Plant Archives Vol. 25, No. 2, 2025 pp. 43-48 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.no.2.008

ASSESSMENT OF GENETIC PARAMETERS FOR YIELD AND YIELD CONTRIBUTING TRAITS IN CASTOR (*RICINUS COMMUNIS* L.)

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(Date of Receiving-24-05-2025; Date of Acceptance-30-07-2025)

ABSTRACT

Castor (*Ricinus communis* L.) is a vital non-edible oilseed crop with substantial industrial and export potential. Castor oil and its derivatives are widely utilized as lubricants in the aerospace and power engine industries, as well as in the manufacture of pharmaceuticals, soaps, cosmetics, varnishes, and other industrial products. The present study was undertaken to estimate genetic parameters such as phenotypic and genotypic coefficients of variation (PCV and GCV), broad-sense heritability, genetic advance as a percentage of the mean and correlation analysis. The results revealed that, for most of the traits, the difference between PCV and GCV was minimal, indicating a relatively low environmental influence and greater genetic control over trait expression. High broad-sense heritability was recorded for the majority of the traits, except for days to 50% flowering and number of effective spikes per plant. This suggests that additive gene action predominates in the inheritance of these traits. Therefore, direct selection for traits such as days to maturity, number of nodes to primary spike, plant height, primary spike length, effective primary spike length, number of effective spikes per plant, number of capsules per spike, seed yield (kg ha{-^{1}), and 100-seed weight (g) would be both effective and advantageous for improving yield potential in castor. Correlation studies revealed that seed yield has shown direct positive association with primary spike length, effective primary spike length and number of capsules per primary spike. Thus, selection for these traits will be effective in yield improvement of castor.

Key Words: Castor, Correlation, GCV, Heritability, PCV, Seed Yield.

Introduction

Castor (*Ricinus communis* L.) is a non-edible oilseed crop belonging to the family Euphorbiaceae. It can be grown either as an annual or a perennial crop, depending on agro-climatic conditions. Castor seeds contain approximately 50–55% oil. The crop is distributed widely across tropical and subtropical regions of the world (Kumar *et al*., 2015; Chaudhari *et al*., 2019), and is believed to have originated in the Ethiopian and Eastern African regions, where high genetic diversity has been observed (Vavilov, 1951; Moshkin, 1986; Rukhsar *et al*., 2017). India is the world's leading producer and exporter of castor oil, accounting for nearly 80% of the global export volume. Within India, Gujarat ranks first in both area and production, followed by Rajasthan, Andhra Pradesh, and Telangana. Despite its significance, castor cultivation in India remains confined to approximately eight lakh hectares, with an average productivity of 1,930 kg/ha (Indiastat, 2025).

Castor oil is rich in ricinoleic acid, a unique hydroxylated fatty acid that imparts valuable industrial properties. Ricinoleic acid not only enhances the lubricating properties of the oil particularly in the aerospace and power engine industries but also makes it highly suitable for biodiesel production, even at low temperatures (Sujatha *et al*., 2008). In addition, castor oil finds diverse applications in the manufacturing of soaps, varnishes, plasticizers, inks, and cosmetics (Ranjitha *et al*., 2019; Morris, 2004).

To meet the rising industrial demand for castor oil,

Table 1: List of hybrids utilised for the study.

S. No.	Hybrid	S. No.	Hybrid
1	PCH720	10	PCH729
2	PCH721	11	PCH730
3	PCH722	12	PCH731
4	PCH723	13	PCH745
5	PCH724	14	PCH746
6	PCH725	15	PCH747
7	PCH726	16	PCH748
8	PCH727	17	PCH749
9	PCH728	18	ICH5 ©
		19	PCH111 ©

there is an urgent need to enhance castor productivity. Although present-day hybrids exhibit high yield potential and resistance to major pests and diseases, further yield improvement remains largely untapped. This highlights the importance of incorporating genetically diverse parental lines and evaluating hybrids derived from such crosses. In this context, the present study of estimation of genetic parameters including phenotypic and genotypic variability, heritability, and genetic advance along with correlation analysis, becomes crucial. These tools enable breeders to understand the inheritance of traits, the extent of environmental influence on trait expression, and the interrelationship among key yield-contributing characters. Though the present study was carried out on hybrids, this will give a basic understanding of the inheritance of traits and their association.

