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Research Article

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

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Abstract
Castor is one of the non - edible oilseed crop cultivated all over the world. Knowledge on genetic divergence is the foremost important tool for the initiation of any successful breeding programme. The present investigation aims to reveals the nature and magnitude of diversity that exist among the 70 castor genotypes based on 11 biometrical traits, using Mahalanobis D^2 statistics. Based on the genetic distance, 70 castor genotypes were grouped into seven different clusters. Among the characters studied, seed yield per plant (45.96 per cent) had major contribution to the total divergence. The maximum inter-clusters distance was recorded between genotypes cluster IV and cluster VI. The maximum intera- cluster distance was observed in the cluster VII (28.28). Thus, selection of genotypes from diverse clusters for future hybridization programme as a parental genotypes will helps to obtain segregants.

Key words
Castor, cluster, inter cluster distance, D^2 statistics, *Ricinus communis* L.

Introduction

Castor (*Ricinus communis* L., 2n = 20, Family: *Euphorbiaceae*) belongs to a mono- specific genus *Ricinus*, which is believed to have a polyphyletic origin with India as one of the centres of diversity. Castor is known for its wider adaptability and is grown in tropical, subtropical and temperate regions of the world. Castor is a non- edible oil - seed crop cultivated around the world because of its commercial importance. Castor oil founds its wider range of applications in pharmaceuticals, lubricants, dyes, paints and varnishes *etc.*, as a raw material. It is cultivated in 30 different countries across the world on commercial scale. India is the world leader in Castor production and export. Area under castor cultivation in India is 8.3 lakh ha , with the production of 14.21 lakh tonnes and average productivity of 1713 kg/ ha (Annual report 2017-2018, IIOR). In India, castor is extensively cultivated in Gujarat, Rajasthan, Telangana, Andhra Pradesh, Tamil Nadu, Madhya Pradesh, Orissa and Karnataka. In Tamil Nadu, the area under castor cultivation is around 5.2 thousand hectare, with production of 1.6 thousand tonnes and average productivity of 311 kg/ ha (Annual report 2017-2018, IIOR). The state productivity is very low as compared to national average. Thus, there is a need to develop high yielding potential hybrids in order to increase the productivity considerably.

A thorough knowledge on genetic diversity will help us to identify diverse genotypes which could be employed as a parents in hybridization programme for developing superior segregants. D^2 analysis was performed among the 70 castor genotypes to study the genetic diversity present among them.

Materials and Methods

The experimental material consisted of 70 castor genotypes. The materials was raised in Randomized Block Design with 2 replications during *rabi* 2017 at Tapioca and Castor Research Station, Yethapur. Each genotypes were sown in 3 rows of 6m long with a spacing of 90 cm × 60 cm.

Necessary agronomic practices were undertaken during crop growth period. Five plants were randomly selected from each plot in each replications for recording observations. 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).Mahalanobis D^2 analysis (Mahalanobis, 1936) was used to estimate genetic divergence among the 70 genotypes. The statistical analysis was performed using software GENRES.

Results and Discussion

Analysis of variance revealed significant differences among the genotypes; for the characters studied indicating presence of variability among the seventy genotypes for the traits under investigation. Mahalanobis D^2 statistics is an effective tool in quantifying the degree of divergence at genetic level and it also provides quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936).

Seventy genotypes were grouped into seven clusters(Table.3), Cluster I is larger and comprised of 53 genotypes, cluster II, III, IV, V and VI comprised of 2 genotypes each and cluster VII found to have 7 genotypes. These results are in conformation with the results stated by Patel *et al.*(2010) . The distribution of genotypes into different clusters indicated the genetic diversity doesn't rely upon geographical diversity (Ramesh *et al.* 2012).

The intra and inter cluster distances among seven clusters were computed and are presented in Table 4**.** The intra-cluster distance ranges from 6.09 (cluster II) to 28.28 (cluster VII), indicating that the genotypes present in the cluster VII have a wide range of diversity within the cluster and low intra-cluster distance in the cluster II indicated the presence of minimal diversity among the genotypes. The maximum inter-cluster distance was observed between cluster IV and cluster VI (46.24) followed by cluster I and cluster VI (44.24). Comparatively minimal inter-cluster distance was recorded between cluster II and cluster IV (11.57). Hence these results ascertain the fact that crosses between genotypes of distant cluster will yield heterotic segregants in future breeding programme.

The per cent contribution towards total divergence by all the 11 characters are presented in the Table 5. Seed yield per plant (45.96%) contributed maximum towards genetic divergence Sevagaperumal *et al.*(2000) and Chauhan (2017) followed by 100 seed weight (18.63%), plant height (11.42%), total number of capsules (9.23%), oil content (4.92%), primary spike length (4.63%), total number of spikes per plant (2.98%), days to 50 per cent maturity (1.32%), days to 50 per cent flowering (0.70%) and divergence is least contributed by two traits namely number of nodes upto primary spike(0.08%) and effective length of primary spike (0.08%).

Cluster means were worked out for seven clusters and are presented in the Table 6. Cluster I recorded high mean for plant height (86.89), number of nodes upto primary spike (17.07) and oil content (45.05). Cluster VI recorded high values for effective length of primary spike (45.05), number of capsules on primary spike (83.12) and 100 seed weight (55.85). Cluster VII recorder high values for yield per plant (120.54).

