al.*, 1987).

While studying the genetics of resistance in soybean to the peanut root-knot nematode (*Meloidogyne arenaria*) using crosses of susceptible genotype 'CNS' with 3 resistant genotypes, Jackson, PI 200538 and PI 230977. Luzzi *et al.* (1995 a) reported that resistance was inherited in quantitative nature. They further reported that PI 200538 had genes for resistance to *M. arenaria* that were not the same as in Jackson and PI 230977.

Luzzi *et al.* (1995 b) studied inheritance of resistance in soybean to javanese root-knot nematode (*Meloidogyne javanica*) involving a susceptible genotype 'CNS' in crossing with three resistant genotypes Gordon, PI 80466 and PI 230977 and reported that resistance was quantitatively inherited and each resistant parent might be having genes for resistance at different loci or different

alleles at the same loci. Heritability estimates for the three crosses ranged from 48 to 76 %.

Pankaj et al. (1995) studied inheritance of resistance to the pathotype 1 of cyst nematode (*Heterodera avenae*). F₁ progenies of both the cross combinations were resistant indicating dominant nature of gene. Segregation of progenies into 3 resistant and 1 susceptible ratio in F₂ revealed that resistance was governed by single dominant gene.

2.2 YIELD AND ITS COMPONENTS :

2.2.1 Gene action :

The nature and magnitude of gene action governing the inheritance of quantitative characters could be of great importance to the plant breeder in selecting the appropriate breeding procedure.

Fisher (1918) was first to give the concept of genetic variation and its partitioning into additive, dominance and epistatic components as under :

1. An additive genetic variance (σ^2_A) arises from the additive effect of genes summed at all segregating loci and is fixable in nature.

2. Dominance genetic variance (σ^2_D) arises from an intraallelic interaction of gene at segregating loci and is non-fixable type variation.
3. Epistatic genetic variance arises from an interallelic interaction of genes at two or more segregating loci and is also a non-fixable type variation.

Hayman (1958), and Jinks and Jones (1958) partitioned this component of genetic variation into three types of interactions viz., (i) additive x additive (effect due to interaction between homozygous gene pairs e.g. AA and BB), (ii) additive x dominance (interaction between AA and Bb or Aa and BB) and (iii) dominance x dominance (effect arising due to interaction between Aa x Bb).

Bhapkar and Cruz (1967) studied the inheritance of oil content in a cross of two parents and revealed that F₁ mean oil content was higher than those of the parents. The F₂ population showed continuous variation with mean being more towards the F₁. showed involvement of large number of genes with epistatic effects indicating possibilities of selecting lines with higher oil content.

Varisai and Stephen (1967) studied inheritance of number of nodes upto main inflorescence and observed additive gene action for this trait.

Hooks *et al.* (1971) found both additive and non-additive gene actions important for the expression of days to flower, number of effective branches/plant, number of nodes upto primary and secondary racemes, seed weight and oil content. However, only non-additive gene effects were involved in the expression of seed yield in castor.

Giriraj (1973) studied combining ability in a diallel set of six varieties of castor and reported dominance and overdominance for yield and partial dominance for length of primary raceme, number of capsules on primary raceme, 100 seed weight and oil content.

Giriraj *et al.* (1973) studied combining ability through a diallel and found both additive and non-additive genetic components playing role for yield, length of primary spike, number of capsules on primary spike, 100 seed weight and oil content in castor.

Genetic analysis of yield components through a diallel involving 4 parents carried out by Ramaswamy and Menon (1973) revealed that additive component (d) was highest for 100 seed weight, size of capsules and number of capsules. The analysis further showed the presence of partial dominance for number of racemes/plant, oil content, number of capsules and 100 seed weight.

Giriraj *et al.* (1974) studied nature of inheritance of five quantitative traits and found overdominance for yield and oil content and partial dominance for length of primary raceme, number of capsules on primary raceme and 100 seed weight. It was further suggested that recurrent selection should be used to improve the mean performance of the parents.

Kandaswami (1977) observed highly significant gene interactions for number of branches, number of racemes, length of main raceme, length of pistillate region of raceme, total number of capsules and seed yield in a line x tester analysis in castor indicating that these characters were not predominantly additive in nature. He suggested exploitation of hybrid vigour as a suitable breeding method to improve seed yield in castor.

Yadava *et al.* (1978) studied combining ability in a diallel set of eight genetically divergent inbred lines of castor and observed predominance of non-additive variance over additive genetic variance governing the inheritance of seed yield, the former being four times greater than the latter. The perfect correspondence between the sca effect of a cross and its heterotic value further revealed that *per se* performance of a cross and its sca effect would be two important criteria for exploitation of hybrid vigour.

Singh and Yadava (1981) analysed an 8 x 8 half diallel cross in castor and found partial dominance for flowering, complete dominance for maturity and over dominance for yield. Both additive and non-additive types of gene action were found important and variances for gca and sca were significant for these three characters. They concluded that the cross having parents of genetically divergent groups exhibited higher sca effects for these traits.

Singh and Srivastava (1982) investigated six yield related traits in 30 F₁ hybrids obtained by crossing 11 lines from U.S.A., 3 lines from India and 1 line from U.S.S.R with testers Tarai 4 and Type 3 and observed that dominance effects were predominant for number of effective branches/plant, days to flowering, length of main spike, length of pistillate region of main raceme, number of capsules/plant and seed yield/plant.

In an 8 x 8 partial diallel cross of castor involving dwarf, medium and tall inbreds, Singh and Yadav (1982) revealed that the plant height was under the control of both additive and non-additive type of genetic variances with more preponderance of the former. Dwarfness was governed by a recessive gene with very high narrow sense heritability suggested the prospects of breeding dwarf varieties of castor without sacrificing much yield.

While studying inheritance of seed yield/plant and components of genetic variability in F₁ generation through a 5 x 5 diallel, Alba and Greco (1983) observed that both additive and non-additive genetic variances were important for seed yield.

Bhatt and Reddy (1983) studied combining ability of an 8 x 8 diallel in castor and revealed that both fixable and non-fixable components were of equal importance for days to flower, while the latter was predominant for number of capsules/spike and yield. They further advocated the use of biparental matings with reciprocal recurrent selection, to exploit both fixable and non-fixable components for further improvement in yield.

Kandasamy *et al.* (1983) studied combining ability through line x tester analysis involving diverse parents in castor and observed predominance of non-additive genetic variance for number of branches, number of racemes and length of pistillate region of raceme. They further revealed that the general combining ability (gca) alone had greater effect on yield and its components while specific combining ability (sca) had little influence on seed yield.

Patel *et al.* (1984) carried out line x tester analysis involving 3 pistillate lines and 18 pollen parents in castor for earliness and its related traits and revealed the predominance of additive gene action for days to flower,

days to maturity and nodes upto main spike. For exploitation of earliness in hybrids it was suggested to select parents having lower nodes upto main spike.

Swarnlata *et al.* (1984) studied inheritance of yield and its components in castor through a diallel involving 17 diverse varieties and observed predominance of additive gene action for plant height, number of nodes to flower, length of primary raceme and 100 seed weight. Whereas predominance of non-additive gene action for number of capsules on primary spike and seed yield/plant.

Narkhede *et al.* (1985) conducted combining ability analysis for yield and its components in castor through diallel mating. The variance components due to general combining ability (gca) and specific combining ability (sca) were highly significant for seed yield, plant height, length of primary raceme, number of effective spikes/plant, number of capsules/primary raceme, number of nodes upto primary raceme, number of secondary branches/plant and number of tertiary branches/plant indicating the presence of both additive and non-additive gene actions for the control of these traits. However, greater magnitude of gca variance suggested the predominance of additive gene action.

Patel *et al.* (1985) studied variability in 44 entries involving 32 F₁'S and their 12 parents and observed additive gene action for seed yield and number of

capsules/plant whereas non-additive gene action for 100 seed weight, plant height upto main raceme, effective branches/plant and days to flowering in castor.

Bhatt and Reddy (1986) studied six crosses of castor for seven yield components and reported significant epistatic interactions for days to flower, number of nodes to main raceme, plant height upto main raceme, number of racemes and seed yield. However, predominance of fixable gene effects for most of the characters suggested bulk population and mass pedigree methods for enhancing seed yield whereas biparental matings with reciprocal recurrent selection could be exploited for both fixable and non-fixable genetic components of yield and its attributes in castor.

Patel *et al.* (1986) studied combining ability for seed yield and its attributes through line x tester analysis involving 4 pistillate lines and 15 pollen parents in castor. They reported the preponderance of non-additive gene action for yield/plant and number of capsules on main spike, whereas additive gene action was predominant for nodes upto main spike, length of main spike, effective spikes/plant and 100 seed weight.

Pathak *et al.* (1986) studied genetic architecture of oil content through an 11 x 11 diallel cross analysis and reported that both additive and non-additive gene effects

were important, however, non-additive gene effects was predominant for the inheritance of oil content.

A line x tester analysis involving 4 pistillate lines and 8 pollen parents was carried out for yield and its attributes in castor by Dangaria *et al.* (1987). They observed predominance of non-additive gene action for yield, number of capsules/plant and effective branches/plant and additive gene action for length of main raceme, effective length of main raceme and 100 seed weight.

Fatteh *et al.* (1987) studied combining ability for seed characters through line x tester analysis and reported predominance of additive gene action for 100 seed weight, seed length, seed width, thickness of seed and endosperm percentage. However, predominance of non-additive gene action was observed for oil content.

Gene effects for some quantitative characters in castor studied by Narkhede *et al.* (1987), revealed predominance of additive gene effects for plant height and length of spike, dominance gene effects for number of effective spikes, number of primary and secondary racemes and yield/plant and epistatic gene effects for number of nodes upto main raceme and capsule number/main raceme.

Pathak and Dangaria (1987) observed preponderance of additive type of gene action for days to flower, days to

maturity, nodes upto main raceme, plant height upto main raceme, length of main raceme, capsules on main raceme, effective branches/plant and 100 seed weight while studying combining ability for yield and its components in castor using diallel set of 11 parents. The study further showed predominance of non-additive gene action for seed yield. In view of the preponderance of additive gene action, single plant selection in segregating generations in crosses involving high general combiners with high sca effects was advocated.

Fatteh *et al.* (1988) studied combining ability through line x tester analysis and reported that the gene effects for seed yield, capsules/main spike and effective branches/plant were largely non-additive and for days to 50 % flowering, nodes upto main raceme and plant height upto main raceme were predominantly additive.

Pathak *et al.* (1988) studied gene effects through generation means using four inbred lines, their three F₁'S, F₂'S and back crosses in castor and found that additive, additive x additive and dominance x dominance effects were more important for seed yield, whereas dominance x dominance for days to flowering, only additive effects for total and effective branches and all gene effects were found important for plant height upto main raceme, length of main spike and 100 seed weight.

Dobariya *et al.* (1989) investigated combining ability and mode of inheritance for oil content through 12 x 12 partial diallel cross and reported that both additive as well as non-additive gene action were involved in the inheritance of seed oil content with predominant role of non-additive gene action. They further suggested use of specific combinations for the exploitation of heterosis for seed oil content in castor.

Pathak *et al.* (1989) carried out line x tester analysis for seed yield and its components and observed that additive genetic variance predominantly governed the expression of days to flowering, days to maturity, number of total and effective branches and 100 seed weight, whereas non-additive genetic variance chiefly controlled the inheritance of seed yield, plant height, number of nodes upto primary spike, length of primary spike and number of capsules on primary raceme.

While studying combining ability for earliness and its related traits in castor through a 10 x 10 diallel set, Mehta *et al.* (1991 b) reported preponderance of additive gene action for days to 50 % flowering, days to maturity, number of nodes upto main raceme and plant height upto main raceme.

Patel *et al.* (1991) studied variability in 14 diverse entries of castor and reported additive gene action

for 100 seed weight, plant height upto main raceme, length of primary raceme and seed yield and non-additive gene action for oil content.

Dhapke *et al.* (1992) examined 35 entries of castor to judge the genetic diversity between different lines for various characters. They revealed that number of branches, number of capsules on main raceme, length of pistillate region, number of capsules and seed yield/plant were mainly influenced by additive gene action.

Dobariya *et al.* (1992) studied combining ability for seed yield and its components through a 12 x 12 diallel cross analysis and reported the role of non-additive gene action in the control of seed yield and additive gene action for length of main raceme, effective length of main raceme, effective branches/plant, number of capsules on main raceme, number of capsules/plant and 100 seed weight.

Patel (1992) investigated inheritance of yield and its components through generation mean analysis involving 5 diverse parents of castor. He observed both additive as well as non-additive gene effects for seed yield, number of capsules on main raceme, number of total and effective branches/plant, plant height and days to flowering in different crosses. It was suggested to explore the possibility of commercial hybrids or alternatively to follow

cyclic method of breeding to evolve desirable ideotypes of castor suitable for specific farming conditions.

Goyani *et al.* (1993) studied inheritance of oil, hull content and seed yield through a 6 x 6 diallel set in castor. They reported the predominant role of additive genetic variance in the inheritance of oil content and seed yield.

Natarajan *et al.* (1993) studied the nature of combining ability and gene action for yield and its components through a 5 x 5 partial diallel analysis and observed that both additive and non-additive gene actions were responsible for seed yield, length of main raceme and pistillate region.

Sudhakar *et al.* (1995) studied combining ability through line x tester analysis involving 13 parents and reported best general as well as specific combiner for different traits. They further observed that gca effects of parents were in accordance to mean performance for yield suggesting that per se performance of the parents could be effectively used as selection criteria.

Vindhiyavarman and Ganesan (1995) studied combining ability using line x tester analysis and reported that non-additive type of gene action was predominant for seed yield, effective number of spikes/plant, length of main

spike, effective length of main spike and number of capsules/plant, whereas additive type of gene action was important for number of nodes upto main spike.

2.2.2 Heterosis and inbreeding depression

Heterosis has been considered as one of the important break through in the field of plants and animal breeding.

The term, heterosis, refers to a phenomenon in which F_1 population obtained by crossing of two genetically dissimilar individuals shows increase or decrease in vigour over mid-parental value (Heterosis) and/or over better parental value (Heterobeltiosis).

Usually, the term heterosis and hybrid vigour are used synonymously. However, there is great controversy over these two words. Hybrid vigour refers to increased vigour and size while heterosis refers to increased vigour as well as decreased vigour (i.e. weakness) of hybrids. Thus, the term heterosis has wider coverage than the term hybrid vigour.

In 1763, hybrid vigour was first reported in artificial tobacco (*Nicotiana* spp.) hybrids by J.G. Kolreuter. East (1908) and Shull (1908) studied the effects of cross and self fertilization in maize and finally Shull (1914) gave the term "Heterosis" to the developmental

stimulus resulting from the union of different gametes and hybrid vigour to the manifest effects of heterosis. Stebbins (1959) defined heterosis for crop plants as greater adaptedness to human needs which has been obtained in a particular environment through artificial selection followed by hybridization. Subsequently, many workers advanced several explanations to heterosis like dominance (Davenport, 1908), over dominance (East, 1908 and Shull 1908) and Epistasis (Jones, 1917 and Jinks and Jones, 1958), Fonseca and Patterson (1968) described heterosis as an improvement of heterozygotes in relation to better parent. Mather and Jinks (1971) defined heterosis as the amount by which the mean of an F_1 family exceeds its better parent.

Inbreeding occurs by mating individuals that are related by ancestry. Inbreeding depression is observed in F_2 and in later generations. The extent of depression even in the same crop varies from character to character and from generation to generation. The extent of depression also depends upon the number of parents involved in the original cross as well as relationship between two parents crossed. Generally, depression is rapid in first few generations and slows down in later generations. The major cause of rapid depression from F_1 to F_2 is the breakdown of specific gene combinations for heterosis in F_1 as a consequence of segregation in F_2 generation.

Usually, the phenotypic consequences of inbreeding in cross fertilizing species are reduction in plant height and size, loss of vigour, seed production capacity, fitness, yield potential and the appearance of the abnormalities. The appearance of lethal and sublethal alleles and increase in homozygosity are its genetic consequences.

White (1918) observed a higher amount of seeds in F₁ castor than either of the parents.

Claassen and Hoffman (1950) suggested the use of pistillate lines for producing F₁ hybrid seeds.

In a study of 22 single cross castor hybrids Zimmerman and Van Horn (1953) reported 87 to 132 % heterosis for seed yield over their better parent.

Narayan (1958) studied the production of hybrid castor seed and observed 2.7 to 277.0 % higher yield in F₁ over the better parent and maximum average increase of 22.9 % seed yield in F₁ over the better parent.

Stein (1958) observed a marked increase in yield over higher yielding parent together with considerable increase in vegetative vigour. However, increased yield was attributed to increased number of seeds/raceme in the hybrid over better parent.

Pathak and Dikshit (1961) studied heterosis for various stages of growth and development through 30 F₁'S derived from various combinations of 13 parents. They observed positive as well as negative heterosis and heterobeltiosis for germination and rate of formation of leaves whereas only positive heterosis was found for plant height of 20 days old seedlings.

Sindagi (1964) studied manifestation of hybrid vigour in 15 F₁'S during early seedling stage using combinations of 17 parents and observed high heterotic effects for number of leaves, plant height and leaf index.

Ankineedu and Kulkurni (1965) studied the exploitation of heterosis for seed yield and observed that all F₁ hybrids yielded more than their respective better parents and standard variety HC 6. They found highest heterosis (56.58 %) for seed yield/plant in a cross between indigenous and exotic lines.

Satyabalan et al. (1965) studied hybrid vigour in castor using six hybrids and reported significant positive heterosis for number of racemes/plant (68.70 %) and seed yield/plant (76.62 %).

In a study of hybrid vigour through 54 hybrids of castor involving nine pistillate lines with 20 monoecious lines, Gopani et al. (1968) observed positive heterosis over

better parent for seed yield/plant, number of effective branches/plant, plant height, number of capsules on main raceme and oil content. However, they noticed negative heterosis over better parent for 100 seed weight. Hybrid TSP 10R x JI 15 proved significantly better yielder than other hybrids and inbreds and released for general cultivation as GCH 3 in Gujarat.

Varisai et al. (1969) studied hybrid vigour through top crosses of castor using six Egyptian inbreds and TMV 1 as tester and reported positive heterosis over better parent for number of effective branches, length of pistillate region of raceme, length of main raceme, total number of capsules and seed yield/plant. However, they observed negative heterosis for number of days to first flowering and days to maturity which would be helpful in deciding earliness of the crop.

In a study of heterosis through 13 hybrids of castor derived through top crosses of five Russian and eight indigenous inbreds and TMV 1 as tester, Varisai et al. (1970) noticed expression of hybrid vigour for number of racemes, number of capsules/plant and seed yield.

Hooks et al. (1971) studied heterosis in 21 hybrids derived through 7 x 7 half diallel analysis of castor and reported significant effect of heterosis for seed yield.

Kabariya and Gopani (1971) Studied the performance of the parents, the F₁ and F₂ generations of GCH 3 (TSP 10 R x JI 15) and observed significant heterosis in F₁ over mid parental value for number of capsules on the main spike, percentage of pistillate flower and seed yield. However, significant reduction in heterosis for number of capsules on main spike and percentage of pistillate flowers in F₂ as compared to F₁ generations was observed. They also observed that there was increase in number of nodes and plant height in F₂ over F₁ mean and mid-parental values.

Gopani *et al.* (1972) studied hybrid vigour in five hybrids of castor in comparison with open pollinated variety S 20 for two years at six locations and noticed higher yield of hybrids than the variety S 20. However, none of the hybrids had higher oil content than variety S 20.

Giriraj *et al.* (1973) studied heterosis in a diallel of six varieties of castor and reported heterosis for seed yield in the crosses of HC 6 x Gujarat monospike and Gujarat monospike x cimarron.

Yadava *et al.* (1978) studied heterosis using 8 x 8 diallel crosses of castor and reported seven F₁ out of 28, exhibited positive and high heterosis (20 to 314 %) over better parent and mid-parental value for seed yield.

Kaul and Prasad (1983) studied heterosis through crosses between dwarf and tall inbreds of castor and found heterosis over their respective better parent for seed yield ranging from 80 to 194 %. They further observed that heterosis for seed yield was due to the heterosis for main spike length and number of capsules on primary spike.

In a study on heterosis and genetic architecture of oil content through an 11 x 11 diallel cross analysis of castor, Pathak *et al.* (1986) observed thirteen crosses exhibiting significant heterosis over better parents. However, twenty five crosses exhibited significant heterosis over mid parent.

Bhatt and Reddy (1987) studied genetic divergence among 8 parents through D^2 and canonical analysis and observed heterosis in all 56 F_1 populations. They further suggested that the importance of genetic diversity among parents used in hybrid breeding programme.

Dangaria *et al.* (1987) studied magnitude of heterosis for seed yield and its attributes in 32 hybrids derived through line x tester analysis involving 4 pistillate lines and eight pollen parents. They observed heterosis over better parent, ranging from -13.30 to 88.57 % for seed yield, -38.96 to 59.83 % for spike length, -31.85 to 97.50 % for number of capsules/plant, -27.27 to 9.26 % for 100 seed weight, -18.12 to 29.85 % for nodes upto main spike and -6.90 to 175.18 % for plant height.

