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Research Note

Exploring agro-morphological variation, genetic diversity, and trait associations in castor (*Ricinus communis* L.) genotypes

Yamanura[1*], R. Mohan kumar[1], Prashanth. A. Sangannavar[2] and B. Boraiah[1]

[1]All India Co-ordinated Research Project on Castor, Zonal Agricultural Research Station, University of Agricultural Sciences, GKVK, Bengaluru – 560 065, Karnataka, India
[2] Research Co-ordination Section, Central Silk Board, Ministry of Textiles, Govt. of India, Bengaluru – 560 068, Karnataka, India
***E-Mail** : yaman3181aug8@gmail.com

Abstract
The current study involved 40 castor genotypes and revealed significant variation in agro-morphological traits among them. Genetic estimates showed higher values, alongside a narrow range of genotypic and phenotypic coefficients of variance for key traits such as seed yield, plant height, 100-seed weight, effective primary spike length, and number of capsules on primary spikes, indicating a favorable scope for selection. Out of the ten analysed traits, four exhibited a positive direct effect, while six showed a negative direct effect on seed yield per plant. Maximum positive direct effects were observed for total length of primary spike, days to maturity of primary spike, percent oil content, and hundred-seed weight. Hence, genotypes possessing these traits could play a pivotal role in breeding elite cultivars within improvement programme. The seed yield per plant, plant height, 100-seed weight, effective primary spike length, and number of capsules on primary spikes showed high estimates for both GCV and PCV, indicating substantial variability with minimal environmental influence. This suggests that these traits offer a strong opportunity for selection and breeding, as the genetic variability in these traits is more significant than environmental factors. Most quantitative traits studied exhibited high heritability and high genetic advance, indicating that these traits are largely controlled by additive genetic effects, which is favourable for selection.

Keywords: *Ricinus communis*, Correlation analysis, Genetic variability

Castor (*Ricinus communis* L.) is a widely cultivated non-edible oilseed crop. As castor oil is used for manufacture of lubricant, soaps, refined oil, perfumed hair oil, ointments, cosmetics, varnishes, synthetic resins, printing inks, carbon paper and processed leather, the crop has immense industrial application (Mutlu and Meier, 2010). Castor being a deep-rooted drought tolerant crop, suites well to arid and semi-arid regions of India (Naidu *et al*., 2015). It is mainly produced in India (88%). However, China, Brazil, Russia, Thailand, Ethiopia and Philippines also contribute to the global production (Yamanura and Kumar, 2020). In India, it is presently, cultivated in over 8.35 lakh ha, with a production of 12.2 lakh tones of castor seed and productivity of 1600 kg ha^{-1} (ICAR-IIOR, 2020). Despite the phenomenal gain in productivity of castor over the past few years, the task of meeting out its market demand is still a formidable task due to growing global demand. Interestingly, different castor growing regions of India exhibits significant variation in productivity. This could be due to several factors, with the main challenge being the absence of high-performing genotypes that can thrive in diverse environments (Kumar *et al*., 2021).

Genetically diverse parents tend to produce more favourable gene combinations, leading to higher heterosis. This makes it crucial to identify parents with significant

genetic divergence from the existing germplasm for use in future breeding programs. Hence, we initiated the characterization of germplasm accessions within our available pool. It ensures optimal use of the characterized germplasm by end users and helps distinguish unique accessions within a species.

Germplasm collections without passport data has meagre utility (<1%) in crop improvement or germplasm utilization in breeding. Of late, germplasm collections with complete representation of genetic diversity in the form of minicore have been developed in many crops (~1% of the core collection) (Upadhyaya *et al*., 2010; Muniswamy *et al*., 2014). Minicore approach has been an effective methodology to enrich and increase crop improvement programmes by providing a focused, efficient, and cost-effective way to study and utilize genetic diversity. It streamlines the research process and facilitates faster progress in breeding, which is crucial for addressing the demands of a rapidly changing agricultural landscape. Similarly, in castor, morphological characterization offers a means of access to the larger collections for further exploration and also helps in proper assessment of genetic diversity, association mapping, population structure and targeted gene mining. It will direct to better utilization of diverse germplasm for developing broad based genotypes / cultivars, especially in the situation like climate change.

