ROLE OF GENETIC VARIABILITY AND THEIR ASSOCIATED CHARACTERON YIELD ATTRIBUTING TRAITS IN CASTOR (*Ricinus communis* L.) GERMPLASM LINES

Abstract

Castor(*Ricinus communis* L.) is an industrially important non-edible oil seed crop with limited genetic variation.It is consequently important to diversify the genetic base to utilize the diversity. The primary objective of this study was to assess the extent and significance of variability among castor genotypes concerning yield and its associated traits. A study with two hundred germplasm lines along with four checks on genotypes on variability, correlation, and path coefficient was carried out for nine traits. TheGCV and PCV values indicated the presence of broad variation for all characters except for days to 50 percent flowering, days to maturity, number of nodes, and oil content. However, high heritability coupled with high genetic advance as percent mean was observed for plant height, days to 50 percent flowering, days to maturity, number of nodes, total length of the primary spike, number of effective spikes, seed weight, and total yield. The character's plant height,number of nodes, total length of the primary spike, number of effective spikes, seed weight, and oil content show a positive significant correlation with the total yield. The path coefficient analysis indicates that the utmost positive direct effect on total yield was exertedby a number of effective spikes per plant.Hence it was concluded that selection for traits total length of the primary spike, number of effective spikes,and 100 seed weight beneficial in yield improvement programs of castor.

Key words: Castor, Variability, Correlation, Path coefficient and yield

INTRODUCTION

Castor (*Ricinus communis* L.) is an industrially important non-edible oilcrop that belongs to the family of Euphorbiaceae and the genus Ricinus. It is a diploid plant with a chromosome number of 2n=20 (Mullualem *et al*., 2017). India is leading in the production and export of castor in the world (Sadaiah*et al*., 2021). Castor seeds contain 45 to 55 percent oil which is the major source of ricinoleic acid an unusual hydroxyl fatty acid that has tremendous industrial significance (Senthilvel *et al*., 2016). The effectiveness of crop improvement initiatives depends on the type and extent of genetic variability present in the crop.To accomplish this, the genotypes must undergo phenotypic assessment, followed by the estimation of trait heritability and their interrelationships. Heritability estimates are vital for discerning the heritable component of variability within the traits. These steps are essential for gaining insights into the heredity aspects and determining the potential for improvement in the crop (Jyothsna *et al*., 2016). To make selection effective the heritability should couple with high genetic advance (Mullualem *et al*., 2017). To achieve the desired yield improvement, it is imperative to genetically enhance traits contributing to yield. Correlation coefficient studies offer valuable insights into the nature and strength of associations among different traits, while path coefficient analysis helps identify direct and indirect effects on other attributes through correlations, establishing causal relationships between variables. These methods play a crucial role in understanding the interplay of traits and guiding targeted crop enhancement strategies (Dapke et al., 2016). Hence the present investigation was undertaken to estimate the of genetic variability and character associations among yield-related traits in the selected castor germplasm lines.

MATERIALS AND METHODS

The experimentwas conducted at the Indian Institute of Oilseeds Research (IIOR), Rajendranagar, Hyderabad. The city is nestled on the Deccan Plateau and is positioned at a 17°15’16’’ N latitude and 78°18’30’’ E longitude during *Kharif*, 2022. Two hundred germplasm lines along with four checks (DCS-9, GC-3, 48-1, PCS-262) with a spacing of 90 cm between the rows and 60 cm between the plants were evaluated in an augmented randomized complete block design by replicating the checks in which each line is sown in a single row of 6.0 m length and allrecommended agronomic practices adopted to raise a good crop.

The observations *viz*., Plant height (cm),days to 50% flowering, days to maturity of primary spike, number of nodes to primary spike, total length of primary spike(cm), number of effective spikes per plant, 100 Seed weight(g), total seed yield/plot(g), oil content (%) were recorded on randomly selected five plants in each genotype and mean values were considered for analysis.

