Combining ability analysis of some newly developed white rust resistant lines of Indian mustard (BRASSICA JUNCEA L. CZERN & COSS).

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ABSTRACT

Combining ability analysis of 6x6 diallele set of crosses in Indian mustard for 9 quantitative traits revealed preponderance of non-additive gene effects for yield per plant, plant height and days to maturity whereas additive gene effect was found to be predominant for the inheritance of rest of characters. The parent NRCM-10, NRCM-56, NRCM-75 and NRCM-85 appeared to be good general combiner for most of the characters. NRCM-10 X NRCM-75 (10.32) recorded highest SCA effect for yield per plant.

KEYWORDS- Brassica juncea, Indian mustard, GCA, SCA, Heterosis.

Introduction

Indian mustard (Brassica juncea) is a self pollinated species, yet in this crop frequent out-crossing occurs which varies from 5 to 30% depending upon the environmental conditions and random variation of pollinating insects. Cytologically Indian mustard is an amphidiploid (2n=36), derived from interspecific cross of *Brassica campestris* (2n=20) and Brassica nigra (2n=16) followed by natural chromosome doubling. These relationships have been confirmed by the artificial synthesis of amphidiploids species by hybridizing basic diploid species and also by analysis of chloroplast and mitochondrial DNA restriction pattern of basic and amphidiploids species. The improved mustard seeds contain 39-44% oil. For International acceptance, erucic acid content should be <2%.In India the area of rape and mustard 5.92Mha, Production 6.78MT and yield 1145kg/ha in 2018- 19. Seed quality, Seed yield and other yield related parameters of Brassica oil seed crop has been tried to improve by several researchers Heterosis is the best way to improve crop varieties. All the high yielding released varieties are highly susceptible to white rust. Heterosis is the interpretation of increased vigor, size, fruitfulness, development speed, resistance to disease and insect pests or climatic vigors, manifested by cross-bred organisms as compared with corresponding inbreds (Shull, 1952; Jinks and Jones, 1958).Development of hybrid cultivars has been successful in many Brassica spp. (Miller, 1999). For the study of inheritance of quantitative characters and evaluation of various possible breeding procedures in heterosis phenomena, the comprehensive study of combining ability is immensely essential (Allard, 1960). Combining ability studies emphasized the preponderance effect of GCA on yield and most of the yield components, indicating the importance of additive gene action (Wos et al., 1999). On the other hand, Pandey et al. (1999) reviewed evidences for the presence of significant SCA effects for yield and yield components, indicating the importance of non-additive gene action. Singh et al. (2005) reported that non-additive genetic effects in addition to additive effects accounted for yield heterosis. In Indian mustard Singh et al. (2006) observed that general and specific combining ability variance were highly significant for almost all the characters and reported that high GCA for 1000 seed weight and oil content. High SCA for seed yield and oil content. Keeping these points in view, the present investigation was undertaken to determine GCA and SCA of parental lines.

Material and method

The experimental material comprised of total six promising white rust resistant lines of Indian mustard (B. juncea) namely NRCM-10, NRCM-21, NRCM-35, NRCM-56, NRCM-75 and NRCM-85. These lines were developed by crossing *B.juncea* genotype with *B. napus for introgression* of White rust resistance to *B.juncea at Directorate of rapeseed –mustard, Sewar, Bharatpur (Raj)*. These lines are nearly isogenic lines.

Development of F1 hybrids

Five rows of six WR lines of mustard of 5m length were sown in the *Directorate of rapeseed –mustard, Sewar, Bharatpur, (Raj)* and maintaining plant to plant and row to row distance 10 cm and 30 cm respectively. Normal agronomic practices were applied in the field. At the flowering, these six lines were cross in all possible combinations under complete diallele system through hand emusculation and controlled pollination. Paper bag were used for avoiding contaminations.

Table 1: White rust resistant lines used in diallele derived from *Brassica napus*.

NRCM-10	BEC107/Hyola401	Resistant
NRCM-21	BEC107/Hyola401//Varuna	Resistant
NRCM-35	GSLI/BIO902	Resistant
NRCM-56	BEC107/NRCG411	Resistant
NRCM-75	NRCG57/RH819	Resistant
NRCM-85	RH819/NPC03//Kranti/GSLI	Resistant

Result and Disscussion

The analysis of variance was carried out for nine characters and showing the significant difference amongst all the parents excepts plant height and main shoot length. While the crosses exhibited significant mean sum of square for all characters except siliqua on main shoot (Vaghela et al. (2011), Patel et al. (2012), Arifullah (2013)). However, parent vs. crosses exhibited significant differences for yield per plant.

The ANOVA for GCA and SCA indicated that variance due to GCA and SCA were highly significant for all the characters. The variance due to SCA is higher than the GCA for yield per plant, plant height and days to maturity indicated that role of non-additive gene action inheritance of these traits Vaghela et al. (2011), Yadav et al. (1993), pradeep et al. (2013).

