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Genetic components of variation for seed yield and its component traits in castor (*Ricinus communis* L.) through diallel analysis

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Abstract
The experimental material consisting of 101 entries comprised of ten parents and their 45 hybrids and 45 F_2s developed through half diallel mating design and one standard check (GCH 7) were evaluated in a randomized block design with three replications. Numerical approach of diallel analysis was used to assess the nature and magnitude of gene action governing the expression of quantitative traits. The t^2 values were found non-significant for all the characters in both the generations, which suggested that assumptions of diallel analysis are fulfilled. The overall results of genetic components of variances for seed yield and other characters revealed that the estimates of dominance component of genetic variance (D) were significant for days to 50% flowering of primary raceme, days to maturity of primary raceme, number of nodes up to primary raceme, length of primary raceme, effective length of primary raceme, number of capsules per plant, 100-seed weight, oil content and seed yield per plant in both F_1 and F_2 generations except for number of nodes up to primary raceme in F_2 and oil content and seed yield per plant in F_1 generation. The components of dominance effects (H_1 and H_2) were significant for all the characters in both the generations except for H_2 in case of effective length of primary raceme in F_2 and number of effective branches per plant in F_1 generation suggesting the prevalence of both these dominance components in the inheritance of all these characters. This suggested the involvement of dominance gene action in the inheritance of these traits. The ratio of total number of dominant to recessive genes (KD/KR) in the parents was greater than one for all the characters in both F_1 and F_2 generations except for oil content, which indicated unequal frequency of recessive and dominant genes with an excess of dominant genes in the parents for these traits. High narrow sense heritability estimates were observed for effective length of primary raceme and 100-seed weight in F_1 generation, moderate heritability was noticed for number of nodes up to primary raceme, length of primary raceme, number of effective branches per plant, number of capsules on primary raceme and oil content in F_1 generation, Remaining characters possessed low estimates of narrow sense heritability.

Keywords: Castor, genetic components, Diallel, numerical approach

Introduction
Castor (*Ricinus communis* L.) belongs to the *Ricinus* monospecific genus of the Euphorbiaceae family and is one of the world's oldest oilseed crops with chromosome number 2n= 20. The name of the genus "Ricinus" comes from the Latin word meaning "dog tick" because of the seed that resembles the prevalent dog pest. Castor plant is regarded to be indigenous to the tropical East African area of Ethiopia. Castor is one of the world's largest non-edible plants of oilseeds. Hayman (1954) [3] identified six hypotheses as the grounds for the additive-dominance model implementation. Among the different mating designs, diallel mating design as suggested by Schmidt (1919) and Hayman (1954a) [3] and elaborated by Griffing (1956) is a useful methodology for combining parents and crosses for their combining ability effects and also for understanding the nature of gene actions. An added advantage of diallel analysis is that it gives overall genetic architecture of the polygenic characters in a single generation. In addition to Griffing's (1956) approach, Hayman (1954a) [3] numerical approach would provide detail account of components of gene effect and related parameters. Therefore, the genetic components of variances *viz.*, D, H_1, H_2, h^2, E and F along with their standard errors and various statistical ratios namely, mean degree of dominance $(H_1/D)^{1/2}$, proportion of positive and negative alleles in the parents, $H_2/4H_1$, proportion of dominant and recessive alleles in the parents $(4DH_1)^{1/2} + F/(4DH_1)^{1/2} - F$, number of gene groups which control the character h^2/H_2 and narrow sense heritability (%) were studied under the present study.

Materials and Methods
The experimental material comprised of a set of 10 diverse parents of castor which were used for half diallel mating design.

The experimental material, consisting of 101 entries including 10 parents, 45 hybrids, 45 F_2s and one standard check (GCH 7) was raised in a Randomized Block Design with three replications at the Main Oilseeds Research Station, JAU, Junagadh during *kharif* 2016-17. Each entry was accommodated in a single row of 7.2 m. length spaced at 90 cm apart with plant-to-plant spacing of 60 cm. Recommended agronomic practices and plant protection measures were adopted timely to raise the healthy crop.

