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Research Article

Genetic divergence analysis of castor (*Ricinus communis* L)

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Abstract

Castor is an important non edible oil seed crop cultivated throughout the world in varied climatic situation, due to its wider adaptability. Genetic diversity plays a foremost role in developing a potent genotype. Hence the present study was attempted to group 68 castor genotypes into different clusters based on Mahalanobis D^2 statistics. Based on genetic distance, 68 castor genotypes were grouped into 14 clusters. Among the 11 biometrical characters studied, seed yield per plant has contributed more to the total divergence. The maximum intra cluster distance was observed in cluster XIV and minimal intra cluster distance was recorded in cluster II. Similarly maximum inter cluster distance was observed between cluster XIII and cluster XIV. The minimal inter cluster distance was observed between cluster III and cluster V. Thus the selection of genotypes from these diverse clusters will help us to arrive at potent segregants in future hybridization programme.

Key words
Castor, Genetic divergence, D^2 statistics, *Ricinus communis* L.

Introduction

Castor (*Ricinus communis* L.) is a cross pollinated crop with a chromosomes number, 2n=20, belongs to the family Euphorbiaceae and it is indigenous to Eastern Africa and originated in Ethiopia. Castor is a monoecious plant and its inflorescence is known as raceme or spike. In the raceme, 30-50% upper portion contains female flowers and 50-70% lower portion possess male flower. Castor is a sexually polymorphic species with different sex forms viz., monoecious, pistillate and pistillate with interspersed staminate flowers (Lavanya, 2002). The crop is grown for its non-edible oil (45-50 percent oil in seeds) which is completely biodegradable and rich (80-90%) in an unusual hydroxy 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. Castor oil is utilized in several fields such as manufacturing lubricants, printing inks, hydraulic fluids, cosmetics, nylon fibres, pharmaceuticals and varnishes etc..,

Success of hybridization and subsequent selection of desirable segregants depends largely on the selection of parents with high genetic variability for different characters. The more diverse the parents, within overall limits of fitness, greater are the chances of obtaining higher amount of heterotic expression in F_1. The use of Mahalanobis D^2 statistic for estimating genetic divergence has been emphasized by Sukla *et al*., (2006). Hence the present investigation was carried out at TCRS, Yethapur to ascertain the value and magnitude of genetic diversity of 68 castor genotypes and to select suitable genotypes for further utilization in breeding programme.

Material and Methods

The experimental material comprised of 68 genotypes (Table 1) evaluated 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). Mahalonobis D^2 analysis (Mahalonobis, 1936) was used to estimate genetic divergence among the 68 genotypes. The statistical analysis was performed using software GENRES.

Result and Discussion

The analysis of variance revealed a significant difference among the 68 genotypes for all the eleven characters indicating the existence of high genetic variability among the genotypes for all the traits. The D^2 values of the genotypes ranged from 33.75 to 1414.51 indicating that the material was quite diverse. Based on genetic distance, the 68 genotypes were grouped into fourteen clusters. (Table.2)

Cluster I, the largest cluster, comprising forty genotypes, followed by cluster XIII with four genotypes. Remaining all clusters (II, III, IV, V, VI, VII, VIII, IX, X, XI, XII and XIV) were comprised with two genotypes each. The distribution of genotypes into different clusters indicated the genetic diversity doesn't depend on geographical diversity (Ramesh et al. 2012). Intra and inter cluster distance were computed and presented in table 3. Intra cluster distance ranges from 5.8 (cluster II) to 28.0 (cluster XIV). This shows that the genotypes present in the cluster XIV shows wide range of diversity and genotypes present in the cluster II shows minimal range of diversity. The maximum inter cluster distance was observed between cluster XIII and cluster XIV (37.6) followed by cluster VIII and cluster XIII (37.1). Minimum inter cluster distance was recorded between cluster III and cluster V (7.7). Genotypes belongs to clusters separated by high genetic distance may be used for hybridization programme to obtain heterotic segregants in future breeding programme. Therefore, genotypes from cluster VIII, XIII and XIV may be used in breeding programmes to exploit heterosis.

The cluster mean values showed wide range of variability among clusters for all the traits under study. The percentage contribution of each cluster towards total divergence is also shown in the Table 5. Highest contributing character towards divergence is seed yield per plant (41.3%) and mean value of the cluster for this character ranged from 47.1 to 125.5 g/ plant (Table 4). Genotypes in the cluster XIV are having the highest mean value for this cluster and lowest was noticed in cluster X. This result is in accordance with those of Jawar Lal and Lavanya (2019).

