

Original Research Article

Variability, Correlation Patterns and Principal Component Analysis (PCA) for Seed Yield and Contributing Traits in Castor (*Ricinus communis* L.)

ABSTRACT:

Castor (*Ricinus communis* L.) is a vital crop for industrial applications in more than 250 products including lubricants, paints, cosmetics, pharmaceuticals etc. This study is an attempt to understand the genetic diversity in 15 male (monoecious) and 15 female (pistillate) advanced breeding lines of castor. 11 quantitative traits were subjected to analysis of variance, correlation analysis, principal component analysis (PCA) and K-means clustering. Significant genetic variability and trait correlations were noticed, revealing opportunities for targeted improvement in castor. Clustering identified six distinct genetic groups, facilitating the identification of diverse parental lines. Principal component analysis elucidated key contributors of variation, enabling informed breeding decisions. This comprehensive study provides a foundation for further improvement in seed yield, oil content and environmental resilience in castor.

Keywords: Castor, Pistillate, monoecious, K-means clustering, Principal component analysis

INTRODUCTION:

Castor is a commercial, non-edible and industrial oil seed crop and member of the Euphorbiaceae family with a diploid chromosome count of $2n=20$. It has extensive genetic variability, with Ethiopia considered as the most probable site of origin and India as an important centre of diversity [1, 2]. Castor's reproductive mechanism is distinct, with cross-pollination facilitated by wind dispersal and monoecious nature [3]. Its seeds contain a unique oil composition, primarily ricinoleic acid, used in various industrial products and as a promising candidate for biodiesel production [4, 5, and 6].

Castor is well-suited for both irrigated and dryland farming in India during the *khariif*/late *khariif* and *rabi* season, requiring minimal irrigation in the post-monsoon period [7]. Castor serves as a contingency crop, providing flexibility in agricultural planning to mitigate disruptions caused by monsoon irregularities. Over the past forty years, collaborative research led by ICAR-IIOR and SAUs has resulted in the development of 15 high-yielding castor varieties and 24 hybrids. The major castor growing states in India include mainly Gujarat and Rajasthan followed by Andhra Pradesh, Tamil Nadu, Karnataka and to some extent in Telangana and Maharashtra. During the period 2022-23, India produced 19.80 lakh tonnes of castor in an area of 10.19 lakh hectares [8]. Over the past forty years, collaborative research led by the Indian Council of Agricultural Research-Indian Institute of Oilseeds Research (ICAR-IIOR) and several State Agricultural Universities (SAUs) has resulted in the development of 15 high-yielding

castor varieties and 23 castor hybrids. These efforts have significantly advanced castor breeding, boosting the productivity and sustainability in the industry.

The efficacy of varietal or hybrid development programmes fundamentally hinges on the magnitude and nature of genetic variability present in breeding lines.

The Indian germplasm repository boasts an impressive array of morphological diversity, mirroring the range of variants found in other centers of origin and tropical and subtropical regions. Twenty-four morphological descriptors have been crafted to characterize castor germplasm accessions. Notably, the native Indian collection predominantly features medium-tall plants with woody stems with red and green colour, accompanied by a varying number of nodes, divergent branching and a waxy stem coating. Furthermore, the leaves exhibit a semi-cup shape, while the racemes are characterized by their medium length, loose, conical shape, medium-sized, non-dehiscent, green and spiny capsules [2].

The genetic diversity studies in castor breeding lines will aid plant breeders in selecting suitable parental lines for breeding programmes. Breeders can develop effective strategies for selection of genotypes by combining genetic variability, genotypic correlation analysis and principal component analysis. There is a need to understand correlation relationships between traits, highlighting potential synergies and trade-offs. Principal Component Analysis (PCA) is required to determine the primary factors contributing to the overall variation. Additionally, K-means clustering analysis can be employed to group the advanced breeding into distinct clusters. The present investigation aims to estimate genetic variability and character associations among yield-related traits in monoecious and pistillate breeding lines of castor.

MATERIAL AND METHODS:

Thirty advanced and stabilized breeding lines of castor, comprising 15 monoecious and 15 pistillate lines, developed by pedigree method at the ICAR-Indian Institute of Oilseeds Research, Hyderabad and SAUs were utilized for genetic diversity study. Prior to evaluation, all the breeding lines underwent six (monoecious) to eight (pistillate) generations of self-pollination at research farm of ICAR-IIOR, Hyderabad under controlled pollination conditions.