Material and Methods

The present investigation was carried out during *kharif*, 2024 at the Regional Agricultural Research Station (RARS), Professor Jayashankar Telangana Agricultural University (PJTAU), Palem, located in Nagarkurnool district, Telangana. The experimental site is situated at 16.51° N latitude and 78.24° E longitude, with an altitude of 545 meters above mean sea level. The experimental material consisted of 19 castor hybrids, including two standard checks (Table 1), developed at RARS, Palem. The hybrids were evaluated in a randomized complete block design (RBD) with two replications. Each genotype was sown in a single row of 6 meters in length, with a spacing of 90 cm between the rows and 60 cm among the plants in a row. Observations were recorded on five randomly selected plants from each genotype for various agronomic and yield-related traits, including days to 50% flowering, plant height (cm), number of nodes to primary spike, primary spike length (cm), effective primary spike length (cm), number of effective spikes per plant, number of capsules per primary spike, seed yield (kg ha^{-1}), and hundred seed weight (g).

The data were subjected to analysis of variance (ANOVA) as per the procedure outlined by Panse and Sukhatme (1985) to determine the significance of genotypic differences. Phenotypic and genotypic coefficients of variation (PCV and GCV) were calculated following the method of Falconer (1981), while broad-sense heritability and genetic advance as a percentage of mean were estimated using the formulas suggested by Allard (1960) and Johnson *et al.*, (1955), respectively. Correlation analysis among traits was performed using the method described by Snedecor and Cochran (1967). All statistical analyses related to genetic parameters (Popat *et al.*, 2020) and correlation studies (Makowski *et al.*, 2022) were carried out using the R software environment.

Results and Discussion

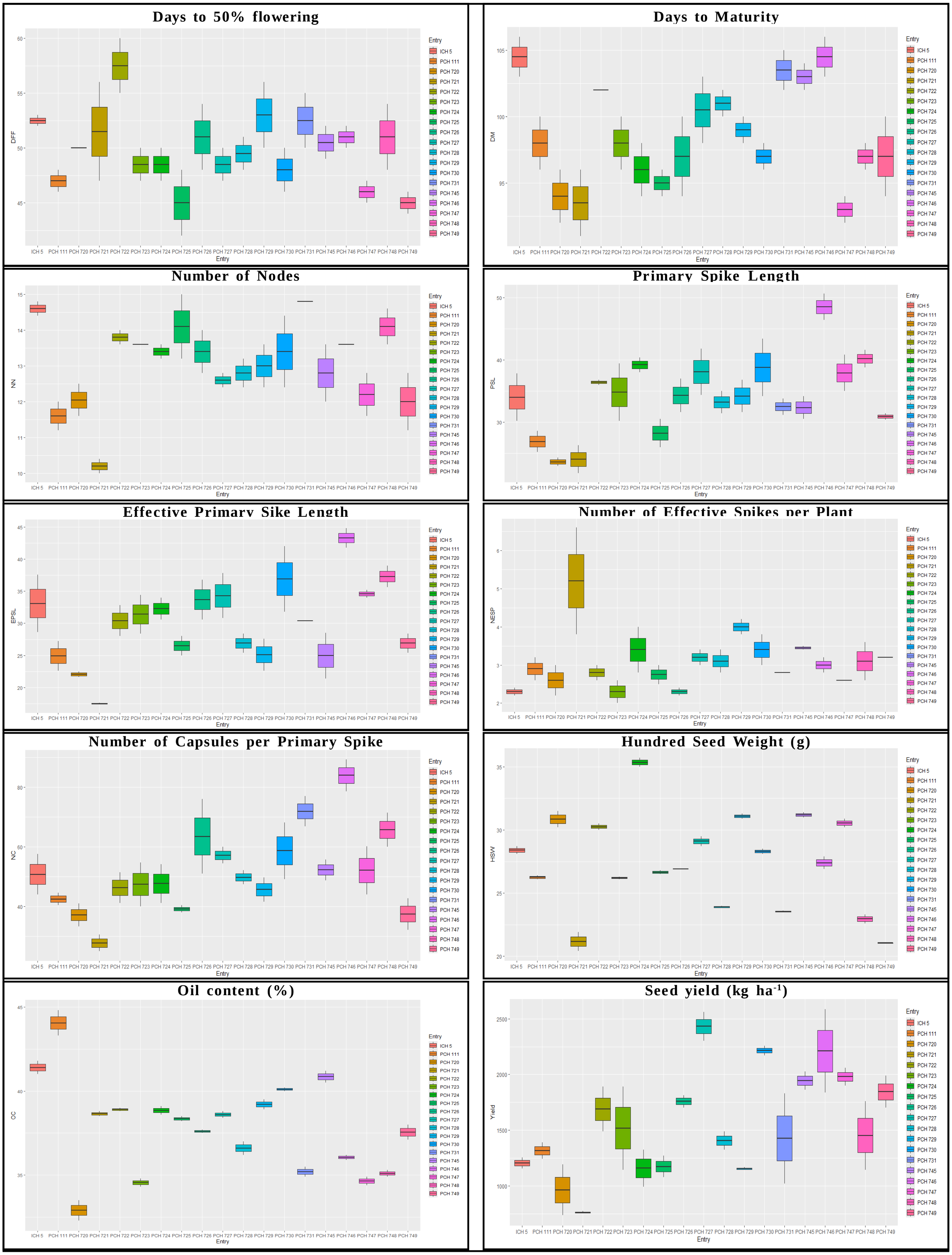
Analysis of variance (ANOVA) revealed that the genotypes differed significantly for all the traits under study (Table 2), indicating the presence of considerable genetic variability in the experimental material. The distribution of genotypes for the observed traits, depicted through boxplots (Fig. 1), further confirmed the extent of variability. Substantial variation was also reflected in the range values of the studied traits (Table 3).

