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Genetic Diversity Studies in Castor (*Ricinus communis* L.) – Review

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ABSTRACT: Castor (*Ricinus communis* L., 2n = 2x = 20), a premier non-edible commercial oilseed crop belonging to the family Euphorbiaceae, plays a pivotal role in global industrial agriculture, with India being the major supplier of castor oil and its derivatives. Castor oil is highly valued due to its unique hydroxylated fatty acid, ricinoleic acid, which enhances its utility as a superior lubricant in high-power engines and facilitates easy conversion into biodiesel, even at low temperatures. In addition to its industrial applications in soaps, printing inks, linoleum, varnishes, and plasticizers, castor oil serves medicinal purposes as a potent laxative and as a therapeutic agent for skin ailments such as sunburn, wrinkles, and stretch marks. The castor oil extraction by-product, known as castor cake, is rich in organic nutrients—containing approximately 6.4% nitrogen, 2.5% P_2O_5, and 1% K_2O, along with essential micronutrients—making it a valuable input for organic farming. Furthermore, castor stems are used as firewood and as raw material for paper pulp production, while its fresh leaves support eri-silkworm rearing and dried leaves function as natural insecticides.

In castor improvement programs, assessing genetic divergence is crucial for selecting superior and diverse parental lines. The Mahalanobis D^2 statistic is a widely used and powerful multivariate tool for quantifying genetic diversity within castor germplasm. Complementing this, Principal Component Analysis (PCA) effectively reduces complex datasets into a smaller number of informative components, enabling the identification of key traits contributing most to overall variation. Additionally, correlation and path coefficient analyses provide insights into the interrelationships among yield and yield-contributing traits, helping breeders to prioritize important characters for selection and to formulate efficient hybridization strategies. Together, these biometrical and multivariate approaches form the foundation for designing robust breeding programs aimed at enhancing castor productivity and genetic improvement.

Keywords: Castor, Ricinus communis, Castor oil, Ricinoleic acid, Castor cake, Genetic divergence, Mahalanobis D^2, PCA, Correlation, Path analysis, Yield traits, Plant breeding.

INTRODUCTION

Castor (*Ricinus communis* L., 2n=2x=20), a premier non-edible commercial oilseed crop, belongs to spurge family commonly known as *Euphorbiaceae*. Castor is believed to have originated in the Ethiopian-East African region. There are four recognized centers of diversity for castor: Ethiopian-Eastern Africa, North-West Africa, South-West Africa and the Arabian Peninsula, and the Indian subcontinent, including China. In India, castor has been known since ancient times and is mentioned in the Sushruta Samhita, a text written over 2,000 years ago (Gangaiah, 2005). It is an important industrial non-edible oilseed crop grown in arid and semi-arid regions worldwide (Govaerts *et al.,* 2000). The genus Ricinus is monotypic, meaning R. communis is the only species, though it exists in different polymorphic forms. Some of these forms have been named *R. macrocarpus* and *R. microcarpus* (Weiss, 2000), but they are not true species since they can intercross and produce fertile offspring. Cytological studies show that all castor varieties are diploids, and it is believed to be a secondary balanced polyploid with a basic chromosome number of x = 5 (Singh, 1976).

The main sex forms in castor are monoecious, pistillate, and interspersed staminate flowers. A sex revertant is a female plant that later develops into a monoecious form. Environmental conditions significantly affect the sex ratio of flowers within a variety. Lower temperatures (around 30°C) during winter favor the development of female flowers, while higher temperatures (around 32°C) during summer and the rainy season promote the formation of male flowers.

The development of fully pistillate lines and the presence of high heterosis for seed yield have helped in hybrid castor breeding in India. Castor plants show different sex forms, including monoecious, pistillate, and hermaphroditic types. Shifriss (1960) classified these into conventional and unconventional types and identified three pistillate mechanisms—N type, S type, and NES type—based on genetic control. Among these, S type pistillate lines are mainly used in hybrid breeding. However, environmental factors can affect sex expression, creating challenges in hybrid seed production. To ensure successful seed production, pistillateness must remain stable across different temperatures. Therefore, selecting the right parent lines through careful evaluation is essential, as a parent's individual performance does not always indicate its potential in hybrid combinations.

India is the global supplier of castor oil and its by-products. India alone produces 18.79 lakh tonnes of castor bean from 10.30 lakh hectares cultivated area with an average productivity of 1824 kg ha^{-1} (INDIASTAT, 2023-24). In India, castor is chiefly grown in the states of Gujarat followed by Rajasthan, Andhra Pradesh, Telangana, Tamil Nadu, Karnataka and Madhya Pradesh. Castor seed contains 48 to 56 per cent oil. Castor oil possesses unique properties that set it apart from other oils, as it does not freeze even at temperatures as low as -12°C to -18°C. Ricinoleic acid is the primary component of castor oil, accounting for over 89% of its total fatty acid content. In addition to ricinoleic acid, castor oil also contains other fatty acids, including oleic acid, linoleic acid, α-linolenic acid, stearic acid, palmitic acid, and dihydroxystearic acid (Omari *et al*., 2015). Due to the presence of substantial quantity of the unusual hydroxylated fatty acid "ricinolate" which enhances its consumption as a *lubricant* in power engines. It can readily be dissolved in alcohol and transformed into *biodiesel* even at low temperatures. It is also used to manufacture soaps, printing inks, linoleum, varnishes and plasticizers. Castor oil is a potent *laxative* and is also a *curing agent* for skin problems *viz*., sunburn, crinkles and stretch symbols, etc. The by-product of castor oil expeller is the *cake* which contains vital organic with nitrogen (6.4%), P_2O_5 (2.5%) and K_2O (1%) including micronutrients for organic farming. The plant stems are used as firewood and to prepare pulp by the paper mills. Beyond this, fresh castor leaves are used to *rear eri* silkworms, while desiccated leaves are used as an insecticide in agriculture.