In other hand GCA is higher than SCA for main shoot length, siliqua on main shoot, siliquae length, seed per plant, oil content and seed weight. The GCA: SCA ratio was less than one for all the characters. This indicated that non- additive component player more role in inheritance of these characters. This is in agreement with the studies of Rao and Gulati (2001) and Patel et al. (1993).

The promising combiners based on per se performances and significant GCA effects (Table 3) were NRCM-10 , NRCM-35, NRCM-56, NRCM-85 for main shoot length, NRCM-10 and NRCM-35 and NRCM-75 for plant height, NRCM-10 and NRCM-85 for siliqua length, NRCM-10 and NRCM-56 for seed per siliqua, NRCM-56, NRCM-75 and NRCM-85 for seed weight. These results accordance with Singh et al. (2005), Singh et al. (2007), Sadanand et al. (2009), Patel et al. (2012) and Gami and Chauhan (2013). NRCM-10, NRCM-56, NRCM-75 and NRCM-85 appeared to be good general combiner for most of the characters. The parents discussed above had high general combining ability and fixable component of gene action additive and additive x additive type of epitasis, these could be successfully exploited by developing homozygous line have used for improved character for which improvement was desired. These parental lines might be utilized for producing the intermatting population in order to get desirable recombinants in Indian mustard.

Out of 15 crosses, 8 crosses had positive significant SCA effect for yield per plant and 7 crosses had negative SCA effect. NRCM-10 X NRCM-75 (10.32) recorded highest SCA effect followed by NRCM-56 X NRCM-75 (6.65), NRCM-35 X NRCM-56 (6.11), NRCM-56 X NRCM-85 (5.29), NRCM-10 X NRCM-85 (5.13), NRCM-10 X NRCM-56 (4.75), NRCM-10 X NRCM-21 (3.26), and NRCM-10 X NRCM-35 (2.65) for yield per plant. The cross NRCM-75 X NRCM-85 (-9.74), NRCM-35 X NRCM-75 (-6.96), NRCM-21 X NRCM-35 (-6.54) and NRCM-21 X NRCM-85 (-5.76) were observed to be record negative significant SCA effect these findings also reported by different workers viz; Dixit et al. (2007), Yadav et al. (2009) Vaghela et al. (2011) and Maurya et al. (2012).

The potentiality of a variety may be judged by comparing performance *per se*, while the combining ability of the parents can be judged by the F_1 values. The potentiality of the cross to be forwarded to next generation is decided on the basis of high mean performance, high GCA of one or both the parents involved in the cross, and with the negative SCA effects.

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Table 1: ANOVA of parents F1's for 9 characters in a 6 parental diallele cross of Indian mustard (mean sum of squares).

Source of variation	df	Yield /plant	Plant height	Main shoot length	Siliquae on main shoot	Siliquae length	Seed/ siliquae	Oil content	Seed weight	Days to maturity
Replication	1	3.89**	175.08**	24.50	172.34*	0.080	14.06**	3.82**	0.354**	14.38**
Diallele progenies	35	0.103	5.26	2.56	21.52	0.064	0.25	0.04	0.003	0.609
Parents	5	70.69**	21.63	31.63	297.36**	11.04**	146.37**	102.57**	15.44**	110.5**
Crosses	29	2.55**	235.34**	60.96**	12.82	0.413**	1.70*	12.26**	0.077*	60.85**
F1	14	0.52**	278.79**	112.68**	419.69**	40.71**	35.68**	28.97**	40.2**	19.33**
rf1	14	15.30**	422.54**	279.49**	738.67**	0.85**	11.42**	1.54**	0.359**	17.83**
f vs l	1	0.55**	26.07	12.03	3.55	0.16**	0.55	1.30**	0.004	2.50
Parent vs crosses	1	0.31**	0.148	19.76	5.95	0.009	0.77	0.34	0.0025	0.149
Error	35	0.06	20.36	11.95	25.92	0.02	0.35	0.12	0.01	1.11

**Significant at p = 0.05; *Significant at p = 0.01

Table 2: ANOVA for combining ability and related statistics of 9 characters in a 6 parental diallel cross of F_1's in Indian mustard

