

**CHARACTERISATION OF CASTOR GERMPASM**  
(*Ricinus communis* L.,)

**By**

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## **DECLARATION**

I, **Mr. M. SRINIVASA RAO**, hereby declare that the thesis entitled “**CHARACTERISATION OF CASTOR GERMPLASM** (*Ricinus communis* L.)”, submitted to **Acharya N. G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** in the major field of **Genetics and Plant Breeding** is the result of original research work done by me. I also declare that any material in the thesis has not been published earlier.

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## **CERTIFICATE**

**Mr. M. SRINIVASA RAO** has satisfactorily prosecuted the course of research and that the thesis entitled “**CHARACTERISATION OF CASTOR GERMPLASM (*Ricinus communis* L.)**” submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part thereof has not been previously submitted by his for a degree of any university.

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## LIST OF SYMBOLS AND ABBREVIATIONS

ANOVA	:	Analysis of variance
ARS	:	Agricultural Research Station
CV	:	Coefficient of variation
GA	:	Genetic advance
GAM	:	Genetic advance as percent of mean
GCV	:	Genotypic coefficient of variation
NS	:	Non-significant
PCV	:	Phenotypic coefficient of variation
RARS	:	Regional Agricultural Research Station
S	:	Significant
UAS	:	University of Agricultural Sciences
%	:	Per cent
<sup>0</sup> C	:	Degree Celcius
Df	:	Degrees of freedom
<i>et al.,</i>	:	and others
F <sub>1</sub>	:	First generation hybrid of a cross
g	:	Grams
h <sup>2</sup> b	:	Heritability in broad sense
h <sup>2</sup> n	:	Heritability in narrow sense
Kg/ha	:	Kilogram per hectare
No.	:	Number
<i>viz.,</i>	:	Namely
2D	:	Two dimensional
3D	:	Three dimensional

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### **ABSTRACT**

An investigation on Characterization of Castor Germplasm was carried out during *kharif*, 2008-2009 at Agricultural College farm, Bapatla with 54 genotypes of castor (*Ricinus communis* L.) germplasm.

The genotypes were characterized for 12 morphological characters *viz.*, stem colour, types of inter nodes on stem, plant branching pattern, petiole colour, lamina colour, bloom, type of inflorescence, colour of stigma, capsule type, spike shape, spike compactness and seed colour as per DUS guidelines of castor.

The mean, variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of yield component traits with seed yield per plant upto 180 days were studied for 28 characters *viz.*, days to 50% flowering of primary raceme, stem length to primary raceme, number of nodes to primary raceme, total length of primary raceme, effective length of primary raceme, days to 80% maturity of primary raceme, number of secondary branches per plant, days to 50% flowering of secondary raceme, number of nodes to secondary raceme, stem length to secondary raceme, total length of secondary raceme, effective length of secondary raceme, days to 80% maturity of secondary raceme, number of tertiary branches per plant, days to 50% flowering of

tertiary raceme, number of nodes to tertiary raceme, stem length to tertiary raceme, effective length of tertiary raceme, days to 80% maturity of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, L / B ratio of seed, harvest index, seed yield per plant at 120 days, seed yield per plant upto 150 days and seed yield per plant upto 180 days.

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the modifying effect of the environment in association with the characters at genotypic level. High PCV coupled with high GCV observed for traits *viz.*, days to 50% flowering of primary raceme, stem length to primary raceme, nodes to primary raceme, total length of primary raceme, effective length of primary raceme, nodes to secondary raceme, stem length to secondary raceme, total length of secondary raceme, effective length of secondary raceme, tertiary branches per plant, stem length to tertiary raceme, effective length of tertiary raceme, seed yield per plant at 120 days, seed yield per plant up to 150 days, and seed yield per plant up to 180 days. High heritability coupled with high genetic advance as per cent of mean was observed for all the traits except for days to 80% maturity of tertiary raceme, oil content, L / B ratio and harvest index indicates operation of additive gene action in inheritance of these traits.

Correlation study indicated that total length of primary raceme, effective length of primary raceme, total length of secondary raceme, effective length of secondary raceme, tertiary branches per plant, nodes to tertiary raceme, stem length to tertiary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, harvest index, seed yield per plant at 120 days, and seed yield per plant up to 150 days showed significant positive association with seed yield per plant upto 180 days. So improvement in seed yield is possible by taking above characters in the selection scheme.

Path coefficient analysis revealed that harvest index, seed yield per plant up to 150 days, tertiary branches per plant and 100 seed weight of primary raceme exerted highest direct positive effect and positive significant association with seed yield per plant upto 180 days.

The results of multivariate analysis revealed that the presence of considerable genetic divergence among the 54 genotypes studied and grouped into 9 clusters as per  $D^2$  analysis and 8 clusters in case of principal component analysis was at random, which suggested that geographical isolation might not be the only factor causing genetic diversity.

By Mahalanobis'  $D^2$  statistic, it could be inferred that the traits effective length of tertiary raceme, days to 50 percent flowering of tertiary raceme, stem length to tertiary raceme, seed yield per plant at 120 days contributed maximum towards genetic divergence. Based on the intra and inter-cluster distances among the groups, suggestions were made to attempt crosses to obtain new desirable recombinants in castor between the genotypes of clusters VI and IX followed by clusters I and IX.

Principal component analysis identified five principal components (PCs), which contributed 89.39 per cent of cumulative variance. The population with high PC 1 values was characterized by effective length of tertiary raceme, where as population with high PC 2 values was characterized by seed yield per plant at 120 days. In PC 3 characters like harvest index showed maximum weightage.

Agglomerative cluster analysis showed that wide genetic distance exists between clusters III and IV followed by clusters III and VI. Therefore during hybridization programme selection of parents from these clusters will produce superior segregants. Dendrogram obtained by cluster analysis showed the sub-grouping of genotypes within the cluster which is not possible through  $D^2$  analysis.

## CHAPTER I

### INTRODUCTION

Castor (*Ricinus communis L.*) with  $2n=20$ , an important industrial non edible oil seed crop belongs to the family *Euphorbiaceae* and indigenous to Eastern Africa. Its oil is being used in various industries for manufacturing of lubricants, synthetics and resins, and fibres; in soap industry; in textile industry for dyeing and fining; ointments; cosmetics; for plasticizing oil cloth and artificial leather. It is also being used for medicinal and lighting purpose. Castor meal and hulls are used as fertilizer and preparation of good quality, active carbon, respectively.

Castor is cultivated in an area of about 1.41 million hectares in world with an annual production of 1.39 million tones. India is the world's principal producer of castor and ranks first in both area and production in the world. Besides meeting the domestic demands, in the year 2008-09, India exported castor oil worth of Rs. 1821.57crores. Castor productivity in India is more than the world average and it ranks first among the major producing countries viz., China and Brazil (AICRP on Castor, DOR 2006). In India, castor crop occupies an area of about 7.86 lakh hectares with a production of 10.53 lakh tones and the productivity of 1338 kg/ha. In Andhra Pradesh, it is grown in area of 1.99 lakh ha with production of 1.29 lakh tones. The productivity level of castor in Andhra Pradesh is poor (648 kg/ha) compared to that of Gujarat (1977 kg/ha). (Indiastat 2009).

Plant breeders are constantly using various biometrical techniques to have a greater understanding of nature of gene action for various quantitative traits to plan an effective breeding programme for the improvement of seed yield and oil yield. There is always a need for replacing the existing varieties with high yielding varieties of various maturity durations coupled with biotic and abiotic stress tolerance and quality in order to meet the ever increasing demand for the various value added products.

Before launching any breeding programme, a thorough knowledge of the nature and magnitude of genetic variability, heritability, genetic advance, genetic divergence and association of character in a crop species is essential. Even in the association of the characters information regarding the direct and indirect effects contributing by each character to yield will be an added advantage for crop improvement.

Morphological characterization of seed, seedling and plant would generally be considered for varietal identification. Introduction of Plant Variety Protection under General Agreement on Trade and Tariff (GATT) necessitated the need for precise genotypic characterization with clear Distinctiveness (D), Uniformity (U), Stability (S). The concept of DUS was fundamental to the characterization of the variety as a unique creation. It is essential to secure Plant Breeder's Rights (PBR) and it also generates official description of a variety. Information on DUS characters of the parental lines generated in castor is not documented until now. Hence, there is a need to characterize castor genotypes.

Assessment of variability present in any crop species is essential pre requisite for formulating an effective breeding programme. The existing variability can be used to further enhance the yield level of the cultivars following the appropriate breeding strategies. Estimation of genetic variability does not give a clear indication of the possible improvement that can be achieved through selection and it should be used in conjunction with heritability and genetic advance. Studies on genotypic coefficient of variation enables to compare the amount of variability present in different characters. Heritability is the measure of transmission of characters from generation to generation and estimates of heritability may be of some help to the breeder in selecting superior individuals and successfully utilizing them in breeding programme.

Correlation is the measure of the mutual relationship between two variables. It is a measure of the degree of closeness and the linear relationship between the two variables. The study of correlations may help the plant breeder to know how the improvement of one character will bring simultaneous improvement in other characters.

Path coefficient analysis is a standardized regression coefficient and measures the direct influence of one variable upon another. Direct selection for yield is not reliable approach since it is influenced by the environment. Therefore it is essential to identify the component characters through which yield can be improved.

The nature and magnitude of genetic divergence available in a species is essential for selection of desirable parents for hybridization. Mahalanobis'  $D^2$  statistic is an

effective tool in quantifying the degree of genetic divergence present in the material at genotypic level. It provides a quantitative measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1936).

The study on above aspects is essential to identify superior genotypes. The crosses between the genotypes with maximum genetic divergence would be responsible for improvement as they are likely to yield desirable recombinants in the progeny.

Hence an attempt has been made in the present investigation with the following objectives.

1. To study variability for yield and yield components.
2. To study the character association, direct and indirect effects of yield components on yield.
3. To estimate the genetic divergence in available germplasm to find out the important characters contributing to the genetic divergence.

## CHAPTER II

### REVIEW OF LITERATURE

Castor is one among the oilseeds which is having a high potential for non edible oil but lesser research work has been done for its potential exploitation. The literature available on the main objectives of the present study has been comprehensively reviewed under the following heads.

2.1 Morphological characterization

2.2 Variability, heritability and genetic advance as per cent of mean

2.3 Genetic divergence

2.4 Correlations

2.5 Path analysis

#### **2.1 MORPHOLOGICAL CHARACTERISATION**

Varietal identification and genuineness of variety are very important during the development, maintenance and multiplication of new varieties, parental lines and hybrids. According to guidelines of International Union for the Protection of New Varieties (UPOV) each variety should have distinctiveness, uniformity and stability (DUS) *i.e.*, a new crop variety has to be distinct from other existing varieties and uniform in its characteristics which are genetically stable across the locations. Hence, continuous release of castor varieties and hybrids by Central and State Varietal Release Committee has warranted to develop techniques for varietal identification during

different crop growth stages and at post harvest, which would help to determine the extent of genetic purity.

The literature available on these aspects on castor is very meager. Hence, an attempt has been made to review the literature on important oil seed crops on these aspects.

Muhammad *et al.* (1971) developed a key for the identification of 154 castor cultivars based on their crop duration. The 120 genotypes were distinguished into 3 distinct types comprising of 16 short duration (< 150 days), 53 medium duration (151-195 days) and 51 long duration (> 196 days).

Jagdish *et al.* (1994) studied key diagnostic characters under field and laboratory conditions to distinguish sunflower parental lines and hybrids based on branching pattern, plant height, seed colour, shape, *etc.* and found that characters, seed colour, shape and number of leaves on main stem varied with genotypes studied.

Anita (1995) classified sunflower genotypes using seed characters *viz.*, seed shape, colour, 100-seed weight, seed size and plant characters like leaf shape, colour, margin, stem pubescence, branching, number of nodes, number of branches per plant, petiole colour, length of the petiole, plant height and head diameter.

Varier *et al.* (1999) identified four hybrids of castor and their parents based on seed shape, mottling on seed coat, shape and size of micropyle.

Rajendra Prasad *et al.* (2003) characterized ten hybrids of sunflower along with parental lines using morphological characters *viz.*, leaf size, leaf colour, leaf angle between lower part of petiole and stem, hairiness on leaf, petiole pigmentation, stem pigmentation, ray flower colour, shape, disc flower colour, bract shape, plant height, seed size, seed shape, seed length and seed base colour *etc.*

Rajeswari (2004) characterized and evaluated 16 genotypes of sunflower using 10 morphological characters *viz.*, leaf size, leaf colour, leaf angle between lower part

of petiole and stem, petiole pigmentation, ray flower colour, disc flower colour, branching, type of branching, seed shape, seed base colour and eight yield contributing characters *viz.*, plant height, days to 50 per cent flowering, days to maturity, head diameter, number of filled seeds per head, 100 seed weight, seed yield/plant and oil content.

In a study, twenty nine castor genotypes including varieties, parental lines and hybrids were characterized for their morphological characters, response to chemical tests and molecular characterization. The study identified 22 groups from 29 genotypes studied, of which 18 groups were constituted by single genotypes only; rest of the genotypes could be grouped into four groups. Most of the hybrids were similar to their parent except RCH 1 which is similar to its female parent VP-1 (NSP 2004, Technical Bulletin No. 25).

Characterisation is a part of the “Passport information” and has become an integral part of the permanent plant information record of germplasm. For describing each accession for its individual identity, 23 highly heritable and easily distinguishable morphological descriptors were developed in castor. Characterisation has helped in identification of rare localized and distinct morphotypes *e.g.* purple colour morphotype, papaya leaf type, which are useful as genetic markers. In addition, large morphological variability present in germplasm for leaf size, capsule colour and size, seed shape, colour and size *etc.* was also identified (AICRP on Castor, DOR 2006).

Malles (2007) characterized and evaluated 55 castor germplasm lines for 30 morphological characters. *VIZ.*, hypocotyl anthocyanin pigmentation, anthocyanin pigmentation of young emerging leaves, waxy bloom on upper side of leaf, waxy bloom on lower side of leaf, stem waxy bloom, stem colour, type of internodes on stem, length of 4<sup>th</sup> leaf from top (cm), time of flowering of primary spike (days), number of nodes on main stem, leaf shape, number of lobes on leaf, lacination of leaf,

petiole length (cm), petiole surface, plant branching pattern, location of branches, type of flowers on primary raceme, capsule spininess, capsule spine length, capsule length (cm), plant height upto primary spike, weight of 100 seeds (g), spike shape, spike compactness, seed shape, seed coat colour, seed mottling, seed caruncle, and oil content (%)

## **2.1 VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN**

### **2.1.1 Variability**

The information on the nature and magnitude of variability for both quantitative and qualitative traits in any crop species plays a major role in formulating an effective breeding programme and its success. Economic traits, which are polygenetically controlled and highly influenced by environment, determine the success in breeding programme through their genotypic variability. It is therefore essential to partition the over-all variability (total variability) into heritable and non-heritable components. Knowledge on the magnitude of heritability coupled with nature and extent of variability in the breeding material gives an idea for effective genetic improvement through selection. High PCV and GCV for a character indicate high variability in that population for that character (Singh, 1998).

The available literature on variability in *Ricinus communis* L. was presented in Table 1.

### **2.1.2 Heritability and Genetic advance as per cent of mean**

Hanson *et al.* (1956) defined heritability in broad sense as the ratio of genotypic variance to the total genetic variance in the non-segregating populations. Heritability ( $h^2$ ) measures the relative amount of heritable portion of the variability, while genetic

advance (GA) indicates the amount of progress that can be expected with selection in a character. Johnson *et al.* (1955) reported that estimates of both heritability and genetic advance are more useful in the choice of selection method rather than heritability or genetic advance alone. High heritability coupled with high genetic advance indicates additive gene effect (Johnson *et al.*, 1955) and improvement could be made for that character by simple selection based on phenotypic performance. Low genetic advance irrespective of high or low heritability leads to non-additive gene action (Panse, 1957) and improvement of that trait by simple selection may not be rewarding (Verma *et al.*, 1987).

The available literature on heritability and genetic advance in *Ricinus communis* L. is presented in Table 2.

## **2.3 GENETIC DIVERGENCE**

### **2.3.1 Mahalanobis' $D^2$ analysis**

A knowledge on the nature and the magnitude of genetic variability present in the crop species will play an important role in formulating a successful breeding programme. It has been known that greater the genetic variability present in the plant population greater will be the chances of obtaining the desirable gene combinations.

Mahalanobis'  $D^2$  statistics is an effective tool in quantifying the degree of genetic divergence at the genotypic level and provides measure of association between geographic distribution and genetic diversity based on generalized distance (Mahalanobis, 1928).

Divergence analysis is performed to identify the diverse genotypes for hybridization purposes. Clustering by  $D^2$  statistic is useful in this matter. The genotypes grouped together are less divergent than the ones, which fall into different

clusters. Three important points are to be considered while selecting genotypes for hybridization purpose.

- 1) Choice of the particular cluster from which genotypes are to be used as parents.
- 2) Selection of particular genotype from selected cluster.
- 3) Relative contribution of characters towards total divergence.

Clusters separated by largest statistical distance ( $D^2$ ) show maximum divergence (Singh and Chaudhary, 1977).

The available literature indicated that limited research work has been carried out on genetic divergence in castor. Hence the literature pertaining to other oilseed crops are also presented below.

Using  $D^2$  analysis and canonical analysis Singh and Srivastava (1978) studied 17 varieties of castor and grouped into seven clusters. Close relation observed between genetic divergence and geographical diversity.

Ratinaswamy and Jagathesan (1983) conducted a study to determine genetic diversity in sesame using Mahalanobis'  $D^2$  and canonical analysis. The results indicated that genetic divergence was not influenced by seasonal changes, absence of relationship between the divergence of parents as measured by generalized distance and extent of superiority of  $F_1$ 's over their better parents.

Bhatt and Reddy (1987) estimated genetic diversity in castor by using Mahalanobis'  $D^2$  statistic and canonical analysis and observed 26 clusters formed from 50 varieties. The geographical distribution is not related to genetic diversity. The traits

*viz.*, seed yield per plant, seed weight, node number and plant height were the main contributors towards genetic divergence.

Sodani *et al.* (1990) assessed the genetic divergence of 99 lines of taramira and grouped them into 13 clusters. Grouping of lines into different clusters was not related to their geographic origin. Pods per plant, seed yield per plant, seed yield per plot and test weight contributed maximum towards divergence.

Using Mahalanobis'  $D^2$  statistic Sharma and Mehta (1991) grouped 50 soybean cultivars into 10 and 8 clusters when grown in monoculture and intercropped with maize, respectively. Some cultivars had similar clustering patterns in both the cropping systems, while others showed inconsistent clustering patterns. The study showed no association between geographical origin and clustering pattern.

Ghatge and Kadu (1993) grouped 58 strains of soybean into 7 clusters by using Mahalanobis'  $D^2$  statistic. The clustering pattern revealed that genetic diversity was not necessarily associated with geographical diversity.

Kumar and Nadarajan (1994) grouped 64 soybean genotypes of diverse origin into 11 clusters and observed that the genotypes from different geographical locations were grouped into a single cluster, while the genotypes of the same geographical origin were grouped into different clusters indicating that the genetic diversity is not associated with geographical origin.

Using Mahalanobis'  $D^2$  statistic, Dobhal (1995) grouped 65 soybean genotypes for 12 yield components into 17 clusters. No linear relationship between geographic and genetic divergence was observed. Canonical analysis revealed higher contribution of yield per plant, number of pods per plant, pods per cluster, pod length and seeds per pod towards the total genetic divergence.

Muppidathi *et al.* (1995) assessed genetic divergence of 121 inbreds of sunflower by using Mahalanobis'  $D^2$  statistic and grouped them into 9 clusters. Grouping of clusters was not related to their geographic origin. Seed yield, head diameter and self-fertility percentage contributed maximum towards total genetic divergence.

Mahalanobis'  $D^2$  statistic conducted in 60 indigenous and exotic soybean genotypes by Sharma *et al.* (1995). The 60 genotypes were grouped into 6 clusters. No significant relationship between geographical origin and genetic diversity was observed. On the contrary, the genotypes originating at the same place showed wide genetic diversity.

Bera and Das (1999) grouped 28 genotypes of groundnut into 5 clusters at two locations *viz.*, Midnapur and Purulia. The first two clusters accounted for about 55% and 70% of total variability for Midnapur and Purulia, respectively. Pod yield per plant, harvest index and 100 seed weight were major contributors towards total genetic divergence. The genotypes grouped together were of diverse origin for both locations and cluster composition. Intercluster genetic divergence varied with change in location.

Chakrabarty and Banu (1999) studied 16 pistillate castor genotypes for their genetic divergence and grouped them into five clusters. The study revealed that the pistillate base in castor has diversified considerably and could be exploited in hybrid breeding programmes.

Sevagaperumal *et al.* (2000) grouped 36 castor genotypes into 10 clusters by using Mahalanobis'  $D^2$  statistics. The study revealed that single plant yield contributed maximum followed by plant height and 100 seed weight towards the total genetic divergence. The study suggested that hybridization between the genotypes from the cluster seven (TRC207, TRC223 and Bhagya) and nine (TMV 3 and Aruna) with

maximum inter cluster distance are responsible for resulting highly heterotic hybrids and show wide spectrum of variability in subsequent segregation generations. The results clearly indicated that there is no parallelism between the geographic diversity and genetic diversity in castor.

Mahalanobis'  $D^2$  statistic conducted in 19 genotypes of castor by Venkataramaiah *et al.* (2000). The 19 genotypes were grouped into 8 clusters. No significant relationship between geographical origin and genetic diversity was observed. Considerable genetic variability observed in the material which led to genetic diversity.

Lakshamma *et al.* (2002) studied 68 diverse genotypes of castor for genetic diversity. Their studies revealed that intra cluster distance was maximum for cluster V. Inter cluster distance was the highest between clusters II and III, cluster II and V and clusters II and VI. Depending upon the intra cluster distance, cluster mean value and mean performance, cross combinations involving RG 1633 x RG 173, RG 1633 x RG 1611, RG 1611A and VP-1 x RG 1633 were suggested to achieve novel recombinants and superior population having high seed yield. The genotype TNHAP 179 (cluster XV), and 1149-2-1 (cluster XVII), were selected for intermating among themselves to produce wider segregation.

Using Mahalanobis'  $D^2$  statistic, Rogde *et al.* (2003) grouped 36 genotypes of sesame into 7 clusters. The clustering pattern indicated that there was no relationship between genetic diversity and geographic diversity. Number of seeds per capsule, harvest index and oil content contributed more towards total divergence.

Roy and Ali (2003) reported  $D^2$  analysis of 18 sunflower hybrids and grouped them into 8 clusters. Among the characters studied, days to 50 % flowering and days

to maturity contributed maximum (19.61 %), to the genetic diversity, followed by a contribution of yield per plot (14.4 %).

Komaraiah *et al.* (2004) evaluated 101 sunflower genotypes for their genetic divergence using  $D^2$  analysis and grouped them into 10 clusters. The number of filled seeds per head contributed highest towards genetic divergence followed by plant height, number of unfilled seeds, days to maturity, oil content, seed yield, days to 50 per cent flowering, number of leaves and head diameter.

Rao (2004) grouped 72 sesame genotypes into 10 clusters by using multivariate  $D^2$  statistic. The study indicated that capsules per plant, days to maturity, 1000 seed weight and seed yield contributed maximum towards total genetic divergence.

Anuja Gutha *et al.* (2005) evaluated 35 genotypes of castor for genetic diversity using Mahalanobis'  $D^2$  statistic and grouped them into six clusters. The number of capsules on main spike contributed maximum towards genetic divergence followed by plant height and 100-seed weight. Hierarchical cluster analysis resulted into six clusters containing one to twenty four genotypes. The best clusters with regard to seed yield and oil content were cluster V and IV.

Using multivariate analysis, Thirumala Rao *et al.* (2005) studied the degree of divergence in 94 sunflower genotypes for 10 characters. The study revealed that genetic diversity and geographical diversity are not related. The characters contributed maximum to genetic divergence are plant height, oil content and test weight.

Ravi *et al.* (2006) evaluated 66 genotypes of sunflower and grouped them into 9 clusters. The genotypes grouped into various clusters revealed that there was no relationship between geographical distribution and genetic diversity. The traits seed set under self pollination, total dry matter per plant and seed yield per plant contributed more towards genetic divergence.

Singh *et al.* (2006) studied 23 genotypes of Indian mustard for genetic diversity and grouped them into five clusters. The study revealed that intra cluster distance was maximum for cluster I. Inter cluster distance was highest between cluster II and IV, cluster IV and I. On the basis of  $D^2$  analysis, it would be desirable to cross the parents from cluster I and II with that of cluster III(vaibhar), IV (seta) and V(sej-2) to achieve novel recombinants and superior population having high seed yield.

Solanki *et al.* (2006) estimated genetic diversity in Indian mustard by using Mahalanobis'  $D^2$  statistic and observed six clusters from 32 genotypes. The results showed that geographical diversity was not necessarily a direct cause of genetic diversity. Plant height contributed maximum to the total divergence (40.5) followed by days to maturity.

Srinivas *et al.* (2006) grouped 45 sunflower genotypes into 9 clusters by using Mahalanobis'  $D^2$  static. Days to maturity, 100 seed weight and leaf area index contributed maximum towards total genetic divergence.

Wang *et al.* (2007) explored the potential possibility of using castor for bio-diesel production. Out of 1034 accessions, they have selected 48 accessions as source for bio-energy in the USA. The evaluation for divergence was done with Amplified Fragment Length Polymorphism (AFLP) and DNA markers.

Allan *et al.* (2008) studied worldwide genetic diversity in 200 individuals comprising 41 castor bean accessions and assessed using amplified fragment length polymorphisms (AFLPs) and simple sequence repeats (SSRs). The study found that despite surveying five continents and 35 countries, genetic diversity in castor bean germplasm is relatively low compared to estimates of genetic diversity in other plant species.

Kanchan Kumari and Rao *et al.* (2008) grouped 90 diverse linseed genotypes into 9 clusters by using Mahalanobis'  $D^2$  statistic. The inter cluster distance was maximum

clusters VI and VII followed by clusters VI and IX and clusters III and VI. Based on inter cluster distance and cluster means the genotypes from clusters VI and VII could be selected for hybridization programme to obtain high heterotic expression and also to recover desirable transgressive segregants.

Using multivariate analysis Manjaya *et al.* (2008) studied the nature of divergence in 55 soybean genotypes for 9 characters. The characters contributed to genetic diversity are days to maturity, harvest index, plant height and 100 seed weight.

Using Mahalanobis'  $D^2$  statistic Patel *et al.* (2008) grouped 60 genotypes of sesamum into clusters. No relationship between geographical diversity and genetic divergence was observed. Branches per plant, plant height and seed yield per plant contributed more towards total divergence.

### **2.5.2 Principal component analysis and cluster analysis**

Principal component analysis was carried out to transform the interdependent traits into a set of independent traits as well as to reduce the dimensionality of the data structure (Banfield ,1978) . It is defined as a method of data reduction to clarify the relationship between two or more characters into limited number of uncorrelated new variables. The reduction is achieved by linear transformation of the original characters into a new set of uncorrelated variables known as Principal Components (PCs).

Brown (1991) used Principal Component, Hierarchical Cluster Analysis for the data from seven of the nine regions of Regional Cotton Variety Tests across the U.S. cotton belt. The 3D plots displayed results of the principal component analysis, while results from Ward's minimum variance clustering were presented as dendrograms.

Altaher and Singh (2003) estimated genetic divergence in 40 genotypes of upland cotton by using Principal Component Analysis. Clustering based on PCA scores

separated the genotypes into six clusters. Cluster II was the largest cluster with 28 genotypes from different agro-climatic zones, indicating that geographical diversity is not always associated with the genetic diversity.

Anuja Gutha *et al.* (2005) evaluated for genetic diversity in 35 castor genotypes. Principal component analysis identified three principal components which explained 77.7% variability in castor. The principal component analysis enabled loading of similar type of variables on common principal component. Genotypes RG 2854, RG2777, RG 2850 and RG 279 (based on PC 1 axis) were found better performers.

Karunakar Raju *et al.* (2005) used cluster analysis and PCA to estimate genetic divergence in 80 genotypes of upland cotton. Five principal components, which had a cumulative variation 74.48% formed the basis for divergence of genotypes into nine clusters.

Muraleedhar *et al.* (2005) assessed the genetic divergence among 50 genotypes of tetraploid cotton using PCA and cluster analysis. The five principal components, which had a cumulative variation of 89.22% formed the basis for divergence of genotypes into eight clusters.

Based on multivariate analysis, Bahia *et al.* (2008) determined the genetic divergence using cluster analysis and principal components analysis. Three groups were formed, and the one which comprised the more divergent cultivar Mirante 10, is not recommended for hybridization due to its low performance. The promising combinations were those found between Sipeal 28 X BRS 149 Nordestina and EBDA MPA 17 X BRS 149 Norstina, due to the dissimilarity and the best average performance of these genotypes.

Vijaya Laxmi (2008) used cluster analysis and PCA to estimate genetic divergence in 72 genotypes of upland cotton. The PCA identified seven principal components which contributed 87.47% of cumulative variance. The population with high PC<sub>1</sub> values were characterized by high number of bolls per plant, where as population with high PC<sub>2</sub> values were characterized by boll weight.

## **2.4 CORRELATIONS**

Correlation refers to the degree and direction of association between two or more variables. Correlation studies are useful in developing an effective basis of phenotypic selection in plant populations. Yield is polygenically controlled character with low heritability hence direct selection is not effective. Yield improvement could be achieved by indirect selection. Further, knowledge of genetic correlations among the characters contributing to the yield leads to the most effective method of selection. By this way combinations of favorable characters could be brought out by minimizing the retarding effect of antagonistic relations. When attempts are made to establish correlations, it is essential to calculate the coefficient of correlation between the characters of interest with an account for the type of variability *viz.*, environmental, genotypic and phenotypic.

### **2.4.1 Association of component characters with yield**

The literature available on association of yield component characters with yield was presented in Table 3.

### **2.4.2 Association among yield component characters**

The literature on the association among the yield component characters was presented in Table 4.

## CHAPTER - III

### MATERIALS AND METHODS

The present investigation was carried out during *khariif* 2008-09 at Agricultural College Farm, Bapatla, Guntur (Dt.), Andhra Pradesh, located at an altitude of 5.4m MSL, 15°54`N latitude and 80°90`E longitude. The soil is black cotton type with clay texture. The material used and methods adopted in the present investigation are briefly described below.

#### 3.1 MATERIAL

The experimental material used in the present study comprised 54 diverse genotypes of *Ricinus communis* (L.) obtained from Regional Agricultural Research Station (RARS), Palem. The list of genotypes are presented in Table7.

#### 3.2 METHODS

##### 3.2.1 Experimental Details

The details of experimental techniques followed for the present investigation are furnished in Table 8. The experiment was conducted in a randomized block design with two replications. Each genotype was sown in three rows of 3 m length with a row to row spacing of 90 cm and plants spaced at 60 cm within a row. Recommended package of practices was adopted to raise a good crop.

A basal dose of 60 Kg N/ha, 40 Kg P<sub>2</sub>O<sub>5</sub>/ha, 30 Kg K<sub>2</sub>O/ha and 60 Kg N/ha was applied 30 days after sowing. Irrigation, weeding and plant protection operations were taken up as and when needed during the crop growth. The racemes of genotypes were

harvested as and when the colour of capsules changed from green to yellowish brown and few capsules started drying.

### **3.2.2 Record of Observations**

Ten plants of each genotype in each replication were chosen at random and labeled for recording observations. Single plant observations were recorded on 28 quantitative characters and the mean of the ten plants was used for statistical analysis and 12 qualitative characters were observed. The characters considered for present investigation are listed below.

#### **3.2.2.1 Quantitative characters**

##### **3.2.2.1.1 Days to 50% flowering of primary raceme**

Days taken from the date of sowing to the date of initiation of flowering of primary spike were recorded when 50 percent of the plants had initiated flowering.

##### **3.2.2.1.2 Plant height upto primary raceme (cm)**

Plant height was recorded in centimeters from ground level up to the base of the primary spike.

##### **3.2.2.1.3 Number of nodes upto primary spike**

Total number of nodes on the main shoot, from the ground level up to the point where the main spike emerged was recorded.

#### **3.2.2.1.4 Total length of primary raceme (cm)**

The length of primary spike was recorded in centimeters from where it was emerged to the tip of the spike at the maturity.

#### **3.2.2.1.5 Effective length of primary raceme (cm)**

The length of primary spike recorded in centimeters from where capsules have actually formed to the tip of the spike

#### **3.2.2.1.6 Days to 80% maturity of the primary raceme**

The number of days taken by each genotype's primary raceme to turn 80 % of its capsules from green to light yellow was recorded.

#### **3.2.2.1.7 Number of secondary branches per plant**

The total numbers of secondary branches having effective spikes were recorded.

#### **3.2.2.1.8 Days to 50% flowering of secondary raceme**

Days taken from the date of sowing to the date of initiation of flowering of secondary spike were recorded when 50 percent of the plants had initiated flowering.

#### **3.2.2.1.9 Number of nodes to secondary raceme**

Total number of nodes present on each effective secondary branch was recorded and taken mean of all the secondary branches.

#### **3.2.2.1.10 Plant height to secondary raceme (cm)**

Plant height was recorded in centimeters from the base of the primary raceme to the base of the secondary raceme.

#### **3.2.2.1.11 Total length of secondary raceme (cm)**

The length of secondary spike recorded in centimeters from where it was emerged to the tip of the spike.

#### **3.2.2.1.12 Effective length of secondary raceme (cm)**

The length of secondary spike recorded in centimeters from where capsules have actually formed to the tip of the spike.

#### **3.2.2.1.13 Days to 80% maturity of the secondary raceme**

The number of days taken by each genotype's secondary raceme to turn 80 % of its capsules from green to light yellow was recorded.

#### **3.2.2.1.14 Number of tertiary branches per plant**

The total numbers of tertiary branches having effective spikes were recorded.

#### **3.2.2.1.15 Days to 50% flowering of tertiary raceme**

Days taken from the date of sowing to the date of initiation of flowering of tertiary spike were recorded when 50 percent of the plants had initiated flowering.

#### **3.2.2.1.16 Number of nodes to tertiary raceme**

Total number of nodes present on each effective tertiary branch was recorded and taken mean.

#### **3.2.2.1.17 Plant height to tertiary raceme (cm)**

Plant height was measured in centimeters from secondary raceme to the base of the tertiary raceme.

#### **3.2.2.1.18 Effective length of tertiary raceme (cm)**

The length of tertiary spike recorded in centimeters from where capsules have actually formed to the tip of the spike.

#### **3.2.2.1.19 Days to 80% maturity of the tertiary raceme**

The number of days taken by each genotype's tertiary raceme to turn 80 % of its capsules from green to light yellow was recorded.

#### **3.2.2.1.20 100 - seed weight primary raceme (g)**

One hundred randomly selected seeds from the bulk of the seed yield of primary raceme were weighed after thorough sun drying at an optimum moisture level of 10%.

#### **3.2.2.1.21 100 - seed weight secondary raceme (g)**

One hundred randomly selected seeds from the bulk of the seed yield of secondary raceme were weighed after thorough sun drying at an optimum moisture level of 10%.

#### **3.2.2.1.22 100 - seed weight tertiary raceme (g)**

One hundred randomly selected seeds from the bulk of the seed yield of tertiary raceme were weighed after thorough sun drying at an optimum moisture level of 10%.

#### **3.2.2.1.23 Oil content (%)**

Oil content in seeds was estimated using machine (NIR) at Agricultural College, Bapatla and expressed as per cent.

#### **3.2.2.1.24 L/B ratio of the seed**

Length and breadth was measured with the help of verniere calipers in centimeters and ratio was taken.

#### **3.2.2.1.25 Harvest index**

The ratio of seed yield per plant to the biological weight per plant. (Capsule weight + plant dry weight) expressed as a percentage of each plant .

$$HI = \frac{\text{Single plant seed yield (g)}}{\text{Total plant dry weight (g)}} \times 100$$

#### **3.2.2.1.26 Seed yield upto 120 days (g)**

Seed yield was obtained from ten individual plants, picking wise at 120 days after sowing and expressed in g/plant.

#### **3.2.2.1.27 Seed yield upto 150 days (g)**

Seed yield was obtained from ten individual plants, up to 150 days after sowing and expressed in g/plant.

#### **3.2.2.1.28 Seed yield upto 180 days (g)**

Seed yield was obtained from ten individual plants, up to 180 days after sowing and expressed in g/plant.

### **3.2.2.2 Qualitative characters**

Morphological characters were recorded as per National Test guidelines for DUS on castor. The qualitative characters were recorded as visual assessment by a single observation of a group of plants or parts of plants (VG) or individual plants or parts of plants (VS). The quantitative characters are measured by a single observation of a group of plants or parts of plants (MG) or single plants or parts (MS). It was ensured that the number of aberrant plants or parts of plants should not exceed 5 per cent in the genotype.

#### **3.2.2.2.1 Stem colour**

Stem colour was observed before flowering stage and grouped as green, red, and dark red.

#### **3.2.2.2.2 Type of internodes on stem**

It was observed visually on group of plants before flowering stage and grouped as condensed and elongated (normal).

#### **3.2.2.2.3 Plant branching pattern**

It was observed visually on group of plants at flowering stage and grouped as convergent and divergent type.

#### **3.2.2.2.4 Petiole colour**

Petiole colour was observed before flowering stage and grouped as green, green with reddish tinge, red and dark red.

#### **3.2.2.2.5 Lamina colour**

Lamina leaf colour was observed before flowering stage and grouped as green, dark green and green with reddish tinge.

#### **3.2.2.2.6 Bloom**

It was observed visually on group of plant in emerging fresh leaves and grouped no bloom, single bloom, double bloom, and triple bloom.

#### **3.2.2.2.7 Type of inflorescence**

It was observed visually on group of plants at flowering stage and grouped as monoecious, interspersed staminate flowers (ISF)

#### **3.2.2.2.8 Colour of the stigma**

It was observed visually on group of plants at flowering stage and grouped as pink, red and dark red.

#### **3.2.2.2.9 Capsule type**

Capsule spiniess was observed visually on group of plants at dough grain stage and grouped as non spiny and spiny.

#### **3.2.2.2.10 Spike shape**

Spike shape was observed visually on group of plants at dough grain stage and grouped as umbrella, cylindrical and conical stage.

#### **3.2.2.2.11 Spike compactness**

It was observed at dough grain stage and grouped as loose, semi-compact, compact.

#### **3.2.2.2.12 Seed colour**

Seed colour was observed after harvest and grouped as marron, brown, deep chocolate.

### **3.3 Statistical Analysis**

The data in respect of various characters were subjected to the following statistical techniques.

#### **3.3.1 Analysis of variance**

The analysis of variance for each character was done as per the standard statistical procedure given by Cochran and Cox (1950) for randomized block design.

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

where,

- $Y_{ij}$  = Performance of the  $j^{\text{th}}$  genotype in the  $i^{\text{th}}$  block.  
 $\mu$  = general mean  
 $b_i$  = effect of  $i^{\text{th}}$  block  
 $t_j$  = effect of  $j^{\text{th}}$  genotype  
 $e_{ij}$  = random error associated with  $i^{\text{th}}$  block and  $j^{\text{th}}$  genotype.

The analysis of variance for each character was carried out as indicated below:

Source of Variation	d.f.	SS	MSS	F. ratio
Replications	r-1	RSS	RSS/r-1 [ $Mr = \sigma_e^2 + \sigma_r^2$ ]	$M'r/M'e$
Treatments (Genotypes)	g-1	TrSS	TrSS/g-1 [ $Mg = \sigma_e^2 + \sigma_g^2$ ]	$M'g/M'e$
Error	(r-1) (g-1)	ESS	ESS/(g-1) (r-1) [ $Me = \sigma_e^2$ ]	
Total	(rg-1)	TSS		

- where ,  $r$  = Number of replications  
 $g$  = Number of genotypes  
 $df$  = Degrees of freedom  
 $SS$  = Sum of squares  
 $MSS$  = Mean sum of squares  
 $\sigma_e^2$  = Error variance

$\sigma_r^2$	=	Variance due to replications
M'r	=	Mean sum of squares due to replications
M'g	=	Mean sum of squares due to genotypes
M'e	=	Mean sum of squares due to error

The test of significance was carried out against the corresponding error degrees of freedom by using 'F' table values given by Fisher and Yates (1963)

### 3. 3.2 Estimation of genetic parameters

#### 3. 3.2.1. Coefficient of variation

Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953).

$$\text{Phenotypic standard deviation } (\sigma_p) = \sqrt{\sigma_p^2} = \sqrt{\sigma_g^2 + \sigma_e^2}$$

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\bar{X})} \times 100$$

$$\text{Genotypic standard deviation } (\sigma_g) = \sqrt{\sigma_g^2}$$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\bar{X})} \times 100$$

Categorization for GCV and PCV based on the range of variation as reported by Subramanian and Menon (1973) was followed.

Low	=	Less than 10%
Moderate	=	10-20%
High	=	More than 20%

### 3.3.2.2. Heritability in broad sense [ $h^2(b)$ ]

Heritability in broad sense was estimated as per Allard (1960).

$$h^2(b) = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

The range of heritability in broad sense [ $h^2(b)$ ] was classified as suggested by Johnson *et al.* (1955).

Low	=	Less than 30%
Moderate	=	30-60%
High	=	More than 60%

### 3.3.2.3. Genetic advance (GA)

This was estimated as per the formula proposed by Lush (1940) and Johnson *et al.* (1955).

$$GA = K \times \sigma_p \times h^2(b)$$

Where,

K = Selection differential at 5 per cent selection intensity  
which accounts to a constant value 2.06

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

$\sigma_p$  = Phenotypic standard deviation

### 3.3.2.4. Genetic advance as per cent of mean (GAM)

$$\text{GAM} = \frac{\text{GA}}{\text{Grand mean } (\bar{X})} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et. al.* (1955).

Low	=	Less than 10%
Moderate	=	10 - 20%
High	=	More than 20%

### 3.3.3 GENETIC DIVERGENCE

#### 3.3.3.1. Mahalanobis D<sup>2</sup> analysis

The data collected on different characters were analysed through Mahalanobis D<sup>2</sup> analysis to determine the genetic divergence among the genotypes (Mahalanobis, 1928).

D<sup>2</sup> value between i<sup>th</sup> and j<sup>th</sup> genotypes for 'P' characters was calculated as

$$D_{ij}^2 = \sum_{t=1}^P (Y_i^t - Y_j^t)^2$$

where,

$Y_i^t$  is uncorrelated mean value of i<sup>th</sup> genotype for 't' characters

$Y_j^t$  is uncorrelated mean value of j<sup>th</sup> genotype for 't' characters

$D_{ij}^2$  is D<sup>2</sup> between i<sup>th</sup> and j<sup>th</sup> genotypes.

### 3. 3.3.1.1 Test of significance

Variances were calculated for all the characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1967). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for differences in the mean values of a number of correlated variables with regard to the pooled effect of characters was carried out using 'V' statistic, which in turn utilizes Wilk's criterion ' $\Lambda$ '. The sum of squares and sum of products of error and error + variety, variance and covariance matrix were used for this purpose. The estimation of Wilk's criterion was done using the following relationship.

$$\Lambda = \frac{[E]}{[E+V]} = \frac{\text{Determinant of error matrix}}{\text{Determinant of error + variety matrix}}$$

where,

$\Lambda$  = Wilk's criterion

[E] = Determinant of error matrix sum of squares and sum of products matrix.

[E+V] = Determinant of error + variety sum of squares and sum of product matrix.

$$V_{(Stat)} = -m \log_e \Lambda = -[n - (p+q+1)/2] \log_e \Lambda$$

where,

$$m = n - (p + q + 1) / 2$$

p = number of characters (28)

$q = \text{number of varieties} - 1$  (or d.f. for varieties) (53)

$n = \text{degrees of freedom for error} + \text{varieties}$

and  $\log_e \hat{\epsilon} = 2.3026 \log_{10} \hat{\epsilon}$

Accordingly,  $V_{(Stat)}$  value is 4690.900

$V_{(Stat)}$  is distributed as  $\chi^2$  with  $pq$  ( $28 \times 53 = 1484$ ) degrees of freedom in the present study. The tabulated value of  $\chi^2$  for 1484 degrees of freedom is 1054.747 at 5 per cent level which is lower than the calculated  $\chi^2$  value (4690.900).

### 3.3.3.1.2 Transformation of correlated variables

In the present model, computation of  $D^2$  values was reduced to simple summation of the differences in mean values of various characters of the two genotypes *i.e.*  $\sum d^2_i$ . Therefore, transformation of correlated variables into uncorrelated ones was done before working out the  $D^2$  values. Transformation was done using pivotal condensation method.

### 3.3.3.1.3 Computation of $D^2$ values

For the given combination of 'i' and 'j' genotype, the mean deviation *i.e.*  $Y_i^t - Y_j^t$  for  $t = 1, 2, \dots, p$  variables are computed and the  $D^2$  values were calculated as already given using the following formula.

$$D_{ij}^2 = \sum_{t=1}^p (Y_i^t - Y_j^t)^2$$

where

$Y_i^t = \text{uncorrelated mean value of } i^{\text{th}} \text{ genotype for character } t.$

$Y_j^t = \text{uncorrelated mean value of } j^{\text{th}} \text{ genotype for character } t.$

$D_{ij}^2$  is  $D^2$  between  $i^{\text{th}}$  and  $j^{\text{th}}$  genotype.

#### 3.3.3.1.4 Testing the significance of $D^2$ values

The  $D^2$  value obtained for a pair of population is taken as calculated value of  $\chi^2$  and is tested against the tabulated value of  $\chi^2$  for P degrees of freedom where P is the number of characters considered. In the present study P is 28. The tabulated value of  $\chi^2$  at 5 per cent level of significance for 28 degrees of freedom being 45.41 is lower than calculated values of  $D^2$  (Table 15) which clearly shows that most of  $D^2$  values are significant.

#### 3.3.3.1.5 Contribution of individual characters towards divergence

In all combinations each character was ranked based on their contribution towards divergence between two entries ( $d_i = Y_i^t - Y_j^t$ ). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where, P is the total number of characters. Percentage contribution towards genetic divergence was calculated using the following formula.

$$\text{Percentage contribution of character} = x = \frac{N \times 100}{M}$$

where,

N = Number of genotype combinations where the character was ranked first.

M = All possible combinations of number of genotypes considered.

### **3.3.3.1.6 Grouping of genotypes into various clusters**

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster should, at least on an average, show a smaller  $D^2$  value than those belonging to different clusters. For this purpose  $D^2$  values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1977). To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest  $D^2$  value from the first two populations was added. Similarly the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average  $D^2$ , that population was not considered for including in that cluster. The genotypes of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued until all the genotypes were included into one or other cluster.

### **3.3.3.1.7 Average intra-cluster distance**

For the measurement of intra-cluster distance, the formula used was  $\Sigma D^2_i/n$  where,  $\Sigma D^2_i$  was the sum of distances between all possible combinations (n) of the populations included in a cluster.

### **3.3.3.1.8 Average inter-cluster distance**

Clusters were taken one by one and the distances from other clusters were calculated. The distance between two clusters was the sum of  $D^2$  values between the members of one cluster to each of the members of the other cluster divided by the product of number of genotypes in both the clusters under consideration.

$$\text{Average inter-cluster distance} = \frac{D^2}{(n_1 \times n_2)}$$

where,  $n_1$  and  $n_2$  are number of genotypes of two clusters.

$D^2$  = Distance between two cluster.

### 3.3.3.2 Principal Component Analysis and Cluster Analysis

Principal Component Analysis was carried according to the procedure described by Banfield (1978). The PCA can be performed on two types of data matrices viz., variance – covariance matrix and correlation matrix. With characters of different scale, a correlation matrix standardizing the original data set is preferred. If the characters are of same scale, a variance – covariance matrix can be used. In the present study, PCA was performed on the correlation matrix of traits, thereby removing the effects of scale (Jackson, 1991).

#### 3.3.3.2.1 Eigen values and eigen vectors

The eigen values and eigen vectors were computed from data matrix. Eigen values define the amount of total variation that is displayed on principal components. The proportion of variation accounted for each principal component (PC) is expressed as the eigen value divided by the sum of the eigen values.

$$\text{Per cent variance explained for PC1} = \frac{\text{Eigen value (PC1)}}{\text{Sum of eigen values}}$$

The eigen vector (loading) defines the correlation of each variable with the principal components.

The principal components were identified by following procedure.

The  $j^{\text{th}}$  principal component ( $Y_j$ ) of the observation  $X$  is the linear combination given as follows:

$$Y_j = A_{1j}X_1 + \dots + A_{pj} X_p$$

Where,

$A_{ij}$  are found such that  $Y_j$  is uncorrelated  $Y_1, Y_2, \dots, Y_{j-1}$  the  $j^{\text{th}}$  largest variance. The  $A_{ij}$  are the elements of the normalized eigen vector associated with largest  $j^{\text{th}}$  eigen value. The variance of the  $j^{\text{th}}$  principal component is  $\lambda_j$  and the total system variance trace  $(S) = \lambda_1 + \lambda_2 + \dots + \lambda_p$ . The importance of the  $j^{\text{th}}$  principal component is given by

$$\frac{\lambda_j}{\text{Trace (S)}}$$

This is informative about the proportion of total variation that can be accounted for the  $i^{\text{th}}$  principal component. The correlation between the  $i^{\text{th}}$  original variable  $X_i$  and the  $j^{\text{th}}$  principal component  $Y_j$  is given by

$$\rho(X_i, Y_j) = \frac{A_{ij} \sqrt{\lambda_j}}{\sqrt{S_i}}$$

Where  $S_i$  is the standard deviation of  $X_i$ .

Thus, a principal component is linear function of the test variables given as follows

$$\text{Principal component} = ax_1 + bx_2 + \dots + hx_8$$

Where, a,b,... are coefficients and  $x_1, x_2 \dots$  etc., are the variables in such a way that the principal component has a unit variance as reported by Ehrenberg (1985).

The PCA scores for each genotype under concerned PCs were computed and utilized to derive a 2D or 3D (dimensional) scatter plot of individuals.

### **3.3.3.2.2 Cluster analysis**

In the present study Agglomerative hierarchical clustering technique was followed as given by Anderberg (1993).

#### **1. Obtaining data matrix**

The PCA scores for 54 genotypes were used as input for clustering because principal component analysis provides variable independence and balanced weighting of traits, which leads to an effective contribution of different characters on the basis of respective variation.

