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Yamanura

All India Co-ordinated Research Project on Castor, Zonal Agricultural Research Station, University of Agricultural Sciences, GKVK, Bengaluru, Karnataka, India

R Mohan Kumar

All India Co-ordinated Research Project on Castor, Zonal Agricultural research Station, University of Agricultural Sciences, GKVK, Bengaluru, Karnataka, India

Study of genetic variability, path coefficient and genetic diversity in castor (*Ricinus communis* L.)

Yamanura and R Mohan Kumar

Abstract

An investigation on genetic variability of castor through multivariate analysis was undertaken at All India Co-ordinated Research Project on Castor, Zonal Agricultural research Station, University of Agricultural Sciences, GKVK, Bengaluru during *khari*f 2019-20. This study involved 33 genotypes [20 hybrids, 12 parents and a check (ICH-66)]. The outcome of the study indicated the existence of high degree of variability among the study materials. High heritability coupled with high combining ability were noticed for the characters such as days to 50% flowering, days to maturity, plant height to primary raceme, nodes counts to primary spike, volume and seed weight, effective spikes numbers and seed yield. Further, correlation analysis indicated the strong and positive association between seed yield and oil content (0.717**), hundred seed weight (0.679**), hundred volume weight (0.527**), number of capsules per primary raceme (0.443**), effective length of primary spike (0.245**), total length of primary spike (0.216*) and number of effective spikes per plant (0.012). The residual effect was 0.73 and 0.63 at phenotypic and genotypic level, respectively in the present investigation. Thus, present study also indicated the influence of some extraneous traits associated with seed yield in castor in addition to yield attributing factors indicated in this study.

Keywords: Castor, correlation, genetic diversity, genetic advance, heritability and path analysis

Introduction

Castor (*Ricinus communis* L.) is the oldest non-edible oilseed crop recently turned out to be an important commercial crop of tropical, sub-tropical and warm temperate part of the world (Weiss, 2000) [30]. It is being cultivated in about 30 diverse countries on saleable scale, among these India, Brazil, China, Russia, Thailand and Philippines are the most vital castor growing countries. India is world leader in area, 12.2 lakh tonnes of castor is being produced from 7.62 lakh ha with an average yield of 1.6 t ha⁻¹ (ICAR-IIOR 2020) [10]. The seeds of castor contain about 40 to 60 per cent oil that is rich in triglycerides, principally *ricinolein*. Castor oil has great industrial value as it is used for the makeup of soaps, refined and perfumed hair oil, printing inks, varnishes, synthetic resins, carbon paper, lubricant, ointments, cosmetics and processed leather. India blessed with huge land mass of ideal tropical conditions for castor crop (Naidu *et al.*, 2015) [16] and is one of the biggest producers of castor seed (Yamanura and Kumar, 2019). The productivity of castor in India is also high as compared to other countries (ICAR-IIOR 2020) [10]. However, there is a great scope and huge responsibility on India to produce and meet out the global demand of castor (Yamanura and Kumar 2019). Castor largely being a rainfed crop in the vagaries of climate change the seed yield in castor is directly or indirectly influenced by several factors, out of which sex expression *i.e.*, percent pistillate whorls is very important (Aher *et al.*, 2015) [1]. Castor being the highly cross-pollinated species with peculiar sex mechanism, there is a need for development of stabilized cultivars for commercial cultivation with higher femaleness. Therefore, tapping the opportunity of heterosis exploitation is order of the day to enhance yield per unit area in castor. Yield is a complex character which depends upon many determining traits hence, the information on degree of association between yield and its component character is prerequisite for crop improvement. Hence, a study of genetic variability of seed yield and its components characters among available germplasm provides a strong basis for selection of desirable genotypes for augmentation of yield and other agronomic characters. Heritability and genetic advance are also important selection parameters. It will help the plant breeder in selecting the elite genotype from diverse population. To assess the magnitude of correlations for various characters with yield would be immense help in the indirect selection for the improvement of yield.

Corresponding Author:

Yamanura

All India Co-ordinated Research Project on Castor, Zonal Agricultural research Station, University of Agricultural Sciences, GKVK, Bengaluru, Karnataka, India

Seed yield is influenced by its various components directly and/or indirectly via other traits that create a complex situation before a breeder for making desirable selection (Movaliya *et al.*, 2018) [15]. The phenotypic correlation indicates the extent of observed relationship between the two characters while genotypic correlation provides information about linkage for the gene controlling the pair of characters. Therefore, the correlation co-efficient at genotypic and phenotypic levels were considered, however, they do not provide the exact picture of direct and indirect cause of such association, which can be cleared through path analysis. Thus, path analysis is very useful to pin point the important yield components which can be utilized for recommending selection indices. In the present studies an attempt was made to obtain such information in castor with available genotypes.

Materials and Methods

The experimental material consists of 33 entries, which includes 20 hybrids, 12 parents and a check (ICH-66) were obtained from the ICAR-IIOR, Hyderabad, India. The present investigation was laid out by randomized complete block design (RCBD) with three replications during *kharif*, 2019-20 at All India Co-ordinated Research Project on Castor, Zonal Agricultural Research Station, GKVK, Bengaluru.

The complete set of 33 entries was sown in a single row of 6.0-meter length was assigned to each genotype with 10 dibbles having 60 cm intra and 90 cm inter row spacing. All recommended agronomic practices and plant protection measures were followed for raising normal crop. The observations were recorded on five randomly selected plants for twelve traits *viz.*, DFF: Days to 50 per cent flowering, DMPS: Days to maturity of primary spike, PH: Plant height (cm), NN: Number of nodes up to primary spike, TLPS: Total Length of primary spike (cm), ELPS: Effective Length of primary spike (cm), NC: Number of capsules on primary spike, NES/P: Number of effective spikes per plant, HSW: 100 seed weight (g), HVW: 100 Volume weight (g), SY: Seed yield per plant (g), OC: Oil content (%). The observations for days to 50 per cent flowering and maturity were recorded on plot basis.

