

## Gene Action, Combining Ability, Genetic Parameters and Character Association Studies in Castor (*Ricinus communis* L.)

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### ABSTRACT

Castor (*Ricinus communis* L.) is an important non-edible oilseed crop of India. In 2021-22, castor is cultivated under an area of 0.8m. ha with a productivity of 2.2 t/ha. India contributes more than 80% of world requirement of castor oil and its derivatives. To meet the growing oil demand it is imperative to identify or to develop cultivars with high oil yield. The present study of combining ability, genetic parameters will be helpful in understanding the gene action associated with the traits and to identify better combiners to yield superior hybrids. Analysis of variance studies revealed that significant variation exists in the ma-

terial understudy. Higher estimates of SCA variance were observed than the GCA variance except for seed yield indicating preponderance of non-additive gene action in governing the traits. Significant gca effects were observed in SKP-84 and ICS-142 for seed yield and PPL-1001, SKI-215, DCS-86, PCS-327 and Kiran for oil content. Significant sca effect was observed for the crosses viz., M-574 x Kiran, PPL-1001 x SKI-215 and SKP-84 x JI-244 for total yield. Correlation studies revealed that, seed yield has recorded significant positive association with primary spike length, effective primary spike length and number capsules per primary spike whereas days to 50% flowering has shown significant positive association with number of nodes to primary spike. Heritability and genetic advance as per cent of mean studies indicated preponderance of non-additive gene action in governing the traits. Hence development of high yielding hybrids by exploiting hybrid vigour will be an effective method of crop improvement in castor.

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### INTRODUCTION

Castor (*Ricinus communis* L.) belongs to the family Euphorbiaceae and grows abundantly in tropical and sub-tropical countries (Weiss 2000). It is an industrially important crop because of its high seed oil content. Castor seed contains nearly 48% oil and ricinoleic acid is the major fatty acid component present in the

oil. India is the leading producer of castor with an area of 8 lakh ha. Production of 15 lakh tones and productivity of 1902 kg ha<sup>-1</sup> (FAOSTAT 2020) with exports of almost 80% of its total castor production. Castor oil is used as an efficient lubricant for high-speed engines and as an ingredient in soaps, shampoo, shoe polish, candles and ointments (Morris 2004, Gouri Shankar *et al.* 2010).

To meet the growing requirement of the industries, it is imperative to breed high yielding cultivars in castor. Knowledge of gene action of economically important traits and identification of suitable breeding methods are essential for castor improvement (Panera *et al.* 2018). In general, economically important traits viz., seed yield and oil content were observed to be governed by many genes (Cockerham 1961, Dube *et al.* 2018). The emphasis of castor breeding programs in India is majorly focused on higher seed yield, oil content and resistance to pests and diseases (Lavanya *et al.* 2006). Castor, being a cross pollinated crop emphasis was laid much on hybridization involving single and multiple crosses from different sources to develop improved hybrids with several traits superiority by exploiting heterosis.

Development of superior cultivars depends on genetic diversity of parental lines and combining ability of the parents involved in crossing programs (Lavanya and Chandramohan 2003, Ramana *et al.* 2005). The parents with known per se performance may result in generation of superior hybrid combinations. Further combining ability is a powerful tool to select good combiners and in turn involving the same as parental lines in hybridization programs to develop improved cultivars (Giriraj *et al.* 1973). Thus study on gene action and combining ability along with the knowledge of genetic parameters for any given trait will be much more helpful for a breeder to understand inheritance of a trait, to identify the parental lines with good combining ability and in turn to develop desirable cross combinations (Patel *et al.* 2015, Delvadiya *et al.* 2018).