#### **2. Standardizing the data matrix**

To compare the similarities among the genotypes, the data matrix was standardized using a standardizing function i.e., Q analysis. The data matrix was standardized in cluster analysis to make the characters contribute more equally to the similarities among genotypes and to nullify the arbitrarily affect of the units chosen for measuring the attributes among the genotypes.

Column standardizing function CA-Q analysis was carried by following formula

$$Z_{ij} = \frac{\overline{X_{ij}} - X_j}{S_{ij}}$$

$$\text{Where } \overline{X_j} = \sum_{i=1}^n X_{ij} / n$$

$$\text{Where } S_{ij} = \frac{\sum_{i=1}^n X_{ij} / n}{n-1}$$

Where,  $i$  = no.of genotypes i.e., 54 in this case

$j$  = total number of variables i.e., 28 in this case

The resulting data after standardization is unit less and have mean zero and variance one.

### 3. Computing the resemblance matrix

A resemblance coefficient, which measures the overall resemblance (the degree of similarity or distance) between a pair of genotypes, was computed. Here 54 genotypes were taken in data matrix and therefore resemblance coefficient was computed for total 1431 combinations i.e.,  ${}_{54}C_2$  ways.

The data matrix was transformed to distance matrix (resemblance matrix) based on the dissimilarity coefficients using squared Euclidean distance method.

$$\text{Squared Euclidean distance [ } d_{ij} \text{]} = \sum_{K=1}^P (X_{ik} - X_{jk})^2$$

Where,

$P$  = number of genotypes i.e., 54

$X_{ik}$  = value of  $i^{\text{th}}$  genotype for  $k$  PCA scores

$X_{jk}$  = value of  $j^{\text{th}}$  genotype for  $k$  PCA scores

#### **4. Execution of the clustering method**

Distance matrix was converted into dendrogram by using Ward's method where the distance between two clusters is the sum of squares between two clusters summed over all variables. At each stage in the clustering procedure within cluster sum of squares is minimized over all partitions obtained by combining 2 clusters from previous stage.

##### **3.3.3.2.3 Complete linkage diagram**

This was one of the hierarchical methods as classified by Everitt (1974), starts with the computation of the 'distance' or similarities of each individual with every other individual. A comparison of such similarity coefficients among the pairs of individuals or objects finally leads to a tree diagram, referred as 'Dendrogram'. For the dendrogram, the clusters of homogeneous units can be identified.

Sorenson (1948) first developed the method of complete linkage dendrogram. This method was based on the distance matrix  $D$ . Computation of a similarity measurement between all possible pairs of  $D^2$  values would result in an 'n' symmetrical matrix (where n is the number of genotypes). Similarity measurement was nothing but correlation coefficient between the variables. Any coefficient  $C_{ij}$  in the matrix gives the resemblance between i and j. The next step is to arrange the objects into a hierarchy. So objects (genotypes) were associated with other groups which they most closely resemble and so on until all the objects have been placed into a complete classification scheme (Sneath and Sokal, 1973).

The essential features of this particular method of cluster analysis could be summarized as follows:

1. The correlation coefficient was used as a similarity measure.
2. Highest similarities were clustered or linked first.

3. Two objects (genotypes) could be connected only if they had mutually highest correlation with each other.
4. After two objects (genotypes) were clustered, their correlations with all other objects were averaged.

### 3.3.4 CORRELATIONS

Phenotypic and genotypic correlations were worked out by using the formula suggested by Falconer (1964).

Phenotypic coefficients of correlation ( $r_p$ )

$$r(x_i, x_j)_p = \frac{Cov(x_i, x_j)_p}{\sqrt{V(x_i)_p \cdot V(x_j)_p}}$$

where,

$r(x_i, x_j)_p$  = Phenotypic correlation between  $i^{\text{th}}$  and  $j^{\text{th}}$  character.

$Cov(x_i, x_j)_p$  = Phenotypic covariance between  $i^{\text{th}}$  and  $j^{\text{th}}$  character

$V(x_i)_p$  = Phenotypic variance of  $i^{\text{th}}$  character

$V(x_j)_p$  = Phenotypic variance of  $j^{\text{th}}$  character

Genotypic coefficient of correlation ( $r_g$ )

$$r(x_i, x_j)_g = \frac{Cov(x_i, x_j)_g}{\sqrt{V(x_i)_g \cdot V(x_j)_g}}$$

Where,

$r(x_i, x_j)_g$  = Genotypic correlation between  $i^{\text{th}}$  and  $j^{\text{th}}$  character.

$Cov(x_i, x_j)_g$  = Genotypic covariance between  $i^{th}$  and  $j^{th}$  character

$V(x_i)_g$  = Genotypic variance of  $i^{th}$  character

$V(x_j)_g$  = Genotypic variance of  $j^{th}$  character

### **Z transformation for genotypic correlation**

Since the t table can be used only for testing the null hypothesis  $p=0$ . It is unsuited for testing other null hypothesis, such as  $p= 0.5$ , or  $p_1=p_2$ , or for making confidence statement about  $p$ , when  $p \neq 0$  the shape of the distribution of  $r$  changes, becoming skew.

A solution to these problems was provided by Fisher (1921) and as quoted by Snedecor and Cochran (1967) who devised a transformation from  $r$  to a quantity  $z$ , distributed normally with standard error.

$$\sigma_z = \frac{1}{\sqrt{(n-3)}}$$

Practically independent of the value of the correlation in the population from which the sample is drawn, the relation of  $r$  to  $z$  is given by

$$z = \frac{1}{2} [\log_e(1+r) - \log_e(1-r)]$$

#### **3.3.4.1 Test of significance**

Significance of correlation coefficients was tested by comparing phenotypic and genotypic correlation coefficients with the table values (Fisher and Yates, 1963) at

(n-2) degrees of freedom at 5% and 1% level where 'n' denotes the number of genotypes tested.

### 3.3.5 Path coefficient analysis

Path coefficient analysis, suggested by Wright (1921) and elaborated by Dewey and Lu (1959) was used to calculate the direct and indirect contribution of various traits towards seed yield.

For estimation of various direct and indirect effects, a set of simultaneous equations were formed:

$$\begin{aligned}
 r_{1y} &= P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \dots + r_{1k} P_{ky} \\
 r_{2y} &= r_{21} P_{1y} + P_{2y} + r_{23} P_{3y} + \dots + r_{2k} P_{ky} \\
 r_{iy} &= r_{i1} P_{1y} + P_{iy} + r_{i3} P_{3y} + \dots + r_{ik} P_{ky} \\
 r_{ky} &= r_{k1} P_{1y} + P_{k2} P_{2y} + r_{k3} P_{3y} + \dots + r_{kk} P_{ky}
 \end{aligned}$$

where ,

$r_{1y}$  to  $r_{ky}$  = Coefficient of correlation between causal factors 1 to K and dependant character Y.

$r_{1k}$  to  $r_{k-1,k}$  = Coefficient of correlation among causal factors

$P_{1y}$  to  $P_{ky}$  = Direct effects of characters 1 to k on character Y.

The above equations were written in a matrix form as under

$$\begin{array}{ccc}
 \mathbf{A} & & \mathbf{B} & & \mathbf{C} \\
 \\
 \begin{bmatrix} r_{1y} \\ r_{2y} \\ \cdot \\ \cdot \\ r_{ky} \end{bmatrix} & = & \begin{bmatrix} 1 & r_{12} & r_{13} & \cdot & \cdot & \cdot & r_1 \\ r_{21} & 1 & r_{23} & \cdot & \cdot & \cdot & r_2 \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ r_{k1} & r_{k2} & r_{k3} & \cdot & \cdot & \cdot & 1 \end{bmatrix} & & \begin{bmatrix} p_{1y} \\ p_{2y} \\ \cdot \\ \cdot \\ p_{ky} \end{bmatrix}
 \end{array}$$

Then  $B=(C)^{-1} A$

$$\text{Where } (C)^{-1} = \begin{bmatrix} C_{11} & C_{12} & \cdot & \cdot & \cdot & C_{1k} \\ C_{21} & C_{22} & \cdot & \cdot & \cdot & C_{2k} \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ C_{k1} & C_{k2} & \cdot & \cdot & \cdot & C_{kk} \end{bmatrix}$$

Then the direct effects were calculated as follows,

$$P_{1y} = \sum_{i=1}^k C_{1i} \cdot r_{iy}$$

$$P_{2y} = \sum_{i=1}^k C_{2i} \cdot r_{iy}$$

$$P_{ky} = \sum_{i=1}^k C_{ki} \cdot r_{iy}$$

### 3.3.5.1 Residual effect

In plant breeding it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual

effect measures the role of other possible independent variables which were not included in the study on the dependent variable. The residual effect is estimated with the help of direct effects and simple correlation coefficients.

$$1 = P^2 R_y + \sum P_{iy} r_{iy}$$

Where,  $P^2 R_y$  is the square of residual effect.

**Table 7: Source of castor (*Ricinus communis*L.) genotypes**

<b>S.No.</b>	<b>Name of the genotype</b>	<b>source</b>
1	PPL 101	RARS, Palem
2	PPL 102	RARS, Palem
3	PPL 103	RARS, Palem
4	PPL 104	RARS, Palem
5	PPL 105	RARS, Palem
6	PPL 106	RARS, Palem
7	PPL 107	RARS, Palem
8	PPL 108	RARS, Palem
9	PPL 109	RARS, Palem
10	PPL 110	RARS, Palem
11	PPL 111	RARS, Palem
12	PPL 112	RARS, Palem
13	PPL113	RARS, Palem
14	PPL 114	RARS, Palem
15	PPL 115	RARS, Palem
16	PPL 116	RARS, Palem
17	PPL 117	RARS, Palem
18	PPL 118	RARS, Palem
19	PPL 119	RARS, Palem
20	PPL 120	RARS, Palem
21	PPL 121	RARS, Palem
22	PPL 122	RARS, Palem
23	PPL 123	RARS, Palem
24	PPL 124	RARS, Palem
25	PPL 125	RARS, Palem
26	PPL 126	RARS, Palem
27	PPL 128	RARS, Palem
28	PPL 129	RARS, Palem
29	PPL 130	RARS, Palem
30	PPL 131	RARS, Palem
31	PPL 132	RARS, Palem
32	PPL 133	RARS, Palem
33	PPL 134	RARS, Palem
34	PPL 135	RARS, Palem
35	PPL 136	RARS, Palem
36	PPL 137	RARS, Palem
37	PPL 138	RARS, Palem
38	PPL 139	RARS, Palem
39	PPL 140	RARS, Palem
40	PPL 141	RARS, Palem
41	PPL 142	RARS, Palem
42	PPL 143	RARS, Palem
43	PPL 144	RARS, Palem
44	PPL 145	RARS, Palem
45	PPL 147	RARS, Palem
46	PPL 148	RARS, Palem
47	PPL 149	RARS, Palem

48	PPL 150	RARS, Palem
49	PPL 151	RARS, Palem
50	DPC 9	DOR, Hyderabad
51	M 574	DOR, Hyderabad
52	PCH 80	RARS, Palem
53	PCH 111	RARS, Palem
54	KIRAN	RARS, Palem

RARS : Regional Agricultural Research Station

DOR : Directorate of Oilseeds Research

PPL : Palem Pistilate Line

DPC : DOR Pistilate Castor

PCH : Palem Castor Hybrid

**Table 8: Experimental details of the present investigation.**

Location	:Agricultural College Farm Bapatla, Andhra Pradesh
Season	: <i>Kharif</i> , 2008
Entries	:54 castor ( <i>Ricinus communis</i> L.) genotypes
Design	:Randomized Block Design
Replications	:2
Plot size	:8.1 sqm
Spacing	:90 cm between rows and 60 cm within rows
Row length	:3m
Number of plants/replication	:15
Fertilizers	:120N:40P <sub>2</sub> O <sub>5</sub> :K <sub>2</sub> O kg ha <sup>-1</sup> (60 Kg N as basal dose and 60 Kg N was applied 30 days after sowing)
Plant protection	:Need based plant protection measures were taken up against pest and diseases.



## **CHAPTER IV**

### **RESULTS**

The experimental results obtained from the present study on 28 characters *viz.*, Days to 50% flowering of primary raceme, plant height up to primary raceme, number of nodes up to primary raceme, total length of primary raceme, effective length of primary raceme, days to 80% maturity of the primary raceme, number of secondary branches per plant, days to 50% flowering of secondary raceme, number of nodes to secondary raceme, plant height to secondary raceme, total length of secondary raceme, effective length of secondary raceme, days to 80% maturity of the secondary raceme, number of tertiary branches per plant, days to 50% flowering of tertiary raceme, number of nodes to tertiary raceme, plant height to tertiary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, days to 80% maturity of the tertiary raceme, oil content, L/B ratio, harvest index, seed yield up to 120 days, seed yield up to 150 days and seed yield up to 180 days, pertaining to 54 genotypes of castor are presented here under.

### **ANALYSIS OF VARIANCE**

The analysis of variance for all the 28 characters was furnished in Table- 9. The analysis of variance revealed significant differences for all the characters studied.

The results obtained are presented under the following headings.

4.1 Morphological characterization

4.2 Variability, heritability and genetic advance as per cent of mean

4.3 Correlations

4.4 Path analysis

4.5 Genetic divergence

#### **4.1 MORPHOLOGICAL CHARACTERIZATION**

Fifty four castor genotypes were characterized based on their morphological characters as per DUS guidelines of castor (Table:11).

##### **4.1.1 Stem colour**

Three types of stem colour was observed *viz.*, green, red and dark red. Twenty one genotypes *viz.*, PPL-101, PPL-105, PPL-106, PPL-108, PPL-110, PPL-115, PPL-122, PPL-129, PPL-132, PPL-133, PPL-134, PPL-135, PPL-138, PPL-141, PPL-144, PPL-148, PPL-149, PPL-150, PPL-151, GCH-4 and KIRAN had dark red stem, while DPC-9, M-574, PCH-80 and PCH-111 had green stem, remaining twenty nine genotypes had red stem (Fig. 1).

#### **4.1.2 Type of inter nodes on stem**

Forty three genotypes have elongated type of internodes and eleven genotypes *viz.*, PPL-105, PPL-111, PPL-112, PPL-119, PPL-133, PPL-134, PPL-149, DPC-9, M-574, PCH-111 and KIRAN were condensed type of internodes (Fig. 2).

#### **4.1.3 Plant branching pattern**

Two types of branching patterns were observed *viz.*, convergent and divergent. The genotypes PPL-108, PPL-109, PPL-115, PPL-120, PPL-121, PPL-122, PPL-123, PPL-128, PPL-130, PPL-134, PPL-135, PPL-136, PPL-137, PPL-145, PPL-150 and GCH-4 were divergent while the remaining genotypes were convergent (Fig. 3).

#### **4.1.4 Petiole colour**

Petiole colour observed in the genotypes were green, green with reddish tinge, red and dark red. The genotypes PPL-103, PPL-109, PPL-112, PPL-113, PPL-114, PPL-117, PPL-118, PPL-120, PPL-123, PPL-131, PPL-132, PPL-136 and PPL-137 were green with reddish tinge where as PPL-108, PPL-110, PPL-129, PPL-134, PPL-135, PPL-141 and PPL-148 were dark red. The genotypes DPC-9, M-574, PCH-80, PCH-111 were green and the remaining genotypes were red (Fig. 4).

#### **4.1.5 Lamina colour**

Genotypes were grouped into three groups based on lamina colour – dark green, green and green with reddish tinge. The genotypes PPL-110, PPL-116, PPL-121,

PPL-123, PPL-125, PPL-133, PPL-134, PPL-138, PPL-148, PPL-149, PPL-151 and KIRAN showed green with reddish tinge where as PPL-105, PPL-106, PPL-107, PPL-108, PPL-115, PPL-122, PPL-129, PPL-132, PPL-136, PPL-140, PPL-142, PPL-143 and PPL-147 were dark green. Remaining genotypes had green colour (Fig. 5).

#### **4.1.6 Bloom**

The genotypes PPL-141 and PPL-147 were triple bloom while PPL-117 and PPL-126 were single bloom and the rest of the genotypes are double bloom type (Fig. 6).

#### **4.1.7 Type of Inflorescence**

Most of the genotypes had interspersed staminate flowers except PPL-117 and PPL-125 which were monoecious (Fig. 7).

#### **4.1.8 Colour of stigma**

Three types of stigma colours were observed pink, red and dark red. Fourteen genotypes *viz.*, PPL-106, PPL-110, PPL-117, PPL-119, PPL-122, PPL-125, PPL-126, PPL-132, PPL-135, PPL-138, PPL-143, PPL-144, M-574 and KIRAN were dark red. Eleven genotypes *viz.*, PPL-102, PPL-107, PPL-111, PPL-113, PPL-118, PPL-121, PPL-131, PPL-137, PPL-139, PPL-140 and PPL-145 were pink and the remaining genotypes were red (Fig. 8).

#### **4.1.9 Capsule type**

Most of the genotypes had spiny capsules except PPL-112, PPL-113, PPL-120, and Kiran which were non spiny (Fig. 9).

#### **4.1.10 Spike shape**

Three types of shapes were observed *viz.*, conical, cylindrical and umbrella. The genotype PPL-126 was umbrella shaped. The genotypes PPL-111, PPL-112, PPL-113, PPL-130, PPL-132, PPL-141, PPL-142, GCH-4 and PCH-111 were cylindrical. And the remaining genotypes had conical spike shape (Fig. 10).

#### **4.1.11 Spike compactness**

Ten genotypes namely PPL-102, PPL-109, PPL-110, PPL-114, PPL-115, PPL-116, PPL-117, PPL-118, PPL-121 and DPC-9 had compact spike while twenty genotypes *viz.*, PPL-101, PPL-107, PPL-123, PPL-129, PPL-130, PPL-132, PPL-136, PPL-138, PPL-139, PPL-140, PPL-141, PPL-143, PPL-151, PPL-147, PPL-148, PPL-150, GCH-4, PCH-80, PCH-111 and KIRAN had loose spike and the remaining eighteen genotypes showed semi compact spike (Fig. 11).

#### **4.1.12 Seed colour**

Three types of seed colours were observed – maroon, brown and deep chocolate. Ten genotypes *viz.*, PPL-107, PPL-113, PPL-117, PPL-119, PPL-125, PPL-126, PPL-135, PPL-148, DPC-9 and KIRAN had maroon seed colour. While fifteen genotypes *viz.*,

PPL-110, PPL-111, PPL-114, PPL-121, PPL-130, PPL-131, PPL-132, PPL-133, PPL-134, PPL-137, PPL-141, PPL-144, PPL-145, GCH-4 and PCH-80 had deep chocolate colour and the remaining twenty nine genotypes had brown colour (Fig. 14).

## **4.2 MEAN, VARIABILITY, HERITABILITY AND GENETIC ADVANCE**

The estimates of mean, range, phenotypic coefficients of variation (PCV), genotypic coefficient of variation (GCV), heritability ( $bs/h^2$ ) and genetic advance as per cent of mean (GAM) are presented in Table 12. The variability percentages are described character wise here under. The above estimates of PCV and GCV were represented in Fig 15 and 16 respectively.

### **4.2.1 Days to 50% flowering of primary raceme**

This trait varied from 51.00 (GCH 4, PPL 103 and PCH 80) to 116.00days (PPL 147) with a mean value of 66.78 days. The genotypic and phenotypic coefficients of variation were 20.73 and 20.81% respectively and high in magnitude. High heritability (99.19%) and high genetic advance as per cent of mean (42.53) were observed for this trait.

### **4.2.2 Stem length up to primary raceme (cm)**

This trait varied from 48.00 (M-574) to 282.30 cm (PPL 147) with a mean value of 113.31cm. The estimates of both GCV and PCV (34.65 and 34.74%) were high. High

heritability (99.44%) and high genetic advance as per cent of mean (71.18) were observed for this trait. The check variety M-574 showed less stem length to primary raceme (48.00 cm).

#### **4.2.3 Number of nodes up to primary spike**

The range of variation for this character among the genotypes was from 14.00 (Kiran) to 37.40 percent (PPL 147) with a mean of 19.91 percent. The estimated values of GCV and PCV (22.47 and 22.75%) were high. High heritability (97.55%) and high genetic advance as per cent of mean (45.73) was recorded for this trait. The check variety Kiran showed less number of nodes to primary raceme (14.00).

#### **4.2.4 Total length of primary raceme (cm)**

The variation for this character ranged from 24.40 (PPL 113) to 62.4 cm (PPL 123) with an average of 42.86 cm. The estimates of GCV and PCV (20.37 and 20.77%) were high. High heritability (96.21%) and high genetic advance as per cent of mean (41.16) was observed for this trait. The check variety M-574 showed higher total length of primary raceme (47.00 cm).

#### **4.2.5 Effective length of primary raceme (cm)**

The mean effective length of primary spike ranged from 19.4 (PPL 117) to 55.00 cm (PPL 139 and PPL 149) with a mean of 36.97 cm. The estimates of GCV and PCV (24.05 and 24.32%) were high. High heritability (97.80%) and high genetic advance as

per cent of mean (49.0) were recorded for this trait. The check variety DPC-9 showed higher effective length of primary raceme (42.00 cm).

#### **4.2.6 Days to 80% maturity of the primary raceme**

The range of variation for this trait was from 85.50 (PPL 117) to 131.00 days (PPL 149) with a mean of 101.89 days. The estimates of GCV and PCV (11.48 and 11.53%) were moderate. High heritability (99.15%) and high genetic advance as per cent of mean (23.55) were recorded for this parameter. The check variety Kiran showed lower days to 80% maturity of primary raceme (86.00).

#### **4.2.7 Number of secondary branches per plant**

This attribute varied from 1.8 (PPL 150) to 4.4 (PPL 114) with a mean value of 2.61. The estimates of GCV (17.96%) and PCV (19.83%) were moderate. High heritability (82.07%) and high genetic advance as per cent of mean (35.52) were recorded for this trait. The check variety DPC-9 showed more number of secondary racemes per plant (2.7).

#### **4.2.8 Days to 50% flowering of secondary raceme**

This attribute varied from 69.5 (PCH 80) to 140.5 days (PPL 147) with a mean value of 95.13 days. The estimates of GCV (17.07%) and PCV (17.14%) were moderate. High heritability (99.18%) and high genetic advance as per cent of mean (35.03) were recorded for this trait. The check variety Kiran showed lower days to 50% flowering of secondary raceme (76.50)

#### **4.2.9 Number of nodes to secondary raceme**

This attribute varied from 6.3 (PPL 120) to 18.45 (PPL 101) with a mean value of 10.65. The estimates of GCV (24.71%) and PCV (26.26%) were high. High heritability (88.57%) and high genetic advance as per cent of mean (47.92) were recorded for this trait. The check variety Kiran showed less number of nodes to secondary raceme (8.30).

#### **4.2.10 Stem length to secondary raceme (cm)**

The variation for this character was ranged from 35.2 (PPL 117) to 151.9 cm (PPL 140) with an average of 83.20 cm. The estimates of GCV and PCV (34.94 and 35.62%) were high. High heritability (96.21%) and high genetic advance as per cent of mean (70.61) were observed for this trait. The check variety M-574 showed less stem length to secondary raceme (37.00 cm).

#### **4.2.11 Total length of secondary raceme (cm)**

The variation for this character was ranged from 12.85 (PPL 117) to 54.5 cm (PPL 130) with an average of 34.23 cm. The estimates of GCV and PCV (22.99 and 23.32%) were high. High heritability (97.13%) coupled and genetic advance as per cent of mean (46.67) was observed for this trait. The check variety DPC-9 showed highest total length of secondary raceme (42.00 cm).

#### **4.2.12 Effective length of secondary raceme (cm)**

The variation for this character ranged from 15.0 (PPL 105) to 46.0 cm (PPL 130) with an average of 29.11 cm. The estimates of GCV and PCV (24.56 and 24.89%) were high. High heritability (97.33%) and high genetic advance as per cent of mean (49.91) was observed for this trait. The check variety DPC-9 showed highest effective length of secondary spike (38.60 cm).

#### **4.2.13 Days to 80% maturity of the secondary raceme**

The range of variation for this trait was from 101(PPL 136) to 156.50 days (PPL 147) with a mean of 126.0 days. The estimates of GCV and PCV (11.02 and 11.11%) were moderate. High heritability (98.50%) and high genetic advance as per cent of mean (22.54) were recorded for this parameter. The check variety Kiran showed lower days to 80% maturity of secondary raceme (114.00).

#### **4.2.14 Number of tertiary branches per plant**

This attribute varied from 1.1 (PPL 111) to 5.0 (PPL 125) with a mean value of 3.08. The estimates of GCV (31.11%) and PCV (32.24%) were high. High heritability (93.10%) and high genetic advance as per cent of mean (61.84) were recorded for this trait. The check varieties Haritha and DPC-9 showed more number of tertiary racemes per plant (4.00).

#### **4.2.15 Days to 50% flowering of tertiary raceme**

This attribute varied from 87 (PPL 117) to 163.00 days (PPL 147) with a mean value of 120.66 days. The estimates of GCV (14.04%) and PCV (14.08%) were moderate. High heritability (99.45%) and high genetic advance as per cent of mean (28.84) were recorded for this trait. The check variety Kiran showed lower days to 50% flowering of tertiary raceme (103.00).

#### **4.2.16 Number of nodes to tertiary raceme**

This attribute varied from 5.00 (PPL 102) to 12.05 (PPL 104) with a mean value of 8.48. The estimates of GCV (17.69%) and PCV (18.87%) were moderate. High heritability (87.40%) and high genetic advance as per cent of mean (34.16) were recorded for this trait. The check variety Kiran showed less number of nodes to tertiary raceme (7.60).

#### **4.2.17 Stem length to tertiary raceme (cm)**

The variation for this character was ranged from 17.20 (PPL 101) to 97.4 cm (PPL 129) with an average of 49.06 cm. The estimates of GCV and PCV (37.98 and 38.27%) were high. High heritability (98.46%) and high genetic advance as per cent of mean (77.63) were observed for this trait. The check variety Kiran showed less stem length to tertiary raceme (24.00 cm).

#### **4.2.18 Effective length of tertiary raceme(cm)**

The variation for this character ranged from 13.10 (PPL 139) to 31.6 cm (DPC 9) with an average of 20.56 cm. The estimates of GCV and PCV (22.77 and 23.20%) were high. High heritability (96.29%) and high genetic advance as per cent of mean (46.03) were observed for this trait. The check variety DPC-9 showed highest effective length of tertiary raceme (31.60cm).

#### **4.2.19 Days to 80% maturity of the tertiary raceme**

This attribute varied from 119.50 (PPL 128) to 173.00 days (PPL 149) with a mean value of 145.97 days. The estimates of GCV (9.73%) and PCV (9.88%) were low. High heritability (97.04%) and moderate genetic advance as per cent of mean (19.74) were recorded for this trait. The check variety Kiran showed lower days to 80% maturity of tertiary raceme (132.00).

#### **4.2.20 100 seed weight of primary raceme (g)**

The range of variation observed for this character was from 18.21 (PPL 141) to 31.25 g (GCH 4) with a mean of 23.99 g. The estimated values of GCV and PCV (12.33 and 12.66%) were moderate. High heritability (94.80%) and high genetic advance as per cent of mean (24.73) were observed for this trait. The check variety M-574 showed highest 100 seed weight of primary raceme (29.09g).

#### **4.2.21 100 seed weight of secondary raceme (g)**

The range of variation observed for this character was from 17.61 (PPL 129) to 30.90 g (PCH 111) with a mean of 25.24 g. The estimated values of GCV and PCV (12.0 and 12.54%) were moderate. High heritability (91.61%) and high genetic advance as per cent of mean (23.67) were observed for this trait. The check variety M-574 showed highest 100 seed weight of secondary raceme (27.51g).

#### **4.2.22 100 seed weight of tertiary raceme (g)**

The range of variation observed for this character was from 17.67 (PPL 129) to 32.73 g (PCH 111) with a mean of 24.18g. The estimated values of GCV and PCV (13.18 and 13.94%) were moderate. High heritability (89.51%) and high genetic advance as per cent of mean (25.7) were observed for this trait. The check variety DPC-9 showed highest 100 seed weight of tertiary raceme (29.43 g).

#### **4.2.23 Oil content (%)**

This trait ranged from 43.96 (PPL 129) to 51.59 per cent (PPL 143) with a mean of 48.12 percent. The estimates of GCV and PCV (3.65 and 4.12%) were low. High heritability (78.53%) and low genetic advance as per cent of mean (6.67) were recorded for this trait. The check variety Kiran showed highest oil content (51.37%).

#### **4.2.24 L/B ratio of seed**

This attribute varied from 1.30 (DPC 9) to 1.59 (PPL 106) with a mean value of 1.46. The estimates of GCV (3.72%) and PCV (3.99%) were low. High heritability (87.18%) and low genetic advance as per cent of mean (7.16) were recorded for this trait. The check variety Kiran showed highest L/B ratio of the seed (1.49).

#### **4.2.25 Harvest index (%)**

This trait ranged from 30.2 (PPL 147) to 43.1 per cent (DPC 9) with a mean of 36.56 per cent. The estimates of GCV and PCV (8.98 and 9.5%) were low. High heritability (89.37%) and moderate genetic advance as per cent of mean (17.49) were recorded for this trait. The check variety DPC-9 showed high harvest index (43.10%).

#### **4.2.26 Seed yield up to 120 days (g)**

The range of variation observed for this character was from 0 (PPL 102, PPL 141, PPL 147, PPL 148 and PPL 149) to 129.40 g (PPL 103) with a mean of 54.12 g. The estimated values of GCV and PCV (61.64 and 62.62%) were high. High heritability (96.89%) coupled with high genetic advance as per cent of mean (124.99) was observed for this trait. The check variety Kiran showed highest seed yield per plant at 120 days (97.50 g).

#### **4.2.27 Seed yield up to 150 days (g)**

The range of variation observed for this character was from 26.85 (PPL 141) to 184.00 g (PPL 103) with a mean of 102.69 g. The estimated values of GCV and PCV (38.84 and 39.68%) were high. High heritability (95.83%) and high genetic advance as per cent of mean (78.33) were observed for this trait. The check variety DPC-9 showed highest seed yield per plant upto 150 days (147.50 g).

#### **4.2.28 Seed yield up to 180 days (g)**

The range of variation observed for this character was from 60.1 (PPL 112) to 210.5 g (DPC 9) with a mean of 125.97 g. The estimated values of GCV and PCV (24.03 and 25.32%) were high. High heritability (90.06%) and high genetic advance as per cent of mean (46.98) were observed for this trait. The check variety DPC-9 showed highest seed yield per plant upto 180 days (210.50 g).

### **4.4 CORRELATIONS**

The phenotypic and genotypic correlation coefficients between seed yield per plant up to 180 days and yield components and inter relations among them were estimated and presented in Table 13. In general, the results revealed that the genotypic correlations were higher than the phenotypic correlations for almost all the characters under study.

#### **4.4.1 Days to 50% flowering of primary raceme**

This trait showed significant positive association at both genotypic and phenotypic levels with stem length to primary raceme (0.7669\*\* and 0.7628\*\*), nodes to primary raceme (0.8995\*\* and .8876\*\*), total length of primary raceme (0.2573\*\* and 0.2529\*\*), effective length of primary raceme (0.2720\*\* and 0.2723\*\*), days to 80% maturity of primary raceme (0.8519\*\* and 0.8469\*\*), days to 50% flowering of secondary raceme (0.8984\*\* and 0.8924\*\*), nodes to secondary raceme (0.3653\*\* and 0.3437\*\*), stem length to secondary raceme (0.4872\*\* and 0.4739\*\*), days to 80% maturity of secondary raceme (0.8723\*\* and 0.8628\*\*), days to 50% flowering of tertiary raceme (0.8453\*\* and 0.8400\*\*), days to 80% maturity of tertiary raceme (0.7882\*\* and 0.7732\*\*). While this trait showed significant negative association with nodes to tertiary raceme (-0.3086\*\* and -0.2938\*\*), stem length to tertiary raceme (-0.2920\*\* and -0.2881\*\*), 100 seed weight of tertiary raceme (-0.2607\*\* and -0.2441\*), L/B ratio of seed (-0.3641\*\* and -0.3367\*\*), harvest index (-0.6162\*\* and -0.5745\*\*), seed yield per plant at 120 days (-0.7723\*\* and -0.7566\*) and seed yield per plant up to 150 days (-0.7817\*\* and -0.7663\*\*).

#### **4.4.2 Stem Length to primary raceme**

Both at genotypic and phenotypic levels, this trait had significant positive correlation with days to 50% flowering of primary raceme (0.7669\*\* and 0.7628\*\*), nodes to primary raceme (0.7641\*\* and 0.7542\*\*), total length of primary raceme (0.2890\*\* and 0.2817\*\*), effective length of primary raceme (0.2865\*\* and 0.2842\*\*), days to 80% maturity of primary raceme (0.7594\*\* and 0.7537\*\*), days to 50%

flowering of secondary raceme (0.8085\*\* and 0.8010\*\*), nodes to secondary raceme (0.3427\*\* and 0.3149\*\*), stem length to secondary raceme (0.4670\*\* and 0.4572\*\*), days to 80% maturity of secondary raceme (0.8723\*\* and 0.7515\*\*), days to 50% flowering of tertiary raceme (0.7403\*\* and 0.7364\*\*), days to 80% maturity of tertiary raceme (0.7078\*\* and 0.6966\*\*). While this trait showed significant negative association with nodes to tertiary raceme (-0.3189\*\* and -0.3030\*\*), stem length to tertiary raceme (-0.1971\*\* and -0.1944\*), 100 seed weight of tertiary raceme (-0.2245\* and -0.2023\*), harvest index (-0.6306\*\* and -0.5917\*\*) and seed yield per plant at 120 days (-0.5623\*\* and -0.5501\*\*), seed yield per plant up to 150 days (-0.5952\*\* and -0.5816\*\*)

#### **4.4.3 Number of nodes to primary raceme**

Genotypic and phenotypic correlations revealed that this trait had significant positive association with days to 50% flowering of primary raceme (0.8995\*\* and 0.8876\*\*), stem length to primary raceme (0.7641\*\* and 0.7542\*\*), days to 80% maturity of primary raceme (0.8069\*\* and 0.7929\*\*), days to 50% flowering of secondary raceme (0.8192\*\* and 0.8053\*\*), nodes to secondary raceme (0.3469\*\* and 0.3302\*\*), stem length to secondary raceme (0.4107\*\* and 0.3968\*\*), days to 80% maturity of secondary raceme (0.7990\*\* and 0.7805\*\*), days to 50% flowering of tertiary raceme (0.7841\*\* and 0.7722\*\*), days to 80% maturity of tertiary raceme (0.7038\*\* and 0.6777\*\*). While this trait showed significant negative association with nodes to tertiary raceme (-0.3255\*\* and -0.3104\*\*), stem length to tertiary raceme (-0.3754\*\* and -0.3679\*\*), 100 seed weight of tertiary raceme (-0.2145\* and -0.2049\*), L/B ratio of seed (-0.2984\*\* and -0.2818\*\*), harvest index (-0.6003\*\* and -0.5506\*\*),

seed yield per plant at 120 days (-0.6596\*\* and -0.6423\*\*) and seed yield per plant up to 150 days (-0.7258\*\* and -0.7080\*\*).

#### **4.4.4 Total length of primary raceme**

Total length of primary spike had significant positive association at both genotypic and phenotypic levels with days to 50% flowering of primary raceme (0.2573\*\* and 0.2529\*\*), stem length to primary raceme (0.2890\*\* and 0.2817\*\*), effective length of primary raceme (0.9211\*\* and 0.9019\*\*), days to 80% maturity of primary raceme (0.3475\*\* and 0.3408\*\*), days to 50% flowering of secondary raceme (0.4346\*\* and 0.4236\*\*), nodes to secondary raceme (0.3675\*\* and 0.3434\*\*), stem length to secondary raceme (0.3741\*\* and 0.3605\*\*), total length of secondary raceme (0.5835\*\* and 0.5677\*\*), effective length of secondary raceme (0.5177\*\* and 0.5051\*\*), days to 80% maturity of secondary raceme (0.4084\*\* and 0.3985\*\*), days to 50% flowering of tertiary raceme (0.4099\*\* and 0.3964\*\*), effective length of tertiary raceme (0.4259\*\* and 0.4114\*\*), days to 80% maturity of tertiary raceme (0.4652\*\* and 0.4541\*\*), 100 seed weight of primary raceme (0.3039\*\* and 0.2971\*\*), 100 seed weight of secondary raceme (0.2642\*\* and 0.2546\*\*) and oil content (0.3342\*\* and 0.2795\*\*) while this trait showed significant negative association with tertiary branches per plant (-0.2817\*\* and -0.2672\*\*)

#### **4.4.5 Effective length of primary raceme**

Effective length of primary raceme had significant positive association at both genotypic and phenotypic levels with days to 50% flowering of primary raceme

(0.2720\*\* and 0.2723\*\*), stem length to primary raceme (0.2865\*\* and 0.2842\*\*), total length of primary raceme (0.9211\*\* and 0.9019\*\*), days to 80% maturity of primary raceme (0.3334\*\* and 0.3298\*\*), days to 50% flowering of secondary raceme (0.4452\*\* and 0.4384\*\*), nodes to secondary raceme (0.3037\*\* and 0.2980\*\*), stem length to secondary raceme (0 and 3857\*\* and 0.3735\*\*), total length of secondary raceme (0.5902\*\* and 0.5784\*\*), effective length of secondary raceme (0.5770\*\* and 0.5632\*\*), days to 80% maturity of secondary raceme (0.3961\*\* and 0.3891\*\*), effective length of tertiary raceme (0.2874\*\* and 0.2797\*\*), days to 80% maturity of tertiary raceme (0.4709\*\* and 0.4639\*\*), 100 seed weight of primary raceme (0.3308\*\* and 0.3184\*\*), 100 seed weight of secondary raceme (0.3093\*\* and 0.2952\*\*) and oil content (0.3653\*\* and 0.3119\*\*) while this trait showed significant negative association with tertiary branches per plant (-0.3226\*\* and -0.3075\*\*)

#### **4.4.6 Days to 80% maturity of primary raceme**

This trait recorded significant positive association with days to 50% flowering of primary raceme (0.8519\*\* and 0.8469\*\*), stem length to primary raceme (0.7594\*\* and 0.7537\*\*), nodes to primary raceme (0.8069\*\* and 0.7929\*\*), total length of primary raceme (0.3475\*\* and 0.3408), effective length of primary raceme (0.3334\* and 0.3298\*\*), days to 50% flowering of secondary raceme (0.8951\*\* and 0.8891\*\*), nodes to secondary raceme (0.4350\*\* and 0.4087\*\*), stem length to secondary raceme (0.4525\*\* and 0.4414\*\*), days to 80% maturity of secondary raceme (0.9116\*\* and 0.8980\*\*), days to 50% flowering of tertiary raceme (0.8221\*\* and 0.8158\*\*) and days

to 80% maturity of tertiary raceme (0.7987\*\* and 0.7861\*\*) both at genotypic and phenotypic level.

This trait showed significant negative association with nodes to tertiary raceme (-0.2784\*\* and -0.2598\*\*), stem length to tertiary raceme (-0.3275\*\* and -0.3235\*\*), L/B ratio (-0.3022\*\* and -0.2785\*\*), harvest index (-0.6002\*\* and -0.5631\*\*), seed yield per plant at 120 days (-0.7751\*\* and -0.7586\*\*) and seed yield per plant up to 150 days (-0.7767\*\* and -0.7575\*\*) both at genotypic and phenotypic level.

#### **4.4.7 Number of secondary branches per plant**

This trait showed significant positive association both at genotypic and phenotypic level with stem length to secondary raceme (0.2276\* and 0.1980\*) while this trait showed significant negative association with stem length to tertiary raceme (-0.2270\* and -0.2050\*)

#### **4.4.8 Days to 50% flowering of secondary raceme**

This trait showed significant positive association both at genotypic and phenotypic level with days to 50% flowering of primary raceme (0.8984\*\* and 0.8924\*\*), stem length to primary raceme (0.8085\*\* and 0.8010\*\*), nodes to primary raceme (0.8192\*\* and 0.8053\*\*), total length of primary raceme (0.4346\*\* and 0.4236\*\*), effective length of primary raceme (0.4452\*\* and 0.4384\*\*), days to 80% maturity of primary raceme (0.8951\*\* and 0.8891\*\*), nodes to secondary raceme (0.5528\*\* and 0.5244\*\*), stem length to secondary raceme (0.5155\*\* and 0.5059\*\*), days to 80% maturity of secondary raceme (0.9324\*\* and 0.9232\*\*), days to 50%

flowering of tertiary raceme (0.9419\*\* and 0.9351\*\*) and days to 80% maturity of tertiary raceme (0.8790\*\* and 0.8641\*\*) while this trait showed significant negative association with nodes to tertiary raceme (-0.3641\*\* and -0.3444\*\*), L/B ratio (-0.2973\*\* and -0.2740\*\*), harvest index (-0.5468\*\* and -0.5184\*\*), seed yield per plant at 120 days (-0.7536\*\* and -0.7426\*\*) and seed yield per plant up to 150 days (-0.7300\*\* and -0.7131\*\*) at both genotypic and phenotypic level.

#### **4.4.9 Number of nodes to secondary raceme**

Both at genotypic and phenotypic level this trait showed significant positive association with days to 50% flowering of primary raceme (0.3653\*\* and 0.3437\*\*), stem length to primary raceme (0.3427\*\* and 0.3149\*\*), nodes to primary raceme (0.3469\*\* and 0.3302\*\*), total length of primary raceme (0.3675\*\* and 0.3435\*\*), effective length of primary raceme (0.3037\*\* and 0.2980\*\*), days to 80% maturity of primary raceme (0.4350\*\* and 0.4087\*\*), days to 50% flowering of secondary raceme (0.5528\*\* and 0.5244\*\*), stem length to secondary raceme (0.3606\*\* and 0.3369\*\*), days to 80% maturity of secondary raceme (0.4903\*\* and 0.4581\*\*), days to 50% flowering of tertiary raceme (0.5063\*\* and 0.4757\*\*), days to 80% maturity of tertiary raceme (0.4382\*\* and 0.4157\*\*) and 100 seed weight of secondary raceme (0.2188\* and 0.2081\*)

This trait showed significant negative association with nodes to tertiary raceme (-0.2364\* and -0.2066\*), stem length to tertiary raceme (-0.2936\*\* and -0.2771\*\*), L/B ratio (-0.2263\* and -0.1903\*), seed yield per plant at 120 days (-0.3092\*\* and -0.2778\*\*) and seed yield per plant up to 150 days (-0.3084\*\* and -0.2857\*\*)

#### 4.4.10 Stem length to secondary raceme

This trait showed significant positive association with days to 50% flowering of primary raceme (0.4872\*\* and 0.4739\*\*), stem length to primary raceme (0.4670\*\* and 0.4572\*\*), nodes to primary raceme (0.4107\*\* and 0.3968\*\*), total length of primary raceme (0.3741\*\* and 0.3605\*\*), effective length of primary raceme (0.3857\*\* and 0.3755\*\*), days to 80% maturity of primary raceme (0.4525\*\* and 0.4414\*\*), secondary branches per plant (0.2276\* and 0.1980\*), days to 50% flowering of secondary raceme (0.5155\*\* and 0.5059\*\*), nodes to secondary raceme (0.3606\*\* and 0.3369\*\*), total length of secondary raceme (0.2183\* and 0.2128\*), effective length of secondary raceme (0.2621\*\* and 0.2549\*\*) and days to 80% maturity of secondary raceme (0.5558\*\* and 0.5427\*\*) both at genotypic and phenotypic level.

Whereas the same trait showed significant negative association at both genotypic and phenotypic levels with tertiary branches per plant (-0.2095\*\* and -0.2038\*\*), days to 50% flowering of tertiary raceme (-0.5299\*\* and -0.5190\*\*), nodes to tertiary raceme (-0.2457\* and -0.2409\*), stem length to tertiary raceme (-0.2650\*\* and -0.2600\*\*), days to 80% maturity of tertiary raceme (-0.5260\*\* and -0.5266\*\*), 100 seed weight of primary raceme (-0.2856\*\* and -0.2813\*\*), 100 seed weight of secondary raceme (-0.2606\*\* and -0.2388\*), 100 seed weight of tertiary raceme (-0.4412\*\* and -0.4138\*\*), harvest index (-0.5177\*\* and -0.4749\*\*), seed yield per plant at 120 days (-0.4105\*\* and -0.3867\*\*) and seed yield per plant up to 150 days (-0.4946\*\* and -0.44655\*\*).

#### **4.4.11 Total length of secondary raceme**

This trait showed significant positive association with total length of primary raceme (0.5835\*\* and 0.5677\*\*), effective length of primary raceme (0.5902\*\* and 0.5784\*\*), days to 50% flowering of secondary raceme (0.2068\* and 0.2031\*), stem length to secondary raceme (0.2183\* and 0.2128\*), effective length of secondary raceme (0.9382\*\* and 0.9216\*\*), effective length of tertiary raceme (0.5858\*\* and 0.5678\*\*), harvest index (0.2595\*\* and 0.2339\*) and seed yield per plant up to 150 days (0.2094\* and 0.1944\*) both at genotypic and phenotypic level while this trait showed significant negative association with tertiary branches per plant (-0.2067\* and -0.1909\*)

#### **4.4.12 Effective length of secondary raceme**

Effective length of secondary raceme showed significant positive association both at genotypic and phenotypic level with total length of primary raceme (0.5177\*\* and 0.5051\*\*), effective length of primary raceme (0.5770\*\* and 0.5632\*\*), days to 50% flowering of secondary raceme (0.2056\* and 0.2022\*), stem length to secondary raceme (0.2621\*\* and 0.2549\*\*), total length of secondary raceme (0.9382\*\* and 0.9216\*\*), effective length of tertiary raceme (0.5284\*\* and 0.5108\*\*) and days to 80% maturity of tertiary raceme (0.2202\* and 0.2096\*) while this trait showed significant negative association with tertiary branches per plant (-0.2486\*\* and -0.2403\*).

#### **4.4.13 Days to 80% maturity of secondary raceme**

This trait showed significant positive association both at genotypic and phenotypic level with days to 50% flowering of primary raceme (0.8723\*\* and

0.8628\*\*), stem length to primary raceme (0.7594\*\* and 0.7515\*\*), nodes to primary raceme (0.7990\*\* and 0.7805\*\*), total length of primary raceme (0.4084\*\* and 0.3985\*\*), effective length of primary raceme (0.3961\*\* and 0.3891\*\*), days to 80% maturity of primary raceme (0.9116\*\* and 0.8980\*\*), days to 50% flowering of secondary raceme (0.9324\*\* and 0.9232\*\*), nodes to secondary raceme (0.4903\*\* and 0.4581\*\*), stem length to secondary raceme (0.5558\*\* and 0.5427\*\*), days to 50% flowering of tertiary raceme (0.8781\*\* and 0.8696\*\*) and days to 80% maturity of tertiary raceme (0.8937\*\* and 0.8663\*\*) while this trait showed significant negative association with tertiary branches per plant (-0.2222\* and -0.2101\*), nodes to tertiary raceme (-0.3113\*\* and -0.2983\*\*), stem length to tertiary raceme (-0.3115\*\* and -0.3052\*\*), 100 seed weight of tertiary raceme (-0.3245\*\* and -0.3031\*\*), harvest index (-0.5785\*\* and -0.5437\*\*), seed yield per plant at 120 days (-0.8430\*\* and -0.8269\*\*) and seed yield per plant up to 150 days (-0.7724\*\* and -0.7540\*\*) both at genotypic and phenotypic level.

#### **4.4.14 Number of tertiary branches per plant**

Number of tertiary branches per plant showed significant positive association with nodes to tertiary raceme (0.4157\*\* and 0.3780\*\*) both at genotypic and phenotypic level.

While this trait showed significant negative association both at genotypic and phenotypic level with total length of primary raceme (-0.2817\*\* and -0.2672\*\*), effective length of primary raceme (-0.3226\*\* and -0.3075\*\*), stem length to secondary raceme (-0.2095\* and -0.2038\*), total length of secondary raceme (-0.2067\* and -

0.1909\*), effective length of secondary raceme (-0.2486\*\* and -0.2403\*), days to 80% maturity of secondary raceme (-0.2222\* and -0.2101\*), days to 50% flowering of tertiary raceme (-0.2295\* and -0.2217\*) and days to 80% maturity of tertiary raceme (-0.3439\*\* and -0.3236\*\*).

#### **4.4.15 Days to 50% flowering of tertiary raceme**

This trait showed positive significant association with days to 50% flowering of primary raceme (0.8453\*\* and 0.8400\*\*), stem length to primary raceme (0.7403\*\* and 0.7364\*\*), nodes to primary raceme (0.7841\*\* and 0.7722\*\*), total length of primary raceme (0.4099\*\* and 0.3964\*\*), effective length of primary raceme (0.4255\*\* and 0.4182\*\*), days to 80% maturity of primary raceme (0.8221\*\* and 0.8158\*\*), days to 50% flowering of secondary raceme (0.9419\*\* and 0.9351\*\*), nodes to secondary raceme (0.5063\*\* and 0.4757\*\*), stem length to secondary raceme (0.5299\*\* and 0.5190\*\*), days to 80% maturity of secondary raceme (0.8781\*\* and 0.8696\*\*) and days to 80% maturity of tertiary raceme (0.8704\*\* and 0.8549\*\*). This trait showed significant negative association both at genotypic and phenotypic level with tertiary branches per plant (-0.2295\* and -0.2217\*), nodes to tertiary raceme (-0.3178\*\* and -0.2964\*\*), stem length to tertiary raceme (-0.2954\*\* and -0.2907\*\*), 100 seed weight of tertiary raceme (-0.2200\* and -0.2056\*), L/B ratio (-0.2719\*\* and -0.2514\*\*), harvest index (-0.5535\*\* and -0.5241\*\*), seed yield per plant at 120 days (-0.7235\*\* and -0.7117\*\*) and seed yield per plant up to 150 days (-0.7098\*\* and -0.6974\*\*).

#### **4.4.16 Number of nodes to tertiary raceme**

This trait showed significant positive association both at genotypic and phenotypic level tertiary branches per plant (0.4157\*\* and 0.3780\*\*), stem length to tertiary raceme (0.4626\*\* and 0.4265\*\*), 100 seed weight of tertiary raceme (0.3165\*\* and 0.2759\*\*), seed yield per plant at 120 days (0.2981\*\* and 0.2780\*\*) and seed yield per plant up to 150 days (0.3864\*\* and 0.3713\*\*) while this trait showed significant negative association with days to 50% flowering of primary raceme (-0.3086\*\* and -0.2938\*\*), stem length to primary raceme (-0.3189\*\* and -0.3030\*\*), nodes to primary raceme (-0.3255\*\* and -0.3104\*\*), days to 80% maturity of primary raceme (-0.2784\*\* and -0.2598\*\*), days to 50% flowering of secondary raceme (-0.3640\*\* and -0.3444\*\*), nodes to secondary raceme (-0.2364\* and -0.2060\*), stem length to secondary raceme (-0.2457\* and -0.2409\*), days to 80% maturity of secondary raceme (-0.3113\*\* and -0.2983\*\*), days to 50% flowering of tertiary raceme (-0.3178\*\* and -0.2964\*\*) and days to 80% maturity of tertiary raceme (-0.3936\*\* and -0.3934\*\*) both at genotypic and phenotypic level.