Analysis of variance technique described by Panse and Sukhatme (1989) [17] was followed to test the differences among the genotypes for all the traits. The statistical analysis was performed as per randomized block design (RBD) using statistic package Windostat Version 9.3 from *indostat* services, Hyderabad (India). The genotypic and phenotypic components of variance, coefficients of variability, broad sense heritability and genetic advance were estimated as detailed in Rukhsar *et al.* (2018) [25]. The correlation co-efficient were worked out to understand the association among characters by adopting method described by Singh and Chaudhary (1977) and path analysis was done according to the procedure suggested by Dewey and Lu (1959) [5]. Genetic divergence was calculated using Mahalanobis's D2 statistic (1936) [14]. Grouping of the genotypes in different clusters was done by using Tocher's method (1952).

Results and Discussion

The analysis of variance was performed to test the difference amongst parents and hybrids for twelve traits. The results revealed that, highly significant differences among the 33 genotypes for all the characters indicating considerable genetic variation in the material studied (Table 1). A wide range of variation for agronomic parameters in castor was

reported by Anjani (2000) [2], Anjani (2012) [3], Rukhsar *et al.* (2018) [25], Gabriela *et al.* (2019) [8] and Jawahar *et al.* (2019) [11].

The seed quality parameters are the most imperative traits which limit the price of seeds at the time of sale and 100-seed weight gives a clue about boldness of seeds, so higher mean performance is required. ICH-823 recorded significantly higher 100 seed weight (36.09g) over rest and the lowest was observed in case of DCS-108 (13.16g). The values of the volume weight ranged from 42.85 g(DCS-107) to 64.17 g(ICH-1101), Selection of out yielding varieties or hybrids will be possible only when adequate variability exists in the studied material. Hence, the insight into the magnitude of variability existing in a genotype of a crop species is of greatest importance to plant breeding programme, the number of capsules per primary spike ranged from 28.15 (ICH-1098) to 54.66 (DCS-102). DCS-89 recorded significantly higher effective primary spike length (43.67cm) and was statistically comparable ICH-66 (41.56 cm), DCS-94 (39.56cm) and DCS-102 (36.52cm). The variability in oil content ranged from 35.23% (DCS-107) to 49.18% (ICH-824). Among the entries tested ICH-824 was recorded highest oil content (49.18%) which was significantly on par with ICH-1101(47.54%), ICH-1090(47.49%) and ICH-1086 (47.31%) (mean performance table was bulky hence data not given). The result of oil content was incongruence with Shah *et al.*, (2015), Rukhsar *et al.* (2018) [25], Gabriela *et al.* (2019) [8] and other researchers who observed 46.6% to 51.3% of oil content in castor. The range of days to maturity falls between 81 (ICH-404) to 111 (DCS-89).

Genetic variability studies

The coefficient of variation expressed in phenotypic and genotypic levels are used to compare the variability observed among different traits. Hence, knowledge about the variability using parameters like genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) is of paramount importance for an effective breeding programme in crops like castor. Genotypic and phenotypic coefficient of variation (GCV and PCV %), heritability in broad sense and genetic advance (GA% mean) estimates are summarized in Table 1. The higher estimates and close values of GCV and PCV was observed in seed yield/plant, number of effective spikes/plant, plant height, total and effective primary spike length, number of capsules and 100-seed weight offering better scope for selection as there was less influence of environment and suggesting that potential variability available in studied material for these traits. In earlier researchers, *viz* Patel *et al.*, (1991) [20], Lakshamma *et al.*, (2005) [13], Sridhar *et al.*, (2009) [29] and Sarwar *et al.*, (2010) [26], Rukhsar *et al.* (2018) [25], Gabriela *et al.* (2019) [8] were reported higher GCV and PCV for seed yield whereas, lower GCV was found for test weight by Patel *et al.*, (2010) [26].

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) could be partitioned as high (> 20%), moderate (10-20%) or low (< 10%) (Shivanna, 2008) [27]. Based on this, moderate to high GCV and PCV were observed for all the traits studied except oil content and in all the traits, the magnitude of differences between the GCV and PCV was low for all the traits except for total and effective length of primary spikes and number of capsules on primary spikes where it was moderate. The low differences is an indication of low influence of environmental factors on the phenotypic expression of genotypes for the traits and as such

there is high chance of improving these characters through selection based on the phenotypic data. Earlier researchers (Rao *et al.*, 2009; Zhang-Xishun & Yang-Jain, 2006) [24, 33] had reported similar magnitudes of variability in the works on castor. Patel & Jaimini (1988) [18] also reported moderate to high coefficient of variation for most of the traits in castor irrespective of the environment. In a study on the genetic variation of 68 castor lines, Lakshamma *et al.*, (2005) [13] reported high genotypic and phenotypic coefficient of variability for capsule weight per plant, plant height, capsule number and leaf area index. Golakia *et al.*, (2007) [9] observed high PCV for seed yield in his work on castor. Kasim *et al.*, 2019 [12] reported that moderate to high GCV and PCV were observed for ten out of thirteen characters studied and in all the traits, the magnitude of differences between the GCV and PCV was low for all the traits except for the leaf petiole length branches per plant where it was moderate and high respectively.

