Received: 18 Jun 2021 | Revised: 20 Oct 2021 | Accepted: 25 Oct 2021

Electronic Journal of Plant Breeding

Research Article

Genetic parameters, diversity and character association studies in germplasm lines of castor (*Ricinus communis* L.)

K. Sadaiah*[1], G. Neelima[1], Ch. V. Durga Rani[2], V. Divya Rani[1], G. Madhuri[1], N. Nalini[1], M. Sujatha[1], V. Gouri Shankar[3], M. Parimala Kumar[1], C. Lavanya[4], J. Jawahar Lal[4] and Ch. Damodar Raju[1]

[1]**Regional Agricultural Research Station, PJTSAU, Palem, Nagarkurnool, Telangana**
[2]**Director, Institute of Biotechnology, PJTSAU, Rajendranagar, Hyderabad**
[3]**Administrative Office, PJTSAU, Rajendranagar, Hyderabad**
[4]**ICAR- Indian Institute of Oilseeds Research, Rajendranagar, Hyderabad.**
***E-Mail:** sadaiah.kurapati@gmail.com

Abstract
Castor is an important non-edible oilseed crop having huge industrial and export potential. It is used as an efficient lubricant for high-speed engines and as an ingredient in several commodities. There is a critical need to identify or to improve the germplasm lines with desirable characters. In the present study, 82 germplasm lines were evaluated in augmented design to estimate the genetic parameters *viz*., PCV, GCV, heritability and genetic advance as per cent of mean, principal component analysis and correlation studies. Results showed that the difference between PCV and GCV was low indicating less impact of environment on trait expression. Heritability (broad sense) and genetic advance as per cent of mean values were high for all the traits thus role of additive gene action is found important in governing the traits. Cluster analysis studies revealed that all the genotypes were grouped into eight clusters and cluster VIII documented the highest mean values for hundred seed weight and plant yield. The entries PRC-2 and PCS-337 recorded higher hundred seed weights of 56.5 and 48.6 g, respectively and in turn higher yield. These lines can be utilized as parents in the hybrid development programme for yield improvement. Correlation studies revealed that plant yield showed a significant positive association with all the characters except for days to 50% flowering. Thus selection for these traits *viz*., primary spike length, effective primary spike length, the number of effective spikes per plant, the number of capsules per spike and hundred seed weight will be advantageous in attaining higher yields.

Key words: Castor, cluster analysis, correlation, genetic variability, germplasm lines

INTRODUCTION

Castor (*Ricinus communis* L.) is a cross-pollinated monotypic species that belongs to the family Euphorbiaceae. It is distributed across the world throughout tropical and subtropical regions (Kumar *et al*., 2015; Chaudhari *et al*., 2019). It is believed to have been originated from the Ethiopian & Eastern Africa region owing to the high genetic diversity in the regions (Vavilov, 1951; Moshkin, 1986). India is the leading producer and exporter of castor oil in the world and exports almost 80% of its total castor production. However, in India, the area under castor cultivation is confined to only eight lakh hectares with a productivity of 1902 kg/ha (FAOSTAT, 2020). Castor oil has got huge industrial importance due to the presence of ricinoleic acid (up to 85%) which confers distinctive industrial properties to the oil (Anjani, 2012; Nagarajan *et al*., 2019). It is used as an efficient

lubricant for high-speed engines and as an ingredient in soaps, shampoo, shoe polish, candles and ointments (Ranjitha *et al*., 2019; Gouri Shankar *et al*., 2010; Morris, 2004).

To meet the growing requirement of the industries, there is every need to produce high yielding cultivars in castor. Genetic improvement of the crop and development of new genotypes is the most economical way to achieve the demand in castor (Sujatha *et al.,* 2008, Dapke *et al*., 2016; Salihu *et al*., 2017). Identification of genes and genotypes in the available germplasm and incorporation of same in the elite backgrounds is the best way for achieving desirable genetic improvement (Anjani, 2012). By considering the stable demand for castor oil in numerous industries, there is a crucial need to prominently improve the area, production and yield of castor crops. Based on the literature available, limited variability in castor was observed for yield contributing traits and resistance to diseases and pests which has led to limited progress in castor breeding programmes (Weiss, 2000). Estimation of genetic parameters, diversity studies and correlation analysis allows researchers to obtain more information like transmission of traits from one generation to another, the influence of external factors on traits expression and association among yield contributing traits from the material under study (Grobe, 2005).