#### **4.4.17 Stem length to tertiary raceme**

This trait showed significant positive association with nodes to tertiary raceme (0.4626\*\* and 0.4265\*\*), 100 seed weight of tertiary raceme (0.2569\*\* and 0.2316\*\*), L/B ratio (0.2652\*\* and 0.2472\*\*), harvest index (0.2477\*\* and 0.2405\*), seed yield per plant at 120 days (0.2741\*\* and 0.2676\*\*) and seed yield per plant up to 150 days (0.3948\*\* and 0.3854\*\*) while it showed significant negative association with days to 50% flowering of primary raceme (-0.2920\*\* and -0.2881\*\*), stem length to primary

raceme (-0.1971\* and -0.1944\*), nodes to primary raceme (-0.3754\*\* and -0.3674\*\*), days to 80% maturity of primary raceme (-0.3275\*\* and -0.3235\*\*), secondary branches per plant (-0.2270\*\* and -0.2050\*\*), days to 50% flowering of secondary raceme (-0.2850\*\* and -0.2826\*\*), nodes to secondary raceme (-0.2936\*\* and -0.2771\*\*), stem length to secondary raceme (-0.2650\*\* and -0.2600\*\*), days to 80% maturity of secondary raceme (-0.3115\*\* and -0.3052\*\*), days to 50% flowering of tertiary raceme (-0.2954\*\* and -0.2907\*\*) and days to 80% maturity of tertiary raceme (-0.3049\*\* and -0.3038\*\*) both at genotypic and phenotypic level.

#### **4.4.18 Effective length of tertiary raceme**

Genotypic and phenotypic correlations revealed that effective length of tertiary raceme showed significant positive association total length of primary raceme (0.4259\*\* and 0.4114\*\*), effective length of primary raceme (0.2874\*\* and 0.2797\*\*), total length of secondary raceme (0.5858\*\* and 0.5678\*\*), effective length of secondary raceme (0.5284\*\* and 0.5108\*\*), harvest index (0.4671\*\* and 0.4671\*\*) and seed yield per plant up to 150 days (0.3236\*\* and 0.3236\*\*).

#### **4.4.19 Days to 80% maturity of tertiary raceme**

This trait showed significant positive association with days to 50% flowering of primary raceme (0.7882\*\* and 0.7732\*\*), stem length to primary raceme (0.7078\*\* and 0.6966\*\*), nodes to primary raceme (0.7038\*\* and 0.6777\*\*), total length of primary raceme (0.4652\*\* and 0.4541\*\*), effective length of primary raceme (0.4709\*\* and 0.4639\*\*), days to 80% maturity of primary raceme (0.7987\*\* and 0.7861\*\*), days to

50% flowering of secondary raceme (0.8790\*\* and 0.8641\*\*), nodes to secondary raceme (0.4382\*\* and 0.4157\*\*), stem length to secondary raceme (0.5426\*\* and 0.5266\*\*), effective length of secondary raceme (0.2202\* and 0.2096\*), days to 80% maturity of secondary raceme (0.8937\*\* and 0.8663\*\*) and days to 50% flowering of tertiary raceme (0.8704\*\* and 0.84549\*\*) and recorded significant negative association with tertiary branches per plant (-0.3439\*\* and -0.3236\*\*), nodes to tertiary raceme (-0.3936\*\* and -0.3491\*\*), stem length to tertiary raceme (-0.3049\*\* and -0.3038\*\*), 100 seed weight of tertiary raceme (-0.2822\*\* and -0.2632\*\*), harvest index (-0.4721\*\* and -0.4478\*\*), seed yield per plant at 120 days (-0.7595\*\* and -0.7530\*\*) and seed yield per plant up to 150 days (-0.6725\*\* and -0.6428\*\*) both at genotypic and phenotypic level.

#### **4.4.20 100 seed weight of primary raceme**

This trait showed significant positive association with total length of primary raceme (0.3039\*\* and 0.2971\*\*), effective length of primary raceme (0.3308\*\* and 0.3184\*\*), 100 seed weight of secondary raceme (0.8473\*\* and 0.7727\*\*), 100 seed weight of tertiary raceme (0.8191\*\* and 0.7527\*\*), oil content (0.7220\*\* and 0.6385\*\*), harvest index (0.3329\*\* and 0.3312\*\*), seed yield per plant at 120 days (0.3477\*\* and 0.3277\*\*) and seed yield per plant up to 150 days (0.4084\*\* and 0.3799\*\*) both at genotypic and phenotypic level, while it showed significant negative association with stem length to secondary raceme (-0.2856\*\* and -0.2813\*\*) both at phenotypic and genotypic level.

#### **4.4.21 100 seed weight of secondary raceme**

This trait recorded significant positive association with total length of primary raceme (0.2642\*\* and 0.2546\*\*), effective length of primary raceme (0.3093\*\* and 0.2952\*\*), nodes to secondary raceme (0.2188\* and 0.2081\*), 100 seed weight of primary raceme (0.8473\*\* and 0.7727\*\*), 100 seed weight of tertiary raceme (0.8095\*\* and 0.7243\*\*), oil content (0.5502\*\* and 0.4866\*\*), harvest index (0.2360\*\* and 0.2120\*\*), seed yield per plant at 120 days (0.3137\*\* and 0.3045\*\*) and seed yield per plant up to 150 days (0.3121\*\* and 0.3060\*\*) both at genotypic and phenotypic level. While it showed significant negative association with stem length to secondary raceme (-0.2606\*\* and -0.2388\*) both at genotypic and phenotypic level.

#### **4.4.22 100 seed weight of tertiary raceme**

This trait recorded significant positive association with nodes to tertiary raceme (0.3165\*\* and 0.2759\*\*), stem length to tertiary raceme (0.2569\*\* and 0.2316\*), 100 seed weight of primary raceme (0.8191\*\* and 0.7527\*\*), 100 seed weight of secondary raceme (0.8095\*\* and 0.7243\*\*), oil content (0.5012\*\* and 0.4173\*\*), harvest index (0.3867\*\* and 0.3387\*\*), seed yield per plant at 120 days (0.4338\*\* and 0.3984\*\*) and seed yield per plant up to 150 days (0.4591\*\* and 0.4571\*\*) both at genotypic and phenotypic level while it showed significant negative association with days to 50% flowering of primary raceme (-0.2607\*\* and -0.2441\*), stem length to primary raceme (-0.2245\* and -0.2023\*), nodes to primary raceme (-0.2145\* and -0.2049\*), stem length to secondary raceme (-0.4412\*\* and -0.4138\*\*), days to 80% maturity of secondary raceme (-0.3245\*\* and -0.3031\*\*), days to 50% flowering of tertiary raceme (-0.2200\* and -

0.2056\*) and days to 80% maturity of tertiary raceme (-0.2822\*\* and -0.2632\*\*) both at genotypic and phenotypic level.

#### **4.4.23 Oil content**

This trait recorded significant positive association with total length of primary raceme (0.3342\*\* and 0.2795\*\*), effective length of primary raceme (0.3653\*\* and 0.3119\*\*), 100 seed weight of primary raceme (0.7220\*\* and 0.6385\*\*), 100 seed weight of secondary raceme (0.5502\*\* and 0.4866\*\*), 100 seed weight of tertiary raceme (0.5012\*\* and 0.4173\*\*), seed yield per plant at 120 days (0.3086\*\* and 0.3088\*\*) and seed yield per plant up to 150 days (0.3240\*\* and 0.3240\*\*) both at genotypic and phenotypic level.

#### **4.4.24 L/B ratio of seed**

This trait showed significant positive association with stem length to tertiary raceme (0.2652\*\* and 0.2472\*\*), seed yield per plant at 120 days (0.2782\*\* and 0.2592\*\*), seed yield per plant up to 150 days (0.3275\*\* and 0.2948\*\*) both at genotypic and phenotypic level. While it showed significant negative association with days to 50% flowering of primary raceme (-0.3641\*\* and -0.3367\*\*), nodes to primary raceme (-0.2984\*\* and -0.2918\*\*), days to 80% maturity of primary raceme (-0.3022\*\* and -0.2785\*\*), days to 50% flowering of secondary raceme (-0.2973\*\* and -0.2740\*\*), nodes to secondary raceme (-0.2263\* and -0.1903\*) and days to 50% flowering of tertiary raceme (-0.2719\*\* and -0.2514\*\*) both at genotypic and phenotypic level.

#### **4.4.25 Harvest index**

This trait showed significant positive association total length of secondary raceme (0.2595\*\* and 0.2339\*\*), stem length to tertiary raceme (0.2477\*\* and 0.2405\*), effective length of tertiary raceme (0.4671\*\* and 0.4375\*\*), 100 seed weight of primary raceme (0.3329\*\* and 0.3312\*\*), 100 seed weight of secondary raceme (0.2360\* and 0.2120\*), 100 seed weight of tertiary raceme (0.3867\*\* and 0.3387\*\*), seed yield per plant at 120 days (0.6084\*\* and 0.5823\*\*) and seed yield per plant up to 150 days (0.7896\*\* and 0.7391\*\*) both at genotypic and phenotypic level.

While this trait showed significant negative association with days to 50% flowering of primary raceme (-0.6162\*\* and -0.5745\*\*), stem length to primary raceme (-0.6306\*\* and -0.5917\*\*), nodes to primary raceme (-0.6003\*\* and -0.5506\*\*), days to 80% maturity of primary raceme (-0.6002\*\* and -0.5631\*\*), days to 50% flowering of secondary raceme (-0.5468\*\* and -0.5184\*\*), stem length to secondary raceme (-0.5177\*\* and -0.4749\*\*), days to 80% maturity of secondary raceme (-0.5785\*\* and -0.5437\*\*), days to 50% flowering of tertiary raceme (-0.5535\*\* and -0.5241\*\*) and days to 80% maturity of tertiary raceme (-0.4721\*\* and -0.4478\*\*) at both genotypic and phenotypic level

#### **4.4.26 Seed yield per plant at 120 days**

This trait showed significant positive association with nodes to tertiary raceme (0.2981\*\* and 0.2780\*\*), stem length to tertiary raceme (0.2741\*\* and 0.2676\*\*), 100 seed weight of primary raceme (0.3477\*\* and 0.3277\*\*), 100 seed weight of secondary raceme (0.3137\*\* and 0.3045\*\*), 100 seed weight of tertiary raceme (0.4338\*\* and

0.3948\*\*), oil content (0.3088\*\* and 0.2718\*\*), L/B ratio (0.2782\*\* and 0.2532\*\*), harvest index (0.6084\*\* and 0.5823\*\*) and seed yield per plant up to 150 days (0.8480\*\* and 0.8363\*\*) while it showed significant negative association with days to 50% flowering of primary raceme (-0.7723\*\* and -0.7566\*\*), stem length to primary raceme (-0.5623\*\* and -0.5501\*\*), nodes to primary raceme (-0.6596\*\* and -0.6423\*\*), days to 80% maturity of primary raceme (-0.7751\*\* and -0.7586\*\*), days to 50% flowering of secondary raceme (-0.7536\*\* and -0.7426\*\*), nodes to secondary raceme (-0.3092\*\* and -0.2778\*\*), stem length to secondary raceme (-0.4105\*\* and -0.3867\*\*), days to 80% maturity of secondary raceme (-0.8430\*\* and -0.8269\*\*), days to 50% flowering of tertiary raceme (-0.7232\*\* and -0.7117\*\*) and days to 80% maturity of tertiary raceme (-0.7595\*\* and -0.7350\*\*) both at genotypic and phenotypic level.

#### **4.4.27 Seed yield per plant upto 150 days**

This trait showed significant positive association with total length of secondary raceme (0.2094\* and 0.1944\*), nodes to tertiary raceme (0.3864\*\* and 0.3713\*\*), stem length to tertiary raceme (0.3948\*\* and 0.3854\*\*), effective length of tertiary raceme (0.3236\*\* and 0.3120\*\*), 100 seed weight of primary raceme (0.4084\*\* and 0.3799\*\*), 100 seed weight of secondary raceme (0.3121\*\* and 0.3060\*\*), 100 seed weight of tertiary raceme (0.4591\*\* and 0.4175\*\*), oil content (0.3240\*\* and 0.2701\*\*), L/B ratio (0.3275\*\* and 0.2948\*\*), harvest index (0.7896\*\* and 0.7391\*\*) and seed yield per plant at 120 days (0.8480\*\* and 0.8363\*\*) and significant negative correlation with days to 50% flowering of primary raceme (-0.7817\*\* and -0.7663\*\*), stem length to primary raceme (-0.5952\*\* and -0.5816\*\*), nodes to primary raceme (-0.7258\*\* and -0.7080\*\*),

days to 80% maturity of primary raceme (-0.7767\*\* and -0.7575\*\*), days to 50% flowering of secondary raceme (-0.7300\*\* and -0.7131\*\*), nodes to secondary raceme (-0.3084\*\* and -0.2857\*\*), stem length to secondary raceme (-0.4946\*\* and -0.4655\*\*), days to 80% maturity of secondary raceme (-0.7724\*\* and -0.7540\*\*), days to 50% flowering of tertiary raceme (-0.7098\*\* and 0.6974\*\*) and days to 80% maturity of tertiary raceme (-0.6725\*\* and -0.6428\*\*) both at genotypic and phenotypic level.

#### **4.3.28 Seed yield per plant upto 180 days**

This trait showed significant positive association at both genotypic and phenotypic level with total length of primary raceme (0.2970\*\* and 0.2911\*\*), effective length of primary raceme (0.2416\* and 0.2221\*), total length of secondary raceme (0.3694\*\* and 0.3414\*\*), effective length of secondary raceme (0.2696\*\* and 0.2492\*\*), nodes to tertiary raceme (0.2902\*\* and 0.2799\*\*), stem length to tertiary raceme (0.2518\*\* and 0.2382\*\*), effective length of tertiary raceme (0.6119\*\* and 0.5672\*\*), 100 seed weight of primary raceme (0.4001\*\* and 0.3516\*\*), 100 seed weight of secondary raceme (0.3889\*\* and 0.3621\*\*), 100 seed weight of tertiary raceme (0.4683\*\* and 0.4119\*\*), oil content (0.3602\*\* and 0.2757\*\*), harvest index (0.7859\*\* and 0.7153\*\*), seed yield per plant at 120 days (0.5464\*\* and 0.5346\*\*) and seed yield per plant upto 150 days (0.7828\*\* and 0.7682\*\*) while days to 50% flowering of primary raceme (-0.3724\*\* and -0.3581\*\*), stem length to primary raceme (-0.2637\*\* and -0.2512\*\*), nodes to primary raceme (-0.3643\*\* and -0.3504\*\*), days to 80% maturity of primary raceme (-0.3955\*\* and -0.3732\*\*), days to 50% flowering of secondary raceme (-0.2956\*\* and -0.2769\*\*), stem length to secondary raceme (-0.3032\*\* and -0.2755\*\*), days to 80% maturity of secondary raceme (-0.3511\*\* and -

0.3339\*\*), days to 50% flowering of tertiary raceme (-0.2912\*\* and -0.2799\*\*) and days to 80% maturity of tertiary raceme (-0.2542\*\* and -0.2329\*\*) showed significant negative association with seed yield per plant upto 180 days both at genotypic and phenotypic level.

### **GENOTYPIC CORRELATION AFTER Z TRANSFORMATION**

Genotypic correlation after Z transformation showed positive significant association of the characters total length of primary raceme, effective length of primary raceme, total length of secondary raceme, effective length of secondary raceme, tertiary branches per plant, nodes to tertiary raceme, stem length to tertiary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, harvest index, seed yield per plant at 120 days and seed yield per plant up to 150 days with seed yield per plant up to 180 days and negative significant association with days to 50% flowering of primary raceme, stem length to primary raceme, nodes to primary raceme, days to 80% maturity of primary raceme, days to 50% flowering of secondary raceme, stem length to secondary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme and days to 80% maturity of tertiary raceme (Table 14).

## **4.5 PATH COEFFICIENT ANALYSIS**

The direct and indirect effects of different yield components on yield worked out through path analysis at genotypic and phenotypic levels are presented in Table-15 and Table-16.

### **4.5.1 Days to 50% flowering of primary raceme**

The direct contribution of this character on seed yield per plant up to 180 days was negative (-0.0657 and -0.1525) at both phenotypic and genotypic levels, respectively. The indirect effect through nodes to primary raceme (0.1530 and 0.7026), effective length of primary raceme (0.0640 and 0.2877), days to 80% maturity of secondary raceme (0.2507 and 0.5861), days to 50% flowering of tertiary raceme (0.1162 and 0.5588), nodes to tertiary raceme (0.0013 and 0.0480), L/B ratio(0.0881 and 0.0291) were positive while total length of primary raceme (-0.0320 and -0.2331), days to 80% maturity of primary raceme (-0.0177 and -0.3900), 100 seed weight of tertiary raceme (-0.0254 and -0.0261), harvest index (-0.1751 and -0.4910), seed yield per plant up to 150 days (-0.7110 and -0.5200) showed negative effect both at phenotypic and genotypic levels. Days to 50% flowering of secondary raceme (0.0180 and -1.1456), stem length to tertiary raceme (0.0093 and -0.0035), 100 seed weight of primary raceme (0.0251 and -0.0762) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Nodes to secondary raceme (-0.0195 and 0.0685), stem length to secondary raceme (-0.0036 and 0.0345) and seed yield per plant at 120 days (-0.0565 and 0.0729), showed negative indirect effect at phenotypic level and positive indirect

effect at genotypic level. This trait had a negative and significant association with seed yield per plant up to 180 days (-0.3581\*\* and -0.3724\*\*) at both the levels.

#### **4.5.2 Stem length to primary raceme**

The direct contribution of stem length to primary raceme (-0.0294 and 0.3076) on seed yield per plant up to 180 days was negative at phenotypic level and positive at genotypic level. The indirect effect through nodes to primary raceme (0.01300 and 0.5968), effective length of primary raceme (0.0668 and 0.3031), days to 80% maturity of secondary raceme (0.2184 and 0.5103), days to 50% flowering of tertiary raceme (0.1018 and 0.4895), nodes to tertiary raceme (0.0013 and 0.0496), days to 80% maturity of tertiary raceme (0.1167 and 0.0900) were positive at both the levels. While days to 50% flowering of primary raceme (-0.0502 and -0.1170), total length of primary raceme (-0.0356 and -0.2618), days to 80% maturity of primary raceme (-0.0158 and -0.3477), 100 seed weight of tertiary raceme (-0.0210 and -0.0225), harvest index (-0.1679 and -0.4783) seed yield per plant up to 150 days (-0.6569 and -0.4828) were negative at both phenotypic and genotypic levels. Days to 50% flowering of secondary raceme (0.0163 and -1.0446), stem length to tertiary raceme (0.0119 and -0.0045) were positive at phenotypic level and negative at genotypic level. Nodes to secondary raceme (-0.0179 and 0.642), stem length to secondary raceme (-0.0035 and 0.0331), seed yield per plant at 120 days (-0.0411 and 0.0531) were negative at phenotypic level and positive at genotypic level. This trait had a negative significant association with seed yield per plant up to 180 days (-0.2512\*\* and -0.2637\*\*) at both the phenotypic and genotypic levels.

### **4.5.3 Nodes to primary raceme**

The direct contribution of nodes to primary raceme (0.1724 and 0.7811) on seed yield per plant up to 180 days was positive at both phenotypic and genotypic levels. The indirect contribution through days to 80% maturity of secondary raceme (0.2268 and 0.5369), days to 50% flowering of tertiary raceme (0.1068 and 0.5184), nodes to tertiary raceme (0.0014 and 0.0507), days to 80% maturity of tertiary raceme (0.1135 and 0.0895), L/B ratio (0.0098 and 0.0239) were positive at both the levels while days to 50% flowering of primary raceme (-0.0584 and -0.1372), days to 80% maturity of primary raceme (-0.0166 and -0.3694), 100 seed weight of tertiary raceme (-0.0213 and -0.0215), harvest index (-0.1679 and -0.4783), seed yield per plant up to 150 days (-0.6569 and -0.04828) were negative at both phenotypic and genotypic level. Days to 50% flowering of secondary raceme (0.0163 and -1.0446), stem length to tertiary raceme (0.0119 and -0.0045) were positive at phenotypic level and negative at genotypic level. Stem length to primary raceme (-0.0222 and 0.2351), stem length to secondary raceme (-0.0030 and 0.0291), seed yield per plant at 120 days (-0.0480 and 0.0623) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had negative and significant correlation with seed yield per plant upto 180 days (-0.3504\*\* and -0.3643\*\*) at both genotypic and phenotypic level.

### **4.5.4 Total length of primary raceme**

The direct contribution of this character on seed yield per plant up to 180 days was negative (-0.1264 and -0.9059) at both phenotypic and genotypic levels. The indirect contribution through effective length of primary raceme (0.2119 and 0.9744), days to

80% maturity of secondary raceme (0.1158 and 0.2745), days to 50% flowering of tertiary raceme (0.0548 and 0.2710), effective length of tertiary raceme (0.0700 and 0.0303), days to 80% maturity of tertiary raceme (0.0761 and 0.0592), oil content (0.0101 and 0.0297) were positive while days to 50% flowering of primary raceme (-0.0166 and -0.0392), days to 80% maturity of primary raceme (-0.0071 and -0.1591), tertiary branches per plant (-0.0580 and -0.1513) were negative at both phenotypic and genotypic levels. Days to 50% flowering of secondary raceme (0.0086 and -0.5542), effective length of secondary raceme (0.0703 and -0.0846) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to primary raceme (-0.0083 and 0.0889), nodes to secondary raceme (-0.0195 and 0.0689), stem length to secondary raceme (-0.0028 and 0.0265), total length of secondary raceme (-0.1176 and 0.1217), 100 seed weight of primary raceme (-0.0411 and 0.1204), 100 seed weight of secondary raceme (-0.0010 and 0.1470) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had positive and significant correlation with seed yield per plant up to 180 days (0.2911\*\* and 0.2970\*\*) at both phenotypic and genotypic level.

#### **4.5.5 Effective length of primary raceme**

The direct contribution of effective length of primary raceme (0.2350 and 1.0579) on seed yield per plant up to 180 days was positive at both phenotypic and genotypic levels. The indirect effect through days to days to 80% maturity of secondary raceme (0.1131 and 0.2661), effective length of tertiary raceme (0.0476 and 0.0204), days to 80% maturity of tertiary raceme (0.0777 and 0.0599), oil content (0.0113 and 0.0325)

were positive at both the levels. While days to 50% flowering of primary raceme (-0.0179 and -0.0415), total length of primary raceme (-0.1140 and -0.8344), days to 80% maturity of primary raceme (-0.0069 and -0.1526), tertiary branches per plant (-0.0667 and -0.1732), 100 seed weight of secondary raceme (-0.0012 and -0.1721) were negative at both phenotypic and genotypic levels. Days to 50% flowering of secondary raceme (0.0089 and -0.5677), effective length of secondary raceme (0.0784 and -0.0942) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to primary raceme (-0.0084 and 0.0881), nodes to secondary raceme (-0.0169 and 0.0569), stem length to secondary raceme (-0.0028 and 0.0273), total length of secondary raceme (-0.1198 and 0.1231), 100 seed weight of primary raceme (-0.0440 and 0.1310) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had positive and non significant correlation with seed yield per plant upto 180 days (0.2221 and 0.2416) at both the levels.

#### **4.5.6 Days to 80% maturity of primary raceme**

The direct contribution of days to 80% maturity of primary raceme (-0.0209 and -0.4578) on seed yield per plant upto 180 days was positive at phenotypic level and negative at genotypic level. The indirect effect through nodes to primary raceme (0.1367 and 0.6303), effective length of primary raceme (0.775 and 0.3527), days to 80% maturity of secondary raceme (0.2610 and 0.6126), days to 50% flowering of tertiary raceme (0.1128 and 0.5435), nodes to tertiary raceme (0.0011 and 0.0433), days to 80% maturity of tertiary raceme (0.1317 and 0.1016), L/B ratio (0.0097 and 0.0242) were positive at both the levels while days to 50% flowering of primary raceme (-0.0557 and -

0.1299), total length of primary raceme (-0.0431 and -0.3148), harvest index (-0.1717 and -0.4782), seed yield per plant up to 150 days (-0.7028 and -0.5166) were negative both at phenotypic and genotypic levels. Days to 50% flowering of secondary raceme (0.0180 and -1.1414), stem length to tertiary raceme (0.0105 and -0.0039) showed indirect positive effect at phenotypic level and negative indirect effect at genotypic level. Stem length to primary raceme (-0.0222 and 0.2326), nodes to secondary raceme (-0.0232 and 0.0815), stem length to secondary raceme (-0.0034 and 0.0321), seed yield per plant at 120 days (-0.0567 and 0.0732) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had a negative significant correlation with seed yield per plant up to 180 days (-0.3732\*\* and -0.3955\*\*) both at genotypic and phenotypic levels.

#### **4.5.7 Secondary branches per plant**

The direct contribution of secondary branches per plant (0.1080 and -0.1476) on seed yield per plant up to 180 days was positive at phenotypic level and negative at genotypic level. The indirect effect through stem length to tertiary raceme (0.0066 and -0.0027) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to secondary raceme (-0.0015 and 0.0161) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had a positive and non significant correlation with seed yield per plant up to 180 days (0.0306 and 0.0492) at both phenotypic and genotypic level.

#### **4.5.8 Days to 50% flowering of secondary raceme**

The direct effect of days to 50% flowering of secondary raceme (0.0202 and -1.2751) on seed yield per plant up to 180 days was positive at phenotypic level and negative at genotypic level. The indirect effect through nodes to primary raceme (0.1388 and 0.6399), effective length of primary raceme (0.1030 and 0.4710), days to 80% maturity of secondary raceme (0.2683 and 0.6266), days to 50% flowering of tertiary raceme (0.1293 and 0.6227), nodes to tertiary raceme (0.0015 and 0.0567), days to 80% maturity of tertiary raceme (0.1447 and 0.1118), L/B ratio (0.0096 and 0.0238) were positive while days to 50% flowering of primary raceme (-0.0587 and -0.1370), total length of primary raceme (-0.0535 and -0.3937), days to 80% maturity of primary raceme (-0.0186 and -0.4098), harvest index (-0.1580 and -0.4357), seed yield per plant up to 150 days (-0.6617 and -0.4856) were negative both at phenotypic and genotypic levels. Stem length to primary raceme (-0.0236 and 0.2487), nodes to secondary raceme (-0.0298 and 0.1036), stem length to secondary raceme (-0.0039 and 0.0365), seed yield per plant at 120 days (-0.0555 and 0.0712) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had negative and significant association with seed yield per plant upto 180 days (-0.2769\*\* and -0.2956\*\*) both at phenotypic and genotypic levels.

#### **4.5.9 Nodes to secondary raceme**

The direct contribution of nodes to secondary raceme (-0.0568 and 0.1874) on seed yield per plant up to 180 days was negative at phenotypic level and positive at genotypic level. The indirect effect through nodes to primary raceme (0.0569 and

0.2709), effective length of primary raceme (0.0700 and 0.3213), days to 80% maturity of secondary raceme (0.1331 and 0.3294), days to 50% flowering of tertiary raceme (0.0658 and 0.3347), nodes to tertiary raceme (0.0009 and 0.0368), days to 80% maturity of tertiary raceme (0.0696 and 0.0557), L/B ratio (0.0066 and 0.0181) were positive at both the levels. While days to 50% flowering of primary raceme (-0.0226 and -0.0557), total length of primary raceme (-0.0434 and -0.3329), days to 80% maturity of primary raceme (-0.0086 and -0.1992), 100 seed weight of secondary raceme (-0.0008 and -0.1217), seed yield per plant up to 150 days (-0.2650 and -0.2052) were negative both at phenotypic and genotypic level. Days to 50% flowering of secondary raceme (0.0106 and -0.7049), stem length to tertiary raceme (0.0090 and -0.0035) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to primary raceme (-0.0093 and 0.1054), stem length to secondary raceme (-0.0026 and 0.0256) and seed yield per plant at 120 days (-0.0208 and 0.0292) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had negative and non significant association with seed yield per plant upto 180 days (-0.0531 and -0.0417) both at phenotypic and genotypic levels.

#### **4.5.10 Stem length to secondary raceme**

The direct effect of stem length to secondary raceme (-0.0076 and 0.0709) on seed yield per plant upto 180 days was negative both at phenotypic and positive at genotypic level. The indirect effect through nodes to primary raceme (0.0684 and 0.3208), effective length of primary raceme (0.0878 and 0.4080), days to 80% maturity of secondary raceme (0.1577 and 0.3735), days to 50% flowering of tertiary raceme (0.0718

and 0.3504), nodes to tertiary raceme (0.0011 and 0.0382), days to 80% maturity of tertiary raceme (0.0882 and 0.0690), 100 seed weight of secondary raceme (0.0010 and 0.1450) were positive at both levels while days to 50% flowering of primary raceme (-0.0312 and -0.0743), total length of primary raceme (-0.0456 and -0.3389), days to 80% maturity of primary raceme (-0.0092 and -0.2072), tertiary branches per plant (-0.0442 and -0.1125), 100 seed weight of tertiary raceme (-0.0430 and -0.0442), harvest index (-0.1448 and -0.4125), seed yield per plant up to 150 days (-0.4319 and -0.3290) were negative both at phenotypic and genotypic levels. Secondary branches per plant (0.0214 and -0.0336), days to 50% flowering of secondary raceme (0.0102 and -0.6573), effective length of secondary raceme (0.0355 and -0.0428), stem length to tertiary raceme (0.0084 and -0.0032), 100 seed weight of primary raceme (0.0389 and -0.1132) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to primary raceme (-0.0135 and 0.1437), nodes to secondary raceme (-0.0191 and 0.0676), total length of secondary raceme (-0.0441 and 0.0455) and seed yield per plant at 120 days (-0.0289 and 0.0388) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had negative and significant association with seed yield per plant up to 180 days (-0.2755\*\* and -0.3022\*\*) both at phenotypic and genotypic level.

#### **4.5.11 Total length of secondary raceme**

The direct effect of total length of secondary raceme (-0.2072 and 0.2086) on seed yield per plant up to 180 days was negative both at phenotypic and positive at genotypic level. The indirect effect through effective length of primary raceme (0.1359 and 0.6244),

effective length of tertiary raceme (0.0966 and 0.0417), harvest index (0.0713 and 0.2067), seed yield per plant up to 150 days (0.1804 and 0.1393) were positive at both levels while days to 50% flowering of primary raceme (-0.0025 and -0.0060), tertiary branches per plant (-0.0414 and -0.1110) were negative both at phenotypic and genotypic levels. Effective length of secondary raceme (0.1283 and -0.1532) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to secondary raceme (-0.0016 and 0.0155) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had positive and significant association with seed yield per plant upto 180 (0.3414\*\* and 0.3694\*\*) both at phenotypic and genotypic level.

#### **4.5.12 Effective length of secondary raceme**

The direct effect of this trait (0.1392 and -0.1633) on seed yield per plant up to 180 days was positive both at phenotypic level and negative at genotypic level. The indirect effect through effective length of primary raceme (0.1323 and 0.6104), effective length of tertiary raceme (0.0869 and 0.0376), days to 80% maturity of tertiary raceme (0.0351 and 0.0280) were positive both at phenotypic and genotypic levels. While days to 50% flowering of primary raceme (-0.0041 and -0.0098), tertiary branches per plant (-0.0521 and -0.1335) were negative both at phenotypic and genotypic level. Days to 50% flowering of secondary raceme (0.0041 and -0.2621) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to secondary raceme (-0.0019 and 0.0186), total length of secondary raceme (-0.1910 and 0.1957) showed negative indirect effect at phenotypic level and positive indirect effect at

genotypic level. This trait had positive and significant correlation with seed yield per plant upto 180 days (0.2492\*\* and 0.2696\*\*) both at phenotypic and genotypic level.

#### **4.5.13 Days to 80% maturity of secondary raceme**

The direct contribution of days to 80% maturity of secondary raceme (0.2906 and 0.6720) on seed yield per plant upto 180 days was positive both at phenotypic and genotypic level. The indirect effect through nodes to primary raceme (0.1346 and 0.6241), effective length of primary raceme (0.0914 and 0.4190), days to 50% flowering of tertiary raceme (0.1203 and 0.5806), nodes to tertiary raceme (0.0013 and 0.0485), days to 80% maturity of tertiary raceme (0.1451 and 0.1137) were positive both at phenotypic and genotypic level. While days to 50% flowering of primary raceme (-0.0567 and -0.1330), total length of primary raceme (-0.0504 and -0.3700), days to 80% maturity of primary raceme (-0.0188 and -0.4174), tertiary branches per plant (-0.0456 and -0.1193), harvest index (-0.1658 and -0.4610), seed yield per plant up to 150 days (-0.6996 and -0.5138) were negative both at phenotypic and genotypic level. Days to 50% flowering of secondary raceme (0.0187 and -1.1890), stem length to tertiary raceme (0.0099 and -0.0037) showed positive indirect effect at phenotypic and negative indirect effect at genotypic levels. Stem length to primary raceme (-0.0221 and 0.2336), nodes to secondary raceme (-0.0260 and 0.0919), stem length to secondary raceme (-0.0041 and 0.0394), seed yield per plant at 120 days (-0.0618 and 0.0796) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had negative significant correlation with seed yield per plant at 180 days (-0.3339\*\* and -0.3511\*\*) both at phenotypic and genotypic levels.

#### **4.5.14 Number of tertiary branches per plant**

The direct effect of tertiary branches per plant (0.2170 and 0.5370) on seed yield per plant upto 180 days was positive both at phenotypic and genotypic levels. The indirect effect through total length of primary raceme (0.0338 and 0.2552) was positive both at phenotypic and genotypic level effective length of primary raceme (-0.0723 and -0.3413), days to 80% maturity of secondary raceme (-0.0610 and -0.1493), days to 50% flowering of tertiary raceme (-0.0307 and -0.1517), nodes to tertiary raceme (-0.0017 and -0.0647), days to 80% maturity of tertiary raceme (-0.0542 and -0.0437) were negative both at phenotypic and genotypic level. Stem length to secondary raceme (0.0016 and -0.0149), total length of secondary raceme (0.0395 and -0.0431) showed positive indirect effect at phenotypic and negative indirect effect at genotypic levels. Effective length of secondary raceme (-0.0334 and 0.0406) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had positive non significant association with seed yield per plant upto 180 days (0.1763 and 0.1990) both at phenotypic and genotypic level.

#### **4.5.15 Days to 50% flowering of tertiary raceme**

The direct effect of days to 50% flowering of tertiary raceme (0.1383 and 0.6611) on seed yield per plant up to 180 days was positive both at phenotypic and genotypic level. The indirect effect through nodes to primary raceme (0.1331 and 0.6124), effective length of primary raceme (0.0983 and 0.4502), days to 80% maturity of secondary raceme (0.2527 and 0.5901), nodes to tertiary raceme (0.0013 and 0.0495), days to 80% maturity of tertiary raceme (0.1432 and 0.1107), L/B ratio (0.0088 and 0.0218) were

positive both at phenotypic and genotypic levels while days to 50% flowering of primary raceme (-0.0552 and -0.1289), total length of primary raceme (-0.0501 and -0.3713), days to 80% maturity of primary raceme (-0.0171 and -0.3764), tertiary branches per plant (-0.0481 and -0.1232), 100 seed weight of tertiary raceme (-0.0214 and -0.0221), harvest index (-0.1598 and -0.4410), seed yield per plant up to 150 days (-0.6470 and -0.4722) were negative both at phenotypic and genotypic levels. Days to 50% flowering of secondary raceme (0.0189 and -1.2011), stem length to tertiary raceme (0.0094 and -0.0035) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to primary raceme (-0.0217 and 0.2278), nodes to secondary raceme (-0.0270 and 0.0949), stem length to secondary raceme (-0.0040 and 0.0376), seed yield per plant at 120 days (-0.0532 and 0.0683) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had negative and significant correlation with seed yield per plant upto 150 days (-0.2799\*\* and -0.2912\*\*) both at phenotypic and genotypic level.

#### **4.5.16 Nodes to tertiary raceme**

The direct contribution of nodes to tertiary raceme (-0.0044 and -0.1557) on seed yield per plant upto 180 days was negative both at phenotypic and genotypic level. The indirect effect through days to 50% flowering of primary raceme (0.0193 and 0.0471), days to 80% maturity of primary raceme (0.0054 and 0.1274), tertiary branches per plant (0.0820 and 0.2232), 100 seed weight of tertiary raceme (0.02887 and 0.2317), seed yield per plant up to 150 days (0.3445 and 0.2571) were positive both at phenotypic and genotypic levels. While nodes to primary raceme (-0.0535 and -0.2542), days to 80%

maturity of secondary raceme (-0.0867 and -0.2092), days to 50% flowering of tertiary raceme (-0.0410 and -0.2101), days to 80% maturity of tertiary raceme (-0.0585 and -0.0510) were negative both at phenotypic and genotypic level. Stem length to primary raceme (0.0089 and -0.0981), nodes to secondary raceme (0.0117 and -0.0443), stem length to secondary raceme (0.0018 and -0.0174), seed yield per plant at 120 days (0.0208 and -0.0282) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Days to 50% flowering of secondary raceme (-0.0070 and 0.4643), stem length to tertiary raceme (-0.0138 and 0.0055) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had positive significant association with seed yield per plant up to 180 days (0.2799\*\* and 0.2902\*\*) both at phenotypic and genotypic levels.

#### **4.5.17 Stem length to tertiary raceme**

The direct effect of stem length to tertiary raceme (-0.0324 and 0.0120) on seed yield per plant up to 180 days was negative at phenotypic level and positive at genotypic level. The indirect effect through days to 50% flowering of primary raceme (0.0189 and 0.0445), days to 80% maturity of primary raceme (0.0068 and 0.1499), 100 seed weight of tertiary raceme (0.0241 and 0.0257), harvest index (0.0733 and 0.1974), seed yield per plant up to 150 days (0.3576 and 0.2626) were positive both at phenotypic and genotypic levels while nodes to primary raceme (-0.0634 and -0.2932), days to 80% maturity of secondary raceme (-0.0887 and -0.2093), days to 50% flowering of tertiary raceme (-0.0402 and -0.1953), nodes to tertiary raceme (-0.0019 and -0.0720), days to 80% maturity of tertiary raceme (-0.0509 and -0.0388), L/B ratio (-0.0086 and -0.0212) were negative

both at phenotypic and genotypic level. Stem length to primary raceme (0.0057 and -0.0606), nodes to secondary raceme (0.0157 and -0.0550), stem length to secondary raceme (0.0020 and -0.0188), seed yield per plant at 120 days (0.0200 and -0.0259) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Secondary branches per plant (-0.0221 and 0.0335), days to 50% flowering of secondary raceme (-0.0057 and 0.3634) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had positive non significant correlation at phenotypic level and positive significant correlation at genotypic level with seed yield per plant upto 180 days (0.2382 and 0.2518\*\*).

#### **4.5.18 Effective length of tertiary raceme**

The direct contribution of effective length of tertiary raceme (0.1701 and 0.0711) on seed yield per plant up to 180 days was positive both at phenotypic and genotypic level. The indirect effect through effective length of primary raceme (0.0657 and 0.3040), harvest index (0.1334 and 0.3722), seed yield per plant up to 150 days (0.2895 and 0.2153) were positive both at phenotypic and genotypic levels. While total length of primary raceme (-0.0520 and -0.3858) were negative both at phenotypic and genotypic levels. Effective length of secondary raceme (0.0711 and -0.0863) showed indirect effect positively at phenotypic level and indirect effect negatively at genotypic level. Total length of secondary raceme (-0.1177 and 0.1222) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had positive significant correlation on seed yield per plant upto 180 days (0.5672\*\* and 0.6119\*\*) both at phenotypic and genotypic levels.

#### **4.5.19 Days to 80% maturity of tertiary raceme**

The direct effect of days to 80% maturity of tertiary raceme (0.1675 and 0.1272) on seed yield per plant up to 180 days was positive both at phenotypic and genotypic level. The indirect effect through nodes to primary raceme (0.1168 and 0.5497), effective length of primary raceme (0.1090 and 0.4982), days to 80% maturity of secondary raceme (0.2517 and 0.6006), days to 50% flowering of tertiary raceme (0.1182 and 0.5755), nodes to tertiary raceme (0.0015 and 0.0613) were positive both at phenotypic and genotypic level. While days to 50% flowering of primary raceme (-0.0508 and -0.1202), total length of primary raceme (-0.0574 and -0.4214), days to 80% maturity of primary raceme (-0.0165 and -0.3657), tertiary branches per plant (-0.0702 and -0.1847), 100 seed weight of tertiary raceme (-0.0274 and -0.0283), harvest index (-0.1365 and -0.3761), seed yield per plant up to 150 days (-0.5964 and -0.4473) were negative both at phenotypic and genotypic levels. Days to 50% flowering of secondary raceme (0.0175 and -1.1208), effective length of secondary raceme (0.0292 and -0.0360), stem length to tertiary raceme (0.0098 and -0.0037) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to primary raceme (-0.0205 and 0.2177), nodes to secondary raceme (-0.0236 and 0.0821), stem length to secondary raceme (-0.0040 and 0.0385), seed yield per plant at 120 days (-0.0549 and 0.0717) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had negative and significant correlation with seed yield per plant upto 180 days (-0.2329\* and 0.2542\*\*) both at phenotypic and genotypic level.

#### **4.5.20 100 seed weight of primary raceme**

The direct effect of 100 seed weight of primary raceme (-0.1383 and 0.3962) on seed yield per plant up to 180 days was negative at phenotypic level and positive at genotypic level. The indirect effect through effective length of primary raceme (0.0748 and 0.3499), 100 seed weight of tertiary raceme (0.0783 and 0.0821), oil content (0.0231 and 0.0642), harvest index (0.0979 and 0.2653), seed yield per plant up to 150 days (0.3525 and 0.2717) were positive both at phenotypic and genotypic level. While total length of primary raceme (-0.0375 and -0.2753), 100 seed weight of secondary raceme (-0.0031 and -0.4715) were negative both at phenotypic and genotypic level. Stem length to secondary raceme (0.0021 and -0.0202) and seed yield per plant at 120 days (0.0245 and -0.0328) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. This trait had positive and significant association with seed yield per plant upto 180 days (0.3516\*\* and 0.4001\*\*).

#### **4.5.21 100 seed weight of secondary raceme**

The direct effect of 100 seed weight of secondary raceme (-0.0040 and -0.5564) on seed yield up to 180 days was negative both at phenotypic and genotypic level. The indirect effect through effective length of primary raceme (0.0694 and 0.3272), 100 seed weight of tertiary raceme (0.0753 and 0.0811), oil content (0.0176 and 0.0489), harvest index (0.0646 and 0.1881), seed yield per plant up to 150 days (0.2839 and 0.2076) were positive both at phenotypic and genotypic level. While total length of primary raceme (-0.0322 and -0.2393) were negative both at phenotypic and genotypic level. Stem length to secondary raceme (0.0018 and -0.0185) and seed yield per plant at 120 days (0.0227

and -0.0296) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Nodes to secondary raceme (-0.0118 and 0.0410) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. This trait had positive and significant correlation with seed yield per plant upto 180 days (0.3621\*\* and 0.3889\*\*) both at phenotypic and genotypic level.

#### **4.5.22 100 seed weight of tertiary raceme**

The direct effect of 100 seed weight of tertiary raceme (0.1040 and 0.1002) on seed yield per plant upto 180 days was positive both at phenotypic and genotypic level. The indirect effect through days to 50% flowering of primary raceme (0.0160 and 0.0398), oil content (0.0151 and 0.0445), harvest index (0.1033 and 0.3081) and seed yield per plant up to 150 days (0.3873 and 0.3054) were positive both at phenotypic and genotypic levels. While nodes to primary raceme (-0.0353 and -0.1676), days to 80% maturity of secondary raceme (-0.0880 and -0.2180), days to 50% flowering of tertiary raceme (-0.0284 and -0.1455), nodes to tertiary raceme (-0.0012 and -0.0493), days to 80% maturity of tertiary raceme (-0.0441 and -0.0359), 100 seed weight of secondary raceme (-0.0029 and -0.4504) were negative both at phenotypic and genotypic level. Stem length to primary raceme (0.0060 and -0.0691), stem length to secondary raceme (0.0032 and -0.0313) and seed yield per plant at 120 days (0.0295 and -0.0410) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Stem length to tertiary raceme (-0.0075 and 0.0031), 100 seed weight of primary raceme (-0.1041 and 0.3245) showed negative indirect effect at phenotypic level and positive

indirect effect at genotypic level. This trait had positive and significant association with seed yield per plant up to 180 days (0.4119\*\* and 0.4683\*\*).

#### **4.5.23 Oil content**

The direct effect of oil content (0.0361 and 0.0889) on seed yield per plant up to 180 days was positive both at phenotypic and genotypic level. The indirect effect through effective length of primary raceme (0.0733 and 0.3864), 100 seed weight of tertiary raceme (0.0434 and 0.0502), seed yield per plant up to 150 days (0.2506 and 0.2155) were positive both at phenotypic and genotypic level. While total length of primary raceme (-0.0355 and -0.3028), 100 seed weight of secondary raceme (-0.0019 and -0.3062) were negative both at phenotypic and genotypic level. Seed yield per plant at 120 days (0.0203 and -0.0292) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. 100 seed weight of primary raceme (-0.0883 and 0.2861) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait has positive and significant association with seed yield per plant up to 180 days (0.2757\*\* and 0.3602\*\*) both at phenotypic and genotypic levels.

#### **4.5.24 L/B ratio of the seed**

The direct contribution of L/B ratio of the seed (-0.0349 and -0.0800) on seed yield per plant was negative at both phenotypic and genotypic level. The indirect contribution through days to 50% flowering of primary raceme (0.0221 and 0.0555), days to 80% maturity of primary raceme (0.0058 and 0.1383), seed yield per plant up to 150

days (0.2735 and 0.2178) was positive both at phenotypic and genotypic levels. While nodes to primary raceme (-0.0486 and -0.2331), days to 50% flowering of tertiary raceme (-0.0348 and -0.1798) was negative both at phenotypic and genotypic levels. Nodes to secondary raceme (0.0108 and -0.0424), stem length to secondary raceme (0.0009 and -0.0091), seed yield per plant at 120 days (0.0194 and -0.0263) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. days to 50% flowering of secondary raceme (-0.0055 and 0.3791) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had positive and non significant association with seed yield per plant up to 180 days (0.1037 and 0.1227) both at phenotypic and genotypic levels.

#### **4.5.25 Harvest index**

The direct contribution of harvest index (0.3049 and 0.7968) on seed yield per plant upto 180 days was positive both at phenotypic and genotypic level. The indirect effect through days to 50% flowering of primary raceme (0.0378 and 0.0940), days to 80% maturity of primary raceme (0.0118 and 0.2748), effective length of tertiary raceme (0.0744 and 0.0332), 100 seed weight of tertiary raceme (0.0352 and 0.0388), seed yield per plant up to 150 days (0.6857 and 0.5253) were positive both at phenotypic and genotypic level. While nodes to primary raceme (-0.0949 and -0.4689), days to 80% maturity of secondary raceme (-0.1580 and -0.3888), days to 50% flowering of tertiary raceme (-0.0725 and -0.3659), days to 80% maturity of tertiary raceme (-0.0750 and -0.0600), 100 seed weight of secondary raceme (-0.0008 and -0.1313) were negative both at phenotypic and genotypic level. Stem length to primary raceme (0.0174 and -0.1940),

stem length to secondary raceme (0.0036 and -0.0367), seed yield per plant at 120 days (0.0435 and -0.0575) showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level. Days to 50% flowering of secondary raceme (-0.0105 and 0.6972), total length of secondary raceme (-0.0485 and 0.0541), 100 seed weight of primary raceme (-0.0444 and 0.1319) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait has positive and significant association with seed yield per plant upto 180 days (0.7153\*\* and 0.7859\*\*) both at phenotypic and genotypic level.

#### **4.5.26 Seed yield per plant at 120 days**

The direct effect of seed yield per plant at 120 days (0.0747 and -0.0945) on seed yield per plant up to 180 days was positive at phenotypic level and negative at genotypic level. The indirect effect through days to 50% flowering of primary raceme (0.0497 and 0.1178), days to 80% maturity of primary raceme (0.0159 and 0.3549), 100 seed weight of tertiary raceme (0.0411 and 0.0435), oil content (0.0098 and 0.0274), harvest index (0.1775 and 0.4847), seed yield per plant up to 150 days (0.7760 and 0.5641) were positive both at phenotypic and genotypic levels. While nodes to primary raceme (-0.1107 and -0.5152), days to 80% maturity of secondary raceme (-0.2403 and -0.5665), days to 50% flowering of tertiary raceme (-0.0984 and -0.4781), nodes to tertiary raceme (-0.0012 and -0.0464), days to 80% maturity of tertiary raceme (-0.0012 and -0.1746), L/B ratio (-0.0090 and -0.0223) were negative both at phenotypic and genotypic levels. Stem length to primary raceme (0.0162 and -0.1730), nodes to secondary raceme (0.0158 and -0.0580), stem length to secondary raceme (0.0030 and -0.0291) showed positive indirect

effect at phenotypic and negative indirect effect at genotypic levels. Days to 50% flowering of secondary raceme (-0.0150 and 0.9609), stem length to tertiary raceme (-0.0087 and 0.0033), 100 seed weight of primary raceme (-0.0453 and 0.1378) showed negative indirect effect and positive indirect effect at phenotypic and genotypic levels respectively. This trait had positive and significant correlation with seed yield per plant up to 180 days (0.5346\*\* and 0.5464\*\*) both at phenotypic and genotypic level.