Heritability is a good index of the transmission of traits from parents to their offspring (Falconer D.S., 1989). High heritability coupled with high GA were noticed for the characters viz., days to 50% flowering, days to maturity, plant height up to primary raceme, hundred volume and seed weight, number of effective spikes/plant, seed yield/plant and number of nodes up to primary spike which indicated that genotypic variation for the characters is probably attributed to high additive genetic effect. Moderate genetic advance with moderate heritability was observed in percent oil content, total and effective length of primary spike. Whereas, low genetic advance was observed in number of capsules on primary spike, oil content and volume weight. Therefore, selection based on this trait may not yield dividends in greater improvement of castor.

Correlation and path coefficients analysis

Yield is a complex character resulting from interplay of various yield contributing characters, which have positive or negative association with yield and among themselves. To assess the magnitude of correlations for various characters with yield would be immense help in the indirect selection for the improvement of yield. Pearson correlation coefficient was computed. Pearson correlation analysis among yield and its contributing characters are shown in Table 2. There was significant and positive correlation between total length of primary spike and effective length of primary spike (0.991). total length of primary spike showed significant and positive correlation with number of capsules on primary spike (0.977), plant height showed significant and positive correlation with number of nodes per plant (0.954). seed yield per plant was significant and positively associated with percent oil content (0.717**), hundred seed weight (0.679**), hundred volume weight (0.527**), number of capsules per primary raceme (0.443**), effective length of primary spike (0.245**), total length of primary spike (0.216*) and number of effective spikes per plant (0.012) indicating that selection for these traits would lead to higher seed yield per plant automatically. Oil content is positively and significantly correlated with hundred seed weight (0.488**) and hundred volume weight (0.825**) suggested that oil yield can improved through selection for this yield components. Days to 50% flowering and days to maturity are an important trait showed negative significant correlation with seed yield suggested that medium to late maturing should be exploited to enhance yield in castor. As the correlation coefficient are insufficient to

interpret true relationship for an effective manipulation of the traits hence the path coefficient was calculated (Dhedhi *et al.*, 2010 and Golakia *et al.*, 2007) [6, 9]. The path co-efficient analysis is a statistical device developed by Wright (1921) [31]. The analysis takes into account the cause and effect relation between the variable and is unique in partitioning the association into direct and indirect effect through other independent variables. The path co-efficient analysis also measures the relative importance of casual factors involved. Path analysis was carried out for 12 traits on seed yield and shown in Table-3. path coefficient analysis directed that number of effective spikes per plant (0.883) demonstrated utmost positive direct effect on seed yield per plant followed by hundred seed weight (4.928). hence these traits may be directly attributed for the improvement of seed yield and important in the selection of better genotypes.

In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect, permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of other possible independent variables which were not included in the study on the dependent variables. The residual effect is estimated with the help of direct effects and simple correlation coefficients. The residual effect is high which in the present study were 0.73 and 0.63 at phenotypic and genotypic level respectively. The residual effect is high which indicates that besides the trait studied there are some other attributes which contributes for yield.

Genetic diversity analysis

The single trait is not much importance to a plant breeder as the combined merit of number of desirable traits becomes more important when he/she is concerned with a complex trait like seed yield. Therefore, while improving seed yield, selection of parents based on number of characters having quantitative divergence is required (Rukhsar *et al.*, 2018) [25]. Genetic diversity within the castor genotypes was done by Toucher Method for twelve quantitative traits using statistic package Windostat Version 9.3. Based on the cluster analysis, thirty-three genotypes were grouped into different clusters and sub clusters which is presented in Table 4 and Figure 3. The whole thirty-three genotypes divided into eight main clusters. Cluster I consist of 19 genotype which was found to be a largest cluster had sub clusters from A to O followed by Cluster II had seven genotypes which divided into five sub clusters. Whereas, cluster III, IV, VI, VII and VIII consists of one genotype in each cluster and they had solitary entries Viz. DCS-120, DCS-102, ICH-66, DCS-108 and DCS-89 respectively. Cluster V also grouped as solitary but had ICH-1090 and ICH-326 genotypes.

Based on values of inter cluster distance (Table 5), it was found that the highest divergence occurred between cluster II and V (156.96) followed by cluster V and VIII (138.08), cluster I and VIII (110.42) indicating the wider genetic diversity between genotypes of these groups. The cluster VIII involved DCS- 89 which high yielding, cluster II involves DCS-105, DCS-107, DCS-112, and DCS-119 genotypes of pistilata lines M-574, DPC-9 which are cross derivatives of other geographically diverse accessions as per the catalogue of castor germplasm indicating genetic diversity being contributed by geographical diversity or cross combinations involving geographically diverse genotypes (Jawahar *et al.*, 2019) [11]. This was in contradiction to studies like

Chakrabarty and Banu (1999) [4], and Singh and Srivastava (1978) [28] in castor. Hence, selection of parents from these clusters for hybridization programme would help in achieving novel recombinants. On the other hand, the lowest divergence was noticed between clusters III and IV (16.70) indicating close relationship and similarity for most of the traits of the

genotypes in this cluster. The inter cluster distance was higher than the intra cluster distance these results agreed with Ramesh *et al.*, (2012) [21], Jawahara *et al.* (2019) [11] which indicates the existence of substantial diversity among the genotypes.

