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Study on Combining Ability for Selection of Superior Parents and Crosses in Yellow Sarson

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ABSTRACT: Yellow sarson is the premium oilseeds crop because of having high oil content with good shelf quality. The crop has been not explored much as not grown in extensive area across country. Crop is cultivated mostly in northern and eastern part of country. Not much improvement work has been done in yellow sarson and there is ample scope for its improvement and further exploitation. In the present investigation parents were evaluated on the basis of their combining ability and identified to be used as parent in the breeding programme.

Fourteen parents were selected on the basis of their performance and diversity. 10 were taken as female lines and 4 as testers. 40 crosses were made and crosses along with parental line were evaluated on RBD. Results revealed the presence of dominance for all the traits. The average degree of dominance indicated the presence of non-fixable gene action. Narrow sense heritability (h^2n) found low for all the traits which further confirmed the prevalence of non-additive gene action in the expression of traits. Estimates of GCA effects revealed that B-9 was good general combiner for days to maturity. For Plant height and siliqua density, Jhumka and For number of seeds/siliqua and seed yield/plant YS-166 was the best parent while NDYS-116, NDYS-128, NDYS-2018 and NDYS-132 were found to be the good general combiner for siliquae on main raceme, length of main raceme and siliqua length respectively. Out of 40 crosses, one cross had shown significant SCA in desirable direction for days to maturity and siliqua length. Seven crosses were significant in desirable direction for plant height, Siliqua density and seeds per siliqua. For primary branches and seed yield per plant six crosses while for length of main raceme five crosses had shown significant SCA effects. Four crosses were found significant for test weight and siliquae on main raceme. For oil content eighteen crosses were significant in desirable direction. The superior crosses identified based on their SCA effects for yield as well as oil content were having G × G, G × P, G × A, A × P or P × P GCA parents. These results indicate the action of additive × additive, additive × dominance, dominance× dominance gene interactions for expression of these traits. The contribution of interaction of line× tester was found to be higher than the lines and testers for all the Characters except days to maturity, siliquae on main raceme, length of main raceme, siliqua length, seeds/siliqua and 1000-seed weight. A single parent with good GCA for all the agronomic trait was not found, though there were parents with good GCA for many yield contributing traits. Such identified parents can be incorporated in the hybridization programme for improvement of yellow sarson.

Keywords: Yellow sarson, Combining ability, Genetic component.

INTRODUCTION

Brassica crops are being cultivated in 53 countries covering six continents across the globe with a production of oilseed as well as vegetable crop. India contributes 23.23% area and 16.10% production to the world. After soybean, rapeseed-mustard are second largest oilseed crop and contribute about 30 per cent of the total oilseeds production in India. The area, production and productivity of rapeseed-mustard was 6.79 million ha, 9.12 million tones and 1345kg/ha respectively during 2019-20 (Agricultural Statistics at a Glance, 2020).