#### **4.5.27 Seed yield per plant up to 150 days**

The direct effect of this character (0.9278 and 0.6652) on seed yield per plant upto 180 days was positive both at phenotypic and genotypic levels. The indirect effect through days to 50% flowering of primary raceme (0.0504 and 0.1192), days to 80% maturity of primary raceme (0.0159 and 0.3556), effective length of tertiary raceme (0.0531 and 0.0230), 100 seed weight of tertiary raceme (0.0434 and 0.0460), oil content (0.0098 and 0.0288), harvest index (0.2253 and 0.6291) were positive both at phenotypic and genotypic levels while nodes to primary raceme (-0.1221 and -0.5669), days to 80% maturity of secondary raceme (-0.2191 and -0.5190), days to 50% flowering of tertiary raceme (-0.0964 and -0.4693), nodes to tertiary raceme (-0.0016 and -0.0602), days to 80% maturity of tertiary raceme (-0.1077 and -0.0855), 100 seed weight of secondary raceme (-0.0012 and -0.1737) and L/B ratio (-0.0103 and -0.0262) were negative both at phenotypic and genotypic level. Stem length to primary raceme (0.0171 and -0.1831), nodes to secondary raceme (0.0162 and -0.0578), stem length to secondary raceme (0.0036 and -0.0351), seed yield per plant at 120 days (0.0625 and -0.0801), showed positive indirect effect at phenotypic level and negative indirect effect at genotypic level.

Days to 50% flowering of secondary raceme (-0.0144 and 0.9309), total length of secondary raceme (-0.0403 and 0.0437), stem length to tertiary raceme (-0.0125 and 0.0047), 100 seed weight of primary raceme (-0.0526 and 0.1618) showed negative indirect effect at phenotypic level and positive indirect effect at genotypic level. This trait had positive and significant correlation with seed yield per plant upto 180 days (0.7682\*\* and 0.7828\*\*) both at phenotypic and genotypic levels.

### **4.3 GENETIC DIVERGENCE**

The genetic divergence analysis is performed to identify the diverse genotypes for hybridization purposes. Clustering by  $D^2$  statistic is useful in this matter. In the present investigation quantitative assessment of genetic divergence was carried out for all the 28 characters of 54 *Ricinus communis* L. genotypes studied in the present investigation using Mahalanobis'  $D^2$  statistic.

#### **4.3.1 Mahalanobis' $D^2$ analysis**

##### **4.3.1.1 Test with Wilk's ' $\Lambda$ ' criterion**

Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the Wilk's criterion ' $\Lambda$ '. The Wilk's criterion thus obtained was used in calculations of ' $V$ ' statistic. The ' $V$ ' statistic was highly significant indicating that genotypes differed significantly when all the characters were considered simultaneously.

#### **4.3.1.2 Mahalanobis' $D^2$ values**

To estimate the  $D^2$  values, correlated means of characters were transformed into standardized uncorrelated means using pivotal condensation method. The statistical distance ( $D^2$ ) between pairs of genotypes were obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated values of any two genotypes considered at a time. Thus all the possible 1326 combinations and the corresponding  $D^2$  values were obtained.

#### **4.3.1.3 Contribution of different characters towards genetic divergence**

The percent contribution towards genetic divergence by all the 28 contributing characters is presented in table 17. The trait effective length of tertiary raceme (30.40) contributed maximum towards genetic divergence followed by days to 50% flowering of tertiary raceme (16.77), stem length to tertiary raceme (11.25), seed yield per plant at 120 days (10.76), 100 seed weight of tertiary raceme (5.38), harvest index (5.31) stem length to primary raceme (4.12), days to 80% maturity of secondary raceme (3.42), days to 80% maturity of tertiary raceme (2.38), days to 50% flowering of primary raceme (1.96), 100 seed weight of primary raceme (1.68), days to 80% maturity of primary raceme (1.26), seed yield per plant up to 180 days (0.77), seed yield per plant up to 150 days (0.70), days to 50% flowering of secondary raceme (0.63), 100 seed weight of secondary raceme (0.63), total length of secondary raceme (0.56), oil content (0.42), L/B ratio (0.42), effective length of primary raceme (0.35), total length of primary raceme (0.21), nodes to tertiary raceme (0.21), stem length to secondary raceme (0.14), effective length of

secondary raceme (0.14), tertiary branches per plant (0.14), nodes to primary raceme (0.00), secondary branches per plant (0.00) and nodes to secondary raceme (0.00).

#### **4.3.1.4 Grouping of genotypes into various clusters**

The 54 genotypes were grouped into 9 clusters using the Tocher's method with the criterion that the intra-cluster average  $D^2$  values should be less than the inter-cluster  $D^2$  values. The distribution of 54 genotypes into 9 clusters is presented in Table 18. The mutual relationship between the clusters is represented diagrammatically (Fig. 17) by taking average intra and inter cluster  $D^2$  values.

#### **4.3.1.5 Average intra and inter cluster $D^2$ values**

The average intra and inter cluster  $D^2$  values estimated as per the procedure given by Singh and Chaudhary (1977) were presented in the Table 19.

The maximum intra cluster  $D^2$  value was 1737.36 for cluster VIII followed by 1319.266 for cluster V, 865.401 for cluster II, 844.327 for cluster III, 558.559 for cluster VII, 536.741 for cluster I, while it was zero for cluster IV, VI and IX.

Cluster I comprised of 11 genotypes and was closest to cluster VI (1081.344) followed by cluster VIII (1244.966) and it is farthest from cluster IX (20.324.604) followed by cluster VII (10836.892).

Cluster II comprised of 14 genotypes and was nearest to cluster IV (1137.648) followed by cluster III (1391.604) and it is farthest from cluster IX (10242.585) followed by cluster VII (4094.951).

Cluster III comprised of 11 genotypes and was nearest to cluster II (1391.604) followed by cluster I (1527.938) and it is farthest from cluster IX (14648.815) followed by cluster VII (6528.681).

Cluster IV comprised of one genotypes and was nearest to cluster II (1137.648) followed by cluster III (1568.907) and it is farthest from cluster IX (12981.145) followed by cluster VII (6514.107).

Cluster V comprised of 8 genotypes and was nearest to cluster II (1539.001) followed by cluster IV (2442.638) and it is farthest from cluster IX (7813.980) followed by cluster VI (6266.758).

Cluster VI comprised of one genotype and was nearest to cluster I (1081.344) followed by cluster IV (1921.861) and it is farthest from cluster IX (21728.092) followed by cluster VII (12793.441).

Cluster VII comprised of two genotypes and was nearest to cluster V (2525.634) followed by cluster IX (2836.391) and it is farthest from cluster VI (12793.441) followed by cluster I (10836.892).

Cluster VIII comprised of 5 genotypes and was nearest to cluster I (1244.966) followed by cluster III (1632.166) and it is farthest from cluster IX (19061.795) followed by cluster VII (9686.240).

Cluster IX comprised of one genotype and was nearest to cluster VII (2836.391) followed by cluster V (7813.980) and it is farthest from cluster VI (21782.092) followed by cluster I (20324.604).

#### **4.3.1.6 Cluster mean values**

The cluster mean values for 28 characters are presented in Table 21. The data indicated a wide range of mean values between the characters. Days to 50% flowering of primary raceme had a range of 116.00 for cluster IX to 52.00 for cluster VI; stem length to primary raceme varied from 282.30 for cluster IX to 87.40 for cluster VIII; number of nodes up to primary spike ranged from 37.40 for cluster IX to 16.00 for cluster VI; total length of primary spike varied from 51.00 for cluster VII to 19.40 for cluster VI; effective length of primary spike ranged from 48.05 for cluster VII to 19.40 for cluster VI; days to 80 % maturity of primary raceme varied from 129.50 for cluster IX to 85.5 for cluster VI; number of secondary branches per plant varied from 2.99 for cluster II to 2.10 for cluster VI; days to 50% flowering of secondary raceme from 140.50 for cluster IX to 72.00 for cluster VI; number of nodes up to secondary spike ranged from 14.32 for cluster VII to 6.60 for cluster VI; stem length to secondary raceme varied from 116.62 for cluster V to 35.20 for cluster VI; total length of secondary spike varied from 43.70 for cluster VII to 12.85 for cluster VI; effective length of secondary spike ranged from 37.80 for cluster VII to 18.50 for cluster VI; days to 80 % maturity of secondary raceme varied from 156.50 for cluster IX to 107.00 for cluster VI; tertiary branches/plant varied from 4.00 for cluster VI to 2.00 for cluster VIII; days to 50% flowering of tertiary raceme from 163.00 for cluster IX to 87.00 for cluster VI; number of nodes up to tertiary spike ranged from 9.90 for cluster IV to 5.57 for cluster VII; stem length to tertiary raceme varied from 66.79 for cluster I to 30.300 for cluster VII; effective length of tertiary spike ranged from 25.20 for cluster VII to 13.70 for cluster IV; days to 80 % maturity of tertiary raceme varied from 172.5 for cluster VII to 126.00 for cluster VI; 100 seed weight of

primary raceme varied from 26.74 for cluster VII to 20.58 for cluster IX; 100 seed weight of secondary raceme varied from 28.93 for cluster VII to 21.95 for cluster IV; 100 seed weight of tertiary raceme varied from 26.70 for cluster VII to 20.70 for cluster IX; oil content varied from 49.34 for cluster V to 47.00 for cluster IX; L/B varied from 1.52 for cluster VIII to 1.33 for cluster IV; harvest index varied from 38.42 for cluster III to 30.20 for cluster IX; seed yield / plant up to 120 days varied from 91.82 for cluster I to 0.00 for cluster VII, IX; seed yield / plant up to 150 days varied from 139.53 for cluster I to 35.74 for cluster VII; seed yield / plant up to 180 days varied from 142.63 for cluster III to 81.5 for cluster IV.

#### **4.3.2 Application of principal component analysis in genetic divergence**

In principal component analysis on correlation matrix the standardization of columns (characters) created 28 new variables for 54 genotypes without changing their relative positions. These 28 new variables are the principal components (PC1, PC2 .....PC28). Each principal component is a linear combination of the 28 attributes of data matrix. The loading values are scaled or standardized in such a manner that the sum of square of loadings within a principal component is equal to one. The loadings are viewed as weights defining the contribution of characters in respective principal component. Like regression coefficients, loadings sign (+ / -) are indicative of the direction of contribution. But unlike regression, only the relative contributions are important, so all signs can be changed without affecting the analysis (Jackson, 1991).

The loadings for first principal component were chosen so as to make its variance as large as possible. Loadings of second principal component were chosen such that the

variance of PC2 is as large as possible, subject to the constraint that PC1 and PC2 are uncorrelated. The process was continued to create 28 principal components, but PC's having eigen value less than one is not having any practical significance (Legendre and Legendre, 1984).

Principal components (eigen value greater than one), eigen values (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters are presented in Table-22.

In the present studies, the first five principal components with eigen values more than one contributed 89.39 per cent towards the total variability. The principal component with eigen values less than one were considered as non-significant. It was therefore inferred that the essential features of data set had been represented in the first five principal components. The first principal component contributed maximum towards variability (69.15%). Characters *viz.*, effective length of tertiary raceme (0.42), days to 50% flowering of tertiary raceme (0.33), days to 50% flowering of secondary raceme (0.29), 100 seed weight of tertiary raceme (-0.28), explained the maximum variance in first principal component (PC 1) and signifying their importance in plant yield. Positive correlation was observed among effective length of tertiary raceme, days to 50% flowering of tertiary raceme, days to 50% flowering of secondary raceme while 100 seed weight of tertiary raceme showed negative loading value.

The second principle component (PC 2) described 8.72 percent of contribution towards the total variability. Characters *viz.*, seed yield per plant at 120 days (-0.42), stem length to tertiary raceme (-0.41), days to 50% flowering of tertiary raceme (-0.40) and

effective length of primary raceme (-0.32) showed the maximum variance in this principal component.

The third principle component (PC 3) was characterized by 5.08 percent of contribution towards the total variability. Characters viz., harvest index (-0.48), stem length to tertiary raceme (0.43), stem length to primary raceme (0.35) and 100 seed weight of secondary raceme (0.29) showed maximum variance in this principal component. Stem length to tertiary raceme, stem length to primary raceme and 100 seed weight of secondary raceme were positively correlated while harvest index was negatively correlated.

The fourth principal component (PC 4) was characterized by 3.87 percent contribution towards the total variability. Characters viz., days to 80% maturity of tertiary raceme (0.49), days to 80% maturity of secondary raceme (0.39), stem length to primary raceme (-0.37) and days to 50% flowering of tertiary raceme (0.25) showed the maximum variance in this principal component. Days to 80% maturity of tertiary raceme, days to 80% maturity of secondary raceme and days to 50% flowering of tertiary raceme were positively correlated while stem length to primary raceme was negatively correlated.

The fifth principal component (PC 5) was characterized by 2.56 percent contribution towards the total variability. Characters viz., 100 seed weight of secondary raceme (0.45), 100 seed weight of tertiary raceme (0.42), 100 seed weight of primary raceme (0.29) and seed yield per plant up to 180 days (0.28) showed maximum variance in this principal component.

The PCA scores for 54 castor genotypes in the first three principal components were computed. Principal component I, II and III were considered as three axes as X, Y and Z and squared distance of each genotype from these three axes were calculated and presented in Table-23.

These three PCA scores for 54 genotypes were plotted in graph to get two dimensional and three dimensional scatter diagram (Fig - 18 and Fig -19).

### **4.3.3 Cluster analysis**

To group the 54 genotypes into various clusters, agglomerative hierarchical cluster analysis was followed. Principal component scores for genotypes were used as an input for clustering in Ward's minimum variance method. The tree like structure called dendrogram (Fig -10) was constructed based on Euclidean<sup>2</sup> distance computed from PCA scores of genotypes.

The 54 genotypes were grouped into 8 clusters. The distribution of genotypes into 8 clusters is presented in Table-24. The mutual relationship between clusters is represented diagrammatically (Fig -20) by taking average intra- and inter- clusters Euclidean<sup>2</sup> distances.

#### **4.3.3.1 Average intra- and inter- cluster Euclidean<sup>2</sup> distance values**

The average intra- and inter- cluster Euclidean<sup>2</sup> distance were estimated based on Ward's minimum variance and are presented in the Table-25.

By Ward's method, the 54 genotypes were grouped into 8 clusters. Of the 8 clusters formed, cluster III had minimum intra cluster Euclidean<sup>2</sup> distance value of 0

followed by cluster V (978.46), cluster II (1117.12), cluster IV (1321.42), cluster VI (1385.93), cluster VII (1594.63), cluster VIII (1795.49), and cluster I (1906.44). The inter cluster Euclidean2 distances varied from 2408.35 (between cluster V and cluster VIII) to 42169.76 (cluster III and IV). All the inter-cluster Euclidean2 values were lying between these values.

Cluster I was the largest comprised group of 7 genotypes. It was nearest to cluster II (3635.21) followed by cluster VIII (4053.76) and farthest from cluster III (12462.72) followed by cluster IV (12086.22).

Cluster II consisted of two genotypes. It was closest to cluster I (3635.21) followed by cluster III (5672.78) and farthest from cluster IV (22878.71) followed by cluster VI (19122.28).

Cluster III was comprised of one genotype. It was closest to cluster II (5672.78) followed by cluster I (12462.72) and farthest from cluster IV (42169.76) followed by cluster VI (38651.39)

Cluster IV was comprised of 12 genotypes. It was nearest to cluster V (2587.44) followed by cluster VI (2728.87) and farthest from cluster III (42169.76) followed by cluster II (22878.71).

Cluster V was comprised of 7 genotypes, it was closest to cluster VIII (2408.35) followed by cluster VI (2552.64) and farthest from cluster III (30833.2) followed by cluster II (14309.40).

Cluster VI consisted of three genotypes. It was nearest to cluster V (2552.64) followed by cluster IV (2728.87) and farthest from cluster III (38651.39) followed by cluster II (19122.28).

Cluster VII was comprised of 12 genotypes. It was closest to cluster V (2594.37) followed by cluster VIII (2642.78) and farthest from cluster III (22766.89) followed by cluster II (10059.42). Cluster VIII was consisted of 10 genotypes. It was closest to cluster V (2408.35) followed by cluster VII (2642.78) and farthest from cluster III (24300.27) followed by cluster II (9435.23).

#### **4.3.3.2 Cluster means:**

Cluster means were computed for the 28 characters studied on pooled basis and are presented in Table 26.

Cluster I registered high mean value for nodes to secondary raceme (14.38), stem length to secondary raceme (102.45)

Cluster II comprised high mean value for effective length of primary raceme (48.05), effective length of tertiary raceme (25.20), days to 80% maturity of tertiary raceme (172.50) 100 seed weight of primary raceme (26.74) 100 seed weight of secondary raceme (28.93) while it showed low mean value for nodes to tertiary raceme (5.57) stem length to tertiary raceme (30.30), L/B ratio of seed (1.43) seed yield per plant at 120 days (0.00), seed yield per plant up to 150 days (35.74)

Cluster III recorded high mean value for days to 50% flowering of primary raceme (116.00), stem length to primary raceme (282.30) nodes to primary raceme (37.40), days to 80% maturity of primary raceme (129.50), days to 50% flowering of secondary raceme (140.50), days to 80% maturity of secondary raceme (156.50) days to 50% flowering of tertiary raceme (163.00), while it showed low mean value for effective length of primary raceme (29.60), nodes to secondary raceme (7.75), total length of secondary raceme

(27.90)effective length of secondary raceme (21.30), effective length of tertiary raceme (17.20), 100 seed weight of secondary raceme (20.58) 100 seed weight of tertiary raceme (20.70), harvest index (30.20), seed yield per plant up to 180 days (90.50)

Cluster IV comprised high mean value for tertiary branches per plant (3.63), nodes to tertiary raceme (9.42), 100 seed weight of tertiary raceme (27.10), oil content (49.23). While it showed low mean value for days to 50% flowering of primary raceme (53.75), stem length to primary raceme (84.92), days to 50% flowering of secondary raceme (76.83), stem length to secondary raceme (54.80), days to 80% maturity of secondary raceme (110.12), days to 50% flowering of tertiary raceme (100.71), days to 80% maturity of tertiary raceme (128.08).

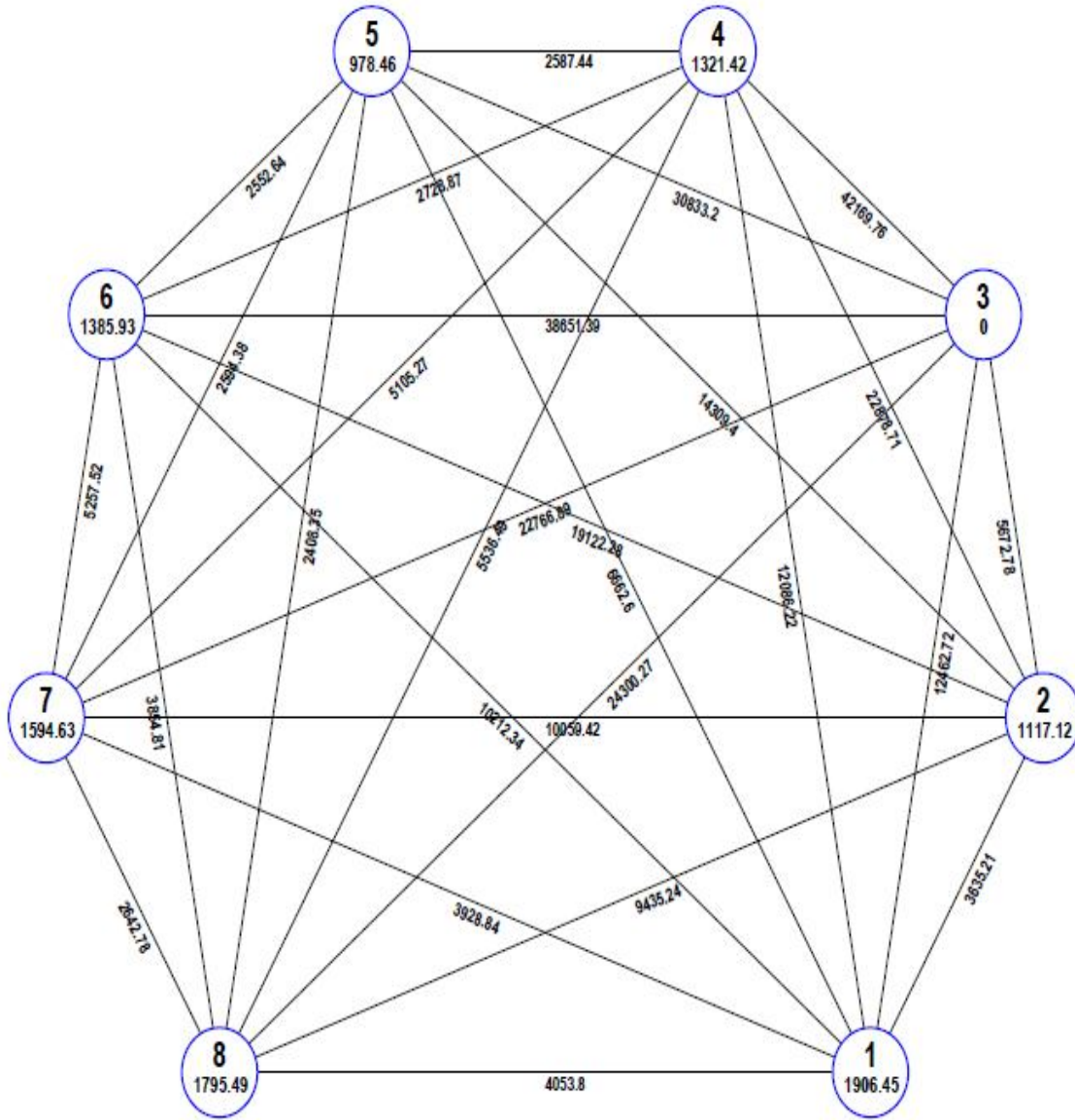
Cluster V registered high mean value for seed yield per plant at 120 days (96.68), seed yield per plant up to 150 days (136.34)

Cluster VI comprised high mean value for total length of secondary raceme (46.50), effective length of secondary raceme (41.30), stem length to tertiary raceme (86.43), L/B ratio of seed(1.50), harvest index (38.46), while it showed low mean value for nodes to primary raceme (15.43), days to 80% maturity of primary raceme (91.00), secondary branches per plant (2.16), tertiary branches per plant (1.83), 100 seed weight of secondary raceme (22.76)

Cluster VII comprised of high mean value for secondary branches per plant (2.96), while it showed low mean value for total length of primary raceme (36.00), oil content (46.43).

Cluster VIII comprised of high mean value for total length of primary raceme (52.66), seed yield per plant up to 180 days (140.36).

**Fig 21: Intra and Inter-cluster distance of 54 castor (*Ricinus communis* L.) genotypes in eight clusters based on Euclidean<sup>2</sup> distances**



Euclidean<sup>2</sup> Distance (Not to the Scale)

**Table 12: Mean, variability, heritability and genetic advance as per cent of mean for yield and yield components in castor (*Ricinus communis* L.)**

S. No.	Character	Mean	Range		GCV (%)	PCV (%)	Heritability (%) (broad sense)	Genetic advance as per cent of mean	
			Minimum	Maximum					
1	Days to 50% Flowering of Pri Raceme	66.78	51.00	116.00	20.73	20.81	99.19	42.53	
2	Stem Length to Pri Raceme (cm)	113.31	48.00	282.30	34.65	34.74	99.44	71.18	
3	Nodes to Pri Raceme	19.91	14.00	37.40	22.47	22.75	97.55	45.73	
4	Total Length of Pri Raceme (cm)	42.86	24.40	62.40	20.37	20.77	96.21	41.16	
5	Effective Length of Pri Raceme	36.97	19.40	55.00	24.05	24.32	97.80	49.00	
6	Days to 80% maturity of Pri Raceme	101.89	85.50	131.00	11.48	11.53	99.15	23.55	
7	Secondary Branches/ Plant	2.61	1.80	4.40	17.96	19.83	82.07	33.52	
8	Days to 50% Flowering of Sec Raceme	95.13	69.50	140.50	17.07	17.14	99.18	35.03	
9	Nodes to Secondary Raceme	10.65	6.30	18.45	24.71	26.26	88.57	47.92	

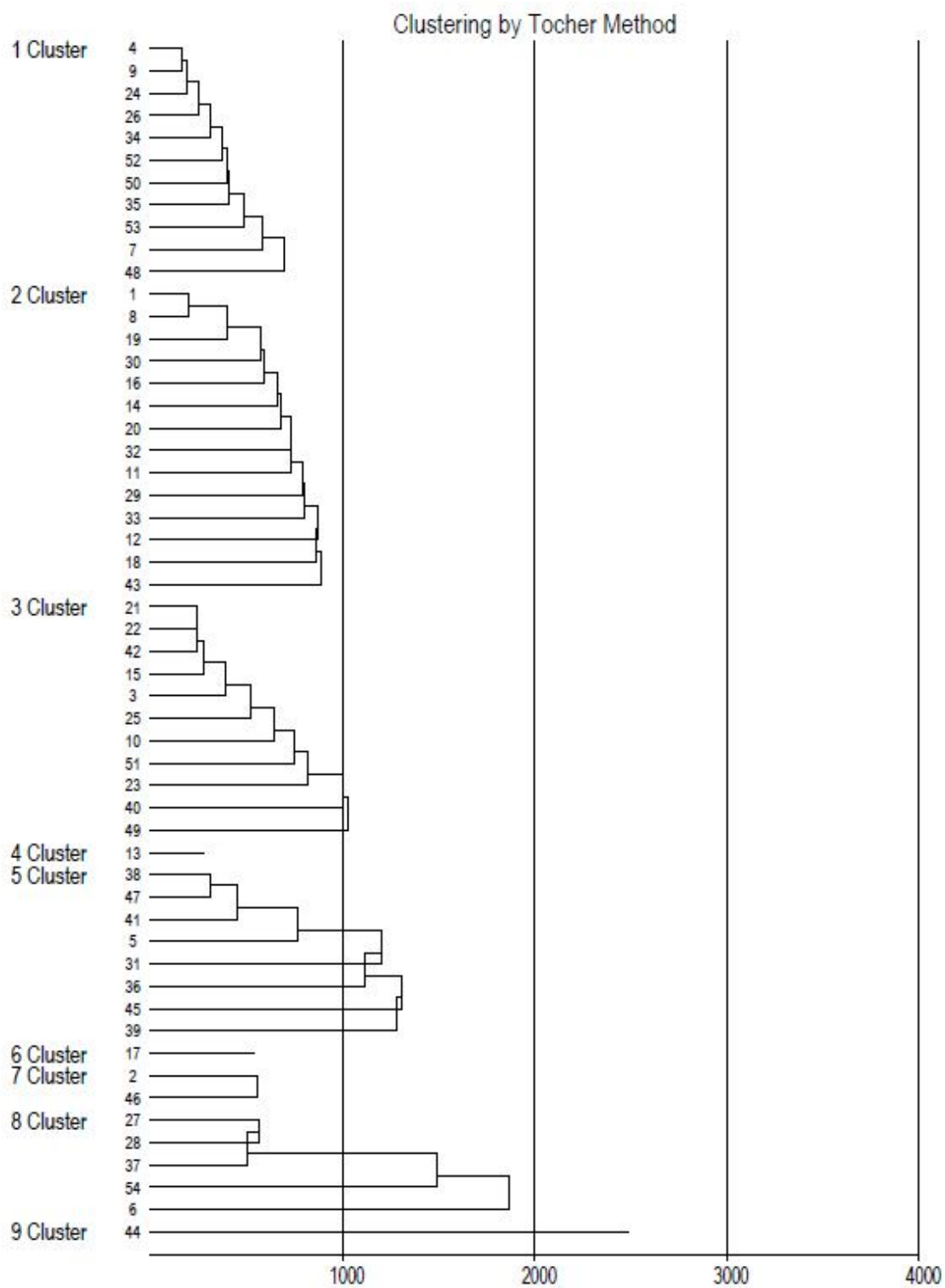
**Table 12: Mean, variability, heritability and genetic advance as per cent of mean for yield and yield components in castor (*Ricinus communis* L.)**

S. No.	Character	Mean	Range		GCV (%)	PCV (%)	Heritability (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum				
10.	Stem Length to Sec Raceme (cm)	83.20	35.20	151.90	34.94	35.62	96.21	70.61
11.	Total Length of Sec Raceme (cm)	34.23	12.85	54.50	22.99	23.32	97.13	46.67
12.	Effective Length Sec Raceme (cm)	29.11	15.00	46.00	24.56	24.89	97.33	49.91
13.	Days to 80% maturity of Sec Raceme	126.00	101.00	156.50	11.02	11.11	98.51	22.54
14.	Tertiary Branches/ Plant	3.08	1.10	5.00	31.11	32.24	93.10	61.84
15.	Days to 50% Flowering of Ter Raceme	120.66	87.00	163.00	14.04	14.08	99.45	28.84
16.	Nodes to Tertiary Racemes	8.48	5.00	12.05	17.69	18.87	87.40	34.16
17.	Stem Length to Ter Raceme (cm)	49.06	17.20	97.40	37.98	38.27	98.46	77.63
18.	Effective Length of Ter Raceme	20.56	13.10	31.60	22.77	23.20	96.29	46.03

**Table 12: Mean, variability, heritability and genetic advance as per cent of mean for yield and yield components in castor (*Ricinus communis* L.)**

S. No.	Character	Mean	Range		GCV (%)	PCV (%)	Heritability (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum				
19.	Days to 80% maturity Of ter Raceme	145.97	119.50	173.00	9.73	9.88	97.04	19.74
20.	100 Seed Wt of Primary Raceme gm	23.99	18.21	31.25	12.33	12.66	94.80	24.73
21.	100 Seed Wt of Secondary Raceme gm	25.24	17.61	30.90	12.00	12.54	91.61	23.67
22.	100 Seed Wt of Tertiary Raceme gm	24.18	17.67	32.73	13.18	13.94	89.51	25.70
23.	Oil Content (%)	48.12	43.96	51.59	3.65	4.12	78.53	6.67
24.	L/B Ratio of Seed	1.46	1.30	1.59	3.72	3.99	87.18	7.16
25.	harvest Index (%)	36.56	30.20	43.10	8.98	9.50	89.37	17.49
26.	Seed Yield/ Plant At 120 Days gm	54.12	0.00	129.40	61.64	62.62	96.89	124.99
27.	Seed Yield/ Plant At 150 Days gm	102.69	26.85	184.00	38.84	39.68	95.83	78.33
28.	Seed Yield/ Plant At 180 Days gm	125.97	60.10	210.50	24.03	25.32	90.06	46.98

**Fig 17: Dendrogram showing relationship among 54 castor (*Ricinus communis* L.) genotypes in nine clusters.**



**Table 1: Review of available literature on variability in Castor (*Ricinus communis L.*)**

S.No	Character	No. of genotypes studied	Range of variability	GCV	PCV	Reference
1.	Days to 50% flowering of primary raceme	65	41.27 - 72.73	18.45	23.08	Dorairaj <i>et al.</i> (1973c)
		35	43.00 - 117.33	24.59	26.03	Rao <i>et al.</i> (1983b)
		44	56.00 - 92.00	10.59	12.36	Patel <i>et al.</i> (1985)
		14	41.75 – 55.25	7.72	8.79	Patel <i>et al.</i> (1991)
		48	56.00-110.00	12.43	13.06	Golakia <i>et al.</i> (2007)
2.	Plant height upto primary spike	154	10.00 – 180.00	-	-	Muhammad <i>et al.</i> (1970)
		65	31.83 – 89.60	-	-	Dorairaj <i>et al.</i> (1973c)
		35	56.66 – 264.00	29.05	-	Muthiah <i>et al.</i> (1982a)
		35	35.06 – 247.20	32.39	34.25	Rao <i>et al.</i> (1983b)
		44	17.30 – 59.90	27.47	31.05	Patel <i>et al.</i> (1985)
		14	28.80 - 93.10	26.69	28.65	Patel <i>et al.</i> (1991)
		10	56.00 – 70.00	7.50	-	Reddy <i>et al.</i> (1999b)
		10	---	71.40	72.00	Reddy <i>et al.</i> (1999c)
		68	---	76.54	77.32	Lakshamma <i>et al.</i> (2005)
		48	40.00-121.50	17.72	19.93	Golakia <i>et al.</i> (2007)
3.	Number of nodes up to primary spike	154	6.00 – 32.00	-	-	Muhammad <i>et al.</i> (1970)
		65	11.00 23.77	-	-	Dorairaj <i>et al.</i> (1973c)
		35	9.00 – 24.33	18.93	-	Muthiah <i>et al.</i> (1982a)
		25	---	29.60	-	Ratnakar (1982)
		35	12.06 – 38.67	33.06	33.44	Rao <i>et al.</i> (1983b)

S.No	Character	No. of genotypes studied	Range of variability	GCV	PCV	Reference
		44	12.00 – 23.10	14.59	16.96	Patel <i>et al.</i> (1985)
		14	12.80 – 19.10	11.56	12.56	Patel <i>et al.</i> (1991)
		10	---	41.80	44.10	Reddy <i>et al.</i> (1999c)
		68	----	44.72	45.42	Lakshamma <i>et al.</i> (2005)
		48	14.70-26.30	12.23	12.84	Golakia <i>et al.</i> (2007)
4.	Total length of primary spike	35	10.00 - 33.00	22.34	-	Muthiah <i>et al.</i> (1982a)
		25	11.00 – 53.00	40.59	-	Ratnakar (1982)
		35	14.21 – 37.05	15.25	24.34	Rao <i>et al.</i> (1983b)
		44	17.80 – 50.75	20.76	27.39	Patel <i>et al.</i> (1985)
		14	32.10 – 71.00	24.06	26.58	Patel <i>et al.</i> (1991)
		9	---	13.00	19.90	Raghu ram Reddy <i>et al.</i> (2000)
		48	25.50 -53.50	13.33	19.34	Golakia <i>et al.</i> (2007)
6.	Effective length of primary raceme	9	----	16.90	22.50	Raghuram Reddy <i>et al.</i> (2000)
		68	---	48.16	50.68	Lakshamma <i>et al.</i> (2005)
		48	25.50 – 53.50	13.63	19.51	Golakia <i>et al.</i> (2007)
7.	Days to maturity of primary raceme	48	96.00-161.00	8.90	9.18	Golakia <i>et al.</i> (2007)

S.No	Character	No. of genotypes studied	Range of variability	GCV	PCV	Reference
8.	Number of secondary racemes	10	0.50 – 1.60	31.90	---	Reddy <i>et al.</i> (1999b)
		10	----	35.40	39.60	Reddy <i>et al.</i> (1999c)
		68	---	46.68	51.00	Lakshamma <i>et al.</i> (2005)
9.	Days to 50% flowering of secondary raceme	10	65.00 – 90.70	7.70	---	Reddy <i>et al.</i> (1999b)
10.	Effective length of secondary spike	68	---	32.13	35.17	Lakshamma <i>et al.</i> (2005)
11.	Number of tertiary racemes	10	0.10 – 0.80	95.80	----	Reddy <i>et al.</i> (1999b)
		10	---	62.70	63.90	Reddy <i>et al.</i> (1999c)
12.	Effective length of tertiary spike	68	----	57.89	61.87	Lakshamma <i>et al.</i> (2005)
13.	Number of spikes/plant	25	3.20 – 12.00	56.25	-	Ratnakar (1982)
		35	1.00 – 4.13	33.44	42.51	Rao <i>et al.</i> (1983b)
		48	1.80 – 13.10	29.51	39.60	Golakia <i>et al.</i> (2007)
14.	100 Seed weight	154	31.00 – 64.90	-	-	Muhammad <i>et al.</i> (1970)
		65	20.30 – 38.30	-	-	Dorairaj <i>et al.</i> (1973c)
		35	45.40 – 118.20	29.07	-	Muthiah <i>et al.</i> (1982a)

S.No	Character	No. of genotypes studied	Range of variability	GCV	PCV	Reference
		25	21.84 – 72.00	56.76	-	Ratnakar (1982)
		35	15.20 – 32.68	17.61	20.71	Rao <i>et al.</i> (1983b)
		44	22.00 – 40.00	12.99	14.08	Patel <i>et al.</i> (1985)
		14	16.15 – 31.98	18.21	18.65	Patel <i>et al.</i> (1991)
		48	20.90 - 46.20	15.10	16.50	Golakia <i>et al</i> (2007)
		9	----	14.80	19.50	Raghuram Reddy <i>et al.</i> (2000)
15.	Oil content	44	46.37 – 53.75	2.67	3.88	Patel <i>et al.</i> (1985)
		14	45.70 – 50.00	2.53	2.81	Patel <i>et al.</i> (1991)
16.	Harvest index	10	25.88 – 32.22	6.73	7.72	Jagtap <i>et al.</i> (2006)
17.	Seed yield/plant	65	9.67 – 73.83	-	-	Dorairaj <i>et al.</i> (1973c)
		4	21.45 – 71.33	-	-	Ramaswamy and Menon (1973)
		35	16.00 – 95.00	43.09	-	Muthiah <i>et al.</i> (1982a)
		25	15.30 – 98.30	26.68	-	Ratnakar (1982)
		35	12.87 – 92.34	41.13	48.29	Rao <i>et al.</i> (1983b)
		44	57.50 – 215.00	24.88	31.07	Patel <i>et al.</i> (1985)
		14	-----	21.20	24.64	Patel <i>et al.</i> (1991)
		10	32.30 – 85.10	31.80	-	Reddy <i>et al.</i> (1999b)
		9	----	28.50	37.90	Raghuram Reddy <i>et al.</i> (2000)
		68	---	39.42	40.11	Lakshamma <i>et al.</i> (2005)
		48	48.50 – 210.00	28.42	35.39	Golakia <i>et al.</i> (2007)

**Table 2: Heritability and genetic advance as per cent of mean in castor (*Ricinus communis* L.)**

S.No	Character	Heritability	Genetic advance as per cent of mean	Reference
1.	Days to 50% flowering primary raceme	63.98	11.08	Dorairaj <i>et al.</i> (1973c)
		96.47	49.80	Rao <i>et al.</i> (1983b)
		73.46	18.66	Patel <i>et al.</i> (1985)
		73.98	13.96	Patel <i>et al.</i> (1991)
		90.57	24.36	Golakia <i>et al.</i> (2007)
2.	Plant height	64.22	18.34	Dorairaj <i>et al.</i> (1973c)
		84.13	54.89	Muthiah <i>et al.</i> (1982a)
		--	63.10	Rao <i>et al.</i> (1983b)
		78.25	50.07	Patel <i>et al.</i> (1985)
		86.80	51.22	Patel <i>et al.</i> (1991)
		74.70	13.30	Reddy <i>et al.</i> (1999b)
		98.00	146.30	Reddy <i>et al.</i> (1999c)
		98.00	156.08	Lakshamma <i>et al.</i> (2005)
79.09	32.47	Golakia <i>et al.</i> (2007)		
3.	Number of nodes up to primary spike	74.24	36.76	Dorairaj <i>et al.</i> (1973c)

S.No	Character	Heritability	Genetic advance as per cent of mean	Reference
		58.90	28.99	Muthiah <i>et al.</i> (1982a)
		75.39	50.71	Ratnakar (1982)
		97.71	67.30	Rao <i>et al.</i> (1983b)
		76.39	26.29	Patel <i>et al.</i> (1985)
		84.70	21.78	Patel <i>et al.</i> (1991)
		90.00	81.80	Reddy <i>et al.</i> (1999c)
		97.00	90.72	Lakshamma <i>et al.</i> (2005)
		90.79	23.79	Golakia <i>et al.</i> (2007)
4.	Total length of primary spike	74.66	52.30	Dorairaj <i>et al.</i> (1973c)
		50.35	33.39	Muthiah <i>et al.</i> (1982a)
		75.72	72.77	Ratnakar (1982)
		39.28	19.70	Rao <i>et al.</i> (1983b)
		57.40	32.40	Patel <i>et al.</i> (1985)
		81.96	44.88	Patel <i>et al.</i> (1991)
		77.30	17.30	Reddy <i>et al.</i> (1999b)
		47.49	18.93	Golakia <i>et al</i> (2007)
5.	Effective length of Primary raceme	90.00	94.29	Lakshamma <i>et al.</i> (2005)
		48.84	19.63	Golakia <i>et al</i> (2007)
		92.90	89.4	Ramesh <i>et al.</i> (2008)
6.	Days to maturity of primary raceme	93.94	17.77	Golakia <i>et al</i> (2007)

S.No	Character	Heritability	Genetic advance as per cent of mean	Reference
7.	Number of secondary spikes	80.00 84.00	65.50 88.01	Raghuram Reddy <i>et al.</i> (1999c) Lakshamma <i>et al.</i> (2005)
8.	Effective length of secondary spike	83.00	60.47	Lakshamma <i>et al.</i> (2005)
9.	Number of tertiaries spikes	96.00	127.30	Raghuram Reddy <i>et al.</i> (1999c)
10.	Effective length of tertiary spike	88.00	111.59	Lakshamma <i>et al.</i> (2005)
11.	Number of spikes /plant	40.98 71.70 61.89 55.82	19.88 98.75 54.20 45.52	Dorairaj <i>et al.</i> (1973c) Ratnakar (1982) Rao <i>et al.</i> (1983b) Golakia <i>et al.</i> (2007)
12.	100 seed weight	82.34 99.67	29.88 59.78	Dorairaj <i>et al.</i> (1973c) Muthiah <i>et al.</i> (1982a)

S.No	Character	Heritability	Genetic advance as per cent of mean	Reference
		99.78	12.29	Ratnakar (1982)
		72.30	30.80	Rao <i>et al.</i> (1983b)
		73.46	14.68	Patel <i>et al.</i> (1985)
		77.03	37.56	Patel and Jaimani (1988)
		95.37	36.64	Patel <i>et al.</i> (1991)
		83.78	28.46	Golakia <i>et al</i> (2007)
13.	Oil content	47.35	3.97	Patel <i>et al.</i> (1985)
		81.60	4.72	Patel <i>et al.</i> (1991)
		91.57	7.81	Kumari <i>et al.</i> (1996)
		96.00	25.5	Ramesh (2008)
14.	Harvest index	75.90	12.08	Jagtap <i>et al</i> (2006)
15.	Yield at 120 days after planting	93.40	96.60	Ramesh <i>et al.</i> (2008)
15.	Seed yield/plant	42.69	41.29	Dorairaj <i>et al.</i> (1973c)
		58.54	67.92	Muthiah <i>et al.</i> (1982a)
		38.48	33.48	Ratnakar (1982)
		72.52	72.10	Rao <i>et al.</i> (1983b)
		64.09	41.03	Patel <i>et al.</i> (1985)
		73.98	37.56	Patel <i>et al.</i> (1991)
		94.00	63.80	Reddy <i>et al.</i> (1999b)
		64.52	47.00	Golakia <i>et al</i> (2007)

**Table 6: Indirect effects of yield components on yield in castor (*Ricinus communis* L.)**

S.No	Character	Effect	Through	Reference
1.	Days to 50 % flowering of primary raceme	Positive	number of nodes plant height, length of primary spike plant height, effective length of primary spike 100 seed weight	Bhatt and Reddy (1981) Mehta and Vashi (1998)  Golakia <i>et al.</i> (2007)
		Negative	100 seed weight number of spikes per plant, 100 seed weight, yield per plant number of nodes, 100seed weight, days to maturity, & effective length of primary raceme days to maturity of main raceme, nodes to main raceme, total length of primary spike	Rao <i>et al.</i> (1983a)  Kumari <i>et al.</i> (1996)  Mehta and Vashi (1998)  Golakia <i>et al.</i> (2007)
2.	Plant height Upto primary raceme	Positive	days to 50% flowering number of spikes per plant, 100 seed weight number of spikes per plant, oil content number of nodes, number of spikes per plant yield per plant, oil content length of primary spike	Bhatt and Reddy (1981) Rao <i>et al.</i> (1983a) Khorgade <i>et al.</i> (1994) Kumari <i>et al.</i> (1996)  Mehta and Vashi (1998)
		Negative	number of nodes, number of spikes per plant, & length of primary spike  days to 50% flowering plant height, 100 seed weight days to 50% flowering, number of nodes, 100 seed weight, days to maturity, effective Spike length of primary raceme	Rao <i>et al.</i> (1983a)  Swarnalatha <i>et al.</i> (1984) Khorgade <i>et al.</i> (1994)  Mehta and Vashi (1998)

S.No	Character	Effect	Through	Reference
3.	Number of nodes up to primary spike	Positive	days to 50 % flowering, plant height, number of spikes per plant, length of primary spike plant height, number of capsules per plant, 100 seed weight plant height, length of primary spike number of spike per plant, number of spikes per plant, oil content	Ananthasayana and Reddi (1981) Muthiah <i>et al.</i> (1982b) Rao <i>et al.</i> (1983a)  Kumari <i>et al.</i> (1996) Mehta and Vashi (1998)  Ramesh and Prasad (2001)
		Negative	plant height, number of spikes per plant, plant height oil content  50% flowering, number of spikes per plant, oil content, seed yield per plant days to 50 % flowering, 100 seed weight plant height, 100 seed weight, days to 50% flowering plant height, no. of secondary branches, effective spike length of P.R, effective spike length of S.R, effective length of T.R  plant height, days to 50% flowering, number of nodes, number of capsules per plant	Rao <i>et al.</i> (1983a) Patel and Jaimani (1991)  Kumari <i>et al.</i> (1996) Mehta and Vashi (1998) Ramesh and Prasad (2001)  Lakshamma <i>et al.</i> (2005)  Ramesh and Prasad (2001)
4.	Total length of primary spike	Positive	number of nodes, number of spikes, 100 seed weight oil content, plant height  days to maturity of main raceme, plant height, nodes to P.R	Rao <i>et al.</i> (1983a) Khorgade <i>et al.</i> (1994) Mehta and Vashi (1998)  Golakia <i>et al.</i> (2007)

S.No	Character	Effect	Through	Reference
		Negative	plant height, number of spikes per plant plant height, number of spikes per plant, 100 seed weight days to 50 % flowering, number of nodes, 100 seed weight, days to maturity, effective length of primary raceme days to flowering of P.R, effective length of P.R, 100 seed weight	Rao <i>et al.</i> (1983a) Khorgade <i>et al.</i> (1994) Mehta and Vashi (1998) Golakia <i>et al.</i> (2007)
5.	Effective spike length of P.R	Positive	oil percentage, 100 seed weight oil content effective sike length of T.R no.of nodes days to maturity, plant height, nodes to P.R total lenth of P.R	Khorgade <i>et al.</i> (1994) Ramesh and Prasad (2001) Lakshamma <i>et al.</i> (2005) Manivel and Manivannan (2006) Golakia <i>et al.</i> (2007)
		Negative	plant height, days to 50% flowering, nodes to P.R, 100 seed weight plant height, No. of nodes, No. of secondary branches, no. of tertiary branches, effective length of secondary raceme days to 50% flowering of P.R, 100 seed weight	Ramesh and Prasad (2001) Lakshamma <i>et al.</i> (2005) Golakia <i>et al.</i> (2007)
6.	80% maturity of primary raceme	positive	effective length of P.R, oil content, 100 seed weight days to 50% flowering of P.R, plant height, effective length of P.R, 100 seed weight	Khorgade <i>et al.</i> (1994) Golakia <i>et al.</i> (2007)

S.No	Character	Effect	Through	Reference
		Negative	length of P.R nodes to P.R, total length of P.R	Khorgade <i>et al.</i> (1994) Golakia <i>et al.</i> (2007)
7.	No. of secondary racemes	Positive	Plant height , effective length of S.R effective length of T.R days to 50% flowering of P.R, nodes to P.R, no. of tertiary branches, oil content, 100 seed weight, effective length of P.R	Lakshamma <i>et al.</i> (2005)  Manivel and Manivannan (2006)
		Negative	no. of nodes, effective length of P.R	Lakshamma <i>et al.</i> (2005)
8.	Effective length of secondary raceme	Positive	effective length of T.R	Lakshamma <i>et al.</i> (2005)
		Negative	plant height, nodes to P.R, No. of secondary branches	Lakshamma <i>et al.</i> (2005)
9.	No. of tertiary racemes	Positive	Days to 50% flowering of P.R, plant height, effective length of P.R, nodes to P.R	Manivel and Manivannan (2006)
		Negative	100 seed weight	Manivel and Manivannan (2006)
10.	Effective length of tertiary raceme	positive	plant height, no. of nodes	Lakshamma <i>et al.</i> (2005)
		Negative	No. of secondary branches, effective length of P.R, effective length of S.R	Lakshamma <i>et al.</i> (2005)
11.	100 seed weight	Positive	number of nodes, number of spikes per plant, oil content	Rao <i>et al.</i> (1983a) Khorgade <i>et al.</i> (1994)

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S.No	Character	Effect	Through	Reference
			number of nodes, effective length of P.R plant height, number of nodes, number of spikes per plant	Mehta and Vashi (1998) Ramesh and Prasad (2001)
			days to flowering of P.R, plant height, effective length of P.R	Golakia <i>et al.</i> (2007)
		Negative	length of primary spike, plant height capsules per plant length of primary spike, plant height capsules per plant days to 50 % flowering, plant height, length of primary spike plant height, number of nodes, number of spikes per plant	Rao <i>et al.</i> (1983a) Khorgade <i>et al.</i> (1994) Mehta and Vashi (1998) Ramesh and Prasad (2001)
			days to maturity of P.R, nodes to P.R, total length of P.R	Golakia <i>et al.</i> (2007)
12.	Oil content	Positive	plant height, seed yield per plant spikes per plant, capsules per plant days 50% flowering of P.R, secondary branches tertiary branches days 50% flowering of P.R, nodes to P.R	Kumari <i>et al.</i> (1996) Ramesh and Prasad (2001) Manivel and Manivannan (2006) Asish <i>et al.</i> (2008)
		Negative	days to 50% flowering, number of nodes, 100seed weight, number of spikes per plant, number of capsules per plant plant height, number of nodes, 100 seed weight plant height, nodes to P.R	Kumari <i>et al.</i> (1996) Ramesh and Prasad (2001) Manivel and Manivannan (2006)