An augmented randomized complete block design (Federer, 1956) was employed to assess genotypic differences among the entries, following the method suggested by Panse and Sukhatme (1964). Genotypic (σ^2g) and phenotypic (σ^2p) variances were calculated using Burton and De vane’s formula(1953), and the variation range was categorized based on Subramanian and Menon's recommendations (1973). Broad sense heritability [h^2 (b)] was determined using the formula by Hanson (1956), and heritability estimations were classified according to Johnson *et al*. (1955). Genetic advance, indicating the projected gain in the next generation, was calculated usingthe formula of Johnson *et al*, (1955). Variance and covariance components for each pair of characteristics were estimated using themethods of Al-Jibouri *et al*, (1958) to calculate phenotypic and genotypic correlation coefficients. The significance of correlation coefficients was tested by comparing the estimated values with table values (Fisher and Yates, 1963) at 5 percent and 1 percent levels. Path coefficient analysis, as proposed by Wright (1921) and detailed by Dewey and Lu (1959), was used to distinguish the direct and indirect effects of independent factors on the dependent variable. Analysis was performed byusing the INDOSTAT method.

RESULTS AND DISCUSSION

1) Genetic variability parameters

Analysis of variance revealed the significant variation among the genotypes for all the traits studied in two hundred germplasm lines. The values of *gcv* and *pcv* were categorized as low (20%) (Subramanian and Menon, 1973). The *gcv*values ranged from 7.03 for oil content to 48.02 for the number of effective spikes (Table 1). High *gcv* valueswere recorded for the traits plant height (28.66),total length of the primary spike (25.38), number of effective spikes (48.02), 100 seed weight (28.94), total yield (34.20) and medium values for the characters days to 50 percent flowering (19.46), days to maturity (13.46), number of nodes (15.53) and oil content (7.03) shows the low *gcv* value.High *pcv* values for the characters plant height (28.78), total length of primary spike (25.56), number of effective spikes (48.68), seed weight (29.36), total yield (34.20), and medium values for the traits days to 50 percent flowering (19.72), days to maturity (13.66), number of nodes (16.88) and oil content (7.32) shows the low *pcv* value.*gcv*valueswere slightly lower than those of *pcv*indicating the minor influence of the environment on the expression of these characters. Results also show the presence of broad genetic variability for all the traits under study except oil content. Similar results can be observed in the findings of Movaliya *et al.* (2018); Chaudhari *et al*. (2016); Mullualem *et al*. (2017); Alhaji *et al.* (2019).

High heritability was found for all the characters under the study with the maximum heritability found in the trait total yield (Table 1). However, only eight among the nine characters studied *viz.,* plant height, days to 50 percent flowering, days to maturity, number of nodes up to primary spike, the total length of the primary spike, number of effective spikes, seed weight, and total yield coupled shows the high heritability coupled with the high genetic advance as percent of mean which indicated a preponderance of additive genetic effect for the characters and there was no environmental influence on the expression and selection for improvement of such characters could be rewarding. Oil content shows high heritability coupled with moderate genetic advance as a percent mean which indicated the presence of both additive and non-additive gene effectsand considerable effect of the environment.High heritability accompanied by moderate genetic advance as a percent mean indicated that the genotypes, under study, were diverse with immensegenetic potential and a further improvement in these traits is possible by practicing a simple selection technique. The results were similar tothe findings of Rukhsar *et al*. (2018); Movaliya *et al*. (2018).

Table 1: Magnitude of variability, heritability, and genetic advance as percent of mean for different characters in the germplasm lines of castor studied during *kharif*, 2022

Trait	**Mean**	**Range**		**GCV**	**PCV**	**h_{BS}**	**GAM**
		Minimum	**Maximum**				
PH	94.96	36.80	178.00	28.66	28.78	99.16	58.87
DFF	68.97	43.00	104.00	19.46	19.72	97.45	39.64
DM	117.19	79.00	160.00	13.46	13.66	97.19	27.38
NN	17.27	10.00	24.60	15.53	16.88	84.63	29.47
TLPS	28.43	14.00	52.00	25.38	25.56	98.58	51.99
NES	12.94	4.00	28.00	48.02	48.68	97.32	97.74
SW	33.10	8.30	59.80	28.94	29.36	97.20	58.87
OC	44.80	27.55	51.46	7.03	7.32	92.42	13.95
TY	815.48	267.4	1698.9	34.01	34.20	98.91	68.78