This study will provide a better view on the symphony of the collection with its genetic diversity by permitting grouping of accessions, identification of valuable germplasm for breeding programmes and development of core collections as earlier opined by Parida *et al*. (2020). A variety of morphological investigations are very much essential for characterization and classification of germplasm. Characterization of accessions is helpful for identification of superior accessions which can be utilized further for breeding programmes. In castor, morphological traits such as seed shape, leaf shape, plant type, types of internodes, branching habits, stem colour, bloom content, spike shape, inflorescence/ spike type, capsule type and seed coat colour are key traits to distinguish genotypes (Lavanya and Gopinath, 2008; Chaudhari *et al.,* 2019). Each of the aforementioned characteristics has their own impact on photosynthesis, crop duration, drought tolerance, insect pest preference, yield and oil quality. Detailing available germplasm for key agro-morphological parameters would help in conceptualization and evolution of elite hybrids and varieties. Hence, a study on assessment of agro-morphology, genetic variability and trait association in castor was undertaken by involving 40 castor genotypes.

The present investigation was carried out at the experiment blocks of All India Co-ordinated Research Project on Castor, Zonal Agricultural Research Station, Gandhi Krishi Vigyan Kendra, University of Agricultural Sciences, Bangalore, Karnataka, India during *Kharif* - 2019-20. The study consisted of 40 castor genotypes which included inbreds (8), preliminary hybrids (18), local collections (9), advanced lines (3) and checks (2). The test genotypes were raised in a randomised complete block design with three replications. The test genotypes were sown in single row plots of 6.0 m length with a spacing of 90 x 60 cm and all recommended package of practices were followed.

Data on 11 qualitative traits and 16 quantitative traits were measured on five randomly chosen plants from each genotype. The quantitative traits observed in this study includes days to 50% flowering of primary spike (DFF), days to maturity of primary spike (DMPS), plant height up to primary spike (PH), number of nodes up to primary spike (NN), total length of primary spike (TLPS), effective length of primary spike (ELPS), number of capsules on primary spike (NC), number of effective spikes per plant (NES/P), 100 seed weight (HSW), percent oil content (OC) and seed yield per plant (SYPP). Similarly, qualitative traits observed were anthocyanin pigmentation on hypocotyl, anthocyanin pigmentation on young emerging leaves, waxy bloom content on upper leaf, waxy bloom content on lower leaf, waxy bloom content on stem, stem colour, type of internodes on stem, leaf shape, leaf laciniation, petiole surface, type of flowers on primary spike, spike shape, spike compactness, spininess of capsules, location of branches, and branching pattern.

The mean values of five randomly selected plants for each genotype were statistically analysed. Phenotypic and genotypic coefficient of variation were computed following the methods proposed by Burton and Devane (1952). As indicated by Sivasubramanian and Menon (1973), GCV and PCV values were categorized as low (1-10%), moderate (11-20%) and high (> 21%). Heritability in broad sense Broad Sense was calculated as a ratio of genotypic variance to the phenotypic variance (Robinson *et al*., 1949). As suggested by Robinson *et al*., 1949, heritability percentages were categorized as low (0-30%), moderate (31-60%) and high (> 61%). Genetic advance was calculated according to the method suggested by Johnson *et al*. (1955). Genetic advance as percentage of mean (GAM) was calculated using the formula of Johnson *et al.* (1955) and was classified into low (0-11%), moderate (11-20%), and high (>20%) categories.

The statistical tool used in the analysis of qualitative traits was the WINDOSTAT software (version 9.3) to perform the analysis of variance (ANOVA), calculate genetic parameters, and apply other relevant statistical methods.