MATERIALS AND METHODS

Eighty diverse germplasm lines including local collections, station germplasm, lines obtained from ICAR-IIOR, Hyderabad and other sources were studied (**Table 1**) along with two checks *viz*., Haritha, Pragathi. The lines were evaluated in an augmented design at the experimental plots of the Regional Agricultural Research Station, Palem during *kharif*, 2019. The experimental location is situated between 16.51° N latitude and 78.24° E longitude at an elevation of 545 meters above mean sea level. Each genotype was raised in a single row of 6 m length with a spacing of 90 × 60 cm. The experimental plot was divided into four blocks and each block contained 22 genotypes along with two checks replicated in all blocks. All the recommended agronomic practices were followed to raise the crop.

The observations on days to 50 % flowering, plant height (cm), the number of nodes to primary spike, primary spike length (cm), effective primary spike length (cm), the number of effective spikes per plant, the number of capsules per spike, yield per plant (g), hundred seed weight (g) were recorded on five plants per genotype. Analysis of variance was performed as described by Panse and Sukhatme (1985). The components of variances were used to calculate phenotypic and genotypic co-efficients of variation as per the formula by Falconer (1981). Besides other genetic parameters *viz*., heritability and genetic advance as per cent of mean was also calculated as suggested by Allard (1960) and Johnson *et al*. (1955), respectively. The cluster analysis was done using DARwin 6 (Perrier and Jacquemoud-Collet, 2006) using Euclidean distance with Unweighted Pair Group Method using Arithmetic means (UPGMA). Correlation analysis was performed as suggested by Snedecor and Cochran (1967). The genetic parameters and histograms were prepared using GenStat for windows 14th edition (VSN International, 2011).

RESULTS AND DISCUSSION

Analysis of variance was carried out for genotypes that showed significant differences for all the traits. This indicates the presence of variability in the material under study. The distribution of material for the traits under study was depicted in the form of a histogram (**Fig.1**) indicating the variability in the material. Considerable variation was also observed through the range in the chosen material (**Table 2**). Days to 50% flowering ranged from 40 to 70 days, plant height ranged from 13.5 to 124 cm, the number of nodes which indicates the earliness of a line ranged from 4 to 18, primary spike length from the basal node of the spike to till tip ranged from 8 to 67.5 cm whereas, effective primary spike length which is calculated as the first capsule from the base till the last capsule of the spike ranged from 2.5 to 67.5 cm, and the number of effective spikes per plant ranged from 2 to 17. Hundred seed weight which can be considered as a direct indicator of plant yield was ranged from 22.3 to 56.3 g. The genotypes, PRC-2 and PCS-337 recorded higher hundred seed weights of 56.5 g and 46.8 g, respectively. These entries can be utilised as an inbred parent for the development of high yielding hybrids or can be evaluated for performance in yield trials to be released directly as varieties. The single plant yield ranged from 15 to 294.2 g among the germplasm lines. The genotypes, PRC-2 and PCS-337 recorded higher seed yields per plant of 294.2 and 288.2 g, respectively which is much higher than the present day cultivars.

In the present study, the phenotypic coefficient of variation (PCV) varied from 11.53 to 56.08 per cent whereas, the genotypic coefficient of variation (GCV) ranged from 11.29 to 45.15 per cent for days to 50% flowering to the number of capsules per spike. Thus the estimates were moderate to high in the material under study (Subramanian and Menon, 1973). For all the traits, the difference between PCV and GCV was very less indicating less influence of environment on the expression of traits (Jaimini, 2002). High PCV and GCV was observed for all the traits except for days to 50% flowering and hundred seed weight which were recorded moderate PCV and GCV estimates.

