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# Genetic Variability and Character Association Studies among Yield Attributing Traits in Genepool Lines of Castor (*Ricinus communis* L.)

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**ABSTRACT: Castor is one of the major industrial oilseed crops with limited genetic diversity. It is therefore important to diversify the genetic base and develop gene pools to harness the diversity and selection efficacy of important morphological traits in crop improvement programs. In this study, fifty castor lines isolated from random mating gene pool and selfed till homozygosity were evaluated for ten phenotypic traits along with two checks. The *gcv* and *pcv* values indicated presence of broad variation for all characters except for days to 50 per cent flowering and days to maturity. However, high heritability coupled with high genetic advance as per cent mean was registered for plant height, number of nodes to primary raceme, primary raceme length, effective primary raceme length, number of effective racemes per plant, number of capsules in primary raceme, 100 seed weight and seed yield. The characters primary raceme length, effective primary raceme length, number of effective racemes, number of capsules in primary raceme and 100 seed weight showed significant positive correlation with seed yield. Path coefficient analysis indicated that days to 50 per cent flowering, days to maturity, number of nodes, primary raceme length, number of effective racemes, number of capsules in primary raceme and 100 seed weight had positive direct effect on seed yield. Hence it was established that selection for traits primary raceme length, number of effective racemes, number of capsules in primary raceme and 100 seed weight should be the basis in yield improvement programmes of castor.**

**Keywords:** Castor, Correlation, gcv, Genetic Advance, Heritability, Path and PCV.

## INTRODUCTION

Castor (*Ricinus communis* L.) is an industrially important non-edible oilseed crop. It belongs to the family *Euphorbiaceae* and has a chromosome number of 2n=20 (Goodarzi *et al.*, 2012). Presently castor crop is cultivated in 30 countries across the globe among which India is leading in production and export (Sadaiah *et al*., 2021). India exports 83 per cent of world's castor oil to China, USA, Japan, Thailand and few European countries (Lokesh *et al*., 2020). Castor seeds contain 45 to55 per cent oil which is the major source of the unusual hydroxyl fatty acid 'ricinoleic acid' that has tremendous industrial significance (Senthilvel *et al*., 2016). It is one of the best sources for the production of biodiesel (Papreja and Mahla 2016). Genetic improvement of any trait requires presence of genotypic variability in the germplasm (Zheng *et al.*, 2010). Hence it is critical to look at the extent of genetic variation present within a crop in order to increase the efficiency of selection. To achieve this, the genotypes have to be subjected to phenotypic evaluation followed by estimation of heritability of the traits and associations of these traits with each other. Heritability estimates are necessary to obtain information on the heritable portion of variability (Jyothsna *et al*., 2016). However, high heritability should be coupled with high genetic advance to make the selection effective (Mullualem *et al*., 2017). To achieve targeted yield enhancement, genetic improvement in yield contributing traits is a must. Studies on correlation coefficient provide information on the nature and strength of associations between various traits while path coefficient analysis allows splitting of the association into direct and indirect effects through other attributes by the correlations thus defining the cause and effect relationship between the variables (Dapke *et al*., 2016). Hence the current investigation aims at estimation of genetic variability and character associations among yield related traits in the selected genepool lines of castor.

## MATERIAL AND METHODS

The experiment was carried out at Regional Agricultural Research Station, Palem situated at 16.5154˚N latitude and 78.2493˚E longitude during *kharif*, 2021. Fifty advanced genepool lines were sown along with two checks (Pragathi for yield attributing traits and DPC-9 for pistillate nature) with a spacing of 90 cm between the rows and 60 cm between the plants in augmented randomized complete block design by replicating the checks five times in which each line is sown in a single row of 6.0 m length. All the agronomic practices and necessary plant protection measures were followed to raise a healthy crop.

