

**“GENETIC VARIABILITY, CORRELATION AND PATH
ANALYSIS FOR YIELD AND ITS ATTRIBUTING
CHARACTERS IN CASTOR (*Ricinus communis* L.)”**

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BY

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**B. A. COLLEGE OF AGRICULTURE
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**GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR
YIELD AND ITS ATTRIBUTING CHARACTERS IN CASTOR**

[*Ricinus communis* L.]

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ABSTRACT

The present investigation entitled “**Genetic Variability, Correlation and Path Analysis for Yield and its Attributing Characters in Castor (*Ricinus communis* L.)**” was carried out at Agricultural Research Station, Anand Agricultural University, Sansoli during *kharif* 2020-21 in a randomized block design with three replications to analyze genetic variability, correlation coefficient and path coefficient analysis in 49 genotypes of castor. The primary objective of the research work was to know about the genetic architecture of various characters under study and their inter-relationship among them. The results revealed that ANDCI 14 is high performing genotype for seed yield based on *per se* performance. The genotype SKI 215 showed highest oil content and also was second highest in seed yield per plant out of total 49 genotypes under study.

Estimates of genotypic coefficient of variation (GCV %) and phenotypic coefficient of variation (PCV %) had been found to be high for the traits number of capsules on main raceme, plant height up to main raceme, effective length of main raceme, effective racemes per plant and seed yield per plant indicating the presence of sufficient variability for these traits. High heritability coupled with high genetic advance as per cent mean were recorded for the characters seed yield per plant, number of capsules on main raceme, plant height up to main raceme, total length of main raceme, effective length of main raceme, effective racemes per plant, 100 seed weight, shelling out turn and oil content.

Highly significant positive correlation for seed yield were found with number of capsules on main raceme ($r_g = 0.8603^{**}$ and $r_p = 0.7362^{**}$), total length of main raceme ($r_g = 0.6796^{**}$ and $r_p = 0.5650^{**}$), oil content ($r_g = 0.6026^{**}$ and $r_p = 0.6014^{**}$) and effective branches per plant ($r_g = 0.4196^{**}$ and $r_p = 0.3708^{**}$). Significantly positive correlation for seed yield was found with nodes up to main raceme ($r_g = 0.3519^*$ and $r_p = 0.1894^*$). The genotypic path coefficient analysis revealed that 100 seed weight (0.7449), nodes up to main raceme (0.7724), number of capsules on main raceme (0.6522) and total length of main raceme (0.7171) shown high and positive direct effect on seed yield.

The trait number of capsules on main raceme not only showed high values for GCV, PCV, heritability and genetic advance as per cent mean but also was highly significant and positively correlated with seed yield per plant. It also exhibited positive and high direct effect on seed yield per plant. Hence, this trait can be used for further genetic improvement and to obtain higher seed yield per plant.



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CERTIFICATE

This is to certify that the thesis entitled “**Genetic Variability, Correlation and Path Analysis for Yield and its Attributing Characters in Castor (*Ricinus communis* L.)**” submitted by **Mr. E. VIJAY KUMAR (Reg. No. 2010119032)** in partial fulfilment of the requirements for the award of the degree of **Master of Science (Agriculture)** in the subject of **Genetics & Plant Breeding** of the Anand Agricultural University, Anand is a record of bonafide research work carried out by him under my personal guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma or other similar title.

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DECLARATION

This is to declare that the whole of the research work reported here in the thesis entitled “**Genetic Variability, Correlation and Path Analysis for Yield and its Attributing Characters in Castor (*Ricinus communis* L.)**” for the partial fulfillment of the requirement for the degree of **Master of Science (Agriculture) in Genetics and Plant Breeding** by the undersigned is the result of investigation done by me under the direct guidance and supervision of **Dr. J. K. Patel**, Associate Research Scientist, Agricultural Research Station, Anand Agricultural University, Sansoli – 387 130 and no part of work has been submitted for any other degree so far.

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LIST OF ABBREVIATIONS AND SYMBOLS

%	:	Per cent
/	:	Per
°	:	Degree
°C	:	Degree Celsius
<	:	Lesser than
>	:	Greater than
AAU	:	Anand Agricultural University
AICRP	:	All India Coordinated Research Projects
ANOVA	:	Analysis of Variance
B.A.C.A.	:	Bansilal Amruthlal College of Agriculture
C. V.	:	Coefficient of Variation
CD	:	Critical Difference
cm	:	Centimeter
CRIDA	:	Central Research Institute for Dryland Agriculture
d.f.	:	Degree of Freedom
E	:	East
<i>et al.</i>	:	et all and others
<i>etc.</i>	:	Etcetera
F ₁	:	Filial generation 1
F ₂	:	Filial generation 2
Fig.	:	Figure
g	:	Gram
GA	:	Genetic Advance
GAM	:	Genectic advance as percent mean
GCV	:	Genotypic Coefficient of Variation
h ²	:	Heritability
ha	:	Hectare

<i>i.e.</i>	:	That is
ICAR	:	Indian Council of Agricultural Research
K ₂ O	:	Potassium oxide
kg	:	Kilogram
kg ha ⁻¹	:	Kilogram per Hectare
min	:	Minute
mm	:	Millimetre
N	:	North
NMR	:	Nuclear Magnetic Resonance
No.	:	Number
NS	:	Non-Significant
P ₂ O ₅	:	Phosphorus pentoxide
PCV	:	Phenotypic Coefficient of Variation
pH	:	Potential of Hydrogen
r	:	Correlation
RBD	:	Randomized Block Design
RCBD	:	Randomized Complete Block Design
r _g	:	Genotypic correlation
r _p	:	Phenotypic correlation
RRTTS	:	Regional Research & Transfer of Technology Stations
S. Em.	:	Standard Error of Mean
SD	:	Standard Deviation
Sr.	:	Serial
var.	:	Variety
<i>via</i>	:	By the means of
<i>viz.,</i>	:	Namely
Σ	:	Summation

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1. INTRODUCTION

Castor (*Ricinus communis* L., $2n = 2x = 20$) belongs to order Euphorbiales and family Euphorbiaceae. It is the sole species in the monotypic genus, *Ricinus* and subtribe, *Ricininae*. It plays an important role as industrially non-edible oilseed crop. It reproduces with a mixed pollination system which favours selfing by geitonogamy but at the same time can be an out-crosser by anemophily or entomophily (Rizzardo *et al.*, 2012).

Castor is one of the oldest cultivated crop, however it contributes to only 0.15% of the vegetable oil produced in the world. The oil produced from this crop is considered to be of importance to the global speciality chemical industry because it is the only commercial source of a Hydroxylated fatty acid. The leaves of castor contain Isoquercetin 2,5-dihydroxy benzoic acid and epicatechin. Castor oil is considered as a reputed remedy for all kinds of Rheumatic affections (Ladda and Kamthane, 2014).

Castor is found throughout India, majorly growing wild on waste land and it also cultivated for its oil seeds. It is a perennial evergreen shrub. The Sanskrit name *Erandah* describes the property of the drug to dispel diseases. It is native to Ethiopian region of tropical East Africa. Castor bean has been introduced and it is cultivated in many tropical and subtropical areas of the world, frequently appearing spontaneously. Ehiopian-East African region is believed to be the probable site of origin because of presence of great diversity in Ethiopia (Moshkin, 1986).

The basic sex forms in castor are monoecious, pistillate and interspersed staminate flower. Sex revertant is a female that turns to monecious at later stages. Environment do cause variation in the sex ratio of flowers within a variety and classified as female (winter, low temperature $< 30^{\circ}\text{C}$) and male (summer, rainy season, high temperature $> 32^{\circ}\text{C}$) promoting environments (Anonymous, 2019).

Oil content of the castor seeds ranges from 40-45% along with 12-16% proteins, 27% carbohydrates and 23-27% fibre. Dehulled varieties contain 60-70% of oil and 18-26% protein. Castor oil is unique as it contents 85-90% ricinolic acid which confers high degree of viscosity and oxidative stability, four times more stable than olive oil. Castor cake contains 6% nitrogen, 2.5% P_2O_5 and 1.5% K_2O . It contains toxic constituents, unfit

for edible purpose, so except to poultry, it cannot be fed to any animals. Castor seed contains an alkaloid called “recinine” which is extremely poisonous.

The various uses and properties of castor oil are ascribed due to the presence of fatty acid called as “ricinolic” acid. Oil is used as lubricant, because of its quality to remain as liquid at low temperature and viscous at high temperature. It is also used in paints, varnishes, textile soaps, cosmetics, nylon, pharmaceuticals, dying, and papermaking. The castor oil is associated with medicinal and veterinary use of obstetrics and dermatology. Used as laxative and a soothing medium for eye diseases, in production of printing inks and artificial leather. It is used as a source for synthetic flower scents and fruit flavours. Castor cake can be used as manure and in anti-termite products. Protein obtained from a castor seed can be used to produce distemper; oil bound water paints, casein plastics and adhesives. Along with bamboo pulp, castor stem pulp can be used for production of papers. Castor leaves can also be used in raising “eri” silkworms.

The castor growing states of India are Gujarat, Rajasthan, Andhra Pradesh, Tamil Nadu, Karnataka and Orissa. During 2019-20, 9.38 lakh ha area was under castor in India which was more by 7.02% than the previous year 2018-19. Among states, Gujarat is leading with 7.02 lakh ha under castor followed by Rajasthan 1.54 lakh ha, Andhra Pradesh 0.33 lakh ha and Telangana 0.27 lakh ha. According to Government 3rd advance estimates, all India castor production in 2019-20 is at 20.60 lakh tonnes (Anonymous, 2020).

According to the second advance estimates of the year 2020-21, Gujarat state for the castor crop has an area of 638.02 (000 ha), production of 1469.30 (000 tonnes) and yield of 2302.91 (kg/ha) (Anonymous, 2021).

The wild and semi-wild castor plants which are not cultivated were seen widespread in its centres of origin and also outside. They represent the immense variability that exists in the species. Castor had been adapted to diverse ecological niches. The ecological heterogeneity, natural selection and its interaction with other evolutionary forces including migration, mutations and genetic drift might have contributed greatly to genetic diversity according to circumstances in the natural niches. Studies on genetic diversity are necessary to explain and categorize the naturally existing variability. The genetic diversity in castor was assessed through agro-morphological

traits and to some extent by molecular techniques. The vast worldwide castor collections that have been reported were poorly studied and barely tapped for castor genetic improvement (Anjani, 2012).

Variability is the main prerequisite for selection. The selection of superior varieties is possible only when there is enough amount of variability present in the gene pool. So, magnitude of variability in gene pool is of prime most importance to take up any breeding programme. The variability present in the population should be hence measured which is possible by various statistical methods like range, SD, variance and CoV. By analysis of these methods we can know the estimates of phenotypic, genotypic and environmental variances which can be further used for estimation of respective coefficient of variation. Hence, the knowledge of variability using the parameters like GCV and PCV is most important for effective breeding programmes in crop like castor (Rukhsar *et al.*, 2018).

Heritability is used to estimate the degree of variation in a phenotypic trait of a population that resulted due to genetic variation between individuals in that population. It is used to measure the response to selection i.e. by estimating heritability of a trait we can know how well the character can be transferred from parents to progeny or from one generation to the next. Hence with knowledge of heritability in crop like castor we can go for selection of traits which have high heritability.

Genetic advance is the improvement in the mean genotype value of selected plants over the parental population. It indicates degree of gain in a character obtained under a particular selection pressure. Heritability estimates combined with genetic advance is more helpful in predicting gain under selection than using heritability estimates alone. The knowledge of these two estimates helps in selecting best genotypes from a diverse population. Hence, these estimates are included in the present study which helps in selection of variety with high yielding characters in crop like castor.

Correlation coefficient is a statistical measure which is used to find degree and direction of relationship between two or more variables. In plant breeding, it is used to measure mutual relationship between various plant characters and determine the characters based on which selection can be made for genetic improvement in yield. Hence, by using correlation coefficient in crops like castor, selection can be made for the

characters with positive and high degree of correlation with yield and its attributing characters.

Path analysis was originally developed by Wright in 1921. This technique was first used for plant selection by Dewey and Lu in 1959. It is simply a standardized partial regression coefficient analysis which splits correlation coefficient into measures of direct and indirect effects of independent variables on the dependent variable (Dewey and Lu, 1959). As path coefficient analysis partitions/divides correlation coefficient into direct and indirect effects of variables, it provides more realistic and dependable inter-relationships between the variables taken into consideration. Hence, with the help of path analysis we can identify the variables which affect the yield contributing traits in castor there by playing a main role in selection of superior genotypes from the taken population.

Objectives:

Keeping all the above facts in view, the proposed investigation has been carried out using 49 genotypes of castor with the following objectives:

- 1) Estimation of the nature and extent of variability present in genotypes with respect to seed yield and it's all traits
- 2) Estimation of genotypic and phenotypic correlations of all traits
- 3) Estimation of direct and indirect effects of various seed yield attributing characters through path coefficient analysis

2. REVIEW OF LITERATURE

Plant breeder is majorly concerned with the improvement of qualitative and quantitative traits in nature. Understanding the genetic architecture of the various characters and the inter relationship between them is necessary. A brief review of work done on variability, correlation and path coefficient analysis in castor have been presented in this chapter under the following headings:

2.1 VARIABILITY

2.2 GENOTYPIC AND PHENOTYPIC CORRELATIONS

2.3 PATH COEFFICIENT ANALYSIS

2.1 VARIABILITY

A critical estimate of genetic variability is required for initiating appropriate breeding procedures in crop improvement programmes. The variability seen in a population could be due to the genetic and environmental factors, Johanssen (1909), who explained the variation in a segregating population into heritable and non-heritable factors and variation within pure line is due to only environmental factors. Later Nelson and Ehle (1909) confirmed Johanssen's work and proved that continuous variation also confirms to Mendelian genetics.

Charles and Smith (1939) had partitioned the genetic variance from total variance by using the estimate of environmental variance in non-segregating population. Heritable variation had been further divided into additive and non-additive components and the non-additive fractions included dominance and inter allelic interaction.

Study of the variability in quantitative characters of castor was conducted by Moshkin and Sachli (1972). They had observed the high phenotypic and genotypic variation in seed weight per plant and the minimum in oil content.

Patel *et al.* (1991) had conducted an experiment to study variability in 14 genotypes of castor for ten yield components. The maximum genotypic coefficient of variability has been observed for plant height and it was followed by length of main raceme, seed yield, capsules per main raceme and 100 seed weight, indicating their importance in breeding programme for improving the crop yield.

Mehta and Vashi (1997) had studied both genotypic and phenotypic variability in 55 genotypes of castor. The phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) was found high for length of pistillate region in the main raceme, number of capsules on the main raceme and seed yield per plant showing a good scope for selection based on improvement of these characters. The close association between GCV and PCV for most of the traits showed that all variability was primarily due to genotypic differences.

Sevugaperumal *et al.* (2000) had conducted an experiment on 36 castor genotypes to estimate phenotypic and the genotypic coefficient of variation. The genotypic variation coefficient was the highest for yield/plant (29.48%) followed by number of racemes/plant (28.6%) and plant height (27.5%). The difference between phenotypic and genotypic variation coefficients was narrow (0.3) for single plant yield.

Lakshmamma *et al.* (2005) conducted an experiment to determine the genetic variation in 68 diverse germplasm lines along with hybrids and cultivars of castor. The maximum phenotypic coefficient of variation and genotypic coefficient of variation were observed for capsule weight/plant, plant height and the number of capsules. The characters viz., plant height, capsule weight, capsule number and leaf area index displayed high heritability and high genetic advance showing the predominance of additive genes in governing the traits. High heritability along with low genetic advance has been observed for inter-nodal length, stem girth, number of secondary and tertiary branches and seed yield, indicating presence of non-additive gene effects. Hence, improvement of these traits may be difficult through selection.

Golakia *et al.* (2007) conducted an experiment on 48 castor genotypes to study the genetic variation present in them. Data was recorded for days to flowering of main

raceme, days to maturity of primary raceme, plant height, nodes up to main raceme, total length of main raceme, effective length of main raceme, total number of capsules on main raceme, number of effective branches per plant, 100-seed weight and seed yield per plant. The analysis of variance indicated significant differences among the genotypes for all the characters indicating considerable amount of variation. The narrow difference between the corresponding estimates of PCV and GCV suggest that the environment had little or no role in the expression of the characters, however, the difference between these two estimates was comparatively wider for effective branches per plant, the total length of main raceme, effective length of the main raceme and seed yield per plant. The high estimates of PCV had been observed for seed yield per plant, effective branches per plant and the number of capsules on main raceme. GCV % was high for effective branches per plant, seed yield per plant and the number of capsules on main raceme. Days to maturity of main raceme, days to flowering of main raceme, number of nodes up to main raceme, 100-seed weight and plant height showed high heritability suggesting low environmental influence and high capability of the characters for transmission to subsequent generations.

Sarwar and Chaudhry (2008) conducted a study on 19 castor mutants and recorded greater than 50% heritability for all the traits but 100 seed weight and capsule weight. Number of capsules per spike and number of spikes showed strong heritability and good genetic advance specifying these traits were been governed by the additive gene action and seed yield can be improved by selection of these characters.

Rao *et al.* (2009) conducted an experiment to evaluate 60 castor genotypes for genetic variability of different traits. They found that genotypes displayed wide range of variation for all characters. The high coefficients of variation have been observed for plant height up to primary spike, test weight and seed yield per plot.

Sridhar *et al.* (2009) conducted an experiment to assess genetic variability present in four F₂ populations of castor. Phenotypic coefficient of variability was higher than the corresponding genotypic coefficient of variability for all the characters under study. High estimates of heritability along with high genetic advance as percentage of mean was observed for the plant height followed by main spike length showing the presence of

additive gene action in these traits. Number of nodes up to primary spike, 100-seed weight and seed yield per plant displayed low to moderate heritability along with low to moderate genetic advance as percentage of mean indicating the preponderance of non-additive gene action in control of these traits.

Patel *et al.* (2010) conducted an experiment to study genetic variability in 41 castor genotypes. They recorded maximum genotypic coefficient of variation and the phenotypic coefficient of variation for trait number of capsules on primary raceme, plant height, seed yield per plant and the number of effective branches per plant. The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters under study, suggesting the role of environmental variance.

Sakure *et al.* (2010) conducted an experiment to study genetic diversity among 22 castor genotypes. The contribution of each trait to total genetic variation was estimated through PCA analysis, first three principal components PCA1 (18.09), PCA2 (15.66) and PCA (11.34) were accounted for 45.09 per cent of total variation. Morphological descriptors had revealed four main clusters of genotypes. The estimation of descriptive statistics for 19 morphological traits revealed the existence of significant level (45.09%) of morphological diversity among 22 castor genotypes. Among the three principal components, maximum variation was contributed by five traits viz., seed colour, bloom, spike length, hypocotyls anthocyanin coloration and the number of nodes. The analysis of variance for quantitative traits revealed significant variation to total genetic diversity. Lowest genetic similarity was observed among the genotypes VP 1 and JI 96 suggesting that both genotypes were genetically diverse and can to be used in genetic improvement program.

Sarwar *et al.* (2010) conducted an experiment to study genetic parameters in 27 castor mutants. They observed higher genotypic coefficient of variation in spikes/plant (19.35%) followed by branches/plant (15.67%) and plant height (15.3%). The lowest GCV estimates were observed for 100 seed weight (3.0%), secondary spike length (4.3%), days to maturity (5.60%) and main spike length (5.8%). The values of phenotypic coefficient of variation (PCV) were greater than genotypic coefficient of variation. GCV was different from PCV as the maximum value was found in spikes/plant (37.2%)

followed by seed yield (30.74%), capsules on secondary spike (29.98%), branches/plant (29.8%) and capsules on main spike (26.63%). Plant height displayed high broad sense heritability (54%) along with high genetic advance (19.8) suggesting that it was governed by additive genes and days to maturity displayed high broad sense heritability (45.10%) along with low genetic advance (6.6) governed by non-additive genes.

