



## Study of Variability in Castor (*Ricinus communis* L.)

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### ABSTRACT

*Castor (Ricinus communis L) belongs to family Euphorbiaceae. It is an industrially important non edible oil seed crop widely cultivated in the arid and semi- arid regions. An insight into the magnitude of variability present in the gene pool of a crop species is of utmost importance to a plant breeder for initiating a judicious plant breeding programme. The coefficients of variation expressed at phenotypic and genotypic levels are generally used for comparing variability present for different characters. Sixty eight castor genotypes were evaluated for studying variability. Analysis of variance revealed high significant difference for all 11 characters, indicating the presence of variability among the 68 genotypes studied. High heritability was recorded for all traits except number of nodes upto primary spike. The high heritability values represent the fact that presence of additive gene action, hence the improvement in those traits could be effective through direct selection. High heritability coupled with high GA was observed for traits plant height, primary spike length, effective length of primary spike, number of capsules per spike, total number of spikes, 100 seed weight and seed yield per plant indicates that heritability is due to additive gene effects and selection may be effective.*

**Key words:** Genetic variability, Heritability and Genetic advance.

### INTRODUCTION

Castor (*Ricinus communis* L.) belongs to family euphorbiaceae. It is an industrially important non edible oil seed crop widely cultivated in the arid and semi- arid regions. Due to monoecious nature of the crop it is mostly cross pollinated crop upto the extent of 50 per cent. It is essentially a semi tropical, intermediate perennial crop, but is has naturalized as annual crop throughout the world. The seed of castor contains more than

45 per cent oil, this oil is rich in (80-90%) in an unusual hydroxyl fatty acid, ricinoleic acid. Castor oil is the only oil soluble in alcohol, presenting high viscosity and requiring less heating than other oils during the production of biodiesel.

An insight into the magnitude of variability present in the gene pool of a crop species is of utmost importance to a plant breeder for initiating a judicious plant breeding programme.

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The coefficients of variation expressed at phenotypic and genotypic levels are generally used for comparing variability present for different characters. Hence, knowledge about the variability parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is of paramount importance for planning a proficient breeding programme.

### MATERIAL AND METHODS

The experimental material comprised of 68 genotypes during Rabi 2015 at Tapioca and Castor Research Station, Yethapur. Seeds of 68 genotypes were sown with a spacing of 90cm X 60 cm. The experiment was arranged in a randomized complete block design with two replications, in three rows plots of 6m length. The recommended agronomical practices and plant protection measures were followed to ensure a normal crop growth. Observations were recorded on five randomly selected plants in each replication.

Observation were recorded for 11 biometrical characters *viz.*, days to fifty per cent flowering, days to fifty per cent maturity, plant height (cm), number of nodes upto primary spike, primary spike length (cm), effective length of primary spike (cm), total number of capsules on primary spike, total number of spikes per plant, 100 seed weight (g), oil content (%) and seed yield per plant (g). Burton (1952) formula was used for estimating Genotypic and phenotypic coefficient of variances.

### RESULT AND DISCUSSION

Analysis of variance revealed high significant difference for all 11 characters, indicating the presence of variability within the 68 genotypes studied. The mean, range, PCV, GCV, heritability and genetic advance as per cent of mean (GAM) were presented in the table 2. It

is easier to interpret from GCV, PCV values that the environmental influence was under control. High PCV and GCV values were recorded for traits like plant height (34.47% and 33.84%), number of capsules on primary spike (28.74% and 28.24%), total spikes per plant (34.57% and 32.20%), 100 seed weight (20.28% and 2.12%) and seed yield per plant (39.13% and 37.30%). Similar results were observed by Patel *et al.*<sup>6</sup>, Abimiku *et al.*<sup>1</sup>, Kote *et al.*<sup>5</sup> and Sami Rukhsar *et al.*<sup>7</sup>.

High heritability was recorded for all traits except number of nodes upto primary spike. The high heritability values represent the fact that presence of additive gene action, hence the improvement in those traits could be effective through direct selection. These results are in accordance with Dorairaj *et al.*<sup>3</sup>, Golakia *et al.*<sup>4</sup> and Patel *et al.*<sup>6</sup>. High genetic advance as per cent of mean was recorded for the traits plant height, number of nodes upto primary spike, length of primary spike, effective length of primary spike, number of capsules on primary spike, total number of spikes per plant, 100 seed weight and seed yield. high GAM values indicates the presence of additive gene action and the traits could be phenotypically selected for their improvement. Days to 50% flowering, days to 50% maturity and oil content have moderate GAM. High heritability coupled with high GA was observed for traits plant height, primary spike length, effective length of primary spike, number of capsules per spike, total number of spikes, 100 seed weight and seed yield per plant indicates that heritability is due to additive gene effects and selection may be effective. Moderate heritability coupled with moderate GA was observed for number of nodes upto primary spike indicates that trait is highly influenced by environmental effects and selection is ineffective.

**Table 1: Analysis of Variance for 11 characters in 68 genotypes in castor**  
Mean sum of squares

Source of Var.	d.f.	Days to 50% flowering	Days to 50% maturity	Plant height	Number of nodes upto primary spike	Primary spike length	Effective length of primary spike	Number of capsules per primary spike	Total number of spike	100 seed weight	Oil content	Yield/ plant
Replication	1	8.50	13.60	1.13	7.89	19.92	1.29	6.77	0.84	1.95	11.17	717.14
Treatments	67	88.20	223.51	1743.14	31.73	166.99	147.50	555.91	17.42	66.87	23.00	2256.00
Error	67	7.05	8.67	32.26	16.00	15.30	8.00	9.88	1.24	0.53	4.74	107.68

**Table 2: Mean, range, variability parameters, heritability and genetic advance for eleven characters in castor**

J	Characters	Mean	Range	PCV (%)	GCV (%)	h <sup>2</sup>	GA %
1	Days to 50 per cent flowering	71.71	52.50-86.00	9.62	8.88	85.19	16.89
2	Days to 50 per cent maturity	108.46	82.00-139.00	9.93	9.56	92.53	18.94
3	Plant height	86.42	36.74-235.42	34.48	33.84	96.37	68.44
4	Number of nodes upto primary spike	16.07	10.50-39.20	30.40	17.45	32.96	20.64
5	Primary spike length	44.94	18.00-64.80	21.24	19.38	83.21	36.41
6	Effective length of primary spike	41.81	22.50-60.70	21.09	19.98	89.70	38.98
7	Number of capsules on primary spike	58.50	35.90-107.40	28.75	28.24	96.51	57.16
8	Total number of spikes	8.83	4.60-17.40	34.57	32.20	86.74	61.78
9	100 seed weight	28.62	19.05-48.20	20.28	20.13	98.44	41.13
10	Oil content	45.56	34.75-51.00	8.17	6.63	65.85	11.09
11	Seed yield per plant	87.85	39.70-193.30	39.13	37.31	90.89	73.27

### CONCLUSION

There is substantial genetic variability exist in castor genotypes. The traits like plant height, primary spike length, effective length of primary spike, number of capsules per spike, total number of spike, 100 seed weight and seed yield per plant were governed by additive gene action and have more scope for selection.

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