Pathak *et al.* (1988) studied heterosis for eleven traits in three separate crosses of castor based on generation means and observed significant positive heterosis for seed yield, plant height, number of capsules on main spike and 100 seed weight, however they recorded highest inbreeding depression for seed yield/plant, followed by 100 seed weight in all the three crosses of castor.

Dobaria *et al.* (1989) studied heterosis in a set of twelve diverse castor genotypes through partial diallel analysis. They observed positive heterosis and heterobeltiosis varied from 2.38 to 7.83 % and 1.95 to 5.91 % respectively for oil content.

In a study on heterosis through a 10 x 10 diallel cross analysis, Mehta *et al.* (1991 a) observed the relative heterosis ranging from -50.75 to 104.75 % and heterobeltiosis ranging from -60.02 to 66.58 % for seed yield/plant. They also reported that high heterosis for seed yield was due to high magnitude of heterosis for number of capsules in main spike, length of pistillate region of main spike, effective branches/plant and seed yield/main spike.

While studying gene effects, heterosis and expected genetic advance as per cent of mean in 4 separate crosses of castor based on generation mean analysis, Patel (1992) observed significant and desirable heterosis and heterobeltiosis for seed yield and its components in

various crosses suggesting the feasibility of the exploitation of hybrid vigour on commercial scale. He also noticed that the crosses showing higher magnitude of heterosis and heterobeltiosis exhibited higher magnitude of inbreeding depression.

2.2.3 Heritability and genetic advance

Heritability in broad sense is the ratio of genotypic variance to the total variance (Phenotypic variance) while in narrow sense, it is the ratio of additive component of variance to the total phenotypic variance. Generally, it refers to the degree to which the variability of metric trait may be transmitted from the parents to the progenies and is the index of transmissibility.

Heritability is a measure of the efficiency of a selection system in separating genotypes to exploit the genetic variability. The estimates of heritability is a useful guide to the plant breeder as they provide the basis for selection on phenotypic performance.

Improvement in the mean genotypic value of the selected families over the base population is known as genetic advance under selection. Statistically, genetic gain is the product of selection differential, phenotypic standard deviation and heritability. Genetic advance under selection depends upon (1) the genetic variability among

different plants or families in the base population (2) the heritability of the character under selection and (3) the intensity of selection, i.e. the proportion of plants or families selected. Genetic advance may also be expressed as per cent of the population mean.

The genetic gain as calculated above is applicable to a mixture of pure lines or clones, but it is not applicable to segregating generation. Therefore, when dealing with segregating populations, heritability in narrow sense is used for estimating expected genetic advance under selection.

Sindagi (1965) studied genotypic variability in the characters like number of branches, number of capsules on main raceme, female portion on main spike, length of main raceme and yield/plant in castor. He observed high heritability for female portion on main spike (77.82 %), number of capsules on main spike (66.80 %) and number of branches (63 %), whereas comparatively low heritability values were obtained for length of main spike (45.78 %) and yield/plant (26.10 %). He further reported high genetic advance as per cent of mean for female portion on the main spike (92.87 %) and number of capsules on main spike (72.87 %).

Stephen *et al.* (1973) studied variability in 60 varieties of castor and reported high heritability with high

genetic advance as per cent of mean for length of pistillate region of raceme, length of raceme and number of nodes upto main raceme, whereas, high heritability with moderate genetic advance as per cent of mean for 1000 seed weight and moderate heritability with high genetic advance as per cent of mean for yield and number of branches. Role of these attributes was considered very important in the selection of parents for improvement of yield in castor.

Ramaswamy and Menon (1973) noticed high heritability for capsule size, seed size and seed weight in a study of 4 x 4 diallel cross analysis in castor.

Giriraj *et al.* (1974) carried out a 6 x 6 diallel cross analysis to study the nature of inheritance of five quantitative traits and observed high heritability value for seed weight, moderate values for length of primary raceme and number of capsules on the primary raceme, whereas low heritability values were observed for seed yield and oil content.

Bhatt and Reddy (1981) studied eight yield attributes in castor and observed estimates of heritability ranging from 0.152 for seed yield to 0.893 for number of nodes upto main raceme. The expected genetic advance was high for plant height and days to flowering.

While studying an 8 x 8 half diallel cross, Singh and Yadava (1981) observed high heritability for days to flower and maturity and low for seed yield in castor.

Muthiah *et al.* (1982) studied variability and heritable components in seven characters in castor and observed high heritability for 100 seed weight. They also reported high heritability with high genetic advance for plant height and seed yield/plant.

Singh and Yadav (1982) reported very high narrow sense heritability (87.96 %) for dwarfness in a study of 8 x 8 diallel crosses of dwarf, medium and tall inbreds of castor.

Kaul and Prasad (1983) studied several crosses between dwarf, moderately tall and tall inbreds of castor and observed highest heritability for number of nodes to the first raceme.

Swarnlata *et al.* (1984) studied a diallel cross involving 17 diverse varieties of castor and observed high heritability for plant height (66 %), number of nodes to flower (83 %) and 100 seed weight (76 %) and low heritability for primary spike length (54 %), number of capsules/primary spike (57 %) and seed yield/plant (40 %).

Patel *et al.* (1985) studied genetic variability in 44 entries involving 32 F₁'s and their 12 parents and observed high to medium heritability combined with high

genetic advance for seed yield/plant and number of capsules/plant and high heritability with low genetic advance for 100 seed weight, plant height upto main raceme, effective branches/plant and days to flowering.

Patel and Jaimini (1988) evaluated 40 diverse genotypes of castor under irrigated and rainfed conditions and observed moderate to high heritability and genetic advance for number of capsules on primary raceme, number of branches/plant, plant height and 100 seed weight whereas, heritability and genetic advance were low to moderate for seed yield/plant.

Patel et al. (1991) studied variability in fourteen diverse entries of castor and observed high heritability with high genetic advance as per cent of mean for seed weight, plant height, length of primary raceme and seed yield whereas high heritability with low genetic advance for oil content.

Dhapke et al. (1992) studied variability in 35 entries involving 24 F₁'S and 11 parents and observed high heritability estimates coupled with high genetic advance for number of branches, number of capsules on main raceme, length of pistillate region, number of capsules and seed yield/plant.

In a study of generation mean analysis involving 5 diverse parents of castor, Patel (1992) reported high to

moderate heritability coupled with high to moderate genetic advance for days to flowering of main raceme, number of nodes upto main raceme, plant height, number of total and effective branches, length of main raceme, number of capsules in main raceme and seed yield/plant. It can be improved upon by following selection in succeeding segregating generations. He also noticed low heritability coupled with low genetic advance for oil content and 100 seed weight, suggested slow improvement in these important traits.

Goyani *et al.* (1993) observed high narrow sense heritability for seed yield/plant (34 %) and also reported medium heritability for hull content (12 %) and oil content (23 %) in a study of inheritance of oil, hull content and seed yield in castor.

MATERIALS AND METHODS

CHAPTER III

MATERIALS AND METHODS

The present investigation on "Genetics of resistance to reniform (*Rotylenchulus reniformis*) nematode, yield and yield components in castor" was carried out during kharif, 1995-96 at the Departments of Plant Breeding and Nematology, B.A. College of Agriculture, Gujarat Agricultural University, Anand Campus, Anand. Geographically Anand is situated at 22°-35'N latitude and 72°-55'E longitude with an altitude of 45.1 m above mean sea level. The soil of experimental site is sandy loam, alluvial in origin and poor in organic matter content (coarse sand 1.3%, fine sand 63%, silt 15% and clay 20%). It is poor in total nitrogen, moderate in available phosphorus and potash. It is very deep well drained and retains moisture fairly. It is neutral to slightly alkaline in reaction and responds well to manuring and irrigation. The meteorological data for the cropping season are presented in Appendix I.

The details of experimental materials used and the techniques adopted in present investigation are described below :

3.1 EXPERIMENTAL MATERIALS :

The experimental materials consisted of seven inbred lines of castor (*Ricinus communis* L.) viz., 48-1,

SPS 43-3, ARUNA, VP 1, TMV 5, SKI 12 and SKI 49 selected from the germplasm maintained at the Main Castor Research Station, Gujarat Agricultural University, Sardar Krushinagar. The important features of these inbred lines are given below :

Sr. No.	Inbred line	Pedigree	Important features
1.	48-1	Selection from local (Hyderabad)	Mahogany stem, medium tall, flat leaves, double bloom, non-spiny capsules, semi-compact spike and resistance to wilt.
2.	SPS 43-3	(VI 9 x JM 6)F ₂ irradiation single plant selection (S.K.Nagar)	Green stem, tall plant, flat leaves, double bloom, spiny capsules and semi-compact spike.
3.	ARUNA	Selection from mutants of HC 6 (Rajendranagar)	Mahogany stem, medium tall, flat leaves, double bloom, spiny capsules and semi-compact spike.
4.	VP 1	(TSP 10RxJI 15)F ₂ x (JP 5 x 26006)F ₂ (Vijapur)	Green stem, dwarf, cup shape leaves, triple bloom, spiny capsules, compact spike and 100 % pistillate line.
5.	TMV 5	Selection from 1158 x 3.2 (Tamil Nadu)	Red stem, medium dwarf, flat leaves, triple bloom, spiny capsules and loose spike.
6.	SKI 12	(HC 8 x 413-19) JH 20 (S.K.Nagar)	Mahogany stem, medium tall, flat leaves, triple bloom, spiny capsules and semi-compact spike.
7.	SKI 49	(SKP 4 x SPS 43-3) x (SKP 2 x SKP 6) (S.K.Nagar)	Green stem, tall, flat leaves, double bloom, spiny capsules and semi-compact spike.

Selection of parents :

Parents were selected on the basis of their reaction to reniform nematode (*Rotylenchulus reniformis*) as per the procedure given in Section 3.2 and classified as follows :

Sr. No.	Genotype	Mean number of females of reniform nematode/plant	Reaction
1.	48-1	7.00	R
2.	SPS 43-3	4.00	R
3.	ARUNA	14.00	MR
4.	VP 1	13.60	MR
5.	TMV 5	25.00	S
6.	SKI 12	27.00	S
7.	SKI 49	39.00	HS

Scale used for classification : (Anon.,1990)

Females/plant	Category
0	Highly Resistant (HR)
1 to 10	Resistant (R)
11 to 20	Moderately Resistant (MR)
21 to 30	Susceptible (S)
> 30	Highly Susceptible (HS)

Eleven crosses viz., (I) SPS 43-3 x 48-1, (II) 48-1 x ARUNA, (III) 48-1 x TMV 5, (IV) SPS 43-3 x SKI 49, (V) VP 1 x ARUNA, (VI) VP 1 x TMV 5, (VII) ARUNA x SKI 49, (VIII) TMV 5 x SKI 12 (IX) SKI 12 x SKI 49 (X) ARUNA x TMV 5 and (XI) ARUNA x SKI 12 were developed during kharif, 1994-95. Subsequently, these F₁'s were selfed and backcrossed to obtain F₂, B₁ and B₂ generations during summer, 1995. The entire experimental material comprised parents (P₁ and P₂), F₁, F₂, B₁ (F₁ x P₁) and B₂ (F₁ x P₂) generations of all eleven crosses which were studied during kharif, 1995-96. The details on experimental materials are presented in Table 3.1.

Table 3.1 : The details of the experimental materials

Cross	No.	Material	Generation
I	i	SPS 43-3	P ₁
	ii	48-1	P ₂
	iii	(SPS 43-3 x 48-1)	F ₁
	iv	(SPS 43-3 x 48-1) F ₁ selfed	F ₂
	v	(SPS 43-3 x 48-1) x SPS 43-3	B ₁
	vi	(SPS 43-3 x 48-1) x 48-1	B ₂
II	i	48-1	P ₁
	ii	ARUNA	P ₂
	iii	48-1 x ARUNA	F ₁
	iv	(48-1 x ARUNA) F ₁ selfed	F ₂
	v	(48-1 x ARUNA) x 48-1	B ₁
	vi	(48-1 x ARUNA) x ARUNA	B ₂
III	i	48-1	P ₁
	ii	TMV 5	P ₂
	iii	48-1 x TMV 5	F ₁
	iv	(48-1 x TMV 5) F ₁ selfed	F ₂
	v	(48-1 x TMV 5) x 48-1	B ₁
	vi	(48-1 x TMV 5) x ARUNA	B ₂

contd..

Cross	No.	Material	Generation
IV	i	SPS 43-3	P ₁
	ii	SKI 49	P ₂
	iii	(SPS 43-3 x SKI 49)	F ₁
	iv	(SPS 43-3 x SKI 49) F ₁ selfed	F ₂
	v	(SPS 43-3 x SKI 49) x SPS 43-3	B ₁
	vi	(SPS 43-3 x SKI 49) x SKI 49	B ₂
V	i	VP 1	P ₁
	ii	ARUNA	P ₂
	iii	VP 1 x ARUNA	F ₁
	iv	(VP 1 x ARUNA) F ₁ selfed	F ₂
	v	(VP 1 x ARUNA) x VP 1	B ₁
	vi	(VP 1 x ARUNA) x ARUNA	B ₂
VI	i	VP 1	P ₁
	ii	TMV 5	P ₂
	iii	VP 1 x TMV 5	F ₁
	iv	(VP 1 x TMV 5) F ₁ selfed	F ₂
	v	(VP 1 x TMV 5) x VP 1	B ₁
	vi	(VP 1 x TMV 5) x TMV 5	B ₂
VII	i	ARUNA	P ₁
	ii	SKI 49	P ₂
	iii	ARUNA x SKI 49	F ₁
	iv	(ARUNA x SKI 49) F ₁ selfed	F ₂
	v	(ARUNA x SKI 49) x ARUNA	B ₁
	vi	(ARUNA x SKI 49) x SKI 49	B ₂
VIII	i	TMV 5	P ₁
	ii	SKI 12	P ₂
	iii	TMV 5 x SKI 12	F ₁
	iv	(TMV 5 x SKI 12) F ₁ selfed	F ₂
	v	(TMV 5 x SKI 12) x TMV 5	B ₁
	vi	(TMV 5 x SKI 12) x SKI 12	B ₂
IX	i	SKI 12	P ₁
	ii	SKI 49	P ₂
	iii	SKI 12 x SKI 49	F ₁
	iv	(SKI 12 x SKI 49) F ₁ selfed	F ₂
	v	(SKI 12 x SKI 49) x TMV 5	B ₁
	vi	(SKI 12 x SKI 49) x SKI 12	B ₂
X	i	ARUNA	P ₁
	ii	TMV 5	P ₂
	iii	ARUNA x TMV 5	F ₁
	iv	(ARUNA x TMV 5) F ₁ selfed	F ₂
	v	(ARUNA x TMV 5) x ARUNA	B ₁
	vi	(ARUNA x TMV 5) x SKI 49	B ₂

contd..

Cross	No.	Material	Generation
XI	i	ARUNA	P ₁
	ii	SKI 12	P ₂
	iii	ARUNA x SKI 12	F ₁
	iv	(ARUNA x SKI 12) F ₁ selfed	F ₂
	v	(ARUNA x SKI 12) x ARUNA	B ₁
	vi	(ARUNA x SKI 12) x SKI 12	B ₂

3.2 SCREENING OF PARENTS FOR REACTION TO RENIFORM NEMATODE (*Rotylenchulus reniformis*) :

The parents were subjected to reniform nematode in pots as follows :

3.2.1 Soil sterilization and disinfestation of pots :

Sandy loam soil (Coarse sand 1.3 %, fine sand 63 %, silt 15 % and clay 20 %) was collected from the nearby fields of the Department of Nematology, B.A.College of Agriculture, Anand Campus, Anand. It was passed through two mesh sieve and filled in an aluminium tray of 45 cm x 30 cm x 15 cm size for steam sterilization at 1.4 kg/cm² pressure for three hours. This sterilized soil was used for pot experiment after cooling. Earthen pots (11 cm diameter and 8 cm height) were washed with water and disinfested with 4 % formaldehyde (formalin 40 EC) solution. The pots were left open for 15 minutes for formalin to evaporate before being used for experiment.

3.2.2 Extraction of reniform nematode (*Rotylenchulus reniformis*) :

Soil samples collected from the rhizosphere of susceptible castor plants sown for maintaining pure culture of *Rotylenchulus reniformis* were kept on a tissue paper (21 cm x 21 cm) supported by a wire gauze of 30 mesh over a plastic dish (24 cm x 24 cm). Enough water was added to the plastic dish to moisten the soil (Petridish Assembly Method, Chawla and Prasad, 1974). After 24 hours, the nematode suspension was collected from the dish and the number of nematodes/ml of the suspension was determined by counting with the help of stereo binocular microscope. The nematodes thus obtained from pure culture were used for inoculating experimental materials.

3.2.3 Sowing of parents and inoculation of nematodes:

Disinfested pots were arranged in complete randomized design with five repetitions on R.C.C. platform in net house ($30^{\circ} \pm 2^{\circ}$). Three seeds of each entry were seeded in the centre of each pot and watered regularly. On germination (2-3 cm height), one plant in each pot nearly of equal size at 2 leaf stage was maintained and the others were removed carefully with roots without disturbing the one to be maintained. Approximately two hundred nematodes (about 1-2 ml culture suspension) were inoculated in the rhizosphere area by making a ring around collar region of

the plant. The ring was filled with soil immediately and the pots were watered regularly.

3.2.4 Observations recorded :

After 12 days of inoculation, plants in each pot were carefully removed and roots washed free of soil particles by holding under running tap water. The roots were then stained with 0.1 % boiling acid fuchsin lactophenol and washed again under tap water to remove excess stain and then kept in pure lactophenol overnight (Franklin, 1949). The stained roots were examined under the stereo binocular microscope for counting the total number of female reniform nematodes/plant.

3.3 CROSSING PROGRAMME :

For crossing programme, inbred lines were sown during kharif, 1994-95. The standard agronomic practices were followed to raise the materials under irrigated condition. Female parents were hand emasculated and bagged before opening of the flower. In the male parents, all opened flowers were clipped off prior to bagging. On emergence of stigma (next day), pollen grains collected from desired male parents were dusted over the emasculated flowers of female parents. In male parents, bagging was carried out to obtain uncontaminated pollen grains for pollination. After pollination, the plants were tagged and

labelled. VP 1 inbred line being 100 % pistillate line, selfing was done in late reverted spikes for obtaining seeds.

3.4 EXPERIMENTAL DESIGN :

The experiment was laid out in a compact family block design with three replications during kharif, 1995-96. Different crosses formed the family blocks, whereas six generations of each cross represented individual plots within family. A single replication had one row of each of the parents and F₁ generations, two rows of the back crosses and four rows of each of the F₂ generation. There were ten plants in a row.

Evaluation of nine selected crosses for reaction to reniform nematode was carried out in pots as per the procedure described in section 3.2, during January to April, 1996. However, six crosses were evaluated for yield and its components, under field conditions with inter and intra row spacings of 90 cm and 60 cm respectively. Sowing of the experiment was carried out on September 4, 1995.

Recommended agronomic practices in vogue alongwith necessary plant protection measures were timely adopted for successful raising of the crop.

The details of nine crosses studied for reaction to reniform nematode and six crosses for seed yield and its components are as follows :

(A) List of crosses studied for reaction to reniform nematode (Pot study)

Cross I : SPS 43-3 x 48-1
Cross II : 48-1 x ARUNA
Cross III : 48-1 x TMV 5
Cross IV : SPS-43-3 x SKI 49
Cross V : VP 1 x ARUNA
Cross VI : VP 1 x TMV 5
Cross VII : ARUNA x SKI 49
Cross VIII : TMV-5 x SKI 12
Cross IX : SKI 12 x SKI 49

(B) List of crosses studied for seed yield and its components (Field study)

Cross I : 48-1 x ARUNA
Cross II : 48-1 x TMV 5
Cross III : VP 1 x ARUNA
Cross IV : VP 1 x TMV 5
Cross V : ARUNA x TMV 5
Cross VI : ARUNA x SKI 12

3.5 CHARACTERS STUDIED :

3.5.1 Reaction to reniform nematode :

In six generations of each of the nine crosses, number of female reniform nematodes was counted per plant and recorded as mentioned under section 3.2.

3.5.2 Yield and its components :

Five plants each in P_1 , P_2 and F_1 , ten plants each in B_1 and B_2 and 20 plants each in F_2 populations were randomly selected and tagged for recording observations. Detailed procedure adopted for recording observations is given below :

1. Days to flowering of main raceme :

The number of days from the date of sowing to the date of flowering of the main raceme on individual plant basis were considered as days to flowering.

2. Number of nodes upto main raceme :

Total number of nodes from cotyledonary node to the base of main raceme were counted and recorded at the time of maturity.

3. Plant height :

The plant height was measured in centimeters from the base of plant to the base of primary raceme at maturity.

4. Number of total branches/plant :

Total number of branches were counted at the time of maturity.

5. Number of effective branches/plant :

The branches bearing capsules were considered as effective branches and were counted at the time of maturity.

6. Length of main raceme :

The length from originating node to the tip of the main raceme was measured in centimeters at the time of harvest.

7. Number of capsules on main raceme :

Total number of capsules on main raceme were counted at maturity.

8. Seed yield/plant :

All the effective racemes/plant were threshed together and cleaned seeds were weighed in grams.

9. 100 seed weight :

Random sample of hundred seeds was taken from the produce of each of the selected plant and weighed. The weight was recorded in grams.

