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Research Article

Genetic analysis of diverse castor (*Ricinus communis* L.) genotypes based on seed related morphometric traits

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Abstract
Diverse source of early genotypes is obligatory for breeding high yielding early castor (*Ricinus communis* L.) cultivars. One hundred and twenty-five medium duration genotypes including three checks were evaluated for the presence of genetic diversity and variability. Genetic distance, variance components and correlation coefficients were estimated for seven seed related quantitative traits. Significant genotypic differences were observed among the collections for these traits. High heritability and high genetic advance were noticed for seed length, seed breadth, Length/Breadth ratio, shelling percentage, 100 seed weight and seed yield per plant, thus mode of gene action reported was additive. Genetic diversity analysis based on dendrogram, phenogram and circular form grouped the entries into seven groups and it computed inter and intra cluster distance. Principal Component Analysis (PCA) revealed that the first three components cumulatively accounted for 72.57 per cent of the total variation. Seed yield per plant showed a significant association with shelling percentage and 100 seed weight. Also, direct effects were high and positive through seed breadth, Length/Breadth ratio and 100 seed weight. The promising genotypes identified (ICIRG 2272103 and RG 1673) and the information generated would be useful for breeding early/medium cultivars as well to understand the physiological mechanism related to earliness in castor.

Keywords: Castor, Multivariate analysis, Correlation, Genetic diversity, Variability

INTRODUCTION

Castor (*Ricinus communis* L., 2n = 2x = 20) is an economically valuable non-edible oilseed crop which was once called as a wasteland colonizer but gained importance because of the commercial significance of its seed oil. Although generally known as “castor bean”, this plant is not a legume (Weiss, 2000). It is utilized as a raw material in the industrial sector and also as a medicine and biodiesel (Anjani *et al.,* 2014). World’s major producing countries are India (18.42 lakh tonnes), Mozambique (0.85 lakh tonnes), China (0.27 lakh tonnes), Brazil (0.14 lakh tonnes) and Myanmar (0.12 lakh tonnes). India meets more than 80% of the demand of castor oil, thereby enjoying a dominant position in the World Castor scenario (Source: www.agriwatch.com). It is grown in arid and semi-arid regions of the world experiencing erratic rainfall and could thrive well in low fertile soils with minimum input

(Milani and Nobrega, 2013). The importance of castor oil lies in the fact that it is the only commercial source of ricinoleic acid, a hydroxylated fatty acid (Severino *et al.*, 2012). Greater variation was reported among the castor genotypes for morphological traits *viz*., sex expression, seed color, bloom type, stem color etc., (Milani and Nobrega, 2013) because of the cross-pollinated nature of the crop. Among the phenotypic traits, seed related traits are important in the correct identification of genotypes among the larger collection and for maximizing the seed yield. Seed oil content is very high ranging from 48 to 60 per cent (Brigham, 1993) but it is cumbersome to improve the oil content beyond a certain limit. Besides, castor oil manufacturers in India can extract 45 to 46 per cent of the oil content. The rest oil content retains with the cake residues. Also augmenting seed oil percentage needs an advanced biotechnological procedure. Hence, the best imperative method to improve overall production is to increase the seed yield.