Heritability provides information about the extent to which a particular genetic character can be transmitted to successive generations (Mangi *et al*., 2010). However, heritability value alone cannot provide information on the amount of genetic progress that would result from the selection of the best individuals. Johnson *et al*. (1955)

Table 1. List of castor genotypes used for the study

S.NO.	Genotype	Source	S.No.	Genotype	Source
1	RG 3829	Bheemda, Barmer, Rajasthan	42	RG 361	Tindivanam, Tamilnadu
2	RG 1869	DOR, Hyderabad	43	RG 66	Dantiwada, Gujarat
3	RG 2795	Cuddalore, Tamilnadu	44	RG 980	Dantiwada, Gujarat
4	RG 3864	Bersamada, Jodhpur, Rajastha	45	RG 937	Dantiwada, Gujarat
5	RG 1346	Unknown	46	RG 1218	Unknown
6	RG 1927	Lampara,Kamrup (dist),Assam	47	RG 1034	Unknown
7	RG 3678	ARS, Mandor, Rajasthan	48	RG 1081	USA
8	RG 3674	ARS, Mandor, Rajasthan	49	RG 1081 R	Derived from RG 1081
9	RG 3926	Nethda, Jodhpur, Rajasthan	50	RG 1282	Unknown
10	RG 1382	Unknown	51	RG 22	Hungery
11	RG 3067	Morgrdh-6,Anjar(Tq), Kutch, Gujarat	52	RG 1145	Unknown
12	RG 3810	Pandherpura, Maharashtra	53	RG -1117	Tindivanam,Tamilnadu.
13	RG 2687	Andhra Pradesh	54	RG -1151	Nigeria
14	RG 3834	Khararatoram, Barmer, Rajasthan	55	RG- 1741	DOR, Hyderabad
15	RG 2539	Unknown	56	RG- 1941	Meghalaya
16	RG 2714	Andaman &Nicobar Islands	57	RG- 1954	Assam
17	RG 840	IARI,RRS,Hyderabad	58	RG 1511	Palem, TS
18	RG 2364	Tindivanam,TNAU,Tamilnadu	59	RG 3408	Chinndwara, MP
19	RG 1069	USA	60	RG 3491	ARS, Mandore, Rajasthan
20	RG 3671	ARS, Mandor, Rajasthan	61	RG 3508	ARS, Mandore, Rajasthan
21	RG 3927	Nethda, Baavdi, Jodhpur, Rajasthan	62	RG 3527	ARS, Mandore, Rajasthan
22	RG 3676	ARS, Mandor, Rajasthan	63	RG 3533	ARS, Mandore, Rajasthan
23	RG 3675	ARS, Mandor, Rajasthan	64	RG 3705	Pipli, Bavnagar dist, GJ
24	RG 3667	ARS, Mandor, Rajasthan	65	RG 3728	Adilabad, TS
25	RG 3815	Gelaluas, Jodhpur, Rajasthan	66	RG 3736	Adilabad, TS
26	RG 3939	S.K.Nagar, Gujarat	67	RG 3761	Tamilnadu
27	RG 3836	Gangla, Sodokebasti, Barmer, RJ	68	RG 3772	Tamilnadu
28	RG 1083	Unknown	69	RG 3799	Tamilnadu
29	RG 3672	ARS, Mandor, Rajasthan	70	RG 631	Dantiwada, Gujarat
30	RG 3204	NBPGR, New Delhi	71	RG 981	Dantiwada, Gujarat
31	RG 3814	Gelaluas, Jodhpur, Rajasthan	72	PRC 2	Palem, TS
32	RG 2593	Chandrakot,Doda (dist),J & k	73	RG 3454	Unknown
33	RG 211	Former USSR	74	PCS 337	Palem, TS
34	RG 919	Dantiwada	75	RG 3160	Samakiya ,Kutch, Gujarat
35	RG 3833	Khararatoram, Barmer, Rajasthan	76	RG 3457	Unknown
36	RG- 1341	Unknown	77	RG 3477	Unknown
37	RG 3866	Kedra, Kodhpur, Rajasthan	78	RG 408	Dantiwada, Gujarat
38	RG 3677	ARS, Mandor, Rajasthan	79	RG 1294	Unknown
39	RG 3673	ARS, Mandor, Rajasthan	80	RG 2497	Unknown
40	RG 3680	ARS, Mandor, Rajasthan	81	Haritha*	Variety developed at RARS, Palem
41	RG 1253	Unknown	82	Pragathi*	Variety developed at RARS, Palem