PH - Plant height up to primary raceme (cm),DFF – Days to 50 percent flowering, DM - Days to maturity, NN - Number of nodes up to primary raceme, TLPS–Total length of the Primary spike (cm), NES - Number of effective spikes per plant, SW –100 seed weight (g), OC- Oil content (%) and TY –Total Seed yield per plot (g). PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation, h_{BS}- Heritability at broad sense, GAM- Genetic advance as a percent mean

2) Character association studies

Seed yield is a multifaceted trait influenced by numerous characteristics. Breeders seek genetic diversity in these traits to identify favourable types. In this investigation, correlations and path coefficient analyses were employed to explore the associations among yield-related traits and their connection to overall yield.

Yield is a multifaceted trait influenced by various contributing characters that can exhibit positive or negative associations both with yield and among themselves. The extensive correlations computed using the Pearson correlation coefficient offer valuable insights for indirect selection strategies to enhance overall yield. The results of the Pearson correlation analysis depict relationships between yield and its contributing characters (Table 2, Figure 1).

The results revealed that the traits plant height (0.2505^{**}), number of nodes up to primary spike (0.4202^{**}), total length of the primary spike (0.3451^{**}), number of effective spikes (0.8470^{**}), seed weight (0.6301^{**}), oil content (0.4964^{**}) have the significant positive correlation with the seed yieldindicating that these attributes were influencing more on seed yield in castor and therefore important for bringing improvement in seed yield. A non-significant positive correlation was registered for the days to maturity (0.0394) while days to 50 percent exhibiteda non-significant negative correlation with seed yield which is highly useful in developing short-duration varieties that require negative selection for flowering without compromising the seed yield. These kinds of correlations were similar to the findings of Movaliya *et al.* (2018); Ruksar *et al*. (2018); Reddy *et al*. (2022).

To gain a comprehensive understanding and enable effective manipulation of the characters, path coefficients were employed alongside correlation coefficients. Path analysis allows for the dissection of correlations into direct and indirect effects, providing insights into the relative significance of the causal factors involved (Dewey and Lu, 1959). In the present study, nine characters were taken and partitioned into direct and indirect effects using seed yield per plot as a dependent variable. The information about the direct and indirect effects of eight variables on seed yield per plot intwo hundred germplasm linescastor is described below (Table 3, Figure 2).

The number of effective spikes per plant (0.7136), seed weight (0.1356), and total length of the primary spike have a high positive direct effect on seed yield while oil content (0.0542), days to maturity (0.0478) and plant height (0.0341) have a low positive direct effect on seed yield. Due to the positive direct effect on seed yield these traits can be considered for the crop improvement program of castor. Days to 50 percent flowering(-0.0622) and number of nodes (-0.0117) have negative direct effects due to negative indirecteffects of other traits.Patel *et al*. (2016); Rukhsar *et al*. (2018); Alhaji *et al*. (2019) findings were similar to the present study.