Castor cultivars are classified as early (< 45 days), medium (45 to 65 days), late (66 to 85 days) and very late (>85 days) based on days to 50 % flowering available on standard Distinctiveness, Uniformity and Stability (DUS) guidelines on castor by Protection of Plant Varieties and Farmer's Rights Authority, Govt. of India (PPV & FRA, 2012) (https://www.plantauthority.gov.in/crop-dus-guidelines). Castor cultivars are also classified as early (120 to 140 days), medium (140 to 160 days) and late (>160 days) maturity types based on the maturity of primary raceme (Weiss, 1983; Atsman, 1989). Castor is mainly grown as a six–eight months duration crop. Moisture stress occurs at around 60 to 65 days after planting that coincides with flowering and capsule formation stages in the castor. Water deficit during the productive phase decreases the yield in any crop. Early/medium maturing cultivars prevent the crop from facing moisture stress during the productive phase. Castor seed development was defined by Moshkin (1986) using four phases (i) formation of capsules and seeds(ii) milky (iii) waxy and (iv) complete ripeness. The duration between these phases should not be reduced to attain proper physiological maturity and hence the better way to breed early varieties is to select the parents with less duration in the vegetative phase with early flowering. Longer duration and lower productivity make them unfit for commercial cultivation and hence the prime objective of castor breeding is to develop varieties with early seed maturation and increased yield (Milani and Nobrega, 2013). Hence, the promising option would be the breeding of early to medium flowering and maturing varieties without compromising yield as it lessens water and input use and makes the crop to fit in multiple cropping systems.

Castor is normally a monoecious crop with pistillate flowers on the upper part and staminate flowers on the lower part. Length of female flowers is higher in first order raceme and with the development of subsequent racemes, the staminate portion increases (Zimmerman and Smith, 1966). With the increase in age of the crop and temperature, the male tendency is more (Shifriss, 1956), thus lowering the productivity. Growth habit of the crop ranges from indeterminate annual to perennial shrub depending on climatic zones and soil types. In India, it is cultivated as an annual crop with a growing period of 5 to 6 months to set fruits and maturity and harvest eventually taking another 2 to 3 months (Anjani *et al.,* 2014). In India, the best season for castor cultivation is during *Kharif* (June-July). When varieties with longer duration are sown during the month of June - July, the first harvesting would be done during December – January. The climatic conditions after the first harvest would be unfavorable and not appreciable for commercial cultivation. Also, the interval between subsequent racemes initiation would be longer and there will not be overlapping of growing racemes thus increasing the crop duration and inputs (Severino and Auld, 2013) without a substantial increase in yield levels. Longer duration indeterminate growth habit of castor makes cultivation and harvesting would be carried out throughout the year. Thus, it does not fit well with the cropping system like cereals and pulses. Also, the late order spikes are small, yielding lower compared to the primary and secondary spikes because of the increase in ratio of male flowers throughout the inflorescence. Harvesting is done at multiple pickings up to four (Anjani, 2010) which ultimately increases the cost of labor. For conventional castor production, manual labor has become scarce and expensive and early/ medium flowering varieties/genotypes can address this issue to some extent by minimizing the pickings which will be the added advantage of breeding early/medium maturing cultivars (Yin *et al.,*2019). Genetic diversity and variability are intrinsic and powerful tools in the hands of plant breeders. Studies on genetic diversity utilizing the available germplasms and monoecious lines are necessary to elucidate and categorize the naturally existing variability. Selection of superior varieties or cultivars will be possible only when adequate variability exists in the gene pool. Hence, the insight into the magnitude of variability present in a gene pool of a crop species is of utmost importance for castor genetic improvement. Literatures on castor diversity analysis are few and scarce (Anjani, 2010; Kanti *et al.,* 2015; Senthilvel *et al.,* 2017; Dapke *et al.,* 2016; Ranjitha *et al.,* 2019; Cherukupalli and Mukta, 2021). The study would offer immense value in generating information for castor yield improvement. In this regard, the current study was undertaken to assess the extent of genetic diversity, variability and association among the medium flowering genotypes of castor based on seed related morphometric traits and to generate a data repository to be used in further castor breeding programmes.