10. Oil content :

The oil content was estimated by Nuclear Magnetic Resonance (NMR) instrument for one random sample (Approximately 13.012 g) from the bulk samples of selected plants in P₁, P₂ and F₁. However, eight random samples from bulked F₂ and four random samples from bulked B₁ and B₂ generations were analysed for oil content.

3.6 STATISTICAL ANALYSIS :

Mean values of the observations recorded on randomly selected representative plants (as described in the section 3.5) were calculated. The generation means for each character were subjected to standard statistical analysis to test the significance of differences among various generations studied (Panse and Sukhatme, 1969). Further, analysis of data was done as given below :

3.6.1 Estimation of gene effects from generation means :

Those crosses which showed significant differences among various generations were subjected to generation mean analysis.

3.6.1.1 Scaling test :

Scaling test as described by Hayman and Mather (1955) was used to check the adequacy of the additive

dominance model for different characters in each cross. The adequacy to scale must satisfy two conditions viz., additivity of gene effects and independence of heritable components from non-heritable ones. the test of first condition provides information regarding the absence or presence of gene interactions. A, B, C and D tests were made using the following equations for calculating their values and variances.

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

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

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

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

The variances of the estimates were computed using following formulae :

$$VA = 4 V(\bar{B}_1) + V(\bar{P}_1) + V(\bar{F}_1)$$

$$VB = 4 V(\bar{B}_2) + V(\bar{P}_2) + V(\bar{F}_1)$$

$$VC = 16V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)$$

$$VD = 4 V(\bar{F}_2) + V(\bar{B}_1) + V(\bar{B}_2)$$

The standard error of each test was calculated as square root of variance as under :

$$S.E. (A) = (VA)^{\frac{1}{2}}$$

$$S.E. (B) = (VB)^{\frac{1}{2}}$$

$$S.E. (C) = (VC)^{\frac{1}{2}}$$

$$S.E. (D) = (VD)^{\frac{1}{2}}$$

Significance of scaling test was tested by calculating the 't' test value as below :

$$t(A) = A/S.E.(A)$$

$$t(B) = B/S.E.(B)$$

$$t(C) = C/S.E.(C)$$

$$t(D) = D/S.E.(D)$$

The calculated values of 't' were compared with tabulated values of 't' at 5 % (1.960) and 1 % (2.576) levels of significance. The significance of any one of these scales is taken to indicate the presence of non-allelic interaction.

- (i) D provides a test largely of 'i' (additive x additive) type of interaction.
- (ii) C indicates 'l' (dominance x dominance) type of gene interaction.
- (iii) Significance of C + D relates 'i' (additive x additive) and 'l' (dominance x dominance) type of interaction
- (iv) 'j' (additive x dominance) type of interaction has no effect on C and D but it affects A and B. The test A and B provide evidence on i, j and l type of gene interactions.

3.6.1.2 The estimation of various gene effects :

(a) In presence of non-allelic interactions :

Various gene effects were estimated using six parameter model suggested by Hayman (1958) as under :

Gene effect	Symbol	Method of estimation
Mean	m	$\bar{F}_2$
Additive	d	$\bar{B}_1 - \bar{B}_2$
Dominance	h	$\bar{F}_1 - 4\bar{F}_2 - \frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2 + 2\bar{B}_1 + 2\bar{B}_2$
Additive x Additive	i	$2\bar{B}_1 + 2\bar{B}_2 - 4\bar{F}_2$
Additive x Dominance	j	$2\bar{B}_1 - \bar{P}_1 - 2\bar{B}_2 + \bar{P}_2$
Dominance x Dominance	l	$\bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\bar{B}_1 - 4\bar{B}_2$

Where,

$\bar{P}_1$, $\bar{P}_2$, $\bar{F}_1$, $\bar{F}_2$, $\bar{B}_1$ and $\bar{B}_2$ are the mean values of P_1 , P_2 , F_1 , F_2 , B_1 and B_2 generations, respectively.

The variance of these estimates was obtained using the following formulae :

$$\begin{aligned}
 V_m &= V\bar{F}_2 \\
 V_d &= V(\bar{B}_1) + V(\bar{B}_2) \\
 V_h &= V(\bar{F}_1) + 16V(\bar{F}_2) + \frac{1}{4}V(\bar{P}_1) + \frac{1}{4}V(\bar{P}_2) + 4V(\bar{B}_1) + 4V(\bar{B}_2) \\
 V_i &= 4V(\bar{B}_1) + 4V(\bar{B}_2) + 16V(\bar{F}_2) \\
 V_j &= 4V(\bar{B}_1) + V(\bar{P}_1) + 4V(\bar{B}_2) + V(\bar{P}_2) \\
 V_l &= V(\bar{P}_1) + V(\bar{P}_2) + 4V(\bar{F}_1) + 16V(\bar{F}_2) + 16V(\bar{B}_1) + 16V(\bar{B}_2)
 \end{aligned}$$

Where,

$V(\bar{P}_1)$, $V(\bar{P}_2)$, $V(\bar{F}_1)$, $V(\bar{F}_2)$, $V(\bar{B}_1)$ and $V(\bar{B}_2)$ are the variances of means of P_1 , P_2 , F_1 , F_2 , B_1 and B_2 generations, respectively.

The standard error of each of the gene effect was as follows :

$$S.E. (m) = V(m)^{\frac{1}{2}}$$

$$S.E. (d) = V(d)^{\frac{1}{2}}$$

$$S.E. (h) = V(h)^{\frac{1}{2}}$$

$$S.E. (i) = V(i)^{\frac{1}{2}}$$

$$S.E. (j) = V(j)^{\frac{1}{2}}$$

$$S.E. (l) = V(l)^{\frac{1}{2}}$$

The 't' values were worked out using following formulae :

$$t(m) = m/S.E.(m)$$

$$t(d) = d/S.E.(d)$$

$$t(h) = h/S.E.(h)$$

$$t(i) = i/S.E.(i)$$

$$t(j) = j/S.E.(j)$$

$$t(l) = l/S.E.(l)$$

The test of significance of gene effects was carried out by comparing the calculated values of 't' with the tabulated values of 't' at 5 % (1.960) and 1 % (2.576) levels of significance.

(b) In absence of non-allelic interaction :

In the absence of non-allelic interactions as indicated by non-significance of scaling test, following three parameter model as suggested by Jinks and Jones (1958) was used for estimation of genetic components as mentioned below :

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

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

$$h = 6\bar{B}_1 + 6\bar{B}_2 - 8\bar{F}_2 - \bar{F}_1 - 3/2\bar{P}_1 - 3/2\bar{P}_2$$

The variances of the estimates were computed using following formulae :

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

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

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

The standard errors of the estimates were calculated using following formulae :

$$S.E.(m) = V(m)^{\frac{1}{2}}$$

$$S.E.(d) = V(d)^{\frac{1}{2}}$$

$$S.E.(h) = V(h)^{\frac{1}{2}}$$

The 't' values of different components were worked out using following formulae :

$$t(m) = m/S.E.(m)$$

$$t(d) = d/S.E.(d)$$

$$t(h) = h/S.E.(h)$$

The test of significance of the gene effects was performed by comparing the calculated values with tabulated value of 't' at 5 % (1.960) and 1 % (2.576) levels of significance.

3.6.2 Estimation of heterosis :

Heterosis, expressed as per cent increase or decrease of F₁ over its mid-parent (heterosis) as well as better or superior parent (heterobeltiosis) was computed as follows :

$$\begin{array}{lcl} \text{Relative heterosis (H}_1\%) & & \overline{F_1} - \overline{MP} \\ \text{(Briggle, 1963)} & = & \frac{\text{-----}}{\overline{MP}} \times 100 \end{array}$$

$$\begin{array}{lcl} \text{Heterobeltiosis (H}_2\%) & & \overline{F_1} - \overline{BP} \\ \text{(Hayes et al., 1955)} & = & \frac{\text{-----}}{\overline{BP}} \times 100 \end{array}$$

Where,

$\overline{F_1}$ = Mean performance of the hybrid

$\overline{F_2}$ = Mean performance of the parents ($\overline{P_1}$ and $\overline{P_2}$) of a hybrid

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

The standard error and calculated 't' value for test of significance for heterosis and heterobeltiosis were calculated as under :

Standard Error :

$$\begin{array}{l} \text{S.E. } (\overline{F_1} - \overline{MP}) \\ \text{(Standard error for } = \sqrt{3Me/2r} \\ \text{relative heterosis)} \end{array}$$

S.E. ($\bar{F}_1 - \bar{BP}$)
 (Standard error for heterobeltiosis) = $\sqrt{2Me/r}$

Where,

Me = Error mean square

r = Number of replications

't' test :

$$t(H_1) = \frac{\bar{F}_1 - \bar{MP}}{S.E.(F_1 - MP)} \quad \dots \quad \text{for heterosis}$$

$$t(H_2) = \frac{\bar{F}_1 - \bar{BP}}{S.E.(F_1 - BP)} \quad \dots \quad \text{for heterobeltiosis}$$

The test of significance of the relative heterosis and heterobeltiosis was carried out by comparing the calculated value of 't' with the tabulated value 't' at 5 % (1.960) and 1 % (2.576) levels of significance.

3.6.3 Estimation of inbreeding depression :

Inbreeding depression was computed by using the following formulae :

$$\text{Inbreeding depression (\%)} = \frac{\bar{F}_1 - \bar{F}_2}{F_1} \times 100$$

$$\begin{aligned} &\text{S.E. } (\bar{F}_1 - \bar{F}_2) \\ &(\text{Standard error for inbreeding depression}) = \sqrt{2Me/r} \end{aligned}$$

$$t(\bar{F}_1 - \bar{F}_2) \text{ ('t' test for inbreeding depression)} = \frac{\bar{F}_1 - \bar{F}_2}{S.E.(F_1 - F_2)}$$

Where,

$\bar{F}_1$ = Mean performance of the F_1

$\bar{F}_2$ = Mean of the F_2

Me = Error mean square

r = Number of replications

The test of significance of the inbreeding depression was performed by comparing the calculated value with the tabulated value of 't' at 5 % (1.960) and 1 % (2.576) levels of significance.

3.6.4 Estimation of heritability :

3.6.4.1 Heritability in broad sense :

The broad sense heritability was calculated by using the formula suggested by Allard (1960) as follows :

$$h^2(b) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

$h^2(b)$ = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

3.6.4.2 Heritability in narrow sense :

Heritability in narrow sense was calculated by using the formula suggested by Allard (1960) as follows :

$$h^2(n)(\%) = \frac{\sigma^2_A}{\sigma^2_p} \times 100$$

Where,

$h^2(n)$ = Heritability in narrow sense

σ^2_A = Additive genetic variance (d)

σ^2_p = Phenotypic variance

3.6.5 Estimation of expected genetic advance under selection :

The expected genetic advance at 5 % selection intensity was estimated by using following formula suggested by Allard (1960).

$$G.A. = K.h^2(n).\sigma_p$$

Where,

$h^2(n)$ = Heritability in narrow sense

σ_p = Phenotypic standard deviation

K = Selection differential (K=2.06 at 5 % selection pressure)

$$G.A. \text{ as percentage of mean} = \frac{G.A.}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = Population mean

RESULTS AND DISCUSSION

CHAPTER IV

RESULTS AND DISCUSSION

The results obtained in the present investigation have been presented and discussed under the following sub heads :

4.1 Gene action

4.2 Heterosis and inbreeding depression

4.3 Heritability and genetic advance

4.1 GENE ACTION :

4.1.1 Resistance to reniform nematode :

Among the nine crosses studied, seven crosses (I,II,III,IV,VI,VII and VIII) showed significant differences among their respective generations (Appendix II).

(a) Mean performance :

The parents of Cross I were at par (Table 4.1) but the F_1 mean was significantly lower than the parental means suggesting the involvement of non-additive gene action in the expression of this trait. Significant difference between F_1 and F_2 generation means revealed the involvement of non-additive gene action. The mean value of B_1 and P_1 generations were significantly different, while the B_2 mean was at par with the recurrent parent P_2 indicating the influence of non-additive gene action on this trait.

Table 4.1 : Mean values of number of reniform female nematodes/plant
for six generations in nine crosses of castor

Crosses	Generations						S.Em.	C.D. (0.05)	C.V. %
	P ₁	P ₂	F ₁	F ₂	B ₁	B ₂			
I	5.93	6.02	3.50	10.97	4.78	6.01	0.13	0.39	3.50
II	5.87	12.53	8.73	11.38	8.30	8.95	0.62	1.98	11.70
III	8.97	18.43	11.60	12.75	9.80	10.98	1.14	3.60	16.38
IV	9.10	27.73	17.20	16.63	12.32	16.52	0.53	1.65	4.99
V	14.27	12.90	12.83	13.94	14.83	14.97	0.58	NS	7.25
VI	13.57	19.53	16.80	17.33	16.22	18.77	0.78	2.45	7.91
VII	15.27	22.63	18.97	22.90	18.27	20.64	1.06	3.34	9.27
VIII	21.97	23.73	22.27	23.10	21.77	24.22	0.41	1.29	3.10
IX	20.73	21.93	20.57	22.13	21.70	22.30	0.69	NS	5.52

Table 4.2 : Estimates of scaling tests and gene effects for number of reniform female nematodes/plant

Crosses	Gene effects														
	Scaling tests					Six parameter model					Three parameter model				
	A	B	C	D	m	d	h	i	j	l	m	d	h		
I	0.12	2.51**	24.92**	11.14**	10.97**	-1.24**	-24.76**	-22.29**	-2.39**	19.66**	-	-	-		
II	2.00	-3.37**	9.64**	5.50**	11.38**	-0.65	-11.47**	-11.01**	5.37**	12.37**	-	-	-		
III	-0.97	-8.07**	0.41	4.72	12.75**	-1.18	-11.55	-9.45	7.10**	18.48*	-	-	-		
IV	-1.67	-11.90**	-4.73	4.42**	16.63**	-4.20**	-10.06**	-8.84**	10.23**	22.41**	-	-	-		
VI	2.07	1.20	2.61	-0.33	-	-	-	-	-	-	15.89**	-2.98**	4.84		
VII	2.30	-0.31	15.77**	6.89**	22.90**	-2.38**	-13.76**	-13.77**	2.61	11.78**	-	-	-		
VIII	-0.70	2.43*	2.18	0.22	23.10**	-2.45**	-1.03	-0.45	-3.13*	-1.29	-	-	-		

* and ** indicate significance at 5 and 1 % levels of significance, respectively.

However, the B₁ mean was inbetween the F₁ and recurrent parent (P₁) and also differed significantly from each of them indicating additive genetic control for this trait.

Cross II, revealed significant difference between the mean of the parents (P₁ and P₂) for this trait and the F₁ mean value while being in between the parental values also differed significantly from either of its parents suggesting that additive gene action was involved in the expression of this trait. However, significant difference between F₁ and F₂ generation means indicated the involvement of non-additive gene action. The mean values of both backcross progenies, B₁ and B₂ were at par with the mean values of the F₁ generation while both differed significantly from mean of their respective recurrent parent.

The difference between the mean of the parents of Cross III was significant for this trait. The mean of F₁ generation was intermediate to the mean of the parents but was at par with P₁ mean suggesting the involvement of non-additive gene action in the inheritance of this trait. However, parity of the mean values of F₁ and F₂ generations indicated the involvement of additive gene action in the expression of this trait. The mean values of B₁ and B₂ generations were at par with each other as well as with the mean values of their F₁ and F₂ generations which also indicated additivity of the genes.

Parents of Cross IV, differed significantly between themselves for this trait. The mean of F₁ generation was intermediate to the mean of the parents and differed significantly from them. The means of F₁ and F₂ were at par. The mean values of B₁ and B₂ generations differed significantly among themselves and were inbetween the F₁ mean and corresponding recurrent parent. These all suggested the influence of additive gene action for the expression of this trait.

The difference between mean values of the parents of Cross VI was significant. The F₁ mean was intermediate to the parental means and differed significantly from them. The means of F₁ and F₂ generations were at par. The mean value of B₁ was inbetween the means of P₁ and F₁ but was at par with the F₁ mean. However, B₂ mean was at par with its recurrent parent P₂. These findings suggested the involvement of both additive and non-additive gene actions in the expression of this trait.

Cross VII revealed significant difference between the parents for this trait and the F₁ mean value while being inbetween the parental values also differed significantly from either parents suggesting the involvement of additive gene action in the expression of this trait. The mean of the F₂ generation differed significantly from the mean of the F₁, indicating that non-additive gene action governed the

expression of this trait. The mean values of B₁ and B₂ generations were at par with each other and also with their respective recurrent parent.

The parents of Cross VIII differed significantly. The mean of the F₁ was inbetween the mean values of the parents, while was at par with the better parent P₁, suggesting the involvement of non-additive gene action. The parity of the mean values of F₁ and F₂ generations suggested that the additive genes were involved in the expression of this trait. The mean values of B₁ and B₂ generations were significantly different from each other, while were at par with their respective recurrent parental means.

(b) Gene effects :

The estimates of scaling tests (Table 4.2) were significant for Crosses I, II, III, IV, VII and VIII indicating the presence of non-allelic interaction for this trait. However, Cross VI showed non-significant scaling test suggesting involvement of only intra-allelic interaction for the expression of resistance to reniform nematode.

The partitioning of genetic components of variance summarised in Table 4.2 revealed that in Cross I, all the gene effects were found significant for the expression of this trait, where dominance, additive x additive and dominance x dominance gene effects were of higher magnitude

in that order. Barring additive, all other gene effects were found significant in Cross II. Where, dominance x dominance, dominance and additive x additive gene effects were greater in magnitude followed by additive x dominance in that order. In Cross III, additive x dominance and dominance x dominance components were significant, the latter being higher in magnitude. All the gene effects viz., additive, dominance and epistatic were highly significant in Cross IV, where the magnitude of dominance x dominance was highest, next in order being additive x dominance, dominance and additive x additive. Thus, predominance of non-additive gene action was observed in which dominance and dominance x dominance components were in opposite direction, indicating the presence of duplicate type of epistasis. In Cross VI, only additive gene effect was found significant. In case of Cross VII, additive, dominance and epistatic (additive x additive and dominance x dominance) gene effects were observed to be highly significant. The opposite signs of dominance and dominance x dominance indicated that the interactions were on balance and mainly of duplicate epistasis in nature. In Cross VIII all the estimates barring additive and additive x dominance were found non-significant. Significant additive effect in negative direction was noted in Crosses I, IV, VI, VII and VIII.

Plant parasitic nematodes are real threat to successful and profitable cultivation of castor crop. The

involvement of additive gene effect in the expression of resistance to reniform nematode in Cross I, IV, VI, VII and VIII in desirable negative direction suggested that the isolation of homozygous recombinants having desirable level of resistance to reniform nematode from the segregating population of these crosses would be feasible and thus selection would be an appropriate breeding method for the improvement of this trait. Duplicate epistasis coupled with significant negative (additive x additive) effects, revealed by Cross I, II, IV and VII indicated the possibility of obtaining genotypes with higher level of resistance to reniform nematode in advance segregating generations.

4.1.2 Yield and its components :

4.1.2.1 Days to flowering of main raceme :

Among the six crosses studied only I, III, V and VI had significant variation among their entries for this trait (Appendix III).