India is one of the centers of diversity, where significant genetic variation exists across diverse ecosystems (Anjani, 2012). Castor is primarily cultivated as a hybrid in India, offering significantly higher yields than inbred lines or traditional varieties (Birchler *et al*., 2003). Genetic diversity assessment before hybrid development can enhance the exploitation of heterosis commercially cultivated castor varieties used for hybrid seed production are highly susceptible to changing climatic conditions and emerging pests/pathogens due to their shared ancestry and the monotypic nature of the Ricinus genus (Shaw *et al*., 2017). To overcome this challenge and improve yield potential, it is essential to explore new genetic resources from germplasm and integrate them into elite breeding backgrounds. The development of high-yielding varieties or hybrids requires substantial genetic diversity at both the gene and genotype levels. Genetic diversity plays a crucial role in genetic improvement and serves as a fundamental criterion in plant breeding programs. The success and longevity of cultivated castor varieties depend on the broad genetic base employed in breeding efforts. To effectively tackle climate challenges and ensure sustainable production, castor breeders must have access to and utilize a wide range of genetic diversity (Galluzzi *et al*., 2020). This emphasizes the need to augment genetic resources through germplasm collection, multiple crosses, and similar approaches, followed by thorough characterization and utilization in breeding programs. Given castor's monoecy-protogyny nature facilitating allogamy mechanism, substantial genetic variation can be expected, making it imperative to characterize germplasm based on genetic diversity (Allan *et al.*, 2008). The Mahalanobis D^2 statistic is a potent tool for quantifying genetic divergence within a population. Divergent genotypes can arise from collection across diverse eco-geographical regions or through combination breeding techniques. This powerful approach aids in identifying genetically distinct individuals and is instrumental in plant breeding programs for developing improved cultivars adapted to varying environmental conditions (Mahalanobis, 1936).

The success of plant breeding hinges on the existing genetic variability within the crop (Zheng *et al*., 2010). Assessing and estimating genetic variability in the germplasm is crucial before initiating any crop improvement program or selecting appropriate breeding techniques. This analysis aids in developing high-yielding and high-quality cultivars, ultimately increasing production. Heritability plays a key role in determining the transmissibility of traits to future generations, which is vital for selecting component traits to improve yield. Heritability estimates, along with genetic advances, are more reliable in predicting the genetic gain achieved via selection compared to heritability estimates alone.

Correlation studies between yield and yield-contributing traits are valuable for breeders to design hybridization programs and evaluate individual plants in segregating populations. Path coefficient analysis further aids in assessing the relative contributions, both direct and indirect, of each component trait to overall yield. By identifying cause-and-effect relationships and measuring their relative significance, path coefficient analysis provides valuable insights. Combining correlations with path coefficient analysis enables the quantification of direct and indirect influences of one characteristic on another. These combined approaches are essential tools for effective genetic improvement and breeding strategies in castor.

Future studies on castor should include testing more genotypes from different areas to find good types for yield and other useful traits. Castor varieties should be tested in many locations to see how they grow under different climates and soils. Important traits like drought tolerance, pest and disease resistance, and oil content need more attention because they help farmers. There is also a need to develop new varieties and hybrids by using diverse and promising parents. Collecting, conserving, and regularly evaluating germplasm will help increase the genetic diversity and support future castor improvement.

Variability in terms of variances and co-efficient of variation

Sevugaperumal *et al*. (2000) studied 36 castor genotypes to assess the phenotypic and genotypic coefficients of variation. The genotypic variation coefficient was maximum for single plant/yield followed by number of spikes/plant and plant height. The difference between phenotypic and genotypic variation coefficients was narrow for single plant yield.

Lakshmamma *et al*. (2005) assessed the genetic variation in 68 diverse germplasm lines along with hybrids and cultivars of castor.The maximum phenotypic coefficient of variation and genotypic coefficient of variation were observed for capsule weight/plant, plant height and number of capsules. The characters *viz.*, plant height, capsule weight, capsule number and leaf area index displayed high heritability and genetic advance implying the predominance of additive genes in governing the traits. High heritability coupled with low genetic advance were observed for inter-nodal length, stem girth, number of secondary and tertiary branches and seed yield, indicating role of non-additive gene effects and therefore selection for these traits may not be rewarding.

Sarwar and Chaudhary (2008) investigated, a set of 19 castor seed genotypes, subjected to gamma irradiation in M_4 generation for genetic analysis. Notably, traits such as 100 seed weight and capsule weight displayed heritability of over 50%. The genetic analysis revealed the presence of additive gene action in traits such as the number of capsules per primary spike, followed by the total length of the primary spike and the number of primary spikes per plant and traits like the number of capsules per spike, total spike length, and total number of primary spikes exhibited strong heritability and significant genetic advancement.

Elena and Rodrguez (2009) studied variability for spike, capsule and seeds characters in 13 genotypes of castor. Variability was reported based on qualitative and quantitative traits: spike (shape, compaction, length of primary spike, number of capsules per spike, weight of seeds per spike, number seed per spike) and seeds (weight of 100 seeds, weight of 100 capsule, oil content).

Sarwar *et al.* (2010) studied genetic parameters in 27 castor mutants and observed that the highest genotypic coefficient of variation (GCV) was found for spikes per plant, followed by branches per plant and plant height. The traits with the lowest GCV were 100-seed weight, secondary spike length, days to maturity, and main spike length. The phenotypic coefficient of variation (PCV) was consistently higher than the GCV for all traits. The highest PCV was recorded for spikes per plant, followed by seed yield, capsules on the secondary spike, branches per plant, and capsules on the main spike.