Second highest contributing character towards divergence is 100 seed weight (19.5%) and mean value of the cluster ranged from 38.8 to 21.73 g. Genotypes in the cluster IX are having the highest mean value for this character and lowest was recorded by cluster XI. Number of capsules per spike contributes 18.6 % contribution towards divergence and the mean value ranged from 39.35 to 71.8. The highest mean value was recorded in the genotypes of cluster IX and the lowest was in the cluster X. The characters viz., oil content (4.8 per cent), days to 50 per cent maturity (6.7 per cent), total number of effective spikelet (4.1 per cent), length of the primary spikelet (1.7 per cent), plant height (1.6 per cent), effective length of primary spikelet (1.3 per cent), days to 50 per cent flowering (0.4 per cent) and number of nodes (0.04 per cent) also contributed towards the genetic divergence. Considering the importance of genetic distance among the cluster, this study suggest the genotypes of major divergence contributing clusters in seed yield per plant (cluster XIV – TMV 5 & MCI 3) , 100 seed weight (cluster XIII – DPC 15 & JC 10) and number of capsules per plant (cluster IX –SM-1 & DCS 107) may be used in hybridization programmes.

References

Mahalanobis, P., On the generalized distance in statistics. Proceedings of National Institute Science, **2**:49-55. (1936).

Lavanya, C., Sensitivity of sex expression and sex variation in castor (*Ricinus communis* L.) to environmental changes. Indian Journal of Genetics and Plant breeding. **62** (3): 232-237. (2002).

Ramesh, M., Lavanya, C., and Rao, M.B., Genetic divergence in some indigenous and exotic germplasm lines of castor (Ricinus communis L) under rainfed conditions, Indian Journal of Dryland Agriculture Research and Development, **27**:79-83. (2012)

Shukla V, Singh S, Singh H and Pradhan SK 2006. Multivariate analysis in tropical japonica "New plant type" rice (Oryza sativa L.). Oryza **43**(3): 203-207. (2006)

Jawahar Lal J and Lavanya C,. Pattern of genotypic diversity in indigenous castor (*Ricinus communis* L.) genotypes, International Journal of Current Microbiology and Applied Sciences, **8(**1): 2465-2471.(2019).

Table 1. List of genotypes selected for D^2 analysis

Sl. No.	Name of the genotype	Sl. No.	Name of the genotype	Sl. No.	Name of the genotype
1	DPC 17	24	GP 537	47	M619-1
2	DPC 21	25	GP 783	48	JI 330
3	GEETHA	26	GP 759	49	SKP 84
4	GPJI 263	27	GP 674	50	DCS 105
5	GPJI 387	28	GP 705	51	JP 96
6	GPSKI 341	29	GP 62	52	SKI 352
7	GPJI 361	30	GP 487	53	SKI 215
8	GPJI 417	31	GP 493	54	MCI 7
9	GPJI 402	32	GP 640	55	SM-1
10	GPJI 420	33	GP 568	56	DCS 107
11	GPJI 220	34	JI 397	57	TMV 6
12	GPJI 415	35	SKI 335	58	DCS 106
13	GPJI 251	36	MCI 9	59	JC 12
14	GPJI 370	37	MOHANUR LOCAL	60	SKI 301
15	GPJI 334	38	MCI 8	61	SKI 304
16	GP 500	39	JC 8	62	48-1
17	GPRG 3748	40	MCI 11	63	TNPT 4
18	GP 471	41	JP 65	64	JC 26
19	GPJI 423	42	MCI 14	65	DPC 15
20	GPRG 1941	43	GP 778	66	JC 10
21	GP 101	44	RG 43	67	TMV 5
22	GP 432	45	DPC 9	68	MCI 3
23	GP 680	46	DCS 94		

Source: Tapioca and Castor Research Station, Yethapur.

Table 2. Composition of D^2 clusters in castor

Cluster no.	Number of genotypes	Name of the genotypes
I	40	DPC 17, DPC 21, GEETHA, GPJI 263, GPJI 387, GPSKI 341, GPJI 361, GPJI 417, GPJI 402, GPJI 420, GPJI 220, GPJI 415, GPJI 251, GPJI 370, GPJI 334, GP 500-2, GPRG 3748, GP 471-3, GPJI 423, GPRG 1941, GP 101, GP 432, GP 680, GP 537, GP 783, GP 759, GP 674, GP 705, GP 62, GP 487, GP 493, GP 640, GP 568, JI 397, SKI 335, MCI 9, MOHANUR LOCAL, MCI 8, JC 8, MCI 11
II	2	JP 65, MCI 14
III	2	GP 778, RG 43
IV	2	DPC 9, DCS 94
V	2	M 619-1, JI 330
VI	2	SKP 84, DCS 105
VII	2	JP 96, SKI 352
VIII	2	SKI 215, MCI 7
IX	2	SM -1, DCS 107
X	2	TMV 6, DCS 106-1
XI	2	JC 12, SKI 301
XIII	4	SKI 304, 48-1, TNPT 4, JC 26
XIII	2	DPC 15, JC 10
XIV	2	MCI 3, TMV 5