Sridhar *et al.* (2010) conducted an experiment in 95 genotypes of castor to estimate the genetic variability present among them. Highly significant differences among genotypes were observed for the all the characters under study. Genotypic and phenotypic variances displayed wide variation for seed yield and its attributes. The GCV and PCV % were high for plant height, number of capsules/spike, effective spike length, seed yield and primary spike length. High heritability was recorded in 100 seed weight, days to 50% flowering, days to maturity, plant height and seed yield indicating additive gene action for these characters. The characters plant height, seed yield, number of capsules and effective spike length can be improved as they contain high heritability along with high genetic advance.

Patel *et al.* (2011) carried out an experiment to evaluate 11 castor inbred lines for variability and character association analysis. Analysis of variance showed significant differences among the genotypes for all traits under study. High GCV and PCV had been recorded for wilt incidence (%), seed yield per plant, stem length and number of branches per plant. Moderate heritability along with low to moderate genetic advance has been exhibited by number of capsules on primary spike and the effective raceme length.

Abimiku *et al.* (2012) conducted an experiment to determine the variability present in nine castor accessions. Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) estimates for two locations had been observed in 9 characters (leaf area, panicle length per plant, days to 50% flowering, days to 50% maturity, plant height, 100 seed weight, capsule per plant, seed yield/plant and seed yield/hectare). The estimates of broad sense heritability had ranged from 48-92% for seed yield. The 100 seed weight, the number of capsules per plant, seed yield/plant and seed yield/hectare had high genetic component which were shown by GCV of 73.08%, 78.25%, 82.59% and 58.78% respectively, while seed yield/hectare had the highest

heritability value of 92.0%. These characters had also high values for the genetic advance (GA).

Ramesh *et al.* (2012) had carried out an experiment to analyze genetic variability for yield and its components among 64 castor genotypes. The trait seed yield at 120 days after sowing exhibited highest phenotypic coefficient of variability (50.2%). The highest genotypic coefficient of variability was observed for seed yield at 150 days after sowing (49.50%).

Radhamani and Ushakumari (2013) had conducted out an experiment to assess variability present in 45 castor genotypes for nine biometrical traits along with four physiological traits. They observed that the germplasm varied significantly for all the characters under study. The estimates of phenotypic and genotypic variances were worked out for all the traits. While considering the biometrical traits, high GCV estimates were noticed for the number of capsules on primary spike, plant height, single plant yield and primary spike length.

Tewari and Kumar (2013) had studied 37 genetically diverse genotypes of castor (*Ricinus communis* L.) including two checks to identify the nature and magnitude of variability. The analysis of variance indicated that highly significant differences were present among the genotypes for all the characters under study. The highest genotypic coefficient of variation (GCV %) and phenotypic coefficient variation (PCV %) were observed for plant height, seed yield per plant and number of effective spikes per plant. The maximum and minimum heritability estimates were noted for plant height (95.70%) and oil content (32.85%), respectively. Genetic advance was high for seed yield per plant (64.47), the number of effective spikes per plant (51.23), number of nodes to primary raceme (51.23), number of capsules in primary raceme (44.62) and moderate for plant height (34.91) and the days to 50% flowering (22.18), but the estimates were low for days to maturity (11.08), 100-seed weight (14.28), volume weight (3.41) and oil content (2.46). High heritability along with high genetic advance has been observed for plant height, number of capsules on primary raceme and seed yield per plant.

Alemaw *et al.* (2014) conducted an experiment to study the phenotypic variability in Ethiopian castor accessions. The 105 accessions have been arranged in RCBD with 3

replications. The data was recorded and statistically analysed for 12 phenotypic traits. The accessions had shown a great range of variation for days to flowering (52 to 148), days to first maturity (118 to 217), days to second maturity (142 to 237), node length (2 to 32 cm), inflorescence length (13 to 74 cm), number of nodes per plant (5 to 26), plant height (89 to 356), number of branches per plant (1 to 9), number of inflorescences per plant (1 to 26), number of capsules per plant (10 to 350), number of seeds per plant (30 to 990), 100 seed weight (21 to 99 g). They found out that the number of nodes per plant followed by number of capsules and seed weight had the highest estimates of genetic coefficient of variability, heritability and genetic advance and the days to maturity of main raceme recorded low GCV, PCV and genetic advance estimates.

Patel and Patel (2014) conducted an experiment on 43 castor (*Ricinus communis* L.) genotypes to estimate variability present among them. Variability parameters were estimated for seed yield (g/plant) and yield component characters. Highest phenotypic coefficient of variability (PCV %) was displayed for the seed yield after 120 days of planting (33.53%). The highest genotypic coefficient of variability (GCV %) value was recorded for seed yield after 120 days of sowing (28.12%). The highest heritability had been recorded by seed specific gravity (90.35%) followed by the number of nodes up to primary spike (82.23%), plant height up to primary spike (76.32%), number of capsules on primary spike (70.84 %) and seed yield after 120 days of sowing (70.3%). The genetic advance as per cent of mean was highest for seed yield at 210 days after sowing (114.6%) then followed by seed yield at 180 days after sowing (78.05%), seed yield at 150 days after sowing (50.96%), number of capsules on primary spike (40.14%) and seed yield after 120 days of sowing (34.11%). The character seed yield showed high variability, heritability and genetic advance as per cent mean.

Goodarzi *et al.* (2015) analyzed genetic diversity of twelve accessions of castor. Result showed significant differences in the characters like length of stem, moist and dry weight, 100 seed weight on primary raceme, leaf area, dry weight, female flower length, male flower length, the secondary and tertiary raceme weight, oil percentage. Analysis of variances revealed significant differences among the accessions. Results pertaining to mean comparison showed that there was a great variability in main stem length among

accessions that varied from 34.1 cm (accession 2) to 69.2 cm (accession 11). Among studied accessions, accession 11 had the maximum value for main stem fresh weight and main stem dry weight traits while accession 2 possess minimum value. Mean comparison manifested that the accessions had variable female flower length which varied from 29.6 cm (accession-1) to 13.5 cm (accession-2). Also, there was a greater variability for male flower length, which varied from 14.9 cm (accession 11) cm to 4.2 cm (accession 8).

Torres *et al.* (2015) conducted an experiment to study variability parameters for oil content % in seven castor genotypes. The results displayed that the experimental coefficient of variation ranged least for the oil content (7.7%) and highest for the number of capsules on main raceme (35.0%). Genotypic coefficient of variation (GCV) varied from oil content (0.4%) to 100-seed weight (35.40%), which indicated that among the characters that are evaluated, number of capsules and 100-seed weight are the ones which showed greater variability.

Chaudhari *et al.* (2016) conducted a study in 72 castor (*Ricinus communis* L.) genotypes to estimate variability parameters for seed yield (g/plant) and yield component characters. The genotypic and phenotypic coefficient of variation has been recorded high for effective spike per plant (GCV 31.92%, PCV 33.49%) followed by the number of capsules on primary spike (GCV 25.07 %, PCV 27.64 %) and plant height up to primary raceme (GCV 23.53%, PCV 25.75%). High heritability with high genetic advance was observed for effective spikes per plant followed by effective primary spike length, plant height up to primary raceme, seed yield per plant, number of capsule on primary spike, number of nodes up to primary raceme. Effective spikes per plant had revealed high variability, heritability and genetic advance as per cent mean.

Dapke *et al.* (2016) conducted an experiment to evaluate the genetic variability present in 61 castor genotypes for eleven traits. The GCV and PCV were found to be high for the number of effective branches per plant (31.28%, and 31.07%, respectively) followed by number of capsules on main raceme (27.79%, and 28.06%, respectively) and seed yield per plant (20.78%, and 21.32%, respectively). The higher magnitude of PCV when compared with GCV for the traits under the study suggested the role of environmental variance.

Mullualem *et al.* (2017) studied phenotypic variability and association of traits among yield and yield-related traits in 48 castor (*Ricinus communis* L.) accessions. Analysis of variance showed that there was high significant difference among the accessions for maximum of the characters studied. For all traits, phenotypic coefficient of variation was greater than genotypic coefficient of variation. The difference between GCV and PCV for 100-seed weight (25% and 23% respectively) and days to second maturity (6.52% and 5.32% respectively) has been noticed to be narrow indicating a lesser extent of environmental influence.

Movaliya *et al.* (2018) had studied PCV and GCV of castor genotypes. High PCV was observed for plant height up to main raceme (35.26%), number of effective branches per plant (31.85%), seed yield per plant (26.89%) and number of capsules on main raceme (25.28%). While oil content (2.10%), days to maturity of main raceme (6.68%), shelling out turn (13.14%) and days to 50% flowering of main raceme (13.59%) had low PCV, 100-seed weight (23.98%), effective length of main raceme (23.13%), length of main raceme (20.25%) and number of nodes up to primary raceme (19.76%) showed moderate PCV. High GCV was observed for plant height up to main raceme (35.26%), number of effective branches per plant (30.35%), seed yield per plant (24.44%), number of capsules on main raceme (23.42%), 100-seed weight (22.16%) and effective length of main raceme (21.45%). While the oil content (1.75%), days to maturity of main raceme (5.63%) and shelling out turn (10.67%) had very low GCV. The length of main raceme (17.68%), number of nodes up to main raceme (16.42%) and days to 50% flowering of main raceme (12.64 %) exhibited moderate GCV.

Rukhsar *et al.* (2018) studied the variability of castor in 15 genotypes for 13 characters. The higher estimates and close values of GCV % and PCV % were observed for seed yield per plant, the number of capsules on main raceme, 100-seed weight and plant height up to main raceme offering better scope in selection as there was less environmental influence. High heritability coupled with high GA % were noticed for the characters viz., 100-seed weight , number of capsules on main raceme, seed yield per plant, plant height up to main raceme, total and effective length of main raceme which suggesting that genotypic variation for the traits is probably attributed to high additive genetic effect. Moderate heritability along with the moderate genetic advance was

observed for shelling out turn. While, low genetic advance was observed in the characters viz., days to 50% flowering with low heritability while the days to maturity and oil content having high heritability. Therefore, if selection is based on this trait it may not yield dividends in greater improvement of castor.

Alhaji *et al.* (2019) has conducted an experiment to evaluate the genetic variability among ten castor genotypes which were arranged in randomized complete block design with three replications. The analysis of variance results displayed significant differences among the genotypes for all the traits under study. The seed yield (kg/ha) was found to be ranged between 411.11 kg/ha and 1140.00 kg/ha with an average of 852.19 kg/ha. High (> 20%) genotypic and phenotypic coefficient of variations had been observed for days to 50 % flowering (26.78%, 27.22%), effective racemes per plant (47.63%, 53.93%), number of capsules on raceme (22.30%, 27.77%) and effective length of raceme (22.59%, 29%).

Nagarajan *et al.* (2019) evaluated 68 castor genotypes for studying variability. Analysis of variance revealed high significant difference for all 11 characters indicating the presence of variability within 68 genotypes studied. High PCV and GCV values were recorded for traits like plant height (34.47% and 33.84%), number of capsules on primary spike (28.74% and 28.24%), total spikes per plant (34.57% and 32.20%), 100 seed weight (20.28% and 2.12%) and seed yield per plant (39.13% and 37.30%).

Sowmya *et al.* (2019) evaluated 23 genotypes of castor from CRIDA germplasm at field conditions. Data on seed yield and its four components i.e., capsule number, number of nodes, number of branches and capsule weight were noted. The phenotypic variance was greater than the genotypic variance for all the traits. Highest phenotypic variance was recorded for the capsule number (2455.5) followed by capsule weight (1778.8) and seed yield (860.3). Lowest phenotypic variance has been observed for number of branches (3.48). Similarly the phenotypic coefficient of variation (PCV %) had been also greater than genotypic coefficient of variation (GCV %) for all the morphological and yield characters. The highest PCV % was found for the seed yield (46.14%), capsule weight (44.86%) capsule number (42.30%), number of branches (32.50%) and number of nodes (23.85%). High heritability has been recorded for seed

yield (99.1%), capsule weight (99.4%), capsule number (99.4%), number of nodes (84.1%) and moderate heritability has been observed for number of branches. Genetic advance as percent of mean (GAM) was highest for capsule number (115.57%), seed yield (94.17%), capsule weight (91.88%), number of nodes (41.22%) and number of branches (30.48%). High heritability coupled with high GAM was observed for capsule weight, capsule number, number of nodes and seed yield. Moderate heritability (45.8 %) with high GAM (30.4 %) was observed for number of branches.

Patel *et al.* (2020) evaluated 60 castor genotypes for the assessment of genetic variability, heritability and genetic advance as percent mean with respect to 9 characters. High GCV and PCV were recorded for the traits viz., number of capsules on primary raceme, seed yield per plant, number of branches per plant, plant height and total length of raceme. High heritability has been recorded in all the traits. The heritability value displayed the presence of additive gene action and further improvement in these traits would be effective through direct selection. High genetic advance had been recorded for the traits viz., number of capsules, seed yield per plant, effective raceme length, number of branches per plant, plant height up to the primary raceme and total raceme length indicating that these characters are governed by additive gene action and simple phenotypic selection will be rewarding for the improvement of these characters.

2.2 GENOTYPIC AND PHENOTYPIC CORRELATIONS

The concept of correlation coefficient was first given by Galton (1889) which was later elaborated by Fisher (1918).

Dorairaj *et al.* (1973) using 6 inbreds and their 15 F_1 's, worked out correlations among characters within the same generation in 6 inbred and in F_1 's derived from them. Within inbred lines, yield has been positively correlated with length of main raceme, total number of capsules per plant and the length of pistillate region of raceme. But it was negatively associated with days to flowering, duration of the crop and number of nodes on main stem. Within F_1 's yield has been positively correlated with the length of main raceme, number of branches and total number of capsules per plant but negatively correlated with days to first flowering, height of the main stem and number of nodes on main stem.

Mehta and Vashi (1998) carried studies on yield correlations in eleven morphological traits in ten castor genotypes and their 45 hybrid. Result revealed that the seed yield per plant had been strongly and positively correlated with length of main raceme, number of capsules on main raceme, length of pistillate region on main raceme and seed yield per main raceme at genotypic and phenotypic levels.

Ramesh *et al.* (2001) conducted an experiment to study correlation for eight characters in 64 crosses of castor. The genotypic and phenotypic correlation values among yield and its attributes showed that the genotypic correlations were greater than the respective phenotypic correlations in all cases. Seed yield showed significant positive association at phenotypic level with the plant height up to primary spike (0.281**), nodes up to secondary spike and effective length of primary spike. Yield per plant had also showed positive but non-significant correlation with the days to maturity and effective spikes per plant.

Kumar *et al.* (2003) conducted an experiment to assess the correlation for yield and its attributing traits in nineteen castor genotypes. Phenotypic and genotypic correlation of yield was significantly positive with the days to 50% flowering, number of capsules, days to maturity and number of racemes per plant while, length of primary spike had significantly positive association at genotypic level.

Manivel and Manivannan (2005) carried an experiment to evaluate 79 genotypes of castor crop under different environmental conditions. Phenotypic correlation coefficient between seed yield and yield components showed that the number of first order branches per plant, number of second order branches per plant, effective length of primary spike, number of spikes per plant, number of capsules per plant and 100-seed weight were significantly and positively correlated with seed yield in all four environments demonstrating their direct role as seed yield component characters.

Golakia *et al.* (2007) conducted an experiment to study correlation between yield and its attributing traits of 48 castor accessions laid out in randomized complete block design with two replications. They results showed that the total length of main raceme, effective length of main raceme and the number of capsules on main raceme has been significantly and positively correlated with seed yield per plant and also among each

other at both genotypic (0.408, 0.399, 0.306, respectively) and phenotypic (0.381, 0.369, 0.265, respectively) levels. This indicated that selection for these characters would lead to improvement in yield. The effective length of main raceme and effective branches per plant were observed to have significant but negative correlation at genotypic level with days to flowering (-0.338, -0.393, respectively) and maturity of main raceme (0.000, -0.071, respectively). This could delay the yield improvement to some extent as the effective length of main raceme had correlated significantly with the seed yield per plant. The 100-seed weight has been found to be independent for seed yield per plant.

Anjani (2008) studied 23 accessions and four checks of castor genotypes. Variance components for 14 traits and correlation coefficients were worked out. Significant genotypic differences had been observed for the traits number of days to 50% flowering, main stem nodes and days to maturity. The results exhibited significant and high positive correlations with each other and low associations with yield and its components. Yield exhibited moderate associations with its components except the 100-seed weight. Cluster analysis grouped the entries into four groups. All 23 accessions displayed stable performance for extra-early maturity. Accessions were identified for high yield, high oil content and high per day productivity.

Gogoi *et al.* (2009) conducted an experiment to study 22 indigenous castor bean genotypes to determine the genotypic and phenotypic correlations. The results showed significant and positive correlations of leaf yield per plant with the leaf area, leaf moisture content, capsules per raceme, raceme length and weight per 100 seeds. The quantitative traits displayed significant and positive correlation coefficients. Leaf yield also displayed significant and positive correlation coefficients among all traits except between leaf moisture content and weight per 100 seeds at genotypic and phenotypic levels

Adeyanju *et al.* (2010) carried out an experiment to study the relationship between oil yield and seven agronomic characters of 28 castor genotypes laid out in randomized complete block design with three replications. The highest positive genotypic correlation had been found between the traits 100 - seed weight and oil percentage ($r = 0.89$), while the significant negative genotypic correlation was found between the traits

days to 50% germination and 100 - seed weight (-0.76). The study revealed that all the traits under study, days to 50% flowering, fruit yield, days to maturity, 100- seed weight, pedicel length and plant height are significantly and positively correlated with the trait oil yield per plant at both phenotypic and genotypic level. The study suggests that oil yield could be improved through selection for the above mentioned yield components.

Dhedhi *et al.* (2010) conducted an experiment to evaluate 29 castor genotypes in randomized block design with three replications to study the correlation between ten quantitative traits in crop grown under irrigated conditions. They observed that the values of genotypic correlation coefficient were higher than those of phenotypic correlation coefficient, indicating the traits studied are under environmental influence. The study displayed that seed yield per plant had positive significant genotypic and phenotypic correlations with 100-seed weight (0.549) and length of primary spike (0.540) while, days to 50 % flowering exhibited negative non-significant correlation with seed yield (-0.73).

Patel *et al.* (2010) conducted an experiment to evaluate 41 castor genotypes for assessment of the correlation in nine characters under study. The results displayed positive and significant correlations between plant height with length of primary raceme, effective branches per plant, number of capsules on primary raceme, 100-seed weight, seed yield per plant and oil content; days to 50% flowering with days to maturity, plant height, length of primary raceme, number of capsules on primary raceme, 100-seed weight; days to maturity with length of primary raceme, plant height, total number of capsules on primary raceme, 100-seed weight; length of primary raceme with 100-seed weight, total number of capsules on primary raceme and seed yield per plant; number of capsules on primary raceme with the 100-seed weight and seed yield per plant.

Rodrigues *et al.* (2010) estimated phenotypic, genotypic and environmental correlations among traits in castor and recorded that there has been positive phenotypic correlation between node number and stem height, stem height and the plant height, stem diameter and 100-seed weight, plant height and stem diameter. There was also positive environmental correlation among stem height and plant height.

Sridhar *et al.* (2010) conducted an experiment in 95 genotypes of castor to assess the correlation among yield and its attributing characters. The results indicated that primary spike length, number of capsules and effective spike length are important productive yield attributing characters as they displayed strong and positive association with seed yield per plant. The characters days to maturity and number of nodes up to main raceme showed significant and positive correlation with seed yield per plant indicating the importance of late maturity and high node number for higher seed yield per plant.

