Original Research Article

Variability,CorrelationPatternsandPrincipalComponent Analysis (PCA) for Seed Yield and Contributing Traits inCastor(*Ricinuscommunis*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 attemptto understand the genetic diversity in 15 male (monoecious) and 15 female (pistillate) advancedbreeding lines of castor.11 quantitative traits were subjected to analysis of variance, correlation analysis, principal componentanalysis (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 keycontributors of variation, enabling informed breeding decisions. This comprehensive study provides afoundation forfurtherimprovement in seedyield,oilcontent,andenvironmentalresilience in castor.

Keywords:Castor, Pistillate,monoecious,K-meansclustering and Principal component analysis

INTRODUCTION:

Castorisacommercial,non-edible,andindustrialoilseedcropandmemberoftheEuphorbiaceae family with a diploid chromosome count of 2n=20. It has extensive genetic variability,withEthiopiaconsideredasthemostprobablesiteoforiginandIndiaasanimportantcentreofdiversity[1, 2]. Castor's reproductive mechanism is distinct, with cross-pollination facilitated by wind dispersaland monoecious nature [3]. Its seeds contain a unique oil composition, primarily ricinoleic acid, used invariousindustrialproductsandasapromising candidate for biodieselproduction[4,5,and6].

Castoriswell-suitedforbothirrigatedanddrylandfarminginIndiaduringthe*kharif*/late*kharifand rabi* season, requiring minimal irrigation in the post-monsoon period [7]. Castor serves as acontingency crop, providing flexibility in agricultural planning to mitigate disruptions caused by monsoonirregularities.Overthepastfortyyears,collaborativeresearchledbyICAR-IIORandSAUshasresultedin the development of 15 high-yielding castor varieties and 24 hybrids.The major castor growing states in Indiaincludemainly GujaratandRajasthanfollowedbyAndhraPradesh,Tamil Nadu,KarnatakaandTelangana. During the period 2022-23, India produced 19.80 lakh tonnes of castor in an area of 10.19lakhhectares[8].

Thegeneticdiversitystudiesincastorbreedinglineswillaidplantbreedersinselectingsuitableparental lines for breeding programmes. Breeders can develop effective strategies for selection of genotypes by combininggeneticvariability,genotypiccorrelationanalysis and principal component analysis.There is a need to understand correlation relationships between traits, highlighting potentialsynergies and trade-offs. Principal Component Analysis (PCA) was required to determine the primaryfactors contributing to the

overall variation. Additionally, K- means clustering analysis was necessitated togroup the advanced breeding into distinct clusters. The presentinvestigation aims to estimate genetic variability and character associations among yield-related traits inmonoeciousandpistillatebreedinglinesofcastor.

MATERIALANDMETHODS:

Thirty advanced and stabilized breeding lines of castor, comprising 15 monoecious and 15pistillate lines, developed at the ICAR-Indian Institute of Oilseeds Research, Hyderabad and SAUswereutilizedfor geneticdiversitystudy.

An experiment was conducted at the ICAR-Indian Institute of Oilseeds Research at Narkhodaresearch 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 24thJuly 2023. The study was conducted inrandomized block design (RBD) with three replications and two rows per genotype with 10 plants perrow 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 primaryspike,100-seed weight (g), oil content (%) and total seed yield per plant were recorded in each replicationfrom five randomly selected plants per breeding line (**Table 1**). All statistical analyses were performedusing INDOSTAT statistical software, INDOSTAT Services, India(http://indostat.software.informer.com/).

RESULTSANDDISCUSSION:

Analysisofvariation: Theanalysisofvarianceshowedsignificantdifferences among the genotypes for all characters. Theestimates of genetic variability, heritability, and genetic advance are presented in **Table 2**. Genotypiccoefficient of variation (GCV) recorded lower than phenotypic coefficient of variation (PCV) for allcharacters, indicating that environmental factors were minimumand phenotypic selection can beeffectively used for improvement. Thecharacterswithhighgeneticvariabilityandphenotypicvariabilitywerenumberofcapsules on primary spike (31.13%, 29.19%), plant height up to primaryspike (26.32%, 27.42%), total seed yield per plant (34.04%, 44.18%), and total number of spikes per plant(23.79%, 36.71%).Thesefindingsareconsistentwithpreviousstudies[9,10,11and12].

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 effectivelength of primary spikes (82.10%). In contrast, moderate heritability estimateswere recorded forhundredseed weight(50.30%)andtotalseedyieldperplant (59.50%),indicatingtheinfluenceofboth geneticandenvironmentalfactors.Theheritability value indicated the presence of additive gene action and further improvement in these traitscould be effective through direct selection. These results are in accordance with the findings of [13, 14and10].

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.).