Patel and Patel (2014) examined the variability parameters for seed yield and its components, finding that the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were moderate for traits including the number of nodes up to the primary spike, the effective and total length of the primary spike, plant height, and the number of capsules on the primary spike per plant.

Torres *et al.* (2015) examine variability parameters for oil content percentage in seven castor genotypes. The results revealed that the experimental coefficient of variation was lowest for oil content and highest for the number of capsules on the main spike. The genotypic coefficient of variation (GCV) ranged from 0.4% for oil content to 35.4% for 100-seed weight, indicating that traits such as the number of capsules and 100-seed weight exhibited the greatest variability among the evaluated characteristics.

Destaw *et al.* (2017) studied on 48 castor germplasm accessions to assess genetic variability among yield and yield-related traits. The analysis of variance showed that traits such as plant height, length of the primary spike, number of capsules per plant, number of secondary branches per plant, length of internode, number of inflorescences per plant, days to second flowering, days to first maturity, days to second maturity, number of seeds per plant, 100-seed weight, and oil content exhibited a high difference between the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), highlighting the significant role of environmental factors in the expression of these traits.

Rukhsar *et al.* (2018) evaluated genetic variability in 15 castor genotypes for 13 traits, including days to flowering, days to maturity, number of nodes up to the primary spike, plant height up to the primary spike, length of the primary spike (total and effective), number of capsules on the primary spike, number of effective spikes, seed yield per plant, 100-seed weight, and oil content. Their findings revealed that the highest genotypic and phenotypic coefficients of variation (GCV and PCV) were observed for the number of capsules on the primary spike. For traits like the number of capsules on the primary spike, seed yield per plant, plant height up to the primary spike, and 100-seed weight, the GCV and PCV values were nearly equal, suggesting these traits are less influenced by environmental factors and offer greater potential for selection, indicating the presence of substantial variability in the germplasm.

Alhaji *et al.* (2019) assessed the genetic variability in 10 castor genotypes, which were arranged in a randomized complete block design with three replications. High genotypic and phenotypic coefficients of variation (greater than 20%) were observed for several traits, including days to 50% flowering, effective spikes per plant, number of capsules on the spike and effective length of the spike.

Lavanya *et al.* (2022) studied segregating population developed by crossing two pistillate (female) lines of castor *viz.*, IPC-23 and IPC-21.The estimates for phenotypic coefficient of variation (PCV) were slightly higher than the genetic coefficient of variation (GCV) for most the traits, suggesting variation in the traits were primarly due to genetic factors, The difference between PCV and GCV was very small for traits like the number of effective spikes per plant, number of nodes to the primary spike, and moderately small for traits like plant height, total spike length, and effective spike length, indicating that the environment had little effect on these traits. However, the difference between PCV and GCV was much larger for seed yield, meaning environmental factors had a stronger impact on seed yield.

Reddy *et al*. (2022) studied 50 castor lines along with two checks. Except for days to 50 per cent flowering and days to maturity the GCV and PCV values indicated presence of broad variation for all characters.

Chandana *et al*. (a) (2025) Studied 40 castor genotypes and found that traits like total seed yield and number of capsules per primary spike Thus, direct selection for these traits could result in further improvement of grain yield.

HERITABILITY AND GENETIC ADVANCE

Sarwar *et al.* (2010) evaluated 27 desirable castor mutants in the M_5 generation and found that plant height had high broad-sense heritability along with a high genetic advance, indicating that it is controlled by additive genes. In contrast, days to maturity showed high broad-sense heritability but low genetic advance, suggesting it is governed by non-additive genes.

Abimiku *et al.* (2012) studied nine castor accessions to assess heritability and genetic advance. They found relatively high broad-sense heritability for the number of capsules per plant, 100-seed weight, and seed yield per plant, with the exception of branches per plant. Additionally, the number of capsules per plant, 100-seed weight, and seed yield per plant showed high genetic advance.

Ramesh *et al.* (2012) conducted studies on heritability and genetic advance for yield components in 64 castor genotypes. They found that seed yield at 180 days after sowing had the highest heritability, followed closely by seed yield at 150 days after sowing. The highest genetic advance as a percentage of the mean was recorded for seed yield at 150 days after sowing, followed by seed yield at 120 days after sowing, effective spike length and the number of capsules per plant.

Radhamani and Ushakumari (2013) studied heritability and genetic advance in 45 castor germplasm accessions, evaluating nine biometrical traits and four physiological traits. They observed high heritability for both biometrical and physiological traits, suggesting low environmental influence and a strong potential for these traits to be passed on to subsequent generations.

Torres *et al.* (2015) studied heritability and genetic advance in seven castor genotypes and found that traits such as plant height, stem diameter, number of bunches, number of capsules, and 100-seed mass had heritability values greater than 60%, indicating they were less influenced by environmental factors. In contrast, oil content and capsule mass exhibited low heritability, which was attributed to a higher environmental variance relative to genotypic variance, suggesting that these traits were more strongly influenced by the environment.

Dapke *et al.* (2016) estimated heritability and genetic advance in 61 castor genotypes. They found high genetic variability, high heritability, and high genetic advance for traits such as plant height up to the primary spike, number of nodes up to the primary spike, total length of the primary spike, length of the capsule-bearing region of the primary spike, number of effective branches per plant, number of capsules on the primary spike, and seed yield per plant. However, traits like days to flowering, days to maturity, 100-seed weight, and oil content showed lower genetic advance, suggesting that direct selection for the other traits could be more effective.

Destaw *et al.* (2017) investigated heritability and genetic advance in 48 castor genotypes. Their results showed that days to flowering exhibited moderate heritability and moderate genetic advance, while days to second flowering had moderate heritability and high genetic advance. For 100-seed weight, moderate heritability was observed, but with low genetic advance.