The observations *viz*., days to 50 per cent flowering, days to maturity, plant height (cm), number of nodes to primary raceme, primary raceme length (cm), effective primary raceme length (cm), number of effective racemes per plant, number of capsules in primary raceme, 100 seed weight (g) and seed yield (g plot$^{-1}$) at 90, 120 and 150 days after sowing were recorded on randomly selected five plants in each genotype and mean values were considered for analysis.

Analysis of variance for augmented randomized complete block design (Federer, 1956) was performed as per the method suggested by Panse and Sukhatme (1964) to assess genotypic differences between the entries. Genotypic ($\sigma^2$g) and phenotypic ($\sigma^2$p) variances were calculated based on the formula given by Burton (1953) and the range of variation was categorized according to the recommendations of Subramanian and Menon (1973). Formula given by Hanson *et al*. (1956) was used to calculate broad sense heritability [$h^2$ (b)] and the heritability estimations were classified as indicated by Johnson *et al.* (1955). The projected genetic gain in the next generation is given by genetic advance which was calculated by the formula of Johnson *et al.* (1955). The variance and covariance components for each pair of characteristics were estimated by the methods described by Al-Jibouri *et al*. (1958) from which phenotypic and genotypic correlation coefficients were calculated. The estimated values of correlation coefficients were then compared with table values of correlation coefficients (Fisher and Yates, 1963) at 5 per cent and 1 per cent levels of significance in order to test their significance. The correlation coefficients were further divided into direct and indirect effects of independent factors on the dependent variable in path coefficient analysis proposed by Wright (1921) and elaborated by Dewey and Lu (1959). All the above mentioned analyses were performed using INDOSTAT software.

## RESULTS AND DISCUSSION

### *A. Genetic variability parameters*

Analysis of variance indicated significant variations for all characters studied in the fifty genotypes. The *gcv* values ranged from 4.63 for days to maturity to 45.88 for seed yield. The values of *gcv* and *pcv* were categorized as low (<10%), medium (10-20%) and high (>20%) (Subramanian and Menon, 1973) (Table 1). High *gcv* was observed for the traits plant height (33.21), number of effective racemes (27.42), number of capsules in primary raceme (32.14) and seed yield (45.88) while for the characters number of nodes (19.36), primary raceme length (19.83), effective primary raceme length (16.55) and 100 seed weight (11.62) medium *gcv* was noted. Low *gcv* was observed for days to 50 per cent flowering (7.33) and days to maturity (4.63). *pcv* values ranged between 7.54 and 49.65 and high *pcv* was observed for plant height (34.37), number of nodes (21.06), primary raceme length (20.38), number of effective racemes (32.9), number of capsules in primary raceme (32.51) and seed yield (45.88). In case of effective primary raceme length (16.56) and 100 seed weight (12.21) the *pcv* was medium while the traits days to 50 per cent flowering (7.54) and days to maturity (4.91) exhibited low *pcv*. Values of *gcv* were slightly lower than those of *pcv* implying minor influence of environment on the expression of these characters. Results also indicated the presence of broad genetic variability for all the traits under study except days to 50 per cent flowering and days to maturity. Similar results can be observed in the findings of Chaudhari *et al.* (2016); Mullualem *et al.* (2017); Alhaji *et al*. (2019).

Heritability was categorized as low (<30), moderate (30-60) and high (>60) (Johnson *et al*., 1955) and high heritability was observed for all the characters under study (Table 1). However only eight among the ten characters studied *viz*., plant height, number of nodes, primary raceme length, effective primary raceme length, number of effective racemes, number of capsules in primary raceme, 100 seed weight and seed yield showed high heritability coupled with high genetic advance as per cent mean. Thus inheritance of these characters was due to additive gene action and there was no environmental influence on their expression which makes them feasible for direct selection. Days to 50 per cent flowering portrayed high heritability but medium genetic advance indicating presence of both additive and non-additive gene action and so was considerably influenced by the environment. The character days to maturity exhibited high heritability and low genetic advance implying non-additive gene action and high environmental interference in its expression. These results were in accordance with the previous finding of Rukhsar *et al*. (2018); Movaliya *et al*. (2018).