Five competitive plants from parental lines and F_1s and 20 plants from each F_2s from each replication were randomly selected before flowering and tagged for the purpose of recording observations on different characters *viz.*, days to 50% flowering of primary raceme, days to maturity of primary raceme, plant height up to primary raceme (cm), number of nodes up to primary raceme, length of primary raceme (cm), effective length of primary raceme (cm), number of effective branches per plant, number of capsules on primary raceme, 100-seed weight (g), seed yield per plant (g) and oil content (%) (except days to flowering and days to maturity) and their average values were used in the statistical analysis.

Genetic analysis of diallel data genetic components of variation was according to method of Hayman (1954) [3] and Jinks (1954) [4]. The first three assumptions of the additive/dominance genetic model underlying an analysis of the diallel cross Hayman (1954) [3] were tested as follows: (1) diploid segregation; (2) homozygous parents each parent was maintained by inbreeding and was assumed to be homozygous; and (3) no reciprocal differences. The remaining assumptions of the simple additive dominance genetic model (Mather and Jinks, 1982) [6] are (4) independent effect of non- allelic genes (i.e. no epistasis); (5) no multiple allelisam and (6) genes independently distributed between parents. Components of variation of F_1 and F_2 generations were estimated by the formulae of Jinks (1956). Expected statistics for F_2 generation were the same as those of F_1 except that contribution of h^2 was reduced to half because of one generation of inbreeding. Thus, co-efficients of H_1 and H_2, KD/KR ratio and narrow sense heritability were one fourth of F_1, while coefficient of F was reduced to half being second and third degree statistics, respectively (Jinks, 1956; Hayman, 1958 and Mather and Jinks, 1982) [6].

Results and Discussions

The t^2 values were found non-significant for all the characters in both the generations, which suggested that assumptions of diallel analysis are fulfilled (Table 1 and Table 2). The overall results of genetic components of variances for seed yield and other characters revealed that the estimates of dominance component of genetic variance (D) were significant for days to 50% flowering of primary raceme, days to maturity of primary raceme, number of nodes up to primary raceme, length of primary raceme, effective length of primary raceme, number of capsules per plant, 100-seed weight, oil content and seed yield per plant in both F_1 and F_2 generations except for number of nodes up to primary raceme in F_2 and oil content and seed yield per plant in F_1 generation. This suggested the involvement of dominance gene action in the inheritance of these traits. These findings are in agreement with those reported by Panera *et al.* (2018) [8]. The components of dominance effects (H_1 and H_2) were significant for all the characters in both the generations except for H_2 in case of effective length of primary raceme in F_2 and number of effective branches per plant in F_1 generation suggesting the prevalence of both these dominance components in the inheritance of all these characters. Further, the magnitude of H_1 and H_2 components was higher as compared to D component for all the characters in both the generations except H_2 for 100-seed weight in F_1, which was suggestive of the fact that dominance components played a pivotal role in the genetic control of all these traits. The results obtained for genetic components of variance are also in confirmation of predominant role of non-additive gene action observed under the combining ability analysis in the present study. Similar findings were also reported by Patel (1998a) [9] and Patel (1998b) [10] in castor.

The F component was found positive and significant for days to 50 % flowering of primary raceme, days to maturity of primary raceme, length of primary raceme and seed yield per plant in both F_1 and F_2 generations except for length of primary raceme and seed yield per plant in F_2 generation, indicating presence of unequal frequency of dominant and recessive genes for these characters. However, for plant height up to primary raceme, number of nodes up to primary raceme, effective length of primary raceme, number of effective branches per plant, number of capsules on primary raceme, 100-seed weight and oil content in both the generations, the positive and non-significant F component indicated presence of equal frequency of dominant and recessive genes for these characters.

The values of overall dominance effects of heterozygous loci (h^2) were found to be positive and significant for days to 50 % flowering of primary raceme, days to maturity of primary raceme and seed yield per plant in both F_1 and F_2 generations, while for plant height up to primary raceme and number of effective branches per plant in F_2 as well as for 100-seed weight and oil content in F_1 generation. The results suggested that dominant gene effects were mainly attributed to heterozygosity and dominance seeming to be acting in positive direction (unidirectional) for these traits. For the characters *viz.*, plant height up to primary raceme, number of nodes up to primary raceme, length of primary raceme, effective length of primary raceme and number of capsules on primary raceme non-significant values of h^2 indicated that dominance effect for these characters was bi-directional in nature i.e. both dominant and recessive alleles were involved at various loci.