An experiment was conducted at the ICAR-Indian Institute of Oilseeds Research at Narkhoda research farm near Hyderabad, India (17.366°N and 78.478°E). The crop was grown under irrigated conditions in red sandy soil and sowing was carried out on 24th July 2023. The study was conducted in randomized block design (RBD) with three replications and two rows per genotype with 10 plants per row in each replication with the spacing of 90 x 60 cm. Eleven characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of nodes to primary spike, total length of primary spike (cm), effective length of primary spike (cm), number of spikes/plant, number of capsules on primary spike, 100-seed weight (g), oil content (%) and total seed yield per plant were recorded in each replication from five randomly selected plants per breeding line (**Table 1**). All statistical analyses were performed using INDOSTAT statistical software, INDOSTAT Services, India [8].

RESULTS AND DISCUSSION:

Analysis of variation: The analysis of variance showed significant differences among the genotypes for all characters. The estimates of genetic variability, heritability, and genetic advance are presented in **Table 2**. The phenotypic coefficient of variation (PCV) values, which quantify the total variability present in the population, including both genetic and environmental components, were calculated. The number of capsules on primary spike (29.19%), plant height up to primary spike (27.42%), total seed yield per plant (44.18%) and total number of spikes per plant (36.71%) showed high phenotypic coefficient of variation. Whereas, days to 50% flowering (15.28), number of nodes (17.54) and oil content (10.47) showed moderate phenotypic coefficient of variation. These PCV values indicate that total seed yield per plant, total and effective length of primary spike, number of capsules on primary spike and total number of spikes per plant have high variability, while days to 50% flowering, number of nodes and oil content have moderate phenotypic variability.

In contrast, the genotypic coefficient of variation (GCV) values, which quantify the genetic component of variability. High GCV values were recorded for, total seed yield per plant (34.04%), number of capsules on primary spike (31.13%), plant height up to primary spike (26.32%) and total number of spikes per plant (23.79%). However, days to 50% flowering (14.89), number of nodes (16.50), total length (19.84) and effective length (20.92) of primary spike and oil content (15.74) showed moderate range of genotypic variability, whereas, days to 50% maturity and hundred seed weight recorded low genotypic variability. These findings are consistent with previous studies [9, 10, 11 and 12]. Genotypic coefficient of variation (GCV) recorded lower than phenotypic coefficient of variation (PCV) for all characters, indicating that environmental factors were minimum and phenotypic selection can be effectively used for improvement.

High heritability estimates were recorded for days to 50% flowering (95.0%), days to 50% maturity (90.70%), number of nodes (88.50%), total length of primary spikes (84.80%) and effective length of primary spikes (82.10%). High the heritability value indicated the presence of additive gene action and further improvement in these traits could be effective through direct selection. These results are in accordance with the findings of [13, 14 and 10].

In contrast, moderate heritability estimates were recorded for hundred seed weight (50.30%) and total seed yield per plant (59.50%), indicating the influence of both genetic and environmental factors. There are contradictory reports for the heritability of total seed yield per plant [15, 16 and 10] reported high heritability (>60%). Whereas [11, 17] reported low (30%) to moderate (30-60%) heritability in broad sense.