Yellow sarson (*Brassica rapa* var yellow sarson) an important ecotype of rapeseed is one of the three variants of *Brassica rapa* i.e., AA genome and among them it is the highest oil yielding. It is gaining preference due to its higher oil quality which can be attributed to its thin seed coat (Mahanta and Barua, 2020). Moreover, its yellow seed coat colour imparts light coloured clearer oil which is preferred over brown seeded toria and brown sarson (Snehi *et al.*, 2019). As compared to mustard, yellow sarson have high oil content (up to 46 %), and early maturing. It is usually used in crop rotation with various vegetables and sugarcane. Its oil is mainly utilized for cooking purposes and in addition to this; the yellow sarson is mostly preferred as leafy vegetable among all cultivated oilseed crops in India (Chatterjee, 1992). Yellow sarson being autogamous has an advantage over out- breeding toria types. But generally yellow sarson varieties suffer from low productivity due to its high vulnerability towards biotic and abiotic stresses. Therefore well built breeding programmes are required for varietal improvement. For this, the available genetic variability can be explored and selection can be done accordingly in desirable direction. Information on the relative importance of the additive (GCA) and non-additive (SCA) gene actions in a breeding population guides the breeder for effective breeding procedure to follow (Dudley and Moll, 1969). Assessment of combining ability in general and in specific combination provides information regarding the nicking ability of particular genotype thereby the parents can be identified for specific traits and can be utilized in hybridization program to maximize the gain. Combining ability analysis gives knowledge about the nature, and magnitude of genetic variance for components of productivity. Further estimation of combining ability effects would enable to differentiate efficient and productive genotypes for creating more productive resource base. Kempthorne, (1957) proposed line × tester analysis as a beneficial tool for screening the lines with speed and reasonable confidence. An appropriate dynamic representation of the genotypic reactions to the varying environments would be of all most significance in exploiting genetic variation efficiently. Most of the available varieties in the past were developed using simple selection method hence problem of narrow genetic base among the varieties persist. Due to narrow genetic base the expression of heterosis is generally very low. The pre-breeding work in term of identification of parents for different yield attributing traits and development of diverse genetic pool is found rarely in the earlier report. Therefore there is an urgent need to revisit the extent of genetic variability in the yellow sarson along with the identification of parents in general and specific combinations for developing heterotic breeding material.

MATERIALS AND METHODS

The experimental materials consisted of 40 F_1's derived from the crosses of 10 lines *viz.* NDYS-2018, NDYS-107, Binoy (B-9), NDYS-115, Jhumka, YS-166, NDYS-132, NDYS-116, NDYS-128 and NRCYS-0502 as females and 4 testers *viz.* Pant Pili Sarson-1 (PPS-1), NRCYS-0501, Pusa Gold and NYDS-113 as males which were crossed in line × tester mating design. The crosses and their parents were evaluated in a randomized block design with three replications and for 11 traits including days to maturity, plant height, length of main raceme, siliquae on main raceme, siliqua density, number of primary branches, siliqua length, seeds per siliqua, 1000-seed weight, seed yield per plant, and oil content. Observation on oil content was recorded using FT-NIR. The Line × tester analyses model as described by Kempthorne, (1957) are used which provides information about general and specific combining ability of parents and crosses.

RESULTS AND DISCUSSION

A. Analysis of variance

It is reflected from ANOVA table that sufficient variability was found among the treatments (Table 1). Partitioning of treatment into parents, crosses, and parent vs. crosses showed that the variances due to parents and crosses were highly significant for all the traits. However, variance due to parents vs. crosses was highly significant for days to maturity, plant height, number of primary branches, siliquae on main raceme, siliqua length, seeds per siliqua, seed yield per plant and oil content whereas significant variation was observed for siliqua density. Non-significant variations for parents vs. crosses were obtained for length of main raceme and 1000 seed weight.

Table 1: ANOVA for Line × Testers mating design including parents and crosses for 11 different characters in yellow sarson.

Sr. No.	Line	df	Characters										
			DM	PH	LMR	SMR	SD	PB	SL	SS	SY	TW	OC
1.	Replication	2	0.20	22.75	1.54	8.92	0.002	0.04	0.15	0.91	0.49	0.07	0.09
2.	Treatment	53	71.29**	223.41**	48.34**	87.92**	0.01**	3.32**	0.59**	70.86**	7.49**	0.43**	1.96**
3.	Parent	13	106.35**	256.58**	30.89**	59.40**	0.01**	3.08**	0.58**	74.29**	6.11**	0.20**	2.35**
4.	Crosses	39	57.59**	217.34**	55.38**	95.92**	0.02**	3.05**	0.35**	67.91**	6.52**	0.51**	1.75**
5.	Parent vs. Crosses	1	149.72**	29.13**	0.17	146.98**	0.02*	16.99**	9.98**	141.43**	63.04**	0.12	5.16**
6.	Error	106	4.56	18.05	7.85	5.75	0.003	0.19	0.07	1.40	0.25	0.04	0.25

Analysis of variance for combining ability revealed that variances due to lines were significant for all the traits except number of primary branches and oil content while variances due to testers were significant for siliqua length, seeds per siliqua and test weight. Variances due to line × tester were significant for all the traits (Table 2).

