

Original Research Article

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Variability and Genetic Advance for Seed Yield and its Components in Castor (*Ricinus communis* L.) Germplasm of CRIDA under Rain-Fed Conditions in Alfisols

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ABSTRACT

Variability in seed yield of castor genotypes and its association between different yield contributing traits as well as genetic advance were studied during kharif-2012 with 23 CRIDA castor genotypes under rain-fed conditions in alfisols. Superior genotypes for yield and its components were identified. The variability for genotypes was significant for seed yield and all its four components studied viz., number of branches, number of nodes, capsule number and capsule weight. The correlation coefficient analysis revealed that seed yield was highly significantly correlated with capsule number and capsule weight. High heritability with high genetic advance as mean (GAM) was observed for capsule number, capsule weight and seed yield, there by revealing that selection for high capsule number and capsule weight will increase the seed yield in castor. Based on the seed yield performance, twelve genotypes which yielded above 63.57g/pl (average yield of 23 genotypes) were selected for further evaluation of physiological efficiency coupled with seed yield. It was observed that CRC-4 is the only genotype where in the range for five characters was 2-6 ranks, thereby revealing that this is a desirable genotype with higher ranks for all the five characters studied.

Keywords

Castor, Genotypes, Seed yield, Genetic variability, Genetic advance

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Introduction

Castor bean (*Ricinus communis* L.) is a tropical non-edible oil yielding plant of high commercial importance. Castor bean is a monotypic species belonging to the family Euphorbiaceae and has a wide range distribution in both tropical and sub-tropical regions (Dapke *et al.*, 2016). India accounts for a total production of 17.33 lakh tonnes from an area of 11.05 lakh ha and a

productivity of 1568 kg/ha during 2014-2015 (Ramesh *et al.*, 2016). Major castor growing countries include India, Brazil, China, Russia and Thailand (Nagesh Kumar *et al.*, 2015). India is largest producer of castor seed and constitutes about 64% of total global production.

In India, Telangana and Gujarat are well known for castor production and productivity. To develop high yielding castor genotypes that

get fit into the present cropping system, it is important to create the genetic variability for the selection of desirable variant. Castor being a deep rooted crop, it can extract water from considerable depth in the soil. In India castor is normally grown as rain-fed crop in both kharif and rabi seasons.

As seed yield is the principal factor and influenced by various characters directly and indirectly, hence it is essential to know the relationship between them in order to improve the yield potential through its components (Frageria and Kokli, 1997). In this direction, maximum utilization of the desirable characters for the development of an ideal genotype is important in castor (Halilu, 2013).

In castor, most of the yield characters are governed by quantitative genes which in turn influenced by environment. Thus, the efficiency of selection of castor becomes lesser with increase in environmental effects (Dhedi *et al.*, 2010). In order to obtain accurate results, the genotypes of castor have to be evaluated over multilocations/seasons (Patel and Jaimini, 1988). Hence, it is necessary to evaluate the genetic variability present across *Ricinus communis* germplasm from different geographic regions (Hinckley, 2006). Thus, the identification of significant yield contributing parameters are necessary for improving the yield of castor and towards this endeavor, 23 genotypes of castor from CRIDA germplasm were evaluated at field conditions. This identification of better lines would be helpful in the process of improving castor productivity and production.

Materials and Methods

Four hundred accessions of castor germplasm were crossed for more than ten years during an Indo-U.S. project at CRIDA. During Kharif-2012, a field study was conducted with twenty three CRIDA castor genotypes i.e., CRC-1,

CRC-2, CRC-3, CRC-4, CRC-5, CRC-6, CRC-7, CRC-8, CRC-9, CRC-10, CRC-11, CRC-12, CRC-13, CRC-14, CRC-15, CRC-16, CRC-17, CRC-18, CRC-19, CRC-20, CRC-21, CRC-22 and CRC-23 at Hayathnagar Research Farm, Central Research Institute for Dryland Agriculture (ICAR-CRIDA), Hyderabad., the trial was sown on July 14th, 2012 in RBD with three replications. During the crop growth period, the crop received 692 mm rainfall spreading in 36 rainy days (> 2.5 mm) and the crop experienced dry spell of more than 10 days during initiation to maturation of secondaries, and the rains stopped from initiation of tertiaries onwards to maturation of tertiaries.