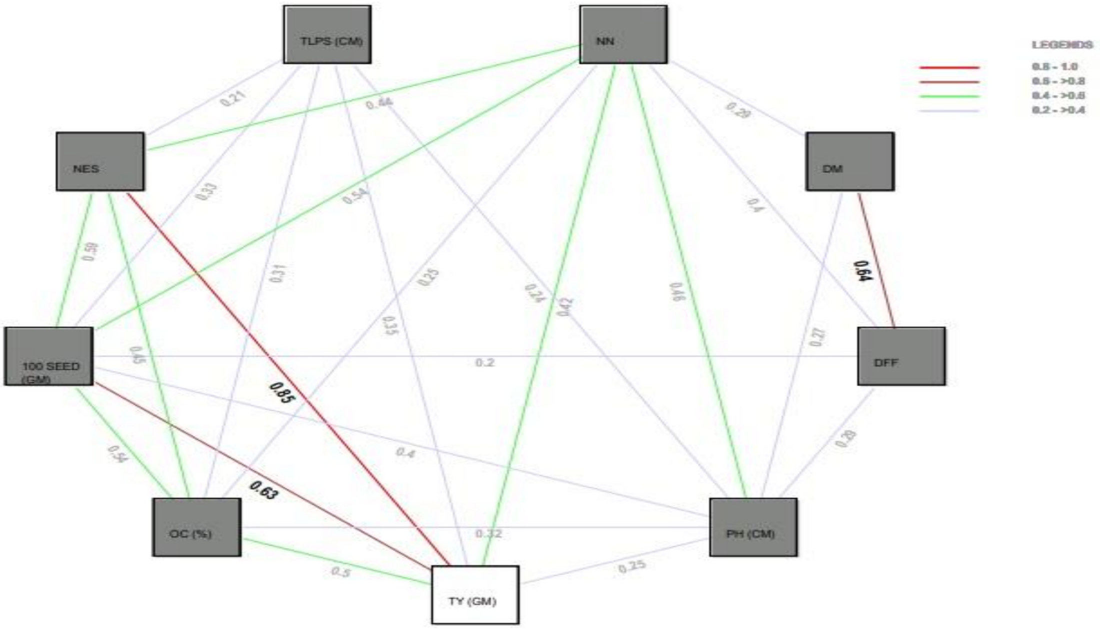

Fig. 1. Phenotypic correlation coefficients among different traits in castor.

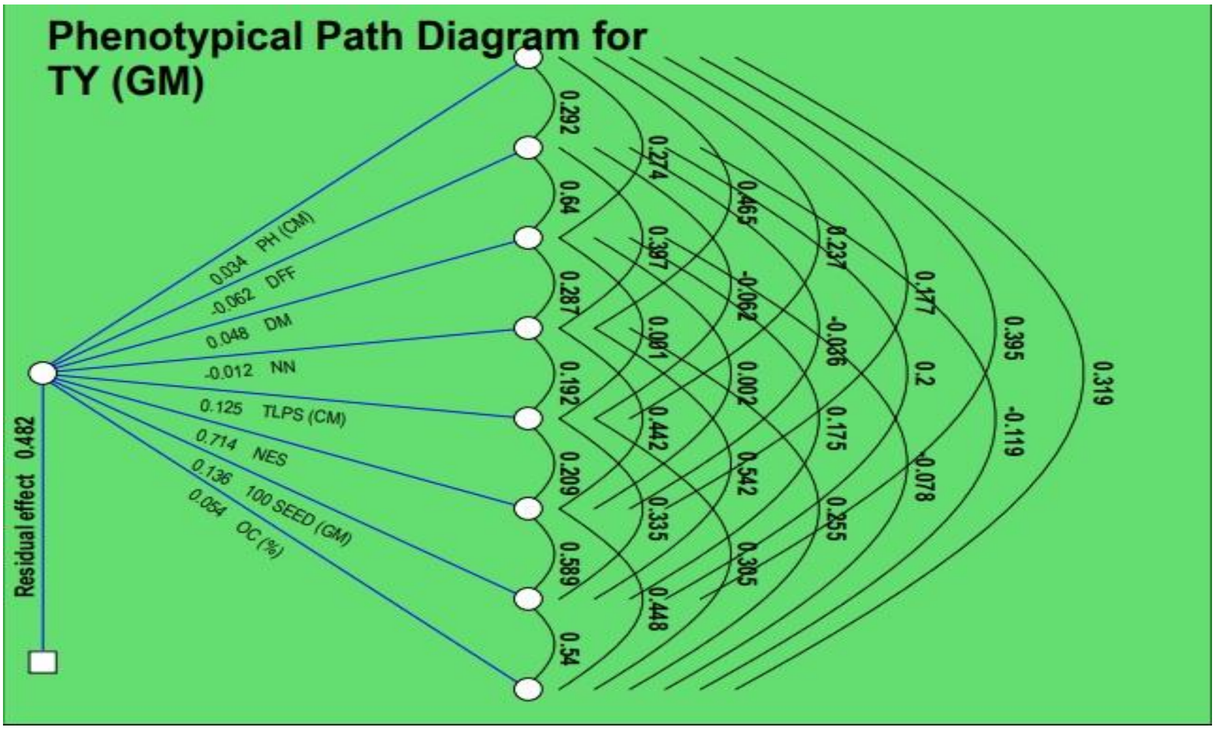

Fig. 2. Phenotypical path diagram of various traits with seed yield per plot in castor.