The environmental component of variation (E) was significant for number of nodes up to primary raceme and oil content in both F_1 and F_2 generations, for length of primary raceme and effective length of primary raceme in F_1 generation and for seed yield per plant in F_2 generation, thereby reflecting the large effect of environmental factors on these traits.

The mean degree of dominance over all loci as estimated by the ratio of $(H_1/D)^{1/2}$ was found to be more than unity for all the characters in both the generations, indicating the role of over dominance gene action in the inheritance of these traits. Similar results were observed by Giriraj *et al*. (1974) [2], Singh and Yadav (1981) [11, 13], Narkhede *et al.* (1985) [7], Dobariya *et al.* (1992) [1], Tank *et al*. (2003) [15], Sodavadiya (2010) [14], Manga and Gila (2015) [5], Patel (1998a) [9], Patel (1998b) [10] and Panera *et al*. (2018) [8].

The ratio of $H_2/4H_1$, which measures the mean frequency of negative and positive genes in the parents, was below its maximum theoretical value (0.25) for all the characters in both the generations except for oil content. The present findings evidenced the asymmetrical distribution of positive and negative genes in the parents. The value of $H_2/4H_1$ was nearly 0.25 for oil content in both F_1 and F_2 generations,

indicating symmetrical distribution of positive and negative genes in the parents for this trait. These findings are in accordance with those reported by Sodavadiya (2010) [14], Manga and Gila (2015) [5], Patel (1998b) [10] and Panera *et al*. (2018) [8] in castor.

The ratio of total number of dominant to recessive genes (KD/KR) in the parents was greater than one for all the characters in both F_1 and F_2 generations except for oil content, which indicated unequal frequency of recessive and dominant genes with an excess of dominant genes in the parents for these traits. Greater than one ratio of KD/KR for oil content suggested higher proportion of recessive genes in the parents for this trait. Patel (1998b) [10] and Panera *et al.* (2018) [8] also reported higher proportion of dominant alleles in the parents for seed yield and its components in castor.

The parameter h^2/H_2 denotes an approximate number of genes or groups of genes controlling the traits i.e. exhibiting dominance. This ratio was greater than unity for days to 50 % flowering of primary raceme, days to maturity of primary raceme and seed yield per plant in both the generations and oil content in F_1 generation suggesting that these characters were controlled by more than two genes or group of genes. For the remaining characters, one gene group with dominant effect was responsible.

High narrow sense heritability estimates were observed for effective length of primary raceme and 100-seed weight in F_1 generation, suggesting that selection based on these attributes would confer rapid improvement. Moderate heritability was noticed for number of nodes up to primary raceme, length of primary raceme, number of effective branches per plant, number of capsules on primary raceme and oil content in F_1 generation, suggesting that breeder can get moderate response while considering above said traits in selection programme. Remaining characters possessed low estimates of narrow sense heritability. Similar results were obtained by Panera *et al*. (2018) [8].

Table 1: Genetic component for days to 50% flowering of primary raceme, days to maturity of primary raceme, plant height up to primary raceme and number of nodes up to primary raceme in castor