Movaliya *et al.* (2018) studied 64 castor genotypes and found that traits such as seed yield per plant, total length of the primary spike, effective length of the primary spike, number of capsules on the primary spike, and oil content exhibited high heritability along with high genetic advance as a percentage of the mean.

Reddy *et al.* (2022) evaluated 50 advanced genepool lines were sown along with two checks, high heritability coupled with high genetic advance as per cent mean was registered for plant height, number of nodes to primary spike, primary spike length, effective primary spike length, number of effective spikes per plant, number of capsules in primary spike, 100 seed weight and seed yield.

Chandana *et al.* (a) (2025) investigated 40 castor genotypes. Their results showed that traits such as effective primary spike length, number of capsules on primary spike, number of effective spikes per plant, 100 seed weight, and total seed yield (kg/ha) exhibited high heritability coupled with high genetic advance as *per cent* of mean, indicating the preponderance of additive gene action and these traits can be effectively improved through simple selection procedures. High heritability but low genetic advance as *per cent* of mean was observed for days to maturity of the primary spike and days to 50% flowering showed high heritability and moderate genetic advance as *per cent* mean. Plant height upto the primary spike and number of nodes to the primary spike showed moderate heritability and genetic advance as *per cent* of mean, Meanwhile, volume weight, final plant stand, and oil content exhibited moderate heritability with low genetic advance as *per cent* of mean.

GENETIC DIVERGENCE

Bezerra and Francisco (2010) investigated the genetic divergence of 11 castor genotypes from the North and North-West regions of Rio de Janeiro, Brazil, based on six quantitative traits. Their multivariate analysis grouped the genotypes into three distinct clusters. Among these, the genotypes Nordestina, IAC 80, Al Guarany, and IAC 226 showed promising potential. They suggested that crossing Al Guarany with IAC 80 would be beneficial for breeding or genetic improvement programs.

Rodrigues *et al.* (2010) characterized 15 castor accessions using morpho-agronomic traits. Four clusters were formed using the Tocher method and hierarchical nearest neighbour clustering based on Euclidean distance. The results of this study suggested that crossings between accessions from Group 1 and Group 3, as well as between Group 2 and Group 4, would be beneficial for further improvement.

Gogoi *et al.* (2011) studied 72 castor accessions collected from the North-Eastern region of India and identified two major clusters of genotypes with varying yield potential. Based on the genetic distance between genotypes in different clusters, contrasting parents may be selected for use in hybridization programs to enhance yield traits.

Benke *et al.* (2012) analyzed genetic divergence in 40 castor genotypes using D^2 statistics. The greatest inter-cluster distance was observed between clusters X and IV, followed by distances between clusters VII and X, IV and III, and III and X. Cluster VII had the lowest mean values for days to flowering and maturity, but the highest values for the effective length of the secondary spike, the number of capsules on the secondary spike, and oil content. Cluster IX exhibited the highest mean values for the number of capsules on the primary spike, total number of capsules, and seed yield per plant. Meanwhile, clusters III, VI, and VIII showed the highest mean values for the effective length of the primary spike, 100-seed weight, and effective length of the tertiary spike, respectively.

Muhammad *et al.* (2015) examined the phenotypic diversity of 63 castor genotypes. The dissimilarity coefficient matrix revealed that the genotype pairs 24816 and 24821, 24821 and 24829, and 21559 and 24821 were the most diverse, showing the highest Euclidean distances. Based on morphological characterization, the subsequent cluster analysis grouped all the genotypes into six major clusters.

Chaudhari *et al.* (2016) investigated the genetic divergence among 72 castor genotypes. The analysis resulted in the formation of eight distinct clusters, with cluster I being the largest, comprising 49 genotypes. Clusters II, IV, VI, VII, and VIII consisted of only one genotype. The greatest divergences were observed between Cluster III and Clusters VIII as well as between Cluster VI and Clusters VIII and II, based on inter-cluster distance. Maximum intra-cluster distance present in Cluster III. In this study effective spike per plant contributes maximum to divergence. These findings suggest that inter-crossing between genotypes from these clusters could lead to improved seed yield and the generation of greater variability. These results highlight the potential for utilizing these clusters to enhance breeding programs and facilitate the development of improved castor varieties.

Silva *et al.* (2017) conducted a genetic divergence analysis in castor using Ward's and Tocher's methods based on Gower's distance. The results revealed the formation of 21 groups based on 13 morpho-agronomic descriptors, including six qualitative and seven quantitative traits, indicating significant variability within the germplasm. Among these groups, some contained promising accessions with desirable agronomic traits, such as precociousness, fruit dehiscence, plant height, and yield.

Rukhsar *et al.* (2018) utilized Mahalanobis D^2 analysis to group 15 castor genotypes into seven distinct clusters. The number of capsules on the main spike emerged as a significant contributor to the overall genetic divergence. Selecting genotypes from diverse clusters, such as Cluster II and V, as well as Cluster II and VII, for hybridization programs can facilitate the generation of novel recombinants.

Nagarajan *et al.* (2019) employed Mahalanobis D^2 statistics to classify a total of 68 castor genotypes into 14 distinct clusters. Among the 11 biometrical variables assessed, seed yield per plant emerged as the most significant contributor to overall divergence. Cluster XIV exhibited the highest intra cluster distance, while Cluster II demonstrated the smallest intra cluster distance. The inter cluster distance was found to be highest between clusters XIII and XIV, whereas the smallest inter-cluster distance was observed between Cluster III and Cluster V. Consequently, the selection of genotypes from these diverse clusters holds promise for facilitating the development of effective segregants in future hybridization programs.

De Oliveira *et al.* (2021) conducted an assessment on 40 castor accessions sourced from Brazil, focusing on 31 morpho-agronomic traits and their reaction to grey mould. The accessions were grouped using the Ward method, which utilized standardized Euclidean distance for quantitative data and the simple coincidence index for qualitative data. Notably, a considerable variation in grey mould reaction was observed among the accessions. Through the clustering analysis, the accessions were categorized into three distinct groups, highlighting the existence of genetic diversity within the studied population.