Table 1: ANOVA and Estimates of genetic parameters for twelve morphological descriptors evaluated by 33 castor genotypes

Source of Variations	DF	DFE	DMPS	PH	NN	TLPS	ELPS	NC	NES/P	SY	HSW	HVW	OC
Replicate	2	18.575**	56.030**	60.246	2.064	124.492*	91.384**	174.139	11.368**	562.131	13.427	16.945	4.262
Treatments	32	98.896**	306.884**	476.006**	9.583**	119.179**	74.358**	126.379**	13.502**	4240.164**	72.81**	88.938**	29.412**
Error	64	2.096	6.488	19.443	0.919	29.567	15.473	57.443	1.232	474.967	6.512	5.816	5.609
Genetic Parameters													
Environmental variance		2.10	6.49	19.44	0.92	29.57	15.47	57.44	1.23	474.97	6.51	5.82	5.61
Environmental coefficient of variation		3.22	2.72	10.71	9.63	14.40	12.70	18.04	15.72	18.63	9.90	4.33	5.37
Genotypical variance		32.27	100.13	152.19	2.89	29.87	19.63	22.98	4.09	1255.07	22.10	27.71	7.93
Genotypic coefficient of variation		12.62	10.68	29.96	17.06	14.47	14.30	11.41	28.64	30.29	18.23	9.45	6.39
Phenotypical variance		34.36	106.62	171.63	3.81	59.44	35.10	80.42	5.32	1730.03	28.62	33.52	13.54
Phenotypic coefficient of variation		13.03	11.02	31.82	19.59	20.42	19.12	21.34	32.67	35.56	20.74	10.39	8.35
h ² (Broad Sense) %		94.00	94.00	89.00	76.18	50.76	56.00	29.65	77.32	73.24	77.54	83.97	59.32
Gen. Advance % Mean		32.29	27.31	74.48	39.22	27.09	28.23	16.10	66.28	68.10	42.30	22.68	12.91
C.V.		3.22	2.72	10.71	9.63	14.40	12.69	18.03	15.72	18.63	9.90	4.33	5.37
S.E.		0.84	1.47	2.55	0.55	3.14	2.27	4.38	0.64	12.58	1.47	1.39	1.37
C.D. 5%		2.36	4.16	7.19	1.56	8.87	6.42	12.36	1.81	35.55	4.16	3.93	3.86
General Mean		45.00	93.73	41.18	9.96	37.76	30.99	42.03	7.06	116.98	25.79	55.71	44.08
Range Lowest		35.33	81.33	25.74	8.00	22.33	21.30	28.15	3.78	33.78	13.16	42.85	35.23
Range Highest		57.33	110.67	77.78	14.22	52.29	43.67	54.66	14.34	189.41	36.09	64.17	49.18
Exp Mean next Generation		56.34	113.70	65.11	13.01	45.74	37.81	47.30	10.71	179.14	34.30	65.56	48.52

*, ** Significant at 5 % and 1 % levels of probability, respectively. DF: Degree of freedom, DFF: Days to 50 per cent flowering, DMPS: Days to maturity of primary spike, PH: Plant height (cm), NN: Number of nodes up to primary spike, TLPS: Total Length of primary spike (cm), ELPS: Effective Length of primary spike (cm), NC: Number of capsules on primary spike, NES/P: Number of effective spikes per plant, SY: Seed yield per plant (g), HSW: 100 seed weight (g), HVW: 100 Volume weight (g), OC: Oil content (%).].

Table 2: Phenotypic (above diagonal) and Genotypic (below diagonal) correlation coefficients between different traits in Castor

	DFF	DMPS	PH	NN	TLPS	ELPS	NC	NES/PT	HSW	HVW	OC
DFF	1.000	0.828**	0.768**	0.694**	0.428**	0.491**	0.254*	0.163	0.145	-0.611**	-0.232*
DMPS	0.827**	1.000	0.648**	0.582**	0.418**	0.439**	0.180	0.215*	0.056	-0.552**	-0.185
PH	0.831**	0.698**	1.000	0.835**	0.524**	0.641**	0.373**	0.406**	0.101	-0.515**	-0.279**
NN	0.810**	0.682**	0.954**	1.000	0.392**	0.486**	0.289**	0.394**	-0.085	-0.586**	-0.425**
TLPS	0.649**	0.647**	0.712**	0.642**	1.000	0.882**	0.676**	0.238*	0.276**	-0.057	0.042
ELPS	0.707**	0.654**	0.833**	0.722**	0.991**	1.000	0.611**	0.350**	0.216*	-0.144	-0.035
NC	0.523**	0.392**	0.704**	0.552**	0.977**	0.951**	1.000	0.160	0.352**	-0.038	0.166
NES/PT	0.222*	0.264**	0.479**	0.501**	0.256**	0.409**	0.126	1.000	-0.273**	-0.153	-0.030
HSW	0.155	0.038	0.115	-0.074	0.307**	0.230*	0.610**	-0.406**	1.000	0.205*	0.501**
HVW	-0.694**	-0.612**	-0.634**	-0.731**	-0.207*	-0.307**	-0.128	-0.213*	0.157	1.000	0.640**
OC	-0.339**	-0.277**	-0.316**	-0.598**	0.012	0.022	0.020	-0.043	0.488**	0.825**	1.000
SY	-0.203*	-0.202*	-0.004	-0.156	0.216*	0.245*	0.443**	0.012	0.679**	0.527**	0.717**

*, ** Significant at 5 % and 1 % levels of probability, respectively. DFF: Days to 50 per cent flowering, DMPS: Days to maturity of primary spike, PH: Plant height (cm), NN: Number of nodes up to primary spike, TLPS: Total Length of primary spike (cm), ELPS: Effective Length of primary spike (cm), NC: Number of capsules on primary spike, NES/P: Number of effective spikes per plant, SY: Seed yield per plant (g), HSW: 100 seed weight (g), HVW: 100 Volume weight (g), OC: Oil content (%).].