Table 2: Correlation coefficients of yield attributing traits in the germplasm lines of castor studied during *kharif*, 2022

	Plant Height (cm)	**Days to 50 % Flowering**	**Days to Maturity**	**Number of Nodes to primary raceme**	**Total Length of the Primary Spike (cm)**	**Number of Effective Racemes**	**100 seed weight (g)**	**Oil content (%)**	**Seed Yield (g)**
Plant Height (cm)	**1**	0.2924**	0.2739**	0.4646**	0.2373**	0.1773*	0.3954**	0.3187**	0.2505**
Days to 50 % Flowering		**1**	0.6395**	0.3970**	-0.0624	-0.0363	0.2002**	-0.1189	-0.0394
Days to Maturity			**1**	0.2873**	0.0008	0.0015	0.1745*	-0.0784	0.0345
Number of Nodes to primary raceme				**1**	0.1922**	0.4424**	0.5424**	0.2548**	0.4202**
Total Length of the Primary Spike (cm)					**1**	0.2086**	0.3346**	0.3051**	0.3451**
Number of Effective Racemes						**1**	0.5893**	0.4475**	0.8470**
100 seed weight (g)							**1**	0.5402**	0.6301**
Oil content (%)								**1**	0.4964**
Seed Yield (g)									**1**

**** Significant at 0.01: *Significant at 0.05**

Table 3: Path coefficient analysis of agro morphological traits in the germplasm lines of castor studied during *kharif*, 2022

	Plant Height (cm)	Days to 50 % Flowering	Days to Maturity	Number of Nodes to primary raceme	Total Length of the Primary Spike (cm)	Number of Effective Racemes	100 seed weight (g)	Oil content (%)
Plant Height (cm)	**0.0341**	0.0100	0.0093	0.0158	0.0081	0.0060	0.0135	0.0109
Days to 50 % Flowering	-0.0182	**-0.0622**	-0.0398	-0.0247	0.0039	0.0023	-0.0125	0.0074
Days to Maturity	0.0131	0.0305	**0.0478**	0.0137	0.0000	0.0001	0.0083	-0.0037
Number of Nodes to primary raceme	-0.0054	-0.0047	-0.0034	**-0.0117**	-0.0023	-0.0052	-0.0064	-0.0030
Total Length of the Primary Spike (cm)	0.0296	-0.0078	0.0001	0.0240	**0.1246**	0.0260	0.0417	0.0380
Number of Effective Racemes	0.1265	-0.0260	0.0011	0.3157	0.1489	**0.7136**	0.4206	0.3194
100 seed weight (g)	0.0536	0.0272	0.0237	0.0736	0.0454	0.0799	**0.1356**	0.0733
Oil content (%)	0.0173	-0.0064	-0.0043	0.0138	0.0165	0.0243	0.0293	**0.0542**
Seed Yield (g)	0.2505	-0.0394	0.0345	0.4202	0.3452	0.8470	0.6302	0.4964
Partial R^2	0.0085	0.0025	0.0016	-0.0049	0.0430	0.6044	0.0855	0.0269

R Square = 0.7675 Residual effect = 0.4822

CONCLUSION

The current investigation on variability parameters, correlation, and path coefficient analyses revealed that the characters length of the primary spike, number of effective spikes, and 100 seed weight largely define the seed yield of the castor. Therefore, it is beneficial to put more focus on these traits in the selection process in order to develop high-yielding varieties and hybrids castor.

FUTURE SCOPE

Through extensive research on GCV (genotypic coefficient of variation), PCV (phenotypic coefficient of variation), heritability, genetic advance as a percentage of mean, correlation, and path coefficient analysis, successfully identified the most desirable traits for enhancing yield in castor. These findings offer valuable insights that can be leveraged to enhance seed yield without compromising other important characteristics such as crop duration and plant architecture in future castor breeding programs. Moreover, the gathered data holds significant potential for selecting superior lines in the development of improved varieties and hybrids, fostering advancements in castor cultivation.

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Conflict of Interest: None.

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