Deepika *et al.* (2022) performed cluster analysis in 62 castor genotypes and grouped the genotypes into eight distinct clusters. The maximum inter- cluster distance was observed between Cluster VI and Cluster VIII, indicating high genetic divergence. Among all clusters, Cluster II exhibited the highest intra-cluster distance, suggesting greater variability within this group. Notably, Cluster VI recorded the highest mean values for 100-seed weight (44.56 g) and seed yield per plant (174 g), making it a promising cluster for selection in castor breeding programs.

Chandana *et al.* (b) (2025) assess 40 castor genotypes and grouped genotypes into six clusters. The highest inter-cluster distance was observed between Clusters IV and VI. The maximum contribution towards genetic divergence was recorded by number of effective spikes per plant followed by effective primary spike length, number of capsules per primary spike, total seed yield, final plantstand and 100 seed weight.

Canonical Root Analysis

Sakure *et al.* (2010) carried out Principal component analysis in 22 castor genotypes and noted that the first three principal components—PCA1 (18.09%), PCA2 (15.66%), and PCA3 (11.34%)—together explained 45.09% of the total variation. Among these, the most variation was contributed by five traits: bloom, spike length, seed colour, hypocotyl anthocyanin coloration, and number of nodes.

Goodarzi *et al.* (2012) carried out a principal component analysis (PCA) on 32 agro morphological traits of 12 Iranian castor bean accessions. The first six principal components had eigenvalues greater than one and together explained 93% of the total variation. The first principal component (PC1) explained 39.4% of the variation, PC2 explained 19.3%, and PC3 explained 13.3%. Seed number on the primary spike, an important yield trait, showed a positive correlation with PC1. Hollow seed number on the primary spike showed a positive correlation with PC2, while oil percentage showed a negative correlation with PC2.

Waluyo *et al.* (2019) studied 22 local castor accessions with two replications in Malang and used PCA to analyze morphological variation. The first three principal components (PC1, PC2, and PC3) explained 86.42% of the total variation. PC1 was strongly linked to capsule and seed size traits. PC2 was related to flowering time, harvesting time, plant height, and stem characteristics. PC3 was associated with inflorescence weight, seed number, and capsule number per plant.

Sadaiah *et al.* (2021) investigated a total of 82 castor germplasm lines for their genetic diversity. Through the PCA analysis, the genotypes were classified into eight distinct clusters, indicating the presence of substantial diversity within the population. Notably, Cluster VIII consisted of genotypes exhibiting the highest mean values for hundred seed weight and plant yield. These findings highlight the potential of Cluster VIII genotypes as valuable contributors to castor breeding program.

Deepak *et al.* (2024) evaluated thirty advanced and stabilized breeding lines of castor, including 15 monoecious and 15 pistillate lines, using a randomized block design (RBD) with three replications. The total genetic variation was analyzed using principal component analysis (PCA). Out of 11 principal components, the first four accounted for about 75.80% of the total variation in the dataset. PC1 explained 26.50%, PC2 explained 20.20%, PC3 explained 15.90%, and PC4 explained 13.20% of the variation. This result shows that the first four components are sufficient to capture most of the variability in the data.

Chandana and Durga Prasad (b) (2025) studied 40 castor genotypes using alpha lattice design. The data were analyzed using principal component analysis (PCA) through GRAPES software and indostat. six principal components were extracted based on mean values, out of which the first five showed a total variation of 85.85%, each having an eigenvalue greater than one. They identified the maximum contributing variables for diversity are *viz.*, number of capsules per primary spike, effective primary spike length, 100 seed weight, total seed yield.

CHARACTER ASSOCIATION AND PATH COEFFICIENT ANALYSIS

Patel *et al.* (2010) evaluated 41 castor genotypes to assess the correlation among nine traits. Their findings showed that seed yield per plant had a highly significant positive correlation with plant height, length of the primary spike, number of capsules on the primary spike, and the number of effective branches per plant.

Abimiku *et al.* (2012) evaluated the character associations between yield and its components across 14 traits in nine castor accessions. The results revealed that the number of spikes per plant, capsules per plant, panicle length, and number of branches showed a significant negative correlation with seed yield.

Ramanjaneyulu and Reddy (2012) conducted a study on correlation and path coefficient analysis in rabi castor. The results indicated that the number of effective spikes per plant, number of spikes per plant, primary spike length, nodes per plant, effective spike length, and number of branches per plant all showed positive direct effects, along with positive genotypic correlations with seed yield. Thus, direct selection for these yield-contributing traits could be beneficial for improving the yield of rabi castor grown under irrigated conditions.

Chaitanya *et al.* (2013) studied character association and path analysis among yield components in 30 castor genotypes. The results showed that 100-seed weight, oil yield per plant, effective length of the main spike, oil content, and number of spikes per plant had a significant positive correlation with seed yield per plant. Path analysis revealed that oil yield per plant, 100- seed weight, number of capsules on the main spike, number of nodes up to the main spike, and days to 50% flowering were the key direct contributors to seed yield in castor.

Tewari and Mishra (2013) studied the relationship between castor seed yield and eight agronomic traits across 30 castor genotypes. The results showed that genotypic correlations generally exhibited more significant differences between character pairs compared to phenotypic correlations. The number of effective spikes per plant and the number of capsules on the primary spike demonstrated the highest significant positive genotypic and phenotypic correlations with seed yield per plant. Path analysis revealed that the number of capsules on the primary spike had a strong positive and highly significant phenotypic direct effect on seed yield per plant.