Abimiku *et al.* (2012) carried out an experiment to determine the character association between fourteen yield and yield attributing characters of nine castor genotypes arranged in randomized complete block design with three replications. They noted that days to 50% flowering had highly positive correlation ($r = 0.496^{**}$) with days to 50% maturity and days to 50% maturity displayed a highly positive correlation ($r = 0.393^{**}$) with 100-seed weight but had negative correlation (-0.318) with seed yield. This analysis showed that the accessions that mature early had comparatively lower seed weight and higher seed yield than those that mature late.

Ahmed *et al.* (2012) conducted an experiment to study correlations and other genetic parameters for the seed yield and its contributing traits in M_4 and M_5 generations of gamma irradiated castor. Phenotypic correlation analysis for the M_4 generation showed that days to maturity had positive and highly significant correlation with plant height (0.6479), while main spike length exhibited positive and highly significant correlation with number of capsules (0.5816). Capsule yield had significant and positive correlation with seed yield (0.4555). Number of spikes per plant also displayed positive association with seed yield. The studies on M_5 generation showed that number of capsules of main spike had highly significant and positive correlation with length of spike (0.8247). The number of spikes per plant had positive and significant association with capsule yield (0.5509). Capsule yield showed a positive and significantly high correlation with seed yield (0.8131). Number of spikes per plant displayed significantly positive correlation with the seed yield (0.486).

Shah *et al.* (2013) conducted an experiment to evaluate 18 castor (*Ricinus communis* L.) genotypes (hybrids/varieties/parental lines) for seed, oil quality and fatty acid profile. Maximum 100 seed weight (37.70 g) had been observed for 48-1 genotype and maximum oil content (50.70%) had been recorded by SKP 84 pistillate line. Hundred seed weight exhibited a positive correlation with kernel % ($r=0.472^*$) and seed oil content displayed positive correlation with kernel oil content ($r=0.664^{**}$).

Tewari and Kumar (2013) conducted character association study in 37 genetically diverse genotypes consisting of two checks i.e. Chandraprabha and T-3. They observed that number of capsules on primary raceme and the number of effective spikes per plant exhibited highly significant and positive correlation with seed yield.

Tewari and Mishra (2013) studied the relationship between castor seed yield and eight agronomic traits in 30 castor genotypes arranged in completely randomized block design with three replications. The highest positive genotypic correlations observed for seed yield were with number of capsules in primary raceme (1.019^{**}) and number of effective spikes per plant (0.965^{**}). Seed yield per plant also displayed positive and significant association with 100 seed weight and oil content at genotypic level (0.262^* and 0.287^{**}) while, it was negatively correlated with number of nodes to primary raceme and days to maturity (0.274^{**} and 0.319^* respectively). Oil content had significant and positive association with number of capsules in primary raceme at both genotypic and phenotypic levels while, number of effective spikes per plant at genotypic level only. The number of capsules indicated a positively significant correlation with effective spikes per plant and 100 seed weight.

Kanti *et al.* (2015) conducted an experiment to assess genotypic correlations between 18 agro-morphological traits. Plant height showed high significant positive correlation with number of nodes on the main stem. Both number of nodes and plant height showed highly significant positive associations with days to 50% flowering, days to maturity and seed yield per plant after 150 days of planting, while it had high negative correlation with the length of primary raceme with capsules and number of secondary racemes per plant. Days to 50% flowering exhibited significant high positive association with days to maturity. The trait days to maturity exhibited highly significant positive

correlation with 100-seed weight and seed yield at 150 days after planting. Days to maturity exhibited a low positive significant correlation with total seed yield per plant and days to 50% flowering showed significant negative correlation with seed yield at 120 days after planting. Correlations between total seed yield per plant and the seed yield per plant after 120, 150, 180 and 210 days of planting were found significant and positive. Oil content showed no significant correlation with seed weight, days to maturity and days to 50% flowering.

Dapke *et al.* (2016) conducted an experiment to study the correlation for ten quantitative characters in 61 genotypes of castor (*Ricinus communis* L.) laid out in randomized block design with three replications under irrigated conditions during *rabi* season. Correlation studies displayed that seed yield had positive significant genotypic and phenotypic correlations with plant height, total length of primary spike, number of effective branches per plant, length of capsule bearing region of primary spike, the number of capsules on primary spike and oil content indicating the importance of the component traits for yield. Only the trait number of nodes up to primary spike displayed significant negative correlation with seed yield. The trait number of capsules on primary spike had displayed positive and significant genotypic correlation with 100-seed weight and length of capsule bearing region of primary spike, while it showed significant negative genotypic and phenotypic correlation with the trait number of nodes up to primary spike.

Mullualem *et al.* (2017) studied association of traits among yield and yield-related traits in castor (*Ricinus communis* L.) accessions. A total of 48 castor accessions were evaluated. The results showed that seed yield had positive and significant phenotypic and genotypic association with number of capsules, number of seeds per plant, length of inter node, number of primary branches per plant, number of secondary branches per plant and number of inflorescence per plant. Oil content had showed positive and significant genotypic correlation with seed yield. Seed yield was highly positively and significantly correlated with number of primary branches per plant ($r = 0.488$), number of seeds per plant ($r = 0.413$), number of secondary branches per plant ($r = 0.376$) and length of inter node ($r = 0.279$). It was weakly but positively correlated with number of capsules per plant ($r = 0.318$) and number of inflorescence per plant ($r = 0.180$).

Movaliya *et al.* (2018) studied correlation and variability for the seed yield and its attributes in castor. The results revealed that there was significant positive correlation of seed yield per plant and number of capsules on main raceme, total length and effective length of main raceme and oil content. Seed yield per plant exhibited highly significant and positive correlations at both genotypic and phenotypic levels with total length of main raceme ($r_g = 0.501$, $r_p = 0.455$), effective length of main raceme ($r_g = 0.520$, $r_p = 0.488$) and number of capsules on main raceme ($r_g = 0.459$, $r_p = 0.426$). Oil content ($r_g = 0.306$, $r_p = 0.241$) had also displayed positively significant correlation with seed yield per plant at genotypic level while it was non-significant at phenotypic level indicating that these characters were influencing more on seed yield and could be useful in improvement of seed yield.

Sowmya *et al.* (2019) conducted an experiment to study the correlation among seed yield and its attributing traits for 23 castor genotypes of CRIDA under rain-fed conditions in alfisols. The study showed that seed yield has been highly significant and positively correlated at genotypic and phenotypic level with capsule weight (0.985 ** and 0.979**) and the capsule number (0.930** and 0.924**). Capsule weight and capsule number had also exhibited significant positive correlation among each other (0.965** and 0.959**).

Mohanty *et al.* (2020) conducted a field experiment during *kharif* 2018 with fifteen genotypes of castor at AICRP on Castor, RRTTS, Odisha to study the relationship between castor seed yield with its nine component traits. Among the nine traits, oil content, number of effective spikes/plant, number of capsules per primary spike and plant height showed significant positive correlation with seed yield per plant at genotypic and phenotypic level, suggesting possibility of improving these characters simultaneously. Number of capsules on primary raceme showed positive and significant association with effective length of primary spike. Highly positive phenotypic correlations on seed yield per plant were exhibited by the number of capsules per primary spike, oil content and the number of effective spikes per plant.

2.3 PATH COEFFICIENT ANALYSIS

The concept of partitioning of correlation into direct and indirect effects through path analysis was originally developed by Wright (1921) and later the technique was first used for plant selection by Dewey and Lu (1959).

Sachli (1986) carried out an experiment to study the associations between seed yield per plant and two groups of yield associated traits. The principal and indirect selection criteria were established. Main yield determining character was number of seeds per plant. Despite their correlation with yield, the traits seed yield from central inflorescence, plant height and the number of lateral inflorescences only influenced yield per plant indirectly.

Mehta and Vashi (1998) carried out studies on yield correlations in eleven morphological characters in ten castor genotypes and their 45 hybrid. Result revealed that length of main raceme exhibited the maximum direct effect on seed yield per plant which was followed by number of capsules in main raceme, seed yield and 100 seed weight. It was observed that the emphasis should be given to these characters in breeding to obtain high yielding genotypes of castor.

Sevugaperumal *et al.* (2000) had conducted an experiment on 36 castor genotypes to estimate path coefficient. The results displayed that days to 50% flowering showed the highest direct effect on seed yield. Number of nodes up to primary raceme exhibited the negative direct effect on seed yield. Plant height, number of nodes up to primary raceme and number of capsules in primary raceme had significant indirect effect on days to 50% flowering. Yield was indirectly influenced by the traits number of capsules on the primary raceme, days to 50% flowering and number of racemes per plant.

Ramesh *et al.* (2001) conducted an experiment to study path coefficient for eight characters in 64 crosses of castor. The analysis displayed that plant height showed direct effect on yield at both phenotypic and genotypic levels. The trait 100 seed weight showed a negative direct effect on yield at genotypic level and positive direct effect at phenotypic level.

Kumar *et al.* (2003) conducted an experiment to study path coefficient analysis in nineteen castor genotypes. The results revealed that days to 50% flowering has more direct effect on the seed yield. This was followed days to maturity, total number of capsules on primary raceme, 100 seed weight and number of racemes per plant. The trait number of nodes up to primary raceme displayed negative direct effect on seed yield. They observed that days to 50% flowering, plant height, days to maturity, number of racemes per plant and number of capsules on primary raceme showed negative indirect effect on the seed yield through number of nodes up to primary raceme.

Lakshmamma *et al.* (2005) conducted an experiment to study path coefficient analysis in 68 diverse lines along with hybrids and cultivars of castor. The results revealed that effective length of the tertiary spike exhibited the highest direct effect towards seed yield per plant followed by total dry matter, capsule weight per secondary spike, total number of capsules per primary spike and the capsule weight per tertiary spike.

Golakia *et al.* (2007) has investigated about path coefficients of 48 castor accessions laid in randomized complete block design with two replications. The results revealed that the total length of the main raceme had the highest and positive direct effect followed by days to flowering of main raceme. Where, highest and negative direct effect was expressed by effective length of main raceme followed by days to maturity of main raceme. The direct effects of remaining characters were found negligible.

Ramanjaneyulu and Reddy (2012) carried studies on path coefficient analysis in *rabi* castor. The result displayed that the traits number of spikes per plant, total number of effective spikes per plant, the primary spike length, effective spike length, nodes per plant and number of branches per plant showed positive direct effects coupled with positive genotypic correlation with seed yield of castor. Therefore, direct selection of these yield attributing characters might be helpful to enhance the yield of *rabi* castor which is grown under irrigated conditions.

Chaitanya *et al.* (2013) studied correlation and path analysis among yield and yield attributing traits in 30 genotypes of castor. Path analysis displayed that oil yield per plant, number of capsules on main spike, 100 seed weight, effective length of main spike,

the number of nodes up to main spike and days to 50% flowering exhibited the direct influence for seed yield in castor.

Tewari and Mishra (2013) carried an experiment to observe the path coefficient analysis of eight agronomic characters in 30 castor genotypes arranged in completely randomized block design with three replications. The results revealed that capsules on primary raceme had significant positive direct path coefficient with seed yield. The direct effect of plant height up to primary raceme, number of nodes up to primary raceme, days to maturity of spike and 100 seed weight were observed to be negatively associated. Number of capsules on the primary raceme with the highest genotypic correlation coefficient with seed yield per plant (0.540) and the days to 50% flowering showed the highest direct path coefficient with seed yield per plant (0.568). The highest indirect effect of number of capsules on primary raceme was *via* number of effective spikes per plant (0.537). The highest total indirect effect (0.964) was *via* number of capsules on primary raceme which was followed by indirect effect of number of effective spikes per plant *via* number of capsules on primary raceme (0.505).

Torres *et al.* (2015) conducted experiment to evaluate path coefficient analysis of morphological description on oil content of the seven castor genotypes. The result displayed that the direct and indirect selection of genotypes with stem diameter, plant height, number of branches and seed weight is promising to select genotypes containing high oil content.

Dapke *et al.* (2016) conducted an experiment to study the correlation and path analysis for ten quantitative characters in 61 genotypes of castor (*Ricinus communis* L.) laid out in randomized block design with three replications under irrigated conditions during *rabi* season. The results revealed that traits plant height up to primary spike (0.027), number of node up to primary spike, (0.039), days to maturity (0.08), total length of primary spike (0.054) and 100-seed weight (0.06) exhibited positive low direct effects on seed yield. While, length of capsule bearing region of primary spike (-0.043) and days to 50% flowering of primary spike (-0.117) exhibited negative low and high direct effects on the seed yield respectively.

Nagarajan *et al.* (2019) evaluated 68 castor genotypes for studying path coefficient analysis. The results displayed that total number of spikes showed highest positive total indirect effect (0.386) *via* days to 50% flowering, primary spike length and days to 50% maturity. Number of capsules on primary spike showed second highest positive total indirect effect (0.366) *via* plant height, seed weight and number of nodes up to primary spike. Effective length of the primary spike showed positive indirect effect (0.225) *via* plant height, number of nodes up to primary spike, number of capsules on primary spike and 100 seed weight. Oil content exhibited positive total indirect effect (0.224) *via* number of capsules on primary spike, days to 50% maturity, plant height, effective length of primary spike, total number of spike and 100 seed weight. Primary spike length shows positive total indirect effect (0.209) *via* effective length of primary spike, days to 50% maturity, plant height, number of nodes up to the primary spike, number of capsules and 100 seed weight. The traits 100 seed weight, plant height and number of nodes up to the primary spike exhibited positive indirect effects (0.186, 0.164 and 0.143 respectively). The traits days to 50% flowering and days to 50% maturity exhibited negative total indirect effect (-0.028 and -0.013 respectively). But the negative total indirect effect was low and negligible.

Mohanty *et al.* (2020) conducted an experiment during *kharif* 2018 with 15 genotypes of castor at AICRP on Castor, RRTTS, Odisha to study path coefficient analysis of nice component traits on seed yield and among them. The results of path coefficient analysis displayed that the trait number of capsules per primary spike had shown higher positive direct effect on seed yield. Since the number of capsules in primary spike, oil content and number of effective spikes per plant were showing high positive correlations with seed yield per plant and also having higher positive direct effect on seed yield. These three characters can be used as the selection criteria in breeding for obtaining higher seed yield in castor.

Yamanura and Kumar (2020) conducted an experiment to study path coefficients in 33 genotypes [20 hybrids, 12 parents and a check (ICH-66)]. Path coefficient analysis directed that the number of effective spikes per plant (0.883) exhibited positive direct effect on seed yield per plant followed by 100 seed weight (4.929). Hence these traits

could be directly attributed for the improvement of seed yield and would be important in the selection of better genotypes.

3. MATERIALS AND METHODS

The present investigation was conducted to assess the genetic variability, correlation and path coefficient analysis in castor. The study has been carried out at Agricultural Research Station, Anand Agricultural University, Sansoli during *kharif* 2020-21. Sansoli is situated at 22°81' N Latitude and 72°75' E Longitude with an elevation of 33 meters above the mean sea level. The soil of experiment site is sandy loam, the typical “goradu” and alluvial in origin. Maximum and minimum temperature was recorded around 41.90 °C and 15.90 °C, respectively. The climatic condition of the area represents the sub-tropical with semi-arid climate. Sansoli receives rainfall around 293 to 1658 mm with average precipitation of 744 mm.

3.1 EXPERIMENTAL MATERIAL

The experimental material consisted of 49 genotypes of castor (*Ricinus communis* L.) representing different geographic origin (Table 3.1). The pure seeds of these genotypes were obtained from various research stations.

3.2 EXPERIMENTAL DETAILS

Forty nine genotypes of castor were sown in a randomized block design in three replications during *kharif* 2020-21. Each line was sown in a single row plot of 6.0 m length with spacing of 120 x 60 cm. The genotypes had been randomly allotted to the plots in each replication. The experiment was surrounded by two guard rows to avoid damage and border effect. All the recommended agronomical practices along with necessary plant protection measures were followed timely for the successful raising of crop.

3.3 CHARACTERS STUDIED

Five competitive plants were randomly selected from each experimental unit in all the replications and were used to record the observations for seed yield as well as its components characters excluding days to 50% flowering and days to maturity. The traits days to 50% flowering and days to maturity had been recorded on plot basis.

Mean values were computed and used for the statistical analysis. The following observations were recorded:

(1) Days to 50% flowering of main raceme

Days were counted on plot basis from the date of sowing to the date on which main raceme of 50% plant attain approximately 3 to 5 cm length.

(2) Days to maturity of main raceme

Days required to reach the physiological maturity of main raceme from date of sowing were calculated.

(3) Nodes up to main raceme

The total number of nodes from cotyledonary node to the base of main raceme had been counted at the time of maturity.

(4) Plant height up to main raceme (cm)

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

(5) Total length of main raceme (cm)

The length from originating node to apex of the main raceme were measured in centimeters at the time of maturity and considered as total length of main raceme.

(6) Effective length of main raceme (cm)

The length of capsule bearing part of main raceme was measured in centimeters at the time of maturity.

(7) Number of capsules on main raceme

The total number of capsules born on main raceme was counted at the time of maturity.

(8) Effective branches per plant

The total number of branches bearing raceme was counted and recorded at the time of maturity.

(9) 100 seed weight (g)

Random sample of 100 - seed was taken from each plant and the weight of the each sample was recorded in grams.

(10) Shelling out turn (%)

A well mixed 100 g capsules weighed on electronic balance from each plant was manually threshed and shelling outturn was calculated.

(11) Seed yield per plant (g)

The entire effective branches per plant were threshed together and cleaned-dried seed were weighed in grams on electronic balance.

(12) Oil content (%)

Oil content was estimated by Nuclear Magnetic Resonance (N.M.R.) technique. For this a random sample of fifty grams of seed was used from bulk seed of each genotype in each replication.

Table 3.1 List of genotypes and their source used in present study

Sr. No.	Genotypes	Source
1	48-1	IIOR, Hyderabad
2	DCS 100	
3	DCS 103	
4	DCS 105	
5	DCS 109	
6	DCS 119	
7	ANDCI 8	RRS, AAU, Anand
8	ANDCI 9	
9	ANDCI 14	
10	ANDCI 10-01	
11	ANDCI 10-05	
12	ANDCI 10-12	
13	JI 35	JAU, Junagadh
14	JI 244	
15	JI 340	
16	JI 357	
17	JI 368	
18	JI 390	
19	JI 397	
20	JI 417	

21	JI 421	JAU, Junagadh
22	JI 424	
23	JI 428	
24	JI 437	
25	JI 440	
26	JI 442	
27	JI 446	
28	JI 448	
29	MI 1	ARS, Mandor
30	MI 2	
31	MI 4	
32	MI 10	
33	MI 16	
34	MI 27	
35	MI 33	
36	SH 10	SDAU, Sardarkrushinagar
37	SKI 64	
38	SKI 90	
39	SKI 215	
40	SKI 315	
41	SKI 322	
42	SKI 346	
43	SKI 351	
44	SI 3	ARS, AAU, Sansoli
45	SI 4	
46	SI 5	
47	SI 8	
48	SI 9	
49	SI 14	

3.4 STATISTICAL ANALYSIS

The data obtained from the germplasm with respect to the various traits mentioned above were statistically analyzed for the various parameter viz., genetic variability, genotypic and phenotypic correlation and path coefficient analysis by following methods:

- 3.4.1 Analysis of variance
- 3.4.2 Variability parameters
- 3.4.3 Correlation
- 3.4.4 Path analysis

3.4.1 Analysis of Variance

The analysis of variance for randomized block design (RBD) was done for each character as per Panse and Sukhatme (1985). The statistical model to be used for analysis of variance is based on the following linear model.

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} =Yield of i^{th} genotype in j^{th} replication

μ = General mean

g_i = Effect of i^{th} genotype

r_j = Effect of j^{th} replication

e_{ij} = Uncontrolled random error associated with i^{th} genotype in j^{th} replication

Table 3.2 ANOVA for Experimental Design

Source of variation	df	M.S.S.	Expected Mean Square
Replication	(r-1)	MS_r	$\sigma_e^2 + g \sigma_r^2$
Genotypes	(g-1)	MS_g	$\sigma_e^2 + r \sigma_g^2$
Error	(r-1) (g-1)	MS_e	σ_e^2
Total	(rg-1)		

Where

r = number of replications

g = number of genotypes

Significance of replication mean sum of square (MS_r) and genotype mean sum of square (MS_g) was tested against error mean sum of square (MS_e).