MATERIALS AND METHODS

Plant material for the experiment was selected based on days to 50 % flowering and 125 medium flowering castor

genotypes which are monoecious lines, germplasms, inbreds and varieties were raised in Randomized Block Design with two replications. Traditionally, castor is grown as a *Kharif* crop. However, with the introduction of new, early and high yielding varieties and hybrids, its cultivation is extended to *Rabi* and summer seasons. Also, due to the effect of monsoon and heavy rain during *Kharif* 2020, the research was carried out in the experimental farm at Tapioca and Castor Research Station (TCRS), Yethapur during *Rabi* 2020. The research station was located within the geographical coordinates 11º 35′ N latitude and 78º 29' E longitude and at an altitude of 282 meters above mean sea level. Field preparation was done as per the improved cultivation method and fertigation measures had been taken at appropriate intervals. Agronomic management practices and crop protection measures were properly followed during the entire growth period. Seven quantitative traits were observed *viz.,* days to 50 % flowering (days), seed length (cm), seed breadth (cm), Length/Breadth ratio, 100 seed weight (g), shelling outturn (%) and seed yield per plant (g). Genetic diversity among 125 castor genotypes was assessed using cluster analysis and PCA. Cluster analysis was performed based on Euclidean distance using the Ward method, inter and intra cluster distance were computed. In order to find out the more significant set of variables, PCA was performed and eigen values and percentage of variance contributed by each PCs were calculated. Basic descriptive statistics (including mean, standard error, minimum value, maximum value, coefficient of variation, standard deviation, skewness and kurtosis) were determined using R software version 4.1.1. Genetic variability estimates, heritability and genetic advance which are the selection parameters for augmenting yield were also analyzed. Classification of PCV and GCV were done as suggested by Sivasubramanian and Madhavamenon (1973). Heritability and genetic advance over mean were categorized as given by Johnson *et al.* (1955). Castor genotypes were subjected to Pearson's correlation analysis to determine the relationship between the traits and in order to unravel the true picture of association, path analysis was also done supporting correlation.

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among the genotypes (**Table 1**). Developing early/medium flowering and maturing cultivars has been historically a demand in castor breeding programs (Anjani, 2010; Passos *et al.,* 2010; Severino *et al.,* 2012; Solanki and Joshi, 2000; Sridhar *et al.,* 2010). Development of high yielding early cultivars is a challenge as early flowering and maturity are generally associated with lower productivity (Anjani, 2010). In regions with short growing seasons or in tropical areas, early maturity is a valuable trait that suits well for multiple cropping systems (Yin *et al.,* 2019). Duration for reproductive growth should not be reduced to ensure proper seed filling and hence, vegetative growth must be condensed while concentrating on earliness breeding. The major obstacle in breeding early/medium maturing genotypes is the presence of a negative correlation between maturity duration and seed yield (Yin *et al.,* 2019). Although the flowering time of castor can be influenced by temperature and other cultivation factors like water, nutrients, etc., it is mainly determined by a genetic factor (Yin *et al.,* 2019). The experimental material consisted of germplasm accessions, inbreds and monoecious lines which were all developed with a common genetic background of Indian origin. Kernel L/B ratio, 100 seed weight and shelling percentage had an influence over the total seed yield per plant (Yu *et al.,* 2019). Studies on variability and diversity based on seed related metric traits aids in the selection and indirect yield improvement. Hence, it is imperative to understand the genetic mechanisms behind the early/medium flowering genotypes in castor. This eventually enhances the seed yield among the early/medium maturing cultivars for making them suitable to climate resilience breeding.

Estimates like a mean sum of squares, measures of dispersion (standard deviation, standard error) and higher order statistics (skewness and kurtosis) are given in **Table 1**. Skewness was positive and significant for 100 seed weight, shelling percentage and seed yield per plant. Peakedness was positive and significant for days to 50 % flowering which was termed leptokurtic. Positive

Table 1. Analysis of variance (ANOVA) and descriptive statistics for seven seed related quantitative traits of 125 medium flowering castor genotypes

Trait	MSS	Mean	SE	SD	Skewness	Kurtosis
Days to 50 % flowering	6.26 **	57.15	0.32	3.53	-0.14	2.32 *
Seed length	0.02 **	1.17	0.01	0.13	0.23	2.42
Seed breadth	0.01 **	0.68	0.01	0.09	0.12	2.36
Length/Breadth ratio	0.04 **	1.73	0.02	0.19	0.19	2.52
100 seed weight	48.35 **	30.91	0.60	6.68	0.47 *	3.01
Shelling percentage	121.19 **	62.74	0.97	10.82	0.47 *	3.65
Seed yield per plant	1857.5 **	111.55	3.83	42.83	0.79 **	3.23