Table1.Meansof11agro-morphologicaltraitsin30breeding lines

ENTRY	DFF	DM	PH	NN	TLP	ELP	TS	TC	OC	HSW	TY
K22-1	53.3	109.3	121.4	15.7	65.1	63.0	4.1	71.7	42.3	26.3	148.7
K22-5	53.7	105.0	86.6	15.3	58.4	54.2	1.9	78.1	38.3	25.4	102.1
R22-14	54.7	100.0	65.9	14.0	38.1	34.8	3.3	52.1	44.1	22.1	81.4
K22-19	53.7	97.7	86.6	15.1	44.9	32.3	3.7	49.7	41.1	22.7	105.2
K22-26	59.7	103.0	78.5	15.6	44.6	41.8	2.6	71.5	45.6	28.6	119.0
K22-35	54.3	101.3	72.9	14.5	55.7	45.4	4.0	54.9	41.7	21.4	114.9
K22-38	54.7	100.7	56.9	13.7	35.7	31.9	4.7	47.9	47.9	25.3	115.2
K22-39	55.3	90.7	60.9	13.1	63.3	53.4	4.3	67.9	38.6	18.3	102.2
K22-43	54.0	102.3	62.2	13.8	42.3	35.2	5.5	47.1	43.5	22.1	125.1
K22-45	55.7	103.0	60.2	13.9	35.9	31.0	5.7	51.2	46.1	18.3	123.0
K22-46	55.0	99.3	79.0	15.3	43.0	32.6	4.5	53.7	37.4	18.3	122.8
K22-47	56.3	106.3	102.3	15.5	40.6	33.8	4.6	30.2	43.0	21.8	77.3
K22-48	59.0	97.7	102.8	16.6	42.5	38.3	3.9	46.7	43.5	22.9	98.0
K22-49	56.0	101.0	80.6	13.5	41.5	37.7	5.3	38.7	39.0	23.1	103.4
ICS-164	49.3	100.3	104.6	17.7	47.0	42.9	3.7	81.7	41.1	22.1	178.7
IPC-41	38.0	103.0	63.6	11.8	50.5	45.4	3.9	40.5	47.7	17.9	73.7
DPC-25	59.7	104.7	60.5	19.0	64.7	60.1	2.2	67.5	39.2	21.6	62.2
IPC-46	48.0	110.3	86.5	18.3	54.6	40.5	3.2	50.4	48.1	26.5	79
DPC-22	62.3	108.7	70.3	16.6	40.0	39.9	2.0	70.0	38.3	21.3	48.2
JP-96	48.7	111.0	75.5	15.1	46.2	42.9	2.3	43.2	47.4	29.1	58.7
IPC-47	47.7	110.7	53.2	17.1	51.7	43.9	1.9	43.7	38.5	25.6	53.2
IPC-44	39.7	93.3	70.7	12.7	33.4	30.9	2.7	51.3	46.2	28.0	74.8
JP-86	62.3	108.0	50.7	16.8	36.9	35.4	2.7	40.7	46.4	28.3	47.5
M-619	62.7	105.7	56.2	21.1	49.3	49.2	2.7	46.1	35.6	17.4	39.5
IPC-48	39.3	94.7	69.0	8.2	50.6	48.2	2.0	79.9	44.8	16.8	70.6
IPC-31	61.7	108.3	43.9	17.4	31.4	29.8	2.6	40.0	38.3	22.1	46.7
IPC-49	45.0	98.0	45.7	13.9	40.7	39.1	1.9	37.2	38.3	34.8	59.1
IPC-53	42.3	98.0	61.4	12.5	36.3	34.7	2.9	43.1	44.3	20.1	58.9
IPC-52	38.0	93.0	49.3	12.0	36.9	33.5	2.9	55.4	37.1	18.7	69.3
IPC-51	38.7	100.7	54.9	13.1	40.6	37.5	4.1	53.6	46.2	25.7	113

DFF- Days to 50% flowering, DM - Days to maturity of primary spike, PH - Plant height (cm), NN –Number of nodes up to primary spike, TLP – Total length of primary spike (cm), ELP – Effective Lengthof primary spike (cm), NS - Number of spikes, NC-Number of capsules in Primary spike, HSW- Hundredseedweight(g.),OC-Oilcontent(%),TY-Totalseedyield(g.).

Table 2. Mean, range, variability parameters, heritability and genetic advance

Characters	Mean	Range		PCV(%)	GCV(%)	h ²	GA%
		Min.	max				
DFF	51.96	38	62.67	15.28	14.89	95.0	29.86
DM	102.19	90.67	111	5.56	5.29	90.7	10.39
PH	71.09	43.96	121.40	27.45	26.32	92.0	52.00
NN	14.97	8.20	21.13	17.54	16.50	88.5	31.99
TLP	45.41	31.43	65.13	21.54	19.84	84.80	37.62
ELP	40.78	29.83	63.00	23.09	20.92	82.10	39.05
NS	53.52	30.20	81.73	29.19	31.13	66.40	39.95
NC	3.39	1.87	5.67	36.71	23.79	71.90	54.39
HSW	23.08	16.80	34.80	22.17	8.19	50.30	23.01
OC	42.31	35.57	48.13	10.47	15.74	61.10	13.18
TY	89.03	39.47	178.70	44.18	34.06	59.5	54.11