(a) Mean performance :

In Cross I, parents (P₁ and P₂) differed significantly but F₁ was at par with the early flowering parent P₁, indicating that the expression of days to flowering in this population was influenced by non-additive gene action (Table 4.3). The parity of the mean values of the F₁ and F₂ generations suggested the involvement of

Table 4.3 : Mean values of days to flowering of main raceme, number of nodes upto main raceme, plant height (cm), number of total branches/plant and number of effective branches/plant for six generations in six crosses of castor

Crosses	Generations						S.Em.	C.D. (0.05)	C.V. %
	P ₁	P ₂	F ₁	F ₂	B ₁	B ₂			
Days to flowering of main raceme									
I	74.69	87.89	73.96	77.10	72.50	71.84	2.23	7.01	5.05
II	71.28	64.55	63.44	66.68	71.75	62.95	2.67	NS	6.92
III	63.67	81.04	62.17	63.57	60.78	68.78	2.24	7.05	5.81
IV	63.78	66.75	61.99	64.39	61.48	62.62	2.99	NS	8.17
V	80.68	63.82	66.91	65.20	70.36	65.30	3.18	10.01	8.01
VI	86.50	65.59	70.70	71.00	74.22	68.09	2.61	8.21	6.21
Number of nodes upto main raceme									
I	21.47	23.74	21.45	20.74	19.56	19.13	0.52	1.64	4.28
II	20.94	17.06	17.50	18.15	19.71	15.25	0.68	2.16	6.42
III	17.07	23.91	15.74	16.51	15.10	18.59	0.41	1.29	3.83
IV	15.94	16.00	15.02	15.94	15.86	15.28	0.78	NS	8.60
V	22.94	19.09	18.20	17.92	18.65	16.95	0.67	2.12	6.31
VI	22.95	16.48	20.90	19.87	19.85	18.55	0.60	1.90	5.28
Plant height (cm)									
I	141.33	154.00	129.65	118.99	100.86	106.43	8.47	26.68	11.71
II	147.38	97.73	103.51	114.76	149.94	85.09	4.84	15.26	7.22
III	26.63	150.04	83.07	62.20	39.84	95.88	1.60	5.06	3.64
IV	29.56	83.14	63.97	63.55	48.18	68.94	1.71	5.37	4.96
V	168.24	85.46	106.52	102.59	109.33	100.23	6.25	19.70	9.66
VI	167.54	75.61	119.83	117.57	133.45	103.56	5.55	17.50	8.04
Number of total branches/plant									
I	19.48	19.50	19.75	17.33	19.45	17.12	1.18	NS	11.26
II	16.24	16.47	19.84	19.01	16.70	15.14	1.06	NS	10.81
III	12.17	19.30	25.37	21.18	14.50	22.93	1.68	5.27	15.06
IV	12.72	16.00	14.45	14.85	12.07	18.43	0.89	2.81	10.48
V	16.06	17.24	21.35	18.37	17.71	18.49	1.82	NS	17.36
VI	14.88	12.30	22.42	15.45	17.85	16.07	1.56	4.90	16.12
Number of effective branches/plant									
I	12.70	12.09	13.03	13.21	15.78	13.11	1.42	NS	10.05
II	12.69	14.20	16.11	15.67	13.43	12.59	0.81	2.54	9.89
III	10.36	14.13	23.48	19.03	12.17	19.73	1.66	5.25	17.49
IV	11.34	13.89	12.87	11.32	10.12	13.88	0.90	NS	12.72
V	10.64	14.99	16.39	14.93	13.57	13.32	1.39	NS	17.21
VI	9.78	10.20	18.01	11.65	13.50	13.06	1.32	4.15	17.95

Table 4.4 : Estimates of scaling tests and gene effects for days to flowering of main raceme, number of nodes upto main raceme, plant height (cm), number of total branches/plant and number of effective branches/plant

Crosses	Gene effects													
	Scaling tests				Six parameter model						Three parameter model			
	A	B	C	D	m	d	h	i	j	l	m	d	h	
Days to flowering of main raceme														
I	-3.64	-18.18**	-2.09	9.87	77.10**	0.67	-27.06*	-19.73	14.53	41.55*	-	-	-	-
III	-4.28	-5.68	-14.75	-2.40	-	-	-	-	-	-	67.56**	-8.69**	-10.56	-
V	-6.87	-0.12	-17.52	-5.27	-	-	-	-	-	-	61.72**	8.43**	8.74	-
VI	-8.76	-0.11	-9.50	-0.32	-	-	-	-	-	-	75.41**	10.45**	-12.94	-
Number of nodes upto main raceme														
I	-3.79**	-6.93**	-5.16**	2.78**	20.74**	0.43	-6.72**	-5.57**	3.14	16.29**	-	-	-	-
II	0.99	-4.05**	-0.38	1.34	18.15**	4.46**	-4.19	-2.68	5.04**	5.74	-	-	-	-
III	-2.60*	-2.48*	-6.42**	-0.67	16.51**	-3.48**	-3.41	1.34	-0.12	3.74	-	-	-	-
V	-3.85*	-0.39	-3.76	0.24	17.92**	1.70*	-1.79	-0.47	-3.46	4.71	-	-	-	-
VI	-4.15**	-0.29	-1.77	1.33*	19.87**	1.30**	-1.48	-2.67*	-3.86**	7.10*	-	-	-	-
Plant height (cm)														
I	-69.27**	-70.80**	-78.67**	30.70	118.99**	-5.57	-79.42*	-61.41	1.53	201.48**	-	-	-	-
II	48.98**	-31.07*	6.89	-5.51	114.76**	64.85**	-8.02	11.02	80.05**	-28.93	-	-	-	-
III	-30.01**	-41.35**	-94.03**	-11.33	62.20**	-56.04**	17.41	22.67	11.34	48.70*	-	-	-	-
IV	2.83	-9.24	13.56	9.98*	63.55**	-20.76**	-12.34	-19.97*	12.07*	26.38	-	-	-	-
V	-56.11**	8.48	-56.39*	-4.38	102.59**	9.10	-11.58	-8.76	-64.58**	38.87	-	-	-	-
VI	-20.80	11.69	-12.54	-1.71	-	-	-	-	-	-	118.16**	45.96**	-4.04	-
Number of total branches/plant														
III	-8.54**	1.20	2.53	4.94	21.18**	8.44**	-0.24	-9.87	-4.87**	17.22	-	-	-	-
IV	-3.04	6.41	1.77	-0.80	-	-	-	-	-	-	12.77*	-1.64*	6.65	-
VI	-1.61	-2.59	-10.23	-3.01	-	-	-	-	-	-	7.57*	1.29*	16.68	-
Number of effective branches/plant														
II	-1.93	-5.12*	3.56	5.31	15.67**	0.84	-7.95	-10.61	3.18	17.66	-	-	-	-
III	-9.51**	1.85	4.68	6.17	19.03**	-7.56**	-0.10	-12.34	-5.68**	20.00	-	-	-	-
VI	-0.78	-2.09	-9.40	-3.26	-	-	-	-	-	-	3.46*	-0.21	18.20	-

* and ** indicate significance at 5 and 1 % levels of significance, respectively.

additive gene action in the expression of this trait. The mean value of B₁ was at par with the means of P₁ and F₁. Whereas, B₂ mean was significantly different from the mean value of P₂ but it was at par with the F₁ mean.

Significant difference was observed between the two parents of Cross III but F₁ mean was at par with the early flowering parent P₁, indicating that the expression of days to flowering in this population was influenced by non-additive gene action (Table 4.3). However, non-significant difference between the mean values of F₁ and F₂ generations indicated the presence of additive gene action. The mean values of B₁ and B₂ generations differed significantly. B₁ mean was at par with its parents P₁ and F₁ while mean value of B₂ was inbetween the mean values of F₁ and its recurrent parent.

Cross V revealed significant differences between the mean of the parents (P₁ and P₂). The F₁ mean differed significantly from the mean of parent P₁ but was at par with the mean values of P₂ and F₂ generations indicating the presence of additive gene action for the expression of this trait. The B₁ generation mean being inbetween the mean values of the P₁ and F₁ also indicated that additive gene action did influence this trait. However, the mean of B₂ generation was at par with the mean of B₁ as well as with that of the F₁ and recurrent parent, P₂.

Significant variation was observed between the parents of Cross VI. The F₁ mean was intermediate to parents but was at par with early flowering parent P₂ as well as F₂ generations. The mean value of B₁ generation was inbetween the mean values of F₁ and P₁ but differed significantly from its recurrent parent. The mean of B₂ generation was inbetween the F₁ and P₂ means but was at par with both the parents. These results indicated the influence of additive gene action in the expression of this trait.

(b) Gene effects :

Significant scaling tests revealed the presence of non-allelic interaction in the inheritance of days to flowering in Cross I. Whereas, non-significant scaling tests for Cross III, V and VI indicated the presence of only intra-allelic interactions for the expression of this trait (Table 4.4).

The estimates of gene effects for days to flowering of main raceme in Cross I (Table 4.4) indicated that dominance and heterozygote interaction (dominance x dominance) were involved in the expression of this trait. The opposite signs of dominance and dominance x dominance gene effects revealed that the interactions were balanced and mainly of duplicate epistatic in nature. Highly significant additive gene effect observed for Cross III in

negative direction indicated early flowering whereas its positive direction for Cross V and VI suggested late flowering.

The present findings are akin to the results obtained by Patel *et al.* (1984), Fatteh *et al.* (1988), Pathak *et al.* (1989) and Mehta *et al.* (1991). Predominance of non-additive gene effects have been reported by Singh and Srivastava (1982), Bhatt and Reddy (1986) and Pathak *et al.* (1988) for the expression of days to flowering. Whereas involvement of both additive as well as non-additive gene effects for the expression of days to flowering have been observed by Hooks *et al.* (1971), Singh and Yadava (1981), Bhatt and Reddy (1983) and Patel (1992).

The results of the present study revealed that days to flowering of main raceme is controlled by non-additive gene effects in Cross I, (suggesting the possibility of recovering early flowering recombinants) in segregating populations of this cross. The sole involvement of additive gene effect in the expression of this trait in Crosses III, V and VI suggested that the isolation of homozygous recombinants with desired days to flowering from the segregating populations of these crosses would be feasible and thus straight selection would be an appropriate breeding method for improvement of this trait.

4.1.2.2 Number of nodes upto main raceme :

Among the six crosses studied all crosses except Cross IV showed significant variation among their respective generations (Appendix III).

(a) Mean performance :

The parents of Cross I differed significantly (Table 4.3) but the F₁ mean was at par with better parent, P₁ indicating that the expression of number of nodes upto main raceme in this population was influenced by non-additive gene action. However, parity of the mean values of F₁ and F₂ generations suggested the involvement of additive gene action in the expression of this trait. The means of B₁ and B₂ generations differed significantly from their respective recurrent parent but were at par with each other.

In Cross II, parents (P₁ and P₂) differed significantly for this trait. The F₁ mean was at par with the parent, P₂ having lower number of nodes, indicating that the expression of this trait was governed by non-additive gene action. The parity of the mean values of F₁ and F₂ generations suggested that additive genes governed this trait. The mean values of B₁ and B₂ generations differed significantly among themselves but were at par with the means of their respective recurrent parent suggesting the involvement of non-additive gene action in the expression of this trait.

Significant difference was observed between the two parents of Cross III. The mean node numbers of F₁ plants were significantly lower than the mean values of both the parents, suggesting the involvement of non-additive gene action for the expression of this trait. However, the parity observed between the mean values of F₁ and F₂ generations indicated the influence of additive gene action in the inheritance of this trait. The mean values of B₁ and B₂ differed significantly from each other as well as with their respective recurrent parent.

The parents of Cross V differed significantly. The mean of F₁ differed significantly from P₁ mean but it was at par with the mean value of P₂ and F₂ generations indicating the presence of additive gene action for the expression of this trait. The B₁ generation mean being inbetween the mean values of the P₁ and F₁ also indicated that additive gene action did influence this trait. However, the mean value of B₂ generation was at par with B₁ mean as well as with its parent P₂ and F₁.

Cross VI exhibited significant differences between the mean of the parents (P₁ and P₂) for this trait and the F₁ mean value while being inbetween the parental values also differed significantly from either of its parents suggesting that additive gene action was involved in the expression of this trait. The non-significant differences between F₁ and

F₂ generations further revealed the involvement of additive gene action in the expression of this trait. The mean of B₁ and B₂ generations were at par with each other, while differed significantly from their respective recurrent parent.

(b) Gene effects :

The estimates of scaling test (Table 4.4) revealed that non-allelic interactions were present in Cross I, II, III, V and VI whereas it was absent in Cross IV (Table 4.4).

The partitioning of genetic components of variation for number of nodes upto main raceme (Table 4.4) indicated that in Cross I, all gene effects barring additive and additive x dominance, were found highly significant wherein dominance x dominance gene effect was greater in magnitude, next in order being dominance and additive x additive gene effects. The opposite signs of dominance and dominance x dominance effects indicated the presence of duplicate epistasis in the inheritance of this trait. Cross II revealed the importance of additive and additive x dominance gene effects for the inheritance of this trait. Additive gene effect was solely involved in the expression of this trait in Cross III and V. All gene effects except dominance were found significant in Cross VI.

Predominance of additive gene action for the expression of number of nodes upto main raceme has been

reported by several workers. Varisai and Stephen (1967), Patel *et al.* (1984), Swarnlata *et al.* (1984), Narkhede *et al.* (1985), Patel *et al.* (1986), Pathak and Dangaria (1987), Fattah *et al.* (1988), Mehta *et al.* (1991) and Vindhiyavarman and Ganesan (1995). However, Narkhede *et al.* (1987) and Pathak *et al.* (1989) reported predominance of non-additive gene effects in the inheritance of number of nodes upto main raceme. While, Hooks *et al.* (1971) reported the role of additive alongwith non-additive gene effects for this trait. Present findings with respect to different crosses are in good agreement with these reports.

The involvement of additive gene effect in the expression of number of nodes upto main raceme in Cross III and V suggested that the isolation of homozygous recombinants with reduced nodes upto main raceme from the segregating population of these crosses would be feasible and thus selection would be an appropriate breeding method for improvement of this trait. However, in Cross II and VI additive as well as non-additive gene effects while in Cross I only non-additive gene effects controlled this trait. The type of gene action responsible for the inheritance of this trait revealed that homozygous recombinants alongwith desired number of nodes could be developed by following reciprocal recurrent selection or *inter se* crossing of desired segregants keeping adequate population size.

4.1.2.3 Plant height :

The data revealed significant differences for the trait in all six crosses (Appendix III).

(a) Mean performance :

There were no significant differences among the mean plant height of both parents (P_1 and P_2) and F_1 generations in Cross I (Table 4.3). The non-significant difference between F_1 and F_2 generations revealed involvement of additive gene action in the expression of this trait. The mean values of B_1 and B_2 generations were at par with each other, while significantly lower than the means of their respective recurrent parents P_1 and P_2 .

In Cross II, parents (P_1 and P_2) differed significantly (Table 4.3) whereas, the F_1 mean was at par with P_2 indicating that the expression of plant height in this population was influenced by non-additive gene action. However, the parity of mean values of F_1 and F_2 generations, suggested the involvement of additive gene action in the expression of this trait. The mean values of B_1 and B_2 generations differed among themselves while were at par with their respective recurrent parents P_1 and P_2 suggesting the involvement of non-additive gene action in the expression of this trait.

Cross III revealed significant difference between the mean of the parents (P_1 and P_2) for this trait and the F_1 mean value while being inbetween the parental values also differed significantly from either parents suggesting that additive gene action was involved in the expression of this trait. The mean of F_2 generation was significantly lower than the mean of the F_1 indicating that non-additive gene action governed the expression of this trait. The mean values of B_1 and B_2 generations differed significantly with each other as well as with their parents, their means being intermediate to the F_1 and the respective recurrent parent.

The parents of Cross IV differed significantly for plant height among themselves as well as from F_1 generation (Table 4.3). The F_1 mean was inbetween the parental values suggesting the importance of additive gene action in the expression of this trait. The F_2 mean was at par with the F_1 mean further the influence of suggested additive gene effect on the inheritance of this trait in this population. The B_1 and B_2 means differed significantly from each other. The B_1 mean was inbetween the P_1 and F_1 mean values and differed significantly from them as well as from B_2 . These findings revealed the involvement of both additive and non-additive gene effects for the expression of this trait in this population.

The parents of Cross V differed significantly between themselves (Table 4.3). The F_1 mean value while being inbetween the parental values also differed significantly from either of its parents. The F_1 mean was at par with the mean of F_2 generation while B_1 mean was at par with the mean of B_2 generation. The mean value of B_1 and P_1 generations were significantly different, while the B_2 mean was at par with the recurrent parent, P_2 . These results indicated involvement of both additive as well as non-additive gene actions in the expression of plant height.

Significant difference was observed between the parents of Cross VI. The F_1 mean differed significantly from the mean values of both the parents and was intermediate to the parental means, suggesting the involvement of additive gene action in the expression of this trait. The parity of the mean values of F_1 and F_2 generations also emphasized the influence of additive gene effect on this trait. The means of B_1 and B_2 generations differed significantly from each other and also with their respective recurrent parent. The B_1 and B_2 means were inbetween the means of the F_1 and their respective recurrent parent, however they were at par with the F_1 mean suggesting additivity of the genes for this trait.

(b) Gene effects :

The estimates of scaling tests (Table 4.4) showed the presence of non-allelic interactions in the inheritance of plant height in all the crosses except Cross VI.

The partitioning of genetic variance (Table 4.4) revealed that dominance and dominance x dominance gene effects were involved in the expression of this trait in Cross I. However, opposite signs of these gene effects indicated the balance for these interactions and were mainly of duplicate epistasis in nature. Additive and additive x dominance were found to be significant in Cross II, where additive x dominance gene effect was greater in magnitude followed by additive gene effect. In Cross III, additive as well as heterozygote interaction (dominance x dominance) governed the expression of this trait, additive gene effect being higher in magnitude and was followed by dominance x dominance gene effects. Barring dominance and dominance x dominance, all other type of gene effects were found significant in Cross IV for the expression of plant height, where additive and additive x additive gene effects were of higher magnitude followed by additive x dominance. In Cross V, only epistatic (additive x dominance) gene effect was found significant. However, additive effect was solely involved in the inheritance of this trait in Cross VI.

Swarnlata *et al.* (1984), Narkhede *et al.* (1987), Pathak and Dangaria (1987), Fatteh *et al.* (1988), Mehta *et al.* (1991) and Patel *et al.* (1991) have reported the predominance of additive gene effect for plant height, while Patel *et al.* (1984), Patel *et al.* (1985) and Pathak *et al.* (1989) have shown the influence of non-additive gene effects in the expression of this trait. However, additive effect alongwith non-additive effects were reported by Singh and Yadav (1982), Narkhede *et al.* (1985), Pathak *et al.* (1988) and Patel (1992).

Involvement of additive effect in Cross VI advocated the use of pedigree method of selection in segregating population for the improvement of this trait. Both additive and non-additive gene effects observed for plant height in Cross II, III and IV, suggested biparental mating approach or reciprocal recurrent selection method as most appropriate breeding method in utilizing both the type of gene effects. As the main additive effect was in desirable negative direction in Cross III and IV, favourable response may be observed by selection of desirable segregants and their *inter se* crossing keeping adequate population size.

4.1.2.4 Number of total branches/plant :

Among the six crosses studied, only Crosses III, IV and VI showed significant variation for this trait (Appendix III).

(a) Mean performance :

The parents of Cross III differed significantly (Table 4.3). The F₁ mean exceeded the mean values of both the parents indicating the presence of overdominance. The F₂ mean was at par with the F₁ mean, suggesting the involvement of additive gene effect in the inheritance of this trait in this population. However, the means of B₁ and B₂ generations were significantly different from each other but were at par with their respective recurrent parents indicating influence of non-additive gene effects in the expression of this trait.

In Cross IV, parents differed significantly from each other (Table 4.3). The mean of F₁ was inbetween the parental means and was at par with either of them, suggesting the presence of additive component for this trait. The F₂ mean at par with the F₁ mean further revealed the role of additive gene action in the expression of this trait. The mean values of B₁ and B₂ differed significantly with each other while were at par with their respective recurrent parent suggesting the importance of non-additive gene effects for the expression of this trait.

The mean values of parents were at par for total number of branches/plant in Cross VI (Table 4.3). The F₁ mean was significantly higher than the parental mean values as well as from the F₂ mean, indicating that non-additive

gene effect did influence the expression of this trait in this population. The parity of the mean values of B₁ and B₂ generations with each other as well as with their respective recurrent parents indicated that non-additive gene effect did control this trait.

(b) Gene effects :

The estimates of scaling test (Table 4.4) were significant in Cross III suggesting the presence of non-allelic interactions in this cross, while non-significant scaling tests in Cross IV and VI indicated the absence of non-allelic interactions in these crosses.

The partitioning of genetic components of variance (Table 4.4) indicated that additive and epistatic (additive x dominance) gene effects in Cross III, while only additive gene effect in Crosses IV and VI governed the expression of total number of branches/plant. The contribution of main effect (additive component) was higher as compared to first order interactions.

The present findings are in conformity with the results reported by Pathak *et al.* (1988), Pathak *et al.* (1989) and Dhapke *et al.* (1992) who reported the importance of additive gene effect for this trait whereas predominance of non-additive gene effects was reported by Kandaswamy (1977) and Kandasamy *et al.* (1983) for total number of

branches/plant. Patel (1992) reported involvement of both additive as well as non-additive gene effects for this trait.

The importance of additive effect along with non-additive effect in Cross III suggested that *inter se* crossing of desired segregants keeping adequate size of population would be a better choice to take the maximum advantage of nature of gene effects governing the total number of branches/plant. The involvement of additive gene effect in Cross IV and VI suggested that pedigree method of selection would be appropriate to improve this trait in the population.

4.1.2.5 Number of effective branches/plant :

Out of six crosses studied Crosses II, III and VI showed significant variation among their respective generations for this trait (Appendix III).

(a) Mean performance :

The mean values of parents of Cross II were at par (Table 4.3) and F₁ mean was at par with the mean value of parent P₂ indicating the presence of non-additive gene effect. The F₂ mean was at par with the F₁ mean, suggesting the involvement of additive gene effect in the inheritance of this trait in this population. The means of B₁ and B₂ generations were at par with each other and were also at par

with their respective recurrent parents indicating influence of non-additive gene effects in the expression of this trait.

The parents of Cross III were at par while, the F₁ plants were significantly superior to either of the parents suggesting the presence of overdominance. The parity of the mean values of F₁ and F₂ generations suggested the involvement of additive gene action in the expression of this trait. The mean values of B₁ and B₂ generations differed significantly. The parity of the mean values of B₁ and P₁ generations suggested the involvement of non-additive gene action in the expression of this trait. However, the B₂ mean was inbetween the mean values of P₂ and F₁, but was at par with F₁ mean indicated presence of additivity of the genes for this trait.

In Cross VI, difference between the mean values of parents were found non-significant (Table 4.3). The F₁ mean was significantly higher than the parental mean values and F₂ mean, indicating that non-additive gene effect did influence the expression of this trait in this population. The B₁ and B₂ means were inbetween their respective parents but were at par with their recurrent parents, P₁ and P₂.