*Check varieties

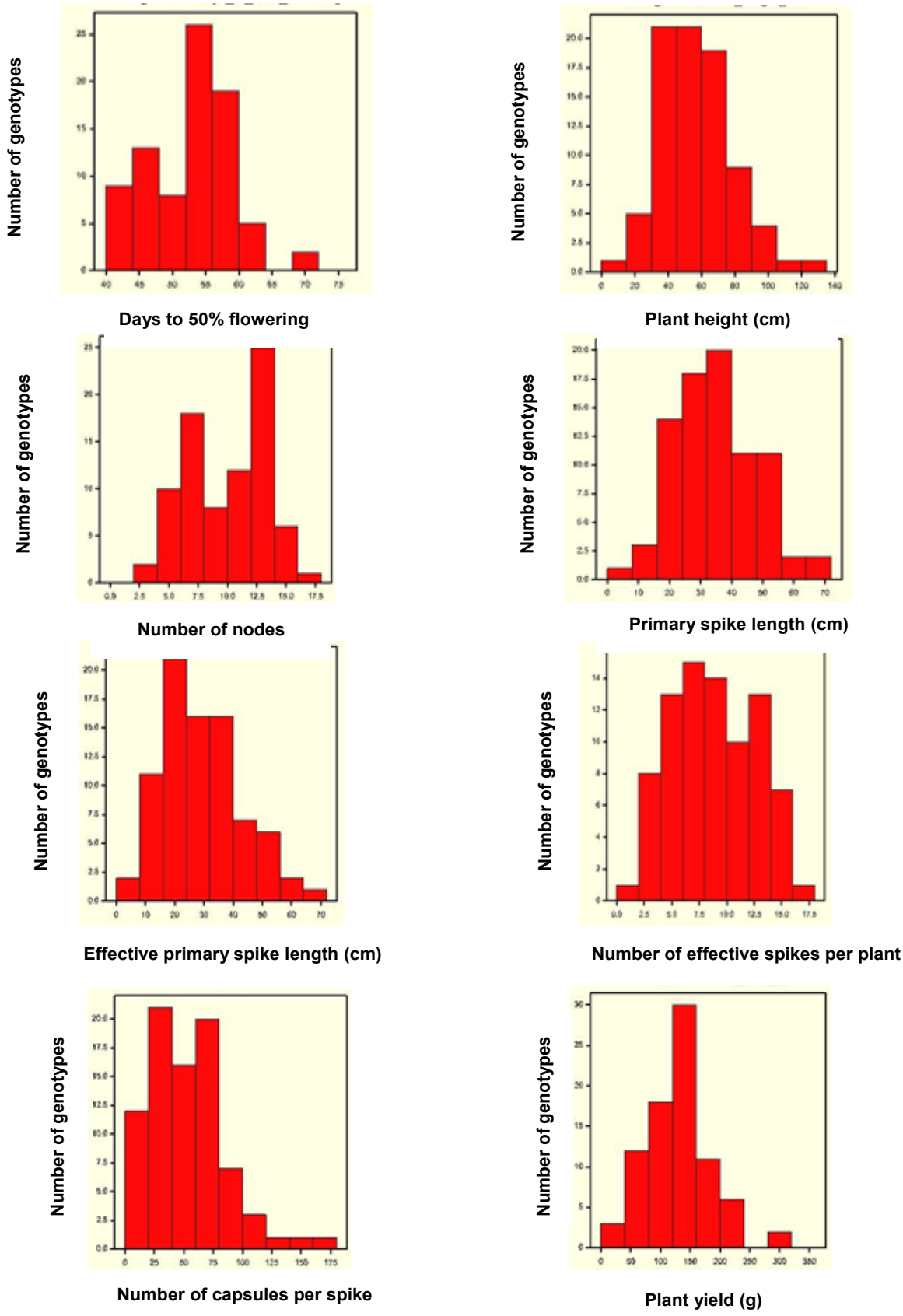

Fig. 1. Histogram depicting the spread of germplasm lines for the traits under study

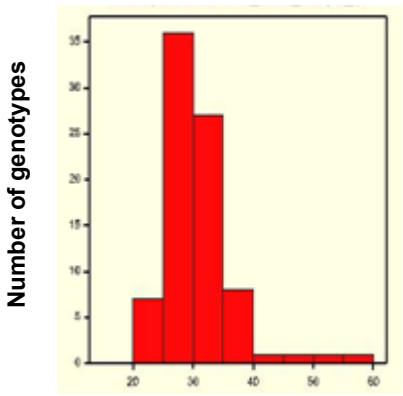

Fig. 1. Histogram depicting the spread of germplasm lines for the traits under study

reported that heritability estimates along with genetic advances would be more successful in predicting the effectiveness of selecting the best individuals. Genetic advance, which estimates the degree of gain in a trait obtained under given selection pressure, is an important parameter that guides the breeder in choosing a selection programme (Hamdi *et al*., 2003). High heritability and high genetic advance for a given trait indicate that it is governed by additive gene action and, therefore, provides the most effective condition for selection (Tazeen *et al*., 2009).

In the present material, the heritability (broad sense) ranged from 37.05 to 98.17 per cent for the traits number of effective spikes per plant to hundred seed weight, respectively (**Table 2**). The genetic advance as per cent of mean ranged from 22.77 to 74.87 for the traits days to 50% flowering to the number of capsules per primary spike (**Table 2**). Higher heritability values were observed for all the traits except for primary spike length, effective primary spike length and the number of effective spikes per plant where higher genetic advance as per cent of mean values was recorded for all the traits (Johnson *et al*., 1955) which indicate the influence of additive gene action in governing the traits resulting in simple phenotypic selection will be helpful in improving and fixing the traits in succeeding generations (Anjana *et al*., 2018). The above mentioned traits *viz*., primary spike length, effective primary spike length and the number of effective spikes per plant recorded moderate heritability and high genetic advance as per cent of mean suggesting the considerable impact of the environment in governing the inheritance of traits.

Diversity studies help in understanding the divergence in the material under study. In the present study, DARwin Software (Perrier and Collet, 2006) was utilised to identify variation in the material under study. Genotypes were grouped into eight clusters (**Table 3**) based on Euclidean distance. Cluster I had 22 genotypes and was considered as the largest in the present study followed by cluster II with 18 genotypes. Further, cluster III was grouped with 7 genotypes, cluster IV contains 11 genotypes, 10 genotypes were grouped in cluster V, cluster VI, VII and cluster VIII had 11, 1 and 2 genotypes, respectively. Cluster mean values (**Table 4**) for yield and yield contributing characters revealed that cluster VIII recorded a higher mean yield of 292.20 g / plant and also recorded a higher average hundred seed weight of 51.6 g.