* P <= 0.05; ** P <= 0.01

MSS – Mean sum of square; SE – Standard Error; SD – Standard deviation

skewness indicated complementary gene action for 100 seed weight, shelling percentage and seed yield per plant. For days to 50 % flowering, the population was leptokurtic (very peaked with positive value). Dhanalakshmi *et al.* (2018) reported skewness and kurtosis for different traits in castor. For the traits with positive skewness and leptokurtic curve, the genetic gain would be exploited by intense selection. The phenotypic coefficient of variance (PCV), Genotypic coefficient of variance (GCV), Broad sense heritability (h^2), Genetic advance (GA) and Genetic advance as per cent of mean (GAM) was computed and presented in **Table 2**. For most of the traits, PCV and GCV were of the medium category whereas h^2 and GAM were high. For days to 50 % flowering, high heritability and medium GAM was observed. The results indicated the existence of sufficient variation among the genotypic collection. Greater PCV values indicated the influence of the environment on different traits. High heritability and high genetic advance were noticed for most of the traits, thus a mode of gene action noticed was additive. Thus, for those traits selection of genotypes may be effective. Variability studies in castor had been reported by Patel and Patel (2014), Priya *et al.* (2018), Alhaji *et al.* (2019), Nagarajan *et al.* (2019), Ilo *et al.* (2020) and Cherukupalli and Mukta (2021).

An illustration on cluster analysis using seed related traits is given in **Fig. 1**. Cluster size and membership

Table 2. Genetic variability estimates for 125 medium flowering castor genotypes

Trait	GCV (%)	GCV category	PCV (%)	PCV category	h^2 (%)	h^2 category	GA	GAM	GAM category
Days to 50 % flowering	6.08	Low	6.13	Low	98.64	High	7.12	12.47	Medium
Seed length	10.66	Medium	10.76	Medium	98.11	High	0.25	21.77	High
Seed breadth	13.27	Medium	13.3	Medium	99.44	High	0.19	27.29	High
Length/Breadth ratio	10.52	Medium	10.75	Medium	95.65	High	0.37	21.22	High
100 seed weight	19.67	Medium	21.2	High	86.1	High	11.64	37.66	High
Shelling percentage	17.12	Medium	17.32	Medium	97.79	High	21.92	34.93	High
Seed yield per plant	38.63	High	38.73	High	99.45	High	88.65	79.47	High

PCV - Phenotypic coefficient of variance; GCV - Genotypic coefficient of variance; h^2 - Broad sense heritability; GA - Genetic advance and GAM - Genetic advance as percent of mean.