(b) Gene effects :

Significant scaling test (Table 4.4) for Crosses II and III and non-significant scaling test for Cross VI

indicated the presence and absence of non-allelic interactions, respectively for the expression of effective branches/plant.

The estimates on gene effects for effective branches/plant (Table 4.4) revealed that barring mean, all other estimates were found non-significant in Cross II and VI. The genic complementation among the genes in the expression of this trait might have resulted in non-significance of any of the gene effect. Additive and digenic interaction (additive x dominance) were found to be significant in Cross III.

Several workers like Kandaswamy (1977), Singh and Srivastava (1982), Kandasamy *et al.* (1983), Patel *et al.* (1985) Dangaria *et al.* (1987), Narkhede *et al.* (1987), Fatteh *et al.* (1988), Vindhiyavarman and Ganesan (1995) reported the predominant role of non-additive gene action in the expression of this trait. However, many workers like Patel *et al.* (1986), Pathak and Dangaria *et al.* (1987), Pathak *et al.* (1988), Pathak *et al.* (1989), Dhapke *et al.* (1992), Dobariya *et al.* (1992) and Sudhakar *et al.* (1995) noted predominant role of additive gene action for the expression of this trait. While Narkhede *et al.* (1985) and Patel (1992) reported non-additive gene action alongwith additive gene action for the inheritance of number of effective branches/plant.

Number of effective branches is an important attribute of seed yield/plant. The involvement of additive gene effect alongwith non-additive gene effect in Cross III, suggested that cyclic method of breeding (recurrent selection) could be profitably utilized to take advantage of both additive and non-additive type of gene actions for the improvement of this trait.

4.1.2.6 Length of main raceme :

Out of the six crosses studied, Crosses I, II, III and VI showed significant variation for this trait (Appendix III).

(a) Mean performance :

In Cross I, parents (P_1 and P_2) differed significantly between themselves. The F_1 mean was at par with the better parent, P_1 . The mean length of main raceme of F_2 plants was significantly lower than the F_1 mean. The mean of B_1 and B_2 generations were at par with each other and with their respective recurrent parent. These findings revealed that both additive as well as non-additive gene actions were important in the expression of this trait.

The parents of Cross II were at par (Table 4.5). The parity of the mean values of F_1 and F_2 generations as well as B_1 and B_2 generations emphasized the influence of additive genes for the expression of this trait. The mean

Table 4.5 : Mean values of length of main raceme (cm), number of capsules on main raceme seed yield/plant (g), 100 seed weight (g) and oil content (%) for six generations in six crosses of castor

Crosses	Generations						S.E.m.	C.D. (0.05)	C.V. %
	P ₁	P ₂	F ₁	F ₂	B ₁	B ₂			
Length of main raceme (cm)									
I	63.50	56.29	65.70	58.70	61.18	60.88	1.53	4.83	4.35
II	63.70	64.79	65.56	62.39	61.40	59.62	1.08	3.41	2.99
III	63.78	60.48	61.35	62.51	58.56	62.76	0.83	2.62	2.34
IV	63.06	67.36	64.32	61.00	64.03	69.28	2.01	NS	5.38
V	57.39	63.45	63.46	60.37	61.89	65.38	1.63	NS	4.56
VI	58.99	65.87	72.30	67.15	64.19	67.88	2.08	6.55	5.45
Number of capsules on main raceme									
I	60.64	68.17	71.42	53.78	67.77	55.34	3.76	11.85	10.37
II	59.85	66.69	71.47	69.51	59.25	66.37	2.38	7.49	6.29
III	66.57	71.01	63.15	56.08	55.50	58.11	2.39	7.52	6.69
IV	69.50	72.64	75.79	72.64	77.95	77.08	1.56	4.92	3.64
V	64.90	69.15	66.27	63.82	61.68	68.19	2.32	NS	6.12
VI	65.47	70.90	76.99	73.03	73.62	76.36	1.78	5.62	4.25
Seed yield/plant (g)									
I	154.50	174.30	176.90	174.80	228.37	215.15	8.92	28.12	8.25
II	153.05	166.88	197.64	212.09	210.56	192.73	9.31	29.32	8.54
III	115.68	171.20	208.76	178.74	124.19	207.99	12.15	38.27	12.54
IV	129.67	156.83	172.12	165.52	128.55	195.09	6.13	19.32	6.73
V	165.26	169.47	179.85	162.89	223.40	181.00	12.41	NS	11.54
VI	163.14	175.87	269.44	181.52	182.46	204.77	10.54	33.22	9.31
100 seed weight (g)									
I	27.56	20.50	27.17	24.74	25.05	27.71	0.67	2.12	4.59
II	28.50	22.92	26.03	30.94	29.17	23.28	1.39	4.39	9.00
III	23.22	21.00	24.58	23.06	22.07	23.14	0.49	1.54	3.70
IV	24.67	23.00	24.01	22.69	25.69	23.33	0.74	NS	5.39
V	20.83	22.21	21.53	20.27	21.21	21.07	0.68	NS	5.58
VI	20.50	29.08	26.00	22.66	23.03	25.96	0.75	2.35	5.27
Oil content (%)									
I	43.70	42.57	42.54	43.54	43.80	43.40	0.21	0.65	0.82
II	43.51	42.73	42.73	43.24	43.70	41.48	0.12	0.36	0.48
III	38.95	44.18	43.64	42.26	40.53	42.02	0.38	1.19	1.57
IV	38.45	41.53	40.98	40.57	38.98	40.13	0.41	1.29	1.77
V	42.21	43.66	41.93	42.11	43.00	42.71	0.24	0.75	0.97
VI	42.40	39.12	42.27	42.53	42.79	43.21	0.51	1.60	2.09

Table 4.6 : Estimates of scaling tests and gene effects for length of main raceme (cm), number of capsules on main raceme, seed yield/plant (g), 100 seed weight (g) and oil content (%)

Gene effects														
Crosses	Scaling tests				Six parameter model						Three parameter model			
	A	B	C	D	m	d	h	i	j	l	m	d	h	
	Length of main raceme (cm)													
I	-6.85	-0.24	-16.41	-4.66	-	-	-	-	-	-	50.58**	3.61**	17.36	
II	-6.46**	-11.10**	-10.04	3.76	62.39**	1.78	-6.20	-7.52	2.32	25.08*	-	-	-	
III	-8.02	3.69	3.08	3.70	-	-	-	-	-	-	69.54**	1.65*	-19.92	
VI	-2.92	-2.41	-0.86	2.24	-	-	-	-	-	-	66.90**	-3.44**	-4.41	
Number of capsules on main raceme														
I	3.48	-28.90**	-56.50**	-15.54	53.78**	12.43	38.09	31.08	16.19	-5.65	-	-	-	
II	-12.82	-5.39	8.57	13.39	-	-	-	-	-	-	90.05**	-3.42**	-63.58	
III	-18.71*	-17.93**	-39.54**	-1.45	56.08**	-2.61	-2.75	2.89	-0.39	33.75	-	-	-	
IV	10.61*	5.72	-3.15	-9.74	72.64**	0.87	24.21	19.48	-0.70	-35.81	-	-	-	
VI	4.68	4.84	1.69	-3.91	-	-	-	-	-	-	60.41**	-2.67**	33.93	
Seed yield/plant (g)														
I	125.34**	79.11**	16.60	-93.92**	174.80**	13.22	200.33**	187.85**	23.09	-392.30**	-	-	-	
II	70.44	20.94	133.19**	20.90	212.10**	17.84	-4.13	-41.81	24.75	-49.58	-	-	-	
III	-76.05*	36.06	10.58	25.29	178.74**	-83.80**	14.76	-50.57	-56.06*	90.56	-	-	-	
IV	-44.68**	61.22**	31.34	7.40	165.52**	-66.53**	14.07	-14.80	-52.95**	-1.74	-	-	-	
VI	-67.65**	-35.76	-151.82**	-24.20	181.52**	-22.31	148.34*	48.41	-15.95	55.00	-	-	-	
100 seed weight (g)														
I	-4.62	7.76	-3.44	-3.29	-	-	-	-	-	-	17.45**	3.53**	19.43	
II	3.81	-2.38	20.29	9.43	-	-	-	-	-	-	44.58**	2.79**	-35.99	
III	-3.67*	0.69	-1.15	0.91	23.06**	-1.07	0.65	-1.82**	-2.18**	4.79	-	-	-	
VI	-0.44	-3.16	-10.94**	-3.67*	22.66**	-2.93*	8.56**	3.35*	2.72	-3.75	-	-	-	
Oil content (%)														
I	1.35*	1.68**	3.58**	0.27	43.74**	0.40	-1.14	-0.54	-0.33	-2.49	-	-	-	
II	1.16**	-2.58**	1.20	1.31	43.24**	2.21**	-3.05*	-2.61	3.74**	4.03*	-	-	-	
III	-1.53	-3.79**	-1.38	1.97**	42.26**	-1.48**	-1.86	-3.94**	2.26	9.26**	-	-	-	
IV	-1.47	-2.24*	0.35	2.03**	40.57**	-1.15**	-3.06**	-4.05**	0.77	7.76**	-	-	-	
V	1.86**	-0.16	-1.29	-1.49**	42.11**	0.29	1.98**	2.99**	2.01**	-4.69**	-	-	-	
VI	0.92	5.04**	4.05	-0.95	42.53**	-0.42*	3.41*	1.90	-4.12**	-7.85**	-	-	-	

* and ** indicate significance at 5 and 1 % levels of significance, respectively.

values of B₂ and P₂ generations were significantly different, while the B₁ mean was at par with the recurrent parent P₁ indicating the influence of non-additive gene action on this trait.

Significant difference was observed between the parents of Cross III (Table 4.5). The F₁ mean was inbetween the parental means, while it was at par with the mean values of parents and F₂ generations, suggesting the involvement of additive gene action in the expression of this trait. The mean values of B₁ and B₂ generations differed significantly between themselves. The B₁ mean was at par with the mean value of its non-recurrent parent P₂ whereas it was significantly different from its recurrent parent and F₁ means. The B₂ mean was at par with the mean value of F₁ and its recurrent parent, P₂.

The parents of Cross VI differed significantly for this trait. The mean of F₁ was at par with mean value of the P₂ indicated the involvement of non-additive gene effect for the expression of this trait. However, non-significant differences between the mean values of F₁ and F₂ generations revealed influence of additive gene action. The B₁ mean was inbetween the mean values of P₁ and F₁ but was at par with the P₁ mean. Present findings revealed the involvement of both additive and non-additive gene effects for the expression of length of main raceme in this population.

(b) Gene effects :

The estimates of scaling test (Table 4.6) revealed that non-allelic interactions were absent in Cross I, III and VI whereas it was present in Cross II.

The partitioning of genetic components of variation (Table 4.6) revealed that additive effect was solely involved in the expression of this trait in Crosses I, III and VI whereas in Cross II only epistatic (dominance x dominance) effect controlled the inheritance of this trait.

The present findings are in close agreement with the results obtained by Swarnlata *et al.* (1984), Patel *et al.* (1986), Dangaria *et al.* (1987), Narkhede *et al.* (1987), Pathak and Dangaria (1987), Patel *et al.* (1991), Dobariya *et al.* (1992) and Sadhukar *et al.* (1995) who observed the role of additive gene effect in the expression of this trait, while Giriraj *et al.* (1974), Kandaswamy (1977), Singh and Srivastava (1982), Narkhede *et al.* (1985), Bhatt and Reddy (1986), Pathak *et al.* (1989) and Vindhiyavarman and Ganesan (1995) who reported the predominant role of non-additive gene effects for the inheritance of length of main raceme. However, Giriraj *et al.* (1973), Pathak *et al.* (1988) and Natarajan (1993) reported the importance of additive alongwith non-additive gene effects for the inheritance of length of main raceme.

The additive effect involved in the expression of this trait in Crosses I, III and VI indicated that development of homozygous recombinants having desired length of main raceme could be developed by selection. As non-additive gene effects played major role in Cross II, it would be desirable to adopt *inter se* crossing between the desirable recombinants keeping adequate population size to improve this important yield attribute.

4.1.2.7 Number of capsules on main raceme :

The data revealed significant differences for the trait in all crosses except Cross V (Appendix III).

(a) Mean performance :

The parents of Cross I were at par (Table 4.5). The F₁ mean was at par with both the parents. The F₂ mean was significantly lower than the mean value of F₁ generation. The B₁ and B₂ means differed significantly with each other. The mean value of B₁ was inbetween the F₁ and P₁ means. The mean value of B₁ was at par with its recurrent parent P₁ while B₂ mean was significantly different to its recurrent parent P₂ as well as F₁. These findings revealed the involvement of both additive and non-additive gene effects for expression of number of capsules on main raceme in this population.

The difference between the parents of Cross II was non-significant for this trait (Table 4.5). The F₁ mean was at par with better parent P₂, indicating the presence of non-additive gene effects for this trait. However, parity of the mean values of the F₁ and F₂ generations suggested the involvement of additive gene action in the expression of this trait. The mean values of B₁ and B₂ generations were at par with each other and also with their respective recurrent parents further revealed the involvement of additivity.

Cross III exhibited non-significant difference between the parents, P₁ and P₂. The F₁ mean was at par with the mean value of P₁ but differed significantly from the parent P₂. The mean of F₁ was at par with the F₂ mean, suggesting the involvement of additive gene action for this trait. The mean values of B₁ and B₂ generations were at par with each other but differed significantly with their respective recurrent parents.

In Cross IV, parents (P₁ and P₂) were at par. The F₁ mean was at par with mean values of better parent, P₂ and F₂ generation. The mean value of B₁ was significantly different from the mean of recurrent parent however was at par with the F₁ mean. The B₂ mean was at par with the mean of P₂ and F₁ generations. These findings suggested the involvement of both additive and non-additive gene effects for the expression of this trait.

The mean values of parents (P_1 and P_2) of Cross VI did not differ significantly between themselves. The F_1 mean exceeded the mean value of both the parents indicating the presence of overdominance. The parity of F_1 and F_2 means suggested that additive gene effect was involved in the inheritance of this trait in this population. The mean value of B_1 was inbetween the F_1 and P_1 means but was at par with the F_1 mean while B_2 mean was at par with the mean of P_2 and F_1 generations.

(b) Gene effects :

The estimates of scaling tests were significant in Crosses I, III and IV, suggesting the presence of non-allelic gene interactions for the inheritance of this trait, while non-significant scaling tests in Crosses II and VI indicated the absence of non-allelic gene interactions in the expression of number of capsules on main raceme (Table 4.6).

Barring mean, all other estimates were found non-significant in Cross I, III and IV (Table 4.6). The genic complementation of the genes influencing the inheritance of this trait might have resulted in the non-significance of any of the gene effect. Additive gene effect was solely involved in the expression of number of capsules on main raceme in Cross II and VI.

The present findings of Cross II and VI are akin to the results obtained by Pathak and Dangaria (1987), Dhapke *et al.* (1992) and Dobariya *et al.* (1992) who reported the presence of additive gene action for the number of capsules on main raceme. The presence of genic complementation observed in Cross I, III and IV in present study were also reported earlier by Patel (1992) for expression of this trait. Giriraj (1973), Giriraj *et al.* (1974), Bhatt and Reddy (1983), Swarnlata *et al.* (1984), Patel *et al.* (1986), Narkhede *et al.* (1987), Fattah *et al.* (1988) and Pathak *et al.* (1989) reported the importance of non-additive gene action for the inheritance of this trait, whereas Giriraj *et al.* (1973), Narkhede *et al.* (1985) and Patel (1992) observed the presence of both additive as well as non-additive gene effects for this trait.

Number of capsules on main raceme is the important yield attributing character in castor. The involvement of additive gene effect in the expression of this trait suggested that the isolation of homozygous recombinants having more number of capsules on main spike from segregating populations would be feasible and thus selection would be an appropriate breeding method for improvement of this trait.

4.1.2.8 Seed yield/plant :

Out of six crosses studied, Cross I, II, III, IV and VI showed significant variation among their respective generations for this trait (Appendix III).

(a) Mean performance :

There were no significant differences among the mean seed yield of the P_1 , P_2 and F_1 plants in Cross I (Table 4.5). The parity of the mean values of F_1 and F_2 generations suggested the involvement of additive gene action in the inheritance of this trait in this population. The mean seed yield of B_1 and B_2 were significantly higher than the mean seed yield of their respective recurrent parent indicating the influence of non-additive gene action on this trait.

The mean values of parents were at par for this trait in Cross II (Table 4.5). The F_1 mean was significantly higher than the better parent, P_2 indicating the presence of overdominance. The F_1 mean was at par with the mean of F_2 generation while B_1 mean was at par with B_2 generation emphasizing that additive gene effect did influence the expression of this trait. The mean seed yield of B_1 was significantly higher than its recurrent parent, P_1 , while, B_2 mean was at par with P_2 . These findings revealed the involvement of both additive as well as non-additive gene

actions in the expression of seed yield/plant in this population.

In Cross III, the mean seed yield of the parents differed significantly. The F₁ mean was at par with the high yielding parent, P₂ indicating that the expression of seed yield in this population was influenced by non-additive gene action (Table 4.5). However, the parity of F₁ and F₂ means suggested the involvement of additive gene effect in the inheritance of this trait. The mean values of B₁ and B₂ generations were significantly different from each other. The mean values of B₁ and B₂ generations were at par with their respective recurrent parents.

The parents of Cross IV differed significantly between themselves. The F₁ mean was at par with the high yielding parent, P₂ and also with the mean of F₂ generation. The mean value of B₁ was significantly different from the mean value of F₁ but was at par with recurrent parent, P₁. The B₂ mean differed significantly from the means of F₁ and P₂. These findings suggested the involvement of both additive and non-additive gene actions for the expression of mean seed yield in this population.

Cross VI exhibited non-significant difference between the parents, P₁ and P₂. However, significantly higher mean value of F₁ than the mean values of both the parents indicated the presence of overdominance. The F₂ mean

was significantly lower than the mean value of F_1 , suggesting the involvement of non-additive gene action for the expression of this trait. The mean values of B_1 and B_2 were inbetween the mean values of F_1 and their respective recurrent parents. However, both were at par with mean values of their respective recurrent parents, suggesting that non-additive gene action was involved in the expression of seed yield.

(b) Gene effects :

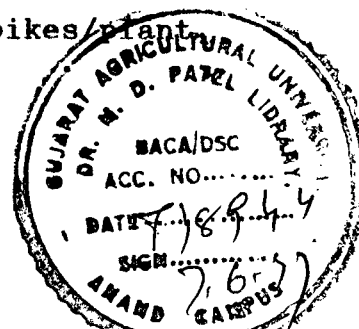
The estimates of scaling tests (Table 4.6) were significant for all the five crosses, indicating the presence of non-allelic interactions for this trait.

The estimates of gene effects for seed yield in Cross I (Table 4.6) revealed that all gene effects except additive and additive x dominance were significant. Here, dominance x dominance gene effect was greater in magnitude, next in order being dominance and additive x additive effects. The opposite signs of dominance and dominance x dominance effects indicated the presence of duplicate epistasis in the inheritance of this trait. In Cross II, barring mean, all other estimates of gene effects were found non-significant. The genic complementation among the genes in the expression of this trait might have resulted in non-significance of all the gene effects. Additive and epistatic (additive x dominance) gene effects were involved in the

inheritance of this trait in Crosses III and IV. In Cross VI, dominance effect was solely involved in the inheritance of this trait.

The present findings are akin to the results obtained by Giriraj *et al.* (1973), Singh and Yadava (1981), Alba and Greco (1983), Narkhede *et al.* (1985), Pathak *et al.* (1988), Patel (1992) and Natarajan *et al.* (1993) who reported the role of both additive and non-additive gene effects in the expression of this trait, while Kandaswamy (1977), Kandasamy *et al.* (1983), Patel *et al.* (1985), Patel *et al.* (1991), Dhapke *et al.* (1992) and Goyani *et al.* (1993) reported the importance of additive gene effects for the inheritance of this trait. However, Giriraj (1973), Hooks *et al.* (1971), Giriraj *et al.* (1974), Yadava *et al.* (1978), Singh and Srivastava (1982), Bhatt and Reddy (1983), Swarnlata *et al.* (1984), Bhatt and Reddy (1986), Patel *et al.* (1986), Narkhede *et al.* (1987), Pathak and Dangaria (1987), Fatteh *et al.* (1988), Dobariya *et al.* (1989), Pathak *et al.* (1989), Dobariya *et al.* (1992), Sudhakar *et al.* (1995) and Vindhiyavarman and Ganesan (1995) observed the role of non-additive gene effects in the expression of seed yield/plant.

Seed yield is the ultimate economical product in castor. It is influenced by several yield attributes like length of main raceme, number of effective spikes/plant



number of capsules on main raceme and 100 seed weight etc. The results of the present study revealed that seed yield was controlled by both additive as well as non-additive gene effects in Crosses III and IV. Hence cyclic method of breeding could be profitably utilized to take advantage of both additive and non-additive type of gene actions for the improvement of this trait. However, in view of the important role of non-additive gene action in Cross I and of dominance gene effect in Cross VI governing the importance of this trait, exploitation of hybrid vigour on commercial scale would be one of the important practical propositions.

4.1.2.9 100 seed weight :

Among the six crosses studied only Crosses I, II, III and VI showed significant variation for 100 seed weight (Appendix III).