3.4.2 Variability Parameters

The phenotypic, genotypic and error variance were estimated as follows:

$$\sigma_e^2 = M_e$$

$$\sigma_g^2 = (MS_g - MS_e)/r$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,

r = Number of replications

g = Number of genotypes

MS_g = Mean sum of square due to genotype

MS_r = Mean sum of square due to replication

MS_e = Mean sum of square due to error

σ_e^2 = Error variance

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

The standard error of mean (S.E.m.) was calculated using following formula:

$$S.E.m. = \sqrt{\frac{\sigma_e^2}{r}}$$

The critical difference (CD) for comparing mean of any two genotypes was computed using following formula:

$$C.D. = S.E.m. \times \sqrt{2} \times t_{0.05}$$

Where,

‘t’ = Table value of ‘t’ at 5% level of significance and error degree of freedom.

The coefficient of variation (CV) was determined as per under

$$\text{Coefficient of variation (C.V. \%)} = \frac{\sqrt{\sigma_e^2}}{\bar{X}} \times 100$$

Where,

$\bar{X}$ = mean of the characters

3.4.2.1 Phenotypic coefficient of variation,

Phenotypic coefficient of variation will be used to measures the magnitude of phenotypic variation present in a particular character and was estimated by the formula suggested by Burton (1952).

$$\text{Phenotypic coefficient of variation} = \text{PCV (\%)} = \frac{\sqrt{\sigma_p^2}}{\bar{X}} \times 100$$

Where,

σ_p^2 = Phenotypic variance

$\bar{X}$ = General mean

3.4.2.2 Genotypic coefficient of variation,

Genotypic coefficient of variation measures the magnitude of genotypic variation present in a particular character and was estimated as per the formula suggested by Burton (1952).

$$\text{GCV (\%)} = \frac{\sqrt{\sigma_g^2}}{\bar{X}} \times 100$$

Where,

σ_g^2 = Genotypic variance

$\bar{X}$ = General mean

GCV and PCV were classified as suggested by Sivasubramanian and Madhavmenon (1973)

Table 3.3 GCV and PCV classification

S. No	Classification	Range
1	Low	Less than 10%
2	Moderate	10 – 20%
3	High	More than 20%

3.4.2.3 Heritability (Broad sense)

Heritability in broad sense, which is the ratio of genotypic variance (σ_g^2) and phenotypic variance (σ_p^2) are calculated by using the formula suggested by Allard (1960).

$$\text{Heritability } (h_b^2) = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

h^2 = Heritability percentage in broad sense.

σ_g^2 = Genotypic Variance and

σ_p^2 = Phenotypic Variance.

Heritability values are categorized as low, moderate and high (Robinson *et al.*, 1949) and are given below.

Table 3.4 Classification of heritability estimates

S. No	Classification	Range
1	Low	Less than 30%
2	Moderate	30 – 60%
3	High	More than 60%

3.4.2.4 Genetic advance (GA)

The expected genetic advance at 5% selection intensity was estimated as

per the formula suggested by Allard (1960).

$$GA = k \times \sigma_p \times h^2_{(b)}$$

Where,

GA = Genetic advance under selection

K = Selection differential (value of k at 5% selection intensity is 2.06)

σ_p = Phenotypic standard deviation

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

3.4.2.5 Genetic advance as percent of mean (GA as % mean)

The genetic advance expressed as per cent of mean was calculated as under:

$$\text{Genetic advance \% of mean} = \frac{\text{Genetic advance (GA)}}{\text{Mean of character } (\bar{x})} \times 100$$

Where,

$\bar{X}$ = General mean

The estimates of genetic advance were classified as (Johnson *et al.*, 1955) low, moderate and high as stated below.

Table 3.5 Classification of estimates of genetic advance

S. No	Classification	Range
1	Low	Less than 10%
2	Moderate	10-20%
3	High	More than 20%

3.4.3 Correlation

It is the degree of association of the trait with yield as well as traits which

attribute the yield. It was calculated as per the procedure given by Singh and Chaudhary (1977).

$$r_p = \frac{\text{Covariance X.Y.(P)}}{\sqrt{\text{Variance X(P).Variance Y(P)}}}$$

Where,

r_p = Phenotypic correlation between character X and Y

$$r_g = \frac{\sigma_{gij}}{\sqrt{\sigma_{gi}^2 \sigma_{gj}^2}}$$

Where,

r_g = Genotypic correlation between character X and Y

Correlation Coefficients between Different Parameters

The procedure used for estimating covariance components between different pairs of observations was the same as that for analysis of variance, except that the sum of square and mean square were replaced by sum of products and mean products, respectively. The different estimates of covariance were determined according to the method specified by Galton (1889) and reviewed by Singh and Chaudhary (1985).

σ_{gij} = Genotypic covariance between i^{th} and j^{th} character

σ_{pij} = Phenotypic covariance between i^{th} and j^{th} character

$\sigma_{pij} = (\sigma_{gij} + \sigma_{eij})$

σ_{eij} = Environmental covariance between i^{th} and j^{th} character

The estimates of covariance and variance were used in computing genotypic and phenotypic correlation coefficient.

Table 3.6 Analysis of co-variance with expected mean sum of cross products

Sources of variation	Degree of freedom	Sum of cross products	Mean sum of cross products (MSCP)	Expected mean sum of cross products
Replications	(r-1)	SCP _r	MSCP _r	$\sigma_{eiej} + g\sigma_{rirj}$
Genotypes	(g-1)	SCP _g	MSCP _g	$\sigma_{eiej} + r\sigma_{gigj}$
Error	(r-1)(g-1)	SCP _e	MSCP _e	σ_{eiej}
Total	(rg-1)	-		

(a) Genotypic covariance (σ_{gigj}) was estimated as follows:

$$\sigma_{gigj} = (\text{MSCP}_g - \text{MSCP}_e) / r\text{MSCP}$$

MSCP = Mean sum of cross products

(b) Phenotypic covariance (σ_{pipj}) was estimated as follows:

$$\sigma_{pipj} = \sigma_{gigj} + \sigma_{eiej}$$

3.4.3.1 Genotypic correlation coefficients (r_{gigj})

The genotypic correlation is mainly caused by pleiotrophy and linkage action of gene and r_{gigj} was estimated as suggested by Hazel *et al.* (1943).

$$r_{gigj} = \frac{\hat{\sigma}_{g_i g_j}}{\sqrt{\hat{\sigma}_{g_i}^2 \times \hat{\sigma}_{g_j}^2}}$$

Where, r_{gigj} = Genotypic correlation coefficient between i^{th} and j^{th} character

$\hat{\sigma}_{g_i}^2$ & $\hat{\sigma}_{g_j}^2$ = Genotypic variance of i^{th} and j^{th} character, respectively

3.4.3.2 Phenotypic correlation coefficients (r_{pipj})

$$r_{pipj} = \frac{\hat{\sigma}_{p_i p_j}}{\sqrt{\hat{\sigma}_{p_i}^2 \times \hat{\sigma}_{p_j}^2}}$$

Where,

r_{pipj} = Phenotypic correlation coefficient between i^{th} and j^{th} character

$\hat{\sigma}_{pi}^2$ & $\hat{\sigma}_{pj}^2$ = Phenotypic variance of i^{th} and j^{th} character, respectively

3.4.4 Path Analysis

Path coefficient is a standardized partial regression coefficient, which measure the direct and indirect influence of one variable upon another thereby permitting the separation of the correlation coefficient in to the component of direct and indirect effects.

The path coefficient analysis was carried-out according to the method suggested by Dewey and Lu (1959). Genotypic correlation coefficients of 10 variables with seed yield per plant were used to estimate the path coefficients for the direct effects of various independent characters on yield. The direct effects designated as ‘P’ were calculated by increasing the underlying correlation matrix as per Doolittle method described by Steel and Torrie (1960).

Direct effect of x_1 on y = P_{x_1y}

Where,

y = effect

x_1 = cause

P_{x_1} is Path coefficient of x_1 on y .

Similarly, Indirect effect of x_1 via x_2 on y = $P_{x_2y} \cdot r_{x_1x_2}$

Where,

P_{x_2y} – Path coefficient of the component character x_2 on y

$r_{x_1x_2}$ – Genotypic correlation between x_1 and x_2

$$r_{ny} = p_{ny} + r_{n2} p_{2y} + r_{n3} p_{3y} + \dots + r_{nx} p_{xy}$$

Where,

r_{ny} = Correlation coefficient between one casual factor and dependent character
i.e. yield.

P_{ny} = Path coefficient between the character and yield.

$r_{n2}, r_{n3} \dots r_{nx}$ = Represents the correlation coefficient between that character and each other
yield component in turn.

$$\begin{matrix} \begin{bmatrix} r_{1y} \\ r_{2y} \\ r_{ny} \end{bmatrix} & = & \begin{bmatrix} 1 & r_{12} & \dots & \dots & r_{1n} \\ r_{21} & 1 & \dots & \dots & r_{2n} \\ r_{n1} & r_{n2} & \dots & \dots & 1 \end{bmatrix} & \begin{bmatrix} a \\ b \\ n \end{bmatrix} \\ \text{Matrix-A} & & \text{Matrix-B} & & \text{Matrix-C} \end{matrix}$$

Where,

[A] = Correlation matrix between yield and biometrical characters

[B] = Correlation matrix between different biometrical characters

[C] = Path coefficient matrix where $a = P_{1y}$, $b = P_{2y}$ and so on.

The value of [C] matrix can be obtained as under,

$$[A] = [B] [C]$$

Thus,

$$[B]^{-1} [A] = [C]$$

The path value means the direct effects were calculated as follows,

$$P_{iy} = \sum c_{i1} r_{iy}$$

Multiplication of direct path and respective correlation coefficient between those two traits yielded indirect effects of a certain character via other character.

$$\text{Indirect effect} = r_{ij} \times p_{ij}$$

Where,

$$i \text{ and } j = 1 \text{ to } n$$

The residual effect is a composite variable that includes all other unaccounted factors affecting yield per plant in this study and is assumed to be independent of the remaining variables. It was calculated as under:

$$\text{Residual effect (x)} = (1 - R^2)^{0.5}$$

Where,

$$R^2 = p_{1y} r_{1y} + p_{2y} r_{2y} + \dots + p_{ny} r_{ny}$$

The estimates of path analysis were classified as (Lenka and Mishra, 1973) low, negligible, moderate, high and very high as stated below.

Table 3.7 Classification and range of estimates of path analysis

S. No	Classification	Range
1	Negligible	0.0 to 0.09
2	Low	0.1 to 0.19
3	Moderate	0.20 to 0.29
4	High	0.3 to 0.99
5	Very high	More than 1

4. RESULTS AND DISCUSSION

The experimental results obtained from the present study “Genetic Variability, Correlation and Path Analysis for Yield and its Attributing Characters in Castor (*Ricinus communis* L.)” are presented under the following aspects:

4.1 ANALYSIS OF VARIANCE

4.2 MEAN PERFORMANCE

4.3 VARIABILITY STUDIES

4.4 CORRELATION COEFFICIENTS

4.5 PATH COEFFICIENT ANALYSIS

4.1 ANALYSIS OF VARIANCE

The statistical analysis was done for all the twelve characters as per randomized block design (RBD). The mean sums of squares due to various sources of variation for different traits are given in table 4.1.

The analysis of variance displayed that mean squares due to genotypes were highly significant for all the 12 characters suggesting the presence of sufficient amount of variability present in the experimental material. The genotype mean sum of square for characters having high significance ($p < 0.01$) are days to 50% flowering of main raceme, days to maturity of main raceme, nodes up to main raceme, plant height up to main raceme, total length of main raceme, effective length of main raceme, number of capsules on main raceme, effective branches per plant, 100 seed weight, shelling out turn (%), seed yield per plant and oil content (%).

The wide range of variation present is useful to the breeder for selection of superior and desired genotypes in further crop improvement programme.

Table 4.1 Analysis of variance (mean sum of squares) for various characters in castor

Sr. No.	Characters	df	Mean Sum of Squares		
			Replications	Genotypes	Error
			2	48	96
1	Days to 50% flowering of main raceme		21.07**	20.04**	2.03
2	Days to maturity of main raceme		13.88	229.31**	20.31
3	Nodes up to main raceme		0.07	7.71**	2.38
4	Plant height up to main raceme		235.17*	891.76**	72.47
5	Total length of main raceme		41.15	552.00**	42.36
6	Effective length of main raceme		28.84	542.57**	42.01
7	Number of capsules on main raceme		3.64	951.13**	58.71
8	Effective branches per plant		0.87	7.73**	0.97
9	100 seed weight		1.74	101.94**	5.40
10	Shelling out turn		9.15	380.76**	33.68
11	Seed yield per plant		101.68	6202.94**	391.60
12	Oil content		2.70	124.60**	10.21

*, ** Significant at P = 0.05 and P = 0.01 levels of probability, respectively

4.2 MEAN PERFORMANCE

The mean performances for 49 genotypes of castor for 12 observations are presented in Table 4.2.

4.2.1 Days to 50% flowering of main raceme

The days to 50% flowering ranged from 39 (JI 368, JI 442,) to 52.67 days (JI 428). The average days to 50% flowering were 43.8 days. It can be observed that all the genotypes displayed significant differences for days to 50% flowering and it indicates the presence of adequate amount of variability for this character.

4.2.2 Days to maturity of main raceme

The days to maturity of main raceme ranged from 110 (JI 397) to 144.67 days (JI 357), with a general mean of 125.89 days. The genotype JI 397 showed the minimum days to maturity of main raceme (110 days). The genotype JI 357 showed the maximum number of days to maturity of main raceme (144.67 days) and was statistically at par with genotype JI 35.

4.2.3 Nodes up to main raceme

From the data, it was observed that the trait nodes up to main raceme ranged from 11 to 19.33 in number with general mean of 16.43. The genotype SKI 322 had significantly the highest number of nodes (19.33). The inbred line JI 397 recorded the least number of nodes up to main raceme (11).

4.2.4 Plant height up to main raceme (cm)

The plant height up to main raceme ranged from 45.78 to 122.33 cm with a general mean of 70.62 cm. The genotype SKI 322 showed the maximum plant height up to main raceme (122.33) and the genotype JI 448 showed minimum value for plant height up to main raceme (45.78) and was statistically at par with genotypes JI 446 and 48-1.

Table 4.2 Mean values of genotypes for different characters in castor

Genotype	Name	DF	DM	NPR	PH	SL	ESL	NC	EB	SW	SOT	SY	OC
1	48-1	43.67	128.67	16.33	45.89	62.67	51.67	46.94	7.56	29.51	55.36	139.33	33.23
2	DCS 100	41.33	140.00	17.00	71.00	57.22	44.67	49.84	5.44	36.54	56.00	147.67	33.24
3	DCS 103	43.00	114.33	17.67	50.00	93.33	81.67	65.64	7.56	28.52	81.14	143.33	28.60
4	DCS 105	43.00	123.00	16.00	62.33	84.00	84.00	40.92	5.33	31.90	81.07	97.00	25.29
5	DCS 109	43.33	132.00	17.67	72.22	90.33	76.89	121.77	6.79	30.25	77.33	218.00	41.68
6	DCS 119	49.33	133.33	17.00	71.44	76.11	75.45	83.23	6.72	31.54	61.49	94.93	31.75
7	ANDCI 8	43.00	123.33	15.67	66.67	65.89	50.33	49.28	5.44	33.64	47.52	114.00	34.80
8	ANDCI 9	46.67	119.33	18.33	67.78	61.55	61.55	52.99	9.67	26.06	45.98	130.20	26.60
9	ANDCI 14	46.33	117.67	16.33	84.67	88.33	72.67	106.64	7.66	30.76	46.69	285.00	38.83
10	ANDCI 10-01	45.67	118.00	18.50	91.67	87.00	49.33	80.66	3.20	25.18	58.41	215.72	37.10
11	ANDCI 10-05	42.00	112.67	15.33	58.89	61.07	56.65	48.65	5.67	29.52	53.13	141.87	25.19
12	ANDCI 10-12	41.67	122.67	12.33	55.00	73.00	64.22	61.64	4.44	38.34	51.55	103.00	39.27
13	JI 35	46.33	142.67	18.00	81.34	56.67	54.67	42.06	4.44	22.72	51.75	92.63	24.50
14	JI 244	46.33	121.67	18.22	61.33	58.11	44.78	57.34	7.67	38.23	60.59	150.56	39.01
15	JI 340	43.00	131.33	18.33	75.00	74.17	74.17	61.73	7.56	26.32	37.79	131.00	27.61
16	JI 357	40.33	144.67	14.67	62.00	94.57	54.50	78.26	6.50	36.01	48.62	213.00	40.28
17	JI 368	39.00	125.00	15.67	57.33	56.00	46.33	50.17	7.78	28.53	62.82	133.27	30.40
18	JI 390	44.33	130.33	15.33	67.00	66.00	50.34	52.60	4.10	39.80	53.10	143.33	37.69
19	JI 397	41.33	110.00	11.00	86.78	50.37	46.44	42.98	2.44	40.38	44.93	84.30	20.33
20	JI 417	42.00	118.33	15.00	74.67	69.33	65.52	48.66	5.78	37.48	57.57	119.80	34.67
21	JI 421	42.00	131.00	16.34	52.22	84.22	56.67	83.35	6.10	40.46	48.64	196.30	38.76
22	JI 424	45.00	114.67	15.22	61.00	64.53	53.00	58.51	5.10	43.70	73.85	168.30	38.59
23	JI 428	52.67	119.33	15.88	76.33	66.97	66.97	52.02	6.75	34.64	77.53	140.37	33.25
24	JI 437	42.67	115.00	19.00	102.48	89.89	70.00	84.18	5.43	30.44	65.09	216.93	38.41
25	JI 440	41.67	113.67	15.95	54.16	87.00	52.17	77.78	7.56	31.05	45.15	196.83	29.91
26	JI 442	39.00	127.33	16.67	51.41	59.00	53.67	52.87	5.45	30.64	55.30	133.33	30.93
27	JI 446	43.00	119.67	14.67	45.89	58.77	49.22	56.08	6.10	39.39	62.97	144.40	39.22
28	JI 448	42.33	118.33	15.11	45.78	65.90	45.00	64.93	5.44	36.09	48.91	167.30	36.13

Results and Discussion

29	MI 1	45.67	123.33	17.55	76.45	72.67	57.33	71.53	8.10	39.18	47.17	206.45	41.50
30	MI 2	46.33	128.00	17.22	50.78	42.78	33.33	37.81	7.10	19.79	60.38	103.87	19.55
31	MI 4	45.67	142.33	18.00	82.11	74.33	74.33	48.46	3.44	24.14	82.15	131.33	24.90
32	MI 10	42.00	130.67	17.33	55.22	60.52	60.52	47.95	4.78	35.53	62.81	144.33	36.18
33	MI 16	44.33	131.00	16.89	60.00	83.33	69.33	76.79	6.67	26.67	55.43	146.20	27.50
34	MI 27	43.00	133.33	16.67	74.33	54.11	41.34	62.87	5.10	39.55	63.17	178.44	40.33
35	MI 33	42.33	129.33	16.50	98.11	54.33	40.00	54.14	2.56	44.62	51.03	111.60	45.30
36	SH 10	43.00	141.33	17.50	89.61	63.00	53.67	52.37	4.56	26.53	52.43	145.17	35.39
37	SKI 64	43.33	128.00	14.30	60.72	59.00	33.55	43.73	3.44	31.96	28.40	89.53	30.52
38	SKI 90	43.33	124.67	16.33	67.00	74.00	42.00	66.33	6.56	39.33	66.82	176.00	41.20
39	SKI 215	44.00	141.33	17.00	81.22	92.33	55.55	94.84	7.56	30.46	47.20	246.53	46.49
40	SKI 315	41.33	122.67	15.95	59.00	76.44	57.11	58.98	5.44	40.36	56.55	167.30	40.26
41	SKI 322	46.67	131.67	19.33	122.33	52.47	48.11	51.48	6.44	31.74	51.74	151.90	31.21
42	SKI 346	44.33	117.33	16.11	63.89	56.00	42.22	40.29	2.56	24.64	66.45	97.90	25.23
43	SKI 351	42.33	125.67	18.67	89.30	55.78	32.33	54.90	4.78	33.62	61.27	127.80	31.99
44	SI 3	45.33	130.67	17.00	89.52	77.33	73.11	54.33	3.33	26.75	53.65	107.13	27.96
45	SI 4	48.33	126.33	15.33	113.05	85.67	81.11	64.44	6.11	31.90	61.36	174.90	31.46
46	SI 5	45.00	115.33	17.33	73.11	85.22	79.33	70.96	6.44	26.72	55.02	172.33	26.83
47	SI 8	40.00	117.67	17.23	69.11	83.00	66.33	87.67	6.44	25.78	60.63	229.33	43.79
48	SI 9	46.33	124.67	15.33	53.67	56.00	54.67	46.09	5.43	33.69	46.71	85.07	33.95
49	SI 14	43.67	135.33	14.34	79.78	64.07	56.00	48.84	4.78	33.91	42.88	128.50	33.06
Maximum value		52.67	144.67	19.33	122.33	94.57	84.00	121.77	9.67	44.62	82.15	285.00	46.49
Minimum value		39.00	110.00	11.00	45.78	42.78	32.33	37.81	2.44	19.79	28.40	84.30	19.55
Mean		43.80	125.89	16.43	70.62	69.89	57.22	61.36	5.74	32.54	56.81	150.68	33.67
CD (0.05)		2.31	7.30	2.49	13.79	10.54	10.50	12.41	1.59	3.76	9.40	32.07	5.17
CV%		3.25	3.57	9.37	12.05	9.31	11.32	12.48	17.15	7.14	10.21	13.13	9.48

DF: Days to 50% flowering, DM: Days to maturity, NPR: Nodes up to main raceme, PH: Plant height up to main raceme, SL: Total length of main raceme,

ESL: Effective length of main raceme, NC: Number of capsules on main raceme, EB: Effective branches per plant, SW: 100 seed weight, SOT: Shelling out

turn (%), SY: Seed yield per plant, OC: Oil content (%)

4.2.5 Total length of main raceme (cm)

The data had shown significant differences among all the inbred lines for this trait and it ranged from 42.78 to 94.57 cm with a general mean of 69.89 cm. The genotype JI 357 had the longest primary raceme (94.57) and the genotype MI 2 had the shortest total length of primary raceme.