Table 3: Path coefficient analysis showing direct and indirect effects of different traits on seed yield per plant in 33 castor genotypes

Character	Level	DFF	DMPS	PH	NN	TLPS	ELPS	NC	NES/PT	HSW	HVW	OC	SY
DFF	P	-0.3176	-0.2631	-0.2438	-0.2203	-0.1362	-0.1562	-0.0809	-0.0520	-0.0462	0.1942	0.0738	-0.1527
	G	0.2990	0.2474	0.2487	0.2423	0.1943	0.2117	0.1566	0.0665	0.0466	-0.2076	-0.1015	-0.2031
DMPS	P	0.0110	0.0132	0.0086	0.0077	0.0055	0.0058	0.0024	0.0029	0.0007	-0.0073	-0.0024	-0.1618
	G	0.4078	0.4928	0.3440	0.3363	0.3190	0.3227	0.1934	0.1303	0.0187	-0.3018	-0.1368	-0.2020
PH	P	0.2374	0.2005	0.3092	0.2584	0.1623	0.1985	0.1153	0.1256	0.0314	-0.1595	-0.0865	0.0421
	G	1.9235	1.6147	2.3129	2.2084	1.6470	1.9274	1.6302	1.1099	0.2669	-1.4605	-0.7316	-0.0041
NN	P	-0.0433	-0.0364	-0.0522	-0.0625	-0.0245	-0.0304	-0.0181	-0.0246	0.0053	0.0367	0.0266	-0.1245
	G	-2.1142	-1.7802	-2.4905	-2.6084	-1.6771	-1.8843	-1.4406	-1.3085	0.1949	1.9081	1.5623	-0.1565
TLPS	P	-0.0961	-0.0938	-0.1176	-0.0880	-0.2242	-0.1978	-0.1517	-0.0535	-0.0619	0.0129	-0.0094	0.1929
	G	0.0003	0.0003	0.0003	0.0003	0.0004	0.0004	0.0004	0.0001	0.0001	-0.0001	0.0000	0.2163
ELPS	P	0.1287	0.1150	0.1679	0.1273	0.2308	0.2616	0.1598	0.0917	0.0566	-0.0377	-0.0092	0.2178
	G	-1.2163	-1.1251	-1.4318	-1.2412	-1.7040	-1.7181	-1.6354	-0.7031	-0.3963	0.5285	-0.0388	0.2454
NC	P	0.0106	0.0075	0.0155	0.0121	0.0282	0.0255	0.0417	0.0067	0.0147	-0.0016	0.0069	0.2517
	G	0.7269	0.5446	0.9781	0.7664	1.3566	1.3209	1.3877	0.1751	0.8478	-0.1778	0.0283	0.4431
NES/P	P	0.0208	0.0274	0.0517	0.0502	0.0304	0.0446	0.0204	0.1273	-0.0348	-0.0195	-0.0039	0.0423

	G	0.1964	0.2335	0.4236	0.4429	0.2265	0.3613	0.1114	0.8828	-0.3587	-0.1886	-0.0385	0.0121
HSW	P	0.0729	0.0280	0.0508	-0.0426	0.1382	0.1083	0.1766	-0.1370	0.5006	0.1026	0.2508	0.5192
	G	0.0524	0.0128	0.0388	-0.0251	0.1036	0.0776	0.2056	-0.1367	0.3365	0.0529	0.1643	0.6795
HVW	P	-0.1806	-0.1630	-0.1523	-0.1733	-0.0170	-0.0425	-0.0113	-0.0452	0.0605	0.2953	0.1892	0.4062
	G	-0.7968	-0.7028	-0.7246	-0.8394	-0.2384	-0.3530	-0.1470	-0.2452	0.1805	1.1475	0.9471	0.5275
OC	P	0.0036	0.0028	0.0043	0.0065	-0.0006	0.0005	-0.0026	0.0005	-0.0077	-0.0098	-0.0154	0.4205
	G	0.3179	0.2601	0.2963	0.5611	-0.0117	-0.0211	-0.0191	0.0408	-0.4574	-0.7732	-0.9368	0.7178
Partial R2	P	0.0485	-0.0021	0.0130	0.0078	-0.0432	0.0570	0.0105	0.0054	0.2599	0.1200	-0.0065	
	G	-0.0607	-0.0995	-0.0096	0.4081	0.0001	-0.4216	0.6148	0.0107	0.2286	0.6053	-0.6725	

R SQUARE = 0.6038 and RESIDUAL EFFECT = 0.728(Phenotypical) and 0.6295 (Genotypical), Bold and diagonal shows the direct effects, DFF: Days to 50 per cent flowering, DMPS: Days to maturity of primary spike, PH: Plant height (cm), NN: Number of nodes up to primary spike, TLPS: Total Length of primary spike (cm), ELPS: Effective Length of primary spike (cm), NC: Number of capsules on primary spike, NES/P: Number of effective spikes per plant, SY: Seed yield per plant (g), HSW: 100 seed weight (g), HVW: 100 Volume weight (g), OC: Oil content (%)].