(a) Mean performance :

The mean values of parents differed significantly for this trait in Cross I (Table 4.5). The F_1 mean was at par with better parent P_1 indicating that the expression of this trait in this population was influenced by non-additive gene action. The mean of the F_2 generation was significantly lower than the mean of F_1 , suggesting the importance of non-additive gene action for the inheritance of this trait. The mean values of B_1 and B_2 generations

differed significantly between themselves, and also from the mean values of their respective recurrent parent.

In Cross II, parents (P_1 and P_2) differed significantly. The mean of the F_1 was observed to be inbetween the parental means but was at par with them. Significantly higher value of F_2 mean than F_1 mean suggested the involvement of non-additive gene action for the expression of this trait. The mean values of B_1 and B_2 generations differed significantly between themselves, while they were at par with their respective recurrent parent and F_1 means.

Cross III exhibited significant difference between the parents, P_1 and P_2 . The mean of the F_1 , while being at par with the mean of better parent, P_1 , was significantly higher than the mean of P_2 . Non-significant difference observed between the means of F_1 and F_2 generations indicated that 100 seed weight was governed by additive gene action. The mean values of B_1 and B_2 generations were at par with each other. The mean value of B_1 was significantly different from the F_1 but was at par with P_1 . The B_2 mean was in between the mean values of P_2 and F_1 , but was at par with the F_1 mean. These findings suggested the involvement both additive and non-additive gene effects in the expression of 100 seed weight.

The mean of the parents in Cross VI differed significantly between themselves as well as from the mean of the F_1 . The mean of the F_1 was intermediate to the mean values of the parents, P_1 and P_2 suggesting the influence of additive gene action in the expression of this trait. Significant lower mean value of F_2 generation than F_1 indicated the involvement of non-additive gene action. The mean values of B_1 and B_2 generations were at par with each other. The mean of B_1 was inbetween the mean values of P_1 and F_1 and also differed significantly from them. The B_2 mean was significantly different from the P_2 but was at par with the F_1 mean.

(b) Gene effects :

The estimates of scaling tests were non-significant for Crosses I and II, suggesting the absence of non-allelic gene interactions in these crosses, while significant scaling tests in Crosses III and VI indicated the presence of non-allelic gene interactions in these population for the inheritance of 100 seed weight (Table 4.6).

Additive gene effect was solely involved in the expression of this trait in Crosses I and II. In Cross III, epistatic (additive x additive and additive x dominance) type of gene effects governed the expression of this trait. Additive, dominance and epistatic (additive x additive)

effects were involved in the expression of this trait in Cross VI.

The present findings of Crosses I and II are in close agreement with the results obtained by Ramaswamy and Menon (1973), Swarnlata *et al.* (1984), Patel *et al.* (1986), Dangaria *et al.* (1987), Fatteh *et al.* (1987), Pathak and Dangaria (1987), Pathak *et al.* (1989), Patel *et al.* (1991) and Dobariya *et al.* (1992) who reported the presence of additive gene action for the expression of 100 seed weight. Giriraj (1973), Giriraj *et al.* (1974) and Patel *et al.* (1985) reported presence of non-additive gene action for this trait. While Hooks *et al.* (1971), Giriraj *et al.* (1973) and Pathak *et al.* (1988) reported the presence of both additive as well as non-additive gene effects for the inheritance of 100 seed weight in castor.

As 100 seed weight being governed by additive and non-additive gene effects in present study, homozygous elite recombinants could be developed following *inter se* crossing of desirable segregants in case of Crosses III and VI, while pedigree method of breeding could be profitably used in Crosses I and II.

4.1.2.10 Oil content :

All the six crosses studied showed significant variation for this trait (Appendix III).

(a) Mean performance :

Significant difference was observed between the parents of Cross I (Table 4.5). The mean of the F₁ differed significantly from the mean of P₁ while was at par with the mean of P₂ indicating that the expression of this trait in this population was influenced by non-additive gene action. The F₂ mean was significantly higher than the mean value of F₁ generation further suggested the influence of non-additive gene action for this trait. The difference between the mean values of B₁ and B₂ generations was non-significant. The mean value of B₁ differed significantly from the F₁ mean but was at par with the recurrent parent P₁. The mean value of B₂ was significantly higher than the mean values of F₁ and P₂ generations.

In Cross II, significant difference was observed between the mean value of the parents. The F₁ mean was at par with P₂ mean indicating the presence of non-additive gene action for the expression of this trait. The mean of the F₂ generation was significantly higher than the mean of the F₁ generation further suggesting the involvement of non-additive gene action in the inheritance of this trait. The means of B₁ and B₂ generation differed significantly between themselves. The mean value of B₂ generation was significantly lower than the mean values of F₁ and recurrent parent, P₂.

The mean of the parents in Cross III differed significantly between themselves. The mean of the F_1 was at par with that of the better parent P_2 , indicating the involvement of non-additive gene action. Significantly lower mean value of F_2 than the mean of F_1 generation further revealed that non-additive gene action governed the expression of this trait. The mean values of B_1 and B_2 generations differed significantly between themselves as well as with their respective recurrent parents. The mean value of B_1 generation was inbetween the mean value of F_1 and its recurrent parent, whereas the mean of the B_2 generation was lower than the means of F_1 and its recurrent parent P_2 .

The parents P_1 and P_2 differed significantly for oil content in Cross IV. The mean of F_1 generation was significantly higher than the mean of P_1 , but was at par with the mean of P_2 , indicating the importance of non-additive gene action for the expression of this trait. However, parity between the mean values of F_1 and F_2 generations revealed the involvement of additive gene action for controlling the inheritance of this trait. The mean values of B_1 and P_1 generations were at par, while, B_2 mean was significantly different from its recurrent parent, P_2 .

The mean value of parents differed significantly for oil content in Cross V. F_1 mean was at par with parent

P₁, indicating that the expression of this trait in this population was influenced by non-additive gene action. However, parity of the mean values of F₁ and F₂ generations suggested the involvement of additive gene action in this trait. The mean values of B₁ and B₂ generations were at par. The B₁ mean was significantly higher than the mean values of F₁ and P₁. The mean value of B₂ was inbetween the means of F₁ and P₂ and was significantly different among them.

Cross VI revealed significant difference between the mean of the parents (P₁ and P₂) for this trait. The F₁ mean was at par with the mean of better parent P₁ indicating that the expression of this trait in this population was influenced by non-additive gene action. The parity of the mean values of the F₁ and F₂ generations suggested that additive gene effect governed this trait. The difference between the mean values of B₁ and B₂ generations was non-significant. The B₁ mean was at par with the mean values of P₁ and F₁ generations. The mean value of B₂ differed significantly from the P₂ mean and was at par with the mean of F₁ generation.

(b) Gene effects :

The significant estimates of scaling tests (Table 4.6) for all six crosses indicated the presence of non-allelic interactions for the expression of oil content.

The estimates of gene effects for oil content in Cross I (Table 4.6) indicated that barring mean, all types of gene effects were found non-significant. This situation indicated that the sets of genes responsible for inheritance of this trait were similar in parental lines. Barring additive x additive, all other gene effects were found significant in Cross II for the expression of this trait, where dominance x dominance gene effect was greater in magnitude followed by additive x dominance, dominance and additive in that order. In Cross III, additive and epistatic (additive x additive and dominance x dominance) gene effects were involved in the inheritance of this trait, where dominance x dominance gene effect was greater in magnitude followed by additive x additive and additive in that order. Barring additive x dominance, all gene effects were found significant in Cross IV where dominance x dominance gene effect was in greater magnitude. In Cross V barring additive, all gene effects were found significant. Barring additive x additive, all gene effects were found significant in Cross VI. The opposite signs of dominance and dominance x dominance effects in Crosses II, IV, V and VI, indicated the presence of duplicate epistasis in the inheritance of this trait. In all crosses studied, dominance x dominance gene effect was found higher in magnitude.

The present findings are akin to the results obtained by Giriraj *et al.* (1973), Pathak *et al.* (1986) and

Dobariya *et al.* (1989) who reported involvement of both additive and non-additive gene effects for the expression of oil content. Goyani *et al.* (1993) observed additive gene effect for this trait, however Bhapkar and Cruz (1967), Giriraj (1973), Giriraj *et al.* (1974), Patel *et al.* (1991) and Patel (1992) reported involvement of only non-additive gene effects for the expression of oil content.

The involvement of additive alongwith non-additive effects for oil content in Crosses II, III, IV and VI whereas the presence of non-additivity alone in Cross II suggested that cyclic method of breeding involving selection of superior genotype and their *inter se* crossing would be more effective for the improvement of this important trait in castor.

4.2 HETEROSIS AND INBREEDING DEPRESSION :

The estimates of heterosis over mid-parent (relative heterosis) and over better parent (heterobeltiosis) in different F₁ hybrids and inbreeding depression in F₂ population for various characters calculated in nine crosses for resistance to reniform nematode and in six crosses for yield and its components in castor are presented in Table 4.7 and 4.8, respectively. The results for each character is presented and discussed in the following paragraphs.

Table 4.7 : Heterosis (M.P. %), heterobeltiosis (B.P. %) and inbreeding depression for resistance to reniform nematode in nine crosses of castor

Crosses		Heterosis (%)		Inbreeding depression (%)
		M.P.	B.P.	
I	SPS 43-3 x 48-1	-41.42**	-40.98**	-68.09**
II	48-1 x ARUNA	-5.11	48.72**	-30.36**
III	48-1 x TMV 5	-15.33	29.32	-9.91
IV	SPS 43-3 x SKI 49	-6.59	89.01**	3.31
V	VP 1 x ARUNA	-5.56**	-0.54	-8.65
VI	VP 1 x TMV 5	1.51	23.80**	-3.15
VII	ARUNA x SKI 49	0.11	23.23*	-20.70*
VIII	TMV 5 x SKI 12	-2.54	1.37	-3.73
IX	SKI 12 x SKI 49	3.56	-0.77	-6.81

* and ** indicate significance at 5 and 1 % levels of significance, respectively

M.P. : Mid parent

B.P. : Better parent

4.2.1 Resistance to reniform nematode :

For this character, parent having less number of females of reniform nematode on infection was considered to be a better parent.

Relative heterosis ranged from -41.42 % (Cross I) to 1.51 % (Cross VI). Highly significant negative heterosis was observed in Cross I (-41.42 %) and Cross V (-5.56 %). Thus, out of nine crosses, only two crosses viz., Cross I and V showed desirable heterosis for resistance to reniform nematode in castor. The estimates of heterobeltiosis for the trait ranged from -40.98 % (Cross I) to 89.01 % (Cross IV). It was found that Cross I (-40.98 %) exhibited highly significant negative heterobeltiosis, whereas Cross II (48.72 %), Cross V (89.01 %), Cross VI (23.80 %) and Cross VII (24.23 %) showed significant positive heterobeltiosis. Thus, out of nine crosses, only Cross I showed desirable heterobeltiosis for resistance to reniform nematode in F₁.

The cross combination, SPS 43-3 x 48-1 (Cross I) depicted the highest magnitude of highly significant negative relative heterosis (-41.42 %) and heterobeltiosis (-40.98 %) with the minimum number (3.50) of females of reniform nematode/plant followed by Cross 48-1 x ARUNA (Cross II) with -5.11 % relative heterosis and 48.72 % heterobeltiosis and 8.73 mean number of females of reniform nematode/plant. The nematode infects the plant through all

periods of its life from germination to maturity makes difficult for its amelioration through plant protection, therefore the breeding of nematode resistant variety/hybrid is most economical and feasible for yield sustainability. To develop resistant hybrids the information on inheritance of resistance to reniform nematode is of paramount importance.

The magnitude of inbreeding depression varied from -68.09 % (Cross I) to 3.31 % (Cross IV). Crosses viz., I (-68.09 %), II (-30.36 %) and VII (-20.70 %) revealed significant negative inbreeding depression, indicating the higher level of infestation of reniform nematode in F₂ population as compared to F₁. The inbreeding depression was found to be positive in Cross III (3.31 %). However, it was non-significant.

4.2.2 Yield and its components :

4.2.2.1 Days to flowering of main raceme :

Heterosis and heterobeltiosis in negative direction are desirable for early flowering. Hence, the early parent of a cross was considered to be a better parent.

The estimates of relative heterosis in six crosses varied from -14.08 % (Cross III) to -5.02 % (Cross IV). Crosses, I and III showed highly significant negative heterosis over their respective mid parental value, whereas

Table 4.8 : Heterosis (M.P. %), heterobeltiosis (B.P. %) and inbreeding depression for various characters in six crosses of castor

Crosses									
Characters	I 48-1 x ARUNA	II 48-1 x TNV 5	III VP 1 x ARUNA	IV VP 1 x TNV 5	V ARUNA x TNV 5	VI ARUNA x SKI 12			
	Heterosis (%)	Heterosis (%)	Heterosis (%)	Heterosis (%)	Heterosis (%)	Heterosis (%)			
	Inbreeding depression (%)	Inbreeding depression (%)	Inbreeding depression (%)	Inbreeding depression (%)	Inbreeding depression (%)	Inbreeding depression (%)			
	M.P.	M.P.	M.P.	M.P.	M.P.	M.P.			
	B.P. resession (%)	B.P. resession (%)	B.P. resession (%)	B.P. resession (%)	B.P. resession (%)	B.P. resession (%)			
	(%)	(%)	(%)	(%)	(%)	(%)			
Days to flowering of main raceme	-9.02** -0.98	-6.59 -1.72	-5.11 -14.08**	-2.36 -2.25	-3.87 -7.39	2.56 -7.03	7.79 -0.42		
Number of nodes upto main raceme	-5.11 -0.09	4.57 -7.89	2.58 -3.71	-7.79* -4.89	-5.95 -6.13	1.54 -6.74	26.82** 4.93		
Plant height	-12.20 -8.26	8.22 -15.54**	5.92** -10.87**	25.12** -5.96**	116.41** -13.52**	3.69 -1.44	58.48** 1.89		
Number of total branches/plant	1.33 1.28	13.96 21.31	20.46* 4.18	61.23** 31.45**	16.52 0.63	-2.79 -9.69	23.84 13.96	64.97** 50.67**	31.09**
Number of effective branches/plant	5.12 2.83	-1.38 19.82**	13.45 2.73	91.75** 66.17**	18.95 2.02	-7.34 12.04	8.91 27.89	9.34* 80.28**	76.57** 35.31**
Length of main raceme (cm)	9.63** 3.46	10.65** 2.05	1.19 4.84*	-3.81* -1.89	-4.51 5.16	0.02 4.87	16.74** 9.76*	7.12	
Number of capsules on main raceme	10.89 4.77	24.69** 12.96**	7.17 2.74	-8.20 -11.07*	11.20* 6.64	4.34 4.16	-1.13 3.70	12.91** 8.59**	5.14
Seed yield/plant (g)	7.60 1.49	1.19 23.55**	18.43* -7.31	45.54** 21.94*	14.38 20.15**	9.75 3.83	7.46 9.43	58.96** 53.20**	32.63**
100 seed weight (g)	13.07** -1.40	8.94* 1.24	-8.67 -16.79*	5.86* 6.18*	0.73 -2.68	5.50 0.05	-3.06 5.85	4.88 -10.59**	12.85**
Oil content (%)	-1.38* -2.65**	-2.35** -0.90**	-1.79** -1.19**	4.99** -1.22	3.16* 2.48*	-2.53 1.00	-2.34** -3.96**	-0.43 3.70*	-0.31 -0.62

* and ** indicate significance at 5 and 1 % levels of significance, respectively

M.P. = Mid parent, B.P. = Better parent

Cross II (-6.59 %), Cross IV (-5.02 %), Cross V (-7.39 %) and Cross VI (-7.03 %) exhibited non-significant negative relative heterosis, indicating reduction in days to flowering as compared to respective mid parental value. The estimates of heterobeltiosis for the trait ranged from -2.81 % (Cross IV) to 7.79 % (Cross VI). It was also observed that the Crosses viz. I, II, III and IV recorded desirable negative heterobeltiosis indicating their earlier flowering than their respective better parent. Varisai *et al.* (1969) and Patel (1992) reported negative heterosis for days to flowering of main raceme in castor which is in confirmity with the present findings.

The estimates of inbreeding depression observed in F₂ generations ranged from -5.11 % (Cross II) to 2.56 % (Cross V). Crosses viz., I (-4.25 %), II (-5.11 %), III (-2.25 %), IV (-3.87 %) and VI (-0.42 %) showed negative inbreeding depression. Whereas V (2.56 %) showed positive inbreeding depression revealed the early flowering in F₂ population over F₁ population. These results are in agreement with the findings of Patel (1992) who reported positive and negative inbreeding depression for this trait.

4.2.2.2 Number of nodes upto main raceme :

For this character, parent having less number of nodes upto main raceme was considered as better parent.

The estimates of relative heterosis in different crosses varied from -23.18 % (Cross III) to 6.01 % (Cross VI). Highly significant negative heterosis observed in Cross III (-23.18 %) was desirable in nature. The estimates of heterobeltiosis observed for the character ranged from -7.79 % (Cross III) to 26.82 % (Cross VI). Significant negative heterobeltiosis was observed in Cross III (-7.79%), indicating less number of nodes upto main raceme in F₁ than its better parent. Whereas, Cross V (13.11 %) and Cross VI (26.82 %) showed significant positive heterobeltiosis. Cross III (VP 1 x ARUNA) recorded significant relative heterosis and heterobeltiosis in negative direction for this trait with lower (15.74) number of nodes upto main raceme followed by Cross IV (VP 1 x TMV 5) with -5.77 % relative heterosis, -5.95 % heterobeltiosis and 15.02 number of nodes upto main raceme, which indicated superiority of F₁ over mid-parent and better parent. Dangaria *et al.* (1987) and Patel (1992) reported negative to positive range of relative heterosis and heterobeltiosis, similar to the results reported here.

The estimates of inbreeding depression in F₂ population ranged from -6.13 % (Cross IV) to 4.93 % (Cross VI). All six crosses showed non-significant inbreeding depression.

4.2.2.3 Plant height :

The estimates of heterosis over mid parental values ranged from -16.03 % (Cross V) to 13.52 % (Cross IV). Cross II (-15.54 %), Cross III (-5.96 %) and Cross V (-16.03 %) showed highly significant negative heterosis which indicated the reduction of plant height in F₁ than the mid-parental value. However, Cross IV (13.52 %) showed highly significant positive heterosis. The value of heterobeltiosis ranged from -8.26 % (Cross I) to 211.94 % (Cross III). It was observed that all crosses except Cross I (-8.26 %) showed highly significant positive heterobeltiosis for this trait indicating an increase in plant height of F₁S than their respective better parents. The present results are in agreement with the findings of Gopani *et al.* (1968), Dangaria *et al.* (1987) and Patel (1992) who reported high negative heterobeltiosis for this trait in castor. High negative heterosis has also been observed for plant height by several workers like Pathak and Dikshit (1961), Sindagi (1964), Pathak *et al.* (1988) and Patel (1992).

The estimates of inbreeding depression in F₂ population ranged from -10.87 % (Cross II) to 25.12% (Cross III). Cross II (-10.87 %) revealed highly significant negative inbreeding depression whereas Cross III (25.12 %) showed highly significant positive inbreeding depression. Crosses viz., I, IV, V and VI also showed positive

inbreeding depression, but were non-significant. Positive inbreeding depression indicated reduction in plant height in F₂ generation. These results of the present study are in conformity with those of Kabaria and Gopani (1971), Pathak *et al.* (1988) and Patel (1992) who reported negative and positive inbreeding depression.

4.2.2.4 Number of total branches/plant :

The values of relative heterosis varied from 0.63% (Cross IV) to 61.23% (Cross III). Cross III (61.23%), Cross V (28.23 %) and Cross VI (64.97 %) showed significant positive heterosis which was indicated by an increase in number of total branches/plant in F₁ than the mid-parental value. Crosses viz., I, II and IV showed positive heterosis but were non-significant. The estimates of heterobeltiosis observed for the character ranged from -9.69 % (Cross IV) to 50.67 % (Cross VI). Cross II (20.46 %), Cross III (31.45 %) and Cross VI (50.67 %) showed significant positive heterobeltiosis for this trait, however, Cross I (1.28 %) and Cross V (23.84 %) showed positive heterobeltiosis but were non-significant. Thus, it was suggested that all hybrids except Cross IV (-9.69 %) had more number of total branches/plant than their respective better parent. Hence, this trait could be improved by exploitation of hybrid vigour. The present findings are akin to the results obtained by Patel (1992) who reported high positive heterosis for this trait.

The estimates of inbreeding depression observed in F₂ germination ranged from -2.79 % (Cross IV) to 31.09 % (Cross VI). All crosses except IV, manifested positive inbreeding depression, while Cross VI (31.09 %) showed highly significant negative inbreeding depression (-2.79 %) indicating an increase in number of total branches/plant in F₂ generation. Patel (1992) also observed significant reduction in heterosis in F₂ for number of branches/plant over F₁ mean and mid-parental values.