### *B. Character associations*

The character associations of nine morphological characters with seed yield were assessed through correlation and path coefficient analyses (Table 2) (Fig. 1). The results revealed that primary raceme length (0.4251**), effective primary raceme length (0.2931*), number of effective racemes (0.5943**), number of capsules in primary raceme (0.5457**) and 100 seed weight (0.5251**) showed significant positive correlation with seed yield. Significant negative correlation with seed yield was noted for days to maturity (-0.3952**) while days to 50 per cent flowering (-0.1135), plant height (-0.2679), number of nodes up to primary raceme (-0.2329) exhibited non-significant negative associations. Therefore these lines are highly useful in developing short duration varieties suitable for mechanical harvesting which require negative selection for flowering and plant height traits without compromising seed yields. These kinds of associations between the traits were previously noted by Goodarzi *et al.* (2015); Dapke *et al*. (2016); Silva *et al*. (2017); Salihu *et al*. (2018).

Path coefficient analysis revealed that days to 50 per cent flowering (0.0493), days to maturity (0.0452), number of nodes up to primary raceme (0.0101), primary raceme length (0.0934), number of effective racemes (0.6996), number of capsules in primary raceme (0.6094) and 100 seed weight (0.2239) showed positive direct effect on seed yield (Table 3) (Fig. 2). So selection for these traits is highly recommended for yield enhancement in castor. The character effective primary raceme length showed negative direct effect on seed yield despite a significant positive correlation which may be due to negative indirect effects from days to maturity (-0.0015), plant height (-0.0040), number of nodes (-0.0005), primary raceme length (-0.0160), number of effective racemes (-0.0004), number of capsules in primary raceme (-0.0082) and 100 seed weight (-0.0007). Rukhsar *et al.* (2018); Salihu *et al*. (2018); Alhaji *et al.* (2019) also have observed similar direct and indirect effects of yield attributing traits on seed yield.

**Table 1: Magnitude of variability, heritability and genetic advance for different agro-morphological characters in castor genepool lines**

| Trait | Mean | Range | | *gcv* | *pcv* | $h_{BS}$ | GAM |
|---|---|---|---|---|---|---|---|
| | | Minimum | Maximum | | | | |
| **DFF** | 53.77 | 43.00 | 65.00 | 7.33 | 7.54 | 94.53 | 14.71 |
| **DTM** | 102.95 | 95.00 | 122.00 | 4.63 | 4.91 | 89.22 | 9.03 |
| **PH(cm)** | 103.05 | 29.60 | 226.80 | 33.21 | 34.37 | 93.37 | 66.21 |
| **NN** | 13.89 | 8.20 | 23.20 | 19.36 | 21.06 | 84.52 | 36.72 |
| **PRL(cm)** | 52.54 | 34.80 | 98.50 | 19.83 | 20.38 | 94.69 | 39.81 |
| **EPRL(cm)** | 44.95 | 31.20 | 57.00 | 16.55 | 16.56 | 99.92 | 34.14 |
| **NR** | 4.07 | 1.00 | 8.40 | 27.42 | 32.9 | 69.47 | 47.15 |
| **NC** | 57.86 | 25.80 | 58.13 | 32.14 | 32.51 | 97.69 | 65.53 |
| **TW(g)** | 28.12 | 21.00 | 37.00 | 11.62 | 12.21 | 90.66 | 22.83 |
| **PY(g)** | 656.07 | 119.14 | 1783.98 | 45.88 | 49.65 | 85.38 | 87.45 |

*gcv*- Genotypic coefficient of variation, *pcv*- Phenotypic coefficient of variation, $h_{BS}$- Heritability in broad sense, GAM - Genetic advance as per cent of mean, DFF – Days to 50 per cent flowering, DTM - Days to maturity, PH - Plant height up to primary raceme (cm), NN - Number of nodes up to primary raceme, PRL - Primary raceme length (cm), EPRL - Effective primary raceme length (cm), NR - Number of effective racemes per plant, NC - Number of capsules in primary raceme, TW – 100 seed weight (g) and PY - Seed yield per plot (g).