Correlation studies provide information on the nature and magnitude of association between pairs of traits,

Table 2. Genetic parameters for yield and yield related traits in castor germplasm lines

Trait	Mean	Range	h^2 (%)	GA as per cent mean	GCV (%)	PCV (%)
DFF	52.70 ± 1.22	40.00 – 70.00	95.93	22.77	11.29	11.53
PH (cm)	57.40 ± 8.66	13.50 – 124.00	80.95	57.69	31.13	34.60
NN	10.60 ± 0.70	4.00 – 18.00	95.39	61.03	30.34	31.06
PSL (cm)	35.60 ± 9.40	8.00 – 18.00	45.67	33.89	24.35	36.03
EPSL (cm)	30.49 ± 10.40	2.50 – 67.5	43.03	40.33	29.76	45.37
NESPP	9.08 ± 2.85	2.00 – 17.00	37.05	30.19	24.08	39.56
NC	54.20 ± 18.03	7.00 – 167.00	64.81	74.87	45.15	56.08
YP (g/ plant)	133.16 ± 25.07	15.00 – 294.20	77.17	62.72	34.62	39.41
HSW (g)	30.42 ± 0.76	22.30 – 56.50	98.17	37.39	18.31	18.48

DFF: Days to 50% flowering, PHT: Plant height, NN: Number of nodes to primary spike, PSL: Primary spike length, EPSL: Effective primary spike length, NESPP: Number effective spikes per plant, NC – number of capsules per primary spike, TY: Total yield per plant, HSW: Hundred seed weight.

Table 3.Grouping of germplasm lines into eight clusters

Cluster	Number of genotypes	Name of Genotypes
I	22	RG 919, RG 3672, RG 2593, RG 3491, RG 3833, RG 1218, RG 937, RG 1954, RG 1346, RG 3408, RG 3829, RG 2687, RG 1294, RG 1069, RG 1741, RG 3866, RG 3457, RG 981, RG 3810, RG 2795, RG 3761, RG 3533
II	18	RG 2714, RG 3834, RG 2364, RG 3799, RG 3673, RG 3836, RG 3926, RG 3772, RG 3736, RG 3454, RG 980, RG 3477, RG 3677, RG 3814, RG 1151, RG 2497, RG 1081, RG 1081 R
III	7	RG 1341, RG 211, RG 1382, RG 3675, RG 3160, RG 3728, RG 3815
IV	11	RG 631, RG 3680, RG 3508, RG 3705, RG 3676, RG 1083, RG 3678, RG 1145, RG 2539, RG 1282, RG 3671
V	10	RG 1511, RG 361, RG 22, RG 3067, RG 1869, RG 1117, RG 1034, RG 66, RG 1253, RG 3674
VI	11	RG 408, Pragathi, Haritha, RG 3667, RG 1941, RG 1927, RG 3927, RG 3527, RG 3204, RG 3939, RG 3864
VII	1	RG 840
VIII	2	PRC 2, PCS 337

Table 4. Cluster means of eight clusters for yield and yield related traits in castor germplasm lines

Cluster	DFF	PHT	NN	PSL	EPSL	NESPP	NC	TY	HSW
I	53.14	46.32	8.45	27.52	22.34	9.61	27.34	117.75	29.52
II	52.61	60.58	10.61	35.92	28.69	9.14	57.72	138.90	30.90
III	54.57	44.57	9.00	25.43	19.00	7.64	48.14	183.70	33.00
IV	53.91	69.64	12.27	40.59	36.18	9.18	73.50	78.39	28.91
V	55.30	40.95	8.70	24.30	18.50	8.30	23.45	57.86	29.42
VI	48.59	74.12	13.71	51.68	49.15	9.44	86.82	192.57	29.21
VII	59.00	76.00	15.00	51.50	51.50	6.50	167.00	44.60	29.03
VIII	55.00	59.70	15.50	44.85	36.10	7.15	53.35	291.20	51.65