Morphological characterization of castor genotypes exhibited vast variation in both qualitative and quantitative traits. The frequency distribution for different qualitative traits like anthocyanin pigmentation on hypocotyl and young emerging leaves, bloom content in different

plant part, stem colour, type of flowers on primary raceme and node pattern on trunk are shown in **Fig. 1**. After germination, young seedlings sometimes show pigmentation. If anthocyanin pigmentation is present, it tends to reoccur in the young leaves and produces red or mahogany-coloured stems. This characteristic can serve as a useful morphological marker in the seed production process. However, in this study anthocyanin pigmentation on hypocotyl was observed in 75% of the genotypes and 80% had pigmentation on young emerging leaves. Bloom content on plant parts decides the drought tolerance and pest reaction (Lavanya and Gopinath, 2008). The presence of waxy bloom on the plant indicates a higher degree of drought tolerance and is less attractive to sucking pests. In the present study, only 10% of the genotypes had waxy bloom on all parts of the plant. These genotypes belonged to the triple bloom group, and included MI-55, MI-85, BCH-43, and BCH-59. Similarly, 10% of the genotypes were free from waxy content and these were grouped under zero bloom category (BCG-10, BCG-11, BCG-15, HCG-21). The colour of the stem was observed to be of mahogany type in 75% followed by green in 20% and red in 5% of the genotypes. They did not exhibit variation for leaf shape, leaf lascination and petiole surface. About 57.50% genotypes were observed to have elongated nodes with pistillate flowers on primary raceme and 42.5% had condensed nodes on stem with monoecious flowers on primary spike. The frequency distribution for the traits *viz.,* spike shape, spike compactness, spininess on capsules, location of branches and branching pattern are displayed in **Fig. 1**. For spike shape, conical shape was observed to be predominant (50%) followed by cylindrical (40%) and umbrella type (10%). For spike compactness trait, 62.50% were observed to be compact, 32.50% semi compact and 5% were of loose types. The dense spininess on the capsules displayed maximum (75%) followed by sparse (17%) and non-spiny genotypes (7.5%) which are less prone to gray mould disease caused by *Botryticinia ricini.* About 62.5% of the genotypes were observed to be of top branching type with convergent branching habit. The morphological characterization in castor germplasm accessions were earlier attempted by several researchers (Lavanya and Gopinath, 2008; Rukhsar *et al*., 2017). Chaudhari *et al*. (2019) showed the importance of morphological characterization for simple and convenient identification of genotypes in seed production activities to maintain the purity of seeds.

Analysis of variance demonstrated significant differences among the genotypes for all observed traits. Most characteristics displayed considerable variability **(Table 1)**. The significant differences among genotypes across all traits suggest ample opportunity to select promising genotypes for yield improvement. These results align with the findings of Ramesh *et al*. (2016), who studied 22 heat-tolerant Recombinant Inbred Lines (RILs) of wheat. Knowledge about the variability among traits estimated using genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are of importance for an effective breeding programme in crops like castor. GCV and PCV, heritability in broad sense and genetic advance (GA% mean) results are summarized in **Table 2**. The higher estimates and close values of GCV and PCV was observed for seed yield/plant, plant height, 100-seed weight, effective primary spike length and number of capsules on primary spikes offering better scope for selection as there was less influence of environment and suggesting that potential variability available in studied material for these traits. Lakshmamma *et al*. (2005), Sarwar *et al.* (2010), Patel *et al*. (2010), Rukshar *et al.* (2018), Gabriela *et al.* (2019) and Yamanura and Kumar (2020b) also reported higher GCV and PCV for seed yield whereas, lower GCV was reported for test weight by Patel *et al*. (2010). High GCV and PCV were observed for all the traits investigated except for days to maturity of primary spike which was moderate and oil content found to be low and the extent of differences between GCV and PCV was low for all the traits investigated. The lower difference of GCV and PCV is a major sign of low influence of environmental factors on the phenotypic expression (Rao *et al*., 2009). Patel and Jaimini (1988) also reported moderate to high coefficient of variation for many of the traits in castor irrespective of the environment. Based on study of 68 castor lines, Lakshmamma *et al*. (2005) indicated high GCV and PCV for capsule weight per plant, capsule number, plant height and leaf area index. Alhaji *et al*. (2019) reported high genotypic and phenotypic coefficients of variation (above 20%) for several days to 50% flowering, number of branches per plant , number of effective racemes per plant , effective raceme length , number of capsules per raceme and height at maturity. Additionally, moderate genotypic coefficients of variation (between 10% and 20%) were observed for traits like height at flowering, leaf petiole length, stem girth, and 100 seed weight. These results suggest that certain traits exhibit substantial genetic variation, providing a good potential for breeding and genetic improvement, while others show moderate variation, indicating potential for selection with a less pronounced impact. Yamanura and Kumar (2020b) reported higher and closely aligned estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in several key traits, including seed yield per plant, number of effective spikes per plant, plant height, total and effective primary spike length, number of capsules, and 100-seed weight. These findings suggest a favourable scope for selection as the influence of environmental factors was limited, indicating substantial inherent variability within the studied material for these traits.