Parameters	Days to 50% flowering of primary raceme		Days to maturity of primary raceme		Plant height up to primary raceme (cm)		Number of nodes up to primary raceme	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
D	38.80* ± 3.18	39.10* ± 5.13	184.74* ± 23.69	184.30* ±37.20	89.79 ±46.45	106.56 ± 70.27	0.07 ± 0.50	0.27* ± 0.43
H_1	74.53* ± 6.77	475.63* ± 43.69	495.77* ± 50.43	2313.51* ±316.73	643.10*± 98.88	3030.91* ±598.31	7.74* ± 1.07	20.08* ± 3.67
H_2	57.76* ± 5.75	328.23* ± 37.13	329.93*± 42.86	1861.53*± 269.19	397.80*± 84.04	1846.27*± 508.50	4.35** ± 0.91	14.18* ± 3.12
F	44.59* ± 7.34	115.12* ± 23.68	283.63* ± 54.66	479.15* ± 171.66	126.99 ± 107.18	292.12 ± 324.27	0.23 ± 1.16	1.30 ± 1.99
h^2	342.61* ± 3.85	538.40* ± 24.85	939.86*± 28.69	1916.67* ± 180.18	11.31 ±56.25	1076.08*± 340.37	0.10 ± 0.61	1.59 ± 2.09
E	1.04 ± 0.95	0.74 ± 1.54	1.59 ± 7.14	2.03 ± 11.21	19.26 ± 14.00	2.48 ± 21.18	0.46* ± 0.15	0.26* ± 0.13
$(H_1/D)^{1/2}$	1.38	1.74	1.63	1.77	2.67	2.66	10.17	4.27
$H_2/4H_1$	0.19	0.17	0.16	0.20	0.15	0.15	0.14	0.17
K_D/K_R	2.41	11.83	2.76	6.51	1.71	3.11	1.36	3.51
h^2/H_2	5.93	1.64	2.84	1.03	0.028	0.58	0.02	0.11
h^2 NS (%)	0.26	0.30	0.28	0.14	0.47	0.52	0.51	0.39
t^2	4.76	3.15	0.11	0.62	4.38	5.04	6.63	5.16

* and ** significant at 5 % and 1 % levels of significance, respectively

Table 2: Genetic component for length of primary raceme, effective length of primary raceme, number of effective branches per plant, number of capsules on primary raceme in castor

Parameters	Length of primary raceme (cm)		Effective length of primary raceme (cm)		Number of effective branches per plant		Number of capsules on primary raceme	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
D	47.49* ± 4.70	49.51* ± 13.04	40.62* ± 4.22	41.79* ± 12.98	0.20 ± 0.32	0.30 ± 0.33	47.88* ± 8.62	51.42*± 12.59
H_1	83.16* ± 10.01	464.02* ± 111.04	47.88* ± 8.98	409.76* ± 110.60	1.57* ± 0.68	9.02* ± 2.89	103.64* ± 18.35	486.68* ± 107.26
H_2	53.30* ± 8.50	406.96* ± 94.37	28.14* ± 7.63	362.46 ± 93.99	0.99 ± 0.58	6.90* ± 2.45	88.12* ± 15.59	382.11* ± 91.16
F	36.02* ± 10.84	54.76 ± 60.18	17.20 ± 9.74	39.03 ± 59.94	0.10 ± 0.74	1.10 ± 1.56	9.22 ± 19.89	106.68 ± 58.13
h^2	0.85 ± 5.69	-0.27 ± 63.17	0.02 ± 5.11	-2.15 ± 62.91	-0.05 ± 0.38	5.64* ± 1.64	-1.10 ± 10.43	1.20 ± 61.01
E	4.03* ± 1.41	2.01 ± 3.93	6.13*± 1.27	4.97 ± 3.91	0.16 ± 0.09	0.06 ± 0.10	4.70 ± 2.59	1.16 ± 3.79
$(H_1/D)^{1/2}$	1.32	1.53	1.08	1.56	2.76	2.70	1.47	1.53
$H_2/4H_1$	0.16	0.21	0.14	0.22	0.15	0.19	0.21	0.19
K_D/K_R	1.80	2.13	1.48	1.85	1.20	4.94	1.14	5.14
h^2/H_2	0.016	-0.001	0.001	-0.006	-0.060	0.81	-0.01	0.003
h^2 NS (%)	0.54	0.20	0.62	0.20	0.45	0.26	0.50	0.20
t^2	2.92	0.14	0.37	0.29	6.12	2.92	1.63	3.82

* and ** significant at 5 % and 1 % levels of significance, respectively

Table 3: Genetic component for 100-seed weight, oil content and seed yield per plant in castor