Table 4: Cluster Means for 12 different agronomic traits in 33 castor genotypes

Traits Cluster	DFF	DMPS	PH	NN	TLPS	ELPS	NC	NES/PT	SY	HSW	HVW	OC
Cluster-1	41.81	87.79	34.19	8.97	35.74	29.14	40.03	6.27	125.93	25.79	58.40	44.84
Cluster-2	50.67	97.81	52.52	11.73	39.13	32.60	45.60	7.52	94.42	26.63	49.35	41.72
Cluster-3	48.00	105.00	41.89	11.22	39.00	31.44	36.33	7.17	71.60	25.88	47.97	40.41
Cluster-4	45.00	101.00	44.55	11.00	48.44	36.52	54.66	10.23	94.14	21.64	55.75	43.32
Cluster-5	43.50	104.83	36.00	8.39	36.44	28.56	42.92	5.73	123.48	28.60	58.72	47.19
Cluster-6	52.33	108.33	64.33	13.67	52.29	41.56	51.33	8.18	170.83	30.72	58.66	43.68
Cluster-7	50.67	105.67	41.00	10.11	35.14	30.41	33.33	9.85	33.78	13.16	53.66	43.02
Cluster-8	53.00	110.67	77.78	13.33	45.44	43.67	45.56	14.34	189.41	26.01	49.79	45.88

Table 5: Cluster composition of Castor genotypes based on quantitative characters

Clusters	Sub clusters	No. of genotypes	Name of Genotypes
I	A	2	ICH-1099, ICH-1100
	B	1	ICH-404
	C	1	ICH-1106
	D	1	ICH-1104
	E	1	ICH-1097
	F	1	DPC-15
	G	2	DCS-104, ICH-824
	H	2	ICH-1101, ICH-1098
	I	2	DPC-9, ICH-1094
	J	1	ICH-1107
	K	1	ICH-1089
	L	1	ICH-1087
	M	1	ICH-1380
	N	1	ICH-1093
O	1	DCS-94	
	TOTAL	19	
II	A	2	DCS-107, DCS-112
	B	1	ICH-1086
	C	1	DCS-119
	D	1	DCS-105
	E	2	ICH-823, ICH-1092
	TOTAL	7	
III	A	1	DCS-120
IV	A	1	DCS-102
V	A	2	ICH-1090, ICH-326
VI	A	1	ICH-66
VII	A	1	DCS-108
VIII	A	1	DCS-89
	GRAND TOTAL	33	

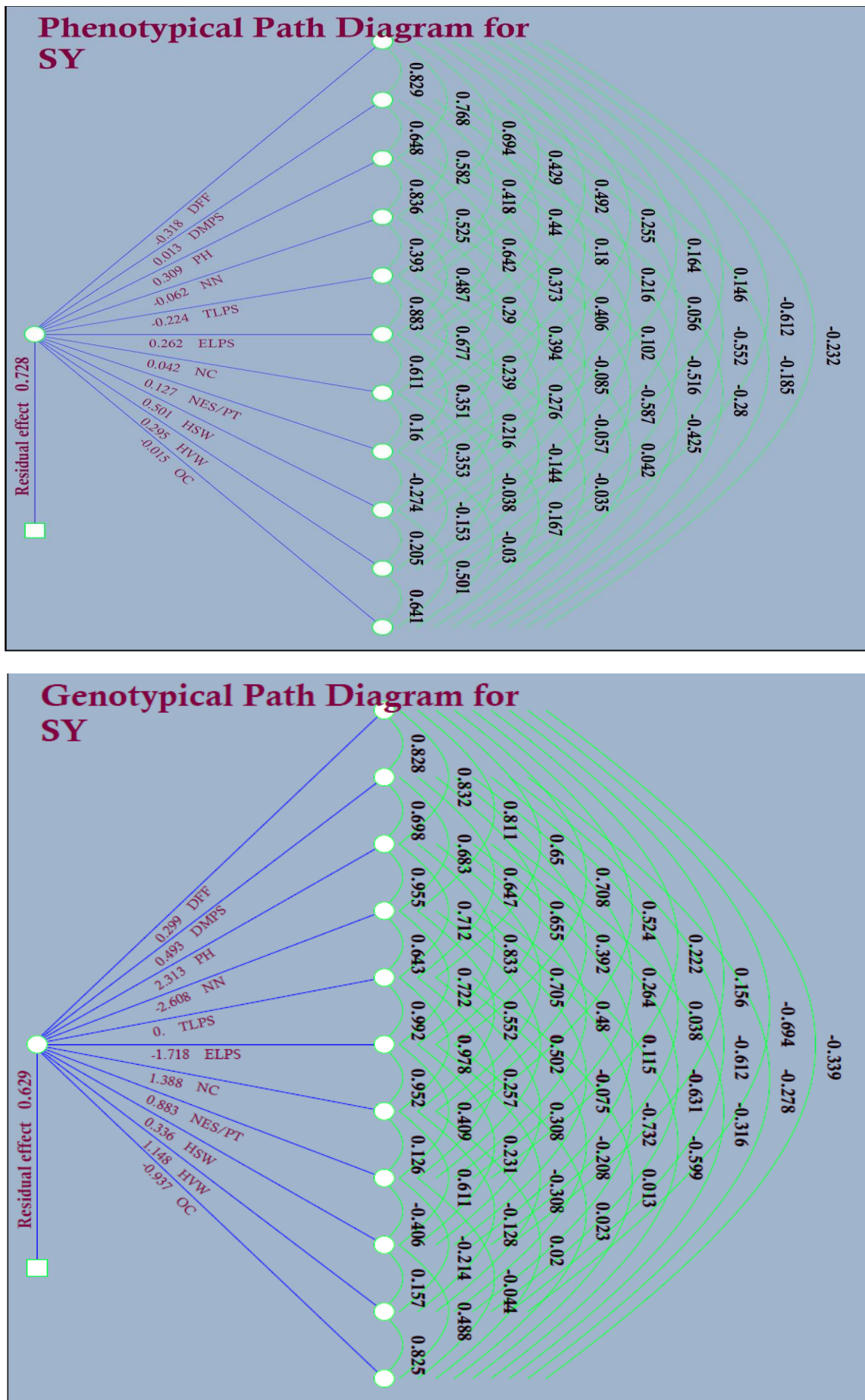


Fig 1: Phenotypical and Genotypical path diagram for seed yield in castor genotypes