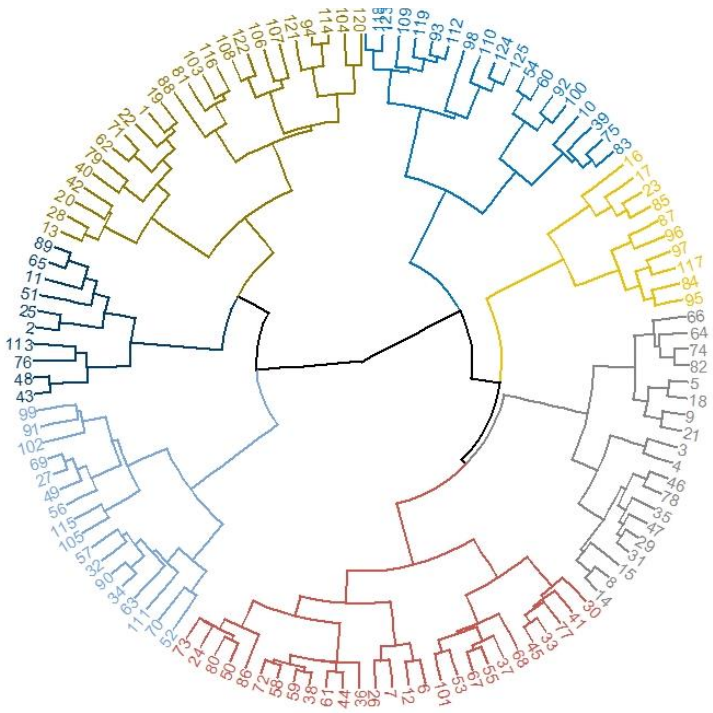

Fig. 1. Circular form of clustering showing the grouping of 125 castor genotypes

were computed and presented in **Table 3**. C4 was the largest cluster with 27 members and C2 and C6 were the smallest with 10 members each. Cluster mean for days to 50 % flowering was low in C1. The genotypes present in C1 are regarded as early flowering and maturing. Regarding the cluster mean values, 100 seed weight and seed yield per plant varied significantly in C3 compared to other clusters (**Table 4**). Cluster distance was maximum in C1, whereas within cluster distance was minimum in C3. Hence, the genotypes present in C1 and C3 could be utilized efficiently in the hybridization programme for developing high yielding heterotic gene pool. C2 and C6 were distantly placed (5.4091) and C4 and C3 were placed close to each other (2.9452) (**Table 5**). Cluster analysis grouped the genotypes based on genetic distance between them and genotypes from diverse clusters could be chosen as parents during the hybridization programme to reap maximum heterosis. On par with Anjani (2010), the results revealed that the cluster formed were irrespective of the geographical origin of the genotypes. The distribution of 125 castor genotypes into seven diverse clusters is indicative of the presence of considerable diversity among these medium flowering collections. This suggests that the generation of additional variability would be possible by inter mating the genotypes from different clusters for which characters need to be mentioned.

PCA revealed maximum variation (34.10%) in the first principal component (PC1) (**Table 6**). The first PC had seed length, seed breadth and 100 seed weight as traits with the highest loadings. The second component accounted for 20.44 per cent variability with the trait Length/Breadth ratio. The PC3 accounted for 18.02 per cent and contributed by shelling percentage whereas days to 50% flowering possessed high loadings in the fourth PC (PC4). Multivariate analysis (PCA) of the genotypic collection revealed that the first three PCs (PC1 to PC3) were separated by Eigen-values >1 and cumulatively accounted for 72.57 per cent of the total variation. The two-dimensional ordination of all the individuals grouped based on their relative contribution to overall variations along with the vectors of the studied traits to assess the relationship between them is given in **Fig. 2**. PCA biplot depicted that the genotype ICIRG 2272103 (98) was well separated from the other and was placed in

Table 3. Cluster size and grouping of 125 medium flowering castor genotypes

Cluster No	Cluster size	Cluster membership
C1	24	GP 674, JI 335, GP 672, SKI 304, MI 173, DCS 105, 48-1, GP 5002, MI 156, SKI 215, MI 200, ICIRG 155, MI 172, GPRG 3748, ICIRG 2612314, GP 680, MI 202, GPJI 415, GPJI 380, MI 210, MI 151, MI 211, GPJI 409, JI 319
C2	10	JC 8, MI 149, RAJASTHAN LOCAL, MCI 11, YTP 1, RG 1673, RG 1608, P 3290, GPRG 297, RG 2787
C3	19	GPJI 356, GPRG 43, GP 699, MI 224, MI 175, MI 169, RG 2819, GP 783, TMV 5, ICS 157, MI 201, MI 221, ICS 154, MI 197, MCI 8, JI 35, SKI 301, RG 392, MCI 3
C4	27	JI 397, TMV 6, MI 180, ICS 186, DCS 85, GPJI 361, GP 471, RG 18, GPJI 346, RG 2722, ICIRG 8982, MI 229, JC 10, RG 2364, RG 1771, ICS 182, SKI 352, MCI 7, GP 568, TNPT 4, JI 330, GP 752, ICIRG 668251, RG 22, MI 170, RG 2104, GP 729
C5	18	GPRG 4713, GP 759, GP 705, GP 487, GPRG 1258, DCS 106, ICIRG 2272103, GP 493, MI 167, MI 168, RG 2822, JI 220, DCS 9, ICIRG 2262962, RG 72, MI 232, GP 789, ICIRG 2262972
C6	10	MI 223, MI 225, RG 1941, ICIRG 1876213, ICIEEGP 6315, ICIRG 261457, ICIRG 1727156, ICIRG 8983, ICIEEGP 7314, MI 230
C7	17	RG 3160, GP 526, MI 152, DCS 107, ICS 161, JC 3, SKI 335, RG 2818, GPSKI 271, ICIRG 27461, RG 1624, ICIRG 27871529, JC 12, GPJI 4262, GPRG 3561, GPJI 378, ICIRG 28004