Table 2: ANOVA for combining ability 11 different characters in yellow sarson.

Sr. No.	Source of variance	df	Characters										
			DM	PH	LMR	SMR	SD	PB	SL	SS	SY	TW	OC
1.	Line	9	185.16**	309.44**	136.25**	266.48**	0.02	4.53	0.69**	193.22**	11.69*	1.46**	1.16
2.	Tester	3	15.53	11.26	30.76	48.69	0.02	1.51	0.95**	115.65**	6.04	0.54*	0.05
3.	Line × Tester	27	19.74**	209.53**	31.16**	44.31**	0.01**	2.72**	0.17**	20.84**	4.85**	0.19**	2.13**
4.	Error	106	4.56	18.05	7.85	5.75	0.003	0.19	0.07	1.40	0.25	0.04	0.25

B. Estimation of component of variances and their magnitude

The results revealed that variances due to SCA were very high in comparison to the variance due to GCA for all the characters which showed preponderance of non-additive gene action for controlling the characters understudy (Table 3). Similar pattern was also noticed in the estimates of σ^2A and σ^2D. Estimates of σ^2D were high as compare to σ^2A which again reflected the major role of non additive gene action. Preponderance of non-additive gene action had also been reported earlier by Rai and Verma (2005); Verma *et al.,* (2009); Rahman *et al.,* (2011); Patel and Patel (2005); Snehi *et al.*, (2020); Tomar *et al.*, (2018). Genetic component analysis for estimation of variability and selection parameter was also reported in Indian mustard (Meena *et al.*, 2016; Adhikari *et al.*, 2018). The range of predictability ratio was from 0.004 (Plant height) to 1.333 (siliqua length). Predictability ratio was found less than 1 for all the traits except siliqua length which indicated involvement of fixable gene action for the trait therefore, simple selection method would be the appropriate breeding methodology. For rest of the traits non-fixable gene action was predominant. In such a situation heterosis breeding would be quite effective. The degree of dominance ranged from 0.866 (siliqua length) to 15.668 (Plant height). For most of the traits the estimate of the degree of dominance (DD) was more than one which showed presence of over dominance while for siliqua length the estimate was less than one which confirmed the involvement of partial dominance for controlling the concern trait. Narrow sense heritability was ranged from 0.30% (Plant height) to 5.16% (length of main raceme). The narrow sense heritability was low for all the traits which further confirm the involvement of non-additive gene action.

Though true over-dominance at specific loci can't be ruled out but the observed levels of over-dominance have generally been traced to mimicking effect of epistasis and linkage which don't warrant the production of only hybrids to exploit heterosis. Under such situations there is every chance of producing inbred lines or populations as good as or even better than hybrids that would obviate the need of costly procedure of producing seed of hybrids on a continuous basis. All the situation falling short of over-dominance, call for development of inbred lines or open pollinated populations in the form of synthetics, composite or improved version of population itself. The existence of over dominance is an indicative of short term gain that can be quickly realized through the development of hybrids and synthetics. Recurrent selection is also an apparent choice when over-dominance is operative. But with partial dominance it is ineffective. However, reciprocal recurrent selection is predicted to be effective regardless of dominance level.

Table 3: Estimates of component of variance and their magnitude for 11 characters in yellow sarson.