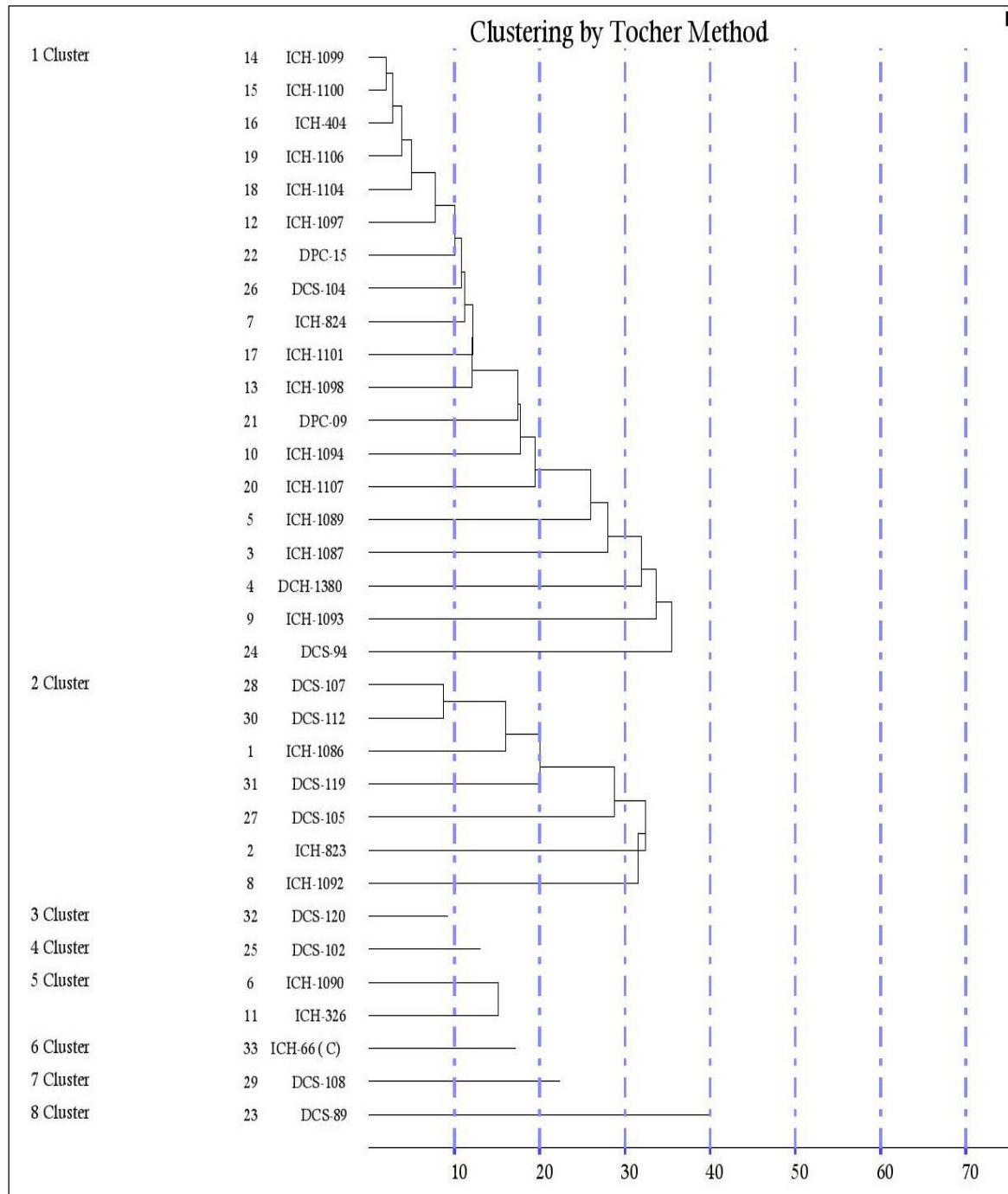


Fig 2: Clustering by Tocher Method for twelve quantitative characters of Castor

Conclusion

From this study it was proved that, high heritability coupled with high GA were noticed for the characters viz., days to 50% flowering, days to maturity, plant height up to primary raceme, hundred volume and seed weight, number of effective spikes/plant, seed yield/plant and number of nodes up to primary spike which indicated that genotypic variation for the characters is probably attributed to high additive genetic effect.

Seed yield per plant was significant and positively associated with percent oil content (0.717**), hundred seed weight (0.679**), hundred volume weight (0.527**), number of capsules per primary raceme (0.443**), effective length of primary spike (0.245**), total length of primary spike (0.216*) and number of effective spikes per plant (0.012) indicating that selection for these traits would lead to higher seed yield per plant automatically, hence it would be sensible

to suggest the breeder who involved in castor breeding to concentrate more on these traits. The residual effect were 0.73 and 0.63 at phenotypic and genotypic level respectively in the present investigation which indicates that besides the trait studied there are some other attributes which contributes for yield.

References

1. Aher AR, Patel KV, Patel MP, Patel JA. Genetic analysis of seed yield and component traits over environments in castor (*Ricinus communis* L.). *Electronic Journal of Plant Breeding*. 2015; 6:141-149.
2. Anjani K. Catalogue of castor, Directorate of Oilseeds Research, Hyderabad, India. 2000, 1.
3. Anjani K. Castor genetic resources: A primary gene pool for exploitation. *Industrial crops and products*. 2012; 35:1-14.