Days to 50% flowering varied from 42 to 60 days, while days to maturity ranged from 91 to 106 days. The number of nodes to the primary spike, a proxy for earliness, ranged from 10 to 15. Primary spike length, measured from the basal node to the spike tip, ranged from 21.8 to 50.6 cm, whereas effective primary spike length (from the first to the last capsule) varied between 17.4 and 44.8 cm. The number of capsules per primary

Table 2: Analysis of variance (ANOVA) for yield and its attributing traits.

Source of Variation	*df*	Mean sum of square									
		DFF	DM	NN	PSL	EPSL	NC	NESP	HSW	OC	Yield
Replication	1	32.23	0.65	0.91	36.41	50.02*	117.08	1.21	0.12	0.13	149038
Genotype	18	18.73*	27.03**	2.50**	71.3**	74.93**	354.06**	0.92*	28.4**	15.07**	419055**
Error	18	8.01	6.65	0.52	11.63	10.81	67.55	0.31	0.22	0.22	73453

Where, DFF-Days to 50% Flowering, DM-Days to Maturity, NN-Number of Nodes to primary spike, PSL-Primary Spike Length (cm), EPSL-Effective Primary Spike Length (cm), NC-Number of Capsules on Primary Spike, NESP-Number of Effective Spikes per Plant, HSW-Hundred Seed Weight (g), OC-Oil Content (%), Yield- Seed Yield (kg ha^{-1})


Days to 50% flowering

Days to Maturity

Number of Nodes

Primary Spike Length

Effective Primary Sike Length

Number of Effective Spikes per Plant

Number of Capsules per Primary Spike

Hundred Seed Weight (g)

Oil content (%)

Seed yield (kg ha^{-1})

Fig. 1: Box plots displaying the performance of different hybrids for different yield contributing traits.

Table 3: Genetic parameters for yield and yield related traits in castor germplasm lines.