DFF-Days to 50% flowering, DM-Days to maturity of primary spike, PH-Plant height (cm), NN-Number of nodes up to primary spike, TLP-Total length of primary spike (cm), ELP-Effective length of primary spike (cm), NS-Number of spikes, NC-Number of capsules in Primary spike, HSW- Hundred seed weight (g.), OC- Oil content (%), TY-Total seed yield (g.). PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation, h²- Heritability at broad sense, GAM- Genetic advance as a percent mean.

Correlation analysis: The correlation analysis revealed various relationships between traits (**Table 3, Figure 1**). Days to 50% flowering showed a significant positive correlation with number of nodes to primary spike (0.6820) and days to 50% maturity (0.4150). Days to 50% maturity had a significant positive correlation with number of nodes to primary spike (0.6328) and 100-seed weight while showing a negative non-significant correlation with total number of spikes, number of capsules on primary spike, and total yield.

Plant height up to primary spike showed a significant positive correlation with total seed yield per plant (0.6053), followed by total length of primary spike, number of capsules on primary spike, effective length of primary spike and number of spikes. Total length of primary spike had a high significant positive correlation with effective length of primary spike (0.9355) and number of capsules on primary spike (0.5348). Effective length of primary spike showed a high significant positive correlation with number of capsules on primary spike (0.6267) and a significant negative correlation with total number of spikes per plant (-0.3417). Additionally, number of spikes per plant was significantly correlated with total seed yield per plant (0.6160) and number of capsules on primary spike had a significant positive correlation with total seed yield per plant (0.4047). Oil content showed no significant correlation with any trait showing that the trait does not have direct association with traits like flowering and plant architecture, similar reports were given by [18,19,20 and 21]. However, hundred seed weight exhibited a significant positive correlation with days to 50% flowering. Total seed yield per plant was significantly correlated with number of capsules per spike (0.6160), plant height to primary spike (0.6053), and number of spikes per plant (0.4047), with a significant negative association with days to 50% maturity.

DFF	DM	PH	NN	TLP	ELP	NS	NC	OC	HSW	TY		
1	0.415		0.682					-0.322			DFF	
	1		0.632						0.309	-0.240	DM	
				0.356	0.268	0.248	0.318				0.605	PH
			1	0.207				-0.375				NN
				1	0.935		0.5348					TLP
					1	-0.341	0.626					ELP
						1			-0.406	0.616		NS
							1			0.404		NC
								1				OC
									1			HSW
										1		TY

Fig.1. Shaded correlation matrix of different traits under study.

Table3 GenotypicCorrelation coefficientsofyieldattributingtraitsintheadvancedbreedinglinesofcastorstudied.

	DFF	DM	PH	NN	TLP	ELP	NS	NC	OC	HSW	TY
DFF	1	0.4150**	0.1351	0.6820 **	0.0636	0.0491	0.1343	0.0056	-0.3226**	-0.0323	0.0111
DM		1	0.1315	0.6328 **	0.1719	0.1669	-0.2066	-0.1715	0.0894	0.3094**	-0.2406*
PH			1	0.1601	0.3565**	0.2689**	0.2483*	0.3181**	0.1000	0.0329	0.6053 **
NN				1	0.2079*	0.1575	-0.2008	-0.0672	-0.3753 *	0.1906	-0.1366
TLP					1	0.9355**	-0.1553	0.5348 **	-0.2547**	-0.1188	0.1773
ELP						1	-0.3417**	0.6267 **	-0.2829**	-0.1053	0.0352
NS							1	-0.2970**	0.2277*	-0.4062**	0.6160**
NC								1	-0.2048*	-0.1924	0.4047 **
OC									1	0.1743	0.0912
HSW										1	-0.1406
TY											1

****Significant at0.01:*Significantat0.05**

DFF- Days to 50% flowering, DM - Days to maturity of primary spike, PH - Plant height (cm), NN -Number of nodes up to primary spike, TLP - Total length of primary spike (cm), ELP - Effective Lengthof primary spike (cm), NS - Number of spikes, NC-Number of capsules in Primary spike, HSW- Hundredseedweight(g.),OC-Oilcontent(%),TY-Totalseedyield(g.).