Rukhsar *et al.* (2018) studied 15 castor genotypes for 13 quantitative traits. It was noted that genotypic correlations were stronger than the corresponding phenotypic correlations for most of the traits, including node position on the primary spike, number of capsules on the primary spike, seed yield per plant, plant height up to the primary spike, and 100-seed weight. Notably, seed yield per plant showed a significant positive correlation with the number of nodes on the primary spike at both the genotypic and phenotypic levels. A significant positive correlation between oil content and 100-seed weight was observed, suggesting that oil yield could be improved by selecting for higher 100-seed weight. Path coefficient analysis identified high direct effects from traits such as shelling percentage, total length of the primary spike, and number of capsules on the primary spike. These traits may play a direct role in enhancing seed yield.

Venkatachalam *et al.* (2019) found that the genotypic and phenotypic correlations were generally similar in magnitude, with genotypic correlations being slightly higher in most cases. The highest significant genotypic correlation was observed between seed yield per plant and the total number of spikes per plant. The total number of spikes had the largest positive total indirect effect, mediated by days to flowering, days to maturity, and primary spike length. Although days to flowering and days to maturity exhibited negative total indirect effects, these were minimal and had little practical significance.

Yamanura and Mohan Kumar (2020) studied 33 genotypes, which included 20 hybrids, 12 parents, and a check variety (ICH-66). Their findings indicated a high level of variability among the genotypes. Correlation analysis revealed a strong positive association between seed yield and several traits, including oil content, 100-seed weight, volumetric weight, number of capsules on the primary spike, effective length of the primary spike, total length of the primary spike and number of effective spikes per plant.

Oke *et al.* (2024) studied 74 castor germplasm accessions and found that Significant positive correlations between the seed yield and leaf length and spike length. The partitioning of the correlations into direct and indirect yield contributors showed positive direct effects for number of internodes to first spike, spike length and height to first spike. Further the findings revealed that selection for long spike early accessions could result in constituting a high yielding breeding population.

Chandana and Durga Prasad. (c) (2025) Studied 40 castor genotypes and found that plant height upto primary spike, effective primary spike length, number of capsules on primary spike and 100 seed weight displayed significant and positive correlation of total seed yield at both phenotypic and genotypic levels. This indicated possibility of simultaneous selection of all these characters for yield improvement.

CONCLUSIONS

The maximum gain yield during breeding depends upon estimates of variability parameters such as GCV, PCV, heritability and genetic advance as % of mean. The estimates of PCV & GCV for traits like number of effective spikes per plant, effective spike length, number of capsules on primary spike and seed yield. Moreover, heritability coupled with genetic advance is usually more informative. In castor, high heritability with high genetic advance as a percentage of the mean was observed for plant height, number of nodes, effective length of primary spike, number of capsules of primary spike clearly indicating the relevance of additive gene action and greater response to phenotypic selection and improvement of such traits could be anticipated. The correlation of the characters is clearly correlated due to a mutual association (positive or negative) with other characters. The yield invariably forms a positive or negative relationship with other traits. Due to the balancing of positive and negative contribution, a superficial association of a trait to yield may appear. As a result, path coefficient analysis seems to be a more effective method for use in selection.

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REFERENCES

Abimiku, O. E., Azagaku, E. D. and Ndor, E. (2012). Genetic variability and correlation studies in some quantitative characters in castor (*Ricinus cummunis* L.) accessions. *Asian Journal of Agricultural Sciences*, *4*(6), 368-372.

Alhaji, K. A., Oliseh, A., Salihu, B. Z. and Kabaraini, M. A. (2019). Studies on genetic variability and trait relationship in castor (*Ricinus communis* L.). *Journal of Plant Development*, *26*, 3-11.

Allan, G., Williams, A., Rabinowicz, P. D., Chan, A. P., Ravel, J. and Kein, P. (2008). Worldwide genotyping of castor bean germplasm (*Ricinus communis* L.) using AFLP's and SSR's. *Genetic Resources and Crop Evolution*, *55*(3), 365-378.

Anjani, K. (2012). Castor genetic resources: A primary gene pool for exploitation. *Industrial Crops and Products*, *35*, 1-4.

Benke, P. and Sakhare, S. (2012). Genetic divergence in castor. *Bioinfolet*, *9*(4), 784-786.

Bezerra, N. and Francisco, V. (2010). Quantitative descriptors to estimative genetic divergence in castor bean (*Ricinus communis* L.) genotype based on multivariate analysis. *Revista Ciência Agronômica*, *41*(2), 294-299.

Birchler, J. A., Auger, D. L. and Riddle, N. C. (2003). In search of the molecular basis of heterosis. *Plant Cell*, *15*, 2236-2239.

Chaitanya, S. K., Venkateswarlu, O., Sekhar, M. R and Reddy, B. V. B. (2013). Character association and path analysis among yield components in castor (*Ricinus communis* L.). *Journal of Oilseeds Research*, *30*(1), 74-76.

Chandana, K., Durga Prasad, A.V.S., Sabitha, N., Raghavendra, M. (2025). (a) Genetic variability studies in castor germplasm (*Ricinus communis* L.). *Biological Forum – An international Journal*, *17*(8), 75-79.

Chandana, K., Durga Prasad, A. V. S. (2025). (b). Multivariate Analysis of Genetic Divergence among Castor (*Ricinus communis* L.) Inbreds using Mahalanobis D2 Statistic. *Agricultural Sciences: Techniques and Innovations*, *4*, 101-110.

Chandana, K., Durga Prasad, A. V. S. (2025). (c). Correlation and Principal Component Analysis of Yield- Related Traits in Castor (*Ricinus communis* L.) Genotypes. *International journal of Plant and Soil science*, *37*(10), 328-336.

Chandana, K., Durga Prasad, A. V. S., Sabitha, N., Raghavendra, M. (2025). (a) Genetic variability studies in castor germplasm (*Ricinus communis* L.). *Biological Forum*, *17*(8), 75-79.