## MATERIALS AND METHODS

The present study consisting of 48 entries viz., three pistillate lines (M-574, PPL-1001 and SKP-84 used

as testers/females) and eleven inbred lines (SKI-215, Kranthi, JI-244, JI-227, ICS-142, ICS-148, ICS-136, DCS-86, DCS-89, PCS-327 and Kiran used as lines/males) and their 33 hybrid combinations developed through line x tester mating design (Kempthorne 1957) along with standard check hybrid ICH-66 were evaluated in a Randomized Block Design with three replications during *kharif*, 2020 at the experimental plots of Regional Agricultural Research Station, PJT-SAU, Palem. The experimental location is situated between 16.51° N latitude and 78.24° E longitude at an elevation of 545 meters above mean sea level. Each entry was sown in a two rows of 6m length with a spacing of 90 × 60 cm. The observations of different agronomic characters viz., days to 50% flowering, days to maturity, 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 spikes per plant, number of capsules on primary raceme, 100-seed weight (g), seed yield per plot (g) and oil content (%) were recorded. The data were analyzed according to ANOVA (Steel and Torrie 1980). General and specific combining ability (GCA and SCA) analysis was done using line × tester method (Kempthorne 1957). Heritability and genetic advance as per cent of mean were also calculated as suggested by Allard (1960) and Johnson *et al.* (1955), respectively. The analysis was done using statistical software INDOSTAT software.

## RESULTS AND DISCUSSION

Analysis of variance revealed that mean square values of genotypes for all the traits were highly significant indicating presence of genetic variability in the material under study (Table 1). All the parents were shown significant effects for all the traits and parents vs hybrids significantly differed for majority of the traits viz., days to 50% flowering, number of capsules, number of effective spikes per plant, hundred seed weight and seed yield indicating considerable heterotic effect for the traits (Dube *et al.* 2018). Mean square values for line effects were significant for number of capsules, number of effective spikes per plant, seed yield and oil content. Variance due to males was higher compared to females except for primary spike length, effective primary spike length, number of effective spikes per plant and seed yield (Patel *et al.* 2015).

**Table 1.** Analysis of variance for different agronomic characters in castor.

Sources of variation	df	DF	DM	PHT	PSL	EPSL
Replications	2	39.53**	98.23**	149.43	65.29	62.28
Genotypes	46	50.06**	42.46**	242.53**	124.71**	127.35**
Parents	13	71.83**	21.25**	460.34**	100.46**	92.70**
Lines	2	211.11**	4.11	130.04	50.04	23.92
Testers	10	47.28**	24.49**	571.45**	112.57**	106.36**
L Vs T	1	38.83**	23.11	9.84	80.15	93.66
P Vs H	1	33.62**	3.2	129.84	88.57	106.26
Crosses	32	41.72**	52.31**	157.56**	135.69**	142.09**
Error	92	3.09	7.66	61.37	25.62	27.11

**Table 1.** Continued.

Sources of variation	NN	NC	NESPP	HSW	GY	OC
Replications	4.17	89.45	14.98**	5.46	3816.25	2.77
Genotypes	12.71**	217.00**	5.22**	31.81**	23732.91**	10.03**
Parents	18.95**	136.62**	2.89*	47.47**	10035.25**	14.32**
Lines	19.11**	279.00**	0.77	93.80**	1559.45	4.32
Testers	20.29**	118.89*	3.40*	42.91**	12732.54**	17.69**
L Vs T	5.21	29.14	2.02	0.41	13.91	0.63
P Vs H	0.1	4062.13**	9.55*	87.53**	341355.53**	13.69
Crosses	10.57**	129.50**	6.03**	23.71**	19371.88**	8.17**
Error	3.05	50.4	1.44	3.01	2945.53	2.34

Where,

DF - Days to 50% flowering, DM - Days to maturity, PHT – Plant height (cm), PSL – Primary spike length (cm), EPSL – Effective primary spike length (cm), NN – Number of nodes to primary spike, NC – Number of capsules per primary spike, NESPP – Number of effective spikes per plant, HSW – Hundred seed weight (g), GY – Seed yield per plot (g plot<sup>-1</sup>), OC – Oil content (%).