Table2.Mean,range,variabilityparameters,heritabilityandgeneticadvance

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-Daysto50%flowering,DM-Daystomaturityofprimaryspike,PH-Plantheight(cm),NN–Numberofnodesuptoprimaryspike,TLP–Totallengthofprimaryspike(cm),ELP–EffectiveLengthofprimaryspike(cm),NS-Numberofspikes,NC-Numberof capsules in Primary spike, HSW- Hundred seed weight (g.) , OC- Oil content (%), TY-Total seed yield (g.). PCV- Phenotypiccoefficient of variation, GCV- Genotypic coefficient of variation, h^2- Heritability at broad sense, GAM- Genetic advance as apercentmean.

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 toprimary spike (0.6820) and days to 50% maturity (0.4150). Days to 50% maturity had a significant positivecorrelation with number of nodes to primary spike (0.6328) and 100-seed weight while showing anegativenon-significantcorrelationwithtotalnumber ofspikes,number ofcapsuleson primaryspike,and totalyield.

Plant height up to primary spike exhibited 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 primaryspike and number of spikes. Total length of primary spike had a high significant positive correlation witheffective length of primary spike (0.9355), number of capsules on primary spike (0.5348). Effectivelength of primary spike showed a high significant positive correlation with number of capsules on primaryspike (0.6267)and significant negative correlation with total number of spikes per plant (-0.3417). Number ofspikesperplantsignificantlycorrelatedwithtotalseedyieldperplant(0.6160).Numberofcapsuleson primary spike also had a significant positive correlation with total seed yield per plant (0.4047). Oilcontentshowedanon-significantpositivecorrelationwithtotalseed yieldandhavenosignificantassociationwith the days to 50% flowering, days to 50 % maturity, number of nodes, plant height, total length ofprimary spike and number of capsules on primary spike. Hundred seed weight exhibited a significantpositive correlation only with days to50%flowering.Totalseedyieldperplantwassignificantlycorrelatedwithnumberofcapsulesperspike(0.6160), plantheighttoprimaryspike(0.6053)andnumberofspikes per plant (0.4047)andhave significant negativeassociationwithdaysto50% maturity.

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.).

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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.Shadedcorrelationmatrixofdifferenttraitsunderstudy.

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 thecharacteristics,groupedtheminto sixclusterswithhighdegreesofsimilarity.Theclustersize ranged from 2 (cluster V) to 11 (cluster II) breeding lines, indicating varying levels of diversity withineach group. The cluster mean differentiated members of each cluster from other clusters, highlightingthe distinctcharacteristicsofeachgroup(**Table5**).

Cluster II and III stood out for their notable characteristics, comprising high-yielding and talllines with late maturity and produced higher number of spikes per plant. In contrast, Cluster IV wascharacterizedbygenotypes with shortheight,longprimaryspikeswithhighernumberofcapsulesonprimaryspike.Clusters V and VI were the pistillate lines withearly flowering and maturity, short stature, fewernodes,highoilcontentandaverageseedyield.In contrast, Cluster I comprisedlate-maturing,shortpistillatelineswitha morenumberofnodesbutlowtotal seedyield per plant.

Table4.Clusteringof30castoraccessionsusingK-clusteringmethodbasedonagro-morphologicaldataset

GroupK	Numberof members	Clustermember
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

Table5.K-ClustermeansFor11agro-morphologicalcharacterstudied.

	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 themaximum variability is crucial in Principal Component Analysis (PCA). According to Rencher (2002), athreshold of 70% variance explained by PCs is recommended. In our analysis, out of 11 the first fourPCs accounted for approximately 75.80% of the total variability in the data set, with PC1 explaining26.50%, PC2 explaining 20.20%, PC3 explaining 15.90%, and PC4 explaining 13.20% (**Table 6**). Thisexceeds the recommended threshold, indicating that the first four PCs are sufficient to capture themajorityofthevariationinthedata.

Alternatively, the Kaiser criterion (1958) suggests retaining PCs with eigenvalues greater than1 (λi> 1), which also supports the retention of the first four PCs. The scree plot further confirms thisdecision, showing a clear break in the slope after the fourth component (**Figure 2**). Therefore, the firstfour PCs were retained for further analysis**.** Simplifying the data while capturing a substantial amountofthevariation.