The average temperature was 30.4°C with minimum and maximum of 15.2°C and 40.0°C respectively (Table 1). Each genotype was sown in 5m length of three rows with plant to plant spacing of 30cm and 1m between rows. At the time of harvest, the observations were recorded on randomly selected five plants from each replication of individual genotype on number of branches up to primaries, number of nodes up to primaries, capsule number, capsule weight and seed yield of three spikes orders i.e., primaries, secondaries and tertiaries.

Genetic analysis

Heritability in broad sense (H^2 or h^2) (Falconer, 1989)

Phenotypic and genotypic correlations (Miller *et al.*, 1958)

Genotypic (σ^2_g) and Phenotypic variances (σ^2_{ph}) (Comstock and Robinson, 1952).

Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) (Singh and Chaudhary, 1985).

Statistical analysis - Analysis of variance (ANOVA)- *STAR* (Statistical Tools For Agricultural Research).

Results and Discussion

Data on seed yield and its four components i.e., number of nodes, number of branches capsule number and capsule weight were recorded for 23 CRIDA castor genotypes for the three spike orders i.e., primaries (first order), secondaries (second order) and tertiaries (third order) during kharif-2012. The mean performance of all the components is presented in Table 2.

Yield and its components

Seed yield (grams per plant-g/pl)

The seed yield of 23 CRIDA castor genotypes ranged from 8.88 g/pl (CRC-23) to 107.4 g/pl(CRC-1) with an average of 63.57 g/pl.

Number of nodes up to primaries (per plant-/pl)

The number of nodes ranged from 11 (CRC-20) to 28.2 (CRC-17) with an average of 19.55/pl. The genotype CRC-1 with high seed yield had 24.3 nodes.

Number of branches up to primaries (per plant)

The number of branches ranged from 2.79 (CRC-16) to 7.75 (CRC-22) with an average branches of 5.74 while CRC-1 recorded 5.56 branches.

Capsule number (per plant)

The capsules of three spike orders ranged from 26.50 (CRC-23) to 225.00 (CRC-5) per plant with an average of 117.13/pl. The high yielding genotype, CRC-1 recorded 174.50 capsules /pl.

Capsule weight (g/pl)

The capsule weight of the genotypes ranged from 15.00 g/pl(CRC-23) to 151.80 g/pl(CRC-

5) with an average of 94.01g/pl. The high yielding genotype, CRC-1 recorded capsule weight of 150 g/pl.

The Analysis of Variance (ANOVA)

ANOVA showed highly significant variability ($p < 0.01$) among the genotypes for all the five parameters studied viz., number of branches, number of nodes up to primaries, capsule number/pl, capsule weight /pl and seed yield /pl and presented in Table 3.

Correlations

Correlation studies provide the association of seed yield with other traits. The genotypic (r_G) and phenotypic correlations (r_p) of all the five parameters are presented in Table 4. The r_G and r_p of seed yield was highly significantly and positively correlated for both capsule weight (0.985 ** and 0.979**) and capsule number (0.930** and 0.924**). Capsule weight and capsule number have also showed significant positive correlation with each other with r_G of 0.965** and r_p of 0.959** respectively. Number of nodes had significant positive r_G (0.462*) with the number of branches.

Genotypic and phenotypic variability, heritability and genetic advance as percent of mean (GAM %)

The variances, coefficient of variations, heritability and genetic advance as percent of mean (GAM) are presented in Table 5.

Genotypic and phenotypic variability

The phenotypic variance was higher than the genotypic variance for all the traits. Highest phenotypic variance was observed for capsule number (2455.5) followed by capsule weight (1778.8) and seed yield (860.3). Lowest phenotypic variance was observed for number

of branches (3.48). Similarly phenotypic co-efficient of variation (PCV) was also higher than genotypic co-efficient of variation (GCV) for all the morphological and yield characters. The highest PCV was found for seed yield (46.14%) followed by capsule weight (44.86%) capsule number (42.30%), number of branches (32.50%) and number of nodes (23.85%).