4.2.2.5 Number of effective branches/plant :

The magnitude of relative heterosis varied from 2.02 % (Cross IV) to 91.75 % (Cross III). All crosses showed positive heterosis, however, Cross II (19.82 %), Cross III (91.75 %) and Cross VI (80.28 %) demonstrated highly significant positive heterosis, indicating increased number of effective branches in F₁ than their respective mid-parental value. Cross III (66.17 %), Cross V (9.34 %) and Cross VI (76.57 %) exhibited significant positive heterobeltiosis suggesting the superiority of F₁S over their respective better parent for number of effective branches/plant. Only Cross IV (-7.34 %) showed negative heterobeltiosis but was non-significant. Highest magnitude of significant positive heterosis over mid-parent and over better parent with maximum number of effective spikes observed in Cross III (23.48) and Cross VI (18.01) indicated

the presence of dominance type of gene effects. Hence, this trait can be improved by exploitation of hybrid vigour. Satyabalan *et al.* (1965), Varisai *et al.* (1970), Mehta *et al.* (1991) and Patel (1992) observed significant positive heterosis for this trait in castor. Heterobeltiosis in positive direction was also noted by Gopani *et al.* (1968) and Varisai *et al.* (1969) for this trait which are in agreement with present findings.

The estimates of inbreeding depression in F₂ generation ranged from -1.38 % (Cross I) to 35.31 % (Cross VI). Cross VI (35.31 %) showed highly significant positive inbreeding depression. All hybrids except Cross I (-1.38 %) exhibited positive inbreeding depression, suggesting the presence of non-additive gene action for the inheritance of this trait in these populations. These results are in close agreement with the findings of Patel (1992) who reported highly significant positive inbreeding depression for this trait.

4.2.2.6 Length of main raceme :

The estimates of relative heterosis for this trait ranged from -1.36 % (Cross IV) to 16.74 % (Cross VI) and heterobeltiosis from -4.51 % (Cross IV) to 9.76 % (Cross VI). Cross I (9.69 %) and Cross VI (16.74 %) exhibited highly significant positive heterosis for this trait, whereas significant positive and negative heterobeltiosis

were observed in Cross VI (9.76 %) and Cross III (-3.81 %), respectively. The cross combination, ARUNA x SKI 12 (Cross VI), depicted the highest relative heterosis (16.74 %) and heterobeltiosis (9.76 %) with the maximum length of main raceme (72.30 cm), indicated the presence of dominance type of gene effects. Hence, this trait can be improved by exploitation of hybrid vigour. Varisai et al (1969), Kaul and Prasad (1983), Dangaria et al. (1987) and Patel (1992) reported positive heterosis over better parent for this trait in castor which is in accordance with the present findings.

The estimates of inbreeding depression varied from -1.89 % (Cross III) to 10.65 % (Cross I). It was observed that Cross I (10.65 %) and Cross II (4.84 %) showed significant positive inbreeding depression causing reduction in length of main raceme in F₂ population. Inbreeding depression in Cross IV (5.16 %), Cross V (4.87 %) and Cross VI (7.12 %) was non-significant but in positive direction. The present results are in agreement with those of Patel (1992) who also observed positive inbreeding depression for this trait.

4.2.2.7 Number of capsules on main raceme :

The magnitude of relative heterosis varied from -8.20 % (Cross III) to 12.91 % (Cross VI). Out of six Crosses, two Crosses viz., II (12.96 %) and VI (12.91 %)

showed highly significant positive relative heterosis for this trait. The estimates of heterobeltiosis ranged from -11.07 % (Cross III) to 8.59 % (Cross VI). Cross VI (8.59 %) exhibited desirable significant positive heterobeltiosis, while Cross III (-11.07 %) showed significant negative heterobeltiosis. High magnitude of relative heterosis and heterobeltiosis with the maximum number of capsules on main raceme (76.99) in Cross VI revealed that this trait can be improved by exploitation of hybrid vigour. The present findings are akin to the results obtained by Kabaria and Gopani (1971), Pathak *et al.* (1988), Mehta *et al.* (1991) and Patel (1992) who observed significant positive heterosis for this trait. However, Gopani *et al.* (1968) and Kaul and Prasad (1983) reported positive heterobeltiosis for this trait in castor.

Inbreeding depression in F₂ generation ranged from 2.74 % (Cross II) to 24.69 % (Cross I). Cross I (24.69 %) and Cross III (11.20 %) showed significant positive inbreeding depression indicating significant reduction in the number of capsules on main raceme in the F₂ population. All crosses exhibited positive inbreeding depression for this trait in present study. These results are in close agreement with the findings of Kabaria and Gopani (1971), Pathak *et al.* (1988) and Patel (1992) who reported significant positive inbreeding depression for number of capsules on main spike.

4.2.2.8 Seed yield/plant :

The magnitude of relative heterosis varied from 7.46 % (Cross V) to 58.96 % (Cross VI). Four cross combinations exhibited significant positive heterosis over mid-parental value. The spectrum of variation in heterobeltiosis was from 1.49 % (Cross I) to 53.20 % (Cross VI). Three hybrids expressed significant positive heterosis over their respective better parent. Cross VI (ARUNA x SKI 12) showed highest relative heterosis (58.96 %) and heterobeltiosis (53.20 %) with the maximum seed yield/plant (269.44 g), followed by Cross III (VP 1 x ARUNA) with 45.54% relative heterosis, 21.94% heterobeltiosis and 208.76 g seed yield/plant and cross II (48-1 x TMV 5) with 23.55 % relative heterosis, 18.43 % heterobeltiosis and 197.64 g seed yield/plant. All hybrids showed positive relative heterosis alongwith heterobeltiosis which suggested the superiority of F₁S over their respective mid-parental and better parental values for seed yield. Great deal of heterotic response over mid and better parental values in Cross combination ARUNA x SKI 12 (Cross VI) revealed real superiority of this hybrid from the commercial point of view. White (1918), Zimmerman and Van (1953), Narayan (1958), Ankineedu and Kulkarni (1965), Satyabalan *et al.* (1965), Varisai *et al.* (1970), Hooks *et al.* (1971), Kabaria and Gopani (1971), Yadava *et al.* (1978), Pathak *et al.* (1988), Mehta *et al.* (1991) and Patel (1992) have also

reported significant positive heterosis for this trait. Heterobeltiosis in positive direction was also noted by Stein (1958), Gopani *et al.* (1968), Varisai *et al.* (1969), Yadava *et al.* (1978), Kaul and Prasad (1983), Dangaria *et al.* (1987) and Patel (1992) for seed yield/plant in castor.

It is evident that highest relative heterosis and heterobeltiosis with the maximum seed yield in the cross combination, ARUNA x SKI 12 (Cross VI) was accompanied by high positive relative heterosis and heterobeltiosis for yield contributing character like number of effective spikes/plant, length of main raceme and number of capsules on main raceme, followed by Cross VP 1 x ARUNA (Cross III) having high positive heterosis and heterobeltiosis for seed yield and yield contributing characters like number of effective spikes and 100 seed weight.

The estimates of inbreeding depression ranged from -7.31 % (Cross II) to 32.63 % (Cross VI). Highly significant positive inbreeding depression was observed in Cross VI only. This cross also noticed the highest heterosis and heterobeltiosis for seed yield suggesting the presence of non-additive gene action in the inheritance of this trait in this population. The present results are in agreement with the findings of Pathak *et al.* (1988) and Patel (1992) who reported the highest inbreeding depression for seed yield/plant.

4.2.9 100 seed weight :

The relative heterosis for this trait ranged from 0.05 % (Cross V) to 13.07 % (Cross I). All crosses exhibited positive heterosis in F₁S over their respective mid-parental value, while Cross I (13.07 %) and Cross II (11.17 %) showed highly significant positive heterosis. The value of heterobeltiosis ranged from -10.59 % (Cross VI) to 5.86 % (Cross III). It was found that only Cross III (5.86 %) exhibited the significant positive heterobeltiosis, which is of desirable nature while rest of the crosses showed negative heterobeltiosis for this trait. The present findings are akin to those of Gopani *et al.* (1968) and Dangaria *et al.* (1987) who reported range of negative to positive heterobeltiosis for this trait. However, Pathak *et al.* (1988) and Patel (1992) reported positive heterosis for this trait.

The magnitude of inbreeding depression varied from -16.79 % (Cross II) to 12.85 % (Cross VI). It was found that Cross I (8.94 %), Cross II (6.18 %) and Cross VI (12.85 %) showed positive significant inbreeding depression, indicating the significant reduction in 100 seed weight in F₂ generation. Cross II (-16.79 %) exhibited negative significant inbreeding depression. The present findings are in agreement with the findings of Pathak *et al.* (1988) and Patel (1992) who reported the significant positive inbreeding depression for 100 seed weight.

4.2.2.10 Oil content :

Results revealed that the heterosis over mid-parental value varies from -2.34 % (Cross V) to 4.99 % (Cross III). Out of six crosses, three crosses viz., III (4.99 %), VI (3.70 %) and IV (2.48 %) showed significant positive heterosis with mean oil content was 43.64 %, 42.27% and 40.57 %, respectively whereas, rest of three crosses showed significant negative heterosis for oil content. The value of heterobeltiosis ranged from -3.96 % (Cross V) to -0.31 % (Cross VI). All the six crosses exhibited negative heterobeltiosis. The present findings are akin to the results obtained by Dobariya *et al.* (1989) and Patel (1992) who reported positive heterosis and heterobeltiosis for this trait, whereas Gopani *et al.* (1968) and Pathak *et al.* (1986) reported significant positive heterobeltiosis for this trait which is not in agreement with the present findings.

Inbreeding depression in F₂ population ranged from -2.35 % (Cross I) to 3.16 % (Cross III). Crosses, III (3.16 %) and IV (1.0 %) showed positive inbreeding depression, while Cross III showed significant positive inbreeding depression in F₂ population for this trait. These results are in agreement with the findings of Patel (1992) who reported significant positive inbreeding depression for oil content.

4.3 HERITABILITY AND GENETIC ADVANCE :

The quantitative traits are not highly heritable. High or low heritability is not rigidly defined, but the following values are generally accepted (Stansfield, 1969).

- (i) Low heritability : < 20 %
- (ii) Moderate heritability : 20 % to 50 %
- (iii) High heritability : > 50 %

The value of expected genetic advance for various characters are usually arbitrarily demarcated into three categories viz., low, moderate and high as follows :

- (i) Low expected genetic advance : 0.01 to 2.00
- (ii) Moderate expected genetic advance : 2.01 to 4.00
- (iii) High expected genetic advance : 4.01 and above

The results obtained on these aspects for different characters in all the nine crosses for resistance to reniform nematode and six crosses for yield and its components are presented and discussed in the following paragraphs.

4.3.1 Resistance to reniform nematode :

The heritability estimates in broad sense ranged from 4.58 % (Cross IX) to 99.27 % (Cross I), whereas the narrow sense heritability ranged from 0.69 % (Cross IV) to 52.82 % (Cross V). It was observed that Cross V and IX

Table 4.9 : Estimates of heritability and genetic advance as per cent of mean for resistance to reniform nematode in nine crosses of castor

Crosses		Heritability (%)		Genetic advance (% of mean)
		Broad sense	Narrow sense	
I	SPS 43-3 x 48-1	99.27	1.99	1.75
II	48-1 x ARUNA	81.51	8.51	4.81
III	48-1 x TMV 5	72.07	7.29	4.11
IV	SPS 43-3 x SKI 49	97.95	0.69	0.49
V	VP 1 x ARUNA	33.34	52.82	14.88
VI	VP 1 x TMV 5	67.73	10.11	2.99
VII	ARUNA x SKI 49	68.36	6.41	2.27
VIII	TMV 5 x SKI 12	62.48	22.38	2.33
IX	SKI 12 x SKI 49	4.58	12.53	1.83

exhibited high narrow sense heritability than their respective broad sense heritability values. This may be due to interactions of environment with gene complex. Cross V expressed moderate broad sense and high narrow sense heritability alongwith high genetic advance which indicated better opportunity for selecting relatively resistant genotypes in segregating populations. The estimates of predicted genetic advance as per cent of mean varied from 0.49 % (Cross IV) to 14.88 % (Cross V). Crosses I, II, III, IV, VI and VII exhibited low narrow sense heritability indicating predominance of non-additive gene action. Cross VIII expressed high broad sense and moderate narrow sense heritability alongwith moderate genetic advance which indicated better opportunity for selecting relatively resistant genotypes in advanced generations. While Crosses II, III, VI and VII expressed high broad sense heritability and low narrow sense heritability coupled with high to moderate genetic advance observed for this trait indicated that some but not significant improvement in the resistance to reniform nematode could be achieved through selection in segregation generations. Very high broad sense heritability and very low narrow sense heritability coupled with low genetic advance in Cross I and Cross IV indicated very little possibility of improving this character by straight selection.

4.3.2 Yield and its components :

4.3.2.1 Days to flowering of main raceme :

The high broad sense heritability was observed in Crosses viz., I (67.26 %), III (77.55 %) and VI (69.98 %), while it was moderate in Crosses II (27.37 %) and V (49.24 %). Narrow sense heritability was moderate in Crosses I (47.97 %) and II (42.73 %) and low in crosses viz., III (3.06 %), V (11.77 %) and VI (18.60 %). Cross I showed moderate narrow sense heritability alongwith high broad sense heritability and high genetic advance as per cent of mean indicated that rapid improvement through straight selection would be possible for developing earliness in castor. High magnitude of broad sense heritability and genetic advance coupled with low narrow sense heritability in Cross VI, while moderate broad sense heritability and moderate genetic advance alongwith low narrow sense heritability in Cross V indicated little possibility of improving this trait following selection in segregating generations. The perusal of data presented in Table 4.10 clearly indicated that the estimates of broad sense heritability in Cross II and IV were lower than their corresponding narrow sense heritability. This is unexpected situation and difficult to explain, but it is significant to note that the differences for this trait among different generations in these Crosses (II and IV) were non-significant for this trait leading to the present results.

The present findings are in close agreement with the results of Bhatt and Reddy (1981), Patel *et al.* (1985) and Patel (1992) who observed high broad sense heritability alongwith high to low genetic advance for this trait. However, Singh and Yadava (1981) observed high narrow sense heritability for days to flowering of main raceme in castor.

4.3.2.2 Number of nodes upto main raceme :

The broad sense heritability for this trait was observed to be high in Crosses viz., I (75.09 %), II (71.78 %), III (95.25 %) , V (79.40 %) and VI (80.03 %). High heritability in broad sense in all Crosses except Cross IV for this trait, revealed greater correspondence between phenotypic and genotypic values. However, low value of narrow sense heritability in all the six crosses revealed the importance of non-additive gene action in the expression of this trait. The data further revealed that the expected genetic advance as per cent of mean was moderate in crosses viz., I (2.09 %), IV (2.71 %) and V (2.19 %), while it was low in Cross II (1.06 %) and Cross VI (0.37 %). High broad sense and low narrow sense heritability coupled with moderate to low genetic advance observed for this trait indicated that no significant improvement in number of nodes upto main raceme could be achieved through selection in segregating generations. In Cross IV, broad sense heritability was lower than the narrow sense heritability, a

situation which is unexpected and difficult to resolve but the differences for this trait among different generations in this cross were non-significant leading to the present results. Kaul and Prasad (1983) and Swarnlata *et al.* (1984) reported high heritability, whereas Stephen *et al.* (1973), Bhatt and Reddy (1981) and Patel (1992) reported high heritability alongwith high and moderate to low genetic advance for number of nodes upto main raceme which are akin to the findings observed under the present study.

4.3.2.3 Plant height :

The estimate of broad sense heritability ranged from 61.72 % (Cross I) to 99.61 % (Cross III). The perusal of results revealed that all six crosses showed high heritability (broad sense) indicating close correspondence between genotypic and phenotypic values due to relatively smaller contribution of environmental effect on this trait in these crosses. However, moderate narrow sense heritability in Cross I (33.95 %) and low narrow sense heritability in rest of the Crosses viz., II (5.02 %), III (0.79 %), IV (2.08 %), V (5.59 %) and VI (1.15 %) observed for this trait revealed greater role of non-additive gene action in the inheritance of this trait. The magnitude of genetic advance varied from 0.62 % (Cross VI) to 11.23 % (Cross I). The high broad sense heritability alongwith moderate narrow sense heritability and high genetic advance

as per cent of mean in Cross I suggested the involvement of additive gene action in the inheritance of this trait and that the selection would be effective for improving this trait in subsequent generations. The expected genetic advance was moderate in Cross II (2.33 %) and Cross V (2.73 %) and low in Crosses viz., III (0.82 %), IV (1.41 %) and VI (0.62 %). Low narrow sense heritability coupled with moderate to low genetic advance in all crosses barring Cross I, indicated that it is difficult to improve the plant height by resorting selection in subsequent segregating generations, as the gene effect involved in these crosses appeared to be non-fixable in nature. Several workers like Bhatt and Reddy (1981), Muthiah *et al.* (1982), Patel and Jaimini (1988), Patel *et al.* (1991) and Patel (1992) reported high heritability alongwith high genetic advance for this trait. However, high broad sense heritability for this trait was observed by Swarnlata *et al.* (1984) and Patel *et al.* (1988) whereas high narrow sense heritability was reported by Singh and Yadav (1982) for this trait.

4.3.2.4 Number of total branches/plant :

The broad sense heritability for this trait was observed to be high in Cross III (72.99 %) and Cross IV (65.35 %), whereas it was moderate in Cross II (37.56 %) and Cross VI (56.06 %). The narrow sense heritability varied from 2.14 % (Cross VI) to 17.76 % (Cross II). The estimates

of genetic advance revealed high genetic advance in Cross II (5.27 %) while, Cross III (3.67 %) and IV (2.72 %) exhibited moderate genetic advance and Cross VI (1.32 %) exhibited low genetic advance. The results on heritability (broad and narrow sense) and genetic advance in Crosses II, III, IV and VI indicated predominant role of non-additive effects and environment in the expression of this trait. The results further revealed that very slow improvement through selection would be possible for evolving castor genotypes with more number of total branches in these populations. In Cross I and V, broad sense heritability was lower than narrow sense heritability. This is an unexpected situation and difficult to explain. The differences among the generations were non-significant in both the crosses for this trait (Appendix III). Sindagi *et al.* (1965) and Dhapke *et al.* (1992) reported high heritability whereas Stephen *et al.* (1973), Patel and Jaimini (1988) and Patel (1992) observed moderate to high heritability alongwith moderate to high genetic advance for this trait. These findings are in agreement with present reports.

4.3.2.5 Number of effective branches/plant :

The broad sense heritability for this trait was observed to be high in Cross III (73.26 %), moderately high in Cross VI (58.21 %) and moderate in Cross II (44.82 %), IV (39.41 %) and V (25.40 %). The narrow sense heritability

varied from 0.88 % (Cross VI) to 25.52 % (Cross II). It is evident from the data that moderate value of heritability (both in broad and narrow sense) observed in Cross II indicated very high influence of additive gene action in the inheritance of this trait. The magnitude of expected genetic advance varied from 0.64 % (Cross VI) to 7.36 % (Cross II). Moderate heritability (narrow and broad sense) with high genetic advance as per cent of mean in Cross II, revealed that selection can be profitably used for improving the number of effective spikes/plant in this cross. However, very low narrow sense heritability coupled with moderate genetic advance in Crosses, viz., III, IV, V and VI indicated that it would be very difficult to improve this trait through straight selection in segregating generations. In Cross I, differences for this trait among different generations were non-significant (Appendix III). Patel *et al.* (1985) and Patel (1992) reported high heritability alongwith low and high genetic advance for this trait in castor, respectively.

4.3.2.6 Length of main raceme :

The estimates of broad sense heritability ranged from 28.85 % (Cross IV) to 66.16 % (Cross III), while narrow sense heritability varied from 0.79 % (Cross III) to 33.14 % (Cross II). It is evident from the data that moderately high values of heritability (both in broad and narrow sense)

observed in Cross II, indicated major role of additive gene action in the inheritance of this trait. High broad sense heritability alongwith low narrow sense heritability were observed in crosses viz., I, III and VI. However, in Crosses IV and V, moderate broad sense and low narrow sense heritability were observed, indicating major role of non-additive gene action in the inheritance of this trait for these crosses. The expected genetic advance was moderate in Cross II (2.66 %) whereas, it was low in Crosses, I (0.33 %), III (0.19 %), IV (0.64 %), V (0.89 %) and VI (0.29 %). Moderately higher heritability (narrow and broad sense) with moderate genetic advance as per cent of mean in Cross II, revealed that selection can be profitably used for improving the length of main raceme in this cross. However, very low narrow sense heritability coupled with moderate to low genetic advance in rest of the crosses, indicated that it would be very difficult to improve this trait through straight selection in segregating generations. Stephen *et al.* (1973), Patel *et al.* (1991) and Patel (1992) reported high heritability alongwith high genetic advance as per cent of mean for this trait. However, moderate heritability for this trait was observed by Giriraj *et al.* (1974) while low heritability was reported by Sindagi (1965) and Swarnlata *et al.* (1984).