Table 4. Cluster mean for six quantitative traits for seven clusters

Cluster number	Days to 50 % flowering	Seed length (cm)	Seed breadth (cm)	Length/ Breadth ratio	100 seed weight (g)	Shelling percentage	Seed yield per plant (g)
C1	53.913	1.037	0.573	1.816	25.865	61.917	104.939
C2	61.250	1.048	0.640	1.645	25.206	57.760	83.419
C3	58.235	1.252	0.745	1.692	38.324	59.624	192.912
C4	56.150	1.326	0.700	1.908	35.517	56.248	95.500
C5	57.455	1.191	0.627	1.904	26.955	84.038	140.118
C6	61.636	1.220	0.767	1.595	30.364	69.337	90.955
C7	55.593	1.163	0.744	1.568	32.400	61.810	91.477

Table 5. Inter and intra cluster distance for seven clusters formed using 125 medium flowering castor genotypes

	C1	C2	C3	C4	C5	C6	C7
C1	2.8014	3.7643	3.8552	3.1316	3.5769	3.9755	3.8531
C2		2.7087	5.1909	3.6221	4.6730	5.4091	3.9723
C3			2.0493	2.9452	3.2825	3.5561	4.6133
C4				2.1894	3.2677	3.5526	3.6196
C5					2.5898	4.5230	4.6194
C6						2.5333	4.3954
C7							2.6798

Table 6. Principal Component Analysis (PCA) of 125 medium flowering castor genotypes

	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Days to 50 % flowering	0.0602	-0.1876	0.3350	**0.9192**	-0.0240	-0.0577	0.0064
Seed length	**0.5194**	0.3266	-0.2134	0.1289	-0.3554	0.3821	-0.5376
Seed breadth	**0.5840**	-0.2799	0.0933	-0.1181	-0.1562	0.3176	0.6578
Length/Breadth ratio	-0.2064	**0.6834**	-0.3371	0.2685	-0.1624	0.0086	0.5274
100 seed weight	**0.5547**	0.1551	-0.1136	-0.0093	0.1515	-0.7951	0.0078
Shelling percentage	-0.0784	0.2576	**0.6842**	-0.2209	-0.6038	-0.2146	0.0028
Seed yield per plant	0.1704	0.4715	0.4888	-0.0591	0.6594	0.2673	-0.0031
Eigenvalue	**2.3871**	**1.4309**	**1.2616**	0.9443	0.6563	0.3158	0.0041
Percentage of variance	34.1008	20.4415	18.0229	13.4905	9.3753	4.5110	0.0581
Cumulative percentage of variance	34.1008	54.5423	72.5652	86.0557	95.4310	99.9419	100