However significant variance due to females were observed for number of effective spikes per plant, seed yield and oil content (Table 2). GCA variance was found significant for number of capsules, number of effective spikes per plant, seed yield, hundred seed weight and oil content indicating significant impact of parental lines on the traits. Instead, SCA variance was found highly significant for all the traits except for number of effective spikes per plant (Ramesh *et al.* 2013, Aher *et al.* 2015, Punewar *et al.* 2017). Thus signifies predominance of non-additive gene action in governing these traits (Ramu *et al.* 2002). The ratio of GCA to SCA variance was less than unity for all the traits except for seed yield thus indicating non-additive effect in governing the traits under study (Ramu *et al.* 2002; Delvadiya *et al.* 2018, Panera *et al.* 2018). However higher significant gca variance for seed yield suggests that selection of superior parental

lines give rise to high yielding hybrid combinations (Solanki and Joshi 2000, Solanki *et al.* 2003)

Estimation of gca effects (Table 3) for parental lines revealed that, females and males showed significant effect for all the traits. However for seed yield, SKP-84 and ICS-142 were found good general combiners compared to other parents. For days to 50% flowering, M-574, Kranthi, JI-244, JI-227 were negatively significant and found early. For earliness, SKI-215, JI-227, ICS-142 were found negatively significant and considered good general combiners for the trait. For oil content, PPL-1001, SKI-215, DCS-86, PCS-327 and Kiran were considered to be good general combiners as the parents were positively significant for the trait.

Sca effects (Table 4) for seed yield were pos-

**Table 2.** Mean square (ANOVA) of general and specific combining ability for different characters in castor.

Sources of variation	df	DF	DM	PHT	PSL	EPSL
Replications	2	27.31**	68.49**	26.41	54.3	42.58
Crosses	32	41.72**	52.31**	157.56**	135.69**	142.09**
Line effects	2	36.37	7.46	240.48	347.78	317.68
Tester effects	10	50.08	69.48	142.47	54.47	66.85
Female x Male	20	38.08**	48.20**	156.81**	155.09**	162.14**
Errors	64	3.01	8.24	45.93	28.8	30.56
Estimates						
Var F		1.00	-0.006	5.42	9.76	8.8
Var M		5.22	6.86	9.01	3.2	4.41
GCA Var		1.91	1.46	6.19	8.35	7.86
SCA Var		11.66**	13.51**	31.81**	43.15**	45.00**
GCA Var/ SCA Var		0.16	0.108	0.194	0.193	0.17

**Table 2.** Continued.

Sources of variation	NN	NC	NESPP	HSW	GY	OC
Replications	1.3	14.61	7.84**	1.97	4014.75	0.87
Crosses	10.57**	129.50**	6.03**	23.71**	19371.88**	8.17**
Line effects	3.12	354.10*	23.75**	26.94	122670.04**	30.02*
Tester effects	13.67	166.84	6.83	36.94	13596.49	10.31
Female x Male	9.76**	88.36	3.86**	16.77**	11929.76**	4.92**
Errors	3.04	54.25	1.18	3.11	3087.23	1.97
Estimates						
Var F	0.002	9.20*	0.67**	0.72	3628.01**	0.84**
Var M	1.18	12.93	0.59	3.77	1183.43	0.88
GCA Var	0.25	10.00**	0.65**	1.37**	3104.17**	0.84**
SCA Var	2.23**	12.65*	0.8	4.58**	2994.74**	0.85*
GCA Var/ SCA Var	0.11	0.79	0.81	0.28	1.03	0.98

Where,

DF - Days to 50% flowering, DM - Days to maturity, PHT - Plant height (cm). PSL - Primary spike length (cm), EPSL - Effective primary spike length (cm), NN - Number of nodes to primary spike, NC - Number of capsules per primary spike, NESPP - Number of effective spikes per plant, HSW - Hundred seed weight (g), GY - Seed yield per plot (g plot<sup>-1</sup>), OC - Oil content (%).

itively significant for M-574 x Kiran, PPL-1001 x SKI-215, SKP-84 x JI-244 thus considered as good specific combiners for the trait. For earliness, PPL-1001 x Kranthi, PPL-1001 x PCS-327 were found to be good specific combiners for the trait. For days to 50% flowering, M-574 x JI-244, M-574 x JI-227, M-574 x DCS-89, PPL-1001 x ICS-148, PPL-1001 x Kiran, SKP-84 x SKI-215, SKP-84 x ICS-136 and SKP-84 x PCS-327 were found good specific combiners for the trait. The parental lines with significant

gca effect for earliness were also yielded significant hybrid combinations for the trait.