Characters	o^2gca	O^2sca	o^2A (D)	o^2D(H)	PR	DD	h^2_{ns} (%)
DM	0.62	5.06	1.24	5.06	0.245	2.020	4.63
PH	0.13	63.83	0.26	63.83	0.004	15.668	0.30
LMR	0.85	12.86	1.7	12.86	0.132	2.750	5.16
SMR	0.39	7.77	0.78	7.77	0.100	3.156	3.65
SD	0.0001	0.02	0.0002	0.02	0.010	10.000	3.00
PB	0.01	0.8	0.02	0.8	0.025	6.325	1.62
SL	0.002	0.003	0.004	0.003	1.333	0.866	1.65
SS	0.08	6.48	0.16	6.48	0.025	6.364	0.65
SY	0.03	1.53	0.06	1.53	0.039	5.050	2.25
TW	0.001	0.05	0.002	0.05	0.040	5.000	1.19
OC	0.006	0.63	0.012	0.63	0.019	7.246	0.94

C. Estimation of GCA effects

Identification of good combiner is the first and foremost step of any successful breeding programme. The success of programme is decided on the basis of choice of genotypes as parents. The estimate of GCA with *per se* performance is an indicator of nicking ability of parents in general. The parent having good GCA effect can serve as better donor as compare to those having poor GCA effect. The results of GCA estimates revealed that none of the parents was good general combiner for all the traits under study (Table 4) whereas parents were found good for more than one character during the study. B-9 and NDYS128 was identified as good general combiner for days to maturity. For Plant height, B-9 and Jhumka while NDYS116, NDYS-128, NDYS-2018 and NDYS-132 were found to be the best parent for length of main raceme, siliquae on main raceme and siliqua length respectively. For number of seeds per siliqua and seed yield per plant YS-166 was emerged out as best parent with desirable significant effect. On the basis of GCA effect, summary of good combiner was prepared and is presented in Table 5. The above identified parents can be used in future hybridization programme targeted to specific trait/traits and ultimately maximum heterosis can be realized.

Table 4: GCA effects of lines and testers for 11 different characters in yellow sarson.

Sr. No.		Characters										
		DM	PH	LMR	SMR	SD	PB	SL	SS	SY	TW	OC
	Lines											
1.	NDYS-2018	0.49	-3.97**	-2.64	-6.26**	0.03**	-0.28	0.45**	1.89**	-1.15**	0.18*	0.07
2.	NDYS-107	2.66**	4.76**	-5.29**	-1.09	-0.08	-0.25	-0.09	3.23**	-1.11**	-0.44**	0.33
3.	B-9	-8.92**	-6.75**	-0.55	-1.76	0.01	-0.63	-0.11	-7.78**	-0.84**	-0.04	-0.70**
4.	NDYS-115	-1.42	0.49	-3.64**	-0.96**	-0.05**	0.99**	-0.15	2.23**	-0.15	-0.68**	-0.53**
5.	Jhumka	-1.34	-9.34**	-1.96	-8.05	0.08**	0.49**	-0.29**	1.48**	-0.87**	-0.18*	-0.22
6.	YS-166	1.33	5.69**	0.83	-0.77	0.02	-0.61**	0.04	4.06**	1.56**	0.04	-0.01
7.	NDYS-132	4.83**	2.71	3.36**	4.66**	-0.00	-0.45*	0.17	-3.44**	0.92**	0.45**	0.25
8.	NDYS-116	0.74	3.43**	1.64	5.14**	-0.03*	-0.49**	0.29**	-5.28**	0.92**	0.14	0.32
9.	NDYS-128	-2.42**	-0.02	4.88**	4.99**	0.02	0.42*	-0.04	2.39**	0.79**	0.27**	-0.15
10.	NRCYS-05-02	4.08**	3.00	3.37**	4.10**	0.01	0.79**	-0.26*	1.23	-0.07	0.26**	0.20
	Testers											
11.	PPS-1	-0.79	-0.31	0.29	-1.51*	0.03*	0.16	-0.01	-2.94**	-0.59*	-0.18**	0.02
12.	NRCYS-05-01	0.24	0.81	-0.33	-0.56	0.00	0.15	0.25**	0.99**	-0.02	-0.00	0.04
13.	Pusa Gold	-0.32	-0.59	1.22	1.28**	0.01	0.01	-0.09	0.86**	0.50**	0.04	0.02
14.	NDYS-113	0.88	-0.09	-1.18	0.79	-0.03*	-0.32**	-0.15	1.09**	0.07	0.14*	-0.08

Table 5: Best parents for different characters identified on the basis of GCA effects.