Heritability and genetic advance are the two major parameters, which provide information about the nature of gene action governing a particular character. High heritability was observed for 100 seed weight (99.70), days required to primary spike maturity (98.30), seed yield

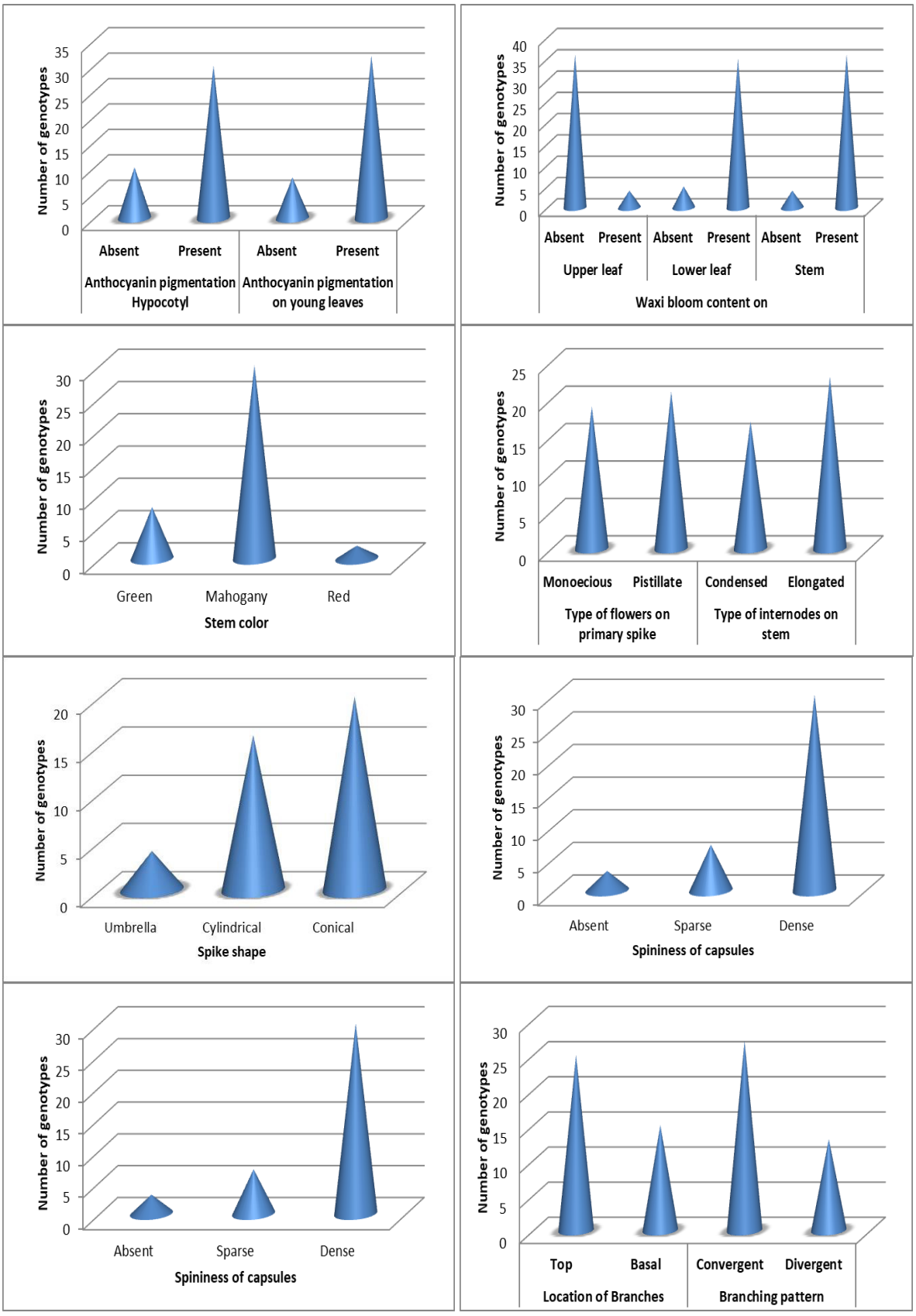

Fig. 1. Frequency distribution of genotypes for qualitative traits

Table 1. Analysis of variance (mean squares) for yield and its components in castor genotypes

#	Source of Variations	Replicate	Treatments	Error
	Degrees of Freedom (DF)	1	39	39
1	Days to 50% flowering of primary spike (DFF)	30.01	217.20**	9.55
2	Days to maturity of primary spike (DMPS)	9.11	442.64**	3.88
3	Plant height up to primary spike (PH)	324.25	2083.39**	101.76
4	Number of nodes up to primary spike (NN)	2.72	17.84**	2.12
5	Total length of primary spike (TLPS)	19.60	280.72**	21.21
6	Effective length of primary spike (ELPS)	76.73	261.07**	24.88
7	Number of capsules on primary spike (NC)	57.19	224.78**	13.72
8	Number of effective spikes per plant (NES/P)	2.95*	3.41**	0.59
9	100 seed weight (HSW)	1.56	271.60**	0.36
10	Percent oil content (OC)	2.10	10.98**	0.53
11	Seed yield per plant (SYPP)	42.52	3762.28**	75.73

Where: [*, ** Significant at 5 % and 1 % levels of probability, respectively,].

Table 2. Variability parameters for eleven quantitative traits in castor genotypes

#	Traits	Mean	GCV %	PCV %	Heritability (%)	G A (%) of Mean
1	Days to 50% flowering of primary spike (DFF)	49.79	20.47	21.39	91.60	40.35
2	Days to maturity of primary spike (DMPS)	102.21	14.49	14.62	98.30	29.59
3	Plant height up to primary spike (PH)	80.23	39.23	41.20	90.70	76.96
4	Number of nodes up to primary spike (NN)	13.62	20.58	23.19	78.70	37.61
5	Total length of primary spike (TLPS)	43.18	26.38	28.46	85.90	50.38