Diversity analysis: The study employed K-means clustering to categorize genotypes into distinct groups, as presented in **Table 4**. This method identified patterns and relationships among the characteristics, grouped them into six clusters with high degrees of similarity. The cluster size ranged from 2 (cluster V) to 11 (cluster II) breeding lines, indicating varying levels of diversity within each group. The cluster mean differentiated members of each cluster from other clusters, highlighting the distinct characteristics of each group (**Table 5**).

Cluster II and III stood out for their notable characteristics, comprising high-yielding and tall lines with late maturity and produced higher number of spikes per plant. In contrast, Cluster IV was characterized by genotypes with short height, long primary spikes with higher number of capsules on primary spike. Clusters V and VI were the pistillate lines with early flowering and maturity, short stature, few nodes, high oil content and average seed yield. In contrast, Cluster I comprised late-maturing, short pistillate lines with a more number of nodes but low total seed yield per plant.

Table 4. Clustering of 30 castor accessions using K-clustering method based on agro-morphological dataset

GroupK	Number of members	Cluster member
I	5	DPC-25, DPC-22, JP-86, M-619, IPC-31
II	11	K22-1, R22-14, K22-26, K22-35, K22-38, K22-43, K22-45, K22-46, K22-49, IPC-46, JP-96
III	4	K22-19, K22-47, K22-48, ICS-164
IV	3	K22-5, K22-39, IPC-47
V	2	IPC-44, IPC-53
VI	5	IPC-41, IPC-48, IPC-49, IPC-52, IPC-51

Table 5. K-Cluster means for 11 agro-morphological character studied.

	DFF	DM	PH	NN	TLP	ELP	NS	NC	OC	HSW	TY
1Cluster	61.73	107.07	56.33	18.19	44.46	42.88	2.44	52.87	39.55	22.13	48.81
2Cluster	54.00	103.76	76.33	14.86	45.70	39.71	4.10	52.96	43.91	23.72	108.33
3Cluster	54.58	100.50	99.06	16.22	43.73	36.82	3.97	52.08	42.18	22.39	114.78
4Cluster	52.22	102.11	66.90	15.18	57.82	50.51	2.71	63.24	38.46	23.11	85.83
5Cluster	41.00	95.67	66.02	12.57	34.88	32.83	2.80	47.20	45.25	24.03	66.87
6Cluster	39.80	97.87	56.52	11.79	43.85	41.55	2.95	53.31	42.83	22.79	77.13

Principal component analysis: The determination of the optimal number of principal components (PCs) that explains the maximum variability is crucial in Principal Component Analysis (PCA). According to Rencher (2002), a threshold of 70% variance explained by PCs is recommended. In our analysis, out of 11 the first four PCs accounted for approximately 75.80% of the total variability in the data set, with PC1 explaining 26.50%, PC2 explaining 20.20%, PC3 explaining 15.90%, and PC4 explaining 13.20% (**Table 6**). This exceeds the recommended threshold, indicating that the first four PCs are sufficient to capture the majority of the variation in the data.

Alternatively, the Kaiser criterion (1958) suggests retaining PCs with eigenvalues greater than 1 ($\lambda_i > 1$), which also supports the retention of the first four PCs. The scree plot further confirms this decision, showing a clear break in the slope after the fourth component (**Figure 2**). Therefore, the first four PCs were retained for further analysis. Simplifying the data while capturing a substantial amount of the variation.

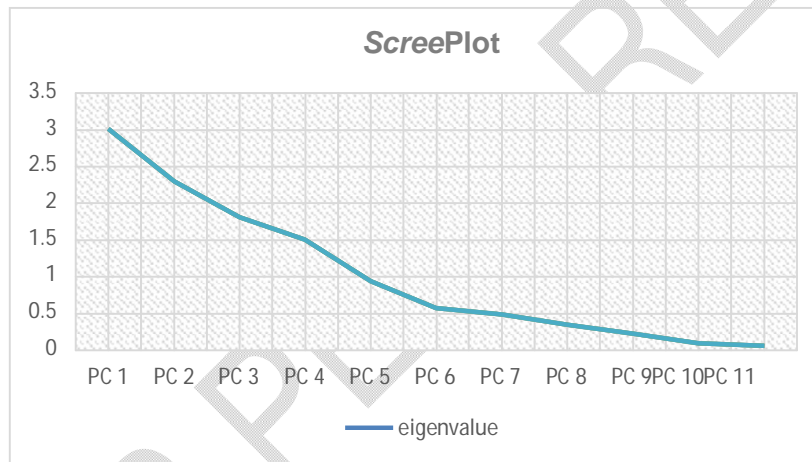


Fig.2. Screeplot of eigenvalues (Variances of principal components).