Table 3. Average intra and inter cluster D2 and D values (within parenthesis) for 68 castor genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	337.43	239.39	250.20	209.80	256.79	232.50	404.64	282.04	280.21	318.58	311.69	856.92	1148.18	418.45
	(18.37)	(15.47)	(15.82)	(14.48)	(16.03)	(15.25)	(20.12)	(16.79)	(16.74)	(17.85)	(17.66)	(29.27)	(33.89)	(20.47)
II		33.75	118.77	141.58	72.55	117.42	92.29	199.94	99.69	145.67	252.80	510.34	757.71	373.74
		(5.81)	(10.90)	(11.90)	(8.52)	(10.84)	(9.61)	(14.14)	(9.99)	(12.07)	(15.90)	(22.59)	(27.53)	(19.33)
III			37.65	87.95	59.62	155.79	211.33	110.25	142.23	142.88	203.02	767.98	1119.15	265.04
			(6.14)	(9.38)	(7.72)	(12.48)	(14.54)	(10.50)	(11.93)	(11.95)	(14.25)	(27.71)	(33.45)	(16.28)
IV				45.48	128.05	132.71	307.99	169.27	204.89	142.46	150.15	802.24	1033.90	251.65
				(6.74)	(11.32)	(11.52)	(17.55)	(13.01)	(14.31)	(11.94)	(12.25)	(28.32)	(32.15)	(15.86)
V					63.63	122.02	141.51	154.89	142.57	116.70	238.11	623.52	921.51	329.13
					(7.98)	(11.05)	(11.90)	(12.45)	(11.94)	(10.80)	(15.43)	(24.97)	(30.36)	(18.14)
VI						70.63	217.73	190.87	152.54	226.63	284.10	567.18	891.34	306.22
						(8.40)	(14.76)	(13.82)	(12.35)	(15.05)	(16.86)	(23.82)	(29.86)	(17.50)
VII							79.56	319.50	179.29	227.08	440.33	459.04	677.44	529.91
							(8.92)	(17.88)	(13.39)	(15.07)	(20.98)	(21.43)	(26.03)	(23.02)
VIII								96.99	193.93	201.77	167.46	998.03	1377.28	317.53
								(9.85)	(13.93)	(14.21)	(12.94)	(31.59)	(37.11)	(17.82)
IX									98.00	306.70	313.82	555.38	910.09	354.36
									(9.90)	(17.51)	(17.72)	(23.57)	(30.17)	(18.82)
X										101.71	180.60	858.92	974.83	421.40
										(10.09)	(13.44)	(29.31)	(31.22)	(20.53)
XI											126.86	1100.92	1195.88	394.84
											(11.26)	(33.18)	(34.58)	(19.87)
XII												554.94	616.16	1014.25
												(23.56)	(24.82)	(31.85)
XIII													511.09	1414.51
													(22.61)	(37.61)
XIV														782.00
														(27.96)

Table 4. Cluster means of 68 castor genotypes for various characters

Cluster	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
I	70.80	107.61	79.01	15.87	43.78	40.84	59.08	8.84	27.78	46.04	83.37
II	68.25	107.50	76.58	15.75	42.45	40.40	48.55	8.25	28.90	43.10	80.80
III	78.50	120.00	203.00	20.27	55.89	50.83	68.33	5.38	38.38	47.85	104.83
IV	70.50	101.00	83.39	15.40	42.90	40.45	69.40	11.65	29.20	47.95	103.45
V	78.25	120.50	90.28	19.05	43.55	41.80	62.35	7.00	27.45	40.78	89.70
VI	76.75	113.25	69.54	19.00	54.90	51.90	67.25	8.35	28.15	41.78	85.70
VII	72.00	109.75	99.21	17.15	51.30	47.60	50.35	6.40	30.73	42.55	61.20
VIII	74.50	109.25	89.08	14.45	51.00	47.28	64.50	10.45	25.30	45.00	102.60
IX	75.75	110.50	92.90	17.95	49.35	45.25	71.80	7.85	38.80	48.50	106.50
X	76.50	105.00	102.70	15.00	39.45	35.25	39.35	6.00	25.98	40.05	47.10
XI	73.25	113.75	106.44	17.40	46.55	42.80	50.65	7.05	21.73	46.53	91.85
XII	73.13	113.13	108.95	15.50	49.30	45.00	57.95	8.95	34.79	45.86	118.95
XIII	59.25	95.50	57.42	11.75	33.80	31.85	44.00	12.95	25.53	45.23	82.45
XIV	72.25	103.25	69.61	14.80	42.70	39.30	55.10	14.40	27.65	47.15	125.50

Table 5. Percentage Contribution of biometrical characters for divergence in 68 castor genotypes

Characters	Number of first rank	Per cent contribution
Days to 50 per cent flowering	8	0.35
Days to 50 per cent maturity	153	6.72
Plant height	37	1.62
Number of nodes upto primary spike	1	0.04
Primary spike length	39	1.71
Effective length of primary spike	29	1.27
Number of capsules on primary spike	423	18.57
Total number of spikes	93	4.08
100 seed weight	444	19.49
Oil content	110	4.83
Seed yield per plant	941	41.31
Total	**2278**	**100.00**

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