6	Effective length of primary spike (ELPS)	36.84	29.50	32.46	82.60	55.22
7	Number of capsules on primary spike (NC)	34.91	29.43	31.28	88.50	57.02
8	Number of effective spikes per plant (NES/P)	5.30	22.38	26.67	70.40	38.69
9	100 seed weight (HSW)	32.42	35.92	35.97	99.70	73.90
10	Percent oil content (OC)	45.94	4.98	5.22	90.70	9.76
11	Seed yield per plant (SYPP)	86.46	49.66	50.67	96.10	100.25

per plant (96.10), days to 50% blooming of primary spike (91.60), plant height and oil content (90.70), capsules number on primary spike (88.50), length of primary spike (85.90) and effective length of primary spike (82.60). Similarly, high genetic advance as percentage of mean was observed for seed yield per plant (100.25), followed by plant height up to primary spike (76.96), 100 seed weight (73.90), number of capsules on primary spike (57.02), effective length of primary spike (55.22) and total length of primary spike (50.38). In the current investigation, all the traits illustrated high heritability indicating low environmental effect and high capacity of the characters to be transmitted to subsequent generations (**Table 2**). All quantitative characters studied had high heritability with high genetic advance except percent oil content, days to maturity of primary spike, 50% flowering of primary spike, number of nodes up to primary spike and number of effective spikes per plant suggesting the predominance of non-additive gene effects. Consequently, selection based solely on these traits may not lead to substantial improvements in castor. Similar reports were earlier made by Yamanura and Kumar (2020b). High heritability (H2 > 60%) coupled with high genetic advance as percentage of mean (GAM > 20%) were observed for seven traits out of thirteen traits examined by Alhaji *et al*. (2019).