PR- Primary raceme, SR- Secondary raceme, TR- Tertiary raceme

**Table 3: Association of yield components with yield in castor (*Ricinus communis L.*)**

S.No	Character	Association	S/NS	P/G	Reference	
1.	Days to 50 %flowering	Positive	NS	-	Bhatt and Reddy (1981)	
				P	Mehta and Vashi (1998)	
			NS	P,G	Golakia <i>et al.</i> (2007)	
			S	-	Jadhav and Deshamukh (2008)	
		Negative	S	-	Dorairaj <i>et al.</i> (1973a)	
				P	Rao <i>et al.</i> (1983a)	
				P	Yadav <i>et al.</i> (2004)	
			Negative	NS	P,G	Ratnakar (1982)
		2.	Plant height upto primary raceme	Positive	S	P,G
					Raju (1981)	
	-				Muthiah <i>et al.</i> (1982b)	
	P,G				Rao <i>et al.</i> (1983a)	
	-				Shinde <i>et al.</i> (1985)	
	P,G				Patel and Jaimani (1991)	
	G				Khorgade <i>et al.</i> (1994)	
	-				Anjani and Reddy (2003)	
	S				Jadhav and Deshamukh (2008)	
	NS			P,G	Golakia <i>et al.</i> (2007)	
Positive	S			-	Yadava and Singh (1973)	
	NS			P	Vindhiyavarman and Manoharan (1994)	
				P	Mehta and Vashi (1998)	
				P	Yadav <i>et al.</i> (2004)	
	Negative			S	P,G	Giriraj <i>et al.</i> (1973)
	Negative	NS	G	Vindhiyavarman and Manoharan (1994)		
		P		Mehta and Vashi (1998)		
3.	Number of nodes up to primary spike	Positive	S	-	Dorairaj <i>et al.</i> (1973a)	
				P	Giriraj <i>et al.</i> (1973)	
				P,G	Muthiah <i>et al.</i> (1982b)	
				P,G	Ratnakar (1982)	
				G	Vindhiyavarman and Manoharan (1994)	
				G	Ramesh and Prasad (2001)	
				P,G	Yadav <i>et al.</i> (2004)	
				Positive	NS	-
				P,G		Bhatt and Reddy (1981)
				P,G		Mehta and Vashi (1998)
				G		Lakshmamma <i>et al.</i> (2005)
		PG		Golakia <i>et al.</i> (2007)		

S.No	Character	Association	S/NS	P/G	Reference
		Negative	S	P,G	Rao <i>et al.</i> (1983a)
		Negative	NS	P,G	Patel and Jaimani (1991)
4.	Total Length of primary spike	Positive	S	-	Dorairaj <i>et al.</i> (1973a,b) Giriraj <i>et al.</i> (1973) - Yadava and Singh (1973) - Bhatt and Reddy (1981) - Muthiah <i>et al.</i> (1982b) P,G Ratnakar (1982) - Rao <i>et al.</i> (1983a) G Khorgade <i>et al.</i> (1994) G Vindhiyavarman and Manoharan (1994) P Mehta and Vashi (1998) G Ramesh and Prasad (2001) - Anjani and Reddy (2003) P Golakia <i>et al.</i> (2007) - Jadhav and Deshamukh (2008)
			NS	G	Golakia <i>et al.</i> (2007)
		Negative	NS	-	Ananthasayana and Reddi (1981)
5.	Effective of length of primary spike	Positive	S	P P	Mehta and Vashi (1998) Golakia <i>et al.</i> (2007)
			NS	G G	Mehta and Vashi (1998) Golakia <i>et al.</i> (2007)
		Negative	NS	P,G	Vindhiyavarman and Manoharan (1994)
6.	Days to maturity	Positive	NS NS	G P,G	Mehta and Vashi (1998) Aswani Kumar <i>et al.</i> (2003)
		Negative	NS	P	Mehta and Vashi (1998)
7.	Oil content	Positive	NS NS	- G	Laureti (1981) Asish <i>et al.</i> (2008)
		Negative	NS	- -	Dorairaj <i>et al.</i> (1973a) Singh <i>et al.</i> (1981)

S.No	Character	Association	S/NS	P/G	Reference
8.	100 seed weight	Positive	S	- P,G P	Raju (1981) Rao <i>et al.</i> (1983a) Yadav <i>et al.</i> (2004)
		Positive	NS	- - P,G P,G	Laureti (1981) Muthiah <i>et al.</i> (1982b) Ratnakar (1982) Patel and Jaimani (1991)
		Negative	S	- G  G	Giriraj <i>et al.</i> (1973) Vindhiyavarman and Manoharan (1994) Yadav <i>et al.</i> (2004)
		Negative	NS	- P,G P,G	Yadava and Singh (1973) Mehta and Vashi (1998) Golakia <i>et al.</i> (2007)
9.	Harvest index	Positive	NS S	G P,G	Jagtap <i>et al.</i> (2006) Ravi <i>et al.</i> (2006)

S      Significant  
 NS     Non Significant  
 P      Phenotypic correlation  
 G      Genotypic correlation

**Table 4: Association among yield components in castor (*Ricinus communis* L.)**

S.No	Character	Association	S/NS	P/G	Reference
<b>1. Association of days to 50 %flowering with</b>					
a.	Plant height	Positive	S	P	Rao <i>et al.</i> (1983a)
				P	Mehta and Vashi (1998)
				-	Yadav <i>et al.</i> (2004)
				P	Golakia <i>et al.</i> (2007)
			NS	G	Golakia <i>et al.</i> (2007)
		Negative	-	G	Ramesh and Prasad (2001)
b.	Number of nodes up to primary spike	Positive	S	P	Mehta and Vashi (1998)
				P,G	Reddy <i>et al.</i> (1999a)
			S	P	Golakia <i>et al.</i> (2007)
			NS	G	Golakia <i>et al.</i> (2007)
		Negative	NS	-	Yadav <i>et al.</i> (2004)
c.	Total length of primary spike	Positive	S	P	Mehta and Vashi (1998)
				P,G	Reddy <i>et al.</i> (1999a)
		Negative	NS	P,G	Golakia <i>et al.</i> (2007)
d.	Effective length of primary raceme	Positive	S	P	Mehta and Vashi (1998)
		Negative	NS	G	Golakia <i>et al.</i> (2007)
			S	P	Golakia <i>et al.</i> (2007)
e.	100 seed weight	Positive	-	G	Ramesh and Prasad (2001)
				S	P,G
		Negative	-	P	Mehta and Vashi (1998)
		Negative	NS	-	Yadav <i>et al.</i> (2004)
f.	Oil content	Negative	S	-	Yadav <i>et al.</i> (2004)
g.	Days to maturity	Positive	S	P	Mehta and Vashi (1998)
			Positive	NS	G
<b>2. Association of plant height with</b>					
a.	Number of nodes upto primary spike	Positive	S	-	Mehta and Vashi (1998)
				-	G
				-	Yadav <i>et al.</i> (2004)
			S	G	Lakshmamma <i>et al.</i> (2005)
			NS	P,G	Golakia <i>et al.</i> (2007)
		Negative	NS	-	Dorairaj <i>et al.</i> (1973a)
			-	-	Ramesh and Prasad (2001)

S.No	Character	Association	S/NS	P/G	Reference
b.	Number of spikes/plant	Positive	-	G	Ramesh and Prasad (2001)
		Positive	NS	P	Rao <i>et al.</i> (1983a)
		Negative	S	-	Dorairaj <i>et al.</i> (1973a)
		Negative	NS	G	Rao <i>et al.</i> (1983a)
c.	Total length of primary spike	Positive	S	-	Dorairaj <i>et al.</i> (1973a) Patel and Jaimani (1991)
		Positive	NS	P,G	Rao <i>et al.</i> (1983a)
			-	P	Mehta and Vashi (1998)
		NS	P,G	Golakia <i>et al.</i> (2007)	
d.	Effective length of primary raceme	Positive	NS	P,G	Golakia <i>et al.</i> (2007)
e.	No. of secondary branches	Negative	NS	G	Lakshmamma <i>et al.</i> (2005)
f.	Effective length of secondary raceme	Positive	NS	G	Lakshmamma <i>et al.</i> (2005)
g.	Effective length of tertiary raceme	Positive	NS	G	Lakshmamma <i>et al.</i> (2005)
h.	100 Seed weight	Positive	S	G	Rao <i>et al.</i> (1983a)
		Positive	NS	P	Rao <i>et al.</i> (1983a)
			-	-	Yadav <i>et al.</i> (2004)
			NS	P,G	Golakia <i>et al.</i> (2007)
	Negative	S	P	Mehta and Vashi (1998)	
		-	G	Ramesh and Prasad (2001)	
i.	Oil content	Positive	-	-	Laureti (1981)
			NS	-	Yadav <i>et al.</i> (2004)
<b>3.</b>	<b>Association of number of nodes up to primary spike with</b>				
a.	Number of spikes/plant	Negative	S	P,G	Ratnakar (1982)
				P,G	Rao <i>et al.</i> (1983a)
		Negative	NS	-	Ananthasayana and Reddi (1981)

S.No	Character	Association	S/NS	P/G	Reference
b.	Total length of primary spike	Positive	S	G	Ratnakar (1982)
		Positive	NS	- P P,G	Ananthasayana and Reddi (1981) Ratnakar (1982) Rao <i>et al.</i> (1983a)
			-	-	Mehta and Vashi (1998)
		Negative	NS NS	- P,G	Dorairaj <i>et al.</i> (1973a) Golakia <i>et al.</i> (2007)
c.	Effective length of primary spike	Positive	S NS	G P,G	Lakshamma <i>et al.</i> (2005) Golakia <i>et al.</i> (2007)
d.	No. of secondary branches	Negative	NS	G	Lakshamma <i>et al.</i> (2005)
e.	Effective spike length of secondary raceme	Positive	S	G	Lakshamma <i>et al.</i> (2005)
f.	Effective spike length of tertiary raceme	Negative	NS	G	Lakshamma <i>et al.</i> (2005)
g.	100 seed weight	Positive	- NS	- - P,G	Giriraj <i>et al.</i> (1973) Ananthasayana and Reddi (1981) Ratnakar (1982)
		Negative	- - S	P,G G -	Rao <i>et al.</i> (1983a) Ramesh and Prasad (2001) Yadav <i>et al.</i> (2004)
		Negative	NS	-	Mehta and Vashi (1998)
h.	Oil content	Negative	NS	-	Yadav <i>et al.</i> (2004)
i.	Harvest index	Positive	NS	P,G	Ravi <i>et al.</i> (2006)
<b>4.</b>	<b>Association of total length of primary spike with</b>				
a.	100 Seed weight	Positive	NS	P,G	Rao <i>et al.</i> (1983a)
		Negative	NS	- P,G P	Ananthasayana and Reddi (1981) Ratnakar (1982) Mehta and Vashi (1998)

S.No	Character	Association	S/NS	P/G	Reference
<b>5.</b>	<b>Association of effective spike length of primary raceme with</b>				
a.	Effective spike length of secondary raceme	Positive	S	G	Lakshamma <i>et al.</i> (2005)
b.	Effective spike length of tertiary raceme	Negative	S	G	Lakshamma <i>et al.</i> (2005)
<b>6.</b>	<b>Association of days to maturity of primary raceme with</b>				
a.	Plant height	Positive	S NS	P,G G P	Aswani Kumar <i>et al.</i> (2003) Golakia <i>et al.</i> (2007) Golakia <i>et al.</i> (2007)
b.	Nodes to primary raceme	Positive	S S NS	P,G P G	Aswani Kumar <i>et al.</i> (2003) Golakia <i>et al.</i> (2007) Golakia <i>et al.</i> (2007)
c.	Total length of primary raceme	Positive	NS NS	G P,G	Mehta and Vashi (1998) Aswani Kumar <i>et al.</i> (2003)
		Negative	S NS	P G	Golakia <i>et al.</i> (2007) Golakia <i>et al.</i> (2007)
d.	Effective length of primary raceme	Positive	NS S	G P	Mehta and Vashi (1998) Mehta and Vashi (1998)
		Negative	S NS	P G	Golakia <i>et al.</i> (2007) Golakia <i>et al.</i> (2007)
e.	100 seed weight	Positive	S NS	P,G P,G	Aswani Kumar <i>et al.</i> (2003) Golakia <i>et al.</i> (2007)
<b>7.</b>	<b>Association of no. of secondary branches with</b>				
a.	Effective length of primary spike	Positive	NS	G	Lakshamma <i>et al.</i> (2005)
b.	Effective length of secondary spike	Positive	NS	G	Lakshamma <i>et al.</i> (2005)
c.	Effective length of tertiary spike	Positive	NS	G	Lakshamma <i>et al.</i> (2005)

S.No	Character	Association	S/NS	P/G	Reference
<b>8.</b>	<b>Association of 100 seed weight with</b>				
a.	Oil content	Positive	S	-	Domingo (1945)
		Positive	NS	-	Singh <i>et al.</i> (1981)
				-	Yadav <i>et al.</i> (2004)
		Negative	-	G	Ramesh and Prasad (2001)

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S      Significant  
 NS     Non Significant  
 P      Phenotypic correlation  
 G      Genotypic correlation

## 2.4 PATH COEFFICIENT ANALYSIS

Path coefficient analysis as devised by Wright (1921) is a standardized partial regression coefficient, which helps in partitioning the correlation coefficient into direct and indirect effects of independent variables on the dependent variable. The path coefficient analysis further helps to elucidate the intrinsic nature of the observed associations and imparts a degree of confidence in the selection scheme adopted for a given situation. It may also help to minimise the number of attributes for which simultaneous selection must be exercised (Dewey and Lu, 1959).

The available literature on direct and indirect effects of yield components on yield in *Ricinus communis* L. was reviewed here under in Tables 5 and 6, respectively

**Table 5: Direct effects of yield components on yield in castor (*Ricinus communis* L.)**

S.No	Character	Effect	Reference
1.	Days to 50% flowering	Positive	Aswani kumar <i>et al.</i> (2003) Yadav <i>et al.</i> (2004) Manivel and Manivannan (2006) Golakia <i>et al.</i> (2007)
		Negative	Patel and Jaimani (1991) Kumari <i>et al.</i> (1996) Mehta and Vashi (1998) Ramesh and Prasad (2001) Asish <i>et al.</i> (2008)
2.	Plant height upto primary spike	Positive	Bhatt and Reddy (1981) Muthiah <i>et al.</i> (1982b) Patel and Jaimani (1991) Kumari <i>et al.</i> (1996) Mehta and Vashi (1998) Aswani kumar <i>et al.</i> (2003) Manivel and Manivannan (2006)
		Negative	Raju (1981) Rao <i>et al.</i> (1983a) Khorgade <i>et al.</i> (1994) Ramesh and Prasad (2001) Yadav <i>et al.</i> (2004)
3.	Number of nodes upto primary spike	Positive	Ananthasayana and Reddi (1981) Muthiah <i>et al.</i> (1982b) Kumari <i>et al.</i> (1996) Yadav <i>et al.</i> (2004)
		Negative	Bhatt and Reddy (1981) Rao <i>et al.</i> (1983a) Patel and Jaimani (1991) Mehta and Vashi (1998) Ramesh and Prasad (2001) Aswani kumar <i>et al.</i> (2003) Golakia <i>et al.</i> (2007)
4.	Total length of primary spike	Positive	Ananthasayana and Reddi (1981) Mehta and Vashi (1998) Ramesh and Prasad (2001) Golakia <i>et al.</i> (2007)
		Negative	Rao <i>et al.</i> (1983a) Khorgade <i>et al.</i> (1994)

S.No	Character	Effect	Reference
5.	Effective length of primary spike	Positive	Ramesh and Prasad (2001) Manivel and Manivannan (2006)
		Negative	Mehta and Vashi (1998) Lakshamma <i>et al.</i> (2005) Golakia <i>et al.</i> (2007)
6.	Days to 80% maturity of primary spike	Positive	----
		Negative	Khorgade <i>et al.</i> (1994) Golakia <i>et al.</i> (2007)
7.	No. of secondary branches/plant	Positive	Manivel and Manivannan (2006)
		Negative	Lakshamma <i>et al.</i> (2005)
8.	No. of nodes up to secondary raceme	Positive	Ramesh <i>et al.</i> (2001)
		Negative	----
9.	Effective length of secondary spike	Positive	----
		Negative	Lakshamma <i>et al.</i> (2005)
10.	No. of tertiary branches	Positive	Manivel and Manivannan (2006)
11.	Effective length of tertiary spike	Negative	Lakshamma <i>et al.</i> (2005)
12.	100 seed weight	Positive	Ananthasayana and Reddi (1981) Bhatt and Reddy (1981) Rao <i>et al.</i> (1983a) Khorgade <i>et al.</i> (1994) Mehta and Vashi (1998) Ramesh and Prasad (2001) Aswani kumar <i>et al.</i> (2003) Manivel and Manivannan (2006)
		Negative	Yadav <i>et al.</i> (2004)
13.	Oil content	Positive	Khorgade <i>et al.</i> (1994) Kumari <i>et al.</i> (1996) Ramesh and Durga Prasad (2001) Manivel and Manivannan (2006) Janamma <i>et al.</i> (2008)
		Negative	Yadav <i>et al.</i> (2004) Asish <i>et al.</i> (2008)

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S.No	Character	Effect	Reference
14.	Harvest index	Positive	Ravi <i>et al.</i> (2006)
15.	Days to maturity	Positive	Muppidathe <i>et al.</i> (1995) Aswani kumar <i>et al.</i> (2003)
		Negative	Ramesh <i>et al.</i> (2001)

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**Table – 27: Promising genotypes selected for earliness**

S. No.	Character	Range entries	Checks			CD at (5%) level	Promising selections above checks
			DPC-9	M-574	Kiran		
1.	Days to 50% flowering of primary raceme	51.00-116.00	70.00	66.50	53.00	2.50	Nil
2.	Days to 80% maturity or primary raceme	85.50-131.00	96.00	100.50	86.00	2.17	Nil
3.	Days to 50% flowering of secondary raceme	69.50-140.50	101.00	95.00	76.50	2.95	PPL 117
4.	Days to 80% maturity or secondary raceme	101.00-156.50	124.00	124.50	114.00	3.42	PPL 117, PPL 126, PPL 128, PPL 136, PPL 137, PCH-111
5.	Days to 50% flowering of tertiary raceme	87.00-163.00	120.00	119.00	103.00	2.48	PPL 104, PPL 109, PPL 117, PPL 125, PPL 128, PPL 130, PPL 136, PPL 137, PPL 151, GCH 4, PCH 80, PCH 111
6.	Days to 80% maturity or tertiary raceme	119.50-173.00	150.50	143.00	132.00	4.97	PPL 109, PPL 1117, PPL 125, PPL 128, PPL 137

**Table – 28: Promising genotypes selected for yield and yield components**

S. No.	Character	Range entries	Checks			CD at (5%) level	Promising selections above checks
			DPC 9	M-574	Kiran		
1.	Total length of primary raceme	24.40-62.40	44.00	47.00	28.00	3.47	PPL 101, PPL 111, PPL 116, PPL 123, PPL 130, PPL 134, PPL 140, PPL 141, PPL 142, PPL 143, PPL 145, PPL 148, PPL 149, PPL 150
2.	Effective length of primary raceme	19.40-55.00	42.00	37.00	24.00	2.67	PPL 116, PPL123, PPL 130, PPL 139, PPL 140, PPL 141, PPL 142, PPL 143, PPL 148, PPL 149
3.	Number of secondary racemes per plant	1.80-4.40	2.70	2.60	1.90	0.44	PPL 105, PPL 111, PPL 114, PPL 123, PPL 131, PPL 134, PPL 144
4.	Total length of secondary raceme	12.85-54.50	42.00	41.00	24.00	2.71	PPL 123, PPL 130, PPL 140, PPL 143, PPL 149
5.	Effective length of secondary raceme	15.00-46.00	38.60	32.00	21.00	2.37	PPL 130
6.	Number of tertiary racemes per plant	1.10-5.00	4.00	3.10	2.10	0.52	PPL 125, PPL 135, PPL 138
7.	Effective length of tertiary raceme	13.10-31.60	31.60	26.70	18.20	1.84	Nil

**Table – 28: Promising genotypes selected for yield and yield components**

S. No.	Character	Range of entries	Checks			CD at (5%) level	Promising selections above checks
			DPC 9	M-574	Kiran		
8	100 Seed Wt of Primary Raceme	18.21-31.25	22.86	29.09	27.04	1.39	GCH 4
9	100 Seed Wt of Secondary Raceme	17.61-30.90	26.03	27.51	26.85	1.83	PPL 102, PPL 105, PPL 125, PPL 143, GCH 4, PCH 111
10	100 Seed Wt of Tertiary Raceme	17.67-32.73	29.43	25.39	26.63	2.18	GCH 4, PCH 111
11	Oil content	43.96-51.57	48.35	49.40	51.37	1.84	Nil
12	Seed yield per plant at 120 days	0.00-129.40	71.50	43.00	97.50	11.98	PPL 103, GCH 4, PCH 80
13	Seed yield per plant upto 150 days	26.85-184.00	147.50	123.10	121.00	16.68	PPL 103, GCH 4, PCH 80, PCH 111
14	Seed yield per plant upto 180 days	60.10-210.50	210.50	123.00	121.00	20.17	Nil

**Table – 23: PCA scores of 54 genotypes of castor  
(*Ricinus communis* L.)**

<b>S.No</b>	<b>Genotype</b>	<b>PCA I X vector</b>	<b>PCA II Y vector</b>	<b>PCA III Z vector</b>
1	PPL 101	167.421	-81.331	5.741
2	PPL 102	203.390	-93.673	14.054
3	PPL 103	133.416	-90.082	-1.427
4	PPL 104	111.157	-82.040	20.551
5	PPL 105	160.079	-84.100	19.042
6	PPL 106	134.302	-69.738	22.732
7	PPL 107	120.162	-85.602	21.936
8	PPL 108	176.244	-82.285	5.933
9	PPL 109	104.149	-80.915	17.201
10	PPL 110	132.845	-77.710	8.478
11	PPL 111	150.681	-95.484	-7.657
12	PPL 112	139.781	-71.758	1.255
13	PPL 113	137.134	-67.363	13.040
14	PPL 114	150.073	-77.592	-1.479
15	PPL 115	132.384	-91.736	4.615
16	PPL 116	153.563	-96.898	4.420
17	PPL 117	101.463	-64.108	10.856
18	PPL 118	145.970	-72.984	8.263
19	PPL 119	156.761	-81.004	-1.642
20	PPL 120	145.411	-77.976	0.517
21	PPL 121	124.532	-93.430	-4.950
22	PPL 122	123.470	-91.949	4.066
23	PPL 123	137.375	-104.455	13.388
24	PPL 125	105.943	-79.203	20.548
25	PPL 126	121.436	-97.571	11.209
26	PPL 128	106.507	-78.931	14.077
27	PPL 129	113.894	-93.717	17.317
28	PPL 130	114.393	-112.240	11.395
29	PPL 131	147.216	-71.448	10.104
30	PPL 132	158.237	-83.775	9.676
31	PPL 133	182.367	-95.626	8.813
32	PPL 134	151.559	-92.463	7.031
33	PPL 135	144.770	-83.611	9.869
34	PPL 136	104.008	-90.713	13.501
35	PPL 137	97.431	-92.268	25.143
36	PPL 138	178.681	-94.077	12.885
37	PPL 139	114.127	-109.479	25.268
38	PPL 140	154.117	-98.491	20.491
39	PPL 141	181.499	-80.467	18.612
40	PPL 142	145.653	-103.299	12.032
41	PPL 143	146.928	-104.977	16.150
42	PPL 144	131.817	-86.731	5.844
43	PPL 145	143.942	-94.134	2.865
44	PPL 147	246.193	-75.439	22.360
45	PPL 148	189.551	-98.330	18.466
46	PPL 149	211.736	-100.427	14.951
47	PPL 150	151.982	-97.855	16.745
48	PPL 151	121.668	-91.594	15.219
49	DPC 9	141.120	-106.873	-6.597
50	GCH 4	103.833	-95.162	16.872
51	M 574	125.638	-100.396	-3.602
52	PCH 80	100.652	-88.015	14.263
53	PCH 111	96.667	-95.603	13.291
54	KIRAN	96.764	-82.922	-3.116



Table 15: Direct and Indirect effects

character	Days to 50% Flowering of Pri Raceme	Stem Length to Pri Raceme (cm)	Nodes to Pri Racem	Total Length of Pri Raceme cm	Effective Length of Pri Raceme	Days to 80% maturity of Pri Race	Secondary Branches/ Plant	Days to 50% Flowering of Sec Raceme	Nodes to Secondary Racem
	1	2	3	4	5	6	7	8	9
1	<b>-0.0657</b>	-0.0502	-0.0584	-0.0166	-0.0179	-0.0557	-0.0056	-0.0587	-0.0226
2	-0.0224	<b>-0.0294</b>	-0.0222	-0.0083	-0.0084	-0.0222	0.0011	-0.0236	-0.0093
3	0.1530	0.1300	<b>0.1724</b>	0.0241	0.0198	0.1367	0.0296	0.1388	0.0569
4	-0.0320	-0.0356	-0.0177	<b>-0.1264</b>	-0.1140	-0.0431	0.0077	-0.0535	-0.0434
5	0.0640	0.0668	0.0270	0.2119	<b>0.2350</b>	0.0775	-0.0269	0.1030	0.0700
6	-0.0177	-0.0158	-0.0166	-0.0071	-0.0069	<b>-0.0209</b>	0.0004	-0.0186	-0.0086
7	0.0093	-0.0039	0.0185	-0.0066	-0.0124	-0.0018	<b>0.1080</b>	0.0028	0.0180
8	0.0180	0.0162	0.0163	0.0086	0.0089	0.0180	0.0005	<b>0.0202</b>	0.0106
9	-0.0195	-0.0179	-0.0187	-0.0195	-0.0169	-0.0232	-0.0095	-0.0298	<b>-0.0568</b>
10	-0.0036	-0.0035	-0.0030	-0.0028	-0.0028	-0.0034	-0.0015	-0.0039	-0.0026
11	-0.0079	-0.0062	0.0103	-0.1176	-0.1198	-0.0214	0.0132	-0.0421	-0.0303
12	0.0087	0.0048	-0.0085	0.0703	0.0784	0.0143	-0.0141	0.0281	0.0147
13	0.2507	0.2184	0.2268	0.1158	0.1131	0.2610	0.0163	0.2683	0.1331
14	-0.0104	-0.0002	-0.0258	-0.0580	-0.0667	-0.0143	0.0211	-0.0357	-0.0390
15	0.1162	0.1018	0.1068	0.0548	0.0578	0.1128	0.0196	0.1293	0.0658
16	0.0013	0.0013	0.0014	0.0006	0.0002	0.0011	-0.0007	0.0015	0.0009
17	0.0093	0.0063	0.0119	-0.0030	-0.0046	0.0105	0.0066	0.0091	0.0090
18	-0.0051	0.0095	-0.0141	0.0700	0.0476	-0.0005	-0.0175	0.0192	0.0320
19	0.1295	0.1167	0.1135	0.0761	0.0777	0.1317	-0.0041	0.1447	0.0696
20	0.0251	0.0200	0.0166	-0.0411	-0.0440	0.0094	0.0208	0.0069	-0.0214
21	0.0000	-0.0002	-0.0003	-0.0010	-0.0012	0.0000	0.0006	-0.0003	-0.0008
22	-0.0254	-0.0210	-0.0213	0.0073	0.0146	-0.0176	-0.0124	-0.0167	0.0101
23	-0.0023	-0.0017	-0.0024	0.0101	0.0113	-0.0006	-0.0039	-0.0006	0.0039
24	0.0118	0.0036	0.0098	0.0003	-0.0001	0.0097	0.0017	0.0096	0.0066
25	-0.1751	-0.1804	-0.1679	0.0305	0.0018	-0.1717	-0.0056	-0.1580	-0.0338
26	-0.0565	-0.0411	-0.0480	-0.0097	-0.0096	-0.0567	-0.0100	-0.0555	-0.0208
27	-0.7110	-0.5396	-0.6569	0.0283	-0.0186	-0.7028	-0.1047	-0.6617	-0.2650
Seed Yield/plant upto 180 Days	<b>-0.3581**</b>	<b>-0.2512**</b>	<b>-0.3504**</b>	<b>0.2911**</b>	<b>0.2221*</b>	<b>-0.3732**</b>	<b>0.0306</b>	<b>-0.2769**</b>	<b>-0.0531</b>

\*= significant at 5% level, \*\*= significant at 1% level





**Table 16: Direct :**

character	Days to 50% Flowering of Pri Raceme	Stem Length to Pri Raceme (cm)	Nodes to Pri Racem	Total Length of Pri Raceme cm	Effective Length of Pri Raceme	Days to 80% maturity of Pri Race	Secondary Branches/ Plant	Days to 50% Flowering of Sec Rceme
	1	2	3	4	5	6	7	8
1	<b>-0.1525</b>	-0.1170	-0.1372	-0.0392	-0.0415	-0.1299	-0.0142	-0.1370
2	0.2359	<b>0.3076</b>	0.2351	0.0889	0.0881	0.2336	-0.0092	0.2487
3	0.7026	0.5968	<b>0.7811</b>	0.1130	0.0904	0.6303	0.1573	0.6399
4	-0.2331	-0.2618	-0.1310	<b>-0.9059</b>	-0.8344	-0.3148	0.0802	-0.3937
5	0.2877	0.3031	0.1224	0.9744	<b>1.0579</b>	0.3527	-0.1454	0.4710
6	-0.3900	-0.3477	-0.3694	-0.1591	-0.1526	<b>-0.4578</b>	0.0067	-0.4098
7	-0.0137	0.0044	-0.0297	0.0131	0.0203	0.0022	<b>-0.1476</b>	-0.0042
8	-1.1456	-1.0309	-1.0446	-0.5542	-0.5677	-1.1414	-0.0363	<b>-1.2751</b>
9	0.0685	0.0642	0.0650	0.0689	0.0569	0.0815	0.0274	0.1036
10	0.0345	0.0331	0.0291	0.0265	0.0273	0.0321	0.0161	0.0365
11	0.0082	0.0068	-0.0114	0.1217	0.1231	0.0225	-0.0135	0.0431
12	-0.0105	-0.0059	0.0103	-0.0846	-0.0942	-0.0167	0.0193	-0.0336
13	0.5861	0.5103	0.5369	0.2745	0.2661	0.6126	0.0463	0.6266
14	-0.0251	0.0002	-0.0649	-0.1513	-0.1732	-0.0382	0.0616	-0.0924
15	0.5588	0.4895	0.5184	0.2710	0.2813	0.5435	0.1021	0.6227
16	0.0480	0.0496	0.0507	0.0231	0.0096	0.0433	-0.0284	0.0567
17	-0.0035	-0.0024	-0.0045	0.0012	0.0018	-0.0039	-0.0027	-0.0034
18	-0.0019	0.0043	-0.0060	0.0303	0.0204	-0.0004	-0.0078	0.0085
19	0.1002	0.0900	0.0895	0.0592	0.0599	0.1016	-0.0042	0.1118
20	-0.0762	-0.0597	-0.0532	0.1204	0.1310	-0.0304	-0.0617	-0.0202
21	-0.0086	-0.0342	-0.0467	-0.1470	-0.1721	0.0002	0.0984	-0.0501
22	-0.0261	-0.0225	-0.0215	0.0072	0.0145	-0.0177	-0.0122	-0.0169
23	-0.0073	-0.0052	-0.0075	0.0297	0.0325	-0.0029	-0.0150	-0.0018
24	0.0291	0.0087	0.0239	0.0017	-0.0003	0.0242	0.0078	0.0238
25	-0.4910	-0.5024	-0.4783	0.0872	-0.0033	-0.4782	-0.0064	-0.4357
26	0.0729	0.0531	0.0623	0.0134	0.0126	0.0732	0.0157	0.0712
27	-0.5200	-0.3959	-0.4828	0.0131	-0.0128	-0.5166	-0.0913	-0.4856
<b>Seed Yield/plant up to 180 Days</b>	<b>-0.3724**</b>	<b>-0.2637**</b>	<b>-0.3643**</b>	<b>0.2970**</b>	<b>0.2416*</b>	<b>-0.3955**</b>	<b>0.0429</b>	<b>-0.2956**</b>

\*= significant at 5% level, \*\*= significant at 1% level



tor (*Ricinus communis* L.)

Effective Length of Ter Raceme	Days to 80% maturity Of ter Raceme	100 Seed Wt of Primary Raceme (gm)	100 Seed Wt of Secondary Raceme (gm)	100 Seed Wt of Tertiary Raceme (gm)	Oil Content (%)	L/B Ratio of Seed	harvest Index (%)	Seed Yield/ Plant At 120 Days (gm)
18	19	20	21	22	23	24	25	26
0.0040	-0.1202	0.0294	-0.0024	0.0398	0.0125	0.0555	0.0940	0.1178
0.0184	0.2177	-0.0463	0.0189	-0.0691	-0.0180	-0.0336	-0.1940	-0.1730
-0.0661	0.5497	-0.1049	0.0656	-0.1676	-0.0661	-0.2331	-0.4689	-0.5152
-0.3858	-0.4214	-0.2753	-0.2393	-0.0652	-0.3028	0.0187	-0.0992	0.1285
0.3040	0.4982	0.3499	0.3272	0.1531	0.3864	0.0044	-0.0044	-0.1417
0.0023	-0.3657	0.0351	0.0001	0.0808	0.0150	0.1383	0.2748	0.3549
0.0163	0.0049	0.0230	0.0261	0.0180	0.0250	0.0144	0.0012	0.0245
-0.1524	-1.1208	0.0652	-0.1148	0.2145	0.0265	0.3791	0.6972	0.9609
0.0347	0.0821	0.0324	0.0410	0.0234	0.0224	-0.0424	-0.0299	-0.0580
-0.0007	0.0385	-0.0202	-0.0185	-0.0313	-0.0121	-0.0091	-0.0367	-0.0291
0.1222	0.0397	0.0382	0.0350	0.0012	0.0145	-0.0004	0.0541	-0.0041
-0.0863	-0.0360	-0.0265	-0.0125	0.0069	-0.0105	0.0093	-0.0248	0.0147
0.0628	0.6006	-0.1286	-0.0566	-0.2180	-0.0623	-0.1467	-0.3888	-0.5665
-0.0055	-0.1847	-0.0282	0.0444	0.1151	-0.0389	-0.0728	0.0200	0.0775
0.0171	0.5755	-0.0741	0.0178	-0.1455	-0.0306	-0.1798	-0.3659	-0.4781
0.0177	0.0613	-0.0321	-0.0226	-0.0493	-0.0402	-0.0207	-0.0280	-0.0464
0.0003	-0.0037	0.0019	0.0019	0.0031	0.0006	0.0032	0.0030	0.0033
<b>0.0711</b>	0.0088	0.0158	0.0092	0.0093	0.0092	-0.0031	0.0332	0.0067
0.0157	<b>0.1272</b>	-0.0186	-0.0048	-0.0359	-0.0054	-0.0238	-0.0600	-0.0966
0.0879	-0.0579	<b>0.3962</b>	0.3357	0.3245	0.2861	0.0540	0.1319	0.1378
-0.0724	0.0209	-0.4715	<b>-0.5564</b>	-0.4504	-0.3062	-0.0154	-0.1313	-0.1746
0.0131	-0.0283	0.0821	0.0811	<b>0.1002</b>	0.0502	0.0081	0.0388	0.0435
0.0115	-0.0038	0.0642	0.0489	0.0445	<b>0.0889</b>	0.0075	0.0152	0.0274
0.0035	0.0150	-0.0109	-0.0022	-0.0065	-0.0067	<b>-0.0800</b>	-0.0100	-0.0223
0.3722	-0.3761	0.2653	0.1881	0.3081	0.1363	0.0995	<b>0.7968</b>	0.4847
-0.0088	0.0717	-0.0328	-0.0296	-0.0410	-0.0292	-0.0263	-0.0575	<b>-0.0945</b>
0.2153	-0.4473	0.2717	0.2076	0.3054	0.2155	0.2178	0.5253	0.5641
<b>0.6119**</b>	<b>-0.2542**</b>	<b>0.4001**</b>	<b>0.3889**</b>	<b>0.4683**</b>	<b>0.3602**</b>	<b>0.1227</b>	<b>0.7859**</b>	<b>0.5464**</b>

<b>Seed Yield/ Plant At 150 Days (gm)</b>
27
0.1192
-0.1831
-0.5669
-0.0179
-0.0203
0.3556
0.0203
0.9309
-0.0578
-0.0351
0.0437
-0.0203
-0.5190
0.0698
-0.4693
-0.0602
0.0047
0.0230
-0.0855
0.1618
-0.1737
0.0460
0.0288
-0.0262
0.6291
-0.0801
<b>0.6652</b>
<b>0.7828**</b>

**Table- 20: The nearest and the farthest cluster from each cluster based on  $D^2$  values.**

<b>Cluster No.</b>	<b>Nearest cluster with <math>D^2</math> values</b>	<b>Farthest cluster with <math>D^2</math> values</b>
I	VI (1081.344)	IX(20324.604)
II	IV (1137.648)	IX (10242.585)
III	II (1391.604)	IX (14648.815)
IV	II (1137.648)	IX (12981.145)
V	II (1539.001)	IX (7813.980)
VI	I (1081.344)	IX (21728.092)
VII	V (2525.634)	VI (12793.441)
VIII	I (1244.966)	IX (19061.795)
IX	VII (2836.391)	VI (21728.092)

**Note: Values in parentheses indicate  $D^2$  values**

**Table- 10: Mean performance of 28 characters of 54 genotypes in castor ( *Ricinus communis* )**

S. no	Genotype	Days to 50% Flowering of Pri Raceme	Stem Length to Pri Raceme (cm)	Nodes to Pri Raceme	Total Length of Pri Raceme cm	Effective Length of Pri Raceme (cm)	Days to 80% maturity of Pri Race	Secondary Branches/ Plant	Days to 50% Flowering of Sec Raceme	Nodes to Secondary Raceme	Stem Length to Sec Raceme (cm)	Total Length of Sec Raceme (cm)	Effective Length Sec Raceme (cm)	Days to 80% maturity of Sec Raceme	Tertiary Branches/ Plant
1	PPL 101	79.50	133.90	26.10	48.00	41.10	112.00	2.50	111.50	18.45	79.35	23.00	19.50	139.50	1.20
2	PPL 102	81.50	188.10	28.00	44.20	41.10	127.00	2.50	131.00	14.15	95.70	42.40	38.60	151.00	1.70
3	PPL 103	51.00	119.40	16.30	46.80	39.80	94.00	2.00	83.50	12.00	89.65	42.60	33.40	116.00	3.40
4	PPL 104	53.50	99.80	16.60	43.10	35.55	101.00	2.10	76.00	7.25	44.45	33.40	27.60	118.00	3.60
5	PPL 105	77.00	133.10	28.50	44.80	34.70	108.50	3.40	111.50	14.60	87.30	23.60	15.00	145.50	2.20
6	PPL 106	63.50	131.40	20.10	28.05	23.90	104.00	2.30	90.00	13.90	92.10	30.60	27.15	127.50	2.40
7	PPL 107	62.00	100.90	19.00	41.80	37.50	105.50	2.60	86.00	14.00	89.40	36.65	29.50	119.50	2.70
8	PPL 108	83.00	139.10	25.30	46.00	42.00	117.00	3.00	116.00	14.45	90.15	24.80	19.40	145.50	2.20
9	PPL 109	58.50	89.90	17.70	42.75	37.15	95.00	2.20	77.50	8.50	48.80	30.45	25.15	111.50	3.50
10	PPL 110	54.00	96.70	15.30	34.25	27.65	102.50	2.50	91.00	8.20	75.64	24.00	18.30	124.00	2.70
11	PPL 111	64.50	111.40	17.70	53.00	40.40	95.00	3.20	90.50	11.40	67.55	35.60	30.90	122.00	1.10
12	PPL 112	77.00	86.60	21.90	33.50	27.40	106.00	2.90	94.50	10.15	64.30	23.90	23.00	128.00	3.80
13	PPL 113	76.00	103.90	22.00	24.40	22.20	107.00	2.80	92.00	8.15	95.13	21.50	25.00	124.50	3.30
14	PPL 114	64.50	98.50	21.60	27.85	24.35	94.50	4.40	93.00	12.20	99.85	31.35	26.65	128.00	3.70
15	PPL 115	58.50	102.00	21.70	39.75	33.65	94.25	3.10	89.00	10.25	108.85	40.50	36.70	114.50	2.80
16	PPL 116	74.50	110.60	21.26	53.60	46.10	110.00	2.70	103.50	9.25	95.55	33.50	30.00	133.50	3.00
17	PPL 117	52.00	100.40	16.00	25.40	19.40	85.50	2.10	72.00	6.60	35.20	12.85	18.50	107.00	4.00
18	PPL 118	76.00	94.30	24.15	36.00	31.90	116.50	3.10	96.00	7.10	77.40	36.75	32.25	134.00	2.60
19	PPL 119	77.00	112.00	23.20	45.40	38.60	109.00	2.40	96.00	7.80	117.00	30.90	27.50	130.00	3.10
20	PPL 120	74.00	93.30	22.20	32.40	28.20	103.50	2.90	93.50	6.30	80.40	38.50	27.75	129.50	4.30
21	PPL 121	53.00	68.30	15.60	40.30	31.70	96.00	2.00	88.00	11.50	65.95	35.00	28.10	116.00	2.90
22	PPL 122	60.00	90.00	17.30	42.95	36.50	91.00	2.30	84.50	10.95	77.50	36.40	31.50	113.50	3.30
23	PPL 123	62.00	111.90	18.10	62.40	52.50	94.00	3.30	94.00	11.70	107.00	45.90	37.65	129.50	2.20
24	PPL 125	53.00	94.50	16.10	34.00	26.90	92.50	2.60	76.50	8.35	45.85	24.60	17.50	108.00	5.00
25	PPL 126	52.00	110.50	15.90	46.13	42.00	92.50	2.80	84.00	8.55	44.55	24.10	19.50	107.00	3.40
26	PPL 128	51.50	83.80	15.90	28.50	21.70	89.50	2.60	74.00	8.50	64.65	25.50	17.00	108.00	3.50
27	PPL 129	52.50	78.10	14.30	34.60	27.60	90.50	2.10	83.00	9.15	73.05	41.00	37.90	127.00	1.50
28	PPL 130	51.50	76.80	15.10	55.60	47.00	91.50	2.00	87.00	9.00	53.35	54.50	46.00	120.00	2.70
29	PPL 131	74.00	122.70	21.70	45.40	31.80	101.00	3.40	87.50	12.20	127.25	35.10	27.75	130.00	3.70

**Table- 10: Mean performance of 28 characters of 54 genotypes in castor ( *Ricinus communis* L. )**

S.NO	Genotype	Days to 50% Flowering of Pri Raceme	Stem Length to Pri Raceme (cm)	Nodes to Pri Racem	Total Length of Pri Raceme cm	Effective Length of Pri Raceme	Days to 80% maturity of Pri Raceme	Secondary Branches/ Plant	Days to 50% Flowering of Sec Raceme	Nodes to Secondary Raceme	Stem Length to Sec Raceme (cm)	Total Length of Sec Raceme (cm)	Effective Length Sec Raceme (cm)	Days to 80% maturity of Sec Raceme	Tertiary Branches/ Plant
30	PPL 132	75.00	148.90	21.00	38.90	33.40	99.00	2.60	103.50	10.30	139.60	27.55	22.40	131.50	3.90
31	PPL 133	80.50	167.50	25.40	47.35	40.00	110.50	2.30	109.50	10.40	134.35	37.50	35.50	135.50	2.60
32	PPL 134	62.00	137.50	18.00	48.20	42.80	98.50	3.20	91.50	11.50	86.10	37.35	32.00	124.00	4.40
33	PPL 135	74.00	107.50	21.50	37.75	31.88	102.00	3.10	103.00	13.50	77.50	37.65	31.50	126.00	4.70
34	PPL 136	53.50	70.50	16.80	39.45	30.50	90.00	2.50	82.50	11.00	75.80	34.00	28.00	101.00	3.70
35	PPL 137	54.00	87.30	16.60	46.40	38.00	91.50	2.70	76.00	8.75	70.80	33.00	31.00	109.00	3.60
36	PPL 138	77.00	168.60	20.00	45.50	36.90	114.00	2.40	110.00	12.20	65.40	44.00	39.00	141.50	4.80
37	PPL 139	61.00	101.70	16.90	42.70	55.00	91.00	2.40	90.00	8.50	72.95	44.00	40.00	122.50	1.30
38	PPL 140	64.50	133.40	18.30	57.30	53.35	116.00	2.50	107.00	11.10	151.90	45.35	40.35	138.50	2.60
39	PPL 141	83.00	175.70	22.40	53.75	48.40	121.00	2.90	115.00	12.65	151.60	28.40	22.50	151.00	3.80
40	PPL 142	79.00	122.00	20.50	54.00	50.80	102.50	2.30	102.50	7.75	120.05	37.50	33.50	134.00	2.70
41	PPL 143	87.00	107.30	25.00	50.40	48.50	104.50	2.90	108.50	11.50	112.40	45.75	40.00	131.00	1.60
42	PPL 144	54.00	101.90	15.50	40.60	33.00	92.00	3.70	90.00	11.40	108.70	37.00	32.00	116.00	2.80
43	PPL 145	58.00	100.90	23.25	49.40	35.40	103.50	2.50	95.00	10.20	59.50	38.90	28.50	129.50	1.80
44	PPL 147	116.00	282.30	37.40	37.10	29.60	129.50	2.30	140.50	7.75	73.85	27.90	21.30	156.50	3.60
45	PPL 148	92.50	153.30	26.40	53.20	45.60	129.50	2.30	130.50	17.90	109.05	36.60	32.00	154.50	4.40
46	PPL 149	91.00	195.40	23.60	58.00	55.00	131.00	2.00	136.50	14.50	96.93	45.00	37.00	155.00	3.10
47	PPL 150	74.50	129.90	20.50	55.50	51.00	107.50	1.80	108.00	10.50	121.00	38.00	36.20	139.00	1.25
48	PPL 151	59.00	117.30	16.40	40.00	37.00	87.00	2.00	87.50	13.00	90.50	32.00	26.00	112.00	2.80
49	DPC 9	70.00	88.00	17.50	44.00	42.00	96.00	2.70	101.00	12.50	62.35	42.00	38.60	124.00	4.00
50	GCH 4	51.00	90.50	16.80	42.00	38.00	93.50	2.70	77.50	9.20	42.05	31.00	27.20	106.00	3.70
51	M 574	66.50	48.00	16.00	47.00	37.00	100.50	2.60	95.00	11.45	37.00	41.00	32.00	124.50	3.10
52	PCH 80	51.00	81.50	16.50	37.00	31.00	91.00	2.50	69.50	6.50	41.80	36.00	27.00	112.50	4.05
53	PCH 111	52.00	71.00	14.50	40.00	38.00	88.50	2.40	78.00	8.10	39.80	28.00	22.50	107.00	4.20
54	KIRAN	53.00	49.00	14.00	28.00	24.00	86.00	1.90	76.50	8.30	59.00	24.00	21.00	114.00	2.10
	<b>Mean</b>	<b>66.78</b>	<b>113.31</b>	<b>19.91</b>	<b>42.86</b>	<b>36.97</b>	<b>101.89</b>	<b>2.61</b>	<b>95.13</b>	<b>10.65</b>	<b>83.20</b>	<b>34.23</b>	<b>29.11</b>	<b>126.00</b>	<b>3.08</b>
	C.V.	1.87	2.58	3.56	4.04	3.61	1.06	8.40	1.55	8.88	6.93	3.95	4.06	1.36	8.47
	S.E.	0.88	2.07	0.50	1.22	0.94	0.77	0.16	1.04	0.67	4.08	0.96	0.84	1.21	0.18
	C.D. 5%	2.50	5.86	1.42	3.47	2.68	2.17	0.44	2.96	1.90	11.56	2.71	2.37	3.43	0.52
	C.D. 1%	3.34	7.81	1.90	4.63	3.56	2.89	0.59	3.94	2.53	15.40	3.61	3.16	4.57	0.70

**Table- 10 : Mean performance of 28 characters of 54 genotypes in castor ( *Ricinus communis* L. )**

S. no	Genotype	Days to 50% Flowering of Ter Raceme	Nodes to Tertiary Racemes	Stem Length to Ter Raceme cm	Effective Length of Ter Raceme	Days to 80% maturity Of ter Raceme	100 Seed Wt of Primary Raceme (gm)	100 Seed Wt of Secondary Raceme( gm)	100 Seed Wt of Tertiary Raceme (gm)	Oil Content (%)	L/B Ratio of Seed	harvest Index (%)	Seed Yield/ Plant At 120 Days (gm)	Seed Yield/ Plant At 150 Days (gm)	Seed Yield/ Plant At 180 Days (gm)
1	PPL 101	140.00	5.30	17.20	15.70	158.50	24.50	25.80	23.10	48.65	1.42	34.20	27.12	59.11	84.11
2	PPL 102	151.00	5.00	17.60	26.30	172.00	28.29	29.60	27.44	50.09	1.46	32.90	0.00	33.49	111.00
3	PPL 103	104.00	8.00	17.95	24.20	131.50	22.58	25.07	23.75	49.53	1.48	41.30	129.40	184.00	184.00
4	PPL 104	92.00	12.05	61.00	23.40	127.50	24.77	26.47	25.77	49.71	1.46	37.20	78.60	139.70	139.70
5	PPL 105	140.50	9.40	49.85	15.20	161.00	24.82	29.57	26.17	48.13	1.53	35.10	45.30	71.60	118.10
6	PPL 106	106.00	8.10	37.45	21.10	152.00	22.93	22.81	25.21	46.28	1.59	33.70	38.35	75.31	75.30
7	PPL 107	107.00	9.00	55.88	22.80	127.50	28.83	26.65	28.97	50.70	1.43	36.50	79.90	123.50	123.50
8	PPL 108	143.00	7.90	24.10	17.30	164.50	23.06	25.63	22.37	48.30	1.44	35.80	25.65	51.90	114.80
9	PPL 109	91.50	8.80	56.00	18.10	120.00	24.94	26.93	24.41	49.72	1.44	36.80	90.60	127.05	127.30
10	PPL 110	122.00	8.90	43.55	14.20	148.00	21.46	20.95	21.63	46.64	1.53	33.40	24.40	115.00	115.00
11	PPL 111	127.50	6.20	28.25	26.60	156.00	23.53	22.23	20.58	50.36	1.48	41.80	47.50	124.30	175.50
12	PPL 112	122.00	7.70	23.30	14.20	147.50	20.96	23.24	24.26	46.58	1.36	30.80	16.90	40.80	60.10
13	PPL 113	117.00	9.90	46.40	13.70	151.50	20.83	21.95	21.52	47.08	1.33	35.10	14.95	55.38	81.50
14	PPL 114	133.00	10.45	28.35	18.10	128.50	19.70	20.15	20.87	45.90	1.43	32.60	31.05	75.15	112.70
15	PPL 115	113.00	8.05	29.90	24.20	139.50	26.92	26.54	21.17	49.11	1.43	37.50	101.00	129.80	129.80
16	PPL 116	128.50	9.30	53.30	25.60	155.00	24.04	23.14	23.51	47.85	1.47	41.04	51.50	86.00	150.50
17	PPL 117	87.00	6.55	37.00	15.30	126.00	23.72	22.11	24.08	47.17	1.49	34.20	54.30	93.45	93.45
18	PPL 118	118.50	8.25	29.30	15.10	146.00	20.45	20.20	20.33	45.96	1.42	35.10	19.60	65.35	105.30
19	PPL 119	135.00	6.25	22.50	14.20	157.00	20.18	21.52	19.52	46.53	1.39	34.20	23.85	59.65	95.60
20	PPL 120	119.00	8.85	34.15	21.20	145.50	20.31	21.73	21.57	44.18	1.46	35.60	24.75	68.50	105.90
21	PPL 121	115.00	8.95	39.45	24.80	140.00	22.22	23.27	22.00	48.66	1.45	39.00	84.00	128.70	128.70
22	PPL 122	113.00	7.75	45.35	21.40	130.50	22.42	26.63	26.72	44.79	1.51	38.50	89.05	138.50	138.50
23	PPL 123	117.50	10.30	54.50	26.70	144.00	29.45	28.59	28.12	49.40	1.43	39.90	46.60	159.20	159.20
24	PPL 125	103.50	8.75	79.10	15.30	123.50	25.00	29.91	27.33	48.09	1.44	38.50	78.00	119.50	119.50
25	PPL 126	119.50	8.75	70.50	19.20	133.00	26.59	26.87	28.00	49.81	1.43	37.40	101.40	138.50	138.50
26	PPL 128	108.00	8.85	73.85	17.50	119.50	21.10	22.95	25.07	45.86	1.46	37.20	96.10	96.10	96.10
27	PPL 129	110.50	9.05	97.40	22.80	142.00	18.28	17.61	17.67	43.96	1.48	40.00	30.00	123.00	123.00
28	PPL 130	106.50	7.65	85.50	27.00	140.00	23.01	23.79	21.61	47.56	1.51	41.20	61.40	151.70	151.70
29	PPL 131	113.50	8.00	36.00	19.80	151.00	18.42	23.67	18.98	44.85	1.42	36.80	45.00	95.90	143.70