Correlation studies (Table 5) among the traits under study revealed that, seed yield was found positively associated with primary spike length, effective primary spike length and number of capsules per primary spike (Sridhar *et al.* 2010, Ramanjaneyulu and Reddy 2012, Movaliya *et al.* 2018). Thus indicating

**Table 3.** Estimation of general combining ability effects for different agronomic traits in castor.

Parents	DF	DM	PHT	PSL	EPSL	NN	NC	NESPP	HSW	GY	OC
M-574	-0.99**	0.37	2.83*	2.77**	2.63**	0.27	1.25	-0.6**	0.28	-19.78*	-0.99**
PPL-1001	1.10**	0.16	-0.3	-3.57**	-3.41**	-0.33	-3.72**	0.97**	-1.01**	-48.62**	0.91**
SKP-84	-0.11	-0.53	-2.53	0.79	0.78	0.061	2.46	-0.36	0.73*	68.40**	0.09
SE (Lines)	0.3	0.48	1.36	0.88	0.9	0.3	1.23	0.21	0.3	9.44	0.26
CD at 5%	0.61	0.96	2.72	1.76	1.81	0.67	2.46	0.41	0.6	18.87	0.53
SKI-215	1.86**	-1.90*	6.79*	-0.15	-0.76	1.83**	-1.8	1.12**	0.58	-8.25	1.34*
Kranthi	-1.46*	-1.24	-2.84	-4.56**	-5.62**	-1.17*	-3.91	-0.32	-1.49*	-29.78	-0.25
Ji-244	-2.9**	-1.68	0.27	-0.61	0.23	-0.72	3.52	1.01*	1.12	-13.32	-0.11
Ji-227	-3.9**	-3.79**	-8.16**	-1.08	-0.81	-0.94	-4.14	-0.65	-0.12	-22.66	-1.06*
ICS-142	3.86**	-2.35*	1.79	2.89	4.03*	1.38*	5.97*	0.677	-0.03	79.26**	-1.14*
ICS-148	0.53	1.98*	2.59	1.03	2.09	1.05	3.52	-1.43**	4.70**	32.19	-1.69**
ICS-136	2.20**	4.64**	3.01	1.25	1.73	0.82	3.97	-0.32	-1.74**	4.53	-0.77
DCS-86	-0.57	2.53**	0.55	-1.94	-2.3	-1.62**	-0.58	-0.76	1.11	-0.24	1.12*
DCS-89	-0.9	-0.68	1.53	4.70**	3.25	-0.5	4.08	1.121**	0.3	7.51	0.42
PCS-327	-0.79	-1.354	-2.39	-0.94	-0.69	-1.17*	-5.36*	0.12	-2.87**	24.64	1.04*
Kiran	2.09**	3.86**	-3.156	-0.57	-1.16	1.05	-5.25*	-0.54	-1.54**	-73.87**	1.10*
SE (Testers)	0.58	0.92	2.61	1.68	1.73	0.58	2.36	0.4	0.58	18.09	0.51
CD at 5%	1.17	1.84	5.21	3.37	3.46	1.16	4.72	0.79	1.16	36.14	1.02

Where,

DF - Days to 50% flowering, DM - Days to maturity, PHT - Plant height (cm), PSL - Primary spike length (cm), EPSL - Effective primary spike length (cm), NN - Number of nodes to primary spike, NC - Number of capsules per primary spike, NESPP - Number of effective spikes per plant, HSW - Hundred seed weight (g), GY - Seed yield per plot (g plot<sup>-1</sup>), OC - Oil content (%).

improvement in these traits can lead to positive improvement in seed yield. Days to 50% flowering has shown positive significant association with number of nodes (Nagarajan *et al.* 2019). Thus selection for reduced number of nodes to primary spike may give rise to early flowering. Number of nodes also shown

positive significant association with plant height, primary spike length and effective primary spike length. Primary spike length and effective primary spike length were positively correlated with each other and with number of capsules per primary spike and hundred seed weight.