The major aim of crop improvement is to achieve a higher yield. It has been generally accepted that correlation between different characters represents a coordination of physiological processes, which is often achieved through gene linkages. The complex nature of seed yield is majorly influenced by number of component traits. Hence, information on the strength and direction of association of these component traits with seed yield and also inter association among them would be very useful in formulating an effective and viable breeding programme for improvement of seed yield. Character association studies are of great significance in the process of selection

by which simultaneous improvement of more than one character is possible. Correlation coefficients at genotypic level were majorly of higher extent than the corresponding phenotypic level representing the strong association between the characters. Correlation coefficients between different pairs of traits were estimated and not all the traits were correlated to each other or with seed yield (**Table 3**). Highest positive significant correlation was observed between total length of primary spike and effective length of primary spike (0.996). Total length of primary spike depicted significant and positive correlation with number of capsules on primary spike (0.429), plant height showed significant and positive correlation with number of nodes per plant (0.669), total length of primary spike (0.560), effective length of primary spike (0.566), oil content (0.248) and hundred seed weight (0.231). Seed yield per plant was positively associated with total length of primary spike (0.0765), effective length of primary spike(0.0425), oil content (0.289) and hundred seed weight (0.1775) indicating that selection for these traits would lead to higher seed yield per plant (**Table 3**). The traits days to 50 % flowering of primary spike, number of nodes to primary spike and effective spikes per plant were negatively correlated with seed yield per plant, suggesting that medium to late maturing should be selected for improvement in seed yield in castor.

The correlation coefficients between any two traits would not give a complete view of a complex situation like plant yield which is equally determined by a number of traits either directly or indirectly. In such conditions, path coefficient analysis would be valuable, as it permits the partitioning of direct effect and indirect effects through other related traits by partitioning the genotypic correlation coefficient (Dewey and Lu, 1959). Among the 10 traits analysed in the present study , four traits illustrated positive direct effect and six traits showed negative direct effect on seed yield. The maximum positive direct effect was observed for total length of primary spike (1.8104), days to maturity of primary spike (DMPS) (0.355), percent oil content (0.3235) and hundred seed weight (0.1132). Hence, these traits can be directly attributed to the enhancement of seed yield and the selection of superior genotypes. Negative direct effect was recorded for days to 50% flowering (-0.0886), plant height (-0.6286), effective length of primary spike (-0.1746) number of nodes up to primary spike (-0.1596), number of effective spikes/ plant (-0.1107) and number of capsules/plant (-0.1716). Similar opinions were earlier expressed by Gabriela *et al*. (2019) and Lal and Lavanya (2019). The present study exhibited huge variation among the tested genotypes for seed yield as well as yield contributing traits (**Table 4**) which facilitated the selection and forwarding the selected genotypes for its further utilization. These results were in accordance with the reports of Manivel and Hussain (2001).

The study unveiled substantial variation in agro-morphological traits, laying a groundwork for selection and breeding. Notably, seed yield, plant height, 100-seed weight, effective primary spike length, and the number of capsules on primary spikes exhibited a narrow range of both genotypic and phenotypic coefficients of variance. This indicates higher genetic stability for these traits, rendering them less susceptible to environmental influences and these traits can be used to select and develop elite cultivars in breeding programs.