**Table- 10 : Mean performance of 28 characters of 54 genotypes in castor ( *Ricinus communis* L. )**

s.no	Genotype	Days to 50% Flowering of Ter Raceme	Nodes to Tertiary Racemes	Stem Length to Ter Raceme cm	Effective Length of Ter Raceme	Days to 80% maturity Of ter Raceme	100 Seed Wt of Primary Raceme (gm)	100 Seed Wt of Secondary Raceme (gm)	100 Seed Wt of Tertiary Raceme (gm)	Oil Content (%)	L/B Ratio of Seed	harvest Index (%)	Seed Yield/ Plant At 120 Days (gm)	Seed Yield/ Plant At 150 Days (gm)	Seed Yield/ Plant At 180 Days (gm)
30	PPL 132	126.00	6.40	47.25	23.40	150.50	21.99	24.26	22.18	47.14	1.48	32.80	52.20	98.70	136.60
31	PPL 133	144.00	8.60	37.80	26.50	162.50	24.00	25.92	21.60	48.26	1.43	31.45	45.50	90.50	124.50
32	PPL 134	120.50	9.50	48.00	28.10	150.50	23.70	25.35	24.74	47.52	1.53	40.30	44.25	115.90	162.50
33	PPL 135	116.50	9.85	44.45	21.00	134.00	26.83	29.08	25.60	48.54	1.38	39.20	37.00	94.20	144.50
34	PPL 136	108.50	10.25	65.75	15.20	129.00	25.52	25.84	27.00	48.25	1.43	37.30	91.80	118.80	118.80
35	PPL 137	97.00	7.45	90.40	20.60	126.50	27.04	26.44	26.78	47.99	1.57	39.80	84.00	149.50	149.60
36	PPL 138	134.50	9.80	52.80	26.20	156.50	23.64	25.86	23.37	49.87	1.44	32.00	25.70	85.20	123.90
37	PPL 139	124.00	10.95	76.40	13.10	151.00	24.59	26.90	24.77	48.55	1.52	34.20	62.50	104.50	121.30
38	PPL 140	133.50	7.85	42.40	16.20	157.00	26.12	26.62	25.19	47.60	1.47	33.80	51.60	84.30	105.10
39	PPL 141	139.00	9.05	53.15	16.00	166.50	18.21	17.76	18.40	50.25	1.46	30.80	0.00	26.85	78.85
40	PPL 142	124.00	8.55	64.50	26.80	153.00	23.79	23.65	23.34	49.03	1.52	34.20	61.60	98.10	139.50
41	PPL 143	137.00	7.85	62.15	17.20	152.00	26.08	29.88	26.31	51.59	1.47	35.50	41.00	96.00	118.00
42	PPL 144	116.50	7.80	41.40	17.20	141.50	20.19	20.61	20.09	46.19	1.51	36.60	76.00	102.35	102.30
43	PPL 145	120.00	6.30	40.15	28.80	157.50	25.58	26.28	26.68	47.70	1.40	41.30	54.00	122.20	158.20
44	PPL 147	163.00	7.15	53.05	17.20	171.50	20.58	26.11	20.70	47.00	1.45	30.20	0.00	36.00	90.50
45	PPL 148	156.50	10.00	62.50	21.40	170.50	27.49	27.42	27.18	49.76	1.40	32.90	0.00	53.05	136.00
46	PPL 149	156.50	6.15	43.00	24.10	173.00	25.20	28.27	25.97	44.90	1.40	34.80	0.00	38.00	111.00
47	PPL 150	131.50	6.85	49.50	17.50	164.50	24.08	24.62	19.90	49.29	1.42	31.80	16.10	48.50	64.15
48	PPL 151	109.50	7.70	61.50	21.20	145.50	23.45	27.80	23.59	46.82	1.40	36.70	95.90	132.55	132.50
49	DPC 9	120.00	7.95	54.35	31.60	150.50	22.86	26.03	29.43	48.35	1.30	43.10	71.50	147.50	210.50
50	GCH 4	106.50	11.50	61.75	17.80	130.50	31.25	29.42	32.15	51.12	1.49	40.10	118.10	178.10	178.00
51	M 574	119.00	8.70	48.80	26.70	143.00	29.09	27.51	25.39	49.40	1.48	41.80	43.00	123.10	123.00
52	PCH 80	99.00	10.50	63.00	19.80	132.50	26.02	28.06	24.28	50.22	1.52	39.20	109.50	170.50	170.50
53	PCH 111	105.50	11.75	66.50	17.20	142.50	27.97	30.90	32.73	50.55	1.55	40.30	87.60	179.60	179.60
54	KIRAN	103.00	7.60	24.00	18.20	132.00	27.04	26.85	26.63	51.37	1.49	40.80	97.50	121.00	121.00
	<b>Mean</b>	<b>120.66</b>	<b>8.48</b>	<b>49.06</b>	<b>20.56</b>	<b>145.97</b>	<b>23.99</b>	<b>25.24</b>	<b>24.18</b>	<b>48.12</b>	<b>1.46</b>	<b>36.56</b>	<b>54.12</b>	<b>102.69</b>	<b>125.97</b>
	C.V.	1.03	6.56	4.75	4.46	1.70	2.89	3.63	4.51	1.91	1.43	3.10	11.04	8.10	7.98
	SE	0.88	0.39	1.65	0.65	1.75	0.49	0.65	0.77	0.65	0.01	0.80	4.23	5.88	7.11
	CD 5%	2.49	1.12	4.67	1.84	4.97	1.39	1.84	2.19	1.84	0.04	2.27	11.99	16.69	20.17
	CD 1%	3.31	1.49	6.23	2.45	6.62	1.85	2.45	2.92	2.46	0.06	3.02	15.97	22.23	26.87



**Table 11: Morphological characterization of Castor genotypes**

S.no	Entry	Stem colour	Type of internodes	Branching pattern	Petiole colour	Lamina leaf colour	Bloom colour	Type of inflorescence	Colour of stigma	Capsule type	Spike shape	Spike compactness	Seed colour
1	PPL 101	DR	E	C	R	G	DB	IS	R	S	CO	L	B
2	PPL 102	R	E	C	R	G	DB	IS	P	S	CO	C	B
3	PPL 103	R	E	C	GR	G	DB	IS	R	S	CO	SC	B
4	PPL 104	R	E	C	R	G	DB	IS	R	S	CO	SC	B
5	PPL 105	DR	C	C	R	DG	DB	IS	R	S	CO	SC	B
6	PPL 106	DR	E	C	R	DG	DB	IS	DR	S	CO	SC	B
7	PPL 107	R	E	C	R	DG	DB	IS	P	S	CO	L	M
8	PPL 108	DR	E	D	DR	DG	DB	IS	R	S	CO	SC	B
9	PPL 109	R	E	D	GR	G	DB	IS	R	S	CO	C	B
10	PPL 110	DR	E	C	DR	GR	DB	IS	DR	S	CO	C	DC
11	PPL 111	R	C	C	R	G	DB	IS	P	S	CY	SC	DC
12	PPL 112	R	C	C	GR	G	DB	IS	R	NS	CY	SC	B
13	PPL 113	R	E	C	GR	G	DB	IS	P	NS	CY	SC	M
14	PPL 114	R	E	C	GR	G	DB	IS	R	S	CO	C	DC
15	PPL 115	DR	E	D	R	DG	DB	IS	R	S	CO	C	B
16	PPL 116	R	E	C	R	GR	DB	IS	R	S	CO	C	B
17	PPL 117	R	E	C	GR	G	SB.	MON	DR	S	CO	C	M
18	PPL 118	R	E	C	GR	G	DB	IS	P	S	CO	C	B
19	PPL 119	R	C	C	R	G	DB	IS	DR	S	CO	SC	M
20	PPL 120	R	E	D	GR	G	DB	IS	R	NS	CO	SC	B
21	PPL 121	R	E	D	R	GR	DB	IS	P	S	CO	C	DC
22	PPL 122	DR	E	D	R	DG	DB	IS	DR	S	CO	SC	B
23	PPL 123	R	E	D	GR	GR	DB	IS	R	S	CO	L	B
24	PPL 125	R	E	C	R	GR	DB	MON	DR	S	CO	SC	M
25	PPL 126	R	E	C	R	G	.SB	IS	DR	S	UMB	SC	M
26	PPL 128	R	E	D	R	G	DB	IS	R	S	CO	SC	B
27	PPL 129	DR	E	C	DR	DG	DB	IS	R	S	CO	L	B

1. Stem colour – green(G), red(R), dark red(DR).
2. Type of internode – condensed(C), elongated (E).
3. Plant branching pattern – convergent(C), divergent(D).
4. Petiole colour – green(G), green with reddish tinge(GR), red(R), dark red(DR).
5. Lamina leaf colour –green(G), dark green(DG), green with reddish tinge(GR).
6. Bloom – no bloom(NB), single bloom(SB), double bloom(DB), triple bloom(TB).

**Table 11 : Morphological characterization of Castor genotypes**

S.no	Entry	Stem colour	Type of internodes	Branching pattern	Petiole colour	Lamina leaf colour	Bloom colour	Type of inflorescence	Colour of stigma	Capsule type	Spike shape	Spike compactness	Seed colour
28	PPL 130	R	E	D	R	G	DB	IS	R	S	CY	L	DC
29	PPL 131	R	E	C	GR	G	DB	IS	P	S	CO	SC	DC
30	PPL 132	DR	E	C	GR	DG	DB	IS	DR	S	CY	L	DC
31	PPL 133	DR	C	C	R	GR	DB	IS	R	S	CO	SC	DC
32	PPL 134	DR	C	D	DR	GR	DB	IS	R	S	CO	SC	DC
33	PPL 135	DR	E	D	DR	G	DB	IS	DR	S	CO	SC	M
34	PPL 136	R	E	D	GR	DG	DB	IS	R	S	CO	L	B
35	PPL 137	R	E	D	GR	G	DB	IS	P	S	CO	SC	DC
36	PPL 138	DR	E	C	R	GR	DB	IS	DR	S	CO	L	B
37	PPL 139	R	E	C	R	G	DB	IS	P	S	CO	L	B
38	PPL 140	R	E	C	R	DG	DB	IS	P	S	CO	L	B
39	PPL 141	DR	E	C	DR	G	TB	IS	R	S	CY	L	DC
40	PPL 142	R	E	C	R	DG	DB	IS	R	S	CY	SC	B
41	PPL 143	R	E	C	GR	DG	DB	IS	DR	S	CO	L	B
42	PPL 144	DR	E	C	R	G	DB	IS	DR	S	CO	SC	DC
43	PPL 145	R	E	D	R	G	DB	IS	P	S	CO	SC	DC
44	PPL 147	R	E	C	GR	DG	TB	IS	R	S	CO	L	B
45	PPL 148	DR	E	C	DR	GR	DB	IS	R	S	CO	L	M
46	PPL 149	DR	C	C	R	GR	DB	IS	R	S	CO	SC	B
47	PPL 150	DR	E	D	R	G	DB	IS	R	S	CO	L	B
48	PPL 151	DR	E	C	R	GR	DB	IS	R	S	CO	L	B
49	DPC-9	G	C	C	G	G	DB	IS	R	S	CO	C	M
50	GCH-4	DR	E	D	R	G	DB	IS	R	S	CY	L	DC
51	M-574	G	C	C	G	G	DB	IS	DR	S	CO	SC	B
52	PCH 80	G	E	C	G	G	DB	IS	R	S	CO	L	DC
53	PCH 111	G	C	C	G	G	DB	IS	R	S	CY	L	B
54	KIRAN	DR	C	C	R	GR	DB	IS	DR	NS	CO	L	M

7. Type of inflorescence – monoecious(MON), interspersed staminate flowers(IS), pistillate(P).

8. Colour of stigma – pink(P), red(R), dark red(DR).

9. Capsule type – non spiny(NS), spiny(S).

10. Spike shape – umbrella(UMB), cylindrical(CY), conical(CO).

11. Spike compactness – loose(L), semi compact(SC), compact(C).

12. Seed colour – maroon(M), brown(B), deep chocolate(DC).



**Table– 24: Clustering of 54 genotypes of castor (*Ricinus communis* L. ) by Ward’s minimum variance method**

<b>Cluster No.</b>	<b>No. of genotypes</b>	<b>Genotypes</b>
<b>I.</b>	<b>7</b>	PPL 101, PPL 108, PPL 105, PPL 133, PPL 138, PPL 148, PPL 141
<b>II.</b>	<b>2</b>	PPL 102, PPL 149
<b>III.</b>	<b>1</b>	PPL 147
<b>IV.</b>	<b>12</b>	PPL 104, PPL 109, PPL 107, PPL 125, PPL 128, PPL 136, GCH 4, PCH 111, PCH 80, PPL 137, PPL 117, KIRAN
<b>V.</b>	<b>7</b>	PPL 115, PPL 144, PPL121, PPL 122, PPL 103, PPL126, PPL151
<b>VI.</b>	<b>3</b>	PPL 129, PPL 130, PPL 139
<b>VII.</b>	<b>12</b>	PPL 106, PPL 110, PPL 112, PPL 113, PPL 118, PPL 120, PPL 114, PPL 119, PPL 131, PPL 135, PPL 132, PPL 134
<b>VIII.</b>	<b>10</b>	PPL 111, PPL 145, DPC-9, M-574, PPL 116, PPL 142, PPL 143, PPL 123, PPL140, PPL 150

**Table– 15: Clustering of 54 genotypes of castor  
( *Ricinus communis* L., )by Tocher’s method**

<b>Cluster No.</b>	<b>No. of genotypes</b>	<b>Genotypes</b>
<b>I.</b>	<b>11</b>	PPL 104, PPL 109, PPL 125, PPL 128, PPL 136, PCH 80, GCH 4, PPL 137, PCH 111, PPL 107, PPL 151
<b>II.</b>	<b>14</b>	PPL 101, PPL 108, PPL 119, PPL 132, PPL 116, PPL 114, PPL 120, PPL 134, PPL 111, PPL131, PPL 135, PPL 112, PPL 118, PPL 145
<b>III.</b>	<b>11</b>	PPL 121, PPL 122, PPL 144, PPL115, PPL103, PPL 126, PPL 110, M-574, PPL 123, PPL142, DPC-9
<b>IV.</b>	<b>1</b>	PPL 113
<b>V.</b>	<b>8</b>	PPL 140, PPL 150, PPL 143, PPL 105, PPL133, PPL138, PPL 148, PPL 141,
<b>VI.</b>	<b>1</b>	PPL 117
<b>VII.</b>	<b>2</b>	PPL 102, PPL 149
<b>VIII.</b>	<b>5</b>	PPL 129, PPL 130, PPL 139, KIRAN, PPL 106
<b>IX.</b>	<b>1</b>	PPL 147,

**Fig 23: Effective length of primary raceme**

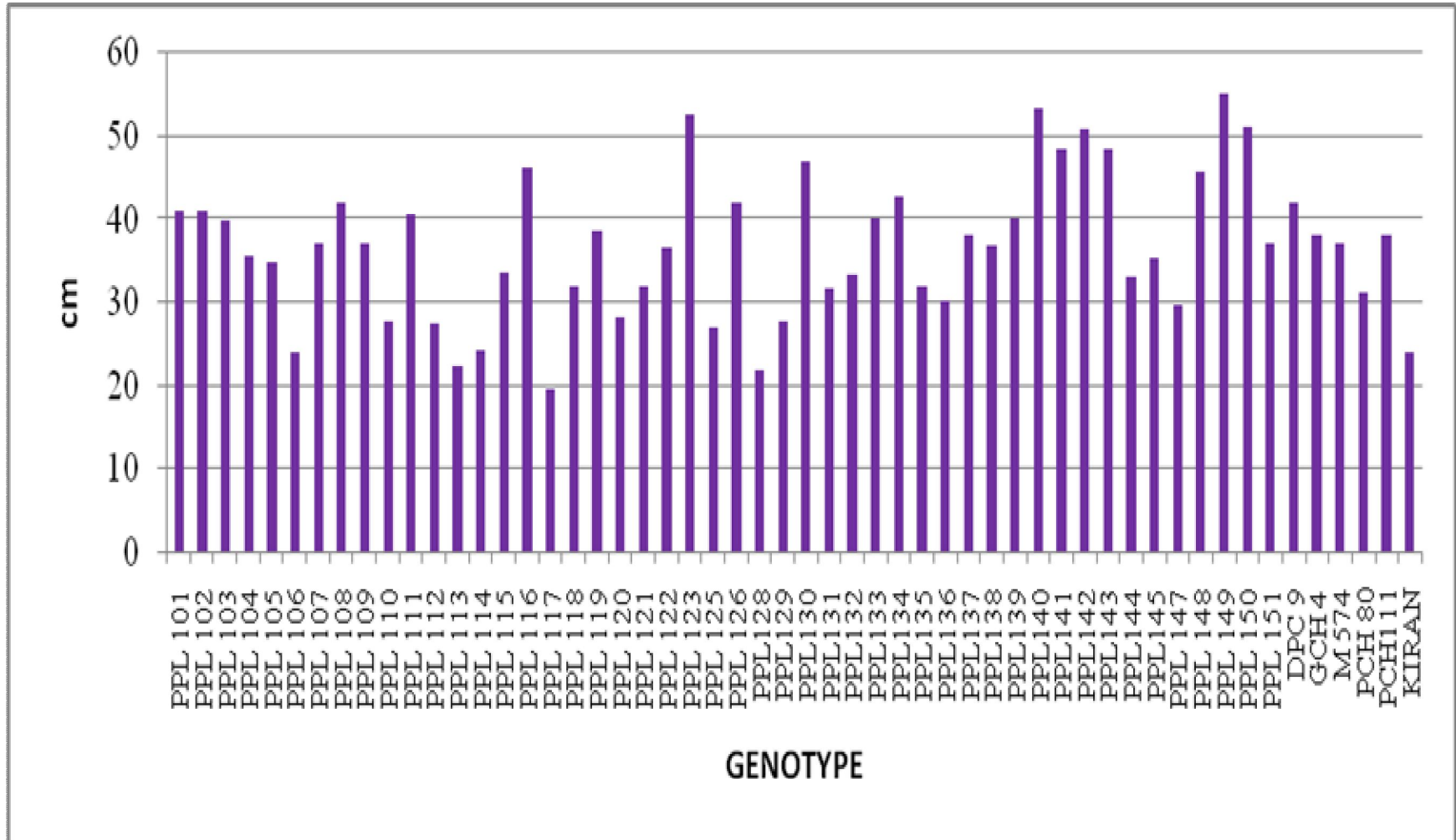
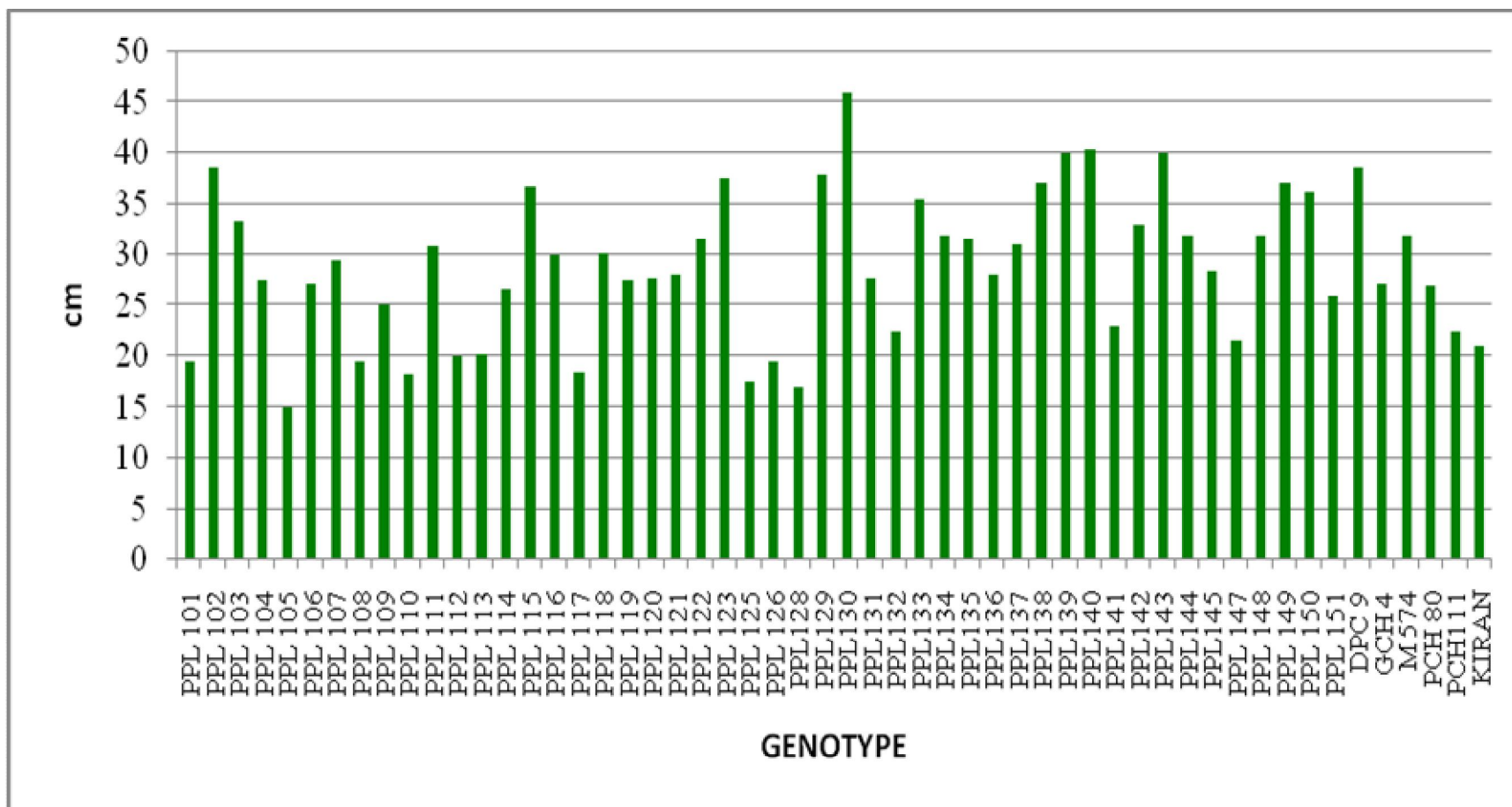
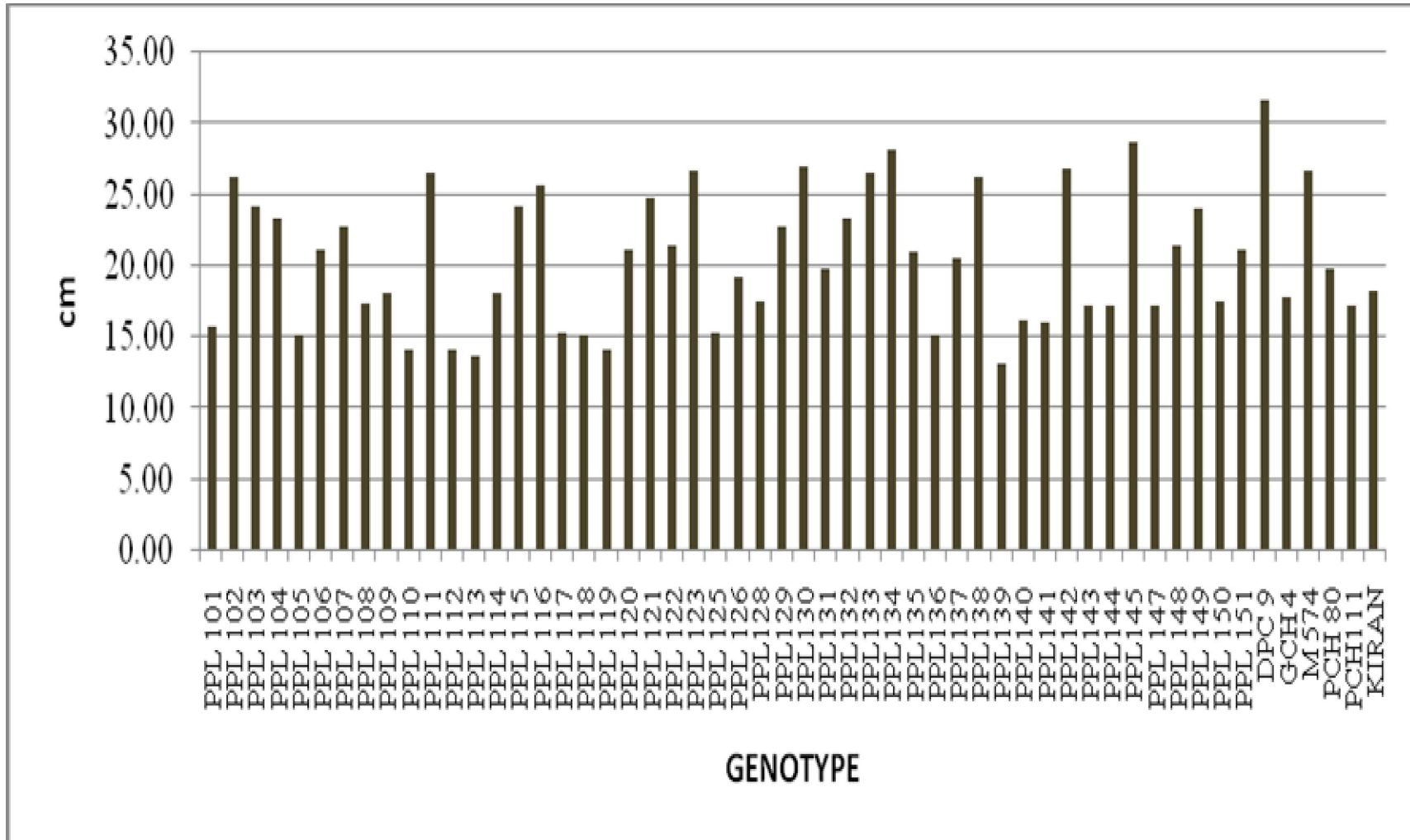


Fig 24: Effective length of secondary raceme



**Fig 25: Effective length of tertiary raceme**



**Fig 26: Number of secondary racemes**

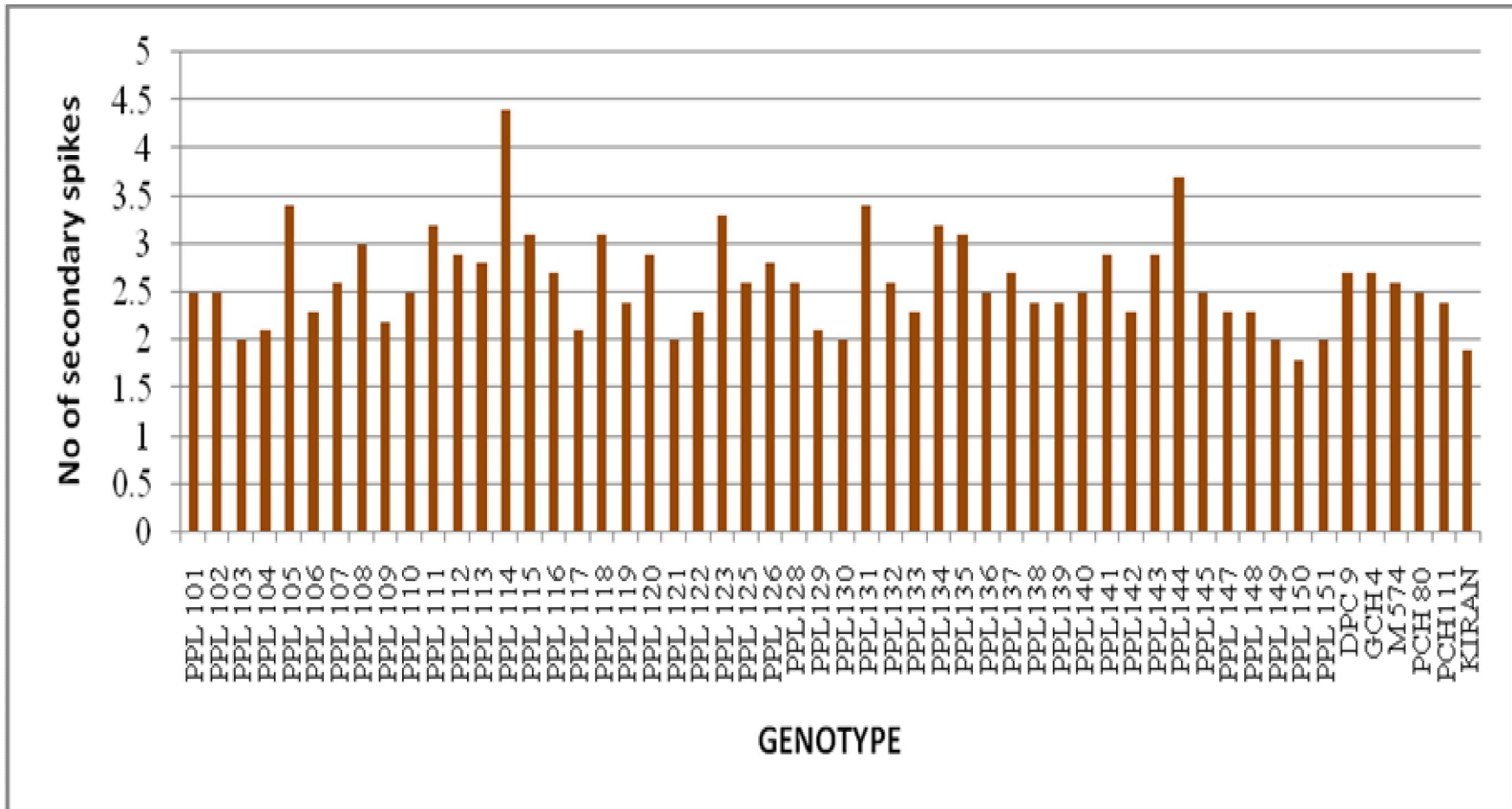


Fig 27: Number of tertiary racemes

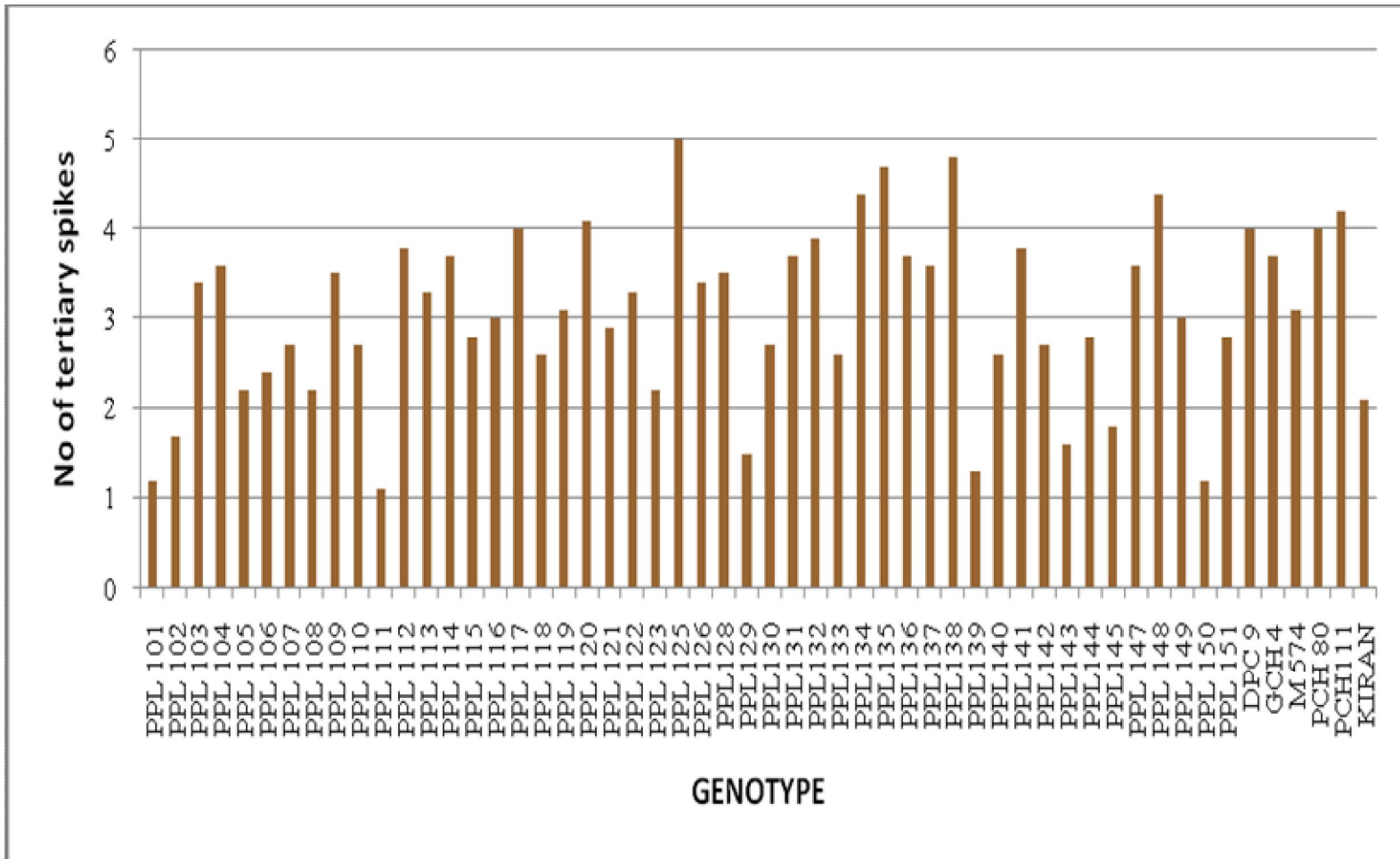
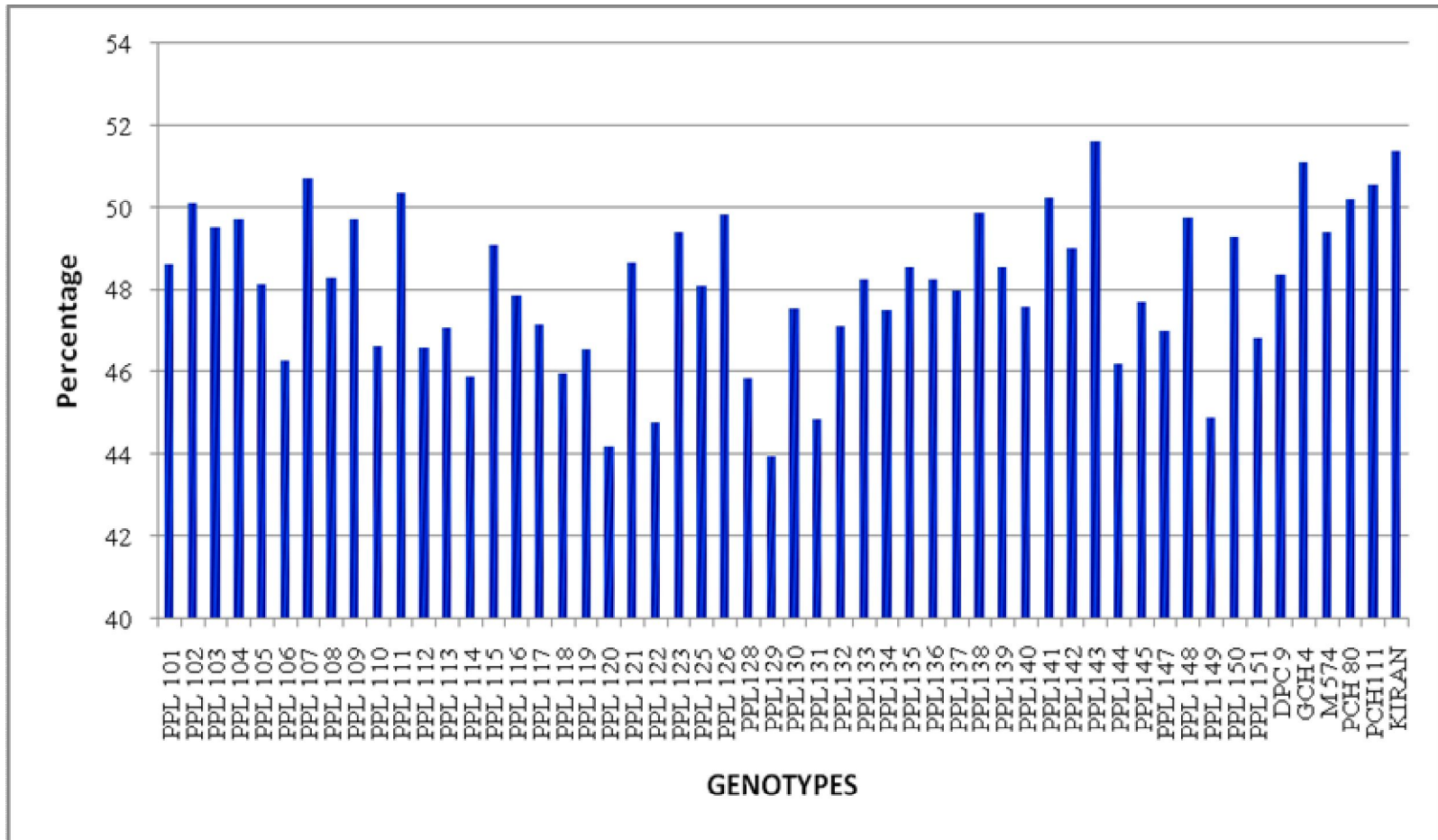


Fig 28: Oil content



**Fig 22: Days to 50% flowering of primary raceme**

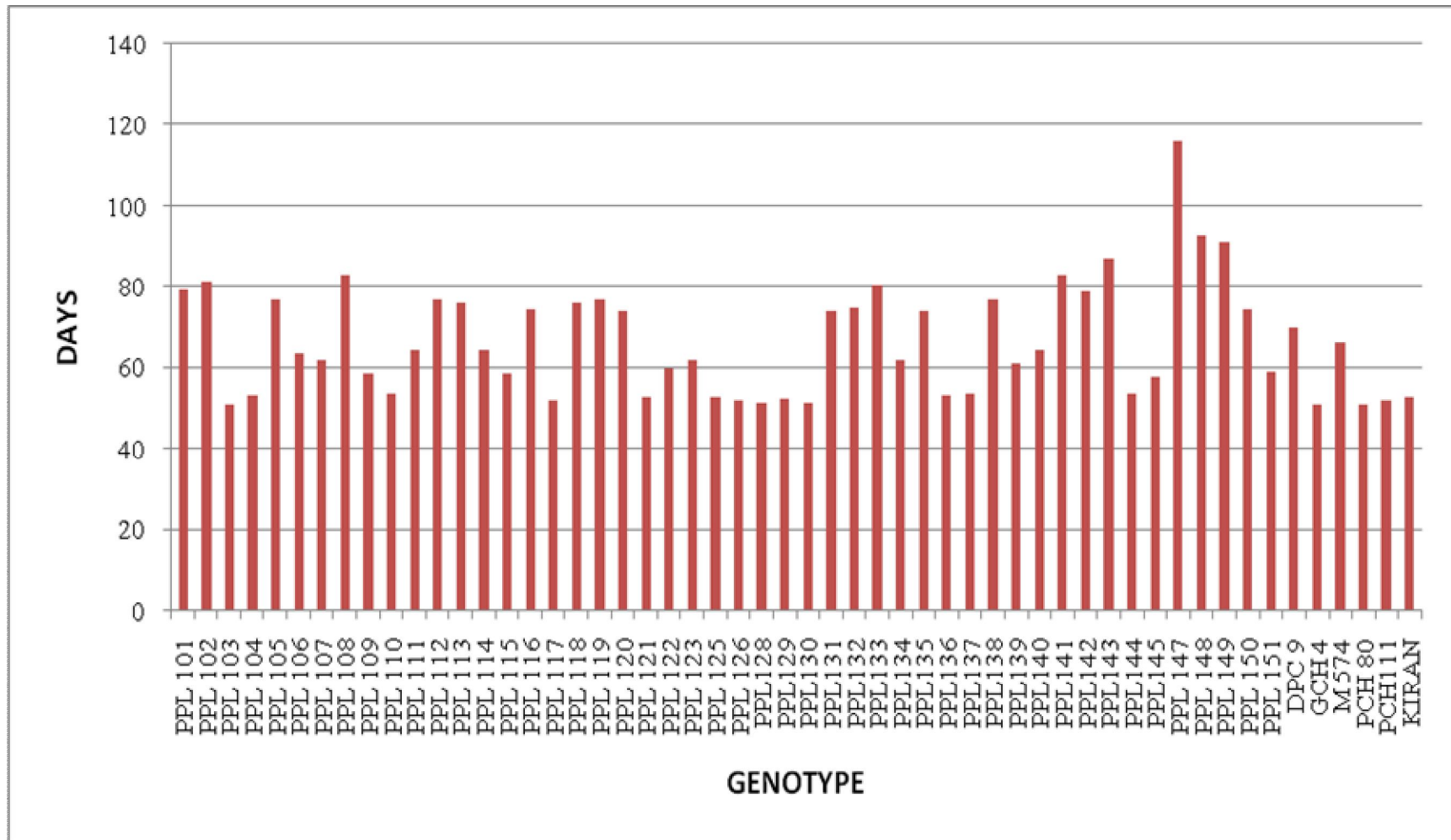
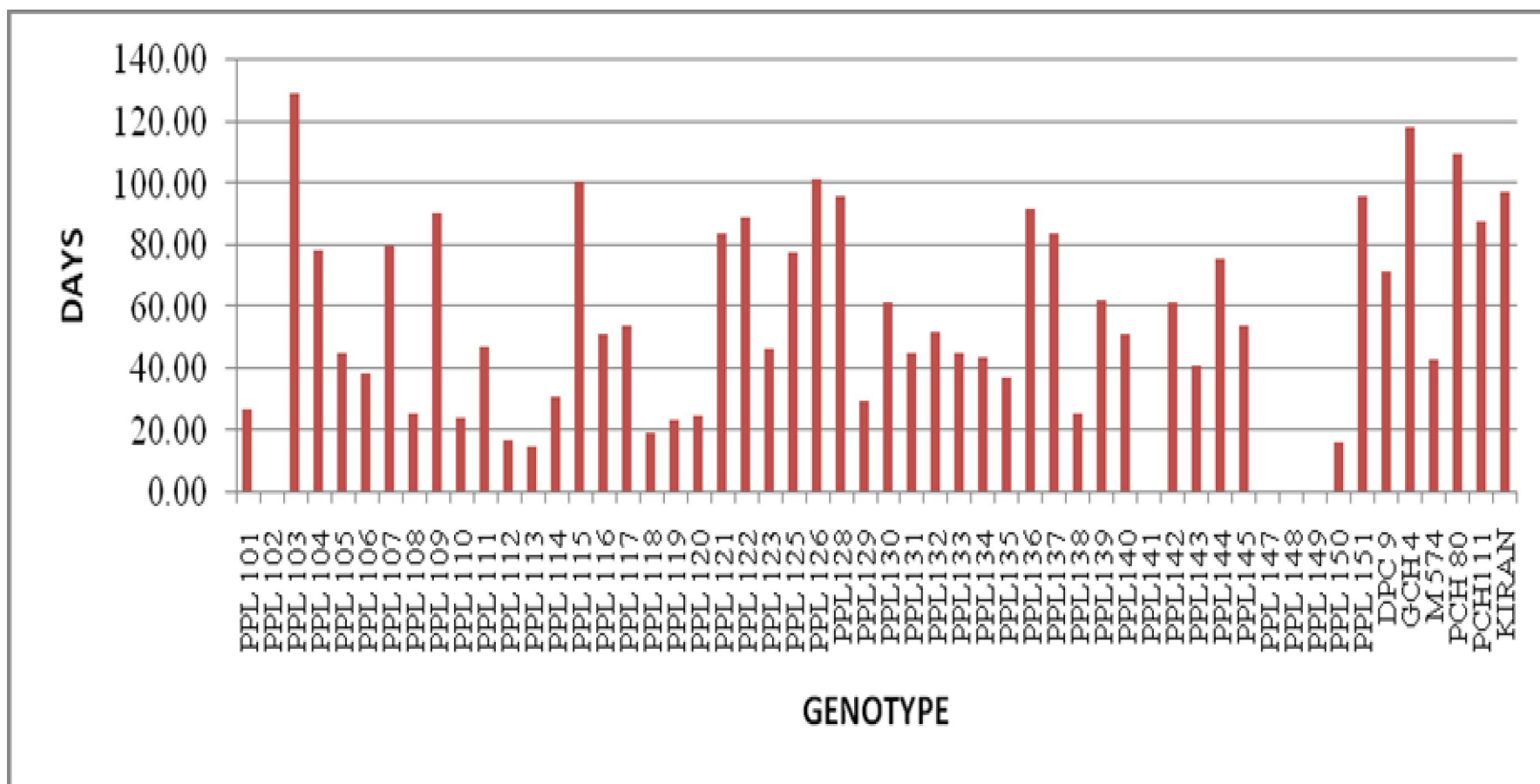