Trait	Mean	Range	H^2 (%)	GAM	GCV (%)	PCV (%)
DFF	49.8	42-60	40.0	6.1	4.6	7.3
DM	98.6	91-106	60.5	5.2	3.2	4.2
NN	13.0	10-15	65.6	12.7	7.6	9.4
PSL	34.1	21.8-50.6	71.9	27.9	16.0	18.8
EPSL	30.1	17.4-44.8	74.7	33.4	18.7	21.7
NC	51.4	25.0-89.2	67.9	39.5	23.2	28.2
NESP	3.0	2.0-6.6	49.6	26.1	17.9	25.5
HSW	27.4	20.4-35.7	98.4	27.9	13.6	13.7
OC	37.8	32.3-44.8	97.0	14.6	7.2	7.3
Yield	1558.9	736.1-2583.3	70.2	46.0	26.6	31.8

Where, H^2 – Heritability, GAM – Genetic Advance as percent of Mean, GCV – Genotypic Coefficient of Variation, PCV – Phenotypic Coefficient of Variation

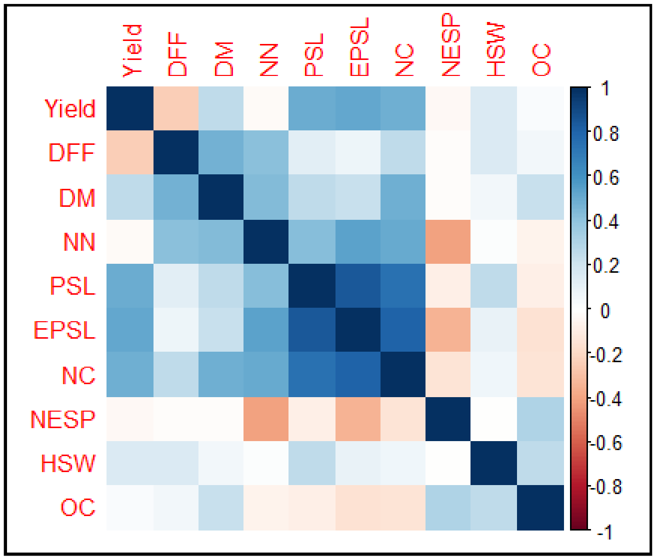


Fig. 2: Pearson's correlation among different traits under study.

spike, a key contributor to yield ranged from 25 to 89.2, and the number of effective spikes per plant varied from 2 to 6.6. Hundred seed weight, a direct indicator of productivity, ranged between 32.3 and 44.8 g. Oil content, an economically important trait in castor, also showed substantial variation from 32.3 to 44.8%. Seed yield varied from 736 to 2,583 kg ha^{-1}, demonstrating high yield diversity among the hybrids (Table 3).

Among the genotypes, PCH-724, though possessing a high hundred seed weight, recorded low yield due to fewer effective spikes and shorter spike length. In contrast, PCH-727 and PCH-730 showed superior yields compared to the checks and other entries under testing, indicating their potential for further evaluation in breeding programs. Notably, PCH-747 emerged as the earliest maturing hybrid with significantly higher yield than the check, followed by PCH-725, which exhibited on-par yield performance. The early maturity of their primary spikes reaching harvestable stage within 95 days allowed completion of the secondary spike harvest within 120–130 days, making these hybrids well-suited for high-density planting systems and compatible with existing cropping systems in Telangana. This enables farmers to cultivate a short-duration castor crop during *kharif*, followed by a *rabi* crop.

In the current study, phenotypic coefficient of variation (PCV) ranged from 4.2% to 31.8%, while genotypic coefficient of variation (GCV) ranged from 3.2% to 26.6% for days to maturity and seed yield, respectively (Table 3). The estimates were generally low to moderate, which is consistent with the findings of Subramanian and Menon (1973). The relatively small differences between PCV and GCV for most traits suggest a lower environmental influence on trait expression, particularly for traits such as number of effective spikes per plant, number of capsules per primary spike, and seed yield highlighting the presence of exploitable genetic variability. These results align with previous studies by Movaliya *et al*., (2018) and Sowmya *et al*., (2019).

Heritability estimates provide insights into the

Table 4: Genotypic correlation among 10 different agronomic characters in castor hybrids evaluated at RARS, Palem during *kharif*, 2024.