Heritability

High heritability was recorded for seed yield (99.1%), followed by capsule number (99.4%), capsule weight (99.4%), number of nodes (84.1%) and moderate heritability was observed for number of branches.

Genetic advance as percent of mean (GAM %)

Genetic advance as percent of mean (GAM) was highest for capsule number (115.57%), followed by seed yield (94.17%), capsule weight (91.88%), number of nodes (41.22%) and number of branches (30.48%). High heritability with high GAM was observed for capsule number, capsule weight, number of nodes (84.1, 41.22) and seed yield. High heritability with high GAM was also observed for. Moderate heritability with high GAM was observed for number of branches (45.8, 30.4).

The ANOVA for yield and its attributes revealed highly significant variability among the twenty three genotypes studied for all the five parameters *viz.*, seed yield, number of primary branches, number of nodes, capsule number and capsule weight.

23 genotypes were classified for high, moderate and low yielding based on values obtained from seed yield. High yielding genotypes ranking from 1 to 7 were classified as high yielders and the yield ranged from 107.4 g/pl (1st rank) to 85.71 g/pl (7th

rank). Moderate yielding genotypes ranking 8 to 15 ranged from 79 g/pl (8th rank) to 52.63 g/pl (15th rank). Low yielders ranking from 16 to 23 ranged from 44.34 g/pl (16th rank) to 8.88 g/pl (23rd rank).

From CRC-1 to CRC-7, other than seed yield, out of the remaining four yield contributing characters studied, it was observed that for number of nodes, instead of 1 to 7 high ranks, it was observed that only 3rd, 4th and 6th ranks were observed for CRC-1, CRC-3, CRC-4 respectively, while 1st, 2nd, 5th and 7th ranks are missing. However, for number of branches, 1st, 3rd, 4th, 5th and 7th ranks are missing for CRC-1 to CRC-7. For capsule number, from CRC-1 to CRC-7, 1st to 8th ranks were observed with 2nd rank missing. Similarly, for capsule weight, from CRC-1 to CRC-7, it was observed that 7th rank is missing.

From the above results, it was observed that CRC-4 is the only genotype where in the range for five characters was 2-6 ranks, thereby revealing that this is a desirable genotype with higher ranks for all the five characters studied. However, among the five characters studied, the top 1-7 ranks for the four characters was revealed by the genotypes CRC-1, CRC-2, CRC-3, CRC-5 revealing that these four genotypes were also desirable after CRC-4. These results showed that the above mentioned four genotypes were top rankers in four characters while for one character (*viz.*, number of nodes) it was moderate. From the remaining high yielding genotypes *viz.*, CRC-6 and CRC-7, the results revealed that these genotypes showed top ranking from 1-7 only for one character *viz.*, capsule weight for former while capsule number for the later respectively.

Similarly, for the genotypes CRC-8 to CRC-15, it was observed that CRC-8, CRC-9, CRC-12, CRC-13 and CRC-14 ranked between 6 to 15 ranks (moderate) for all the three characters

studied revealing them to be moderate genotypes. Whereas, CRC-10 was moderate for only three characters (viz., capsule number, capsule weight and number of nodes) and CRC-11 was also moderate for only three characters (viz., capsule number, capsule weight and number of branches) while CRC-15 was moderate for only two characters studied (viz., capsule number & capsule weight).

For the genotypes from CRC-16 to CRC-23, it was observed that all these genotypes ranked low (16-23) for two yield contributing characters i.e., both capsule number and capsule weight. While with number of nodes and number of branches the genotypes ranked variably with high, moderate and low rankings.

Hence, from the above results of all the genotypes for all the yield parameters studied, it has clearly indicated that the higher seed yield for all the genotypes was obtained due to their higher capsule weight followed by capsule number.