Fig 29: Seed yield per plant at 120 days



**Fig 30: Seed yield per plant upto 150 days**

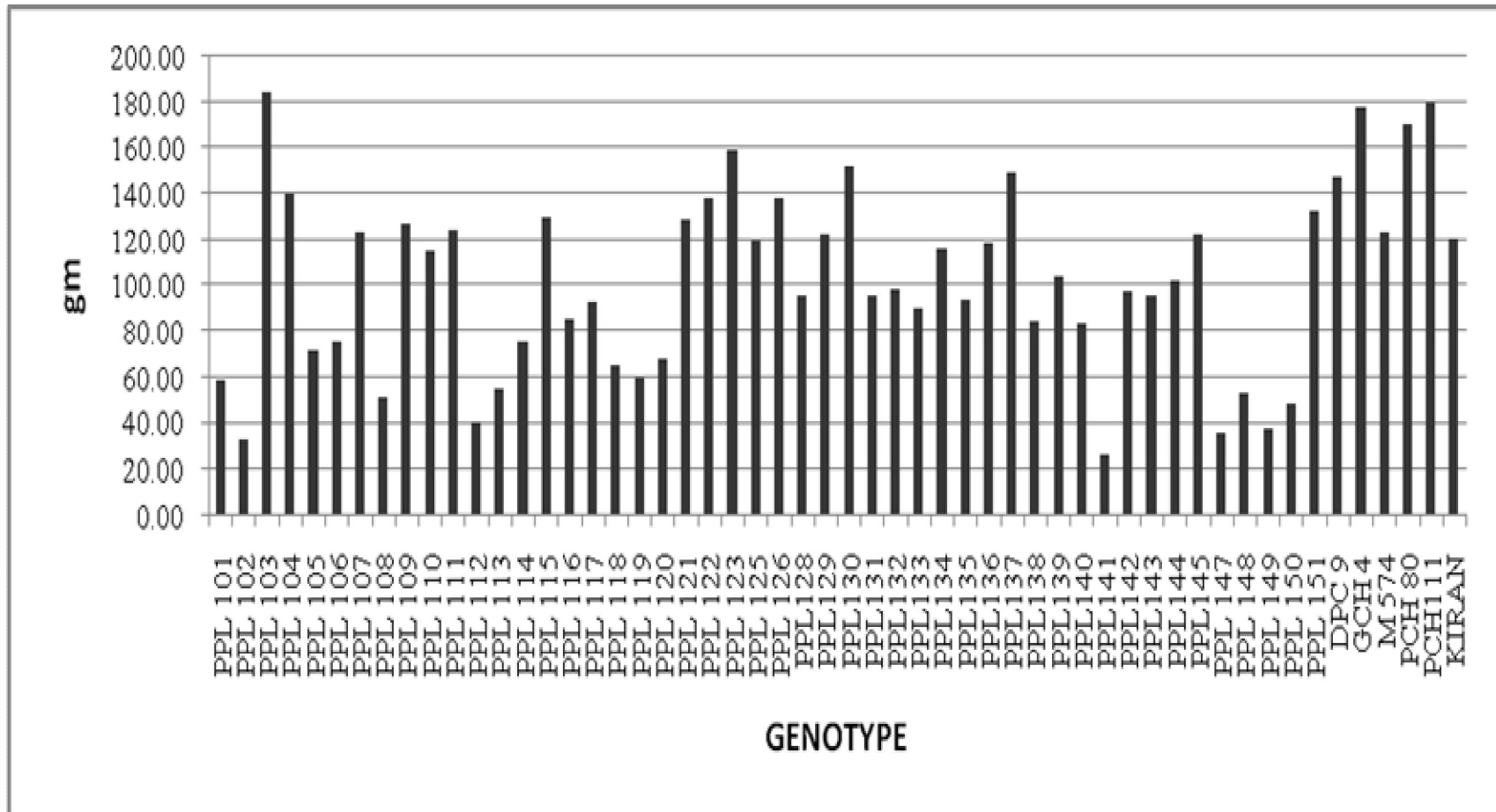


Fig 31: seed yield per plant upto 180 days

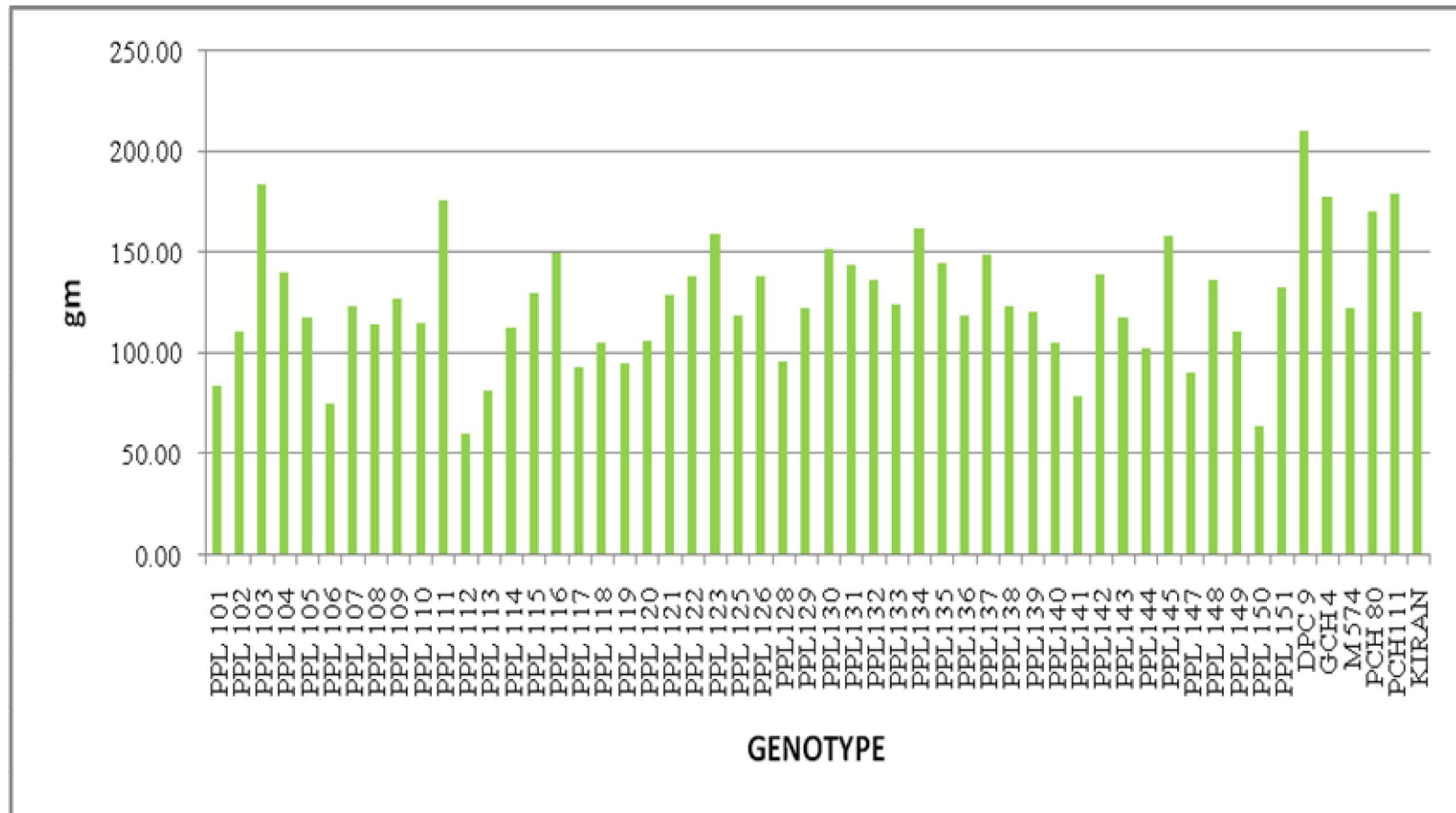
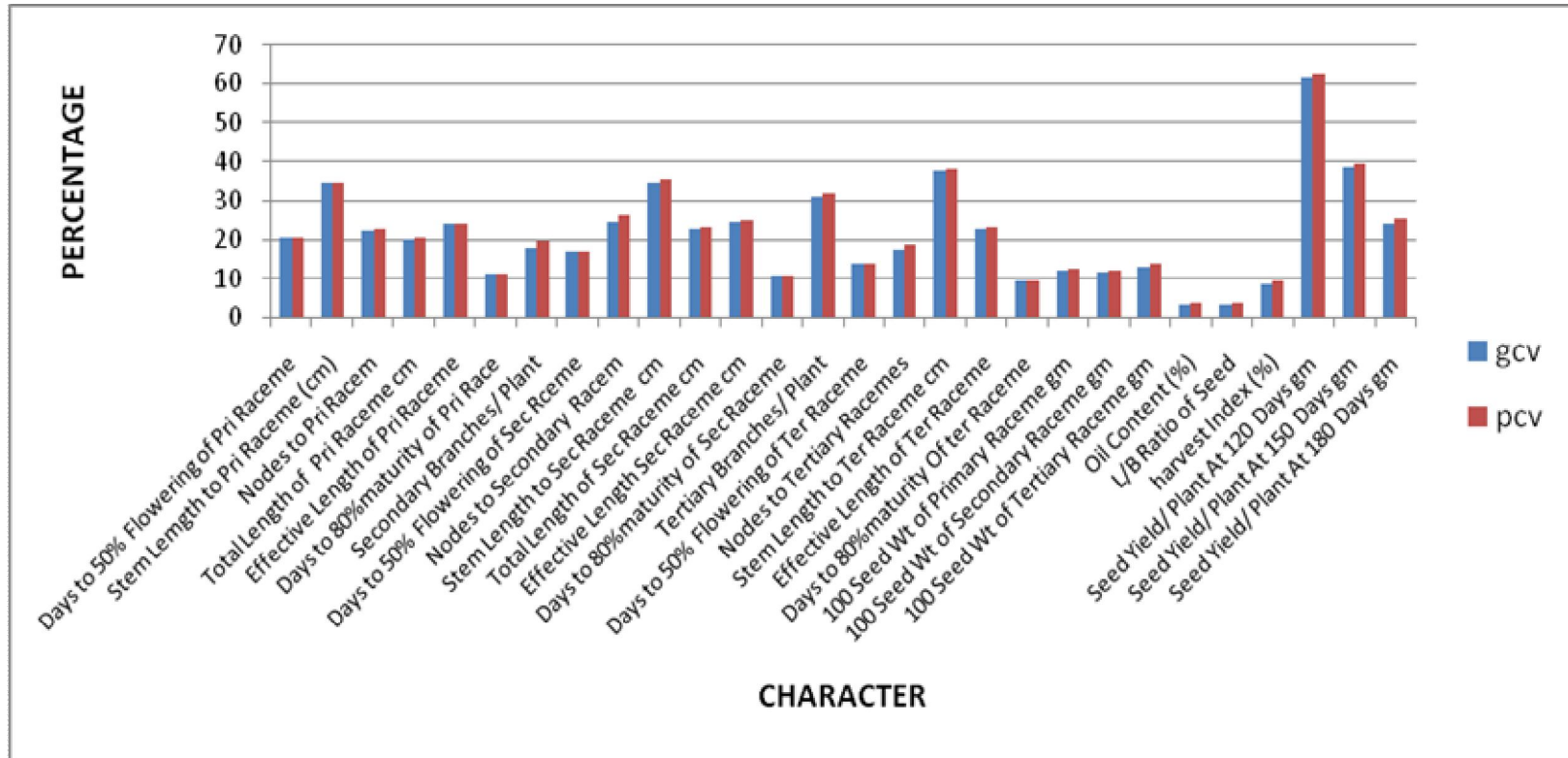
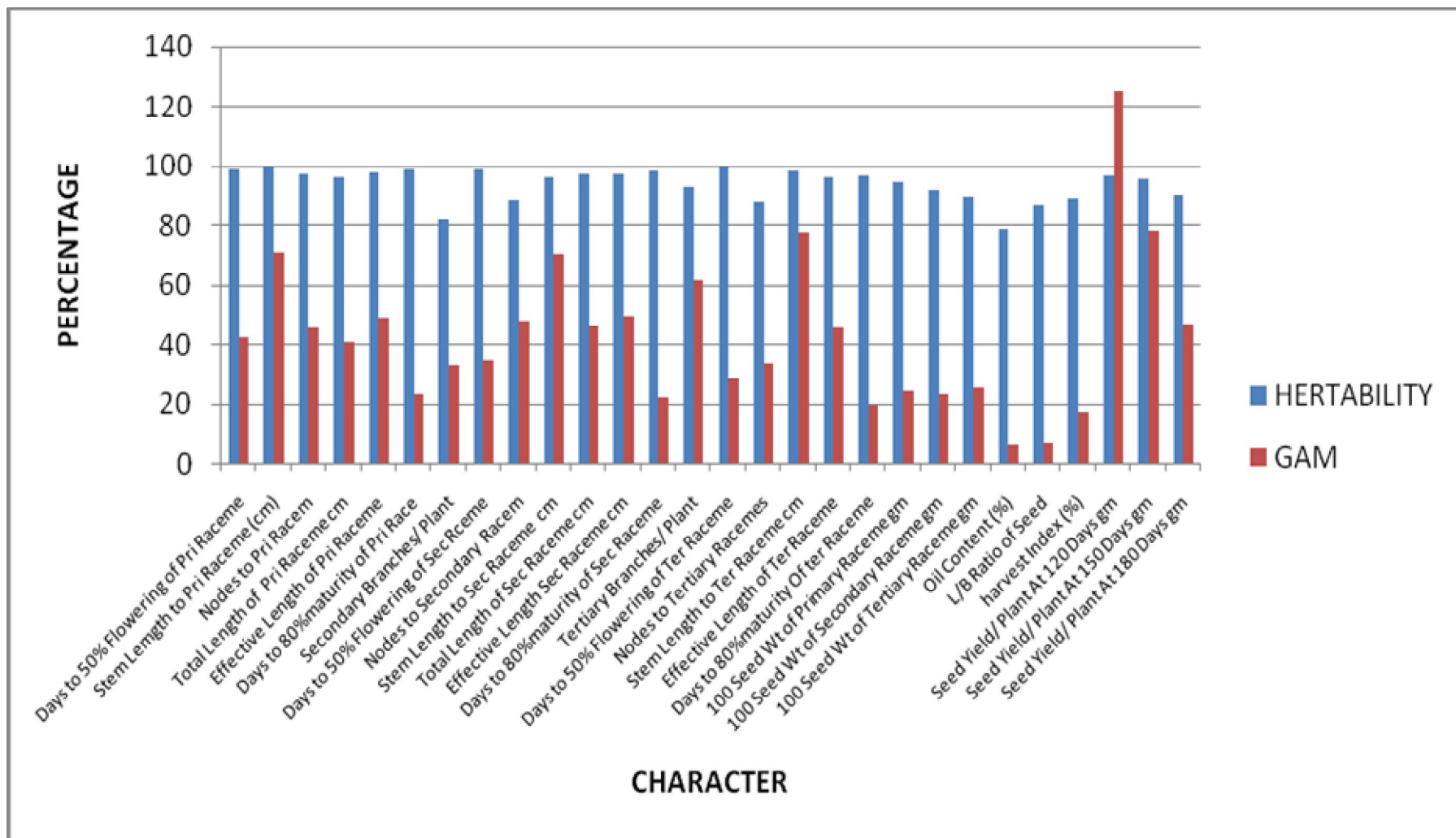


Fig 15: Phenotypic and genotypic coefficients of variation for 28 characters in castor (*Ricinus communis* L.)



**Fig 16: Heritability and genetic advance as per cent of mean (GAM) for 28 charactres in castor (*Ricinus communis*L.)**



**Table 25: Average intra and inter-cluster Euclidian<sup>2</sup> values among eight clusters in 54 of genotypes castor (*Ricinus communis* L.)**

Cluster No.	I	II	III	IV	V	VI	VIII	VIII
I	<b>1906.448</b>	3635.209	12462.72	12086.22	6662.596	10212.340	3928.844	4053.796
II		<b>1117.12</b>	5672.781	22878.71	14309.4	19122.280	10059.420	9435.239
III			<b>0</b>	42169.76	30833.2	38651.390	22766.890	24300.270
IV				<b>1321.419</b>	2587.439	2728.870	5105.269	5536.490
V					<b>978.461</b>	2552.639	2594.378	2408.354
VI						<b>1385.933</b>	5257.520	3854.808
VII							<b>1594.627</b>	2642.784
VIII								<b>1795.494</b>

**Bold and diagonal values indicate intra-cluster distances**

**Table-22 : Eigen values, proportion of the total variance represented by first seven principal components, cumulative per cent variance and component loading of different characters in castor (*Ricinus communis* L.).**

characters	PC <sub>1</sub>	PC <sub>2</sub>	PC <sub>3</sub>	PC <sub>4</sub>	PC <sub>5</sub>
Eigen Value (Root)	51763.56	6528.24	3807.82	2898.02	1916.79
% Var. Exp.	69.153	8.721	5.087	3.872	2.561
Cum. Var. Exp.	69.153	77.875	82.962	86.833	89.394
Days to 50% Flowering of Primary Raceme	0.224	0.051	0.081	0.215	0.181
Stem Length to Primary Raceme (cm)	0.235	0.047	0.357	-0.372	-0.091
Nodes to Primary Raceme	0.054	0.066	0.012	0.120	0.152
Total Length of Primary Raceme (cm)	0.042	-0.230	0.052	-0.026	-0.134
Effective Length of Primary Raceme (cm)	-0.068	-0.319	0.027	0.049	-0.197
Days to 80% maturity of Primary Raceme	0.196	0.063	0.184	0.209	0.027
Secondary Branches/ Plant	0.112	0.149	0.092	-0.080	0.071
Days to 50% Flowering of Secondary Raceme	0.297	-0.133	0.193	-0.021	-0.008
Nodes to Secondary Raceme	0.040	0.094	0.040	-0.145	0.026
Stem Length to Sec Raceme (cm)	0.026	0.026	-0.002	0.109	-0.190
Total Length of Sec Raceme (cm)	0.130	-0.180	0.108	-0.119	0.031
Effective Length Sec Raceme (cm)	-0.039	-0.203	-0.030	-0.065	-0.059
Days to 80% maturity of Secondary Raceme	0.193	0.154	0.104	0.394	0.021
Tertiary Branches/ Plant	-0.033	0.092	-0.026	-0.224	0.153
Days to 50% Flowering of Tertiary Raceme	0.333	-0.409	0.016	0.252	-0.153
Nodes to Tertiary Racemes	0.175	0.055	0.211	0.039	0.131
Stem Length to Tertiary Raceme (cm)	-0.125	-0.411	0.433	-0.153	-0.096
Effective Length of Tertiary Raceme (cm)	0.425	-0.284	-0.172	-0.105	0.266
Days to 80% maturity Of tertiary Raceme	0.059	-0.025	-0.041	0.497	0.021
100 Seed Wt of Primary Raceme (g)	-0.195	-0.076	0.068	-0.140	0.291
100 Seed Wt of Secondary Raceme (g)	0.033	-0.067	0.293	-0.057	0.453
100 Seed Wt of Tertiary Raceme (g)	-0.288	-0.103	0.142	0.228	0.429
Oil Content (%)	-0.209	-0.220	-0.183	0.015	-0.030
L/B Ratio of Seed	-0.119	-0.017	0.084	0.100	0.011
Harvest Index (%)	0.215	-0.062	-0.485	-0.166	0.250
Seed Yield/ Plant At 120 Days (g)	-0.230	-0.421	-0.161	0.109	0.156
Seed Yield/ Plant up to 150 Days (g)	0.199	-0.068	-0.221	-0.118	0.213
Seed Yield/ Plant upto 180 Days (g)	-0.164	0.033	0.179	0.067	0.283

PC= Principal component

**Table 19: Average intra and inter-cluster D<sup>2</sup> values among nine clusters in 54 castor (*Ricinus communis* L.) genotypes**

	I	II	III	IV	V	VI	VIII	VIII	IX
I	<b>536.741 (23.167)</b>	2985.129 (54.636)	1527.938 (39.088)	1885.021 (45.416)	4750.665 (68.925)	1081.344 (32.883)	10836.892 (104.100)	1244.966 (35.284)	20324.604 (142.564)
II		<b>865.401 (29.417)</b>	1391.604 (37.304)	1137.648 (33.729)	1539.001 (39.230)	3651.417 (60.426)	4094.951 (63.991)	2834.842 (53.243)	10242.585 (101.205)
III			<b>844.327 (29.057)</b>	1568.907 (39.609)	2510.182 (50.101)	2480.713 (49.806)	6528.681 (80.800)	1632.166 (40.400)	14648.815 (121.032)
IV				<b>0.000 (0)</b>	2442.638 (49.423)	1921.861 (43.839)	6514.107 (80.710)	2154.031 (46.411)	12981.145 (113.539)
V					<b>1319.266 (36.321)</b>	6266.758 (79.162)	2525.634 (50.255)	4247.663 (65.174)	7813.980 (88.396)
VI						<b>0.000 (0)</b>	12793.441 (113.108)	2039.344 (45.159)	21728.092 (147.404)
VII							<b>558.559 (23.633)</b>	9686.240 (98.418)	2836.391 (53.257)
VIII								<b>1737.736 (41.686)</b>	19061.795 (138.064)
IX									<b>0.000 (0)</b>

**Bold and diagonal values indicate intra-cluster distances, figures in parentheses are D values**

**Table- 21 : Mean values of nine clusters by Tochers's method for 54 genotypes of castor  
( *Ricinus communis* L. )**

cluster	Days to 50% Flowering of Pri Raceme	Stem Length to Pri Raceme (cm)	Nodes to Pri Raceme	Total Length of Pri Raceme (cm)	Effective Length of Pri Raceme (cm)	Days to 80% maturity of Pri Raceme	Secondary Branches/ Plant	Days to 50% Flowering of Sec Raceme	Nodes to Sec Racem	Stem Length to Sec Raceme (cm)	Total Length of Sec Raceme (cm)	Effective Length Sec Raceme (cm)	Days to 80% maturity of Sec Raceme	Tertiary Branches/ Plant
I Cluster	54.455	89.727	16.627	39.545	33.755	93.182	2.445	78.273	9.377	59.445	31.327	25.314	110.227	3.668
II Cluster	72.357	114.086	22.062	42.529	35.380	104.821	<b>2.993</b>	98.214	11.057	90.107	32.489	27.079	130.786	3.107
III Cluster	60.000	96.245	17.245	45.289	38.782	95.932	2.664	91.136	10.568	81.568	36.909	31.023	119.909	3.027
IV Cluster	76.000	103.900	22.000	<b>24.400</b>	22.200	107.000	2.800	92.000	8.150	95.130	21.500	25.000	124.500	3.300
V Cluster	79.500	146.100	23.313	50.975	44.806	113.938	2.562	112.500	12.606	<b>116.625</b>	37.400	32.569	142.063	2.906
VI Cluster	<b>52.000</b>	100.400	<b>16.000</b>	25.400	<b>19.400</b>	<b>85.500</b>	<b>2.100</b>	<b>72.000</b>	<b>6.600</b>	<b>35.200</b>	<b>12.850</b>	<b>18.500</b>	<b>107.000</b>	<b>4.000</b>
VII Cluster	86.250	191.750	25.800	<b>51.100</b>	<b>48.050</b>	129.000	2.250	133.750	<b>14.325</b>	96.313	<b>43.700</b>	<b>37.800</b>	153.000	2.400
VIII Cluster	56.300	<b>87.400</b>	16.080	37.790	35.500	92.600	2.140	85.300	9.770	70.090	38.820	34.410	122.200	<b>2.000</b>
IX Cluster	<b>116.000</b>	<b>282.300</b>	<b>37.400</b>	37.100	29.600	<b>129.500</b>	2.300	<b>140.500</b>	7.750	73.850	27.900	21.300	<b>156.500</b>	3.600

**Bold values are minimum and maximum values**

**Table- 17 : Mean values of nine clusters by Tochers's method for 54 genotypes of castor  
( *Ricinus communis* L. )**

	Days to 50% Flowering of Ter Raceme	Nodes to Tertiary Raceme	Stem Length to Ter Raceme cm	Effective Length of Ter Raceme	Days to 80% maturity Of ter Raceme	100 Seed Wt of Primary Raceme gm	100 Seed Wt of Secondary Raceme gm	100 Seed Wt of Tertiary Raceme gm	Oil Content (%)	L/B Ratio of Seed	harvest Index (%)	Seed Yield/ Plant At 120 Days gm	Seed Yield/ Plant up to 150 Days gm	Seed Yield/ Plant up to 180 Days gm
I Cluster	102.545	9.691	<b>66.793</b>	18.991	129.500	25.990	27.397	27.098	49.003	1.472	38.145	<b>91.827</b>	<b>139.536</b>	139.555
II Cluster	125.929	7.875	34.021	20.650	150.143	22.375	23.734	22.449	47.147	1.434	36.539	35.741	82.690	125.001
III Cluster	116.682	8.518	46.386	23.364	141.318	24.325	25.065	24.513	48.265	1.461	<b>38.427</b>	75.268	133.159	<b>142.636</b>
IV Cluster	117.000	<b>9.900</b>	46.400	<b>13.700</b>	151.500	20.830	<b>21.950</b>	21.520	47.080	<b>1.330</b>	35.100	14.950	55.380	<b>81.500</b>
V Cluster	139.563	8.675	51.269	19.525	161.313	24.305	25.956	23.515	<b>49.344</b>	1.453	32.919	28.150	69.500	108.575
VI Cluster	<b>87.000</b>	6.550	37.000	15.300	<b>126.000</b>	23.720	22.110	24.080	47.170	1.490	34.200	54.300	93.450	93.450
VII Cluster	153.750	<b>5.575</b>	<b>30.300</b>	<b>25.200</b>	<b>172.500</b>	<b>26.745</b>	<b>28.935</b>	<b>26.705</b>	47.495	1.430	33.850	<b>0.000</b>	<b>35.745</b>	111.000
VIII Cluster	110.000	8.670	64.150	20.440	143.400	23.170	23.592	23.178	47.544	<b>1.518</b>	37.980	57.950	115.102	118.460
IX Cluster	<b>163.000</b>	7.150	53.050	17.200	171.500	<b>20.580</b>	26.110	<b>20.700</b>	<b>47.000</b>	1.450	<b>30.200</b>	0.000	36.000	90.500

**Bold values are minimum and maximum values**



**Table - 13 : Estimates of phenotypic (Above d**

character	Days to 50% Flowering of Pri Raceme	Stem Length to Pri Raceme (cm)	Nodes to Pri Racem	Total Length of Pri Raceme cm	Effective Length of Pri Raceme	Days to 80% maturity of Pri Race	Secondary Branches/ Plant	Days to 50% Flowering of Sec Rceme	Nodes to Secondary Racem	Stem Length to Sec Raceme cm
	1	2	3	4	5	6	7	8	9	10
1		0.7628**	0.8876**	0.2529**	0.2723**	0.8469**	0.0859	0.8924**	0.3437**	0.4739**
2	0.7669**		0.7542**	0.2817**	0.2842**	0.7537**	-0.0360	0.8010**	0.3149**	0.4572**
3	0.8995**	0.7641**		0.1398	0.1148	0.7929**	0.1715	0.8053**	0.3302**	0.3968**
4	0.2573**	0.2890**	0.1446		0.9019**	0.3408**	-0.0608	0.4236**	0.3435**	0.3604**
5	0.2720**	0.2865**	0.1156	0.9211**		0.3298**	-0.1146	0.4384**	0.2980**	0.3735**
6	0.8519**	0.7594**	0.8069**	0.3475**	0.3334**		-0.0170	0.8891**	0.4087**	0.4414**
7	0.0930	-0.0300	0.2013	-0.0886	-0.1374	-0.0146		0.0263	0.1669	0.1980**
8	0.8984**	0.8085**	0.8192**	0.4346**	0.4452**	0.8951**	0.0284		0.5244**	0.5059**
9	0.3653**	0.3427**	0.3469**	0.3675**	0.3037**	0.4350**	0.1464	0.5528**		0.3369**
10	0.4872**	0.4670**	0.4107**	0.3741**	0.3857**	0.4525**	0.2276**	0.5155**	0.3606**	
11	0.0391	0.0325	-0.0544	0.5835**	0.5902**	0.1078	-0.0646	0.2068**	0.1578	0.2183**
12	0.0642	0.0363	-0.063	0.5177**	0.5770**	0.1023	-0.1183	0.205**	0.1181	0.2621**
13	0.8723**	0.7594**	0.7990**	0.4084**	0.3961**	0.9116**	0.0689	0.9324**	0.4903**	0.5558**
14	-0.0467	0.0004	-0.1209	-0.2817**	-0.3226**	-0.0711	0.1146	-0.1721	-0.1917	-0.2095**
15	0.8453**	0.7403**	0.7841**	0.4099**	0.4255**	0.8221**	0.1545	0.9419**	0.5063**	0.5299**
16	-0.3086**	-0.3189**	-0.3255**	-0.1485	-0.0614	-0.2784**	0.1826	-0.3641**	-0.2363**	-0.2457**
17	-0.2920**	-0.1971**	-0.3754**	0.0977	0.1477	-0.3275**	-0.2270**	-0.2850**	-0.2936**	-0.2650**
18	-0.0263	0.0598	-0.0846	0.4259**	0.2874**	-0.0050	-0.1102	0.1196	0.1854	-0.0106
19	0.7882**	0.7078**	0.7038**	0.4652**	0.4709**	0.7987**	-0.0333	0.8790**	0.4382**	0.5426**
20	-0.1925**	-0.1506	-0.1343	0.3039**	0.3308**	-0.0766	-0.1557	-0.0511	0.1732	-0.2856**
21	0.0154	0.0614	0.0840	0.2642**	0.3093**	-0.0003	-0.1768	0.0900	0.2188**	-0.2606**
22	-0.2607**	-0.2245**	-0.2145**	0.0719	0.1447	-0.1765	-0.1220	-0.1682	0.1249	-0.4412**
23	-0.0817	-0.0585	-0.0847	0.3342**	0.3653**	-0.0328	-0.1691	-0.0208	0.1197	-0.1710
24	-0.3641**	-0.1093	-0.2984**	-0.0206	0.0041	-0.3022**	-0.0975	-0.2973**	-0.2263**	-0.1280
25	-0.6162**	-0.6306**	-0.6003**	0.1095	-0.0042	-0.6002**	-0.0081	-0.5468**	-0.1597	-0.5177**
26	-0.7723**	-0.5623**	-0.6596**	-0.1418	-0.1339	-0.7751**	-0.1660	-0.7536**	-0.3092**	-0.4105**
27	-0.7817**	-0.5952**	-0.7258**	0.0197	-0.0192	-0.7767**	-0.1373	-0.7300**	-0.3084**	-0.4946**
Seed yield/plant upto 180 days	<b>-0.3724**</b>	<b>-0.2637**</b>	<b>-0.3643**</b>	<b>0.2970**</b>	<b>0.2416*</b>	<b>-0.3955**</b>	<b>0.0429</b>	<b>-0.2956**</b>	<b>-0.0417</b>	<b>-0.3032**</b>

\* = significant at 5% level (0.1890), \*\* = significant at 1% level (0.2468)





**Table- 26 : Mean values of eight clusters by Ward's minimum variance method for 54 genotypes of castor  
( *Ricinus communis* L. )**

cluster	Days to 50% Flowering of Ter Raceme	Nodes to Tertiary Raceme	Stem Length to Ter Raceme cm	Effective Length of Ter Raceme	Days to 80% maturity Of ter Raceme	100 Seed Wt of Primary Raceme gm	100 Seed Wt of Secondary Raceme gm	100 Seed Wt of Tertiary Raceme gm	Oil Content (%)	L/B Ratio of Seed	harvest Index (%)	Seed Yield/ Plant At 120 Days gm	Seed Yield/ Plant up to 150 Days gm	Seed Yield/ Plant up to 180 Days gm
I	142.500	8.579	42.486	19.757	162.857	23.674	25.423	23.170	49.031	1.446	33.179	24.181	62.601	111.466
II	153.750	<b>5.575</b>	<b>30.300</b>	<b>25.200</b>	<b>172.500</b>	<b>26.745</b>	<b>28.935</b>	26.705	47.495	<b>1.430</b>	33.850	<b>0.000</b>	<b>35.745</b>	111.000
III	<b>163.000</b>	7.150	53.050	<b>17.200</b>	171.500	<b>20.580</b>	26.110	<b>20.700</b>	47.000	1.450	<b>30.200</b>	<b>0.000</b>	36.000	<b>90.500</b>
IV	<b>100.708</b>	<b>9.421</b>	61.185	18.433	<b>128.083</b>	26.100	26.877	<b>27.100</b>	<b>49.229</b>	1.481	38.158	88.833	134.733	134.754
V	112.929	8.143	43.721	21.743	137.357	23.481	25.256	23.617	47.844	1.459	38.143	<b>96.679</b>	<b>136.343</b>	136.329
VI	113.667	9.217	<b>86.433</b>	20.967	144.333	21.960	<b>22.767</b>	21.350	46.690	<b>1.503</b>	<b>38.467</b>	51.300	126.400	132.000
VII	120.750	8.512	36.725	18.675	146.833	21.480	22.909	22.201	<b>46.433</b>	1.443	34.967	31.025	79.987	111.558
VIII	125.850	7.985	49.790	24.370	153.250	25.462	25.855	24.845	49.057	1.444	38.424	48.440	108.920	<b>140.365</b>

**Table- 26 : Mean values of eight clusters by Ward's minimum variance method for 54 genotypes of castor  
( *Ricinus communis L.* )**

cluster	Days to 50% Flowering of Pri Raceme	Stem Length to Pri Raceme (cm)	Nodes to Pri Raceme	Total Length of Pri Raceme (cm)	Effective Length of Pri Raceme	Days to 80% maturity of Pri Raceme	Secondary Branches/ Plant	Days to 50% Flowering of Sec Raceme	Nodes to Sec Raceme	Stem Length to Sec Raceme (cm)	Total Length of Sec Raceme (cm)	Effective Length Sec Raceme (cm)	Days to 80% maturity of Sec Raceme	Tertiary Branches/ Plant
I	81.786	153.029	24.871	48.371	41.243	116.071	2.686	114.857	<b>14.379</b>	<b>102.457</b>	31.129	26.129	144.714	3.029
II	86.250	191.750	25.800	51.100	<b>48.050</b>	129.000	2.250	133.750	14.325	96.313	43.700	37.800	153.000	2.400
III	<b>116.000</b>	<b>282.300</b>	<b>37.400</b>	37.100	<b>29.600</b>	<b>129.500</b>	2.300	<b>140.500</b>	<b>7.750</b>	73.850	<b>27.900</b>	<b>21.300</b>	<b>156.500</b>	3.600
IV	<b>53.750</b>	<b>84.925</b>	16.375	37.367	31.475	92.458	2.408	<b>76.833</b>	8.754	<b>54.800</b>	29.121	24.329	<b>110.125</b>	<b>3.637</b>
V	55.357	101.343	16.957	42.361	36.236	92.393	2.557	86.643	11.093	83.671	35.371	29.600	113.571	3.057
VI	55.000	85.533	<b>15.433</b>	44.300	43.200	<b>91.000</b>	<b>2.167</b>	86.667	8.883	66.450	<b>46.500</b>	<b>41.300</b>	123.167	<b>1.833</b>
VII	70.583	111.108	21.054	<b>36.008</b>	30.340	103.625	<b>2.967</b>	94.292	10.108	94.356	31.262	26.771	128.083	3.550
VIII	70.050	106.340	19.812	<b>52.660</b>	45.705	102.950	2.650	100.500	10.735	93.430	40.350	34.770	130.550	2.335

**Table – 9 : Analysis of variance for yield and yield components in 54 genotypes of castor ( *Ricinus communis L.* )**

**Mean sum of squares**

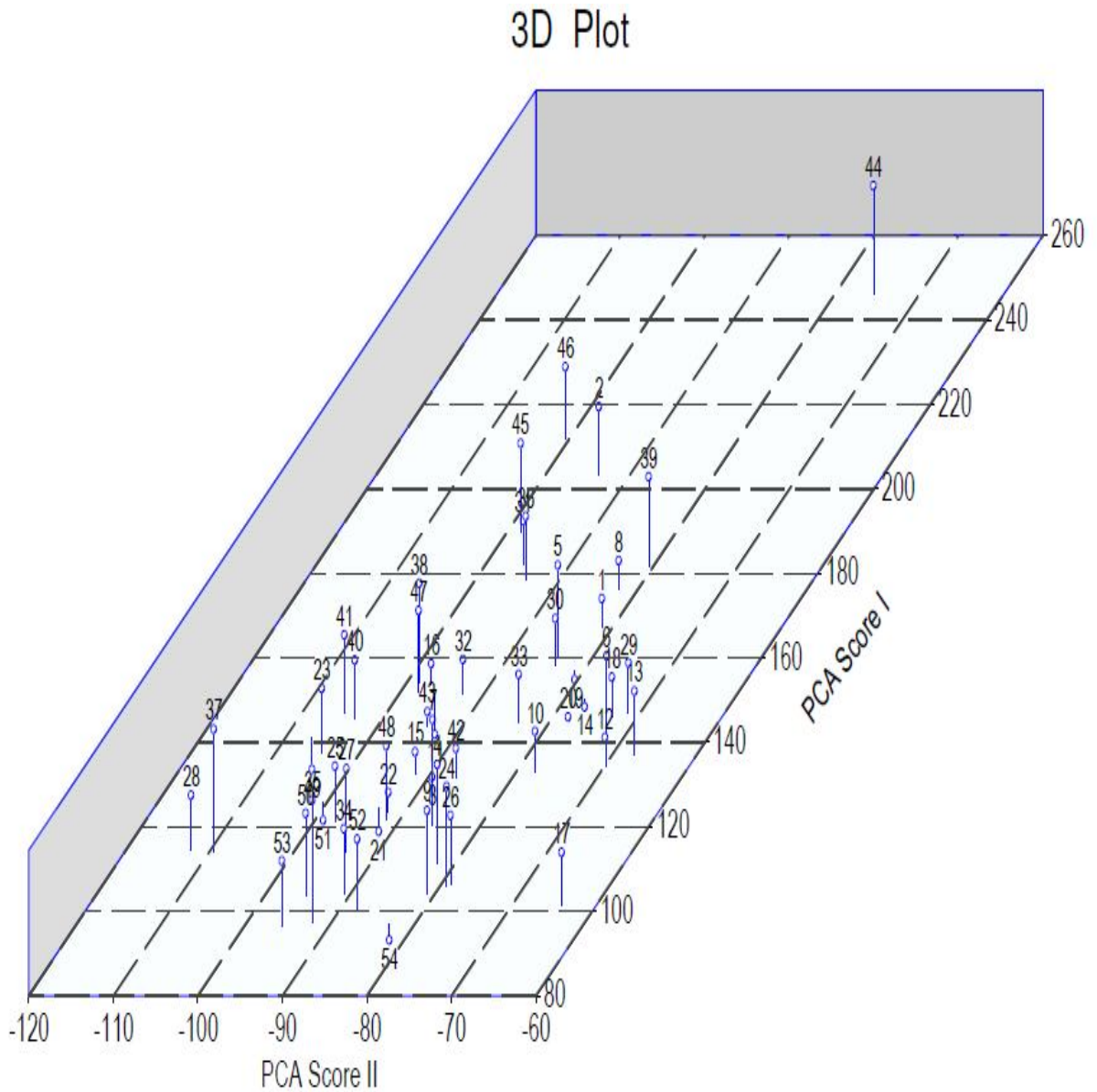
Source	df	Days to 50% Flowering of Primary Raceme	Stem Length to Primary Raceme (cm)	Nodes to Primary Raceme	Total Length of Primary Raceme cm	Effective Length of Primary Raceme	Days to 80% maturity of Primary Raceme	Secondary Branches/ Plant	Days to 50% Flowering of Secondary Raceme	Nodes to Secondary Raceme	Stem Length to Secondary Raceme cm
Replication	1	2.3704	4.0059	0.9502	0.4867	1.6502	1.0208	0.0533	0.5926	3.1008	61.3515
Treatment	53	384.8239**	3091.3206**	40.5637**	155.4486**	159.9686**	274.8849**	0.4881**	529.8525**	14.7476**	1723.8688**
Error	53	1.5590	8.5410	0.5032	3.0001	1.7798	1.1718	0.0481	2.1775	0.8937	33.2270

Source	df	Total Length of Secondary Raceme cm	Effective Length Secondary Raceme cm	Days to 80% maturity of Secondary Raceme	Tertiary Branches/ Plant	Days to 50% Flowering of Tertiary Raceme	Nodes to Tertiary Raceme	Stem Length to Tertiary Raceme cm	Effective Length of Tertiary Raceme	Days to 80% maturity Of tertiary Raceme
Replication	1	9.2459	11.8670	0.0370	0.1337	2.0833	0.1008	14.9261	0.5348	2.6759
Treatment	53	125.6388**	103.5799**	388.8491**	1.8994**	575.4118**	4.8121**	699.6819**	44.6473**	409.4418**
Error	53	1.8257	1.3995	2.9238	0.0679	1.5362	0.3097	5.4306	0.8420	6.1476

Source	df	100 Seed Wt of Primary Raceme gm	100 Seed Wt of Secondary Raceme gm	100 Seed Wt of Tertiary Raceme gm	Oil Content (%)	L/B Ratio of Seed	Harvest index (%)	Seed Yield/ Plant At 120 Days gm	Seed Yield/ Plant up to 150 Days gm	Seed Yield/ Plant up to 180 Days gm
Replications	1	0.0075	0.6196	0.3051	0.7433	0.0005	1.9683	7.7013	49.5049	48.5348
Treatments	53	17.9779**	19.1965**	21.5180**	7.0258**	0.0063**	22.8466**	2261.6694**	3251.4902**	1934.1255**
Error	53	0.4795	0.8397	1.1912	0.8449	0.0004	1.2816	35.7172	69.2328	101.1274

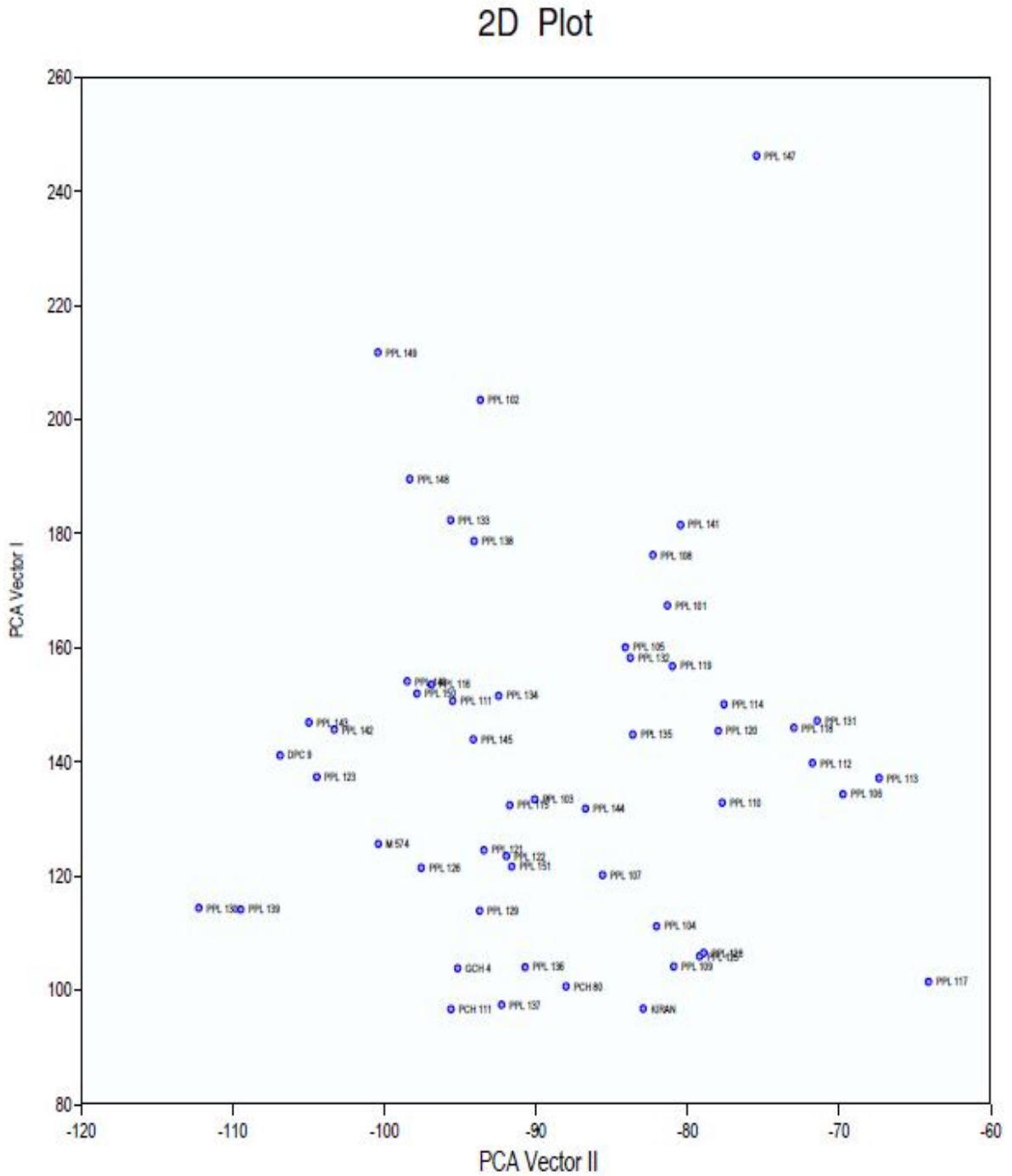


**Fig 19: Three dimensional graph showing relative position of 54 castor (*Ricinus communis* L.) genotypes based on PCA scores.**



Numbers correspondent to the serial number of genotypes as in table 7 (source of genotypes)

**Fig 18: Two dimensional graph showing relative position of 54 castor (*Ricinus communis* L.) genotypes based on PCA scores.**



## **CHAPTER V**

### **DISCUSSION**

Planning and success of any breeding programme largely depends on thorough knowledge of genetic variability present in the available germplasm for the character under improvement. The genotypic coefficient of variation measures the range of genetic variability available in a crop species and also enables to compare the amount of such variability present in different characters. The phenotypic expression of a character is the result of interaction between the genotype and environment. Hence, the total variance needs to be partitioned into heritable and non-heritable to assess the true breeding nature of a particular trait.

The salient features of the results obtained in the present investigation are discussed under the following headings.

5.1 Morphological characterization

5.2 Mean, variability, heritability and genetic advance as per cent of mean

5.3 Correlations

5.4 Path coefficient analysis

5.5 Genetic divergence

#### **5.1 MORPHOLOGICAL CHARACTERISATION**

Varietal testing and release system in all the crops basically concentrates on generating data on parameters like yield, quality, reaction to pests and diseases, agronomic adaptability *etc.* (Tandon, 1992). Introduction of plant variety protection under GATT, necessitated the need for testing of varieties for their Distinctness (D), Uniformity (U) and Stability (S). The DUS test included a detailed botanical examination using a standard list of descriptors. This is intended to remove any

confusion in naming new varieties proposed for registration under plant variety protection (PPV) authority (Mauria, 2005). The guide lines for DUS testing in many crops are developed by UPOV and were used to modify under Indian conditions. Castor, being the native crop of India, guidelines for DUS testing is being developed at Directorate of Oilseeds Research. The present study is an attempt in this direction and helped in standardizing the guidelines of DUS testing in castor.

Among 54 genotypes studied, much variation was found for most of the morphological characters. Stem colour was dark red in 21 genotypes, red in 29 genotypes, and green in 4 genotypes. Type of internodes on stem were condensed in 11 genotypes remaining were elongated. Plant branching pattern was divergent in 16 genotypes remaining 38 genotypes were convergent. Petiole colour was green with reddish tinge in 15 genotypes, dark red in 7 genotypes, 4 genotypes showed green petiole remaining 28 genotypes showed red petiole. Lamina leaf colour was green with reddish tinge in 12, dark green in 13 and green in 29 genotypes. Double bloom in 50 genotypes triple bloom in 2 genotypes and 2 genotypes has single bloom. Type of inflorescence with interspersed staminate flower in 52 genotypes, 2 were monoecious. Colour of stigma was dark red in 14 genotypes, pink in 11 genotypes and red in 29 genotypes. Capsule type was non spiny in 4 genotypes and spiny in 50 genotypes. Spike shape was conical in 44 genotypes, cylindrical in 9 genotypes and umbrella shape in 1 genotype. Compact spike in 10 genotypes, 20 genotypes had loose spike and semi compact in 24 genotypes. Maroon seed colour in 11 genotypes, 15 genotypes had deep chocolate colour and 28 genotypes had brown colour.

The assessment of distinctness can be done by grouping these genotypes into groups. Characteristics suitable for grouping purposes are those which are known from experience and not vary within a variety (Chakrabarty *et al.* 2006). A genotype/variety is considered to be distinct if observations / measurements show it to differ consistently

from all others. Hence, the study is of significance in testing distinctiveness of genotypes. The present findings are in agreement with earlier investigations of Muhammad *et al.* (1971), Jagdish (1994), Varier *et al.* (1999), Rajendra Prasad *et al.* (2003) and Rajeshwari (2004) which showed that morphological characterization helps in identification of genotypes easily.

## **5.2 GENETIC VARIABILITY**

Presence of a wider spectrum of variability in a given crop species will enhance the chance of selecting a desired genotype. The moderate to high GCV indicates a high degree of genetic variability and thus a greater scope for selection as these characters are less influenced by environment. Besides genetic variability, knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted from one generation to next. High heritability indicates that a major part of the phenotypic variability in any character is controlled by additive gene effect, which can be improved by simple selection procedures (Lush, 1940). Heritability also provides information to predict genetic gain obtained by selection. Therefore, for successful improvement of any crop, it is necessary to have a thorough knowledge on the above genetic parameters. The characters with high heritability coupled with high genetic advance further indicate the possibility of making selections in earlier generations.

Burton and Devane (1953) and Swarup and Chaugle (1962) indicated that genetic variability together with the heritability would give a better idea on the amount of genetic advance expected out of selection. The magnitude of heritable variability is the most important aspect of genetic contribution of the breeding material, which has close relationship on its response to selection (Panse, 1957).

The 54 castor genotypes studied in the present investigation differed statistically for all the characters studied. The results obtained on the mean, variability, heritability and genetic advance as per cent of mean are discussed hereunder.

### **Mean, variability, heritability and genetic advance as per cent of mean**

#### **5.2.1 Days to 50% flowering of primary raceme**

The genotypic and phenotypic coefficients of variation were (20.73 and 20.81%) high. These findings are in agreement with those of Rao *et al.* (1983b). High heritability (99.19%) and high genetic advance as per cent of mean (42.53) were observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. Rao *et al.* (1983b), and Golakia *et al.* (2007) reported similar experimental findings in castor.

#### **5.2.2 Stem length up to primary raceme (cm)**

The estimates of both GCV and PCV (34.65 and 34.76%) were high. These findings are in agreement with those of Rao *et al.* (1983b), Patel *et al.* (1985). High heritability (99.44%) and high genetic advance as per cent of mean (71.18) were observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. These findings are in agreement with results reported by Patel *et al.* (1985 and 1991), Reddy *et al.* (1999c), Lakshamma *et al.* (2005), and Golakia *et al.* (2007).

### **5.2.3 Number of nodes up to primary spike**

The estimated values of GCV and PCV (22.47 and 22.75%) were high with a wide range of variability. High heritability (97.55%) coupled with high genetic advance as per cent of mean (45.73) was recorded for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. These findings are in agreement with the results reported by Dorairaj *et al.* (1973c), Ratnakar (1982), Rao *et al.* (1983b), Patel *et al.* (1985 and 1991), Reddy *et al.* (1999c), Lakshamma *et al.* (2005), and Golakia *et al.* (2007).

### **5.2.4 Total length of primary raceme (cm)**

The estimates of GCV and PCV (20.37 and 20.77%) were high. These findings are in agreement with those of (Patel *et al.* 1985, Patel *et al.* 1991). High heritability (96.21%) coupled with high genetic advance as per cent of mean (41.16) was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. Dorairaj *et al.* (1973c), Ratnakar (1982) and Patel *et al.* (1985 and 1991) reported similar experimental findings. The genotypes PPL 101, PPL-111, PPL-116, PPL-123, PPL-130, PPL-134, PPL-140, PPL-141, PPL-142, PPL-143, PPL-145, PPL-148, PPL-149, and PPL-150 can be selected for maximum total length to primary raceme compared with check M-574.

### **5.2.5 Effective length of primary spike (cm)**

The estimates of GCV and PCV (24.05 and 24.32%) were high. These findings are in agreement with those of (Lakshamma *et al.* 2005). High heritability (97.80%) and high genetic advance as per cent of mean (49.00) were recorded for this trait

indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. These findings are in agreement with results reported by Lakshamma *et al.* (2005), and Ramesh (2008). The genotypes PPL-116, PPL-123, PPL-130, PPL-139, PPL-140, PPL-141, PPL-142, PPL-143, PPL-148, and PPL-149 can be selected for higher effective length of primary raceme compared with best check DPC-9.

#### **5.2.6 Days to 80% maturity of the primary raceme**

The estimates of GCV and PCV (11.48 and 11.53%) were moderate. High heritability (99.15%) coupled with high genetic advance as per cent of mean (23.55) was recorded for this parameter indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character.

#### **5.2.7 Number of secondary branches per plant**

The estimates of GCV (17.96%) and PCV (19.83%) were moderate. High heritability (82.07%) and high genetic advance as per cent of mean (33.52) were recorded for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. Raghuram Reddy *et al.* (1999), and Lakshamma *et al.* (2005) reported similar experimental findings in castor. The genotypes PPL-105, PPL-111, PPL-114, PPL-123, PPL-131, PPL-134 and PPL-144 can be selected for higher number of secondary racemes per plant compared with best check DPC-9.

### **5.2.8 Days to 50% flowering of secondary raceme**

The estimates of GCV (17.07%) and PCV (17.14%) were moderate. High heritability (99.18) and high genetic advance as per cent of mean (35.03) were recorded for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. The genotype PPL-117 can be selected for lower days to 50% flowering of secondary raceme compared with best check Kiran.