Highly loaded variables of values >0.5 and eigen values >1 given in bold

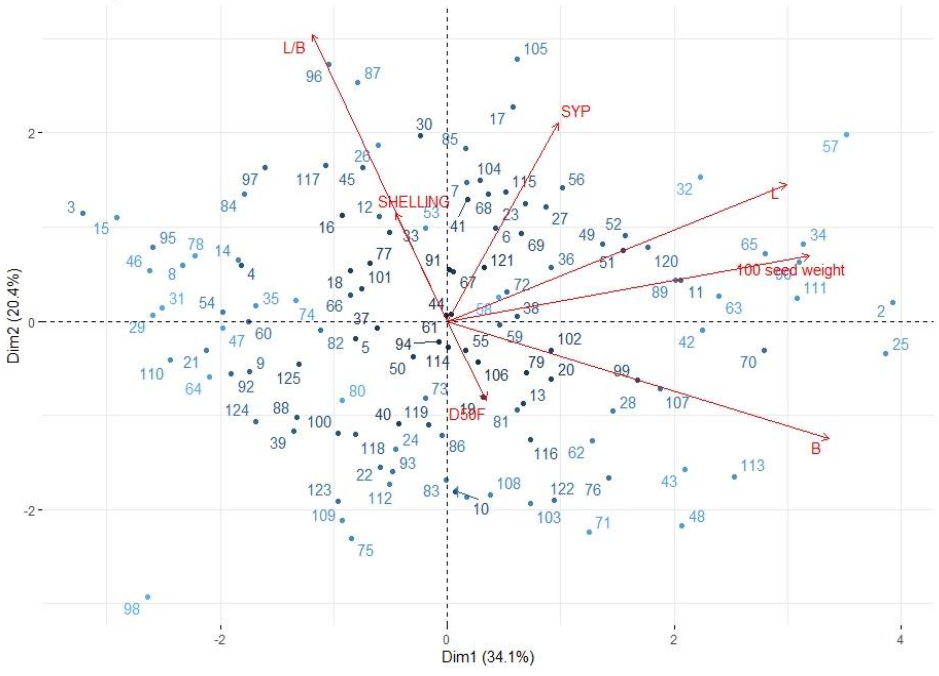

Fig. 2. PCA biplot with vectors of traits and scatter of castor genotype

the lower left portion whereas YTP 1 and RG 1673 (2 and 25) were present on the right corner. The results supported the findings from the cluster analysis that the two genotypes were placed in the same cluster (C2). Also, these genotypes contributed much to the variability which was indicated in light blue in the graph. From PCA, PC1 revealed the maximum variation (34.10 %) and it classified the genotypes based on seed size and weight. PCA analysis indicated that seed size, weight and shelling percentage were the most important descriptors which accounted for more than 50 per cent of the morphological variation expressed among the genotypic collection. Hence, seed related traits especially seed size and weight is important in distinguishing various genotypes of castor. These descriptions from PCA will assist in recording the variability among the castor genotypes.PC1 to PC3 were separated by Eigen-values >1 and cumulatively accounted for 72.57 per cent of the total variation. The high degree of variation reported in the first three PC axes indicates a high degree of variation for these seed related characters. PCA confirmed the results obtained from cluster analysis. PCA aims in determining the most significant character in the data set (Khadivi-Khub *et al.,* 2013). Besides, associations between traits revealed by the vectors of angle emphasized by this method may correspond to the genetic linkage between loci controlling traits or a pleiotropic effect (Rakonjac *et al.,* 2010; Khadivi-Khub *et al.,* 2012). The genotypes identified from the study would be further exposed to genotyping studies to understand the duration behind flower initiation, raceme development, seed filling and seed maturation to breed early varieties/hybrids.