**Table 4.** Estimation of specific combining ability effects for different agronomic traits in castor effect.

Crosses	DF	DM	PHT	PSL	EPSL	NN	NC	NESPP	HSW	GY	OC
M-574 x SKI-215	2.76**	0.51	-0.05	1.99	1.18	0.83	0.41	0.93	0.76	-53.25	0.87
M-574 x Kranthi	2.10*	4.51**	3.13	1.80	2.49	-0.16	-3.47	0.38	-1.06	-7.63	1.33
M-574 x Ji-244	-2.45*	-2.04	-1.87	-7.35*	-7.98**	-0.27	-2.58	-1.61*	-0.25	44.53	0.62
M-574 x Ji-227	-2.12*	1.73	-5.99	-0.30	-0.36	-1.71	9.08*	0.71	-0.97	-7.13	1.04
M-574 x ICS-142	-1.23	-1.34	-2.29	-10.22**	-10.03**	0.61	-3.36	-0.61	-0.66	-93.22**	0.97
M-574 x ICS-148	-0.23	3.29*	-0.12	4.20	5.22	0.61	4.74	-0.50	-0.32	31.34	-1.46
M-574 x ICS-136	4.43**	0.62	14.09**	14.58**	15.38**	4.17**	-0.030	-0.61	2.15*	37.98	-1.62
M-574 x DCS-86	-0.45	-2.93	-9.51*	-7.62*	-7.30	-1.71	3.52	0.82	-2.43*	-36.63	-1.45
M-574 x DCS-89	-2.45*	2.23	3.16	1.03	-0.66	0.17	0.52	-0.06	-0.66	5.30	-1.48
M-574 x PCS-327	-1.89	-2.70	5.42	3.01	1.61	0.17	-3.69	-0.061	4.88**	-11.95	1.24
M-574 x Kiran	1.54	3.92*	-5.97	-1.12	0.45	-2.17**	-5.14	0.606	-1.4	90.65**	-0.08
PPL-1001 x SKI-215	0.01	0.72	4.12	6.80*	6.72*	-0.55	5.05	-0.303	1.09	84.03**	0.09
PPL-1001 x Kranthi	-0.99	-8.27**	-5.88	-3.35	-1.37	-0.88	4.82	-0.192	1.00	-8.14	-1.18
PPL-1001 x Ji-244	3.45**	1.83	1.57	-2.14	-1.54	0.33	1.05	0.808	-0.05	-115.35**	-0.58
PPL-1001 x Ji-227	3.12**	0.94	-2.65	0.53	2.06	1.89	-7.28	-1.19	0.95	42.20	-0.02
PPL-1001 x ICS-142	-1.32	4.17*	3.37	7.06*	6.35*	-0.77	-3.06	-1.52*	0.16	54.77	-1.52
PPL-1001 x ICS-148	-4.32**	0.84	-6.03	-5.95*	-6.47*	-1.77	-3.61	0.25	0.03	-7.81	0.41
PPL-1001 x ICS-136	0.01	0.17	-4.83	-3.54	-4.09	-1.55	4.60	0.47	-3.62**	-27.54	0.39

