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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 recorded 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 D² 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 character and lowest was recorded by cluster XI. Number of capsules per plant type 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


Table 1. List of genotypes selected for D² analysis

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Source: Tapioca and Castor Research Station, Yethapur.
Table 2. Composition of D\(^2\) clusters in castor

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

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

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

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