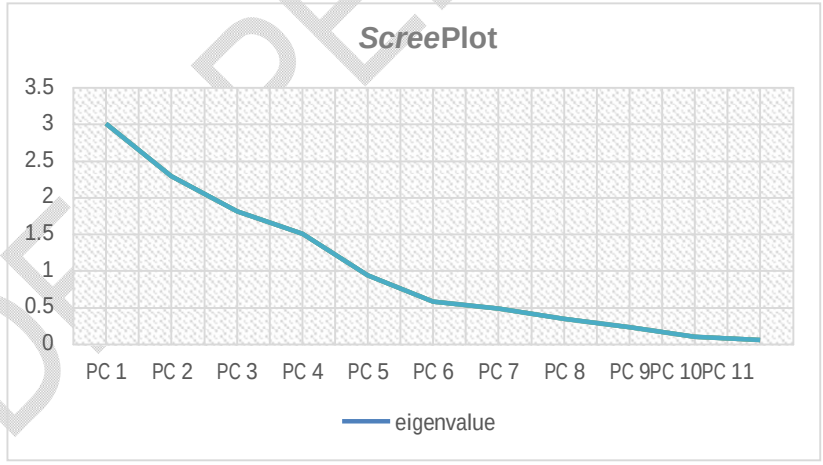

Fig.2.*Scree*plotofeigenvalues(Variancesofprincipalcomponents)

Table6.Principalcomponentanalysisfor11agro-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
Cumulativevariance%	26.50	46.60	62.60	75.80

DFF-Daysto50%flowering,DM-DaystomaturityofprimaryspikePH-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 capturedthe underlying variation pattern in the data.The first component primarily defined by the effective length ofprimary spike as the main contributor followed by total length of primary spike, number of capsules onprimary spike, number of nodes and plant height to primary spike, which were highly correlated andrepresentedthemainsourceofvariationamongthebreeding lines.Thesecondcomponentwascharacterizedbynumberofcapsulesonprimaryspike,totalseedyield,numberof spikesperplantandplant height. The third component highlighted effective length of primary spike, number of capsules onprimary spike and number of spikes per plant as the main contributors of variation, while the fourthcomponent emphasized hundred seed weight, oil content and days to 50% maturity, which were lesscorrelated with the first three components and captured a distinct aspect of the variation. The resultingprincipal component plot (**Figure 3**) displaying a broad dispersion of the 30 parental lines, indicatingsubstantialdiversityamongthem.

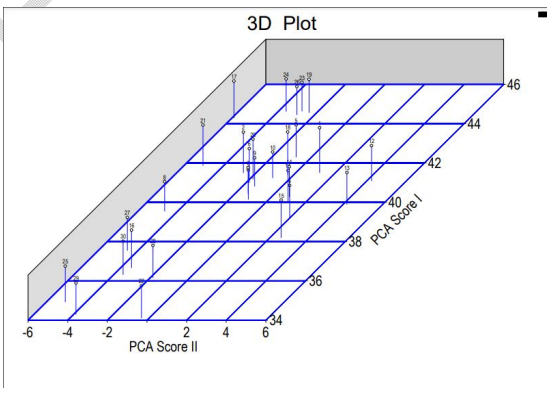

Fig.3.PCAanalysisforthecastorbreedinglines

CONCLUSION:

This study revealed significant genetic variability among the 30 advanced breeding lines of castor for 11 quantitative characters. Early flowering is observed in monoecious lines namely K22-1, K22-5, and K22-19, as well as pistillate lines IPC-41, IPC-51, and IPC-52. Early maturity of primary spike shown by lines K22-19, K22-39, K22-48 (monoecious lines), IPC-44, IPC-52, and IPC-58 (pistillate lines). In terms of plant height, tall stature found in monoecious lines K22-1 and K22-48, as well as in pistillate lines IPC-46, JP-96, and IPC-44, with 17-19 nodes up to primary spike. Condensed internodes were observed in pistillate lines DPC-25, JP-86, M-619, IPC-31, and IPC-51. Long spikes with more number of capsules on the primary spike recorded in monoecious lines K22-1, K22-5, and K22-39, as well as pistillate lines DPC-25, IPC-46 and IPC-48. Further, higher numbers of spikes per plant were found in monoecious lines K22-1 and K22-49, as well as pistillate lines IPC-41, IPC-46, and IPC-51. The monoecious lines K22-26, K22-1, K22-5, and K22-38 exhibited higher oil content and hundred seed weight; total seed yield per plant also observed high in these lines.Similarly, pistillate lines IPC-46, IPC-51, and IPC-41 showed high oil content and more total seed yield per plant making them suitable parental lines for future breeding programmes.

Furthercorrelation analysis revealed key relationships between traits, identified a significant positive association of plant height, number of spikes per plant and number of capsules on primary spike with the total seed yield per plant.Principal component analysis (PCA) Identified primary contributors to variation such as total and effective length of primary spike, number of capsules on primary spike and plant height. K-means clustering divided 30 breeding lines into 6 different clusters based on K- cluster mean. Using the superior advanced breeding lines belonging the divergent clusters as parents in breeding programmes could results in exploitation of maximum heterosis.

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