It could be concluded that the genotype with high yield coupled with other desirable traits like effective primary spike length, plant height, number of capsule on primary spike, total spikes per plant and 100 seed weight could be selected as parents for hybridization programme from cluster I, cluster VI and cluster VII. Inter crossing genotypes from these cluster might results in wide array of variability for exercising effective selection.

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Table 1. Analysis of variance for 11 quantitative characters

Source of variation	df	Mean sum of squares										
		Days to 50 per cent flowering	Days to 50 per cent maturity	Plant height	Number of nodes upto primary spike	Primary spike length	Effective length of primary spike	Number of capsules on primary spike	Total number of spikes	100 seed weight	Oil content	Seed yield per plant
Replication	1	33.983	44.517	24.423	10.560	0.563	3.536	0.423	0.001	0.001	11.280	48.900
Treatment	69	105.077**	146.085**	1687.552**	32.263**	150.546**	174.773**	759.073**	17.125**	107.508**	23.121**	2908.829**
Error	69	7.282	9.854	15.090	15.867	8.718	11.385	14.537	0.878	0.553	5.021	142.711

** at 1 per cent level of significance

Table 2. Mean values for 11 biometrical traits

Characters	Range	General mean	CD (P= 0.05)
Days to 50 per cent flowering	47.5 - 87.5	73.04	5.38
Days to 50 per cent maturity	88.5 - 130	109.4	6.26
Plant height (cm)	36.7 - 171.9	90.3	7.74
Number of nodes upto primary spike	10.7 - 24.1	16.7	7.98
Primary spike length (cm)	29.7 - 72.9	46.5	5.89
Effective length of primary spike (cm)	24.3 - 72.2	43.2	6.73
Number of capsules on primary spike	29.4 - 136.1	60.5	7.6
Total number of spikes	2.9 - 16	8.5	187
100 seed weight (g)	20.6 - 55.9	30.3	1.48
Oil content (%)	36.1 - 50.3	45.5	4.47
Seed yield per plant (g)	34.7- 251.5	100.2	23.83

Table 3. Composition of D^2 clusters for 70 Castor genotypes

Cluster	Number of genotypes	Name of the genotype
I	53	MI 149, MI 174, SKP 61, SKP 59, YRCP 2, DPC 17, M 574, DPC 21, DPC 16, YRCP 1, DPC 18, JP 65, DPC 19, DPC 15, DPC 9, GEETHA, JP 104, M 619-1, SKP 84, JP 96, MI 176, MI 206, MI 207, MI 155, MI 231, MI 170, MI 205, MI 158, GPSKI 338, GPJP 92, GPSKI 332, RG 2364, GPRG 3561, GP 471-3, GP 5502, GPJI 412, GP 415, GP 432, GP 526, GP 672, GP 640, GP 729, SKI 215, SM-1, TMV 6, DCS 100, MCI 14, JC 3, JC 12, RG 27, SKI 335, RG 111, MCI 8
II	2	MCI 9, DCS 107
II	2	JC 8, RG 1771
IV	2	48-1, DCS 94
V	2	SKI 304, MCI 11
VI	2	CO-1, URAMBU LOCAL
VII	7	MOHANUR LOCAL,NPT LOCAL, TMV 5, MCI 3, TNPT 3, RAJASTHAN LOCAL, RG 72

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Table 4. Intra (bold) and Inter cluster distances

Clusters	I	II	III	IV	V	VI	VII
I	**20.025**	16.034	16.734	16.212	20.889	44.294	25.666
II		**6.902**	11.626	11.570	13.234	40.957	21.601
II			**8.148**	13.836	14.940	38.817	21.315
IV				**8.407**	18.353	46.249	23.786
V					**13.005**	34.503	20.972
VI						**15.647**	38.577
VII							**28.280**

Table 5. Contribution of biometrical characters for divergence in 70 castor genotypes

Characters	Number of first rank	Per cent contribution
Days to 50 per cent flowering	17	0.70
Days to 50 per cent maturity	32	1.32
Plant height	276	11.42
Number of nodes upto primary spike	2	0.08
Primary spike length	112	4.63
Effective length of primary spike	2	0.08
Numberof capsules on primary spike	223	9.23
Total number of spikes	72	2.98
100 seed weight	450	18.63
Oil content	119	4.92
Seed yield per plant	1110	45.96
Total	**2415**	**100**

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Table 6. Cluster means for 70 genotypes of Castor for 11 biometrical characters

Cluster	Days to 50 per cent flowering	Days to 50 per cent maturity	Plant height	Number of nodes upto primary spike	Primary spike length	Effective length of primary spike	Number of capsules on primary spike	Total number of spikes	100 seed Weight	Oil content	Seed yield per plant
1	72.20	108.73	86.89	17.07	46.752	43.62	61.54	8.45	28.65	45.05	97.86
2	84.00	109.25	78.75	15.35	40.450	36.90	49.25	7.75	29.30	46.41	98.75
3	67.75	101.25	89.02	15.47	53.400	50.82	57.77	12.47	33.22	47.36	79.25
4	69.75	115.25	87.62	15.05	36.700	33.15	56.70	10.95	26.07	47.52	98.25
5	75.75	117.25	97.97	16.40	40.700	37.50	37.85	7.65	35.45	47.87	101.95
6	77.00	110.50	123.66	21.25	49.050	45.05	83.12	3.55	55.85	47.33	112.05
7	76.71	112.21	108.71	16.63	47.914	43.68	57.27	9.31	34.91	46.48	120.54

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