DFF: Days to 50% flowering, PHT: Plant height (cm), NN: Number of nodes to primary spike, PSL: Primary spike length (cm), EPSL: Effective primary spike length(cm), NESPP: Number effective spikes per plant, NC – number of capsules per primary spike, TY: Total yield per plant (g), HSW: Hundred seed weight(g)

which is useful for the breeder in carrying out multiple trait improvements. In the present study (**Table 5**), no significant correlation was observed for days to 50% flowering with any other traits. Whereas, plant height showed a significant positive correlation with the number of nodes, primary spike length, effective primary spike length, the number of capsules per primary spike and plant yield. The number of nodes to primary spike showed a significant positive correlation with all the yield contributing traits *viz*., primary spike length, effective primary spike length, the number of effective spikes per plant, the number of capsules per primary spike, total yield per plant, hundred seed weight. A significant positive association was observed for primary spike length with effective primary spike length, the number of capsules per primary spike, total yield per plant whereas, effective primary spike length showed a significant positive association with the number of capsules per primary spike and total yield per plant. The number of capsules per primary spike recorded a significant positive association with total plant yield. A significant positive association was also observed between hundred seed weight and total yield per plant. Thus the genotypes with high hundred seed weight *viz*., PCS-337 (46.8 g) and PRC-2 (56.5 g) can be utilized as inbred parents in hybrid seed production or can be directly utilised as a straight variety based on the agronomic performance.

The present study revealed that the entries *viz*., PRC-2 and PCS-337 recorded higher hundred seed weight and higher single plant yield and are diverse compared to the other genotypes. These genotypes can be further utilised in crossing programmes to obtain high yielding cultivars in castor.

Table 5. Phenotypic correlation coefficients of yield and yield related traits in castor germplasm lines

Trait	DFF	PHT	NN	PSL	EPSL	NESPP	NC	TY	HSW
DFF	1.000								
PHT	0.003	1.000							
NN	-0.082	0.759**	1.000						
PSL	-0.120	0.682**	0.701**	1.000					
EPSL	-0.137	0.630**	0.646**	0.919**	1.000				
NESPP	-0.103	0.128	0.283**	0.184	0.127	1.000			
NC	-0.053	0.554**	0.519**	0.700**	0.734**	0.044	1.000		
TY	-0.172	0.213*	0.297**	0.374**	0.340**	-0.008	0.290**	1.000	
HSW	0.113	0.180	0.237*	0.031	-0.009	-0.17	-0.057	0.403**	1.000

DFF: Days to 50% flowering, PHT: Plant height, NN: Number of nodes to primary spike, PSL: Primary spike length, EPSL: Effective primary spike length, NESPP: Number effective spikes per plant, NC – number of capsules per primary spike, TY: Total yield per plant, HSW: Hundred seed weight.

ACKNOWLEDGEMENT

The authors would like to acknowledge the ICAR-Indian Institute of Oilseeds Research for providing the germplasm lines & financial support. The authors would also like to acknowledge PJTSAU for providing technical & financial assistance.

REFERENCES

Allard, R.W. 1960. *Principles of plant breeding*. John Wiley and Sons Inc., New York, USA.

Anjana, P., Pathak, A.R., Madariya, R.B. and Barad, S.H. 2018. Gene action for seed yield and its component traits in castor (*Ricinus communis* L.) using graphical and numerical approach of diallel analysis. *J. Pharmacogn Phytochem*.,**7** (4): 1870-1876.

Anjani, 2012. Castor genetic resources: A primary gene pool for exploitation. *Ind. Crops Prod*., **35**: 1-14. [Cross Ref]

Chaudhari, B.A., Patel, M.P., Dharajiya, D.T. and Tiwari, K.K. 2019. Assessment of genetic diversity in castor (*Ricinus communis* L.) using microsatellite markers. *Biosci. Biotechnol. Res. Asia*., **16** (1): 61-9. [Cross Ref]

Dapke, J.S., Naik, M.R., Vaidya, G.B., Vanve, P. B., Narwade, A.V. and Rajkumar, B.K. 2016. Genetic variability in castor (*Ricinus communis* L.). *European J. Biotechnol. Biosci*., **4**. 39-40.

FAOSTAT, 2020. htpp://faostat.org.

Falconer, D.C. 1981. *An introduction to quantitative genetics*. Longman, New York. 67-68.

Gouri Shankar, V., Venkata Raman Rao, P. and Reddy, V.2010. Heterosis studies in castor (*Ricinuscommunis* L.).*J. Oilseeds Res*., **27**: 95-96.