Chaudhari, D. R., Parmar, V. L., Dube, D. V., Bhakta, R. S., Patel, A. I. and Lodam, V. A. (2016). Genetic variability and divergence study in castor (*Ricinus communis* L.). *Advances in Life Science*, *5*(16), 6418-6422.

Dapke, J. S., Naik, M. R., Vaidya, G. B., Vanve, P. B., Narwade, A. V. and Rajkumar, A. K. (2016). Genetic variability in castor (*Ricinus communis* L.). *European Journal of Biotechnology and Bioscience*, *4*(4), 39-40.

De Oliveira, S. S., Zeffa, D. M., Sartori, M. M., Soares, D. J. and Zanotto, M. D. (2021). Genetic variability in Brazilian castor (*Ricinus communis* L.) germplasm assessed by morpho agronomic traits and gray mold reaction. *Anais da Academia Brasileira de Ciências*, *93*(3), 201-225.

Deepak, K. A., Manjunatha, T., Hemalatha, V. and Chary, D. S. (2024). Variability, Correlation Patterns and Principal Component Analysis (PCA) for Seed Yield and Contributing Traits in Castor (*Ricinus communis* L.). *Journal of Advances in Biology and Biotechnology*, *27*(8), 1217-1227.

Deepika, C., Venkatachalam, S. R., Yuvaraja, A., Arutchenthil, P., Indra, N., Ravichandran, V., Veeramani, P. and Kathirvelan, P. (2022). Seed morphological characterization, genetic diversity and association analysis in late flowering monoecious lines of castor (*Ricinus communis* L.). *Electronic Journal of Plant Breeding*, *13*(2), 574-583.

Destaw, M., Getinet, A., Petros, Y. and Alemu, S. (2017). Phenotypic variability and association of traits among yield and yield-related traits in Castor (*Ricinus communis* L.) accessions at Melkassa, Central Rift Valley of Ethiopia, *African journal of agricultural research*, *12*(52), 3562–356S8.

Elena, M. and Rodrguez, E. (2009). Study of the variability for racemes, fruits and seeds in castor bean (*Ricinus communis* L.) germplasm. *Revista Científica UDO Agrícola*, *9*(4), 764-769.

Galluzzi, G., Seyoum, A., Halewood, M., Lopez Noriega, I. and Welch, E. W. (2020). The Role of Genetic Resources in Breeding for Climate Change: The Case of Public Breeding Programmes in Eighteen Developing Countries. *Plants*, *9*(9), 1129.

Gangaiah, B. (2005). Agronomy Kharif Crops castor. (http://nsdl.nscair.res.in/bitstream/123456789/530/1/Castor++Form atted.pdf).

Gogoi, S. N., Sarma, R. N. and Rajan, R. K. (2011). Genetic diversity of castor (*Ricinus communis* L.). germplasm in north-East region of india. *Indian Journal of Sericulture, 9*(1), 60-62.

Goodarzi, F., Darvishzadeh, R., Hassani, A. and Hassanzaeh, A. (2012). Study on genetic variation in Iranian castor bean (*Ricinus communis* L.) accessions using multivariate statistical techniques. *Journal of medicinal plants Research*. 6(7), 1160-1167.

Govaerts, R., Frodin, D. G. and Radcliffe-Smith, A. (2000). World check list and bibliography of *Euphorbiaceae* (with *pandaceae*). *Redwood Books limited*, Trowbridge, Wiltshire, *13*, 1621.

INDIASTAT, (2023-2024). Agriculture Area and Crops Growth Statistics 2023, 2024 [online] Available at: <https://www.indiastat.com/data/agriculture> [Accessed 18 June 2024].

Lakshmamma, P., Lakshmi, P., Mohan, Y. C. and Lavanya, C. (2005). Genetic variability and character association in castor (*Ricinus communis* L.). *National Journal of Plant Improvement*, *7*(2), 122-126.

Lavanya, C., Manjunatha, T., Senthilvel, S. and Ramya, K. T. (2022). Genetic variability studies of major yield components in segregating population derived from pistillate lines of castor (*Ricinus communis* L.). *Journal of Oilseeds Research*, *39*(3), 174-178.

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

Movaliya, H. M., Chovatia, V. P., Madariya, R. B., Mungala, R. A., Pipaliya, H. R. and Bhuva, S. K. (2018). Study of variability and correlation for seed yield and its attributes in castor (*Ricinus communis* L.). *Journal of Pharmacognosy and Phytochemistry*, *7*(2), 1474-1477.

Muhammad, A., Khurshid, H., Siddiqui, S. U., Ahmad S. J., Ahmad, J. S., Ilyas, M., Khan, A. S., Khan, A., Muhammad, I. I., Noor, S. and Abdul, G. (2015). Estimating spatial population structure through quantification of oil content and phenotypic diversity in Pakistani castor bean (*Ricinus communis* L.) germplasm. *Science, Technology and Development*, *34*(3), 147-154.

Nagarajan, S. and Viswanathan, P. L. (2019). Genetic divergence analysis of castor (*Ricinus communis* L.). *Electronic Journal of Plant Breeding, 10*(2), 754-760.

Oke, C. O. (2024). Morpho-genetic Diversity and Traits Relationship in Castor Germplasm. *Badeggi Journal of Agricultural Research and Environment*, *6*(1), 64-76.

Omari, A., Mgani, Q. A. and Mubofu, E. B. (2015). Fatty acid profile and physico-chemical parameters of castor oils in Tanzania. *Green and Sustainable Chemistry*, *5*, 154-163.

Patel, J. R., M. P., Patel, C. G., Bhatt, R. K. and Bhatt, J. P. (2010). Genetic variability and correlation studies in castor (*Ricinus communis* L.). *International Journal of Agriculture Sciences, 6*(1), 129-131.