source of variation	yield / plant	plant height	main shoot length	Siliquae on main shoot	Siliquae length	Seed/ siliquae	Oil content	Seed weight	Days to maturity
Gca	5.20**	1.31**	21.55**	26.39**	4.64**	4.83**	5.68**	0.17**	7.59**
Sca	6.89**	5.75**	6.89**	15.71**	1.20**	0.53**	4.59**	0.04**	7.84**
error	0.56	0.13	0.74	4.60	0.15	0.02	0.12	0.01	0.04
$\sigma^2 g$	4.34	0.59	20.69	24.43	4.49	4.76	5.11	0.17	6.61
$\sigma^2 s$	6.33	5.62	6.15	11.11	1.05	0.51	4.47	0.03	7.80
V_A	8.68	1.18	41.38	48.85	8.98	9.53	10.21	0.33	13.22
VP	15.01	6.80	47.53	59.96	10.03	10.04	14.68	0.36	21.02
H2	0.58	0.17	0.87	0.81	0.90	0.95	0.70	0.92	0.63
h2	7.89	6.75	7.89	16.71	2.20	1.53	5.59	1.04	8.84
gca:sca	0.60	0.31	0.86	0.77	0.89	0.95	0.71	0.89	0.66
Cvp	37.58	1.39	9.37	11.03	73.19	19.71	9.32	11.83	3.31
Cva	28.58	0.58	8.74	9.96	69.25	19.21	7.77	11.33	2.63

**Significant at p = 0.05; *Significant at p = 0.01

Table 3: Estimates of gca effects of 6 parents for 9 characters in F_1's of a diallel cross in Indian mustard

Parents	yield / plant	plant height	main shoot length	Siliquae on main shoot	Siliquae length	Seed/ siliquae	Oil content	Seed weight	Days to maturity
NRCM-10	-0.25	2.98**	0.89*	0.00	0.36*	0.57**	0.09	-0.63	-1.07
NRCM-21	-0.24	2.62	0.48	-0.02	-0.33	0.56	-0.09	-0.25	0.35
NRCM-35	-0.77	2.03**	1.30**	0.05	-0.78	-0.03	-0.09	-4.78	0.21*
NRCM-56	-0.15	-0.87	0.97*	0.12	-0.81	0.16*	0.02	2.63**	-0.88
NRCM-75	0.84*	1.58**	-1.43	0.13	0.27	-0.21	0.19	3.16**	-0.26
NRCM-85	-0.14	-3.41	1.10*	0.11	0.56**	0.05	-0.05	1.68**	0.10
SE (gi)	0.24	0.11	0.27	0.69	0.12	0.045	0.11	0.032	0.064
SE (gi - gj) ±	0.66	0.31	0.76	1.90	0.34	0.12	0.30	0.088	0.17

**Significant at p = 0.05; *Significant at p = 0.01

Table 4: Estimates of sca effects for 9 characters of 15 F_1's derived from a 6 parents of diallel cross in Indian mustard.

NRCM-10 X NRCM-21	3.26**	4.26**	3.68**	3.89**	0.7**	0.09**	0.89**	0.25**	2.65**
NRCM-10 X NRCM-35	2.65**	2.3**	2.96**	3.26*	0.85**	0.025	0.56*	0.34**	3.98**
NRCM-10 X NRCM-56	4.75**	1.4**	2.35**	4.65**	1.26**	0.06**	0.11	0.1	3.26**
NRCM-10 X NRCM-75	10.32**	-2.56	3.26**	5.8**	1.35**	0.02**	0.94**	-0.5	2.98**
NRCM-10 X NRCM-85	5.13**	2.8**	5.32**	3.68*	0.56*	0.036**	0.55*	-1.23	3.56**
NRCM-21 X NRCM-35	-6.54	1.48**	-3.5	-5.3	1.26**	0.045**	0.66**	0.58**	4.12**
NRCM-21 X NRCM-56	-4.88	3.68**	1.563**	1.69	0.63*	0.23**	0.65**	0.12	4.35**
NRCM-21 X NRCM-75	-1.39	1.36**	2.52**	0.62	0.74**	0.025**	0.24	0.21**	3.59**
NRCM-21 X NRCM-85	-5.76	2.54**	-4.2	6.56**	0.68**	0.075**	0.15	0.45**	2.62**
NRCM-35 X NRCM-56	6.11**	-1.52	5.32**	0.29	0.78**	0.046**	0.35	0.14*	2.36**
NRCM-35 X NRCM-75	-6.96	1.46**	4.26**	7.63**	0.12	0.024	0.38	0.15*	3.95**
NRCM-35 X NRCM-85	-1.39	-2.58	5.8**	-7.56	0.4	0.034**	0.81**	0.26*	3.67**
NRCM-56 X NRCM-75	6.65**	-3.21	6.3**	0.58	0.52*	0.039**	0.22	0.25**	2.85**
NRCM-56 X NRCM-85	5.29**	1.26**	-5.3	5.26**	0.65*	0.029**	0.53*	0.35**	3.64**
NRCM-75 X NRCM-85	-9.74	1.52**	2.3**	4.53**	0.86**	0.042**	0.75**	0.36**	3.26**
SE (sij)	0.45	0.22	0.52	1.29	0.23	0.08	0.21	0.06	0.12
SE (sij - sik)	0.61	0.29	0.70	1.75	0.32	0.12	0.28	0.08	0.16

*Significant at p = 0.05; **Significant at p = 0.01