Characters	Parents					
	1	*Per se* performance	2	*Per se* performance	3	*Per se* performance
DM	B-9	96.67	NDYS-128	107.67	-	-
PH	Jhumka	144.37	B-9	107.26	-	-
LMR	NDYS-116	57.62	NDYS-128	60.58	NDYS-132	56.68
SMR	NDYS-128	11.47	NRCYS-0502	39.53	NDYS-132	38.60
SD	Jhumka	0.74	-	-	-	-
PB	NDYS-115	7.13	NRCYS-0502	7.57	Jhumka	6.67
SL	NDYS-2018	5.77	NDYS-116	6.63	-	-
SS	YS-166	36.67	NDYS-107	31.33	NDYS-128	32.67
SY	YS-166	7.74	NDYS-132	6.84	NDYS-116	7.43
TW	NDYS-132	5.20	NDYS-128	4.83	NRCYS-0502	4.79
OC	NDYS-107	42.73	NDYS-116	42.14	NDYS-132	41.74

D. Specific combining ability effects

The SCA effects of crosses were estimated to know the performance of specific cross for the specific character (Table 6) and accordingly the SCA effects is being utilized through exploitation of heterosis. The result of SCA effects was found that one cross had shown significant SCA in desirable direction for days to maturity and siliqua length. Seven crosses were significant in desirable direction for plant height, Siliqua density and seeds per siliqua. For primary branches and seed yield per plant six crosses while for length of main raceme five crosses had shown significant SCA effects. Four crosses were found significant for test weight and siliquae on main raceme. For oil content eighteen crosses were significant in desirable direction. Out of all the Crosses, NDYS-132 × NDYS-113 (-3.46**) for days to maturity, NDYS-115 × Pusa Gold (-15.79**) for plant height, NDYS-107 × PPS-1 (7.32**) for length of main raceme, B-9 × Pusa Gold (6.10**) for silquae on main raceme, NRCYS-05-02 × Pusa Gold (4.98**), for seeds per siliqua, NDYS-128 × PPS-1 (2.02**) for seed yield per plant, NDYS-107 × PPS-1 (1.84**) for primary branches, NRCYS-05-02 × Pusa Gold (0.44*) for siliqua length, NDYS-107 × NRCYS-05-01 (0.42**) for 1000 seed weight and YS-166 × NDYS-113 (2.12**) for oil content were expressed highest SCA effects in desirable direction. Identification of parents and their specific crosses has also been done and reported by Mall *et al.,* (2010), Gautam *et al.,* (2010); Rahman *et al.,* (2011); Dutta, (2014); Meena *et al.,* (2014); Gami *et al.,* (2015); Meena *et al.,* (2016); Adhikari *et al.,* (2018); Shrimali *et al.,* (2018); Tomar *et al.,* (2018); Lal *et al.,* (2018); Snehi *et al.,* (2019); Mahanta and Barua (2020) for yellow sarson improvement.

Table 6: SCA effect of crosses for 11 different characters in yellow sarson.