Patel, J. K. and Patel, P. C. (2014). Genetic Variability, Heritability and Genetic Advance for yield and yield components in castor genotypes. *International Journal of Plant Science*, *9*(2), 385-388.

Radhamani, T. and Ushakumari, R. (2013). Variability studies in castor germplasm accessions (*Ricinus communis* L.). *Asian Journal of Bio Science, 8*(1), 69-71.

Ramanjaneyulu, A. V. and Reddy, A. V. (2012). Studies on correlation and path coefficient analysis in rabi castor (*Ricinus communis* L.). *Research on Crops*, *13*(3), 1115-1118.

Ramesh, M., Lavanaya, C. and Rao, B. (2012). Genetic divergence in some indigenous and exotic germplasm lines of castor (*Ricinus communis* L.) under rainfed conditions. *Indian Journal of Dry land Agricultural Research and Development*, *27*(2), 79-83.

Reddy, P. S., Priya, P. B., Sadaiah, K., Vanisri, S. and Kumar, C. S. (2022). Genetic Variability and Character Association Studies among Yield Attributing Traits in Genepool Lines of Castor. (*Ricinus communis* L.). *Biological Forum – An International Journal*, *14*(2), 1277-1281.

Rodrigues, H. C., Carvalho, S. P. (2010). Assessment of genetic diversity among castor (*Ricinus communis* L.) through morphological characters. *Revista Ceres*, *57*(6), 773-777.

Rukhsar, M. P., Parmar, D. J. and Kumar, S. (2018). Genetic variability, character association and genetic divergence studies in castor (*Ricinus communis* L.). *Annals of Agrarian Science*, *16*, 143-148.

Sadaiah, K., Neelima, G., Rani, C. V. D., Rani, V. D., Madhuri, G., Nalini, N., Sujatha, M., Shankar, V. G., Kumar, M. P., Lavanya, C and Lal, J. J. (2021). Genetic parameters, diversity and character association studies in germplasm lines of castor (*Ricinus communis* L.). *Electronic Journal of Plant Breeding*, *12*(4), 1134-1141.

Sakure, A. A., HL, D., DR, M., RH, K., & RB, M. (2010). Genetic diversity analysis among castor (*Ricinus communis* L.) genotypes using morphological markers. *Crop Improvement*, *37*(2), 99-104.

Sarwar, G. and Chaudhry, M. B. (2008). Evaluation of castor (*Ricinus communis* L.) induced mutants for possible selection in the improvement of seed yield. *Spanish Journal of Agricultural Research*, *6*(4), 629-634.

Sarwar, G., Ahmed, H. M. and Hussain, J. (2010). Evaluation of castor bean (*Ricinus communis* L.) mutants for genetic parameters and cluster analysis, *48*(3), 289-300.

Sevugaperumal, S., Rangasamy, P. and Muppidathi, N. (2000). Genetic variability, correlation and path coefficient analysis in castor (*Ricinus communis* L.). *Madras Agricultural Journal*, *86*(7/9), 456-459.

Shaw, R. K., Shaik, M., Mir, Z. A., Prasad, M. S. L., Prasad, R. D. and Senthilvel, S. (2017). Establishing a high throughput screening method for large scale phenotyping of castor genotypes for resistance to Fusarium wilt disease. *Phytoparasitica*, *44*(4), 539-548.

Shifriss, O. (1960). Conventional and unconventional systems controlling sex variations in Ricinus. *J. Genet.*, *57*, 573-578.

Silva, S. A., Simoes, K. S., Machado, E. L and Silva, M. S. (2017). Genetic divergence in elite castor bean lineages based on TRAP markers. *Genetics and Molecular Research*, *16*(3), 1-12.

Singh, D. (1976). Castor (*Ricinus communis* L.) (Euphorbiaceae). In: Simmonds N. W., editor. Evolution of Crop Plants. London: Longman. 84-86.

Tewari, N. and Mishra, A. (2013). Correlation and path coefficient analysis of castor (*Ricinus communis* L.) in non-traditional area of central Uttar Pradesh. *International Journal of Genetic Engineering and Biotechnology*, *4*(1), 1-9.

Torres, F. E., Teodoro, P. E., Ribeiro, L. P., Correa, C. C. G., Hernandes, F. B., Fernandes, R. L., Gomes, A. C. and Lopes, K. V. (2015). Correlations and path analysis on oil content of castor (*Ricinus communis* L.) genotypes. *Bioscience Journal*, *31*(5), 1363-1369.

Venkatachalam, S. R., Nagarajan, S., Viswanathn, P. L., Manickam, S. and Ganpathi, N. (2019). Correlation and path coefficient analysis in castor (*Ricinus communis* L.). *International Journal of Pure and Applied Biosciences*, *7*(3), 230-233.

Waluyo, B., Shandila, P., Zanetta, C. U., Saptadi, D. and Ardiarini, N. R. (2019). Character selection by path and principal analysis for enhanced seed size and yield in local castor bean (*Ricinus communis* L.). In *IOP Conference Series: Earth and Environmental Science*, *391*(1), 12062.

Weiss, E. A. (2000). Castor oilseed crops. Oxford, U.K., Blackwell Sciences, 13-52. Wright, S. (1921). The methods of the path coefficients. *The Annals of Mathematical Statistics*, *5*(3), 161-215.

Yamanura, M. and R. Mohan Kumar (2020). Study of genetic variability, path coefficient and genetic diversity in castor (*Ricinus communis* L.). *The Pharma Innovation Journal*, *9*(8), 285-292.

Zheng, L., Qi, J. M., Fang, P. P., Su, J. G., Xu, J. T. and Tao, A. F. (2010). Genetic diversity and phylogenetic relationship of castor as revealed by SRAP analysis. *Wuban Zhiwuxue*, *28*, 1-6.

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