4.2.6 Effective length of main raceme (cm)

The effective length of main raceme ranged from 32.33 to 84.00 cm with a general mean of 57.22 cm. The genotype DCS 105 showed the longest effective length of main raceme (84.00) and the genotype SKI 351 had the shortest effective length of main raceme with length of 32.33 cm, and was statistically at par with genotypes MI 2 and SKI 64.

4.2.7 Number of capsules on main raceme

Number of capsules on main raceme ranged from 37.81 to 121.77 with a general mean of 61.36. The genotype DCS 109 had highest number of capsules on the main raceme (121.77) and the genotype MI 2 had the minimum number of capsules on main raceme (37.81).

4.2.8 Effective branches per plant

The effective branches per plant ranged from 2.44 to 9.67 with a general mean of 5.74. The genotype ANDCI 9 had the highest number of effective branches (9.67) and the genotypes JI 397 showed the minimum number of effective branches (2.44).

4.2.9 100 Seed weight (g)

The 100 seed weight ranged from 19.79 to 44.62 g with a general mean of 32.54 g. The genotype MI 33 showed the highest value for 100 seed weight (44.62 g) and the genotype MI 2 showed minimum value for 100 seed weight (19.79 g).

4.2.10 Shelling out turn (%)

Significant differences were found among genotypes for shelling out turn % which ranged from 28.40 to 82.15%, with a general mean value of 56.81%. The genotype

MI 4 had shown the highest shelling out turn % (82.15%) and the genotype SKI 64 had shown the minimum shelling out turn (28.40%).

4.2.11 Seed yield per plant (g)

The trait seed yield per plant had shown great range of variability and it ranged from 84.30 to 285 g, with a general mean of 150.68 g. The genotype ANDCI 14 had the highest value for seed yield per plant (285 g). The genotype SKI 64 had shown the minimum value (84.30 g) and was statistically at par with genotype SI 9.

4.2.12 Oil content (%)

Castor oil is of great use in industrial, agricultural and pharmaceutical sectors. The data showed that the oil content percentage among genotypes ranged from 19.55 to 46.49% with a general mean of 33.67%. The genotype SKI 215 had the highest oil content (46.49%) and the genotype MI 2 had the minimum oil content (19.55%).

4.3 VARIABILITY STUDIES

Knowledge of genetic parameters is very important for breeding castor with special emphasis on certain characters. Selection based on the yield components is advantageous, if different yield related traits have been well documented (Johnson *et al.*, 1955; Panse, 1957).

Analysis of variance (ANOVA) may not reveal the complete variability and this could be accessed through standardizing the genotypic and phenotypic variances by obtaining coefficient of variability.

The ratio of genotypic variance to the phenotypic variance is known as broad sense heritability. It is expressed in percent. Hence, heritability can be defined as heritable portion of the phenotypic variance. It is an index that can indicate the transmission of characters from parents to their offspring (Falconer, 1989). Genetic advance is the improvement in mean genotypic value of selected plants over the parental population. This is a measure of genetic gain under the selection. Success of genetic advance under selection will depend on three main factors viz., genetic variability, heritability and selection intensity (Allard, 1960).

The estimates of phenotypic (σ_p^2) and genotypic variance (σ_g^2) of each character were obtained from the analysis of variance. The remaining genetic parameters viz., phenotypic coefficient of variation (PCV %), genotypic coefficient of variation (GCV %), heritability in broad sense ($h^2_{(b)}$) and genetic advance as per cent of mean (GA % mean) were calculated from variance components and mean values. All these estimates are presented in table 4.3.

4.3.1 Days to 50% flowering of main raceme

4.3.1.1 Genotypic and phenotypic variance

The low and narrow difference between the estimates of genotypic (6.00) and phenotypic (8.04) variance indicated that, the expression of this trait is highly under the influence of genetic factors.

4.3.1.2 GCV % and PCV %

The GCV (5.59%) and PCV (6.47%) estimates were low and it indicates the presence of low variation for days to 50% flowering in the population. The close estimates of GCV and PCV values indicated that variability was primarily due to genotypic differences.

4.3.1.3 Heritability and genetic advance as percent mean

The heritability (74.70%) is high and genetic advance as per cent mean (9.96%) is low. It suggests that this trait *i.e.* days to 50% flowering of main raceme has limited scope for improvement through selection.

This could be due to lesser magnitude of genetic variation and due to preponderance of the non-additive gene effect hence it might be difficult to improve this trait only through selection

The present findings confirm with Rukhsar *et al.* (2018) who also reported a narrow difference between genotypic and phenotypic variances, low GCV and PCV and

Table 4.3 Estimates of genotypic variance (σ^2_g), phenotypic variance (σ^2_p) and other genetic parameters for different characters in castor

Sr. No.	Characters	σ^2_g	σ^2_p	GCV (%)	PCV (%)	$h^2_{(b)}$ (%)	GA % Mean
1	Days to 50% flowering	6.00	8.04	5.59	6.47	74.70	9.96
2	Days to maturity of main raceme	69.67	89.98	6.63	7.53	77.43	12.02
3	Nodes up to main raceme	1.78	4.15	8.12	12.40	42.82	10.94
4	Plant height up to main raceme	273.10	345.56	23.40	26.32	79.03	42.85
5	Total length of main raceme	169.88	212.24	18.65	20.85	80.04	34.37
6	Effective length of main raceme	166.85	208.86	22.57	25.25	79.89	41.56
7	Number of capsules on main raceme	297.47	356.18	28.11	30.76	83.52	52.92
8	Effective branches per plant	2.26	3.22	26.16	31.28	69.93	45.06
9	100 seed weight	32.18	37.58	17.43	18.84	85.63	33.23
10	Shelling out turn	115.69	149.37	18.93	21.51	77.45	34.32
11	Seed yield per plant	1937.11	2328.71	29.21	32.03	83.18	54.88
12	Oil content	38.13	48.34	18.34	20.65	78.89	33.55

high heritability. Dapke *et al.* (2016) also observed the low estimates of GCV and PCV. Golakia *et al.* (2007), Movaliya *et al.* (2018) and Alhaji *et al.* (2019) also report high heritability.

4.3.2 Days to maturity of main raceme

4.3.2.1 Genotypic and phenotypic variance

The genetic and phenotypic variances are 69.67 and 89.98 respectively. The genotypic variance (69.67) had contributed greatly to phenotypic variance (89.98), which suggests that the variability was mainly due to genetic cause.

4.3.2.2 GCV % and PCV %

The low estimates of GCV (6.63%) and PCV (7.53%) indicates that there is no adequate variability present for this trait. Hence direct selection of this character would be ineffective for further improvement.

4.3.2.3 Heritability and genetic advance as percent mean

From the results it is seen that heritability is high (77.43%) and the genetic advance as percent mean is moderate (12.02%). This suggests the predominance of additive gene effect in expression of this character. Therefore, the selection based on this trait might be great for improvement.

The moderate genetic advance as per cent of mean (12.02%) and high heritability (77.43%) indicate that the trait is governed by both additive and non-additive gene action.

The current findings are in agreement with studies done by Golakia *et al.* (2007), Sarwar *et al.* (2010), Abimiku *et al.* (2012), Dapke *et al.* (2016), Movaliya *et al.* (2018), Rukhsar *et al.* (2018) and Patel *et al.* (2020) who also recorded narrow difference between genotypic and phenotypic variances, low GCV and PCV, high heritability and moderate genetic advance. Alhaji *et al.* (2019) also reported low estimates of GCV and PCV with high heritability. Alemaw *et al.* (2014) recorded low GCV, PCV and genetic advance estimates.

4.3.3 Nodes up to main raceme

4.3.3.1 Genotypic and phenotypic variance

The genotypic and phenotypic variances were 1.78 and 4.15 respectively. The high difference between genotypic variance (1.78) and phenotypic variance (4.15) indicate that phenotypic variation was primarily due to environmental influence.

4.3.3.2 GCV % and PCV %

The estimate of GCV (8.12%) was low and that of PCV (12.40%) was moderate. The difference between GCV and PCV % values indicate that this trait is influenced by environmental effects rather than genetic constitution. Hence, selection for this character would be ineffective in improvement for further generations.

4.3.3.3 Heritability and genetic advance as percent mean

The heritability (42.82%) was moderate and the genetic advance as percent mean (10.94 %) was also moderate.

The low GCV % and moderate PCV % combined with moderate heritability and genetic advance as percent mean indicate that this trait has very little scope for further improvement through selection.

The present findings were in accordance with the studies done by Patel *et al.* (2020) who also recorded low GCV % and moderate PCV % values along with high heritability coupled by high genetic advance as percent mean.

4.3.4 Plant height up to main raceme (cm)

4.3.4.1 Genotypic and phenotypic variance

The genotypic variance was 273.10 and the phenotypic variance was 345.56.

4.3.4.2 GCV % and PCV %

The estimates of GCV (23.40%) and PCV (26.32%) were high. This indicates the presence of ample variability in the population under study.

4.3.4.3 Heritability and genetic advance as percent mean

The heritability (79.03%) and the genetic advance as percent mean (42.85%) were high.

The high GCV and PCV % along with high heritability coupled with high genetic advance as percent mean suggest that, the selection of this character for further improvement would be effective.

These results were supported by Lakshmamma *et al.* (2005), Sridhar *et al.* (2009), Sarwar *et al.* (2010), Radhamani and Ushakumari (2013), Chaudhari *et al.* (2016) and Patel *et al.* (2020).

4.3.5 Total length of main raceme (cm)

4.3.5.1 Genotypic and phenotypic variance

The genotypic and phenotypic variances were 169.88 and 212.24 respectively.

4.3.5.2 GCV % and PCV %

The estimate of GCV (18.65%) was moderate and PCV (20.85%) was high. The moderate value of GCV % indicates the presence of little or no sufficient variability in them. Hence selection of this character for further improvement by selection would be ineffective.

4.3.5.3 Heritability and genetic advance as percent mean

The heritability (80.04%) and genetic advance as percent mean (34.37%) were high.

The present findings were in accordance with Dapke *et al.* (2016), Movaliya *et al.* (2018) and Rukhsar *et al.* (2018) who reported high GCV, PCV, heritability and genetic advance. Golakia *et al.* (2007) observed only high GCV and PCV. Nagarajan *et al.* (2019) and Patel *et al.* (2020) also reported high heritability along with high genetic advance for the said trait.

4.3.6 Effective length of main raceme (cm)

4.3.6.1 Genotypic and phenotypic variance

The genotypic and phenotypic variances were 166.85 and 208.86 respectively.

4.3.6.2 GCV % and PCV %

The estimates of GCV (22.57%) and PCV (25.25%) were high. The values indicate the presence of sufficient variability in the population for this character. Hence, selection for this character would be effective for improvement in further generations.

4.3.6.3 Heritability and genetic advance as percent mean

The heritability (79.89%) and genetic advance as percent mean (41.56%) were high

Therefore this trait with high estimates of GCV and PCV % along with high heritability and genetic advance as percent mean is desirable for selection.

The present results are consistent with Dapke *et al.* (2016), Chaudhary *et al.* (2016), Movaliya *et al.* (2018), Nagarajan *et al.* (2019) and Patel *et al.* (2020) who recorded high GCV, PCV, heritability and genetic advance. Golakia *et al.* (2007) had reported higher estimates of GCV and PCV.

4.3.7 Number of capsules on main raceme

4.3.7.1 Genotypic and phenotypic variance

The genotypic and phenotypic variances were 297.47 and 356.18 respectively. The estimated phenotypic variance (356.18) was greater than genotypic variance (297.47) but the contribution of genotypic variance is greater suggesting that character may be in control of genetic material.

4.3.7.2 GCV % and PCV %

The estimates of GCV (28.11%) and PCV (30.76%) were high. The narrow difference between the estimates of GCV and PCV values suggested very little influence of the environment in expression of this character.

4.3.7.3 Heritability and genetic advance as percent mean

The heritability (83.52%) and genetic advance as percent mean (52.92%) were high.

The value of high genetic advance (52.92%) coupled with high heritability (83.52%) indicated that additive gene effect plays important role in the inheritance of this character. Hence, there would be good response of the selection for improvement of the character. The present findings are in accordance with results reported by Tewari and Kumar (2013), Alemaw *et al.* (2014), Torres *et al.* (2015) and Nagarajan *et al.* (2019).

Golakia *et al.* (2007), Abimiku *et al.* (2012), Dapke *et al.* (2016), Movaliya *et al.* (2018) and Patel *et al.* (2020) also reported higher estimates of GCV, PCV, heritability, and genetic advance. Lakshmamma *et al.* (2005), Ahmed *et al.* (2012), Radhamani and Ushakumari (2013) and Chaudhari *et al.* (2016) also observed high GCV and PCV for capsules on primary raceme. Rukhsar *et al.* (2018) and Alhaji *et al.* (2019) recorded high values for heritability.

4.3.8 Effective branches per plant

4.3.8.1 Genotypic and phenotypic variance

The genotypic and phenotypic variances were 2.26 and 3.22 respectively. The result revealed that the difference between genotypic variance (2.26) and phenotypic variance (3.22) was less indicating that environment play little role in expression of character.

4.3.8.2 GCV % and PCV %

The estimates of GCV (26.16%) and PCV (31.28%) were high.

4.3.8.3 Heritability and genetic advance as percent mean

The heritability (69.93%) and genetic advance as percent mean (45.06%) were high for this trait indicating the variability was due to additive interaction of genes.

Outcome of results were in accordance with report of Sevugaperumal *et al.* (2000), Sarwar and Chaudhry (2008) and Chaudhari *et al.* (2016) who also recorded high heritability coupled with high genetic advance as percent mean.

Dapke *et al.* (2016) and Movaliya *et al.* (2018) reported similar results for heritability and genetic advance. The high genetic advance was reported by Sowmya *et al.* (2019). Patel *et al.* (2020) also recorded high GCV and PCV % with high heritability and genetic advance as percent mean.

4.3.9 100 seed weight (g)

4.3.9.1 Genotypic and phenotypic variance

The genotypic and phenotypic variances are 32.18 and 37.58 respectively.

4.3.9.2 GCV % and PCV %

The estimates of GCV (17.43%) and PCV (18.84%) were moderate. The narrow difference between GCV and PCV values displayed that the character's expression was less affected by environment. The moderate values suggest that there is no or little variability present in them. Hence, further improvement through selection would be not effective.

4.3.9.3 Heritability and genetic advance as percent mean

The heritability (85.63%) and genetic advance as percent mean (33.23%) were high.

The current findings are following Alemaw *et al.* (2014) and Torres *et al.* (2015) who observed moderate GCV and PCV, high heritability and genetic advance. Dapke *et al.* (2016) also recorded moderate GCV and PCV in their study. High heritability and genetic advance were also reported by Sarwar and Chaudhry (2008), Sridhar *et al.* (2009), Alemaw *et al.* (2014), Rukhsar *et al.* (2018) and Movaliya *et al.* (2018).

4.3.10 Shelling out turn (%)

4.3.10.1 Genotypic and phenotypic variance

The genotypic and phenotypic variances were 115.69 and 149.37 respectively.

4.3.10.2 GCV % and PCV %

The value of GCV (18.93%) was low and PCV (21.51%) was high. This indicates that there is less variability in the population under study for this trait. Hence selection of this character in further improvement by selection would be ineffective.

4.3.10.3 Heritability and genetic advance as percent mean

The heritability (77.45%) and genetic advance as percent mean (34.32%) were high.

In contrary Rukhsar *et al.* (2018) found low GCV (8.34 %), moderate PCV (11.10%) high heritability (56.50%) and moderate genetic advance as percent mean (12.94 %).

4.3.11 Seed yield per plant (g)

4.3.11.1 Genotypic and phenotypic variance

The genotypic and phenotypic variances were 1937.11 and 2328.71 respectively.

4.3.11.2 GCV % and PCV %

The GCV (29.21%) and PCV (32.03%) were high suggesting presence of adequate variability for this trait and narrow difference in between them indicated that the environment had less effect on the expression of this trait.

4.3.11.3 Heritability and genetic advance as percent mean

The heritability (83.18%) and genetic advance as percent mean (54.88%) were high. which indicated the predominance of additive gene action in expression of the character and the genotypic ability to transfer the genes to their offspring. Hence, selection can be made in desired direction based on phenotypic performance.

These results are in line with Dapke *et al.* (2016) and Patel *et al.* (2020) who also observed high GCV, PCV, heritability and genetic advance. The high GCV% and PCV% are in accordance with findings of Patel *et al.* (2010), Sarwar *et al.* (2010), Abimiku *et al.* (2012) and Radhamani and Ushakumari (2013). Movaliya *et al.* (2018) also reported high heritability and genetic advance. The high estimates of heritability and genetic advance as

percent mean were earlier reported by Ramesh *et al.* (2012), Tewari and Kumar (2013), Patel and Patel (2014), Chaudhari *et al.* (2016) and Nagarajan *et al.* (2019).

4.3.12 Oil content (%)

4.3.12.1 Genotypic and phenotypic variance

The genotypic and phenotypic variances were 38.13 and 48.34 respectively.

4.3.12.2 GCV % and PCV %

The GCV (18.34%) was moderate and PCV (20.65%) was high. The moderate GCV indicates that there is limited variability present in the population for this character.