Sr. No.	Line	Characters										
		DM	PH	LMR	SMR	SD	PB	SL	SS	SY	TW	OC
1.	NDYS-2018 × PPS-1	-1.46	-0.09	1.46	3.62	-0.02	-0.79*	-0.19	0.11	-1.25**	-0.02	-0.35**
2.	NDYS-2018 × NRCYS-05-01	-1.49	-13.56**	1.75	-1.67	-0.01	-0.91	0.09	0.84	0.36	-0.02	0.32**
3.	NDYS-2018 × Pusa Gold	-3.26	2.92	2.03	-3.64	0.09*	0.42	0.00	-1.02	0.29	-0.02	0.31**
4.	NDYS-2018× NDYS-113	6.21**	10.73**	1.74	1.68	-0.05	1.29**	0.09	0.08	0.60	-0.01	-0.28**
5.	NDYS-107 × PPS-1	1.04	4.57	0.85	7.32**	-0.07	1.84**	0.03	0.78	-1.12**	-0.29	-0.08**
6.	NDYS-107 × NRCYS-05-01	3.01	9.25	0.31	-2.85	0.03	0.05	0.178	-0.49	0.42	0.42**	-0.58**
7.	NDYS-107 × Pusa Gold	-2.09	-1.44	-0.35	-5.08**	0.05	-0.81*	0.05	-3.03**	0.49	0.23	1.31**
8.	NDYS-107 × NDYS-113	-1.96	-12.38**	-0.81	0.61	-0.02	-1.08**	-0.24	2.74**	0.21	-0.36*	-0.65**
9.	B-9 × PPS-1	-1.04	-4.78	0.50	-1.69	0.03	1.12**	-0.09	-0.22	-0.53	0.15	-0.02
10.	B-9 × NRCYS-05-01	-2.08	-4.43	-3.68	-2.11	-0.04	-1.23**	-0.15	1.84	0.25	-0.03	-0.68**
11.	B-9 × Pusa Gold	0.82	5.81	6.10**	5.26**	0.04	0.01	0.06	-3.36**	0.32	-0.08	-0.24**
12.	B-9 × NDYS-113	2.29	3.40	-2.93	-1.46	-0.04	0.09	0.19	1.74	-0.03	-0.03	0.95**
13.	NDYS-115 × PPS-1	-1.54	6.13	3.99	0.45	0.59**	-1.07**	0.01	-1.56	0.29	-0.72**	-0.10**
14.	NDYS-115 × NRCYS-05-01	-1.58	4.52	-4.12	0.68	-0.08*	1.21**	-0.24	-0.16	0.59**	-0.69**	0.79**
15.	NDYS-115 × Pusa Gold	1.99	-15.79**	-4.16	-4.95*	-0.01	-0.35	0.10	-2.69**	-2.14**	0.10	0.15**
16.	NDYS-115 × NDYS-113	1.12	5.14	4.29	3.81	0.03	0.21	0.13	4.41**	1.26**	0.37*	-0.85**
17.	Jhumka × PPS-1	2.37	0.34	-2.29	-3.19	0.00	-0.37*	0.22	0.14	-0.80	-0.29	0.49**
18.	Jhumka × NRCYS-05-01	2.34	-1.98	3.13	-3.14	0.11**	0.88	-0.40	-1.40	0.22	0.09	0.79**
19.	Jhumka × Pusa Gold	-1.09	-0.40	2.58	5.29**	-0.23**	-0.09	0.18	0.73	-0.21	-0.02	-0.67**
20.	Jhumka × NRCYS-05-01	-3.63	2.04	1.04	-3.42	-0.09	-0.42	0.00	0.83	0.79	0.22	-0.61**
