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

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ABSTRACT

In order to assess the genetic divergence among the 41 genotypes accessions in castor, Mahalonobis D^2 statistics was applied. The 41 genotypes were grouped in to 12 clusters where, cluster I was largest containing 27 genotypes followed by cluster IV with 3 genotypes, cluster VI with 2 genotypes and cluster II, III, V, VII, VIII, IX, X, XI and XII with each having single genotype. Based on inter cluster distance, the highest inter cluster distance was observed between cluster IX and cluster XII followed by cluster IV and cluster IX, cluster I and cluster IV and cluster VI and cluster XII. Plant height (20.00 %) was main contributors to the total divergence, which was followed, by 100-seed weight (19.76 %) and number of capsules on primary raceme (17.32 %). The genotypes included in the diverse clusters can be used as promising parents for hybridization programme for obtaining high heterotic response and thus better segregants in castor.

Key words : Castor, Clusters, Genetic diversity

INTRODUCTION

Genetic diversity is of major interest to plant breeder. As more diverse the parents with an overall limit of fitness, the greater is the chance of higher amount of heterotic expression in F1's and greater is the possibility of generating broad-spectrum variability in segregating generations.

Genetic diversity between populations/genotypes indicates the differences in gene frequencies. Multivariate analysis using Mahalanobis D^2 statistics (1936) is valuable tools to study genetic divergence at inter varietal and sub species level in classifying the crop plants. This has been successfully utilized in castor to classify the genotypes and determine their interrelationship by many workers Sevugaperumal *et al*. (2001) and Lakshmamma *et al.* (2002). The present study was carried out to ascertain the nature and magnitude of genetic divergence among 41 castor genotypes.

MATERIALS AND METHODS

Genetic material for the present investigation comprised of 41 castor genotypes. The experiment was carried out in a Randomized Block Design (RBD) with three replications at Agronomy Instructional Farm, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, during August-2004 to March-2005. Sowing of seeds was carried out through dibbling method. Each genotype was grown in single row of 10 dibbles. The distance between two successive rows was 90 cm, while between two dibbles within a row was 60 cm. All the agronomic practices were followed uniformly. The observations were recorded on 5 randomly selected plants and tagged from each genotype in each replication for 9 characters. These data were subjected to divergence analysis (Mahalanobis, 1936) and Tocher's method as described by Rao (1952) for determining group constellation. Average intra and inter cluster distances were estimated as per the procedure outlined by Singh and Chaudhary (1977).

RESULTS AND DISCUSSION

Tocher's method (Rao, 1952) was employed for the formation of clusters. Forty one genotypes were grouped in twelve clusters are presented in Table 1. Cluster I was the largest and comprised of 27 genotypes, which were developed at three research centers *viz.*, Sardarkrushinagar (Gujarat), Junagadh (Gujarat) and Rajendranagar (Andhra Pradesh) followed by cluster IV (3 genotypes), cluster VI (2 genotypes) and clusters II, V, VII, VIII, IX, X and XII each having single genotype were developed at Sardarkrushinagar. Cluster III and cluster XI also included one genotype, each which were developed at Junagadh. This revealed that the genetic diversity had no any relevance with originating centres of the studied genotypes. This could be due to intermingling of gene pool among genotypes by crossing and germplasm exchange programmes. Moreover, the genetic drift and selection in different environments could also cause greater diversity than geographical distance. The results

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Table 1 : Cluster group of 41 genotypes on the basis of D^2 statistics in castor

No. of Cluster	Number of genotypes	Name of genotypes
I	27	JI-263, SKP-112, SKI-80, VI-9, SKI-178, GAUCH-1, SKI-291, VP-1, SKP-93, JI-258, JP-65, SKI-267, GCH-6, SKP-72, GCH-2, SKI-304, GCH-4, 48-1, SKI-293, SKP-6, SH-72, SH-41, SKI-215, SKP-16, SKI-285, SKI-202, GCH-5
II	1	SKP-84
III	1	JI-96
IV	3	SKI-218, SKI-183, SKI-182
V	1	SKP-52
VI	2	SKP-4, SKI-286
VII	1	SKP-108
VIII	1	SKI-147
IX	1	SKI-200
X	1	Geeta
XI	1	JI-35
XII	1	SKI-225

are in accordance with those of Bhatt and Reddy (1987) and Jaimini (2002).

The average intra and inter cluster distance (Table 2) revealed that the genetic diversity among the genotypes in intra-cluster distance was found to be the maximum for cluster I (10.97), followed by cluster IV (10.74) and cluster VI (7.55). The minimum intra-cluster distance was, however, depicted by clusters II, III, V, VII, VIII, IX, X, XI and XII all cluster had 0.0 values. Cluster I in which 27 genotypes are included having considerable intra-cluster distance can be hybridized for obtaining superior inbreds over existing populations through recombination breeding. The maximum inter cluster distance was observed between, cluster IX and cluster XII (28.07), followed by cluster IV and cluster IX (26.41), cluster I and cluster IV (25.27) and cluster VI and cluster XII (25.26). The lowest inter cluster distance was found between cluster II and cluster V (6.89). The results revealed that the genotypes included in clusters I, IV, VI, IX and XII showed the great deal of genetic diversity and the hybridization between the genotypes from cluster IX and cluster XII, cluster IV and cluster IX, cluster I and cluster IV and cluster VI and cluster XII, can provide potential genotypes in the subsequent generations after hybridization. The genotypes from different clusters can also be utilized for development of hybrids, which can give higher yield under diversed agro-climatic conditions.