4.3.2.7 Number of capsules on main raceme :

Broad sense heritability was high in Crosses, viz., III (66.16 %), IV (52.02 %) and VI (59.79 %), while it was moderately high in Cross I (48.32 %) and II (49.21 %) and low in Cross V (12.62 %). Narrow sense heritability varied from 1.32 % (Cross IV) to 94.2 % (Cross V). High magnitude of broad sense heritability and moderately high value of narrow sense heritability alongwith high genetic advance in Cross III revealed the predominant role of additive gene action in the expression of this trait and suggested fair chances for improving number of capsules on main raceme in succeeding generations through selection. Moderately high broad sense heritability and moderately high narrow sense heritability coupled with moderate genetic advance found in Cross I indicated negligible improvement in this trait through selection. Moderately high broad sense heritability alongwith low narrow sense heritability and low genetic advance in Cross II and Cross VI pointed out the predominant role of non-additive gene action in the expression of this trait. Hence, the improvement of this trait through selection would be rather difficult. However, in Cross V, broad sense heritability was low but the narrow sense heritability was high, a situation which is difficult to resolve. High heritability alongwith high genetic advance for this trait was observed by Patel *et al.* (1985), Patel and Jaimini (1988), Dhapke *et al.* (1992) and Patel

(1992). However, moderate heritability was reported by Giriraj et al. (1974), whereas, Swarnlata et al. (1984) reported low heritability for this trait. The present findings are in agreement with these reports.

4.3.2.8 Seed yield/plant :

For seed yield, the broad sense heritability was observed to be high in all the crosses barring Cross V. Narrow sense heritability varied from 9.06 % (Cross II) to 47.36 % (Cross V). It was noticed that the narrow sense heritability was moderate in Crosses viz., I (20.04 %), III (24.84 %), V (47.36 %) and VI (44.12 %), whereas low in Cross II (9.06 %) and IV (10.08 %). High broad sense and moderate narrow sense heritability in Cross I, III and VI clearly suggested the predominant role of additive gene action in the expression of seed yield/plant. However, very low narrow sense heritability in case of Crosses II and IV indicated the involvement of non-additive gene effects in the expression of this trait. The value of expected genetic advance was high in Crosses I (7.76 %), III (15.57 %) and VI (22.06 %), whereas it was moderate in Crosses II (3.56 %) and IV (3.91 %). High heritability in broad sense and moderate narrow sense heritability coupled with high expected genetic advance in Crosses I, III and VI clearly suggested that high seed yield could be fixed within few generations of selection. In case of Crosses II and IV, high

heritability in broad sense and low narrow sense heritability coupled with moderate genetic advance, indicated very little chances of improvement through selection in segregating generation. Moderately high broad and narrow sense heritability alongwith high expected genetic advance in Cross V suggested some scope to fix the character through selection.

High heritability alongwith high genetic advance for seed yield was reported by Patel *et al* (1985), Patel *et al.* (1991), Dhapke *et al.* (1992) and Patel (1992), while moderate heritability accompanied with high genetic advance was observed by Stephen *et al.* (1973). The present findings are in close agreement with these findings. Giriraj *et al.* (1974), Singh and Yadava (1981) and Patel and Jaimini (1988) noted low heritability, whereas Goyani *et al.* (1993) reported high narrow sense heritability for this trait in castor.

4.3.2.9 100 seed weight :

The estimate of broad sense heritability ranged from 26.94 % (Cross V) to 84.05 % (Cross VI), while narrow sense heritability varied from 4.61 % (Cross I) to 39.90 % (Cross III). Crosses I, II, IV and V exhibited very low narrow sense heritability (less than 10 %) indicating predominance of non-additive gene action. The estimates of expected genetic advance varied from 0.62 % (Cross IV) to

5.58 % (Cross VI). Cross III and Cross VI expressed high broad sense and moderate narrow sense heritability alongwith high genetic advance which indicated better opportunity for selection of this trait in advance generations. In case of crosses I and II, high broad sense and very low narrow sense heritability alongwith low genetic advance showed very remote chances of improvement of this trait through selection. Moderate broad sense and low narrow sense heritability alongwith low genetic advance in Cross IV and V suggested that the improvement of this trait through selection would be difficult. Several workers like Ramaswamy and Menon (1973), Giriraj *et al.* (1974), and Swarnlata *et al.* (1984) reported high heritability for this trait. High heritability alongwith high genetic advance was observed by Muthiah *et al.* (1982), Patel and Jaimini (1988) and Patel *et al.* (1991), whereas high heritability alongwith moderate to low genetic advance was observed by Stephen *et al.* (1973) and Patel *et al.* (1985).

4.3.2.10 Oil content :

High broad sense heritability in all the six crosses for this trait revealed greater correspondence between phenotypic and genotypic values. However, low value of narrow sense heritability in all the crosses barring Cross I, revealed the importance of non-additive gene action in the expression of this trait. The estimates of genetic

advance were low in all the six crosses ranging from 0.12 % (Cross VI) to 0.69 % (Cross IV). High broad sense and moderate narrow sense heritability coupled with low genetic advance in Cross I suggested that little improvement could be made through selection in advanced generation for this trait. However, high broad sense heritability with very low narrow sense heritability accompanied by low genetic advance in all the crosses barring Cross I, suggested that improvement in oil content through straight selection would not be possible. The present findings are in close agreement with the results of Patel *et al.* (1991) and Patel (1992) who observed high heritability in broad sense alongwith low genetic advance. Giriraj *et al.* (1974) reported low heritability whereas, Goyani *et al.* (1993) noted medium narrow sense heritability for this trait in castor.

SUMMARY AND CONCLUSION

CHAPTER V

SUMMARY AND CONCLUSION

The present investigation was confined to six generations (P_1 , P_2 , F_1 , F_2 , B_1 and B_2) of eleven crosses viz., I (SPS 43-3 x 48-1), II (48-1 x ARUNA), III (48-1 x TMV 5), IV (SPS 43-3 x SKI 49), V (VP 1 x ARUNA), VI (VP 1 x TMV 5), VII (ARUNA x SKI 49), VIII (TMV 5 x SKI 12), IX (SKI 12 x SKI 49), X (ARUNA x TMV 5) and XI (ARUNA x SKI 12) involving seven inbred lines of castor selected from the germplasm maintained at the Main Castor Research Station, Gujarat Agricultural University, Sardar Krushinagar. The experiment was laid out in a compact family block design with three replications during kharif, 1995-96 at Anand. A replication had one row (consisting of 10 plants) of each of the parents and F_1 generations, two rows of each of the back crosses and four rows of each of F_2 generations following inter and intra row spacing of 90cm x 60cm.

Evaluation of nine crosses for reaction to reniform nematode was carried out in pots during January to April, 1996. However, six crosses were evaluated for days to flowering of main raceme, number of nodes upto main raceme, plant height (cm), number of total and effective branches/plant, length of main raceme (cm), number of capsules on main raceme, seed yield/plant (g), 100 seed weight (g) and oil content (%), under field conditions.

The objectives of the present investigation were to study gene effects through generation mean analysis, magnitude of heterosis in F_1 , inbreeding depression in F_2 , heritability (broad and narrow sense) and genetic advance as per cent of mean. Scaling test as suggested by Hayman and Mather (1955) was used for testing the adequacy of additive-dominance model followed by either six parameter (Hayman, 1958) or three parameter (Jinks and Jones, 1958) model for estimation of gene effects.

Salient features of the results obtained are summarised as under :

The analysis of variance revealed significant differences among different generations for all the characters in all crosses except resistance to reniform nematode in Crosses V and IX (VP 1 x ARUNA and SKI 12 x SKI 49); days to flowering of main raceme, number of nodes upto main raceme, number of effective branches/plant, length of main raceme (cm) and 100 seed weight (g) in cross IV (VP 1 x TMV 5); number of total and effective branches/plant, length of main raceme (cm), number of capsules on main raceme, seed yield/plant (g) and 100 seed weight (g) in Cross V (ARUNA x TMV 5); days to flowering of main raceme and number of total branches/plant in Cross II (48-1 x TMV 5) and number of total and effective branches/plant in Cross I (48-1 x ARUNA).

(i) Gene effects :

(a) Resistance to reniform nematode :

Estimates of gene effects for resistance to reniform nematode revealed that in Crosses I (SPS 43-3 x 48-1) and IV (SPS 43-3 x SKI 49) all gene effects; in Cross II (48-1 x ARUNA) all gene effects excepts additive (d); in Cross III (48-1 x TMV 5) additive x dominance (j) and dominance x dominance (l); in Cross VI (VP 1 x TMV 5) only additive (d); all gene effects barring additive x dominance (j) in Cross VII (ARUNA x SKI 49) and additive (d) and additive x dominance (j) in Cross VIII (TMV 5 x SKI 12) were found significant.

(b) Yield and its components :

Estimates of gene effects using different genetic parameter models showed that in Cross I (48-1 x ARUNA), dominance and dominance x dominance (l) gene effects for days to flowering of main raceme; dominance (h) and additive x additive (i) and dominance x dominance (l) gene effects for number of nodes upto main raceme; dominance (h) and dominance x dominance (l) gene effects for plant height; only additive (d) for length of main raceme and 100 seed weight and dominance (h), additive x additive (i) and dominance x dominance (l) gene effects for seed yield/plant were found significant. Dominance (h) and dominance x dominance (l) gene effects were important for the expression of most of the characters in Cross I (48-1 x ARUNA).

Additive (d) and additive x dominance (j) gene effects for number of nodes upto main raceme and plant height; only additive (d) gene effect for number of capsules on main raceme and 100 seed weight; all gene effects except additive x additive (i) for oil content and dominance x dominance (l) gene effects for length of main raceme were found significant in Cross II (48-1 x TMV 5). The most important gene effects for the expression of most of the characters were additive (d), additive x dominance (j) and dominance x dominance (l) in Cross II.

In Cross III (VP 1 x ARUNA), only additive (d) effect for days to flowering of main raceme, number of nodes upto main raceme and length of main raceme; additive (d) and dominance x dominance (l) for plant height; additive (d) and additive x dominance (j) gene effects for number of total and effective branches/plant and seed yield/plant; additive x additive (i) and additive x dominance (j) gene effects for 100 seed weight and additive (d), additive x additive (i) and dominance x dominance (l) gene effects for oil content were found to be significant. The additive gene effect was found to be largely responsible for the expression of most of the characters in this cross.

The additive, additive x additive (i) and additive x dominance (j) gene effects for plant height; only additive (d) gene effect for number of total branches/plant; additive

(d) and additive x dominance (j) gene effects for seed yield/plant and all gene effects except additive x dominance (j) for oil content were found significant in Cross IV (VP 1 x TMV 5).

In Cross V (ARUNA x TMV 5), only additive (d) gene effect for days to flowering of main raceme and number of nodes upto main raceme; only additive x dominance (j) gene effect for plant height and all gene effects except additive (d) for oil content were found to be significant. For other characters, all gene effects were found to be non-significant in this cross.

The additive gene effect for days to flowering of main raceme, plant height, number of total branches/plant, length of main raceme and number of capsules on main raceme; all gene effects except dominance (h) for number of nodes upto main raceme; only dominance (h) gene effects for seed yield/plant; additive (d), dominance (h) and additive x additive (i) for 100 seed weight and all gene effects except additive x additive (i) for oil content were found to be significant in Cross VI (ARUNA x SKI 12). Additive gene effects appeared to be the most important in controlling the inheritance of most of the characters in this cross.

Overall the results revealed that different types of gene effects controlled the inheritance of the same character in different crosses and for different characters in the same cross.

(ii) Heterosis and inbreeding depression :

(a) Resistance to reniform nematode :

Significant and desirable heterosis over mid parent and better parent were found for resistance to reniform nematode in Cross I (SPS 43-3 x 48-1); significant and desirable heterosis over mid parent was found for this trait in Cross V (VP 1 x ARUNA), while, it was non-significant but in desirable direction in Crosses, II (48-1 x ARUNA), III (48-1 x TMV 5), IV (SPS 43-3 x SKI 49) and VIII (TMV 5 x SKI 12).

The significant inbreeding depression was observed for resistance to reniform nematode in Crosses I, II and VII. Crosses I and II showing high heterosis also showed high inbreeding depression for this trait.

(b) Yield and its components :

Significant relative heterosis in desired direction was observed for days to flowering of main raceme, length of main raceme and 100 seed weight in Cross I (48-1 x ARUNA).

In Cross II (48-1 x TMV 5), plant height, number of effective branches/plant, number of capsules on main raceme and seed yield/plant showed significant and desirable heterosis. However, number of total branches/plant and seed yield/plant exhibited significant desirable heterobeltiosis in this cross.

All characters except length of main raceme and number of capsules on main raceme showed significant and desired relative heterosis, whereas significant and desirable heterobeltiosis was found for number of nodes upto main raceme, number of total and effective branches/plant, seed yield/plant and 100 seed weight in Cross III (VP 1 x ARUNA).

In Cross IV (VP 1 x TMV 5), significant and desirable relative heterosis was found for seed yield/plant and oil content.

Significant and desirable relative heterosis was found for plant height and number of total branches/plant in Cross V (ARUNA x TMV 5), whereas, significant and desirable heterobeltiosis was observed for number of effective branches/plant.

In Cross VI (ARUNA x SKI 12), number of total and effective branches/plant, length of main raceme, number of capsules on main raceme and seed yield/plant showed significant and desirable heterosis and heterobeltiosis. However, oil content exhibited significant desirable relative heterosis only.

Significant inbreeding depression was observed for length of main raceme, number of capsules on main raceme and 100 seed weight in Cross I; plant height and length of main

raceme in Cross II; number of capsules on main raceme, 100 seed weight and oil content in Cross III; number of total and effective branches/plant, seed yield/plant and 100 seed weight in Cross VI.

(iii) Heritability and genetic advance :

(a) Resistance to reniform nematode :

High to moderate magnitude of broad sense heritability coupled with high to moderate genetic advance as per cent of mean were observed for resistance to reniform nematode in Crosses viz., II (48-1 x ARUNA), III (48-1 x TMV 5), V (VP 1 x ARUNA), VI (VP 1 x TMV 5), VII (ARUNA x SKI 49) and VIII (TMV 5 x SKI 12). High to very high broad sense heritability associated with low expected genetic advance were observed for this trait in Crosses I (SPS 43-3 x 48-1) and IV (SPS 43-3 x SKI 49). Narrow sense heritability was generally low in all crosses except Cross VIII (TMV 5 x SKI 12) for this trait.

(b) Yield and its components :

Moderate to high magnitude of broad sense heritability coupled with moderate to high genetic advance observed for seed yield/plant in all the six crosses, for days to flowering of main raceme in all crosses except Crosses III and IV; for number of effective branches/plant in all crosses except Crosses I and VI; for number of nodes

upto main raceme in Crosses I and V; for plant height in Cross I, II and V; for number of total branches in Crosses II, III and IV; for length of main raceme in Cross II; for number of capsules on main raceme in Crosses I and III and for 100 seed weight in Crosses III and VI.

Moderate magnitude of heritability (narrow sense) coupled with high to moderate values of genetic advance observed for seed yield in all Crosses except Crosses II and IV; for days to flowering of main raceme in Crosses I and II; for plant height in Cross I; for number of effective branches/plant in Crosses II and V; for length of main raceme in Cross II; for number of capsules on main raceme in Crosses III and V and for 100 seed weight in Crosses III and VI suggested that these characters can be further improved through selection in advanced generations.

CONCLUSION

Based on the results obtained following conclusions can be drawn :

1. Since, different gene effects were responsible for the inheritance of the same character in different crosses and for the different characters in the same cross, specific handling of individual cross in segregating generations would be advantageous for the improvement of these characters. In general, the

characters controlled by additive gene effect can best be improved by adopting different types of selections. The characters controlled by non-additive gene effect or both additive and non-additive gene effects can successfully be improved by utilizing hybrid vigour or following cycling method of breeding i.e. recurrent selection.

2. Among the various crosses attempted involving diverse parents for degree of resistance to reniform nematodes hybrid combination viz., SPS 43-3 x 48-1 which showed highest magnitude of heterosis (-41.42 %) and heterobeltiosis (-40.98 %) in desired direction can best be exploited for isolating the stable genotypes with acceptable level of resistance to reniform nematode in advance generation.

3. High magnitude and highly significant heterosis and heterobeltiosis observed for seed yield/plant; many of the yield components viz., number of branches/plant (total and effective), length of main raceme, number of capsules on main raceme and 100 seed weight, suggested that hybrids vigour can be profitably used on commercial scale. The hybrid combinations viz., ARUNA x SKI 12 and VP 1 x ARUNA which manifested very high magnitude of heterosis and heterobeltiosis for seed yield, important yield components, earliness and dwarf

plant type can best be exploited for commercial cultivation.

4. High heritability (broad sense) associated with moderate genetic advance recorded for days to flowering of main raceme, number of nodes upto main raceme, plant height, number of total and effective branches/plant, number of capsules on main raceme, seed yield/plant and 100 seed weight indicated that these characters can be further improved through selection in advanced generations.
5. Low narrow sense heritability alongwith low genetic advance observed for oil content indicated that the possibility of improving this characters from the present material is very remote.

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* Original not seen.

APPENDICES

Appendix I : Meteorological data recorded during crop season
(monthly mean)

Month/ Year	Temperature (°C)		Relative humidity(%)		Rain fall (mm)	Wind speed (km/hrs)
	Maximum	Minimum	Morning	Evening		
1995-96						
Sept.	33.66	24.67	90.42	59.80	149.00	4.29
Oct.	35.61	22.23	79.24	42.06	9.60	3.00
Nov.	32.44	14.68	77.47	37.16	0.00	2.52
Dec.	29.25	13.29	80.06	37.04	0.00	3.02
Jan.	27.55	12.41	85.06	42.17	2.20	3.73
Feb.	30.93	12.87	77.01	28.23	0.00	3.18
March	36.38	17.78	65.28	22.91	0.00	3.22
April	37.80	20.14	70.21	25.35	0.00	3.35

Source : Meteorological Observatory, Gujarat Agricultural
University, Anand Campus, Anand

Appendix II : Analysis of variance of six generations for
resistance to reniform nematode in nine
crosses of castor

Cross	Source	d.f.	Mean sum of squares
I	Replication	2	2.662
	Generation	5	96.530**
	Error	10	0.467
II	Replication	2	0.082
	Generation	5	16.799**
	Error	10	1.181
III	Replication	2	0.164
	Generation	5	34.285**
	Error	10	3.922
IV	Replication	2	4.425*
	Generation	5	119.348**
	Error	10	0.827
V	Replication	2	0.218
	Generation	5	2.558
	Error	10	1.023
VI	Replication	2	1.677
	Generation	5	13.248**
	Error	10	1.816
VII	Replication	2	5.292
	Generation	5	25.169**
	Error	10	3.364
VIII	Replication	2	0.007
	Generation	5	3.004**
	Error	10	0.501
IX	Replication	2	0.051
	Generation	5	1.621**
	Error	10	1.417

* and ** indicate significance at 5 and 1 % levels of
significance, respectively

Appendix III: Analysis of variance of six generations for various characters in six crosses of castor

		Mean sum of squares												
Cross	Source	d.f.	Days to flowering of main raceme	Number of nodes upto main raceme	Plant height (cm)	Number of total branches/ plant	Number of effective branches/ plant	Length of main raceme (cm)	Number of capsules in main raceme	Seed yield/ plant (g)	100 seed weight (g)	Oil content (%)		
I	Replication	2	11.859	0.497	116.406	14.830	3.158	17.555	102.245	210.977	15.902**	0.068		
	Generation	5	106.425**	8.138**	1255.863**	4.546	4.845	33.538*	161.551*	2382.987**	22.607**	1.030**		
	Error	10	14.859	0.810	215.125	4.144	6.032	7.043	42.461	238.857	1.362	0.129		
II	Replication	2	99.266*	1.209	303.992*	11.039	17.179**	3.495	40.082	1323.317*	33.082*	0.408**		
	Generation	5	45.469	12.128**	2149.384**	9.724	6.703*	11.796*	74.997**	1721.289**	32.225*	1.821**		
	Error	10	21.355	1.405	70.388	3.467	1.952	3.517	16.967	259.781	5.826	0.040		
III	Replication	2	76.305*	1.555	133.027**	8.679	8.873	23.820**	9.798	1020.492	0.044	0.013		
	Generation	5	170.764**	31.090**	5917.738**	76.518**	76.660**	10.496*	117.178**	4825.530**	4.382**	11.346**		
	Error	10	15.029	0.507	7.726	8.401	8.315	2.070	17.070	442.640	0.716	0.431		
IV	Replication	2	9.879	0.938	13.508	22.169**	10.532*	13.730	40.135*	87.791	6.488	0.465		
	Generation	5	11.123	0.522	1025.423**	15.914**	7.146	26.950	31.084*	1953.334**	3.854	4.212**		
	Error	10	26.883	1.817	8.727	2.390	2.421	12.160	7.310	112.799	1.658	0.503		
V	Replication	2	8.219	0.268	17.813	6.374	2.362	9.058	4.927	454.810	0.628	0.013		
	Generation	5	118.323*	17.046**	2479.269**	9.461	11.699	23.742	23.240	1503.148	1.289	1.275**		
	Error	10	30.257	1.357	117.280	9.983	5.788	7.996	16.145	461.895	1.399	0.171		
VI	Replication	2	98.828*	1.068	128.617	7.310	9.707	21.570	1.571	1954.938*	2.684	0.305		
	Generation	5	162.817**	14.209**	2808.997**	35.066**	26.921*	58.146*	52.149*	4409.114**	28.161**	6.542**		
	Error	10	20.373	1.091	92.542	7.264	5.199	12.955	9.548	333.414	1.675	0.770		

* and ** indicate significance at 5 and 1 % levels of significance, respectively.