**Table 4.** Continued.

Crosses	DF	DM	PHT	PSL	EPSL	NN	NC	NESPP	HSW	GY	OC
PPL-1001 x DCS-86	-0.212	0.94	11.54*	4.62	3.43	2.55*	-3.17	-0.08	4.45**	14.70	0.71
PPL-1001 x DCS-89	2.78**	0.83	3.89	-3.25	-3.59	0.11	-6.17	-63	-1.96	-61.85	0.72
PPL-1001 x PCS-327	4.01**	-4.83**	-4.09	2.19	3.30	0.11	0.27	1.36	-1.95	61.06	-0.63
PPL-1001 x Kiran	-6.54**	2.61	-0.99	-2.97	-4.82	0.55	7.49	1.03	-0.10	-36.07	1.60
SKP-84 x SKI-215	-2.77**	-1.24	-4.06	-8.79**	-7.91*	-0.28	-5.46	-0.63	-1.85	-30.77	-0.97
SKP-84 x Kranthi	-1.11	3.75*	2.75	1.55	-1.12	1.05	-1.35	-0.19	0.06	15.77	-0.15
SKP-84 x JI-244	-1.00	0.20	0.30	9.49**	9.51**	-0.06	1.53	0.80	0.30	70.80*	-0.04
SKP-84 x JI-227	-1.00	-2.68	8.65	-0.22	-1.70	-0.17	-1.79	0.47	0.01	-35.07	-1.01
SKP-84 x ICS-142	2.55*	-2.79	-1.08	3.16	3.68	0.16	6.42	2.14**	0.49	38.44	0.54
SKP-84 x ICS-148	4.55**	-4.13*	6.15	1.75	1.24	1.16	-1.13	0.25	0.29	-23.52	1.04
SKP-84 x ICS-136	-4.44**	-0.798	-9.26*	-11.03**	-11.29**	-2.61*	-4.57	0.14	1.47	-10.44	1.22
SKP-84 x DCS-86	0.66	1.98	-2.02	2.99	3.87	-0.83	-0.35	-0.74	-2.02*	21.93	0.74
SKP-84 x DCS-89	-0.33	-3.13	-7.06	2.21	4.25	-0.28	5.64	0.69	2.62*	56.55	0.76
SKP-84 x PCS-327	-2.11*	7.54**	-1.33	-5.20	-4.92	-0.28	3.42	-1.30	-2.93**	-49.11	-0.61
SKP-84 x Kiran	5.00**	1.31	6.96	4.09	4.37	2.16*	-2.35	-1.63	1.52	-54.58	-1.53
CD @ 95%	2.03	3.19	9.03	5.83	6.00	2.01	8.19	1.38	2.00	62.59	1.77

Where,

DF - Days to 50% flowering, DM - Days to maturity PHT – Plant height (cm) PSL – Primary spike length (cm) EPSL – Effective primary spike length (cm) NN – Number of nodes to primary spike NC – Number of capsules per primary spike, NESPP – Number of effective spikes per plant, HSW – Hundred seed weight (g), GY – Seed yield per plot (g plot<sup>-1</sup>), OC – Oil content (%).

Heritability provides information about the extent of which a particular genetic character can be transmitted to the successive generations (Mangi *et al.* 2010). Heritability estimates along with genetic advance would be more successful in predicting the effectiveness of selecting the best individuals (Johnson *et al.* 1955). Genetic advance, which estimates

the degree of gain in a trait obtained under a given selection pressure, is an important parameter that guides the breeder in choosing a selection program (Hamdi *et al.* 2003). High heritability and high genetic advance for a given trait indicates that it is governed by additive gene action and, therefore, provides the most effective condition for selection (Tazeen *et al.*

**Table 5.** Estimation of character association among different agronomic traits in castor.

	TY	DF	DM	NN	PHT	PSL	EPSL	NCPP	NESPP	HSW	OC
TY	1.000										
DF	0.102	1.000									
DM	-0.089	0.066	1.000								
NN	0.002	0.512**	0.091	1.000							
PHT	-0.090	0.223	0.061	0.760**	1.000						
PSL	0.295*	0.242	0.156	0.499**	0.496**	1.000					
EPSL	0.340*	0.263	0.123	0.479**	0.453**	0.982**	1.000				
NCPP	0.500**	0.023	0.121	0.076	-0.010	0.387**	0.402**	1.000			
NESPP	0.078	0.068	-0.343*	-0.164	-0.095	-0.123	-0.124	0.102	1.000		
HSW	0.042	0.105	-0.014	0.362*	0.292*	0.347*	0.324*	0.023	-0.204	1.000	
OC	-0.032	0.089	-0.111	-0.017	-0.001	-0.239	-0.272	-0.147	0.486**	-0.126	1.000