**Table 2: Correlation coefficients of yield and yield attributing traits in castor gene pool lines.**

| | DFF | DTM | PH | NN | PRL | EPRL | NR | NC | TW | PY |
|---|---|---|---|---|---|---|---|---|---|---|
| **DFF** | 1 | 0.4681** | 0.4311** | 0.4790** | -0.1049 | -0.0620 | -0.3183* | 0.0858 | -0.0911 | -0.1135 |
| **DTM** | | 1 | 0.4544** | 0.3564** | -0.0993 | 0.03808 | -0.3948** | -0.2320 | -0.1521 | -0.3952** |
| **PH** | | | 1 | 0.5546** | -0.1606 | 0.10093 | -0.6214** | 0.3066* | -0.3672** | -0.2679 |
| **NN** | | | | 1 | -0.1365 | 0.00431 | -0.4281** | 0.0786 | -0.1149 | -0.2329 |
| **PRL** | | | | | 1 | 0.5655** | 0.3111* | 0.1361 | 0.2399 | 0.4251** |
| **EPRL** | | | | | | 1 | 0.0861 | 0.2698 | 0.0557 | 0.2931* |
| **NR** | | | | | | | 1 | -0.2194 | 0.3477* | 0.5943** |
| **NC** | | | | | | | | 1 | 0.0322 | 0.5457** |
| **TW** | | | | | | | | | 1 | 0.5251** |
| **PY** | | | | | | | | | | 1 |

DFF – Days to 50 per cent flowering, DTM - Days to maturity, PH - Plant height up to primary raceme (cm), NN - Number of nodes to primary raceme, PRL - Primary raceme length (cm), EPRL - Effective primary raceme length (cm), NR - Number of effective racemes per plant, NC - Number of capsules in primary raceme, TW –100 seed weight (g) and PY - Seed yield per plot (g).

**Table 3: Path coefficients for agro morphological traits in castor gene pool lines.**

| | DFF | DTM | PH | NN | PRL | EPRL | NR | NC | TW |
|---|---|---|---|---|---|---|---|---|---|
| **DFF** | **0.0493** | 0.0194 | 0.0220 | 0.0247 | -0.0046 | -0.0021 | -0.0134 | 0.0048 | -0.0052 |
| **DTM** | 0.0178 | **0.0452** | 0.0198 | 0.0145 | -0.0069 | 0.0021 | -0.0183 | -0.0114 | -0.0073 |
| **PH** | -0.0013 | -0.0013 | **-0.0029** | -0.0016 | 0.0006 | -0.0004 | 0.0018 | -0.0008 | 0.0011 |
| **NN** | 0.0051 | 0.0033 | 0.0056 | **0.0101** | -0.0013 | 0.0002 | -0.0037 | 0.0009 | -0.0012 |
| **PRL** | -0.0087 | -0.0143 | -0.0200 | -0.0123 | **0.0934** | 0.0476 | 0.0354 | 0.0148 | 0.0251 |
| **EPRL** | 0.0013 | -0.0015 | -0.0040 | -0.0005 | -0.0160 | **-0.0313** | -0.0004 | -0.0082 | -0.0007 |
| **NR** | -0.1897 | -0.2832 | -0.4411 | -0.2545 | 0.2649 | 0.0081 | **0.6996** | -0.1111 | 0.2777 |
| **NC** | 0.0598 | -0.1536 | 0.1704 | 0.0539 | 0.0964 | 0.1598 | -0.0967 | **0.6094** | 0.0201 |
| **TW** | -0.0234 | -0.0363 | -0.0880 | -0.0265 | 0.0602 | 0.0052 | 0.0889 | 0.0074 | **0.2239** |
| **PY** | -0.0898 | -0.4223 | -0.3382 | -0.1922 | 0.4867 | 0.1892 | 0.6932 | 0.5058 | 0.5335 |
| **Partial $R^2$** | -0.0044 | -0.0191 | 0.001 | -0.0019 | 0.0454 | -0.0059 | 0.4850 | 0.3082 | 0.1195 |

