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Genetic variability in castor (*Ricinus communis* L.)

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Abstract
The experimental material comprised of 61 castor genotypes were evaluated for assessment of genetic variability, heritability and genetic advance percent mean in respect of eleven characters. The GCV and PCV were of high magnitude for the character number of effective branches per plant followed by number of capsules on primary raceme and seed yield per plant. The magnitude of PCV was higher than GCV for all the characters, suggesting the role of environmental variance. High genetic variability coupled with high heritability and high genetic advance was recorded for all the studied traits except days to 50 percent flowering, days to maturity of primary spike, 100-seed weight, and oil content indicating that direct selection for these traits could be effective.

Keywords: Genetic variability, heritability and genetic advance.

1. Introduction
Castor bean (*Ricinus communis* L.) as an important non-edible oilseed crop (oil content from % 40 to % 60), is a monotypic species in the family *Euphorbiaceae* which has a wide range distribution in tropical and subtropical regions. High genetic diversity of *Ricinus communis* in Ethiopia imply that this species has been originated from Eastern Africa (Vavilov, 1951) [13]. Meanwhile, there are several lands in tropical and subtropical regions undergoing the cultivation of this species. Castor bean is important due to resource of vegetable and medicinal oil. Its oil has several industrial and non-industrial applications (Ogunniyi, 2006) [8]. Considering to increasing demands for castor bean usage in many countries, improvement of genotypes is drawing great attention from plant breeders (Sujatha *et al.*, 2008) [12]. Obviously, genetic variability is same as backbone of any breeding programs that play important role to achieving any success. According to literature, there are limited variability in castor bean for productivity traits and resistance to diseases and pests which led to limit progress in castor bean breeding programmes (Weiss, 2000) [14]. Hence, it is necessary to evaluate the genetic variability present across *Ricinus communis* germplasm from different geographic regions (Hinckley, 2006) [3].

2. Materials and methods
Sixty one castor genotypes comprising of 44 hybrids (Including two checks) and 17 parents of hybrids were evaluated in randomized block design with three replications at college farm Navsari Agricultural University Navsari, Gujarat during *rabi* 2014 under irrigated conditions. Each genotype was planted in 10 rows each accommodating 10 plants in a row-to-row and plant-to-plant spacing being 120 cm and 60 cm, respectively. All the recommended package of practices was adopted besides providing necessary plant protection measures to raise a healthy crop. Observations were recorded on eleven quantitative characters *viz*., days to 50 % flowering of primary spike, days to maturity of primary spike, plant height upto primary spike (cm), number of nodes upto primary spike, total length of primary spike (cm), length of capsule bearing region of primary spike (cm), number of effective branches per plant, number of capsules on primary spike, seed yield per plant (g), 100-seed weight (g) and oil content (%).Genotypic and phenotypic coefficient of variances was estimated based on the formula given by Burton (1952) and heritability and genetic advance were calculated according to Allard (1960) [1].

3. Result and Discussion
Analysis of variance revealed highly significant differences among the genotype for all the characters indicating presence of high amount of variability among the genotypes under study. The range, mean and variability estimates such as GCV, PCV, heritability and genetic advances as per cent of mean are presented in Table 1. While, looking to the estimates of GCV and PCV was greater than GCV indicating that environmental component had been controlled considerably and hence, phenotypic selection can also effectively useful for the improvement. However, the trend of GCV and PCV was same. High GCV and PCV were recorded by the characters number of effective branches per plant (31.28 and 37.07) followed by number of capsules on primary raceme (27.79 and 28.76) and seed yield per plant (20.78 and 21.32). Similar results were recorded by Muthiah *et al*. (1982) [7], Mehta and Vashi (1997) [6]. And Jaimini (2002) [2]. High heritability was recorded all the traits except oil content. The heritability value indicated the presence of additive gene action and further improvement in these traits could be effective through direct selection. The results are in accordance with the findings of Patel and Jaimini (1988) [9], Mehta and Vashi (1997) [6] and Jaimini (2002) [4]. High genetic advance was recorded for number of capsules on primary spike, number of effective branches per plant, seed yield per plant (g) total length of primary spike (cm), length of capsule bearing region of primary spike (cm) and plant height upto primary spike (cm) indicating that these characters are governed by additive genes and simple phenotypic selection will be rewarding for improvement of these characters. The results are in close

conformity with the finding of Patel and Jaimini (1988) [9]. Moderate genetic advance was also observed in seed yield per plant, number of effective branches per plant, length of primary raceme and days to 50% flowering. Low heritability combined with low genetic advance was observed for oil content indicates that the scope for improvement these traits through selection is very much limited and may be attributed to the nonadditive gene action.

Table 1: Mean, range, variability parameters, heritability and genetic advance for eleven characters in castor

Sr. No.	Parameter	Mean	Range	GCV%	PCV%	Heritability	GA (%mean)
1	Day to 50% flowering of primary spike	62.56	54.00-71.00	6.38	7.62	69.96	10.98
2	Days to maturity of primary spike	140.44	120.67-161.00	5.90	6.16	91.48	11.61
3	Plant height upto primary spike (cm)	88.5	41.25-118.97	16.04	16.58	93.61	31.98
4	Number of nodes upto primary spike	13.45	8.17-19.15	14.17	20.51	47.73	20.17
5	Number of effective branches per plant	7.05	3.49-12.01	31.28	37.07	71.2	54.37
6	Total Length of primary spike (cm)	54.93	35.46-78.03	17.25	17.78	94.15	34.49
7	Length of capsule bearing region of primary spike (cm)	50.12	30.74-71.97	19.74	20.55	92.27	39.07
8	Number of capsules on primary spike	69.66	39.08-123.03	27.79	28.76	93.4	55.33
9	Seed yield per plant (g)	185.28	113.10-273.24	20.78	21.32	94.97	41.72
10	100-seed weight (g)	29.47	17.74-36.96	11.41	15.38	54.98	17.42
11	Oil content (%)	48.12	44.42-51.38	2.71	4.53	35.77	3.34

4. Conclusion

The present conclusion revealed substantial genetic variability in the castor germplasm collection and a scope for improvement through selection. The charcters *viz.*, total length of primary spike, length of capsule bearing region of primary spike, number of effective branches per plant, number of capsules on primary spike and seed yield per plant governed by additive gene action that lead more scope for selection as well as population improvement.

5. Referances

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