The genotypic correlation coefficient was calculated for seven quantitative traits in 125 medium flowering genotypes to gain knowledge on association patterns among these traits and is presented in **Table 7**. Seed yield per plant exhibited a very high significant association with shelling percentage and high significance with 100 seed weight. Similarly, significant associations were found among seed length, seed breadth, Length/Breadth ratio and 100 seed weight but the Length/Breadth ratio showed a negative significant association with seed breadth. Correlation among seed length and breadth improves the seed weight thereby increasing the yield. Intercorrelation observed among those traits will indirectly influence the seed yield through selection. To get further insights into a true relationship, the correlation coefficient was divided into direct and indirect effects and is presented in **Table 8**. Path analysis inferred direct effects were high and positive through seed breadth, Length/Breadth ratio and 100 seed weight whereas it was negative and high through seed length. The negative association of seed breadth with the Length/Breadth ratio might be attributed due to moderate

Table 7. Pearson's correlation coefficients for seven seed related biometrical traits

Trait	Days to 50 % flowering	Seed length	Seed breadth	Length/ Breadth ratio	100 seed weight	Shelling percentage	Seed yield per plant
Days to 50 % flowering	1.0000	0.0073	0.0926	-0.1201	-0.0059	0.0304	0.0380
Seed length		1.0000	0.6271***	0.2246*	0.6585***	-0.0730	0.1713
Seed breadth			1.0000	-0.6122***	0.6036***	-0.0670	0.0720
Length/Breadth ratio				1.0000	-0.0940	0.0073	0.0847
100 seed weight					1.0000	-0.1489	0.2592**
Shelling percentage						1.0000	0.2967***
Seed yield per plant							1.0000

* p < 0.05; **p < 0.01; ***p<0.001

Table 8. Direct (diagonal) and indirect effects (off-diagonal) of seed related traits on seed yield per plant

Trait	Days to 50 % flowering	Seed length	Seed breadth	Length/ Breadth ratio	100 seed weight	Shelling percentage	Correlation value for seed yield per plant
Days to 50 % flowering	**0.0503**	-0.0025	0.0289	-0.0470	-0.0023	0.0105	0.0380
Seed length	0.0004	**-0.3393**	0.1953	0.0878	0.2522	-0.0252	0.1713
Seed breadth	0.0047	-0.2128	**0.3114**	-0.2394	0.2312	-0.0231	0.0720
Length/Breadth ratio	-0.0060	-0.0762	-0.1907	**0.3910**	-0.0360	0.0025	0.0847
100 seed weight	-0.0003	-0.2234	0.1880	-0.0367	**0.3830**	-0.0514	0.2592**
Shelling percentage	0.0015	0.0248	-0.0209	0.0029	-0.0570	**0.3454**	0.2967***

Residual effect : 0.2011

negative indirect effects of seed breadth through the Length/Breadth ratio. 100 seed weight exhibited negative moderate indirect effects on seed yield per plant through seed length. Hence, these traits may be directly/indirectly attributed for augmenting total seed yield and aids the breeders to select superior high yielding genotypes in the castor.

The plant material identified would be useful to breeders as a high yielding early/medium parental line and to modify the breeding programmes aimed at developing early/medium maturing cultivars. Genetic diversity existing among 125 medium genotypes is encouraging to create variability for desirable traits by intercrossing them from diverse clusters. The present study also revealed that components of variance, coefficient of variations and heritability obtained could serve as a potent guide for further improvement of castor. The advances in castor improvement are possible through the selection of genotypes with high 100 seed weight and seed yield per plant which showed high values of GCV and PCV coupled with high heritability. Correlation analysis revealed a significant positive correlation between shelling percentage, 100 seed weight and seed yield while a negative correlation was evident between 100 seed weight and days to 50% flowering. Therefore, these traits had to be given due weightage while selecting genotypes for breeding towards earliness and augmenting seed yield. The genotypes ICIRG 2272103 and RG 1673 were notable and can serve as parental lines for earliness coupled with high seed yield in crossing programmes. The accessions RG 1673 and RG 2818 had high 100 seed weight and the seed yield was high in JC 12, RG 3160, GP 526, JC 3, GPJI 378, ICIRG 28004, GPSKI 271 and ICIRG 27461. These genotypes can be used to develop respective trait specific gene pools. They may also be useful for understanding the basic and key physiological aspects pertaining to early flowering and maturity in castor.

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