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Table 3. Phenotypic and genotypic correlation coefficients between different traits in castor

	DFF	DMPS	PH	NN	TLPS	ELPS	NC	NES/ P	HSW	OC	SYPP
DFF	1	0.9020 ***	0.7068 ***	0.8504 ***	0.2837 *	0.2794 *	-0.2133	-0.1744	0.3363 **	0.19	-0.0338
DMPS	0.935**	1	0.6770 ***	0.7467 ***	0.1714	0.1639	-0.2595 *	-0.116	0.4071 ***	0.2856 *	0.021
PH	0.760**	0.710**	1	0.6231 ***	0.5238 ***	0.5254 ***	-0.135	-0.0908	0.2192	0.2474 *	-0.034
NN	1.0057	0.837**	0.669**	1	0.3630 ***	0.3725 ***	-0.1172	-0.1076	0.1781	0.0908	-0.0364
TLPS	0.316**	0.1751	0.560**	0.374**	1	0.9859 ***	0.3707 ***	0.0449	-0.3703 ***	-0.1893	0.0672
ELPS	0.321**	0.1728	0.566**	0.375**	0.996**	1	0.4009 ***	0.0339	-0.3872 ***	-0.2034	0.0345
NC	-0.226*	-0.285*	-0.1565	-0.1528	0.429**	0.464**	1	0.121	-0.5075 ***	-0.3598 **	-0.0912
NES/PT	-0.2094	-0.1376	-0.1105	-0.17	0.0112	-0.0047	0.1567	1	-0.1045	0.0065	-0.0535
HSW	0.350**	0.410**	0.231*	0.2035	-0.398**	-0.425**	-0.541**	-0.1297	1	0.7101 ***	0.1744
OC	0.1697	0.292**	0.248*	0.0858	-0.221*	-0.249*	-0.387**	-0.0121	0.745**	1	0.286*
SYPP	-0.0379	0.0172	-0.0478	-0.0339	0.0765	0.0425	-0.1035	-0.0649	0.1775	0.289**	1

Where: [*, ** Significant at 5 % and 1 % levels of probability, respectively,]; Phenotypic (above diagonal), Genotypic (below diagonal)