### **5.2.9 Number of nodes to secondary raceme**

The estimates of GCV (24.71%) and PCV (26.26%) were high. High heritability (88.57) and high genetic advance as per cent of mean (47.92) were recorded for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character.

### **5.2.10 Stem length to secondary raceme (cm)**

The estimates of GCV and PCV (34.94 and 35.62%) were high. High heritability (96.21%) coupled with high genetic advance as per cent of mean (70.61) was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character.

### **5.2.11 Total length of secondary raceme (cm)**

The estimates of GCV and PCV (22.91 and 23.82%) were high. High heritability (97.13%) coupled with high genetic advance as per cent of mean (46.67) was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving

this character. The genotypes ppl-123, PPL-130, PPL-140, PPL-143 and PPL-149 may be selected for higher total length of secondary raceme compared with best check DPC-9

#### **5.2.12 Effective length of secondary spike (cm)**

The estimates of GCV and PCV (24.56 and 24.89%) were high. These findings are in agreement with those of (Lakshamma *et al.* 2005). High heritability (97.33%) coupled with high genetic advance as per cent of mean (49.91) was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. Lakshamma *et al.* (2005) reported similar experimental findings in castor. The genotype PPL-130 may be selected for effective length of secondary raceme compared with best check DPC-9.

#### **5.2.13 Days to 80% maturity of the secondary raceme**

The estimates of GCV and PCV (11.02 and 11.11%) were moderate. High heritability (98.51%) coupled with high genetic advance as per cent of mean (22.54) was recorded for this parameter indicate the presence of additive and gene action. The genotypes PPL-117, PPL-126, PPL-128, PPL-136, PPL-137 and PCH-111 may be selected for lower days to 80% maturity of secondary raceme compared with best check Kiran

#### **5.2.14 Number of tertiary branches per plant**

The estimates of GCV (31.11%) and PCV (32.24%) were high. These findings are in agreement with those of Reddy *et al.* 1999c. High heritability (93.10%) and high

genetic advance as per cent of mean (61.84) were recorded for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. Raghuram Reddy *et al.* (1999c) reported similar experimental findings in castor. The genotypes PPL-125, PPL-135, and PPL-138 can be selected for more number of tertiary racemes compared with best check DPC-9.

#### **5.2.15 Days to 50% flowering of tertiary raceme**

The estimates of GCV (14.04%) and PCV (14.08%) were moderate. High heritability (99.45%) and high genetic advance as per cent of mean (28.84) were recorded for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. The genotypes PPL-104, PPL-109, PPL-117, PPL-125, PPL-128, PPL-130, PPL-136, PPL-137, PPL-151, GCH-4, PCH-80, and PCH-111 may be selected for lower days to 50% flowering of tertiary raceme compared with best check Kiran

#### **5.2.16 Number of nodes to tertiary raceme**

The estimates of GCV (17.69%) and PCV (18.87%) were moderate. High heritability (87.40) and high genetic advance as per cent of mean (34.16) were recorded for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character.

#### **5.2.17 Stem length to tertiary raceme**

The estimates of GCV and PCV (37.98 and 38.27%) were high. High heritability (98.46%) coupled with high genetic advance as per cent of mean (77.63)

was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character.

#### **5.2.18 Effective length of tertiary spike**

The estimates of GCV and PCV (22.77 and 23.20%) were high. These findings are in agreement with those of Lakshamma *et al.* (2005). High heritability (96.29%) coupled with high genetic advance as per cent of mean (46.03) was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character.

#### **5.2.19 Days to 80% maturity of the tertiary raceme**

The estimates of GCV (9.73%) and PCV (9.88%) were low. High heritability (97.04%) and moderate genetic advance as per cent of mean (19.74) were recorded for this trait indicate the presence of both additive and non-additive gene action. The genotypes PPL-109, PPL-117, PPL-125, PPL-128 and ppl-137 may be selected for lower days to 80% maturity of tertiary raceme compared with check Kiran

#### **5.2.20 100 seed weight of primary raceme (g)**

The estimated values of GCV and PCV (12.33 and 12.66%) were moderate. These findings are in agreement with those of Patel *et al.* (1985 and 1991) and Golakia *et al.* (2007). High heritability (94.80%) coupled with high genetic advance as per cent of mean (24.73) was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for

improving this character. The genotype GCH-4 can be selected for high 100 seed weight of primary raceme compared with best check M-574.

#### **5.2.21 100 seed weight of secondary raceme**

The estimated values of GCV and PCV (12.09 and 12.54%) were moderate. High heritability (91.61%) coupled with high genetic advance as per cent of mean (23.67) was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. The genotypes PPL-102, PPL-105, PPL-125, PPL-143, GCH-4, and PCH-111 can be selected for high 100 seed weight of secondary raceme compared with best check M-574.

#### **5.2.22 100 seed weight of tertiary raceme**

The estimated values of GCV and PCV (13.18 and 13.94%) were moderate. High heritability (89.51%) coupled with high genetic advance as per cent of mean (25.70) was observed for this trait indicates the presence of both additive and non-additive gene action. The genotypes GCH-4, PCH-111 can be selected for high 100 seed weight of tertiary raceme compared with best check DPC-9.

#### **5.2.23 Oil content**

The estimates of GCV and PCV (3.65 and 4.12%) were low which were on par with the results of Patel *et al.* (1985 and 1991). High heritability (78.53%) coupled with low genetic advance as per cent of mean (6.67) was recorded for this trait indicates operation of environmental factors and selection would be ineffective.

#### **5.2.24 L/B ratio of seed**

The estimates of GCV (3.72%) and PCV (3.99%) were low. High heritability (87.18%) and low genetic advance as per cent of mean (7.16) were recorded for this trait revealed the predominance of both additive and non-additive gene action.

#### **5.2.25 Harvest index**

The estimates of GCV and PCV (8.98 and 9.50%) were low which were on par with the results of Jagtap *et al.* (2006). High heritability (89.37%) coupled with moderate genetic advance as per cent of mean (17.49) was recorded for this trait indicates the presence of both additive and non-additive gene action. Jagtap *et al.* (2006) reported similar experimental findings in castor

#### **5.2.26 Seed yield up to 120 days**

The estimated values of GCV and PCV (61.64 and 62.625) were high. These findings are in agreement with those of Rao *et al.* (1983b), Lakshamma *et al.*(2005). High heritability (96.89%) coupled with high genetic advance as per cent of mean (124.99) was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. Patel *et al.*(1991), Reddy *et al.*(1999b) reported similar experimental findings in castor The genotypes PPL-103, GCH-4 and PCH-80 can be selected for higher seed yield per plant at 120 days compared with best check Kiran.

#### **5.2.27 Seed yield up to 150 days**

The estimated values of GCV and PCV (38.84 and 39.68%) were high. High heritability (95.83%) coupled with high genetic advance as per cent of mean (78.33)

was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character. The genotypes PPL-103, GCH-4, PCH-80, and PCH-111 can be selected for higher seed yield per plant upto 150 days compared with check DPC-9.

#### **5.2.28 Seed yield up to 180 days**

The estimated values of GCV and PCV (24.03 and 25.32%) were high. High heritability (90.06%) coupled with high genetic advance as per cent of mean (46.98) was observed for this trait indicate the presence of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving this character.

The genotype PPL-103 was promising for good yield at 120 and 150 days. The genotypes PPL-111, PPL- 123, PPI-130, PPL-140, PPL-142, PPL-143 and PPL-149 were promising for most of the yield and yield attributing characters compared with best checks. These promising genotypes can be further exploited in breeding programmes for generation of high yielding lines.

### **5.4 CORRELATIONS**

Direct selection for yield and yield component traits is not effective as it is a complex quantitative character and it is highly influenced by environment. High genotype and environment interaction will restrict improvement, if selection is based on yield per se. Thus effective improvement in yield may be brought about through selection on yield component characters. Therefore, the correlation between yield and yield components are of considerable importance in selection programme. The aim of correlation studies is primarily to know the suitability of various characters for indirect

selection because selection on any particular trait may bring about undesirable changes in other associated characters (Singh, 1998).

Yield component characters show associations among themselves and also with yield. Unfavorable associations between the desirable attributes under selection may limit genetic advance. Hence, knowledge of associations between the yield and yield components and also among the yield components is essential for planning a sound selection programme ( Falconer, 1964).

In the present investigation, correlation estimates were obtained from 54 genotypes for yield with the yield components of *Ricinus communis* L. are discussed hereunder.

The results indicated that genotypic correlations in general were higher than phenotypic correlations. This may be due to the relative stability of genotypes as majority of them were subjected to certain amount of selection (Johnson *et al.* 1955).

#### **5.4.1 Days to 50% flowering of primary raceme**

This trait showed significant positive association at both genotypic and phenotypic level with stem length to primary raceme, nodes to primary raceme, total length of primary raceme, effective length of primary raceme, days to 80% maturity of primary raceme, days to 50% flowering of secondary raceme, nodes to secondary raceme, stem length to secondary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, days to 80% maturity of tertiary raceme. While it showed significant negative association with seed yield per plant at 120 days. Similar relationships were reported by Rao *et al.* (1983 a), Mehta and Vashi (1998), Reddy *et al.* (1999a), Golakia *et al.* (2007). Jadhav and Deshmukh (2008). Earliness is preferred in castor. As the days to 50% flowering of primary raceme is decreased

remaining 50% flowering of next order racemes decreases, days to 80% maturity of all order raceme also decreases and there by yield at 120 days increases.

#### **5.4.2 Stem length to primary raceme**

Both the genotypic and phenotypic correlations revealed that this trait showed significant positive association with nodes to primary raceme, total length of primary raceme, effective length of primary raceme, days to 80% maturity of primary raceme, days to 50% flowering of secondary raceme, nodes to secondary raceme, stem length to secondary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, days to 80% maturity of tertiary raceme. It indicates that it is possible to improve the above characters with increase in stem length of primary raceme.

This trait showed significant negative association with seed yield/plant at 120 days and seed yield plant upto 150 days which indicates decrease in plant height yield/plant upto 120 and 150 days increases. Similar relationship were reported by Giriraj (1973), Dorairaj *et al.* (1973a), Bhatt and Reddy (1981), Rao *et al.* (1983a), Patel and Jaimani (1991), Yadav *et al.* (2004), Lakshamma *et al.* (2005), Golakia *et al.* (2007).

#### **5.4.3 Number of nodes to primary raceme**

Both the genotypic and phenotypic correlations revealed that this trait showed significant positive association with days to 80% maturity of primary raceme, days to 50% flowering of secondary raceme, nodes to secondary raceme, stem length to secondary raceme, days to 80% maturity of secondary raceme, days to 50% flowering

of tertiary raceme, days to 80% maturity of tertiary raceme. While it showed significant negative association with seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days. Similar reports were given by Rao *et al.* (1983a)

#### **5.4.4 Total length of primary raceme**

This trait showed significant positive association with effective length of primary raceme, days to 80% maturity of primary raceme, days to 50% flowering of secondary raceme, nodes to secondary raceme, stem length to secondary raceme, total length of secondary raceme, effective length of secondary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, effective length of tertiary raceme, days to 80% maturity of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, oil content, seed yield per plant up to 180 days both at genotypic and phenotypic level. It indicates increase in total length of primary raceme can simultaneously increase the effective lengths, 100 seed weights of first and second order racemes and also yield per plant up to 180 days. It showed significant negative association with tertiary branches per plant. Similar findings were reported by Dorairaj *et al.* (1973 a,b), Yadav and Singh (1973), Bhatt and Reddy (1981), Muthiah *et al.* (1982 b), Ratnakar (1982), Rao *et al.* (1983 a), Anjani and Reddy (2003), Jadhav and Deshmukh (2008).

#### **5.4.5 Effective length of primary raceme**

This trait showed positive significant association both at genotypic and phenotypic level with days to 80% maturity of primary raceme, days to 50% flowering of secondary raceme, nodes to secondary raceme, stem length to secondary raceme, total length of secondary raceme, effective length of secondary raceme, days to 80%

maturity of secondary raceme, effective length of tertiary raceme, days to 80% maturity of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, oil content, seed yield per plant up to 180 days. It showed significant negative association with tertiary branches per plant. This is an important attribute which directly influences the yield. These results are in accordance with the findings of Mehta and Vashi (1998), Lakshamma *et al.* (2005), Golakia *et al.* (2007).

#### **5.4.6 Days to 80% maturity of primary raceme**

Both the genotypic and phenotypic correlations revealed that this trait showed significant positive association with days to 50% flowering of secondary raceme, nodes to secondary raceme, stem length to secondary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, days to 80% maturity of tertiary raceme. While it showed negative association with nodes to tertiary raceme, stem length to tertiary raceme, L/B ratio, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days. It indicates that increase in days to 80% maturity of primary raceme increases the duration of the crop and decrease in seed yield per plant at 120 days, up to 150 days and up to 180 days with increase in days to 80% maturity of primary raceme. These results are in accordance with Mehta and Vashi (1998),

#### **5.4.7 Number of secondary branches per plant**

This trait showed significant positive association both at genotypic and phenotypic level with stem length to secondary raceme and non-significant positive association with seed yield per plant up to 180 days. While it showed significant negative association with stem length to tertiary raceme.

#### **5.4.8 Days to 50% flowering of secondary raceme**

This trait showed significant positive association with nodes to secondary raceme, stem length to secondary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, days to 80% maturity of tertiary raceme, Indicates increase in days to 50% flowering of secondary raceme there is increase in the above traits. This trait showed significant negative association with nodes to tertiary raceme, L/B ratio, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days. Indicates decrease in yield per plant at 120 and upto 150 days with increase in days to 50% flowering of secondary raceme.

#### **5.4.9 Number of nodes to secondary raceme**

This trait showed significant negative association with nodes to tertiary raceme, stem length to tertiary raceme, L/B ratio, seed yield per plant at 120 days, seed yield per plant up to 150 days and non significant negative association with seed yield per plant up to 180 days. Indicates the increase in the nodes to secondary raceme there is decrease in yield per plant.

#### **5.4.10 Stem length to secondary raceme**

This trait showed significant negative association with tertiary branches per plant, nodes to tertiary raceme, stem length to tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days indicates increase in stem length to secondary raceme there will be decrease in yield.

#### **5.4.11 Total length of secondary raceme**

This trait showed significant positive association with effective length of secondary raceme, effective length of tertiary raceme, harvest index, seed yield per plant up to 150 days, seed yield per plant up to 180 days both at genotypic and phenotypic level. Indicates increase in total length of secondary raceme there will be increase in yield.

#### **5.4.12 Effective length of secondary raceme**

Effective length of secondary raceme showed significant positive association both at phenotypic and genotypic level with effective length of tertiary raceme, days to 80% maturity of tertiary raceme, seed yield per plant up to 180 days. This trait showed significant negative association with tertiary branches per plant.

#### **5.4.13 Days to 80% maturity of secondary raceme**

Both phenotypic and genotypic correlations revealed that there is strong significant negative association with stem length to tertiary branches, nodes to tertiary raceme, stem length to tertiary raceme, 100 seed weight of tertiary raceme, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days.

#### **5.4.14 Number of tertiary branches per plant**

Number of tertiary branches per plant showed significant negative association with days to 50% flowering of tertiary raceme, days to 80% maturity of tertiary raceme.

#### **5.4.15 Days to 50% flowering of tertiary raceme**

This trait showed significant negative association both at genotypic and phenotypic level with nodes to tertiary raceme, stem length to tertiary raceme, 100 seed weight of tertiary raceme, L/B ratio, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days indicates decrease in seed yield per plant at 120 days, up to 150 days with increase in days to 50% flowering of tertiary raceme.

#### **5.4.16 Number of nodes to tertiary raceme**

Both phenotypic and genotypic correlations revealed that stem length to tertiary raceme, 100 seed weight of tertiary raceme, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days had significant positive association both at phenotypic and genotypic level.

#### **5.4.17 Stem length to tertiary raceme**

This trait showed significant positive association with nodes to tertiary raceme, 100 seed weight of tertiary raceme, L/B ratio, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days at both phenotypic and genotypic level

#### **5.4.18 Effective length of tertiary raceme**

Both the genotypic and phenotypic correlations revealed that this trait showed significant positive association with harvest index, seed yield per plant up to 150 days, seed yield per plant up to 180 days, indicates increase in seed yield per plant up to 150 days, up to 180 days with increase in effective length of tertiary raceme.

#### **5.4.19 Days to 80% maturity of tertiary raceme**

This trait exhibited significant negative association with 100 seed weight of tertiary raceme, harvest index, seed yield per plant at 120 days, up to 150 days, up to 180 days both at genotypic and phenotypic level.

#### **5.4.20 100 Seed weight of primary raceme**

This trait exhibited significant positive association with total length of primary raceme, effective length of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days. These results were in accordance with Domingo (1945), Raju (1981), Rao *et al.* (1983a).

#### **5.4.21 100 Seed weight of secondary raceme**

This trait exhibited significant positive association with total length of primary raceme, effective length of primary raceme, nodes to secondary raceme, 100 seed weight of primary raceme, 100 seed weight of tertiary raceme, oil content, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days. These results were in accordance with Domingo (1945), Raju (1981), Rao *et al.* (1983 a)

#### **5.4.22 100 Seed weight of tertiary raceme**

This trait recorded significant positive association with nodes to tertiary raceme, stem length to tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, oil content, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days. These results were in accordance with Domingo (1945), Raju (1981) and Rao *et al.* (1983 a).

#### **5.4.23 Oil content**

This trait exhibited significant positive association with tlp, effective length of primary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days. These results were in accordance with Lauret (1981), Asish *et al.* (2008).

#### **5.4.24 L/B ratio**

This trait showed significant positive association with stem length to tertiary raceme, seed yield per plant at 120 days, seed yield per plant up to 150 days both at genotypic and phenotypic level.

#### **5.4.25 Harvest index**

This trait showed significant positive association with total length of secondary raceme, stem length to tertiary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, seed yield per plant at 120 days, seed yield per plant up to 150 days, seed yield per plant up to 180 days. These results were in accordance with Ravi *et al.* (2006).

#### **5.4.26 Seed yield per plant at 120 days.**

This trait showed significant negative association with nodes to tertiary raceme, stem length to tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, L/B ratio, harvest index, seed yield per plant up to 150 days.

#### **5.4.27 Seed yield per plant upto 150 days**

This trait showed significant positive association total length of secondary raceme, nodes to tertiary raceme, stem length to tertiary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, L/B ratio, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days.

#### **5.4.28 Seed yield per plant upto 180 days**

This trait showed significant positive association with total length of primary raceme, effective length of primary raceme, total length of secondary raceme, effective length of secondary raceme, nodes to tertiary raceme, stem length to tertiary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, harvest index, seed yield per plant at 120 days, seed yield per plant up to 150 days both at phenotypic and genotypic level. It indicates simultaneous improvement of the above characters can improve the seed yield per plant upto 180 days.

There is significant and positive association existed among the characters days to 50% flowering and 80% maturity of primary, secondary and tertiary racemes. Days to 50% flowering of primary raceme showed significant negative association with seed yield per plant at 120 days and upto 150 days. Obviously decrease in any one of the character would lead to the earliness. These results are in accordance with the findings of Mehta and Vashi (1998), Golakia *et al.* (2007) and Jadhav and Deshmukh (2008).

Phenotypic correlation and genotypic correlation after Z transformation showed significant positive correlation of the characters total length of primary raceme, effective length of primary raceme, total length of secondary raceme, effective length of secondary raceme, tertiary branches per plant, nodes to tertiary raceme, stem length to tertiary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, harvest index, seed yield per plant at 120 days and seed yield per plant up to 150 days with seed yield per plant upto 180 days. Hence improving above characters will improve the yield.

## **5.5 PATH COEFFICIENT ANALYSIS**

The observed correlation between yield and its component character is the net result of the direct and indirect effects of the component character through other yield attributes. The total correlation coefficient between yield and its component characters may sometimes be misleading, as it may be an over or under estimate of its association with other characters. In these cases, direct selection on the basis of correlated response may not be fruitful. For critical evaluation, the correlation coefficient need to be split into direct and indirect effects using path coefficient analysis since, many characters

affect a given trait. Thus, the correlation and path coefficients in combination can give a better insight into cause and effect relationship between different pairs of character.

As a guideline for interpretation of the results of path analysis, the following broad points may be kept in view (Singh and Chaudhary, 1977).

If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective.

If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.

Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed i.e., restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

If correlation coefficient is negative and direct effect is also negative, then we have to drop the selection based on that character.

The residual effect determines how best the causal factors account for the variability of the dependent factor. If the residual effect is high, some other factors which have not been considered here need to be included in this analysis to account fully for the variation in yield.

Based on the above, the characters subjected to correlations were also subjected to path coefficient analysis for estimating the direct and indirect effects so as to formulate a basis for selection in castor. The results are discussed character-wise hereunder.

### **5.5.1 Days to 50% flowering of primary raceme**

This trait exhibited low negative direct effect at phenotypic level and significant negative correlation with seed yield per plant upto 180 days at both phenotypic and genotypic level. It had positive indirect effect through nodes to primary raceme, effective length of primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme, L/B ratio. Because that direct effect is negative and low and even association with seed yield per plant upto 180 days is negative, this trait is of little importance in seed yield improvement. These findings are in agreement with the findings of Rao *et al.* (1983a), Patel and Jamini (1991), Kumari *et al.* (1996), Mehta and Vashi (1998), Ramesh and Prasad (2001), Golakia *et al.* (2007), Ashish *et al.* (2008).

### **5.5.2 Stem length to primary raceme**

This trait exhibited low negative direct effect at phenotypic level and significant negative correlation with seed yield per plant upto 180 days at both phenotypic and genotypic level. It had positive indirect effects through nodes to primary raceme, effective length of primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme, days to 80% maturity of tertiary raceme. Because the direct effect is low and correlation is also negative this trait is of little importance in seed yield improvement. These findings are in agreement with Raju (1981), Rao *et al.* (1983a), Swarnalatha (1984), Khorgade *et al.* (1994), Mehta and Vashi (1998), Ramesh and Prasad (2001), Yadav *et al.* (2004)

### **5.5.3 Nodes to primary raceme**

This character had a positive direct and significant positive phenotypic and genotypic association with seed yield per plant upto 180 days. It had positive indirect effects through days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme, days to 80% maturity of tertiary raceme, L/B ratio. These findings are in agreement with Ananthasayana Reddi (1981), Muthiah *et al.* (1982 b), Rao *et al.* (1983a), Kumar *et al.* (1996), Mehta and Vashi (1998), Yadav *et al.* (2004).

### **5.5.4 Total length of primary raceme**

This character had a negative direct effect and significant positive correlation with seed yield per plant upto 180 days both at phenotypic and genotypic level. It had positive indirect effects through effective length of primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, effective length of tertiary raceme, days to 80% maturity of tertiary raceme, oil content. The indirect effects seem to be the cause of positive correlations. Hence the indirect causal factors are to be considered simultaneously for selection. These findings are in agreement with the findings of Rao *et al.* (1983a), Khorgade *et al.* (1994), Mehta and Vashi (1998), Golakia *et al.* (2007).

Total length of primary raceme showed positive association with seed yield per plant upto 180 days gave negative direct effect. This is in accordance with Khorgade *et al.* (1994). This positive association with seed yield per plant seems to be due to its indirect influence via effective length of primary raceme, days to 80% maturity of secondary raceme, effective length of tertiary raceme, days to 80% maturity of tertiary raceme, oil content. Hence these characters may be given due weightage while practicing the selection for high seed yield in castor.

### **5.5.5 Effective length of primary raceme**

This trait exhibited positive direct effect and significant positive association with seed yield per plant up to 180 days at both phenotypic and genotypic level. The magnitude of the positive indirect effect is greater than negative indirect effects for the characters viz., days to 80% maturity of secondary raceme, effective length of tertiary raceme, days to 80% maturity of tertiary raceme, oil content. Hence, selection through these characters may bring about improvement in yield. These results are in accordance with the findings of Ramesh and Prasad (2001), Manivel and Manivannan (2006).

### **5.5.6 Days to 80% maturity of primary raceme**

This trait exhibited negative direct effect, and significant negative association with seed yield per plant up to 180 days at both genotypic and phenotypic level. It had positive indirect effects through nodes to primary raceme, effective length of primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme, days to 80% maturity of tertiary raceme, L/B ratio. These results are in accordance with Khorgade *et al.* (1994) and Golaki *et al.* (2007).

### **5.5.7 Secondary branches per plant**

This character had low positive direct effect at phenotypic level and non-significant positive association with seed yield per plant up to 180 days both at phenotypic and genotypic level. These results are in accordance with the results of Lakshamma *et al.* (2005), Manivel and Manivannan (2006).

#### **5.5.8 Days to 50% flowering of secondary raceme**

This trait exhibited low positive direct effect at phenotypic level and significant negative association with seed yield per plant upto 180 days both at phenotypic and genotypic level. It had positive indirect effect through nodes to primary raceme, effective length of primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme, days to 80% maturity of tertiary raceme, L/B ratio.

#### **5.5.9 Nodes to secondary raceme**

This trait exhibited negative direct effect at phenotypic level and negative non-significant association with seed yield per plant upto 180 days both at phenotypic and genotypic level. It had positive indirect effects through nodes to primary raceme, effective length of primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme, days to 80% maturity of tertiary raceme, L/B ratio.

#### **5.5.10 Stem length to secondary raceme**

This trait exhibited negative direct effect at phenotypic level and significant negative correlation with seed yield per plant upto 180 days. It had positive indirect effect through nodes to primary raceme, effective length of primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme, days to 80% maturity of tertiary raceme, 100 seed weight of secondary raceme.

#### **5.5.11 Total length of secondary raceme**

This trait exhibited negative direct effect at phenotypic level and significant positive correlation with seed yield per plant upto 180 days. It had positive indirect effect through effective length of primary raceme, effective length of tertiary raceme, harvest index, seed yield per plant up to 150 days.. The magnitudes of positive indirect effects were more. Hence selection through the positive indirect effects may bring about improvement in seed yield per plant upto 180 days.

#### **5.5.12 Effective length of secondary raceme**

This character had a positive direct effect at phenotypic level and significant positive association with seed yield per plant upto 180 days both at phenotypic and genotypic level. It had positive indirect effects through effective length of primary raceme, effective length of tertiary raceme, days to 80% maturity of tertiary raceme. Hence, greater emphasis in selection should be placed on these characters for improvement of yield. These results are in accordance with the results of Lakshamma *et al.* (2005).

#### **5.5.13 Days to 80% maturity of secondary raceme**

This character had positive direct effect and significant negative association with seed yield per plant upto 180 days both at phenotypic and genotypic level. It had positive indirect effects through nodes to primary raceme, effective length of primary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme and days to 80% maturity of tertiary raceme.

#### **5.5.14 Number of tertiary branches per plant**

This trait exhibited positive direct effect and non significant positive association at phenotypic level and significant positive association at genotypic level with seed yield per plant upto 180 days. It had negative indirect effects through effective length of primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme and days to 80% maturity of tertiary raceme. These findings are in agreement with the findings of Manivel and Manivannan (2006).

#### **5.5.15 Days to 50% flowering of tertiary raceme**

This trait exhibited positive direct effect and negative significant association with seed yield per plant upto 180 days both at phenotypic and genotypic level. It had positive indirect effect through nodes to primary raceme, effective length of primary raceme, days to 80% maturity of secondary raceme, nodes to tertiary raceme, days to 80% maturity of tertiary raceme and L/B ratio of seed

#### **5.5.16 Number of nodes to tertiary raceme**

This trait had negative direct effect and significant positive association with seed yield per plant upto 180 days. It had positive indirect effects through days to 50% flowering of primary raceme, days to 80% maturity of primary raceme, tertiary branches per plant, 100 seed weight of tertiary raceme and seed yield per plant up to 150 days.

#### **5.5.17 Stem length to tertiary raceme**

This trait exhibited negative direct effect at phenotypic level and positive non significant association with seed yield per plant upto 180 days. It had positive indirect effects through days to 50% flowering of primary raceme, days to 80% maturity of primary raceme, 100 seed weight of tertiary raceme, harvest index, seed yield per plant up to 150 days. It had negative indirect effects through nodes to primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, nodes to tertiary raceme, days to 80% maturity of tertiary raceme and L/B ratio of seed.

#### **5.5.18 Effective length of tertiary raceme**

This trait exhibited positive direct and positive significant association with seed yield per plant upto 180 days. It had positive indirect effect effective length of primary raceme, harvest index and seed yield per plant up to 150 days. Hence, direct selection for this trait improves the seed yield per plant upto 180 days. These results are in accordance with the results of Lakshamma *et al.* (2005).

#### **5.5.19 Days to 80% maturity of tertiary raceme**

This trait exhibited negative direct effect and negative non-significant association with seed yield per plant upto 180 days. It had positive indirect effects through nodes to primary raceme, effective length of primary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme and nodes to tertiary raceme.

#### **5.5.20 100 seed weight of primary raceme**

This trait exhibited negative direct effect at phenotypic level and positive significant association with seed yield per plant upto 180 days. It had positive indirect

effects through effective length of primary raceme, 100 seed weight of tertiary raceme, oil content, harvest index and seed yield per plant up to 150 days. The indirect effects seem to be the cause of positive correlations. Hence the indirect causal factors are to be considered simultaneously for selection. These findings are in agreement with the findings of Yadav *et al.* (2004), Khorgade *et al.* (1994), Mehta and Vashi (1998), Ramesh and Prasad (2001), Golakia *et al.* (2007).

#### **5.5.21 100 seed weight of secondary raceme**

This trait exhibited negative direct effect at phenotypic level and positive significant association with seed yield per plant upto 180 days. It had positive indirect effects through help, 100 seed weight of tertiary raceme, oil content, harvest index and seed yield per plant up to 150 days. The indirect effects seem to be the cause of positive correlations. Hence the indirect causal factors are to be considered simultaneously for selection.

#### **5.5.22 100 seed weight of tertiary raceme**

This trait exhibited positive direct effect and positive significant association with seed yield per plant upto 180 days. It had positive indirect effect through days to 50% flowering of primary raceme, oil content, harvest index and seed yield per plant up to 150 days. Hence selection through these characters may bring about improvement in yield.

#### **5.5.23 Oil content**

This trait exhibited low positive direct effect and positive significant association with seed yield per plant upto 180 days both at phenotypic and genotypic

level. It had positive indirect effect through effective length of primary raceme, 100 seed weight of tertiary raceme and seed yield per plant up to 150 days. Hence, greater emphasis in selection should be placed on these characters for improvement of yield. These results are in accordance with the findings of Khorgade *et al.*(1994), Kumari *et al.* (1996), Ramesh and Prasad (2001), Manivel and Manivannan (2006), Janamma *et al.* (2008), Ashish *et al.* (2008)

#### **5.5.24 L/B ratio of the seed**

This trait exhibited negative direct effect and positive non significant association with seed yield per plant upto 180 days both at phenotypic an genotypic level. It had positive indirect effect through days to 50% flowering of primary raceme, days to 80% maturity of primary raceme, seed yield per plant up to 150 days..

#### **5.5.25 Harvest Index**

This trait exhibited positive direct effect and significant positive association with seed yield per plant upto 180 days both at phenotypic and genotypic level. It had positive indirect effect through days to 50% flowering of primary raceme, days to 80% maturity of primary raceme, effective length of tertiary raceme, 100 seed weight of tertiary raceme and seed yield per plant up to 150 days. These results are in accordance with the findings of Ravi *et al.* (2006).

#### **5.5.26 Seed yield per plant at 120 days**

This trait exhibited positive direct effect at phenotypic level and significant positive association with seed yield per plant upto 180 days both phenotypic and genotypic level. It had indirect positive effects through days to 50% flowering of

primary raceme, days to 80% maturity of primary raceme, 100 seed weight of tertiary raceme, oil content and seed yield per plant up to 150 days.

#### **5.5.27 Seed yield per plant upto 150 days**

This trait exhibited positive direct effect and positive significant association with seed yield per plant upto 180 days both at phenotypic and genotypic level. It had positive indirect effect through days to 50% flowering of primary raceme, days to 80% maturity of primary raceme, effective length of tertiary raceme, 100 seed weight of tertiary raceme, oil content, and harvest index both at phenotypic and genotypic level.

The path analysis indicated that harvest index, seed yield per plant upto 150 days, tertiary branches per plant and 100 seed weight of primary raceme had significant direct positive association with seed yield per plant upto 180 days.

### **5.3 GENETIC DIVERGENCE**

For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses made between the parents with maximum genetic divergence would more likely yield desirable recombinants in the progenies. However, it is desirable to select suitable genetically divergent parents, based on information about the genetic variability and genetic diversity present in the available germplasm.

Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools to quantify the diversity were available. However, this is an inferential criterion and may not be useful for discrimination among the populations occupying ecologically marginal habitats.

The multivariate analysis using Mahalanobis'  $D^2$  statistic provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. Further selection of diverse parents for hybridization programme can be effective by the identification of characters responsible for the total genetic diversity among the populations (Singh and Chaudhary, 1977).

The multivariate analyses like Mahalanobis'  $D^2$  statistic and principal component analysis provide useful statistical tool for measuring the genetic diversity in a given population with respect of the characters that were considered together. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discriminations between the populations.

### **5.3.1 Mahalanobis' $D^2$ analysis**

The distribution of 54 genotypes into 9 clusters was at random with maximum number of 14 genotypes in cluster II, cluster I and cluster III are the second largest with 11 genotypes followed by cluster V (eight genotypes) cluster VIII (five genotypes), cluster VII (two genotypes).

As could be seen from the results that cluster IV, VI and IX were solitary clusters. The formation of distinct solitary clusters maybe due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity.

The distribution of genotypes indicated that the geographical diversity and genetic diversity were not related. This suggests that there are forces other than geographical seprative such as natural or artificial selection, exchange of breeding material, genetic drift and environmental variation. The results were in accordance

with the findings of Ratinaswamy and Jagathesan (1983), Bhatt and Reddy (1987), Ghatge and Kadu (1993), Venkataramaiah *et al.* (2000), Rodge *et al.* (2003), Thirmula Rao *et al.* (2005), Solanki *et al.* (2006), and Patel *et al.* (2008).

The results revealed that the traits effective length of tertiary raceme followed by days to 50% flowering of tertiary raceme, stem length to tertiary raceme and seed yield per plant at 120 days contributed maximum towards genetic divergence.

The intra and inter cluster  $D^2$  values than revealed that inter cluster  $D^2$  values were greater than intra cluster  $D^2$  values. The maximum inter cluster  $D^2$  value were observed between cluster VI and IX followed by cluster I and IX. Based on these studies crosses may be made between the genotypes of cluster VI *viz* PPL-117 and IX *viz* PPL-147 followed by clusters I *viz* , PPL-104, PPL-109, PPL-125, PPL-128, PPL-136, PCH-80, GCH-4, PPL-137, PCH-111, PPL-107, PPL-151 and IX *viz* PPL-147 to obtain new desirable recombinants in castor. Maximum intra cluster  $D^2$  value was observed in cluster VIII followed by cluster V, cluster II, cluster III and cluster VII and cluster I. The intra cluster  $D^2$  values in cluster IV, VI and IX were zero as they consists of one genotype in each cluster.

The high intra cluster distance in cluster VIII indicates the presence of wide genetic diversity among the genotypes *viz.*, PPL-129, PPL-130, PPL-139, PPL-106, Kiran, cluster mean values showed wide range among the genotypes studied, which indicates the presence of variation among the genotypes studied.

For a successful breeding program selection of genetically diverse parents is an important prerequisite so as to obtain better and desirable recombinants. Similar results were reported by Bhatt and Reddy (1987), and Sevagaperumal *et al.* (2000) in castor.

### 5.3.2 Principal Component Analysis

Results obtained from PCA on the correlation matrix of the traits reduce the dimensionality of the data set by creating five significant principal components having eigen value more than one. The PCA scores for individual genotypes were used for clustering the genotypes as suggested by Anderberg (1993). Results of PCA and cluster analysis are discussed here under.

The first seven principal components with eigen value more than one contributed to 89.39 per cent of the variability amongst 54 genotypes evaluated for 28 traits. Other principal components with eigen values less than one, which were considered non-significant and hence ignored as they are unlikely to have any practical significance. These results are in accordance with the reports of Altaher and Singh (2003) where six principal components were formed to describe the maximum variance of the data set.

The first principal component contributed maximum towards variability (69.153%). Characters *viz.*, effective length of tertiary raceme (0.42), days to 50% flowering of tertiary raceme (0.33), days to 50% flowering of secondary raceme (0.29), 100 seed weight of tertiary raceme (-0.28), explained the maximum variance in first principal component (PC 1) and signifying their importance in plant yield. Positive correlation was observed among effective length of tertiary raceme, days to 50% flowering of tertiary raceme, days to 50% flowering of secondary raceme. While 100 seed weight of tertiary raceme showed negative loading value.

The second principle component (PC 2) described 8.721 percent of contribution towards the total variability. Characters *viz.*, seed yield per plant at 120 days (-0.42), stem length to tertiary raceme (-0.41), days to 50% flowering of tertiary raceme (-0.41) and effective length of primary raceme (-0.32) showed the maximum variance in this principal component.

The third principle component (PC 3) was characterized by 5.087 percent of contribution towards the total variability. Characters *viz.*, harvest index (-0.48), stem length to tertiary raceme (0.43), stem length to primary raceme (0.35) and 100 seed weight of secondary raceme (0.29) showed maximum variance in this principal component. Stem length to tertiary raceme, stem length to primary raceme and 100 seed weight of secondary raceme were positively correlated while harvest index was negatively correlated.

The fourth principal component (PC 4) was characterized by 3.87 percent contribution towards the total variability. Characters *viz.*, days to 80% maturity of tertiary raceme (0.49), days to 80% maturity of secondary raceme (0.39), stem length to primary raceme (-0.37) and days to 50% flowering of tertiary raceme (0.25) showed the maximum variance in this principal component. Days to 80% maturity of tertiary raceme, days to 80% maturity of secondary raceme and days to 50% flowering of tertiary raceme were positively correlated while stem length to primary raceme was negatively correlated.

The fifth principal component (PC 5) was characterized by 2.56 percent contribution towards the total variability. Characters *viz.*, 100 seed weight of secondary raceme (0.45), 100 seed weight of tertiary raceme (0.43), 100 seed weight of primary raceme (0.29) and seed yield per plant up to 180 days (0.28) showed maximum variance in this principal component

The analysis thus identified the maximum contributing variables *i.e.*, days to 50% flowering of tertiary raceme, stem length to tertiary raceme, stem length to primary raceme, 100 seed weight of tertiary raceme and 100 seed weight of secondary raceme.

The PCA scores for 54 genotypes were plotted in graph to get the 2D (PCA I as X axis and PCA II as Y axis) and 3D (PCA I as X axis, PCA II as Y axis and PCA II as

Z axis) scattered diagram. The genotypes of divergent clusters like PPL-117 and PPL-147 scattered far apart in the 2D and 3D plots, while genotypes of similar clusters are placed close to each other in the centre.

### **5.3.3 Cluster analysis**

The principal component scores of genotypes were used as input for clustering procedures in order to group the genotypes into various clusters and to confirm the results of principal component analysis.

Hierarchical clustering (Ward's minimum variance) method was followed to create the tree like structure called dendrogram based on Euclidean2 distance (dissimilarity coefficients). Fifty four genotypes were grouped into eight clusters and distributions of various genotypes into various clusters were random indicating the geographical diversity and genetic diversity were not related. Among all the clusters, cluster IV and VII was the largest on containing 12 genotypes followed by cluster VIII with 10, cluster I and V with 7 each, cluster VI with 3, cluster II with 2, and cluster III with one genotype.

Of the eight clusters formed maximum intra-cluster distance Euclidean2 distance was recorded in cluster I followed by cluster VIII and cluster VII.

The maximum inter-cluster distance was observed between cluster III and cluster IV (42,169.76) followed by cluster III and clusters VI (38,651.39) and cluster III and cluster V (30,833.2). This suggested that there is wide genetic diversity between these clusters. Based on these studies, crosses can be made between genotypes of their clusters to obtain better and desirable segregants.

Results of cluster analysis based on PCA scores were compared with the results of the principle component analysis on a visual aid in desecrating clusters in the 2 D

and 3D scatter diagrams. The genotypes falling in same cluster, which were present closer to each other in scatter diagram.

Brown (1991) Altaher and Singh (2003). Karunakar Raju *et al.* (2005) and Muraleedhar *et al.* (2005) also studied the utilization of principal component analysis with clustering of Ward's method in genetic divergence studies

Out of eight clusters formed, cluster III recorded high days to 50% flowering of primary raceme, stem length to primary raceme, nodes to primary raceme, days to 80% maturity of primary raceme, days to 50% flowering of secondary raceme, days to 80% maturity of secondary raceme, days to 50% flowering of tertiary raceme, and low effective length of primary raceme, nodes to secondary raceme, total length of secondary raceme, effective length of secondary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of tertiary raceme, harvest index, seed yield per plant at 120 days, seed yield per plant up to 180 days. Cluster V recorded high seed yield per plant at 120 days and seed yield per plant up to 150 days. Cluster VIII recorded high mean values for total length of primary raceme, and high seed yield per plant up to 180 days.

Cluster V recorded high cluster mean values for yield at 120 and upto 150 days. So the genotypes present in cluster V *i.e* PPL-103, PPL-115, PPL-121, PPL-122, PPL-126, PPL-144 and PPL-151 may be used in breeding programme for higher seed yield.

#### **5.3.4 Comparative study of D<sup>2</sup> analysis, principal component analysis and cluster analysis**

Mahalanobis' D<sup>2</sup> statistic and Jackson's principal component analysis are the tools for analyzing multivariate data. The advantage of PCA over D<sup>2</sup> analysis is that it reduces the dimensionality of the data set by creating significant principal components

which contributed towards maximum variability of the genotypes. In PCA, standardization of data made attributes to contribute equally towards the divergence studies irrespective of the units taken.

The Principal component analysis sorted only significant principal components out of the only 28 attributes. The contribution of the main characters for variance easily identified by the characters loaded on the PC1 with high loading values. PCA facilitate the in-depth analysis for genetic diversity. In  $D^2$  analysis, effective length of tertiary raceme, followed by, Days to 50% flowering of tertiary raceme stem length to tertiary raceme and seed yield per plant at 120 days contributed maximum for the divergence. While in PCA the characters *viz.*, effective length of tertiary raceme, days to 50% flowering of tertiary raceme significantly loaded in PC1 and contributed more towards variability. It can be concluded that the characters which contributed more towards divergence in  $D^2$  analysis were loaded in PC1 except stem length to tertiary raceme and seed yield per plant at 120 days which showed significant high value in PC2.

The  $D^2$  analysis grouped the 54 castor genotypes into nine clusters, where as PCA grouped them into eight clusters. In  $D^2$  analysis cluster I is the largest with 14 genotypes followed by cluster I and cluster III (11 genotypes) where as in PCA, the cluster IV and cluster VII were the largest comprising of 12 genotypes each, followed by cluster VIII (10 genotypes) and cluster I and V (7 genotypes each).

The pattern of distribution of genotypes into different clusters was at random. Furthermore, the two clustering methods grouped differently and clustering pattern for genotypes are not same. There was one solitary cluster (cluster III) formed in Ward's minimum variance method, where as in case of  $D^2$  analysis cluster IV, cluster VI, and cluster IX represent solitary cluster. Genetic diversity was the outcome of several factors along with geographical diversity. Hence the selection for hybridization should be more based on genetic diversity rather than geographic diversity.

Ward's minimum variance dendrogram (cluster analysis) created sub group within a cluster, so relative position of the genotypes within the cluster can be determined by seeing the dendrogram distance. In case of  $D^2$  analysis, we can only know the intra cluster distance but not the genotypes relative position in the respective cluster.

## **Conclusions**

The following conclusions were drawn from the results and discussion on various aspects of the present study

1. Fifty four genotypes were characterized based on their morphological characters as per DUS guidelines of castor. Characters that had been used for characterization of castor genotypes were stem colour, types of inter nodes on stem, plant branching pattern, petiole colour, lamina leaf colour, bloom, type of inflorescence, colour of stigma, capsule type, spike shape, spike compactness, seed colour.
2. The studies on genetic variability indicated that the castor genotype possessed considerable genetic variability.
3. Correlation study indicated that total length of primary raceme, effective length of primary raceme, total length of secondary raceme, effective length of secondary raceme, tertiary branches per plant, nodes to tertiary raceme, stem length to tertiary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, harvest index, seed yield per plant at 120 days, and seed yield per plant up to 150 days showed significant positive association with seed yield per plant upto 180 days at both genotypic and phenotypic levels. So improvement in seed yield is possible by taking above characters in selection

scheme. Seed yield per plant at 120 days showed significant negative association with days or 50% flowering of primary raceme and days to 80% maturity of primary raceme and as well days to 50% flowering of primary raceme has significant positive association with next order 50% flowerings and days to 80% maturities which indicates decrease in 50% flowerings and 80% maturities of the castor racemes decreases the duration and gradually increase in yield at 120 days.

4. Path coefficient analysis revealed that harvest index, seed yield per plant up to 150 days, tertiary branches per plant and 100 seed weight of primary raceme exerted highest direct positive effect and positive significant association with seed yield per plant upto 180 days.
5. The results of multivariate analysis revealed that the distribution of 54 castor genotype into nine clusters in case of  $D^2$  analysis and into eight clusters in case of principal component analysis was at random indicating that the genetic diversity and geographical diversity were not related.
6. By Mahalanobis'  $D^2$  statistic, it could be inferred that the traits effective length of tertiary raceme, days to 50% flowering of tertiary raceme, stem length to tertiary raceme, seed yield per plant at 120 days, 100 seed weight of tertiary raceme and harvest index contributed maximum towards genetic divergence.
7. Principal component analysis identified five principal components (PCs) which contributed 89.39 per cent of cumulative variance. The populations with high PC 1 values were characterized by effective length of tertiary raceme, where as population with high PC 2 values were characterized by seed yield per plant at 120 days. In PC 3 character like harvest index contributed maximum weightage.

8. Agglomerative cluster analysis showed that wide genetic distances exist between cluster III and IV followed by cluster III and VI. Therefore during hybridization programme, selection of parents from these clusters will produce superior segregants.

## CHAPTER VI

### SUMMARY

The present investigation was carried out during *kharif*, 2008-2009 at Agricultural College Farm, Bapatla with 54 genotypes of castor (*Ricinus communis* L.)

Fifty four genotypes were characterized based on their morphological characters as per DUS guidelines of castor. Characters that had been used for characterization of castor genotypes were stem colour, types of inter nodes on stem, plant branching pattern, petiole colour, lamina leaf colour, bloom, type of inflorescence, colour of stigma, capsule type, spike shape, spike compactness, seed colour.

The mean, variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of yield component traits with seed yield per plant upto 180 days were studied for 28 characters *viz.*, days to 50% flowering of primary raceme, stem length to primary raceme, number of nodes to primary raceme, total length of primary raceme, effective length of primary raceme, days to 80% maturity of primary raceme, secondary branches per plant, days to 50% flowering of secondary raceme, number of nodes to secondary raceme, stem length to secondary raceme, total length of secondary raceme, effective length of secondary raceme, days to 80% maturity of secondary raceme, number of tertiary branches per plant, days to 50% flowering of tertiary raceme, number of nodes to tertiary raceme, stem length to tertiary raceme, effective length of tertiary raceme, days to 80% maturity of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, L/B ratio of seed harvest index seed yield per plant at 120 days, seed yield per plant upto 150 days and seed yield per plant upto 180 days.

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating that the data generated from the above diverse material shall represent wide variability. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficient of variation indicating the modifying effect of the environment in association with the characters at genotypic level. High PCV coupled with high GCV observed for traits days to 50% flowering of primary raceme, stem length to primary raceme, nodes to primary raceme, total length of primary raceme, effective length of primary raceme, nodes to secondary raceme, stem length to secondary raceme, total length of secondary raceme, effective length of secondary raceme, tertiary branches per plant, stem length to tertiary raceme, effective length of tertiary raceme, seed yield per plant at 120 days, seed yield per plant up to 150 days, and seed yield per plant up to 180 days. High heritability coupled with high genetic advance as per cent of mean was observed for all the traits except for days to 80% maturity of tertiary raceme, oil content, L/B ratio, harvest index indicates operation of additive gene action in the inheritance of these traits and improvement of these characters is possible through simple selection.

Correlation study indicated that total length of primary raceme, effective length of primary raceme, total length of secondary raceme, effective length of secondary raceme, tertiary branches per plant, nodes to tertiary raceme, stem length to tertiary raceme, effective length of tertiary raceme, 100 seed weight of primary raceme, 100 seed weight of secondary raceme, 100 seed weight of tertiary raceme, oil content, harvest index, seed yield per plant at 120 days, and seed yield per plant up to 150 days showed significant positive association with seed yield per plant upto 180 days at both genotypic and phenotypic levels. So improvement in seed yield is possible by taking above characters in selection scheme.

Seed yield per plant at 120 days showed significant negative association with days to 50% flowering of primary raceme and days to 80% maturity of primary raceme and as well days to 50% flowering of primary raceme has significant positive association with next order 50% flowerings and days to 80% maturities which indicates decrease in 50% flowerings and 80% maturities of the castor racemes decreases the duration and gradually increase in yield at 120 days.

Path coefficient analysis revealed that harvest index, seed yield per plant up to 150 days, tertiary branches per plant and 100 seed weight of primary raceme exerted highest direct positive effect and positive significant association with seed yield per plant upto 180 days.

The results of multivariate analysis revealed that the distribution of 54 castor genotypes into nine clusters in  $D^2$  analysis and into eight clusters in case of principal component analysis was at random indicating that the genetic diversity and geographical diversity were not related.

By Mahalanobis  $D^2$  statistic, it could be inferred that the traits effective length of tertiary raceme, days to 50% flowering of tertiary raceme, stem length to tertiary raceme, seed yield per plant at 120 days contributed maximum towards genetic divergence. Based on the intra and inter-cluster distances among the groups, suggestions were made to attempt crosses to obtain new desirable recombinants in castor between the genotypes of cluster VI and cluster IX followed by cluster I and IX.

Principal component analysis identified five principal components (PCs), which contributed 89.39 per cent of cumulative variance. The population with high PC1 values was characterized by effective length of tertiary raceme, where as population with high PC2 values were characterized by seed yield per plant at 120 days. In PC3 characters like harvest index showed maximum weightage.

Agglomerative cluster analysis showed that wide genetic distance exists between cluster III and IV followed by cluster III and VI. Therefore during hybridization programme selection of parents from these clusters will produce superior segregants. Dendrogram obtained by cluster analysis showed the sub-grouping of genotypes within the cluster which is not possible through  $D^2$  analysis.

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