21.	YS-166 × PPS-1	0.37	5.04	-3.60	0.19	0.05	-0.00	0.15	-0.72	0.09	0.39*	-0.38**
22.	YS-166 × NRCYS-05-01	1.34	-0.38	0.71	2.15	0.02*	-0.43	0.38	0.68	-0.50	-0.71**	-0.81**
23.	YS-166 × Pusa Gold	0.24	-2.83	3.94**	-2.54	-0.09	0.29	-0.29	2.14**	0.38	0.25	-0.93**
24.	YS-166 × NDYS-113	-1.96	-1.83	-1.05	0.19	0.16**	0.15	-0.24	-2.09**	0.03	0.06	2.12**
25.	NDYS-132 × PPS-1	0.54	-9.37**	2.36	1.59	-0.01	0.24	-0.18	-1.89	-0.63	-0.06	0.21**
26.	NDYS-132 × NRCYS-05-01	2.84	-0.79	1.27	-2.88	-0.06	0.25	-0.03	-1.83	0.67	-0.09	0.73**
27.	NDYS-132 × Pusa Gold	0.07	3.12	-3.17	-0.47	0.03	-1.34**	-0.09	2.31**	-0.06	-0.19	0.29**
28.	NDYS-132 × NDYS-113	-3.46**	7.05**	-0.47	1.76	0.04	0.85	0.30	1.41	0.23	0.36*	-1.28**
29.	NDYS-116 × PPS-1	-0.04	6.51	1.83	-3.28	-0.08*	-0.31	0.20	3.28**	0.57	-0.01	-0.79**
30.	NDYS-116 × NRCYS-05-01	-2.08	2.89	1.89	5.34*	0.10**	0.74*	0.02	1.34	-0.93	0.15	0.59**
31.	NDYS-116 × Pusa Gold	2.49	3.76	-0.44	-1.41	-0.02	0.47	-0.07	0.14	-0.05	0.02	0.44**
32.	NDYS-116 × NDYS-113	-0.38	-13.17**	0.51	-0.65	-0.01	-0.89*	-0.15	-4.76**	0.40	-0.15	-0.24**
33.	NDYS-128 × PPS-1	0.79	-12.71**	-5.03**	-3.66	-0.00	0.43	0.15	1.61	2.02**	0.05	0.33**
34.	NDYS-128 × NRCYS-05-01	0.76	0.98	4.43**	2.89	-0.01	-0.31	0.21	2.34*	-2.45**	0.21	-0.67**
35.	NDYS-128 × Pusa Gold	-0.68	0.98	3.81**	-2.19	-0.07	-0.31	-0.38	-0.19	-0.01	-0.19	-0.24**
36.	NDYS-128 × NDYS-113	-0.88	10.75**	-3.21	2.95	0.08*	0.18	0.01	-3.76**	0.44	-0.06	0.58**
37.	NRCYS-0502 × PPS-1	-1.04	4.36	-2.08	0.65	0.03	-1.07**	-0.31	-1.23	1.36**	0.14	0.69**
38.	NRCYS-0502 ×NRCYS-05-01	-3.08	3.50	4.57**	-1.39	-0.07	-0.25	-0.03	-3.16**	1.35**	0.06	-0.54**
39.	NRCYS-0502 × Pusa Gold	1.49	3.88	-1.03	0.39	0.01	1.71**	0.44**	4.98**	1.00*	-0.12	-0.42**
40.	NRCYS-0502 × NDYS-113	2.62	-11.75**	-1.46	0.35	0.02	-0.39	-0.09	-0.59	-3.71**	-0.08	0.27**