Table 4. *Per se* performance of castor genotype

#	GENOTYPES	DFF	DMPS	PH	NN	TLPS	ELPS	NC	NES/ P	HSW	OC	SYPP
1	BCG-10	64.00	120.50	119.23	15.38	28.23	20.06	18.68	5.17	64.34	51.95	160.29
2	BCG-11	59.00	123.00	108.72	16.56	32.12	27.40	21.50	5.00	67.36	53.93	81.10
3	BCG-15	61.50	126.50	98.40	14.73	22.33	17.96	16.50	4.75	74.15	49.33	93.43
4	HCG-21	65.50	125.50	201.83	16.65	83.56	73.72	37.73	6.77	28.46	44.50	62.48
5	BCG-24	57.00	100.50	150.83	17.12	52.94	47.20	29.56	4.00	26.22	46.01	53.80
6	BCG-25	67.50	129.50	119.16	17.79	52.39	42.26	27.23	3.78	44.42	49.60	53.24
7	BCG-28	59.00	125.00	117.45	15.62	44.62	39.56	36.28	3.50	30.76	46.00	111.01
8	BCG-33	68.00	128.00	111.05	17.66	44.00	40.98	32.06	4.50	36.53	46.05	71.71
9	BCG-35	61.50	109.00	95.06	20.79	48.96	43.60	27.10	5.66	28.27	45.38	91.32
10	MI-52	55.50	110.50	97.28	16.45	47.48	41.12	31.62	5.16	22.78	44.88	63.75
11	MI-54	54.50	104.00	89.77	15.47	49.12	45.74	52.06	3.90	19.09	44.36	57.32
12	MI-55	56.00	107.50	76.13	14.98	59.30	53.45	64.95	3.50	18.71	44.10	52.34
13	MI-71	54.00	90.50	65.51	17.41	56.28	50.18	62.82	6.50	36.46	43.24	80.32
14	MI-73	37.00	81.00	52.48	10.50	29.48	24.46	24.90	5.78	27.12	45.94	55.29
15	MI-83	58.00	111.50	80.16	17.74	61.27	51.83	25.12	4.50	30.35	45.86	211.86
16	MI-85	45.00	88.00	65.66	11.56	50.12	40.59	30.93	4.73	39.21	48.38	61.71
17	ICS-245	55.50	108.00	94.75	15.95	53.29	46.14	33.80	7.69	23.17	46.24	67.42
18	ICS-246	44.50	103.50	70.20	12.68	51.89	45.22	41.18	6.90	26.11	44.01	65.27
19	ICS-252	42.00	88.50	75.08	11.18	49.28	44.23	51.98	6.77	25.64	45.19	60.73
20	BCH-43	52.00	108.00	73.02	13.45	37.15	31.60	28.68	6.63	30.73	43.21	50.73
21	BCH-59	54.50	104.00	51.67	14.62	21.99	15.93	32.16	4.21	31.33	45.14	43.74
22	BCH-70	41.50	84.00	69.57	10.50	57.53	53.00	29.57	4.62	26.36	45.80	84.08
23	BCH-74	42.50	90.50	85.79	10.87	42.26	36.39	36.14	5.56	34.24	45.69	80.51
24	BCH-82	36.00	81.50	70.78	9.50	44.12	37.66	42.68	7.06	32.85	48.20	126.47
25	BCH-84	42.00	93.50	77.87	10.62	48.01	41.83	49.56	3.68	29.88	46.28	162.42
26	BCH-85	53.50	107.50	68.30	15.17	44.87	37.21	30.21	5.05	31.59	44.67	166.12
27	BCH-86	42.50	93.00	54.56	11.23	43.60	35.64	32.74	4.68	33.89	47.76	199.78
28	BCH-88	34.50	83.00	40.50	9.84	29.87	25.74	31.71	6.06	30.06	45.12	90.69
29	BCH-89	35.50	83.00	33.41	10.15	35.43	28.61	30.04	3.09	30.71	44.75	34.39
30	BCH-90	34.00	86.50	43.18	10.11	34.19	27.92	42.67	5.54	23.97	44.92	52.47
31	BCH-95	42.00	96.00	43.80	11.50	34.23	25.36	41.68	6.04	31.59	43.82	100.95
32	BCH-97	42.00	91.50	66.58	11.06	39.82	34.13	31.06	3.06	30.86	43.11	89.61
33	BCH-100	44.00	96.00	66.01	11.87	31.81	26.36	33.64	6.07	30.14	45.93	70.69
34	BCH-101	39.50	89.00	50.55	10.50	37.55	31.42	29.69	6.28	29.04	46.24	124.32
35	BCH-110	35.00	83.50	47.95	10.22	30.31	22.58	28.54	6.16	34.71	45.24	33.27
36	BCH-116	67.00	124.00	103.24	17.51	42.98	37.49	30.22	4.94	33.78	44.79	35.62
37	BCH-117	57.00	110.50	73.69	14.23	35.93	28.70	24.24	4.96	26.62	41.88	70.11
38	DCH-177	37.00	94.50	82.64	10.73	43.06	37.29	43.04	5.06	24.20	47.48	125.12
39	JI-35	46.50	96.50	59.29	11.89	34.81	28.85	37.73	5.71	25.01	44.37	71.90
40	48-1	48.00	112.00	58.30	13.10	41.10	34.40	44.49	9.05	26.21	48.21	91.11
Mean		49.79	102.21	80.23	13.62	43.18	36.84	34.91	5.30	32.42	45.94	86.46
C.V.		6.21	1.93	12.57	10.70	10.67	13.54	10.61	14.51	1.85	1.59	10.07
S.E.		2.19	1.39	7.13	1.03	3.26	3.53	2.62	0.54	0.42	0.52	6.15
C.D. 5%		6.25	3.99	20.40	2.95	9.32	10.09	7.49	1.56	1.21	1.48	17.60
Range Lowest		34.00	81.00	33.41	9.50	21.99	15.93	16.50	3.06	18.71	41.88	33.27
Range Highest		68.00	129.50	201.83	20.79	83.56	73.72	64.95	9.05	74.15	53.93	211.86

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