Maximum capsule weight/pl among the different varieties in castor were obtained due to genetic superiority and it even depends on weather conditions (Koutroubas *et al.*, 1999). Koutroubas *et al.*, (1999, 2000) suggested that lower number of branches in three spike orders resistant to shattering are desirable to develop new varieties in castor.

Golakia *et al.*, (2015) reported that less number of nodes on main stem are the indirect indicators of earliness. Aswani *et al.*, (2003) reported that capsule number is one of the yield contributing traits in castor. Patel *et al.*, (2016) suggested that number of capsules can be taken into contemplation rather than number of nodes up to primary spike for improvements of seed yield in castor. Anastasi *et al.*, (2015) opined that according to the variation in yield components of castor, seed

yield has changed substantially with genotype. Gila and Manga (2015) reported that in castor seed yield/plant varies with the variety.

Uguru (2000) recorded range of 90.2 to 507.2 g/pl of seed yield among six populations of castor. Gobin *et al.*, (2001) reported that the mean seed yield ranged as from 500 kg/hain India to 1000 kg/ha in Thailand and 2500 kg/ha under improved conditions in USA. However, recent report showed that 554 kg/ha was obtained in Brazil, 600 kg/ha in Russian Federations, 621 kg/ha in Romania, 626 kg/ha in Thailand, 667 kg/ha in Sudan, 700 kg/ha in Ukraine, 909 kg/ha in China and 1,266 kg/ha in India (FAO, 2000).

About 878 accessions were identified among Indian collections for desirable traits with 70–80 grams per 100 seed and high seed yield at multiple harvests (Anjani and Hegde, 2007). The average seed yields in India range from 1864 kg/ha in the State of Gujarat to 371 kg/hain the State of Andhra Pradesh, where the crop has been predominantly grown without irrigation on marginal soils (Basappa, 2007).

In Brazil, seed yields have averaged 667 kg/ha over the last 10 yr (CONAB, 2011). The State of Parana has the highest average seed yield in the country (1600 kg/ha) due to better soil fertility and agronomical practices (Silva *et al.*, 2009).

A positive relationship between yield and its components indicates that any improvement in one of the yield components would result in concomitant increase in one or more components (Adeyanju *et al.*, 2010). Both genotypic and phenotypic correlations were of comparable magnitude, the genotypic correlations of all the parameters studied were higher than the phenotypic correlations indicating that these characters were more related genotypically.

Table.1 Weather data during crop growth period- Kharif-2012

	Temperature		RH (relative humidity)	
	Max. (°C)	Min. (°C)	Max (%)	Min (%)
Average	30.4	18.7	89.0	54.0
Minimum	15.2	10.2	59.0	17.0
Maximum	40.0	25.5	100.0	96.0

Total Rainfall = 692 mm

Number of rainy days (>2.5 mm) = 36 days

Table.2 Mean performance of yield and its components of 23 CRIDA castor genotypes during Kharif-2012