R Square = 0.9278 Residual effect = 0.2687

DFF – Days to 50 per cent flowering, DTM - Days to maturity, PH - Plant height up to primary raceme, NN - Number of nodes to primary raceme, PRL - Primary raceme length, EPRL - Effective primary raceme length, NR - Number of effective racemes per plant, NC - Number of capsules in primary raceme, TW –100 seed weight and PY - Seed yield per plot

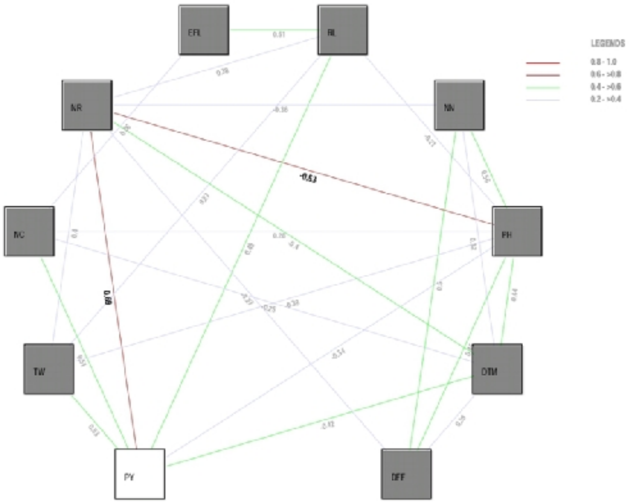

**Fig. 1.** Phenotypic correlation coefficients among different traits in castor.

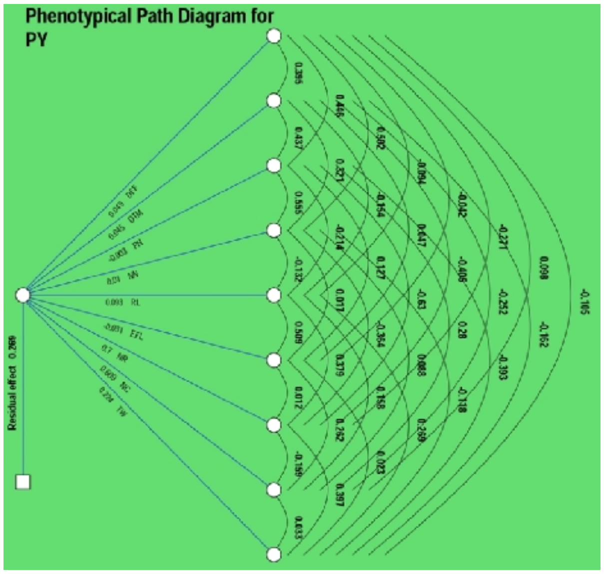

**Fig. 2.** Phenotypical path diagram of various traits with seed yield per plot in castor.

## CONCLUSION

It can be concluded based on the results of variability studies, correlation and path coefficient analyses, that the characters primary raceme length, number of effective racemes per plant, number of capsules in primary raceme and 100 seed weight largely define the seed yield of castor and hence should be prioritized in selection programmes in order to develop high yielding varieties and hybrids.

## FUTURE SCOPE

Through the studies on GCV, PCV, heritability, genetic advance as per cent of mean, correlation and path coefficient analysis the traits that were desirable for improvement in yield were identified. The associations among these traits also became very clear which can be exploited to improve the overall seed yield without compromising on other characters like crop duration and plant architecture in the future castor breeding programmes. The data can also be useful for selecting superior lines for the development of varieties and hybrids.

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**Conflict of Interest.** None.

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