4.3.12.3 Heritability and genetic advance as percent mean

The heritability (78.89%) and genetic advance as percent mean (33.55%) were high.

In contrary Rukhsar *et al.* (2018) found low GCV (3.28%), low PCV (3.88%), high heritability (71.40%) and low genetic advance as percent mean (5.70%).

The above results revealed that all the traits under study displayed significant variation among the genotypes. The genotype ANDCI 14 had the highest seed yield and was elite inbred line based on *per se* performance. The genotype SKI 322 had shown high values for the traits number of nodes up to main raceme and plant height. The genotype DCS 109 had shown high value for the trait number of capsules on main raceme.

The traits plant height up to main raceme, effective length of main raceme, capsules on main raceme, effective branches per plant and seed yield per plant have displayed high values for GCV %, PCV %, heritability and genetic advance as percent mean. So selection based on these characters will be effective for further improvement.

The traits days to 50% flowering, days to maturity of main raceme, nodes up to main raceme, total length of main raceme, 100 seed weight, shelling out turn % and oil content % displayed low to moderate values for GCV %, PCV %, heritability and genetic advance as percent mean. Hence selection based on above mentioned characters for further improvement would be ineffective.

The differences between genotypic and phenotypic variances were narrow for all the characters except nodes up to primary raceme. The narrow difference indicate that environment had little role in expression of these characters.

The trait nodes up to main raceme had shown the genotypic and phenotypic variance 1.78 and 4.15 respectively. The resulting values indicate that this trait is more effected by environment when compared to other traits.

There is less difference between GCV and PCV were observed for most of the traits indicating that the variability was primarily due to genotypic variances *i.e.* additive gene action.

High heritability coupled with high genetic advance as percent mean was observed for the traits *viz.*, plant height up to main raceme, total length of main raceme, effective length of main raceme, number of capsules on main raceme, effective branches per plant, 100 seed weight, shelling out turn, oil content and seed yield per plant. The high estimates indicate that additive gene action played a greater role in governing these characters.

High heritability coupled with low genetic advance as percent mean was observed for the characters days to 50% flowering and days to maturity. These estimates indicate that dominant gene action played a major role in governing these traits.

Low heritability coupled with low genetic advance as percent mean was observed the character nodes up to main raceme. These low values suggested that environment played a major role in governing this character.

4.4 CORRELATION COEFFICIENTS

Yield is a complex character and is the multiplicative end product of many quantitative traits (Whitehouse *et al.*, 1958). Hence selection for improvement in yield on the basis of *per se* performance is not effective.

Success of any crop improvement programme depends on the correlation between yield and its components, both at phenotypic and genotypic level. Correlation is a powerful tool for studying character association and is therefore, very beneficial to facilitate selection for important characters without sacrificing gain in others.

The association between characters that can be directly observed is called phenotypic correlation. The real or true association can be assessed through genotypic correlation, which will eliminate the environmental influence. Genotypic correlation is helpful in construction of the selection indices.

The association among traits may result from linkage, pleiotropy and/or physiological association among characters. Correlation is the net or overall effect of segregating genes. Some genes may increase both the characters resulting in positive correlation, while other genes may increase one character and decrease the other character resulting in negative correlation. Hence it is important to know the interrelationship among various traits in order to accumulate optimum combination of yield attributing characters into a single genotype.

The correlation coefficients were estimated for all the combinations of twelve characters under study at both genotypic (r_g) and phenotypic (r_p) levels. The results are presented in the table 4.4.

4.4.1 Days to 50% flowering of main raceme

The trait days to 50% flowering showed significant positive correlation with nodes up to main raceme at both genotypic and phenotypic levels ($r_g = 0.3078^*$ and $r_p = 0.1962^*$). It showed significant positive correlation at genotypic level and highly significant positive correlation at phenotypic level with plant height up to main raceme ($r_g = 0.3502^*$ and $r_p = 0.2966^*$). Also positive correlation was observed with shelling out turn ($r_g = 0.1975$ and $r_p = 0.1279$), effective branches per plant ($r_g = 0.1666$ and $r_p = 0.1299$) and days to maturity of main raceme ($r_g = 0.0461$ and $r_p = 0.0002$) at both genotypic and phenotypic levels. Positive correlation at genotypic and highly significant positive correlation at phenotypic level were observed with effective length of main raceme ($r_g = 0.2548$ and $r_p = 0.2176^{**}$). Negative correlation at genotypic and positive correlation at phenotypic level were observed with total length of main raceme ($r_g = -0.0166$ and $r_p = 0.0062$) and number of capsules on main raceme ($r_g = -0.0101$ and $r_p = 0.0127$). Negative correlation at genotypic and significant negative correlation at

Table 4.4 Genotypic and phenotypic correlation among different characters in castor

Column		DF	DM	NPR	PH	SL	ESL	NC	EB	SW	OC	SOT	SY
DF	rg	1.0000	0.0461	0.3078 *	0.3502 *	-0.0166	0.2548	-0.0101	0.1666	-0.2016	-0.1751	0.1975	-0.0861
	rp	1.0000	0.0002	0.1962 *	0.2966 **	0.0062	0.2176 **	0.0127	0.1299	-0.1784 *	-0.1670 *	0.1279	-0.0629
DM	rg		1.0000	0.2541	0.2061	-0.0274	-0.0492	-0.0071	-0.0901	-0.1348	0.1288	-0.1228	-0.0544
	rp		1.0000	0.2100 *	0.1244	-0.0528	-0.0768	-0.0169	-0.0650	-0.1082	0.0881	-0.0884	-0.0475
NPR	rg			1.0000	0.3658 **	0.1689	0.1951	0.2651	0.4183 **	-0.6006 **	0.0447	0.2902 *	0.3519 *
	rp			1.0000	0.2684 **	0.1116	0.0877	0.1883 *	0.1927 *	-0.3129 **	-0.0016	0.2007 *	0.1894 *
PH	rg				1.0000	0.0875	0.1253	0.1287	-0.2826 *	-0.0891	0.0451	-0.0511	0.1613
	rp				1.0000	0.0624	0.1534	0.1097	-0.1874 *	-0.0722	0.0375	-0.0116	0.1493
SL	rg					1.0000	0.7331 **	0.8063 **	0.2986 *	-0.1352	0.3106 *	0.1915	0.6796 **
	rp					1.0000	0.6103 **	0.6611 **	0.2350 **	-0.1195	0.2694 **	0.1179	0.5650 **
ESL	rg						1.0000	0.4177 **	0.2955 *	-0.2877 *	-0.1161	0.3651 **	0.1961
	rp						1.0000	0.3239 **	0.1931 *	-0.2399 **	-0.0898	0.2979 **	0.1601
NC	rg							1.0000	0.4111 **	-0.0117	0.5666 **	0.0459	0.8603 **
	rp							1.0000	0.3056 **	-0.0081	0.4955 **	0.0388	0.7362 **
EB	rg								1.0000	-0.1511	0.1182	0.0192	0.4196 **
	rp								1.0000	-0.1459	0.0781	-0.0229	0.3708 **
SW	rg									1.0000	0.6111 **	-0.0841	0.0573
	rp									1.0000	0.4935 **	-0.0307	0.0377
OC	rg										1.0000	-0.0169	0.6026 **
	rp										1.0000	-0.0399	0.6014 **
SOT	rg											1.0000	0.0499
	rp											1.0000	0.0051
SY	rg												1.0000
	rp												1.0000

Note; *,** Significant at 5% and 1% levels respectively

DF: Days to 50% flowering, DM: Days to maturity, NPR: Nodes up to main raceme, PH: Plant height up to main raceme, SL: Total length of main raceme, ESL: Effective length of main raceme, NC: Number of capsules on main raceme, EB: Effective branches per plant, SW: 100 seed weight, SOT: Shelling out turn, SY: Seed yield per plant, OC: Oil content

phenotypic level were observed with the traits 100 seed weight ($r_g = -0.2016$ and $r_p = -0.1784^*$) and oil content ($r_g = -0.1751$ and $r_p = -0.1670^*$). Non-significant negative correlation at both genotypic and phenotypic levels was observed with the trait seed yield per plant ($r_g = -0.0861$ and $r_p = -0.0629$). Negative correlation of days to 50% flowering with seed yield was also recorded by Abimiku *et al.* (2012). Negative correlation of this trait with oil content was also found previously at genotypic level by Sridhar *et al.* (2010).

4.4.2 Days to maturity of main raceme

Days to maturity of main raceme showed positive correlation at genotypic level and significant positive correlation at phenotypic level with the trait nodes up to main raceme ($r_g = 0.2541$ and $r_p = 0.2100^*$). It showed positive correlation at both genotypic and phenotypic level with plant height up to main raceme ($r_g = 0.2061$ and $r_p = 0.1244$), oil content ($r_g = 0.1288$ and $r_p = 0.0881$) and days to 50% flowering of main raceme ($r_g = 0.0461$ and $r_p = 0.0002$). It displayed a negative correlation at both genotypic and phenotypic levels with 100 seed weight ($r_g = -0.1348$ and $r_p = -0.1082$), effective length of main raceme ($r_g = -0.0492$ and $r_p = -0.0768$), seed yield per plant ($r_g = -0.0544$ and $r_p = -0.0475$), shelling out turn ($r_g = -0.1228$ and $r_p = -0.0884$), total length of main raceme ($r_g = -0.0274$ and $r_p = -0.0528$), effective branches per plant ($r_g = -0.0901$ and $r_p = -0.0650$) and number of capsules on main raceme ($r_g = -0.0071$ and $r_p = -0.0169$).

4.4.3 Nodes up to main raceme

Nodes up to main raceme showed highly significant positive correlation at both genotypic and phenotypic levels with plant height up to main raceme ($r_g = 0.3658^{**}$ and $r_p = 0.2684^{**}$). It showed highly significant positive correlation at genotypic and significant positive correlation at phenotypic level with effective branches per plant ($r_g = 0.4183^{**}$ and $r_p = 0.1927^*$). It displayed significant positive correlation at both genotypic and phenotypic levels with seed yield per plant ($r_g = 0.3519^*$ and $r_p = 0.1894^*$), days to 50% flowering of main raceme ($r_g = 0.3078^*$ and $r_p = 0.1962^*$) and shelling out turn ($r_g = 0.2902^*$ and $r_p = 0.2007^*$). At genotypic level it had positive correlation and at phenotypic level it had significant positive correlation with number of capsules on main raceme ($r_g = 0.2651$ and $r_p = 0.1883^*$) and days to maturity of main raceme ($r_g = 0.2541$

and $r_p = 0.2100^*$). It showed positive correlation at both genotypic and phenotypic levels with total length of main raceme ($r_g = 0.1689$ and $r_p = 0.1116$). At genotypic level it had positive correlation and at phenotypic level it had negative correlation with oil content ($r_g = 0.0447$ and $r_p = -0.0016$) and effective length of main raceme ($r_g = 0.1951$ and $r_p = 0.0877$). A highly significant negative correlation was observed at both genotypic and phenotypic levels with 100 seed weight ($r_g = -0.6006^{**}$ and $r_p = -0.3129^{**}$). Highly significant positive correlation of nodes up to main raceme with plant height was also recorded by Kumar *et al.* (2003) and Tewari and Mishra (2013). The highly significant positive correlation with plant height and the significant positive correlation with seed yield was also noted earlier by Sridhar *et al.* (2010).

4.4.4 Plant height up to main raceme (cm)

Plant height up to main raceme had highly significant positive correlation at both genotypic and phenotypic levels with nodes up to main raceme ($r_g = 0.3658^{**}$ and $r_p = 0.2684^{**}$). It had significant positive correlation at genotypic and highly significant positive correlation at phenotypic level with days to 50% flowering of main raceme ($r_g = 0.3502^*$ and $r_p = 0.2966^{**}$). A positive correlation was observed at both genotypic and phenotypic levels with days to maturity of main raceme ($r_g = 0.2061$ and $r_p = 0.1244$), seed yield per plant ($r_g = 0.1613$ and $r_p = 0.1493$), number of capsules on main raceme ($r_g = 0.1287$ and $r_p = 0.1097$), effective length of main raceme ($r_g = 0.1253$ and $r_p = 0.1534$), total length of main raceme ($r_g = 0.0875$ and $r_p = 0.0624$) and oil content ($r_g = 0.0451$ and $r_p = 0.0375$). It displayed significant negative correlation at both genotypic and phenotypic levels with effective branches per plant ($r_g = -0.2826^*$ and $r_p = -0.1874^*$). It had negative correlation at both genotypic and phenotypic level with shelling out turn ($r_g = -0.0511$ and $r_p = -0.0116$) and with 100 seed weight ($r_g = -0.0891$ and $r_p = -0.0722$). High significant positive correlation with nodes upto main raceme at both genotypic and phenotypic levels was also reported by Kumar *et al.* (2003), Movaliya *et al.* (2018) and at only phenotypic level by Ramesh *et al.* (2001). The positive association of this trait with seed yield and its negative association with 100 seed weight had been previously recorded by Sridhar *et al.* (2010). The significant positive correlation at genotypic level and highly significant positive correlation at phenotypic level of this character with days to 50% flowering was reported earlier by Kanti *et al.* (2015).

4.4.5 Total length of main raceme (cm)

Total length of main raceme showed a highly significant positive correlation at both genotypic and phenotypic levels with number of capsules on main raceme ($r_g = 0.8063^{**}$ and $r_p = 0.6611^{**}$), seed yield per plant ($r_g = 0.6796^{**}$ and $r_p = 0.5650^{**}$) and effective length of main raceme ($r_g = 0.7331^{**}$ and $r_p = 0.6103^{**}$). It had significant positive correlation at genotypic and highly significant positive correlation at phenotypic level with oil content ($r_g = 0.3106^*$ and $r_p = 0.2694^{**}$) and effective branches per plant ($r_g = 0.2986^*$ and $r_p = 0.2350^{**}$). It showed positive correlation at both genotypic and phenotypic levels with nodes up to main raceme ($r_g = 0.1689$ and $r_p = 0.1116$), plant height up to main raceme ($r_g = 0.0875$ and $r_p = 0.0624$) and shelling out turn ($r_g = 0.1915$ and $r_p = 0.1179$). It displayed negative correlation at genotypic level and positive correlation at phenotypic level with days to 50% flowering of main raceme ($r_g = -0.0166$ and $r_p = 0.0062$). Negative correlation at both genotypic and phenotypic levels was observed with 100 seed weight ($r_g = -0.1352$ and $r_p = -0.1195$) and days to maturity of main raceme ($r_g = -0.0274$ and $r_p = -0.0528$). The highly significant positive correlation of this trait with effective length of main raceme and seed yield was earlier recorded by Dapke *et al.* (2016). Its highly significant positive correlation with number of capsules on main raceme was noted by Kumar *et al.* (2003), Ahmed *et al.* (2012) and with seed yield was recorded by Dhedhi *et al.* (2010). Positive correlation of total length of main raceme with plant height was also reported earlier by Abimiku *et al.* (2012).

4.4.6 Effective length of main raceme (cm)

Effective length of main raceme had highly significant positive correlation at both genotypic and phenotypic levels with total length of main raceme ($r_g = 0.7331^{**}$ and $r_p = 0.6103^{**}$), number of capsules on main raceme ($r_g = 0.4177^*$ and $r_p = 0.3239^{**}$) and shelling out turn ($r_g = 0.3651^{**}$ and $r_p = 0.2979^{**}$). It displayed positive correlation at both genotypic and phenotypic level with nodes up to main raceme ($r_g = 0.1951$ and $r_p = 0.0877$), seed yield per plant ($r_g = 0.1961$ and $r_p = 0.1601$) and plant height up to main raceme ($r_g = 0.1253$ and $r_p = 0.1534$). It showed positive correlation at genotypic and highly significant positive correlation at phenotypic level with days to 50% flowering of main raceme ($r_g = 0.2548$ and $r_p = 0.2176^{**}$). At both genotypic and phenotypic levels

significant positive correlation was observed with effective branches per plant ($r_g = 0.2955^*$ and $r_p = 0.1931^*$). It showed significant negative correlation at genotypic level and highly significant negative correlation at phenotypic level 100 seed weight ($r_g = -0.2877^*$ and $r_p = -0.2399^{**}$). A negative correlation at both the genotypic and phenotypic levels was observed with oil content ($r_g = -0.1161$ and $r_p = -0.0898$) and days to maturity of main raceme ($r_g = -0.0492$ and $r_p = -0.0768$). Highly significant positive correlation of this trait with total length of main raceme was earlier recorded by Movaliya *et al.* (2018) and Sridhar *et al.* (2010).

4.4.7 Number of capsules on main raceme

Number of capsules had shown highly significant positive correlation at genotypic and phenotypic levels with seed yield per plant ($r_g = 0.8603^{**}$ and $r_p = 0.7362^{**}$), total length of main raceme ($r_g = 0.8063^{**}$ and $r_p = 0.6611^{**}$), oil content ($r_g = 0.5666^{**}$ and $r_p = 0.4955^{**}$), effective length of main raceme ($r_g = 0.4177^{**}$ and $r_p = 0.3239^{**}$) and effective branches per plant ($r_g = 0.4111^{**}$ and $r_p = 0.3056^{**}$). It displayed positive correlation at genotypic and significantly positive correlation at phenotypic level with nodes up to main raceme ($r_g = 0.2651$ and $r_p = 0.1883^*$). A positive correlation at both genotypic and phenotypic level was observed with plant height up to main raceme ($r_g = 0.1287$ and $r_p = 0.1097$) and shelling out turn ($r_g = 0.0459$ and $r_p = 0.0388$). It showed negative correlation at genotypic and positive correlation at phenotypic level with days to 50% flowering of main raceme ($r_g = -0.0101$ and $r_p = 0.0127$). At both genotypic and phenotypic level it had negative correlation with 100 seed weight ($r_g = -0.0117$ and $r_p = -0.0081$) and days to maturity of main raceme ($r_g = -0.007$ and $r_p = -0.0169$). Its highly significant positive correlation with total length of main raceme was reported also by Patel *et al.* (2010) and Abimiku *et al.* (2012) and with seed yield was reported earlier by Kumar *et al.* (2003), Tewari and Mishra (2013) and Dapke *et al.* (2016). Movaliya *et al.* (2018) reported similar highly significant positive correlation with total length of main raceme and positive correlation with shelling out turn %. Negative correlation of this trait with 100 seed weight was reported earlier by Sridhar *et al.* (2010).

4.4.8 Effective branches per plant

Effective branches per plant displayed highly significant positive correlation at

both the genotypic and phenotypic levels with seed yield per plant ($r_g = 0.4196^{**}$ and $r_p = 0.3708^{**}$) and number of capsules on main raceme ($r_g = 0.4111^{**}$ and $r_p = 0.3056^{**}$). It showed highly significant positive correlation at genotypic level and significantly positive correlation at phenotypic level with nodes up to main raceme ($r_g = 0.4183^{**}$ and $r_p = 0.1927^*$). It had significantly positive correlation at the genotypic level and highly significant positive correlation at the phenotypic level with total length of main raceme ($r_g = 0.2986^*$ and $r_p = 0.2350^{**}$). It displayed significant positive correlation at both genotypic and phenotypic levels with effective length of main raceme ($r_g = 0.2955^*$ and $r_p = 0.1931^*$). It displayed positive correlation at both genotypic and phenotypic levels with days to 50% flowering of main raceme ($r_g = 0.1666$ and $r_p = 0.1299$) and oil content ($r_g = 0.1182$ and $r_p = 0.0780$). A significantly negative correlation was observed at both genotypic and phenotypic levels with plant height up to main raceme ($r_g = -0.2826^*$ and $r_p = -0.1874^*$). It showed negative correlation at both genotypic and phenotypic levels with 100 seed weight ($r_g = -0.1510$ and $r_p = -0.1459$) and days to maturity of main raceme ($r_g = -0.0901$ and $r_p = -0.0650$). It showed positive correlation at genotypic level and negative correlation at phenotypic level with shelling out turn ($r_g = 0.0192$ and $r_p = -0.0229$). Its highly significant positive correlation with number of capsules on main raceme was reported earlier by Tewari and Mishra (2013).