4. Chakrabarty SK, Banu SS. Genetic diversity in pistillate lines of castor. *Indian Journal of Agricultural Sciences*, 1999; 69(10):729-730.
5. Dewey JR, Lu KH. A correlation and path coefficient analysis of component of crested wheat seed production, *Agron. J.* 1959; 51:515-518.
6. Dhedhi KK, Ghelani YH, Joshi HJ, Dangaria CJ. Correlation and path coefficient analysis in castor (*Ricinus communis* L.) over environments, *Agric. Sci. Digest.* 2010; 30(4):286-289.
7. Falconer DS. in: *Introduction to Quantitative Genetics*, third ed., Longman, New York, 1989.
8. Gabriela N, da Piedade, Lucas V Vieira, Amanda RP, dos Santos, Deoclecio J Amorim *et al.* Principal Component Analysis for Identification of Superior Castor Bean Hybrids. *Journal of Agricultural Science.* 2019; 11(9).
9. Golakia PR, Kavani RH, Monpara BA. Genetic variation and trait relationship in castor. *National Journal of Plant Improvement.* 2007; 9(1):60-62.
10. ICAR-IIOR. Annual Report 2019, AICRP on Castor, published by Indian Institute of Oilseeds Research, Hyderabad, 2020, 83.
11. Jawahar Lal J, Lavanya C. Pattern of Genotypic Diversity in Indigenous Castor (*Ricinus communis* L.) Genotypes, *Int. J Curr. Microbiol. App. Sci.* 2019; 8(1):2465-2471.
12. Kasim AA, Oliseh A, Salihu BZ, Kabaraini MA. Studies on genetic variability and trait Relationship in castor (*Ricinus communis* L.). *Journal of Plant Development.* 2019; 26:3-11.
13. Lakshamma P, Lakshmi P, Mohan YC, Lavanya C. Genetic variability and character association in castor (*Ricinus communis* L.), *Natl. J Plant Improv.* 2005; 7(2):122-126.
14. Mahalanobis PC. On the generalized distance in statistics, *Proc. Natl. Inst. Sci.* 1936; 2:49-55.
15. Movaliya HM, Chovatia VP, Madariya RB, Mungala RA, Pipaliya HR, Dr. Bhuva SK. Study of variability and correlation for seed yield and its attributes in castor (*Ricinus communis* L.) *Journal of Pharmacognosy and Phytochemistry.* 2018; 7(2):1474-1477.
16. Naidu LGK, Dharumarajan S, Lalitha M, Vasundhara R, Ramamurthy V, Obi Reddy GP *et al.* Identification and delineation of potential castor growing areas in different Agro-eco sub regions of India. *J Oilseeds Res.*, 2015; 32(1):39-48.
17. Panse VG, Sukhatme PV. (Revised by, P.V. Sukhatme, V.N Amble) *Statistical Methods for Agricultural Workers*, ICAR, New Delhi, 1989.
18. Patel PS, Jaimini SN. Variability in castor. *Indian Journal of Agricultural Science.* 1988; 58(1):394-396.
19. Patel JR, Saiyed MP, Patel CG, Bhatt RK, Bhatt JP. Genetic variability and correlation studies in castor (*Ricinus communis* L.), *Int. J Agric. Sci.* 2010; 6(1):129-131.
20. Patel PS, Jaimini SN. Inter-relationship and path analysis of certain quantitative characters in castor (*Ricinus communis* L.) *J Oilseeds Res.* 1991; 8:105-108.
21. Ramesh M, Lavanya C, Brahmeshwar Rao MV. Genetic divergence in some indigenous and exotic germplasm lines of castor (*Ricinus communis* L.) under rainfed conditions. *Indian journal of dryland agricultural research and development.* 2012; 27(2):79- 83.
22. Rao CR. *Advanced Statistical Methods in Biometrical Research*, John Willey and Sons Inc, New York, 1952, 390.
23. Rao PVR, Giri VG, Pachauri DK. Evaluation of castor (*Ricinus communis* L.). *Research on Crops.* 2006; 1(1):699-708.
24. Rao PVR, Shankar VG, Reddy AV. Variability studies in castor (*Ricinus communis* L.). *Research on Crops.* 2009; 10(1):696-698.
25. Rukhsar MP, Patel DJ, Parmar, Sushil Kumar. Genetic variability, character association and genetic divergence studies in castor (*Ricinus communis* L.), *Annals of Agrarian Science.* 2018; 16:143-148.
26. Sarwar G, Ahmed HM, Hussain J. Evaluation of castorbean (*Ricinus communis* L.) mutants for genetic parameters and cluster analysis. *J Agric. Res.* 2010; 48(3):289-300.
27. Shivanna S. Genetic diversity, combining ability and stability analysis of selected castor lines. PhD Thesis, University of Agricultural Sciences, Bangalore, India, 2008.
28. Singh A, Srivastava AN. Genetic diversity in relation to yield and its components in castor. *Indian Journal of Agricultural Sciences.* 1978; 48:25-28.
29. Sridhar V, Dangi, Reddy AV, Sudhakar R, Sankar AS. Genetic variability in F₂ populations of castor (*Ricinus communis* L.). *Int. J Agric. Environ. Biotechnol.* 2009; 2(3):227-229.
30. Weiss EA. *Oilseed Crops*, Oxford, Blackwell Science, 2000, 364.
31. Wright S. Correlation and causation. *J Agril. Res.* 1921; 20:557-585.
32. Yamanura, Kumar RM. An over view of utility, status, retrospective and prospects of castor: A Review. *Mysore Journal of Agricultural Sciences.* 2020; 54(2):14-29.
33. Zhang-Xishun Z, Yang-Jian G. Study on the relationship between genetic distance and heterosis in castor. *Scientia Agricultura Sinica.* 2006; 39(3):633-640.