	Yield	DFF	DM	NN	PSL	EPSL	NC	NESP	HSW	Oil
Yield	1.000	-0.207	0.354	0.271	0.825**	0.840**	0.714**	-0.367	0.107	0.004
DFF		1.000	0.720**	0.240	0.070	-0.136	0.183	0.075	0.146	0.039
DM			1.000	0.648**	0.505*	0.417	0.655**	-0.239	0.043	0.312
NN				1.000	0.523*	0.628**	0.666**	-0.762**	0.197	-0.132
PSL					1.000	0.978**	0.814**	-0.277	0.280	-0.133
EPSL						1.000	0.871**	-0.526*	0.167	-0.195
NC							1.000	-0.533*	0.029	-0.236
NESP								1.000	-0.243	0.329
HSW									1.000	0.146
Oil										1.000

proportion of observed variation that is genetic in nature (Mangi *et al*., 2010); however, heritability alone is not sufficient to predict the response to selection. According to Johnson *et al*., (1955), the combination of heritability and genetic advance is more reliable in assessing the potential of selection. Genetic advance, which measures the expected gain under selection, guides breeders in developing effective improvement strategies (Hamdi *et al*., 2003). In this study, broad-sense heritability ranged from 40.0% to 98.4% across traits, with high heritability observed for all traits except days to 50% flowering and number of effective spikes per plant, suggesting that most traits are predominantly governed by additive gene action and minimally influenced by the environment. Similar trends were reported by Patel *et al*., (2010), Yamanura and Kumar (2020), Patel and Patel (2014), and Chaudhari *et al*., (2018).

Genetic advance as a percentage of mean ranged from 5.2% to 46.0% for days to maturity and seed yield, respectively (Table 3). High genetic advance was recorded for traits such as primary spike length, effective primary spike length, number of capsules per primary spike, hundred seed weight, and seed yield, indicating additive gene action and the feasibility of effective phenotypic selection (Anjana *et al*., 2018). Conversely, lower genetic advance values for traits like days to 50% flowering, days to maturity, number of nodes per plant, and oil content suggest a greater influence of non-additive gene effects.

Traits showing both high heritability and high genetic advance as percent of mean are ideal targets for selection, and in the current study, such traits included primary spike length, effective spike length, number of capsules per spike, hundred seed weight, and seed yield confirming their potential for genetic improvement through direct selection.

Correlation analysis revealed several important trait associations that are critical for improving yield in castor. Yield showed a positive and significant correlation with primary spike length, effective primary spike length, and number of capsules per primary spike, suggesting that these spike-related traits play a crucial role in enhancing productivity (Table 4). A longer primary spike contributes to an increased effective spike length, which in turn supports a greater number of capsules, thereby improving yield potential (Kumar *et al*., 2015; Solanki *et al*., 2004). Moreover, days to 50% flowering was positively associated with days to maturity, indicating that delayed flowering tends to prolong the crop's life cycle. Days to maturity also showed significant positive correlations with number of nodes to primary spike, primary spike length, and number of capsules per primary spike, implying that these vegetative and reproductive traits contribute to extended maturity duration (Kumar *et al*., 2015). A strong association was also found among number of nodes to primary spike, effective primary spike length, and number of capsules, further reinforcing the contribution of robust spike architecture to yield traits. However, negative significant associations were noted between effective spike length and number of effective spikes per plant, likely due to source-sink competition, where longer and more productive spikes may draw more nutrients, limiting the development of additional spikes (Ramesh *et al*., 2012). This competition also likely explains the negative correlation between number of capsules per spike and number of effective spikes, indicating that an increase in productivity per spike might reduce the total number of spikes formed due to physiological or environmental constraints (Solanki *et al*., 2004). These insights provide a valuable framework for selecting complementary traits in castor breeding programs aimed at maximizing yield through balanced spike development (Fig. 2).

Conclusion

The findings of the study indicate that most of the yield-contributing traits exhibit high heritability along with moderate to high genetic advance as a percentage of the mean. This suggests that additive gene action plays a predominant role in the expression of these traits, making them more responsive to selection. Therefore, applying selection pressure on these yield contributing traits would be effective in achieving genetic improvement and in turn higher yields. Additionally, the significant positive correlation observed between these agronomic traits and seed yield implies that improvement in studied traits through selection will directly contribute to an increase in overall seed yield, making them reliable targets in yield enhancement breeding programs.

Acknowledgements

The authors would like to acknowledge the DST SERB TARE for their financial assistance and ICAR-Indian Institute of Oilseeds Research, Hyderabd & or PJTAU for providing technical assistance.

Competing interests: The authors have no relevant financial or non-financial interests to disclose.

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