4.4.9 100 seed weight (g)

Hundred seed weight showed highly significant positive correlation at both genotypic and phenotypic levels with oil content ($r_g = 0.6111^{**}$ and $r_p = 0.4935^{**}$). It had positive correlation at both genotypic and phenotypic levels with seed yield per plant ($r_g = 0.0573$ and $r_p = 0.0377$). A highly significant negative correlation at both genotypic and phenotypic levels was observed with nodes up to main raceme ($r_g = -0.6006^{**}$ and $r_p = -0.3129^{**}$). It showed negative correlation at genotypic and significantly negative correlation at phenotypic level with days to 50% flowering of main raceme ($r_g = -0.2016$ and $r_p = -0.1784^*$). It displayed significant negative correlation at genotypic level and highly significant negative correlation at phenotypic level with effective length of main raceme ($r_g = -0.2877^*$ and $r_p = -0.2399^{**}$). It displayed negative correlation with effective branches per plant ($r_g = -0.1511$ and $r_p = -0.1459$), total length of main raceme ($r_g = -0.1352$ and $r_p = -0.1195$), days to maturity of main raceme ($r_g = -0.1348$ and $r_p = -$

0.1082), shelling out turn ($r_g = -0.0841$ and $r_p = -0.0307$), plant height up to main raceme ($r_g = -0.0891$ and $r_p = -0.0722$) and number of capsules on main raceme ($r_g = -0.0117$ and $r_p = -0.0081$) at both genotypic and phenotypic levels. The highly significant positive correlation of 100 seed weight with oil content was earlier reported by Adeyanju *et al.* (2010) and Dapke *et al.* (2016).

4.4.10 Shelling out turn (%)

Shelling out turn percent showed highly significantly positive correlation at both genotypic and phenotypic level with effective length of main raceme ($r_g = 0.3651^{**}$ and $r_p = 0.2979^{**}$). It had significantly positive correlation with nodes up to main raceme ($r_g = 0.2902^*$ and $r_p = 0.2007^*$) at both genotypic and phenotypic levels. It displayed positive correlation with days to 50% flowering of main raceme ($r_g = 0.1975$ and $r_p = 0.1279$), total length of main raceme ($r_g = 0.1915$ and $r_p = 0.1179$), seed yield per plant ($r_g = 0.0499$ and $r_p = 0.0051$) and number of capsules on main raceme ($r_g = 0.0459$ and $r_p = 0.0388$) at both genotypic and phenotypic levels. It showed negative correlation with days to maturity of main raceme ($r_g = -0.1228$ and $r_p = -0.0884$), 100 seed weight ($r_g = -0.0841$ and $r_p = -0.0307$), plant height up to main raceme ($r_g = -0.0511$ and $r_p = -0.0116$) and oil content ($r_g = -0.0169$ and $r_p = -0.0399$) at both genotypic and phenotypic levels. It showed positive correlation at genotypic level and negative correlation at phenotypic level with the trait effective branches per plant ($r_g = 0.0192$ and $r_p = -0.0229$). Positive correlation of this trait with seed yield per plant was also reported earlier by Rukhsar *et al.* (2018).

4.4.11 Seed yield per plant (g)

Seed yield per plant showed highly significant positive correlation with number of capsules on main raceme ($r_g = 0.8603^{**}$ and $r_p = 0.7362^{**}$), total length of main raceme ($r_g = 0.6796^{**}$ and $r_p = 0.5650^{**}$), oil content ($r_g = 0.6026^{**}$ and $r_p = 0.6014^{**}$) and effective branches per plant ($r_g = 0.4196^{**}$ and $r_p = 0.3708^{**}$) at both genotypic and phenotypic levels. It had significantly positive correlation with nodes up to main raceme ($r_g = 0.3519^*$ and $r_p = 0.1894^*$) at both genotypic and phenotypic levels. It displayed positive correlation with effective length of main raceme ($r_g = 0.1961$ and $r_p = 0.1601$), plant height up to main raceme ($r_g = 0.1613$ and $r_p = 0.1493$), 100 seed weight ($r_g =$

0.0573 and $r_p = 0.0377$) and shelling out turn ($r_g = 0.0499$ and $r_p = 0.0051$) at both genotypic and phenotypic levels. It had negative correlation with days to 50% flowering of main raceme ($r_g = -0.0861$ and $r_p = -0.0629$) and days to maturity of main raceme ($r_g = -0.0544$ and $r_p = -0.0475$) at both genotypic and phenotypic levels. Its highly significant positive correlation with total length of main raceme, number of capsules on main raceme and effective branches per plant were earlier reported by Abimiku *et al.* (2012) and Patel *et al.* (2010). The highly significant positive correlation of seed yield with number of capsules on main raceme and effective branches per plant and oil content was reported by Mohanty *et al.* (2020). Sowmya *et al.* (2019) and Mullualem *et al.* (2017) reported highly significant correlation of seed yield with number of capsules on main raceme. Sridhar *et al.* (2010) reported significantly positive correlation of seed yield with nodes up to primary raceme.

4.4.12 Oil content (%)

Oil content showed highly significant positive correlation with 100 seed weight ($r_g = 0.6111^{**}$ and $r_p = 0.4935^{**}$), seed yield per plant ($r_g = 0.6026^{**}$ and $r_p = 0.6014^{**}$) and number of capsules on main raceme ($r_g = 0.5666^{**}$ and $r_p = 0.4955^{**}$) at both genotypic and phenotypic levels. It had significantly positive correlation at genotypic and highly significant positive correlation at phenotypic level with total length of main raceme ($r_g = 0.3106^*$ and $r_p = 0.2694^{**}$). It showed positive correlation with days to maturity of main raceme ($r_g = 0.1288$ and $r_p = 0.0880$), effective branches per plant ($r_g = 0.1182$ and $r_p = 0.0781$) and plant height up to main raceme ($r_g = 0.0451$ and $r_p = 0.0375$) at both genotypic and phenotypic levels. It had positive correlation at genotypic level and negative correlation at phenotypic level with nodes up to main raceme ($r_g = 0.0447$ and $r_p = -0.0016$). It displayed negative correlation at genotypic level and significantly negative correlation at phenotypic level with and days to 50% flowering of main raceme ($r_g = -0.1751$ and $r_p = -0.1670^*$). It showed negative correlation with effective length of main raceme ($r_g = -0.1161$ and $r_p = -0.0898$) and shelling out turn ($r_g = -0.0169$ and $r_p = -0.0399$) at both genotypic and phenotypic levels. Its highly significant positive correlation with number of capsules on main raceme was earlier reported by Tewari and Mishra (2013) and Mullualem *et al.* (2017). Highly significant positive correlation with 100 seed weight was reported also by Sridhar *et al.* (2010).

Highly significant positive correlation for seed yield were found with total length of main raceme, number of capsules on main raceme, effective branches per plant and oil content. Significantly positive correlation for seed yield was found with nodes up to primary raceme.

Hence, total length of main raceme, number of capsules on main raceme, effective branches per plant, oil content % and nodes up to primary raceme are the most important traits that contributed towards higher seed yield.

4.5 PATH COEFFICIENT ANALYSIS

Seed yield is a polygenic trait influenced by various components directly or indirectly. Indirect selection is more successful than direct selection when the attributes at issue have low heritability and are not easily or reliably observable. The purpose of correlation studies is primarily to know the suitability for indirect selection of different characters. Since selection for one or more traits results in a correlated response for some of the characteristics (Searle, 1965) and the pattern of variation will also be modified (Waddington and Robertson, 1966). Hence, knowledge of genetic association between yield and its components is important.

In the present study eleven characters viz., days to 50% flowering, days to maturity, nodes up to main raceme, plant height up to main raceme (cm), total length of main raceme (cm), effective length of main raceme (cm), number of capsules on main raceme, effective branches per plant, 100 seed weight (g), oil content (%), shelling out turn (%) were selected to partition their genotypic correlation coefficients with seed yield into the direct and indirect effects. The eleven characters are considered as the independent variables and the seed yield was considered as the dependent variable. The genotypic correlation coefficients worked out between seed yield per plant and each of these eleven independent variables and among themselves. The resulting estimates obtained for direct and indirect effects of different traits on seed yield per plant are presented in table 4.5

4.5.1 Days to 50% flowering Vs Seed yield per plant

Days to 50% flowering showed negative correlation with seed yield per plant ($r_g =$

-0.0861). The direct effect of days to 50% flowering was negative and negligible (-0.0341). The indirect effect of days to 50% flowering was positive and moderate *via* nodes up to main raceme (0.2378). It exhibited low and negative indirect effect *via* 100 seed weight (-0.1502) and effective length of main raceme (-0.1306). It had negligible indirect effects *via* other characters on seed yield per plant. The negative and negligible direct effect of days to 50% flowering was reported earlier by Nagarajan *et al.* (2019).

4.5.2 Days to maturity of main raceme Vs Seed yield per plant

The days to maturity of main raceme had negative and non-significant correlation with seed yield per plant ($r_g = -0.0544$). The direct effect of days to maturity of main raceme was negative and negligible (-0.0802). It showed positive and low indirect effect *via* nodes up to main raceme (0.1963) while negative and low indirect *via* 100 seed weight (-0.1004). Its indirect effect *via* remaining characters was negligible on seed yield per plant. Similar estimates were reported earlier by Nagarajan *et al.* (2019) who found negative and negligible direct effect of days to maturity.

4.5.3 Nodes up to main raceme Vs Seed yield per plant

Nodes up to primary raceme showed significantly positive correlation with seed yield per plant ($r_g = 0.3519^*$). The direct effect of nodes up to main raceme was positive and high (0.7724). The indirect effects *via* number of capsules on main raceme (0.1729) and total length of main raceme (0.1211) were positive and moderate while indirect effect *via* effective length of main raceme (-0.1001) was negative and low. The indirect effect *via* 100 seed weight was negative and high (-0.4474). It had negligible indirect effect *via* remaining characters on seed yield per plant. The positive and high direct effect of nodes up to main raceme on seed yield was earlier reported by Tewari and Mishra (2013).

4.5.4 Plant height up to main raceme Vs Seed yield per plant

Plant height up to main raceme had positive association with seed yield per plant ($r_g = 0.1613$). The direct effect of this trait on seed yield was negative and low (-0.1173). It had a positive and moderate indirect effect *via* nodes up to main raceme (0.2825.) Its

Table 4.5 Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effect of different characters on seed yield in castor

Characters	DF	DM	NPR	PH	SL	ESL	NC	EB	SW	SOT	OC	Genotypic correlation with seed yield
DF	-0.0341	-0.0037	0.2378	-0.0411	-0.0119	-0.1306	-0.0065	-0.0155	-0.1502	-0.0213	0.0911	-0.0861
DM	-0.0016	-0.0802	0.1963	-0.0242	-0.0197	0.0252	-0.0045	0.0084	-0.1004	0.0133	-0.0671	-0.0544
NPR	-0.0105	-0.0204	0.7724	-0.0429	0.1211	-0.1001	0.1729	-0.0389	-0.4474	-0.0313	-0.0232	0.3519 *
PH	-0.0119	-0.0165	0.2825	-0.1173	0.0628	-0.0642	0.0841	0.0263	-0.0663	0.0055	-0.0234	0.1613
SL	0.0006	0.0022	0.1305	-0.0103	0.7171	-0.3757	0.5259	-0.0278	-0.1007	-0.0207	-0.1616	0.6796 **
ESL	-0.0087	0.0039	0.1507	-0.0147	0.5256	-0.5125	0.2725	-0.0275	-0.2143	-0.0394	0.0604	0.1961
NC	0.0003	0.0006	0.2048	-0.0151	0.5782	-0.2141	0.6522	-0.0382	-0.0088	-0.0051	-0.2947	0.8603 **
EB	-0.0057	0.0072	0.3231	0.0331	0.2142	-0.1514	0.2681	-0.0929	-0.1125	-0.0021	-0.0615	0.4196 **
SW	0.0069	0.0108	-0.4639	0.0104	-0.0971	0.1474	-0.0077	0.0141	0.7449	0.0091	-0.3178	0.0573
SOT	-0.0067	0.0099	0.2241	0.0061	0.1374	-0.1871	0.0299	-0.0018	-0.0627	-0.1079	0.0088	0.0499
OC	0.0061	-0.0103	0.0345	-0.0053	0.2228	0.0595	0.3696	-0.0111	0.4552	0.0018	-0.5201	0.6026 **

Note: *,** Significant at 5% and 1% levels respectively.

Residual effect = 0.1070

DF: Days to 50% flowering, DM: Days to maturity, NPR: Nodes up to main raceme, PH: Plant height up to main raceme, SL: Total length of main raceme, ESL: Effective length of main raceme, NC: Number of capsules on main raceme, EB: Effective branches per plant, SW: 100 seed weight, OC: Oil content, SOT: Shelling out turn

indirect effect through other characters was negligible on seed yield per plant.

4.5.5 Total length of main raceme Vs Seed yield per plant

It had highly significant positive correlation with seed yield per plant ($r_g = 0.6796^{**}$). The total length of main raceme had positive and high direct effect (0.7171) on seed yield per plant. It displayed high positive indirect effect *via* number of capsules on main raceme (0.5259) and moderate negative indirect effect *via* effective length of main raceme (-0.3757) on seed yield per plant. The indirect effects *via* nodes up to main raceme were low and positive (0.1305) while *via* oil content (-0.1616) and 100 seed weight (-0.1007) were low and negative. Its indirect effect *via* other traits was negligible on seed yield per plant.

4.5.6 Effective length of main raceme Vs Seed yield per plant

The effective length of main raceme had positive association with seed yield per plant ($r_g = 0.1961$). Its direct effect on seed yield per plant was observed to be negative and high (-0.5125). It displayed positive and high indirect effect *via* total length of main raceme (0.5256) and positive moderate indirect effect *via* number of capsules on main raceme (0.2725). The effective length of main raceme had negative with moderate indirect effect *via* 100 seed weight (-0.2143) on seed yield per plant. The indirect effects *via* remaining traits were negligible on seed yield per plant. Golakia *et al.* (2007) had also recorded the highest negative direct effect of effective length of main raceme along with its positive correlation to seed yield per plant. Similar estimates were also reported by Ramesh *et al.* (2001), Lakshamma *et al.* (2005), Ramanjaneyulu and Reddy (2012) and Chaitanya *et al.* (2013).

4.5.7 Number of capsules on main raceme Vs Seed yield per plant

This trait showed highly significant positive correlation with seed yield per plant ($r_g = 0.8603^{**}$). The direct effect of number of capsules on main raceme with seed yield per plant was positive and high (0.6522). The indirect effect of number of capsules on main raceme *via* total length of main raceme was positive with high value (0.5782) and *via* nodes up to main raceme (0.2048) was moderate and positive. The indirect effects *via*

oil content (-0.2947) and effective length of main raceme (-0.2141) were negative and moderate. The indirect effect through other traits was negligible on seed yield per plant. The positive high direct effect and its high indirect effect through total length of main raceme were earlier reported by Dapke *et al.* (2016) and Mohanty *et al.* (2020). Nagarajan *et al.* (2019) also reported its positive and high direct effect on seed yield per plant.

4.5.8 Effective branches per plant Vs Seed yield per plant

The effective branches per plant displayed highly significant positive correlation with seed yield per plant ($r_g = 0.4196^{**}$). Its direct effect on seed yield per plant was negative and low (-0.0929). It had a positive with high indirect effect *via* nodes up to main raceme (0.3231) on seed yield per plant while it showed positive and moderate indirect effects *via* number of capsules on main raceme (0.2681) and *via* total length of main raceme (0.2142). Negative with low indirect effects were observed *via* effective length of main raceme (-0.1514) and 100 seed weight (-0.1125). The indirect effect of effective branches per plant *via* remaining traits was negligible on seed yield per plant.

4.5.9 100 seed weight Vs Seed yield per plant

100 seed weight had a positive association with seed yield per plant ($r_g = 0.0573$). It showed a high with positive direct effect (0.7449) on seed yield per plant. The 100 seed weight had negative with high indirect effect *via* nodes up to main raceme (-0.4639) and oil content (-0.3178). It displayed positive with low indirect effect *via* effective length of main raceme (0.1474). The indirect effect of 100 seed weight *via* remaining traits was negligible on seed yield per plant. Yamanura and Kumar (2020) also reported similar estimates of high and positive direct effect and negative high indirect effect through nodes up to main raceme and oil content of this character on seed yield. Kumar *et al.* (2003) also reported its positive and high direct effect on seed yield.

4.5.10 Shelling out turn Vs Seed yield per plant

The shelling out turn showed positive association with seed yield per plant ($r_g = 0.0499$). The direct effect of this trait was negative and low (-0.1079) on seed yield per plant. The indirect effect of shelling out turn was positive with moderate value *via* nodes

up to main raceme (0.2241) and positive with low value *via* total length of main raceme (0.1374). It showed negative with low indirect effect *via* effective length of main raceme (-0.1871). The indirect effects of this character *via* remaining characters were negligible on seed yield per plant.

4.5.11 Oil content Vs Seed yield per plant

The oil content percentage had highly significant positive correlation with seed yield per plant ($r_g = 0.6026^{**}$). The direct effect of oil content on seed yield per plant was negative and high (-0.5201). The indirect effects of this trait were positive and high *via* 100 seed weight (0.4552) and number of capsules on main raceme (0.3696), while it was positive and moderate *via* total length of main raceme (0.2228). The indirect effects of this trait *via* remaining characters were negligible on seed yield per plant. The negative and high direct of oil content on seed yield was reported earlier by Yamanura and Kumar (2020).

The genotypic path coefficient analysis indicated that 100 seed weight, nodes up to main raceme, number of capsules on main raceme and total length of main raceme exhibited high and positive direct effect on seed yield. Hence we can say that these characters were major components of seed yield. These four characters can be used as the selection criteria in breeding for higher seed yield in castor.

These traits can be directly attributed for improvement of the seed yield and important in selection of better genotypes in castor (Johnson, 1955; Sarwar, 2005). To improve the seed yield, proper attention must be paid to these traits at the time of selection; since they had strong, direct and positive effects on seed yield, they should be directly selected. Remaining characters displayed either negative or negligible direct effects on seed yield.

It was revealed that although oil content showed highly significant positive correlation with seed yield, it had highly negative direct effect on seed yield. The highly significant positive correlation with seed yield was due to its high positive indirect effect *via* number of capsules on main raceme and oil content.

Residual effect (0.1070) indicated that the characters studied were sufficient to explain per cent of the variation in the seed yield.

When correlation coefficient is positive but direct effect is negative, low or negligible, the indirect effects may be the cause of correlation. In such situation, the direct effects are to be considered simultaneously. In some cases, the direct effect is positive and high along with negative correlation, under such circumstances, a restricted simultaneous selection model can be followed *i.e.* restrictions are to be imposed to lower or nullify the undesirable indirect effects to make use of direct effect.

5. SUMMARY AND CONCLUSION

The research work entitled “**Genetic Variability, Correlation and Path Analysis for Yield and its Attributing Characters in Castor (*Ricinus communis* L.)**” was conducted to assess genetic variability, correlation coefficient and path coefficient analysis in 49 genotypes of castor. The primary objective of the research work was to understand the genetic architecture of various characters under study and their inter-relationship among them.

The experimental material of the present study comprised of 49 diverse genotypes of castor. The pure seeds of these genotypes were procured from various research stations. The study had been carried out at Agricultural Research Station, Sansoli during *kharif* 2020-21 in a randomized block design with three replications.

The experimental material was evaluated for twelve quantitative characters viz., days to 50% flowering, days to maturity of main raceme, nodes up to main raceme, plant height up to main raceme, total length of main raceme, effective length of main raceme, number of capsules on main raceme, effective branches per plant, 100 seed weight, shelling out turn, seed yield per plant and oil content.