Where,

DF - Days to 50% flowering, DM - Days to maturity, PHT – Plant height (cm), PSL – Primary spike length (cm), EPSL – Effective primary spike length (cm), NN – Number of nodes to primary spike, NC – Number of capsules per primary spike, NESPP – Number of effective spikes per plant HSW – Hundred seed weight (g) GY – Seed yield per plot (g plot<sup>-1</sup>), OC – Oil content (%).



**Table 6.** Estimation of heritability and genetic advance as per cent of mean for different traits in castor.

	PV	PSD	H <sub>(NS)</sub>	Mean	GA	GAM
TY	10184.94	100.92	0.61	569.41	126.61	22.24
DF	16.51	4.06	0.23	48.03	1.93	4.03
DM	19.00	4.36	0.15	103.25	1.39	1.34
NN	3.76	1.94	0.14	14.07	0.54	3.83
PHT	64.66	8.04	0.19	43.74	3.17	7.26
PSL	68.41	8.27	0.24	25.80	4.16	16.13
EPSL	69.77	8.35	0.23	23.67	3.88	16.39
NCPP	49.46	7.03	0.40	57.31	5.80	10.11
NESPP	2.60	1.61	0.51	5.70	1.69	29.72
HSW	8.34	2.89	0.33	27.62	1.96	7.11
OC	3.34	1.83	0.51	43.67	1.92	4.39

Where,

DF - Days to 50% flowering, DM - Days to maturity, PHT - Plant height (cm); PSL - Primary spike length (cm), EPSL - Effective primary spike length (cm), NN - Number of nodes to primary spike; NC - Number of capsules per primary spike, NESPP - Number of effective spikes per plant, HSW - Hundred seed weight (g), GY - Seed yield per plot (g plot<sup>-1</sup>), OC - Oil content (%).

PV - Phenotypic variance, PSD - Phenotypic standard deviation; H<sub>(NS)</sub> - Heritability narrow sense, GA - Genetic advance, GAM - Genetic advance as per cent of mean, DD - Degree of dominance.

2009).

In the present material, the heritability (narrow sense) ranged from 15 to 61% for days to maturity and total yield, respectively (Table 6). Majority of traits viz., days to 50% flowering (23%), days to maturity (15%), number of nodes (14%), plant height (19%), primary spike length (24%), effective primary spike length (23%) showed low heritability whereas number of capsules (40%), number of effective spikes per plant (51%), hundred seed weight (33%) and oil content (51%) showed moderate narrow sense heritability as it was evident that majority of traits were governed by non-additive gene action through combining ability studies. The results were in contrast with the findings of Patel *et al.* (2010), Rukhsar *et al.* (2018) and Nagarajan *et al.* (2019) wherein high heritability was observed for the above traits. Genetic advance as per cent of mean ranged from 1.34 to 29.72 for days to maturity and number of effective spikes per plant, respectively. For majority of traits the values of genetic advance as per cent of mean are low to moderate except for seed yield (22.24) and number of effective spikes per plant (29.72). Degree of dominance indicates the magnitude of dominance

deviation relative to the additive variance. Higher the degree of dominance value more will be the trait expressibility of the hybrid progeny. In the present cross, degree of dominance value was observed to be more than unity for most of the characters indicating over-dominance expression of these traits except for total yield (0.69) and number of effective spikes per plant (0.78).

As the traits were having low to moderate heritability, genetic advance as per cent of mean and less than unity *gca* to *sca* variance with more than unity of degree of dominance indicates fixation of traits in generations will be difficult and hence hybrid breeding and identifying high heterotic hybrids will result in achieving higher yields.

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