The contribution of individual characters towards the divergence (Table 3) indicated that plant height (20.00 %) was main contributors to the total divergence, which was followed by 100-seed weight (19.76 %) and number of capsules on primary raceme (17.32 %). Other characters like days to 50 per cent flowering (11.46 %), number of effective branches per plant (16.83 %) and seed yield per plant (11.59 %) had moderate whereas, the characters like days to maturity (0.73 %), length of primary raceme (0.98 %) and oil content (1.34 %) had low contribution towards total divergence.The results were akin to the reports of Sevugaperumal *et al*. (2001) and Jaimini (2002).

There was a wide range of variation in the cluster mean values for most of the characters under study (Table 4). Cluster mean showed that the cluster IX had genotype with the maximum values for the earliness and seed yield per plant. Cluster IV had genotypes with the maximum values for plant height and 100-seed weight. Cluster III had superior genotype for length of primary raceme and number of effective branches per plant. Genotypes in cluster XII had good number of capsules on primary raceme and better oil content.

Table 2 : Average intra and inter cluster distance (D = Ĕ D^2)

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	10.97	14.04	14.21	25.27	17.12	15.12	14.95	14.55	13.25	15.45	17.32	23.93
II		0.0	19.15	22.94	6.89	14.69	8.26	11.69	19.69	17.52	18.39	20.52
III			0.0	19.76	20.83	18.66	15.18	13.36	12.85	10.66	16.39	20.74
IV				10.74	21.97	24.25	16.57	17.22	26.41	19.07	23.05	13.85
V					0.0	13.52	8.34	14.62	21.94	18.35	20.82	20.64
VI						7.55	13.71	19.56	17.21	16.93	23.90	25.26
VII							0.0	8.96	19.99	11.87	16.14	15.57
VIII								0.0	19.27	11.62	9.74	14.54
IX									0.0	19.41	22.86	28.07
X										0.0	12.18	18.63
XI											0.0	18.83
XII												0.0

Table 3 : Per cent contribution of different characters to total genetic divergence

Sr. No.	Characters	Number of time character ranked first	Per cent contribution
1.	Days to 50 per cent flowering (No.)	94	11.46
2.	Days to maturity (No.)	6	0.73
3.	Plant height (cm)	164	20.00
4.	Length of primary raceme (cm)	8	0.98
5.	Number of capsules on primary raceme	142	17.32
6.	Number of effective branches per plant	138	16.83
7.	Seed yield per plant (g)	95	11.59
8.	100-seed weight (g)	162	19.76
9.	Oil content (%)	11	1.34
	Total	820	100.00

Table 4: Cluster mean for different characters in castor

Cluster number	Days to 50 % flowering	Days to maturity	Plant height (cm)	Length of primary raceme (cm)	Number of capsules on primary raceme	Number of effective branches	Seed yield per plant (g)	100-seed weight (g)	Oil content (%)
I	59.52	129.30	49.96	35.89	58.75	3.81	139.03	31.51	48.06
II	69.33	142.33	37.64	52.73	79.24	1.10	74.33	33.85	46.99
III	67.00	146.33	86.76	60.01	69.33	6.50	246.33	34.50	48.95
IV	88.78	178.67	132.07	51.83	136.08	3.89	185.89	41.22	48.04
V	82.00	162.67	36.08	49.69	60.44	0.69	83.67	35.97	49.05
VI	76.00	157.67	33.53	25.24	29.73	3.87	40.16	36.67	48.72
VII	81.33	154.67	65.42	57.78	86.58	3.10	80.00	36.19	49.03
VIII	72.67	139.67	90.67	56.40	108.52	2.85	155.67	32.26	46.98
IX	49.33	127.33	57.22	29.00	38.78	3.83	254.67	35.49	43.11
X	85.67	146.33	86.47	51.87	69.50	6.4	108.01	32.27	48.37
XI	78.67	122.00	97.07	44.33	98.47	3.9	163.33	27.10	49.86
XII	95.67	178.33	86.13	48.07	168.00	4.3	200.01	33.50	50.95

Crosses among the diverse parents are likely to yield desirable combinations. Therefore, a crossing programme should be initiated between the genotypes belonging to different clusters. The greater the distance between two clusters, the wider the genetic diversity among the parents to be included in hybridization programme. Parents combining high yield potential with wide genetic diversity are likely to yield superior segregants with in short period. The genotypes with high mean values from any cluster can either straight away be used for adoption or can be used in hybridization for yield improvement.

REFERENCES

Bhatt, D. and Reddy, T.P. (1987). Genetic divergence and heterosis in castor. *Indian J. Bot.*, **10** (1): 21-26.

Jaimini, N. (2002). Genetic variability, association studies, genetic divergence and stability analysis in newly evolved pistillate lines of castor (*Ricinus communis* L.). M.Sc. (Ag.) Thesis, Gujarat Agricultural University, Sardarkrushinagar.

Lakshmamma, P., Reddy, A.V.V. and Mohan, C.Y. (2002). Divergence studies in castor. *Nat. J. Plant Improve.*, **4** (2): 23-25.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proc. Nat. Inst. Sci.*, (Indian). 2: 49-55.

Rao, C.R. (1952). *Advanced Statistical Methods in Biometrical Research*. John Willey and Sons Inc., New York, pp., 363.

Sevugaperumal, S., Rungasamy, P. and Muppidathi, N. (2001). Genetic divergence studies in castor (*Ricinus communis* L.). *Madras Agric. J.*, **87** (4-6): 241-243.

Singh, R.K. and Chaudhary, B.D. (1977). *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi, pp., 304.

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