Genotype	Seed Yield (g/pl) (Rk)	Capsule No./ pl (Rk)	Capsule wt. (g/pl) (Rk)	Nodes No./pl (Rk)	Branches No./ pl (Rk)
CRC-1	107.40 (1)	174.50 (3)	150.00 (2)	24.3(3)	5.56 (13)
CRC-2	106.44 (2)	182.50 (2)	147.80 (4)	18.0 (13)	7.50 (2)
CRC-3	104.92 (3)	172.75 (4)	147.10 (5)	24.1(4)	6.06 (11)
CRC-4	94.36 (4)	167.33 (5)	148.10 (3)	22.3(6)	7.50 (2)
CRC-5	93.85 (5)	225.00 (1)	151.80 (1)	16.0 (15)	6.75 (6)
CRC-6	92.12 (6)	145.50 (8)	133.00 (6)	11.8 (18)	3.00 (20)
CRC-7	85.71 (7)	146.25 (7)	127.50 (8)	19.7(11)	4.83 (16)
CRC-8	79.00 (8)	163.25 (6)	127.80 (7)	16.0 (15)	6.00 (12)
CRC-9	75.89 (9)	130.20 (9)	113.80 (9)	16.8 (14)	7.04 (5)
CRC-10	74.85 (10)	118.8 (10)	100.10 (10)	18.7 (12)	4.33 (17)
CRC-11	64.15 (11)	108.72 (13)	90.50 (13)	15.8 (16)	5.00 (15)
CRC-12	63.92 (12)	110.57 (11)	80.80 (15)	25.3(2)	6.33 (9)
CRC-13	62.45 (13)	109.67(12)	92.10 (12)	16.0 (15)	7.16 (4)
CRC-14	58.80 (14)	106.50 (14)	94.50 (11)	19.8(10)	6.17 (10)
CRC-15	52.63 (15)	103.78 (15)	83.00 (14)	15.9 (17)	4.09 (18)
CRC-16	44.34 (16)	77.67 (18)	64.11 (16)	20.8 (7)	2.79 (21)
CRC-17	41.83(17)	99.46 (16)	59.10 (17)	28.2 (1)	7.30 (3)
CRC-18	34.57 (18)	45.11 (22)	42.00 (21)	20.5 (8)	5.14 (14)
CRC-19	34.00 (19)	58.03 (21)	46.90 (20)	18.0 (13)	3.33 (19)
CRC-20	30.92 (20)	62.00 (20)	50.30 (18)	11.0 (19)	5.00 (15)
CRC-21	25.98(21)	77.17 (19)	48.40 (19)	23.2(5)	6.72 (7)
CRC-22	25.04 (22)	82.83 (17)	48.40 (19)	22.3(6)	7.75 (1)
CRC-23	8.88 (23)	26.50 (23)	15.00 (22)	25.3(2)	6.67 (8)
Average	63.57	117.13	94.01	19.55	5.74
Minimum	8.88	26.5	15.0	11.0	2.79
Maximum	107.4	225.0	151.8	28.2	7.75

1 to 7 ranks-high, 8 to 15 ranks-moderate, 16 to 23 ranks -low

Table.3 ANOVA for yield and yield parameters of 23 castor genotypes during Kharif-2012

Source	DF	Mean sum of squares				
		Seed yield	Capsule number	Capsule weight	Number of nodes	Number of branches
Replication	2	9.729	37.246	1.247	3.291	0.355
Genotype	12	2565.4**	7336.8**	5316.4**	58.4**	6.670**
Error	24	7.766	14.879	9.934	3.469	1.887
CV (%)		4.38	3.29	3.35	9.52	23.93

*Significance at $p < 0.05$ and ** Significance at $p < 0.01$

Table.4 Genotypic and phenotypic correlations of 23 CRIDA castor genotypes during Kharif-2012

		Seed yield	Capsule number	Capsule weight	No. of nodes	No. of branches
No. of nodes	r_G	-0.162	-0.140	-0.206	1.00	0.462*
	r_P	-0.143	-0.122	-0.188	1.00	0.337
No. of branches	r_G	0.069	0.266	0.122		1.00
	r_P	0.046	0.192	0.103		1.00
Capsule number	r_G	0.930**	1.00	0.965**		
	r_P	0.924**	1.00	0.959**		
Capsule weight	r_G	0.985**		1.00		
	r_P	0.979**		1.00		
Seed yield	r_G	1.00				
	r_P	1.00				

*Significance at $p < 0.05$ and ** Significance at $p < 0.01$

Table.5 Co-efficient of variations, variances, heritability and GAM (%) for yield and yield parameters of 23 CRIDA castor genotypes during Kharif-2012

Parameter	Genotypic variance	Phenotypic variance	GCV	PCV	Heritability	GAM (%)
Seed Yield	852.6	860.3	45.93	46.14	0.991	94.17
Capsule Number	2440.6	2455.5	42.17	42.30	0.994	115.57
Capsule Weight	1768.8	1778.8	44.73	44.86	0.994	91.88
No. of Nodes	18.30	21.78	21.87	23.85	0.841	41.22
No. of Branches	1.594	3.48	21.99	32.50	0.458	30.48

The r_G and r_p of seed yield was highly significantly and positively correlated for both capsule weight (0.985 ** and 0.979**) and capsule number (0.930** and 0.924**) which were in concurrence with the results of Ahmed *et al.*, (2012). Similarly, in the present investigation, seed yield and number of primary branches are correlated non-significantly and these results are in agreement with the findings of Aghili *et al.*, (2012) in Lentil. However, Sarwar *et al.*, (2010) reported seed yield in castor had non-significant correlation with number of nodes. Positive and significant genotypic correlation was observed with number of nodes with number of branches (Abimiku *et al.*, 2012) in castor.