Parameters	100-seed weight (g)		Oil content (%)		Seed yield per plant (g)	
	F_1	F_2	F_1	F_2	F_1	F_2
D	15.12* ± 1.64	15.12* ± 3.42	0.16* ± 0.02	0.13 ± 0.19	5833.71* ± 1328.68	3365.54 ± 1867.73
H_1	18.65* ± 3.50	228.26* ± 29.12	0.39* ± 0.04	4.37* ± 1.62	19711.79* ± 2828.22	43080.09* ± 15902.59
H_2	13.93* ± 2.98	180.87* ± 24.75	0.41* ± 0.03	4.35* ± 1.37	14993.53* ± 2403.67	27460.47* ± 13515.43
F	4.32 ± 3.80	24.96 ± 15.78	-0.13 ± 0.04	-0.22 ± 0.87	8418.58* ± 3065.66	11397.15 ± 8618.85
h^2	5.65* ± 1.9	8.56 ± 16.56	2.07* ± 0.02	0.21 ± 0.92	44965.31* ± 1608.92	96191.85* ± 9046.71
E	0.07 ± 0.49	0.07 ± 1.03	0.10* ± 0.006	0.12* ± 0.05	434.44 ± 400.61	2902.61* ± 563.14
$(H_1/D)^{1/2}$	1.11	1.94	1.55	2.80	1.83	1.78

$H_2/4H_1$	0.18	0.19	0.26	0.24	0.19	0.15
K_D/K_R	1.29	2.47	0.58	0.55	2.29	36.39
h^2/H_2	0.40	0.04	4.95	0.04	2.99	3.50
h^2 NS (%)	0.68	0.29	0.40	0.13	0.20	0.28
t^2	0.91	0.50	0.57	4.59	2.07	7.65

* and ** significant at 5 % and 1 % levels of significance, respectively

References

1. Dobariya KL, Dangaria CJ, Patel VJ. Combining ability in a castor diallel. J Maharashtra Agric. Univ. 1992; 17(2):235-238.
2. Giriraj K, Mensinkai SW, Sindagi SS. Components of genetic variation for yield and its attributes in 6x6 diallel cross of castor (*Ricinus communis* L.). Indian J Agric. Sci. 1974; 44(3):132-136.
3. Hayman BI. The theory and analysis of diallel crosses. Genetics. 1954; 39:789-809.
4. Jinks JL. The analysis of continuous variation in a dialle cross of *Nicotiana rustica* varieties. Genetics. 1954; 39:767-788.
5. Manga Gila A. Determination gene action of five yield and yield related characters of selected castor accessions in a 5×5 diallel crosses. Int. J Curr. Res. Aca. Rev. 2015; 3(6):374-379.
6. Mather K, Jinks JL. Biometrical genetics 3rd edition. Chapman and Hall, London, 1982.
7. Narkhede BN, Jadhav MS, Deokar AB. Combining ability analysis in castor. J Maharashtra Agric. Univ. 1985; 10(1):102-103.
8. Panera AV, Pathak AR, Madariya RB, Barad SH. Gene action for seed yield and its component traits in castor (*Ricinus communis* L.) using graphical and numerical approach of diallel analysis. J Pharmaco. and Phyto., 2018; 7(4):1870-76.
9. Patel KA. Genetic architecture of yield and component characters in castor (*Ricinus communis* L.). M.Sc. (Agri.) Thesis (Unpublished) Submitted to Gujarat Agricultural University, Sardarkrushinagar, 1998a.
10. Patel PS. Genetic architecture for sex expression and qualitative and quantitative characters in castor (*Ricinus communis* L.). Ph.D. Thesis (Unpublished) Submitted to Gujarat Agricultural University, Sardarkrushinagar, 1998b.
11. Singh H, Yadav TP. Genetic analysis of days to flowering, maturity and yield in castor. (*Ricinus communis* L.). Haryana Agric. Univ. J Res. 1981; 11(1):54-59.
12. Singh RK, Chaudhary BD. Biometrical Methods in Quantitative Genetic 159. Analysis. 3rd Ed. Ludhiana, New Delhi. Kalyani Publishers, 1985, 318.
13. Singh H, Yadav TP. Genetic analysis of days to flowering, maturity and yield in castor. (*Ricinus communis* L.). Haryana Agric. Univ. J Res. 1981; 11(1):54-59.
14. Sodavadiya PR. Genetic architecture of seed yield and yield attributing traits in castor (*Ricinus communis* L.). Ph.D. Thesis (Unpublished) submitted to Junagadh Agricultural University, Junagadh, 2010. 18.
15. Tank CJ, Jaimini SN, Ravindrababu Y. Combining ability analysis over environments in castor (*Ricinus communis* L.). *Crop Res.* 2003; 26(1):119-125.