The superior crosses identified based on their SCA effects for yield as well as oil content were having G × P, A × A, A × P or P × P GCA parents. These results indicate the operation of additive × additive, additive × dominance, dominance × dominance gene interactions for expression of these traits. Operation of later type of interaction was more prevalent as promising crosses combined low × low GCA parents gesturing towards role of diallel selective mating, heterosis breeding and biparental mating for improvement of those specific crosses (Table 7). There appeared some correspondence between the magnitude of SCA effect and *per se* performance of the promising crosses. Subsequently, pointing the chance of marking superior cross combination based on either of these parameters. Further there was no consistency in the GCA effects of the parents involved in the crosses having significant SCA effects.

Table 7: Prospective cross combinations based on *per se* performance and desirable SCA effects seed yield per plant and oil content (%) and suggesting breeding strategy.

Cross combinations	*Per se* performance	SCA effects	GCA effect of combining parent	Other characters with significant SCA effects	Suggested breeding method
Seed yield per plant (g/plant)					
NDYS-128 × PPS-1	10.01	2.02**	G×P	SS, SL, PB, SMR, LMR	Heterosis breeding/diallel selective mating with selection pressure on SS, PB, SL, SMR & LMR
NRCYS-0502 × PPS-1	8.50	1.36**	P×P	PB, SMR, LMR	
NRCYS-0502 × NRCYS-0501	9.09	1.35**	P×P	SL, PB, LMR	
NDYS-115 × NDYS-113	9.38	1.26**	P×P	SS, SL, PB, LMR	
NRCYS-0502 × Pusa Gold	9.23	1.00*	P×G	SS, SL, PB, SMR, LMR	
Oil content (%)					
YS-166 × NDYS-113	46.01	2.12**	A×P	-	Heterosis breeding/diallel selective mating
NDYS-107 × Pusa Gold	45.65	1.31**	A×P	-	
B-9 × NDYS-113	44.03	0.95**	P×P	-	

E. Contribution of lines, testers and lines × testers

The relative contribution of lines and testers and their interaction gave an indication of about the magnitude ad nature of genetic variability present in material studied. The contribution of lines and testers is reflected in the presence of additive gene action whereas the relative importance of non-fixable gene action can be realized only with the interaction effects.

The contribution of lines, testers and line ×tester interactions for all the traits in yellow sarson are presented in Table 8. Top level input was recorded for days to maturity (74.19%) followed by 1000-seed weight (66.04%), number of seeds per siliqua (65.66%) and length main raceme (64.11%). Lowest contribution was registered for oil content (15.29%). Among the testers highest contribution was noticed in siliqua length (20.74%), number of seeds per siliqua (13.09%) and siliqua density (8.69%). The lowest tester contribution was expressed for oil content (0.24%). The interaction of line × tester was maximum for oil content (84.47%) followed by plant height (66.74%), number of primary branches per plant (61.84%) and siliqua density (55.36%). The contribution of interactions (line ×tester) was found higher than the lines and testers for all the traits except days to maturity, length of main raceme, siliquae on main raceme, siliqua length, seeds per siliqua and 1000-seed weight. The results showed the importance of non-additive gene action for controlling the characters under consideration. These finding were again approved the relative high magnitude of SCA than GCA variance for the traits studied.

Table 8: Contribution of line, tester and their interaction towards total variance.

Sr. No.	Characters	Lines	Testers	Interaction
1.	Days to maturity	74.19	2.07	23.73
2.	Plant height (cm)	32.86	0.39	66.74
3.	Length of main raceme (cm)	56.77	4.27	38.96
4.	Siliquae on main raceme	64.11	3.90	31.98
5.	Siliqua density	35.94	8.69	55.36
6.	No. of primary branches	34.35	3.81	61.84
7.	Siliqua length (cm)	45.11	20.74	34.15
8.	Seeds per siliqua	65.66	13.09	21.24
9.	Seed yield per plant (g)	41.37	7.13	51.51
10.	1000-seeds weight (g)	66.04	8.17	25.79
11.	Oil content (%)	15.29	0.24	84.47

CONCLUSION

On the basis of research finding and discussion obtained from the present investigation, non-additive genetic variance was found to be more prominent as compare to additive genetic variance for most of the characters which suggested perceptible advance of maintaining heterozygosity or restoring it at the end of the breeding programme. Potential parents and crosses have been identified based on relevant multiple parameters. The parents can be utilized as donor for specific trait and crosses can be utilized through heterosis breeding by adopting most appropriate breeding strategies suggested during the study for overall improvement of yellow sarson. A long term breeding programme can also be initiated where the selective parents can be involved for improvement of specific character. Pedigree method can be practiced to have desirable outcome with maximum improvement.

Future scope: Combining ability analysis is an excellent method for identification of parents for development of heterotic cross combinations. During the study parents were evaluated on the basis of their GCA and SCA effects. Parents showed good combining ability for different agro-morphological traits. These identified donors can further be utilized as parents for improvement of seed potential of crop and/or any trait specific breeding programme. The analysis also helps in development of diverse gene pools. Grouping of Germplasm into diverse gene pool is the basis for development of heterotic hybrids. Therefore the identified donor for specific trait will help the breeder in formulation the breeding programme for improvement of crop.

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