Improvement of castor seed yield can therefore, be achieved through selection of these highly correlated characters as increase in mean value of any one of these characters would significantly increase the mean of others (Patel *et al.*, 2016). The variations that existed among the genotypes in the yield components showed that in castor, seed yield could be improved through selection programmes, if genetic information of these characters is known (Gila and Manga, 2015).

While, looking into the estimates of GCV and PCV, it was observed that PCV was greater than GCV indicating the influence of environment and hence phenotypic selection can also be effectively useful for the crop improvement (Patel *et al.*, 2010). Higher GCV and PCV were observed for capsule number (2440.6 & 2455.5) followed by capsule weight (1768.8 & 1778.8) and seed yield (852.6 & 860.3). Higher GCV and PCV for seed yield, capsule number and capsule weight in castor were reported by Udaya *et al.*, (2013) and Lakshamma *et al.*, (2005).

Heritability estimates along with genetic gains are more effective and reliable in predicting

the improvement through selection (Johnson *et al.*, 1955). Heritability which denotes the proportion of genetically controlled variability is very important biometrical tool for guiding plant breeder for adoption of appropriate breeding procedures. The heritability value indicates the presence of additive gene action and further improvement in these traits could be effective through direct selection (Jaimini, 2002). High heritability coupled with high genetic advance, indicate the presence of high additive gene effects suggesting that direct selection for the traits would be beneficial (Panse, 1957). High heritability coupled with moderate genetic advance in the character indicates that the variability was due to both additive and non-additive interaction of genes. The characters exhibited low heritability with moderate genetic advances indicates a non-additive gene effect in governing the characters. Low heritability with low genetic advance indicate the preponderance of non-additive gene action in inheritance of the characters and high influence of environment (John *et al.*, 2016).

High heritability with high genetic advance as mean (GAM) was observed for capsule number, capsule weight and seed yield. These results are in accordance with the findings of Dhapke *et al.*, (1992), Solanki and Joshi (2000) with castor. Similarly high heritability with high genetic advance mean was also observed for number of nodes. Dorairaj *et al.*, (1973) reported high heritability with high genetic advance mean for number of nodes in castor. Plant traits having high variability, high heritability and genetic advance mean would be an effective tool for crop improvement (Aytac and Kinaci, 2009). Hence, for the improvement of seed yield in castor, selection for capsule number and capsule weight could be given priority (Mehta and Vashi, 1998). The emphasis of current breeding programmes in India is mainly

focused on high seed yield in castor (Lavanya *et al.*, 2006; Lavanya and Solanki, 2010) since seed yield is the principal and predominant factor for the development of an ideal genotype, identification of significant yield contributing parameters are necessary for sustaining improved yield (Halilu *et al.*, 2013). Increased interaction between plant breeders and geneticists with supporting scientists such as molecular biologists, plant physiologists, plant nutritionists, entomologists, and plant pathologists would speed the genetic improvement of castor (Severino *et al.*, 2012). Hence, these results revealed that capsule number and capsule weight are the most important traits for the improvement of seed yield in castor.

Hence, these results revealed that capsule number and capsule weight are the most important traits for the improvement of seed yield in castor.

In conclusion, twelve genotypes, out of 23 CRIDA genotypes were selected which yielded above the average yield of 63.57 g/pl for further evaluation. It was observed that CRC-4 is the only genotype where in the range for five characters was 2-6 ranks, thereby revealing that this is a desirable genotype with higher ranks for all the five characters studied. The development of new castor cultivars would be enhanced by selecting capsule weight and capsule number for increasing seed yield.

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