The observations were recorded from five competitive plants which are randomly selected from each experimental unit in all the replications for seed yield and its component characters excluding days to 50% flowering and days to maturity as they were recorded on plot basis. The data has been analyzed at Department of Agricultural Statistics, B. A. College of Agriculture, AAU, Anand.

The salient features of the study are as under:

1. Analysis of variance revealed that the mean sum of squares of genotypes were found to be significant for all the twelve traits indicating that there is sufficient amount of variability present in the genotypes under the study and are genetically diverse.

2. The ANDCI 14 is identified as high performing genotype for seed yield based on *per se* performance. The genotype SKI 215 showed highest oil content and also was second highest in seed yield per plant out of total 49 genotypes under study.
3. High degree of variability was shown by characters like seed yield per plant, number of capsules on main raceme and plant height up to main raceme indicating the presence of wide variation for these characters.
4. Estimates of genotypic and phenotypic variance indicated that, genotypic variance contributed more to the total variance suggesting that variability present in genotypes under the study was mainly due to genetic constitution and it was less influenced by the environment.
5. Estimates of genotypic coefficient of variation (GCV %) and phenotypic coefficient of variation (PCV %) had been found to be high for the traits plant height up to main raceme, effective length of main raceme, number of capsules on main raceme, effective branches per plant and seed yield per plant indicating the presence of sufficient variability for these traits. Hence, direct selection based on these traits could lead to further genetic improvement.
6. Estimates of genotypic coefficient of variation (GCV %) and phenotypic coefficient of variation (PCV %) were found to be either low or moderate for the traits days to 50% flowering, days to maturity, nodes up to main raceme and 100 seed weight indicating that there is little or no sufficient variability present for these traits. Hence, direct selection based on these traits would be ineffective for further genetic improvement.
7. High heritability coupled with high genetic advance as per cent mean were recorded for the characters plant height up to main raceme, total length of main raceme, effective length of main raceme, number of capsules on main raceme, effective branches per plant, 100 seed weight, shelling out turn, seed yield per plant and oil content. These results suggest that additive gene action played a major role in governing these characters.
8. High heritability coupled with low to moderate genetic advance as per cent mean were recorded for the characters days to 50% flowering of main raceme and days

to maturity of main raceme. These results indicate that these characters may be under the influence of both additive and non-additive gene effects.

9. The trait nodes up to main raceme had showed moderate heritability coupled with moderate genetic advance. The result suggests that this trait was majorly under control of non-additive gene action.
10. The correlation studies indicated that seed yield per plant was highly significant and positively associated with total length of main raceme, number of capsules on main raceme, effective branches per plant and oil content.
11. Significant and positive correlation of seed yield per plant was found with the trait nodes up to main raceme.
12. Hence we can say that the traits viz., total length of main raceme, number of capsules on main raceme, effective branches per plant, oil content and nodes up to main raceme have contributed more towards higher seed yield.
13. Highly significant and positive correlation of oil content was observed with 100 seed weight, number of capsules on main raceme and seed yields per plant. These results indicated that oil yield can be improved by selecting bold seeded genotypes as the increase in mean value of the trait would significantly increase oil content.
14. The path coefficient analysis revealed that the traits nodes up to main raceme, total length of main raceme, number of capsules on main raceme and 100 seed weight exhibited high and positive direct effect on seed yield. Hence, we can say that these traits were major components of seed yield.
15. The traits total length of main raceme and number of capsules on main raceme had shown highly significant positive correlation and also high and positive direct effect on seed yield per plant. Hence, more importance should be given to these traits at the time of selection.
16. The residual effect of genotypic path coefficient analysis indicated that the characters studied were sufficient to explain per cent of the variation in the seed yield.

❖ **CONCLUSION**

It can be concluded from the above findings that high GCV and PCV coupled with high heritability and genetic advance as per cent mean was observed for the traits viz., plant height up to main raceme, effective length of main raceme, number of capsules on main raceme, effective branches per plant and seed yield per plant. Hence, we can say that high variability and additive gene action is present for the above mentioned traits. Correlation and path analysis revealed the importance of traits viz., total length of main raceme and number of capsules on main raceme. Therefore importance should be given to these characters. The trait number of capsules on main raceme not only showed high values for GCA, PCA, heritability and genetic advance as per cent mean but also was highly significant and positively correlated with seed yield per plant. It also exhibited positive and high direct effect on seed yield per plant. Hence, this trait can be used for further genetic improvement and to obtain high seed yield per plant.

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Appendix I Mean weekly meteorological data recorded during the crop period *kharif* 2020-21 at Agricultural Research Station, Anand Agricultural University, Sansoli.

Month	Meteorological Standard week	Temperature ($^{\circ}\text{C}$)		Relative Humidity (%)		Rainfall (mm)
		Max.	Min.	Max.	Min.	
September 2020	36	33.9	26.6	89.3	65.1	2.0
	37	33.8	26.5	89.7	65.9	28.0
	38	33.6	25.9	91.1	73.4	36.0
	39	32.1	25.3	91.4	66.3	3.2
	40	33.9	24.9	86.7	52.1	13.2
October 2020	41	35.9	23.0	77.1	38.6	0.0
	42	35.1	26.9	88.4	56.5	10.4
	43	35.3	20.3	79.9	29.6	0.0
	44	34.0	17.6	80.4	30.5	0.0
November 2020	45	33.4	15.8	80.1	29.6	0.0
	46	32.6	19.1	78.9	39.6	0.0
	47	30.4	15.2	80.9	39.1	0.0
	48	30.4	17.6	76.6	41.6	0.0
December 2020	49	32.7	15.1	87.9	36.1	0.0
	50	27.4	17.9	94.1	62.4	16.4
	51	26.6	12.6	82.0	44.3	0.0
	52	26.8	12.3	73.6	36.5	0.0
January 2021	1	25.7	14.9	77.0	48.0	0.0
	2	27.5	16.1	89.0	59.0	0.0
	3	29.2	13.6	91.0	44.0	0.0
	4	26.9	11.1	81.0	38.0	0.0
February 2021	5	28.9	10.9	83.0	31.0	0.0
	6	29.6	11.0	80.0	23.0	0.0
	7	31.8	14.7	82.0	34.0	0.0
	8	32.7	15.6	74.0	27.0	0.0
March 2021	9	34.4	15.2	84.0	27.0	0.0
	10	35.8	16.6	85.0	29.0	0.0
	11	36.4	18.1	75.0	30.0	0.0
	12	36.5	20.0	77.0	36.0	0.0
	13	38.1	19.8	74.0	27.0	0.0

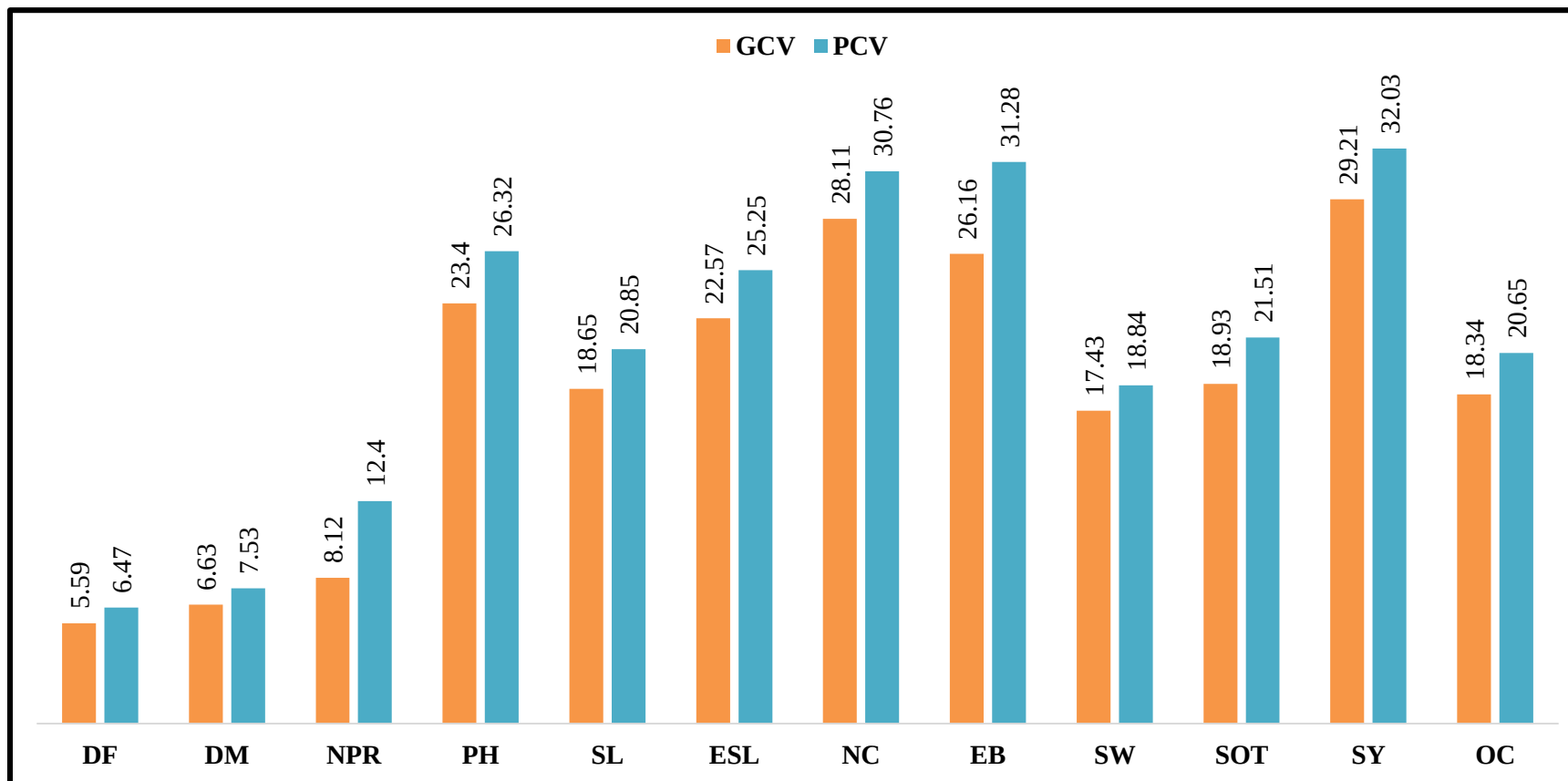


Fig 4.1 Graphical representation of Genotypic and Phenotypic Coefficient of Variation

DF: Days to 50% flowering, DM: Days to maturity, NPR: Nodes up to main raceme, PH: Plant height up to main raceme, SL: Total length of main raceme, ESL: Effective length of main raceme, NC: Number of capsules on main raceme, EB: Effective branches per plant, SW: 100 seed weight, SOT: Shelling out turn (%), SY: Seed yield per plant, OC: Oil content (%)

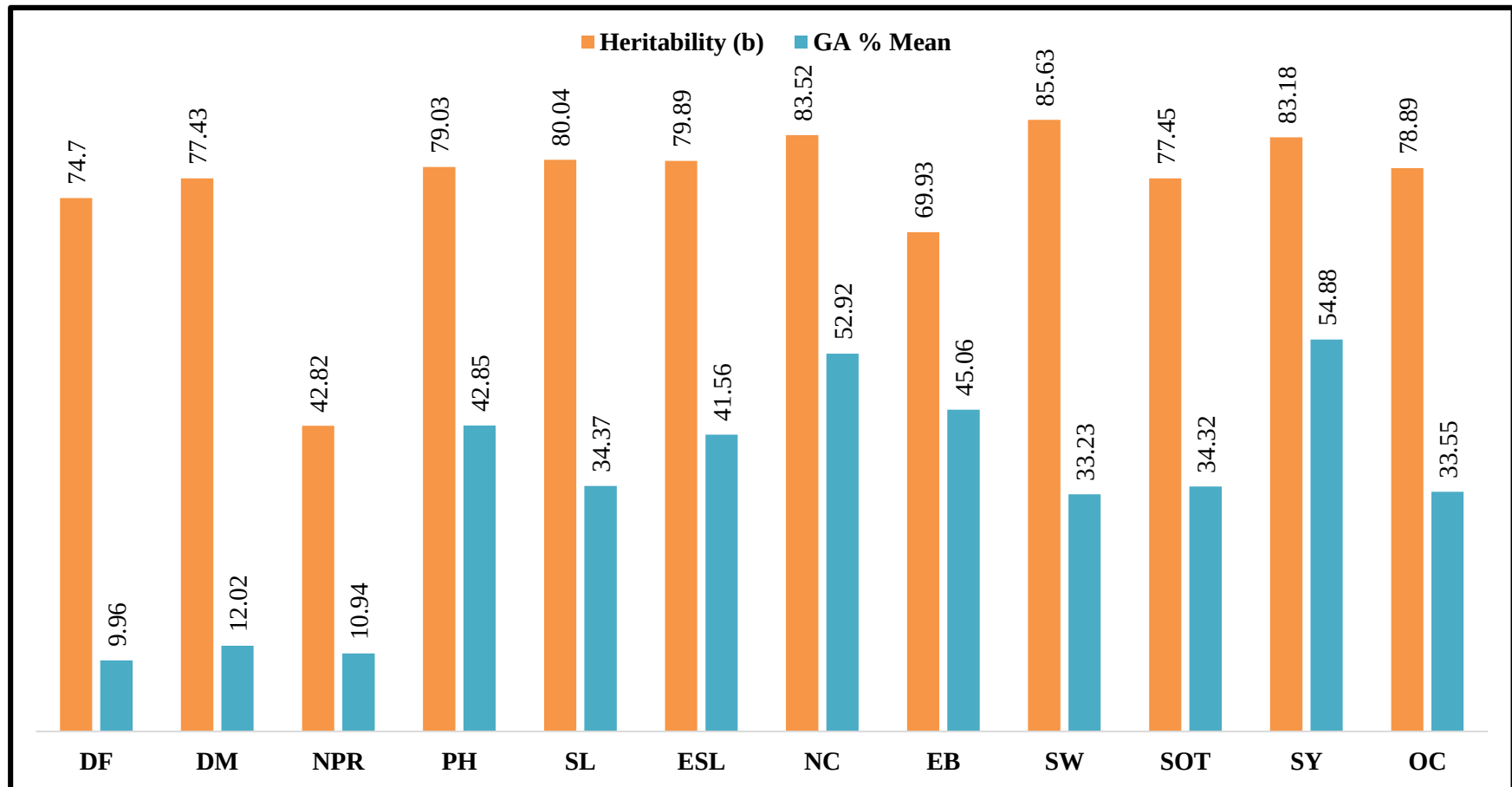


Fig 4.2 Graphical representation of Broad Sense Heritability and Genetic Advance as per cent Mean

DF: Days to 50% flowering, DM: Days to maturity, NPR: Nodes up to main raceme, PH: Plant height up to main raceme, SL: Total length of main raceme, ESL: Effective length of main raceme, NC: Number of capsules on main raceme, EB: Effective branches per plant, SW: 100 seed weight, SOT: Shelling out turn (%), SY: Seed yield per plant, OC: Oil content (%)

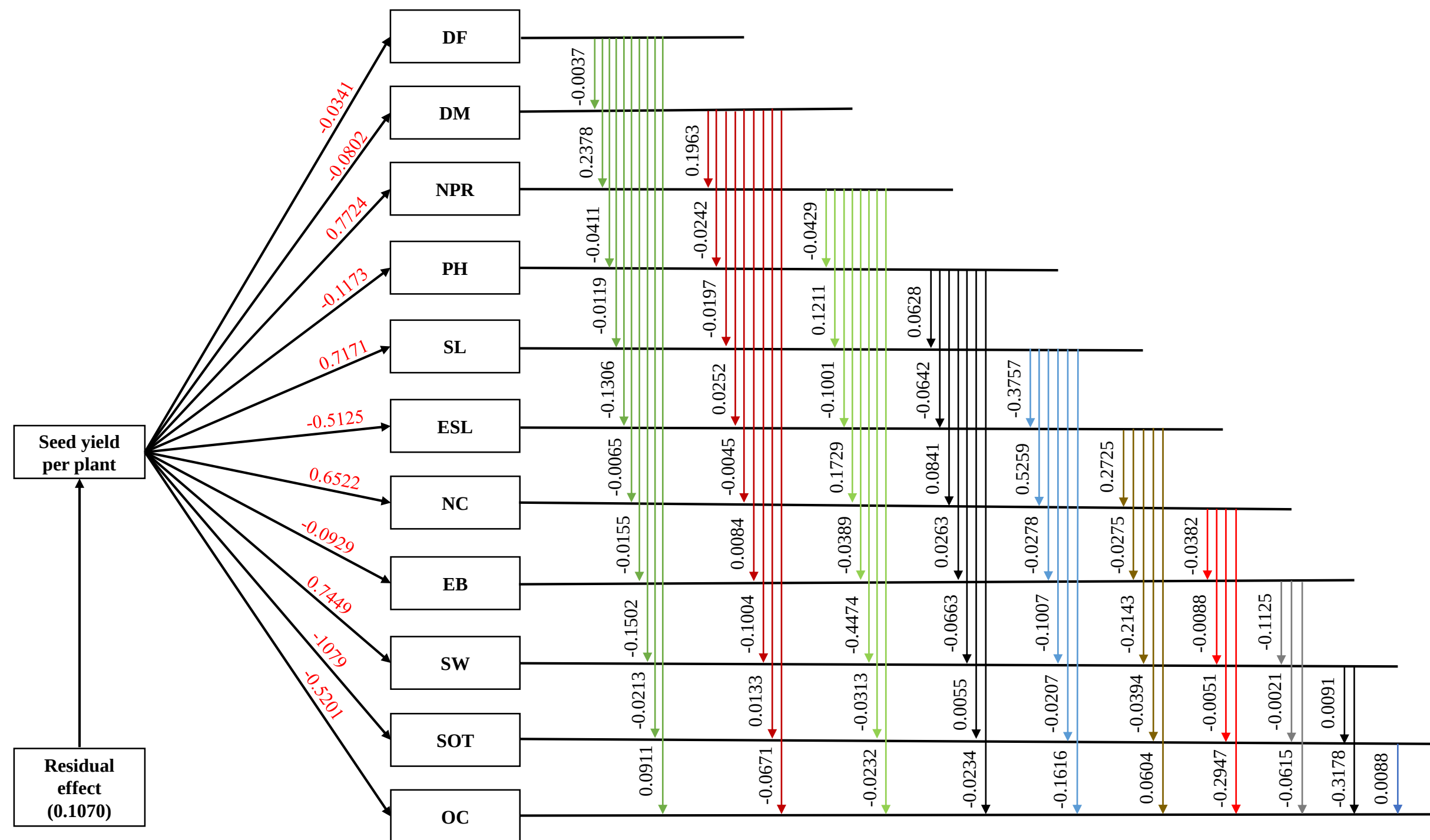


Fig. 4.3 Path diagram showing direct and indirect effects of various characters on seed yield per plant

DF: Days to 50% flowering, DM: Days to maturity, NPR: Nodes up to main raceme, PH: Plant height up to main raceme, SL: Total length of main raceme, ESL: Effective length of main raceme, NC: Number of capsules on main raceme, EB: Effective branches per plant, SW: 100 seed weight, SOT: Shelling out turn (%), SY: Seed yield per plant, OC: Oil content (%)



Plate 3.1 Field view of castor experiment at Agricultural Research Farm AAU, Sansoli (*kharif* 2020-21)



MI 10 (Compact)

JI 428 (Semi-compact)

JI 368 (Semi-loose)

JI 440 (Loose)

Plate 4.1 Variability among racemes of four castor genotypes used in the study



48-1 (Non-spiny)



DCS 109 (Spiny)



JI 397 (Spiny)

Plate 4.2 Variability among capsules of three castor genotypes used in the study



48-1



DCS 109



JI 397

Plate 4.3 Variability among seeds of three castor genotypes used in the study