Grobe, J. R. 2005. *Aplicações da estatística multivariadanaanálise de result adosem experimentos com soloseanimais* (Master's thesis, Universidade Federal do Paraná, Curitiba).

Hamdi, A., El-Chareib,A.A., Shafey, S.A. and Ibrahim, M.A.M. 2003. Genetic variability, heritability and expected genetic advance for earliness and seed yield from selections in Lentil. *Egypt J. Agric. Res*., **81** (1): 125-137.

Jaimini, N. 2002. Genetic variability, association studies, genetic divergence and stability analysis in newly evolved pistillate lines of castor (*Ricinu scommunis* L.). M.Sc. (Ag.) Thesis, Gujarat Agricultural University, Sardarkrushinagar (Gujarat).

Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *J. Agron*., **47** (7): 314-318. [Cross Ref]

Kumar, M.V.N., Gouri Shankar, V., Ramya, V., Bindu Priya, P., Ramanjaneyulu, A.V., Seshu, G. and Reddy, D.V.V. 2015. Enhancing castor (Ricinus communis L.) productivity through genetic improvement for Fusarium wilt resistance – A review. *Ind. Crops Prod*., **67**: 330-335. [Cross Ref]

Mangi, S., Sial, M., Ansari, B., Arain, M., Laghari, K. and Mirbahar, A. 2010. Heritability studies for grain yield and yield components in F_3 segregating generation of spring wheat. *Pak. J. Bot*., **42** (3): 1807-1813.

Morris, J.B. 2004. Phytochemical traits in the genetic resources of castor bean. *Cur. Topics Pl. Biol.,* **5**: 63-67.

Moshkin, 1986. Castor. Amerind publishing, New Delhi, India.

Nagarajan, S., Viswanathan, P.L., Venkatachalam, S.R., Manickam S. and Ganapathi, N. 2019. Genetic divergence analysis of castor (*Ricinus communis* L). *Electronic Journal of Plant Breed*ing, **10** (2): 754-760

Panse, V.G. and Sukhatme, P.V. 1985. Statistical methods for agricultural workers. ICAR, New Delhi.

Perrier, X. and Jacquemoud-Collet, J.P. 2006. DARwin software. http:Darwin.cirad.fr/.

Ranjitha, V., Venkatachalam, S.R., Arutchenthil, P. and Kathirvelan, P. 2019. Genetic divergence in castor (*Ricinus communis* L.). *Electronic Journal of Plant Breed*ing, **10** (2): 766-771.

Salihu, B.Z., Falusi, A.O., Gana, A.S., Adebola, M.O. and Daudu, O.Y. 2017. Estimation of heritability and predicted genotype mean for seed yield of castor (*Ricinuscommunis* L.) using Best Linear Unbiased Prediction (BLUP). *J. Plant Dev*., **24**: 51-65.

Snedecor, G.W. and Cochran, W.G. 1967. *Statistical Methods*. Oxford and IBH Publishing Co., New Delhi. 172-195.

Subramanian, P.S. and Menon, P.M. 1973. Genotypic and phenotypic variability in rice. *Madras Agric. J*., **60**: 1093.

Sujatha, M., Reddy, T.P. and Mahasi, M.J. 2008. Role of biotechnological interventions in the improvement of castor (*Ricinus communis* L.) and *Jatropha curcas* L. *Biotechnol. Adv*., **26**: 424–435. [Cross Ref]

Tazeen, M., Nadia, K. and Farzana, N.N. 2009. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. *J. Food Agric. Environ*.**, 7**(3 & 4): 278-282.

Vavilov, N.I. 1951. The origin, variation, immunity and breeding of cultivated plants. Waltham, MA: Chronica Botanica. [Cross Ref]

VSN International. 2011. GenStat for Windows 14th Edition. VSN International, Hemel Hempstead, UK.

Weiss, E.A. 2000. Oilseed crops. 2nd ed. Blackwell Science, Oxford.-1096.