Table 6. Principal component analysis for 11 agro-morphological traits

Variables	PC1	PC2	PC3	PC4
DFF	0.222	-0.391	-0.231	-0.374
DM	0.21	-0.46	-0.19	0.218
PH	0.297	0.191	-0.445	0.013
NN	0.300	-0.49	-0.148	-0.108
TLP	0.498	0.161	0.115	0.048
ELP	0.500	0.147	0.217	0.116
NS	-0.142	0.207	-0.489	-0.424
NC	0.375	0.336	0.126	0.018
OC	-0.208	0.136	-0.306	0.435
HSW	0.000	-0.185	-0.216	0.643
TY	0.162	0.320	-0.485	0.047
Eigenvalue	3.01	2.296	1.813	1.507
Variance%	26.50	20.20	15.90	13.20
Cumulative variance%	26.50	46.60	62.60	75.80

DFF- Daysto50%flowering, DM-Daystomaturityofprimaryspike, PH-Plantheight(cm), NN-Numberofnodesuptoprimaryspike, TLP- Totallengthofprimaryspike(cm), ELP-EffectiveLengthofprimaryspike(cm), NS-Numberofspikes, NC- NumberofcapsulesinPrimaryspike, HSW- Hundredseedweight(g.), OC- Oilcontent(%), TY- Totalseedyield(g.).

The Principal Component Analysis (PCA) identified four significant components that captured the underlying variation pattern in the data. The first component primarily defined by the effective length of primary spike as the main contributor followed by total length of primary spike, number of capsules on primary spike, number of nodes and plant height to primary spike, which were highly correlated and represented the main source of variation among the breeding lines. The second component was characterized by number of capsules on primary spike, total seed yield, number of spikes per plant and plant height. The third component highlighted effective length of primary spike, number of capsules on primary spike and number of spikes per plant as the main contributors of variation, while the fourth component emphasized hundred seed weight, oil content and days to 50% maturity, which were less correlated with the first three components and captured a distinct aspect of the variation. The resulting principal component plot (**Figure 3**) displaying a broad dispersion of the 30 parental lines, indicating substantial diversity among them.

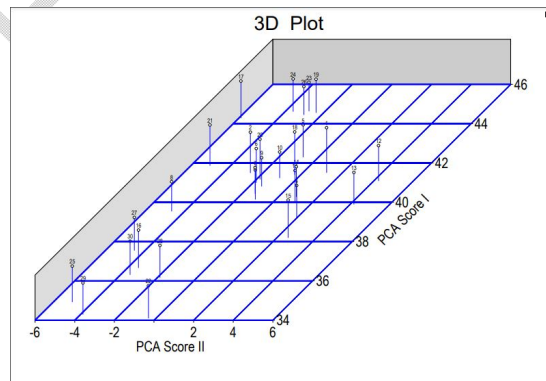


Fig. 3. PCA analysis for the castor breeding lines

CONCLUSION:

This study revealed significant genetic variability among 30 advanced castor breeding lines for 11 quantitative characters. Based on mean performance for 11 traits, K22-1, K22-5, K22-26, K22-39, K22-43, K22-46 and ICS-164 were identified as best monoecious lines, whereas IPC-41, IPC-46, IPC-44, IPC-48, IPC-52 and IPC-58 were identified as best pistillate lines.

Correlation analysis revealed significant positive associations between traits, including plant height, spikes per plant and capsules on primary spike with total seed yield per plant. Principal component analysis (PCA) identified primary contributors to variation, such as primary spike length, capsules on primary spike and plant height. K-means clustering divided the 30 breeding lines into 6 clusters based on K-cluster mean. Using superior lines from divergent clusters as parents could exploit maximum heterosis in breeding programmes.

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