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Short Communication

Triple test cross analysis for metric traits in yellow *sarson* (*Brassica rapa* var. yellow *sarson* Prain) across environments

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Various biometrical designs have been used in different crops to estimate various types of gene effects. In most of the designs, it is assumed that non-allelic interactions are absent, where as the fact is often contrary to the assumption. The information on genetics, especially on epistatic gene effects, of important characters in yellow *sarson* (*Brassica rapa* var. *yellow sarson* Prain), an autogamous crop is meagre. The triple test cross technique which especially tests the non-allelic interactions and also provides equally precise estimates of the additive and dominance components of genetic variation, has been used for genetic analysis of seed yield, oil content and component traits in yellow *sarson* across environments

Two true breeding testers SSK 92-13 (L_1) and NDYS-2 (L_2), and their F_1 (L_3) were crossed individually with 20 diverse strains of yellow *sarson* (NDYS-38, NDYS 44, NDYS-9502, NDYS-9503, NDYS-9506, NDYS-9508, NDYS-9509, Benoy, MYSL-203, MYSL-204, YSC-26, YSC-32, YSC-53, YSC-56, YSC-58, NRCY-5, NRCY-7, YST-151, RAUDYS-81-9 and BIO-YS-1) as females to produce L_{1i}, L_{2i} and L_{3i} families, respectively. Of the two testers, NDYS-2 is a carmel seeded, white rust resistant, high yielding variety developed through gamma irradiation at NDUAT, Faizabad, and SSK-92-13 is a yellow seeded, high yielding strain developed at S. K. Nagar, Gujarat. These two testers thus represent diverse origin. The experimental material comprising of three testers (L_1, L_2, L_3) and 20 L_{1i}, L_{2i} and L_{3i} families each was evaluated in randomized complete block design with three replications during 2000-01 in three environments, two of which were under irrigated conditions- first at CRS Masodha (E1) and second at Kumarganj (E2), and third under rainfed condition at CRS Masodha (E3). Each family was assigned a single row of 3 m length spaced at 30 cm with plants spaced at 15 cm. Observations recorded on 10 randomly selected plants/ replication for 11 metric traits viz. days to flowering (DF), days to maturity (DM), plant height (PH), primary branches/plant (PB), siliquae/plant (SP), seeds/siliqua (SS), 1000-seed weight (TW), biological yield (BY), seed yield /plant (SY), harvest index (HI) and oil content (OC) were subjected to triple test cross analysis [1].

The pooled analysis of variance for 11 characters over three environments, showed highly significant differences due to treatments, hybrids, parents and lines for all the characters indicating wide genetic diversity among genotypes for the various characters (Table 1).

Table 1. Combined ANOVA for different characters of yellow *sarson* in triple test cross analysis over environments

Source of variation	df	DF	DM	PH	PB	SP	SS	TW	BY	SY	HI	OC
Environment	2	5.03**	2.66**	16.34**	3.63**	5.65	7.73*	0.75**	0.49	0.25	2.64**	0.12
Treatment	82	74.81**	30.90**	439.18**	3.44**	979.72**	70.82**	0.37**	83.62**	41.97**	7.89**	3.15**
Hybrids (H)	59	20.70**	17.91**	421.44**	1.49**	484.02**	58.32**	0.29**	55.58**	1.82**	4.63**	2.51**
Parents (P)	22	131.10**	48.72**	426.10**	4.05**	795.83**	99.00**	0.34**	61.54**	2.19**	3.57**	4.61**
Lines (L)	19	98.91**	53.49**	414.51**	3.61**	796.17**	108.12**	0.38**	57.22**	1.88**	2.77**	3.77*
Testers (T)	2	3.00**	20.70**	523.56**	3.25**	732.82**	0.05	0.20	73.28**	2.84**	12.09**	7.08*
P_1+P_2 *vs* F_1	1	0.02	20.17**	774.46**	2.08**	889.79**	0.02	0.02	33.44**	3.68**	1.25	0.01
P_1 *vs* P_2	1	6.00**	14.52**	14.52**	3.74**	279.25**	0.06	0.37	101.98**	0.77*	22.52**	14.16**
L *vs* T	1	998.99**	14.03*	450.96**	13.88**	915.39**	123.52**	0.01	120.10**	6.87**	1.62	15.54**
H *vs* P	1	2029.15**	406.59**	1770.87**	105.11*	34270.86**	188.45**	5.74**	2227.00**	252.58**	295.81**	9.21*
Error	164	0.37	0.50	2.79	0.25	3.70	1.80	0.07	1.34	0.15	0.57	2.18

*,** Significant at 5% and 1% probability levels, respectively.

Table 2. Detection of epistasis for seed yield and its component characters in yellow *sarson* over environments

Characters		Mean sum of squares					
		[i] type epistasis	[j+1] type epistasis	Total epistasis	[i] type epistasis × environment	[j+1] type epistasis × environment	Total epistasis × environment
	df	1	19	20	2	38	40
DF	E_1	24.07	33.65**	33.17**	6.02	8.81	8.67
	E_2	355.27	10.95*	28.17**	88.82**	4.86	9.06
	E_3	19.27	11.44	11.83*	4.82	6.22	6.15
	Pooled	37.35	5.93**	7.51**	9.36**	1.46	1.85
DM	E_1	12.15	47.45*	45.68**	3.04	5.24	5.13
	E_2	106.67	24.98**	29.07**	26.67	3.64	4.79
	E_3	510.62	4.59	29.88**	127.60	4.12	10.30
	Pooled	27.57	9.84**	10.73**	6.89*	1.39	1.66
PH	E_1	21945.94	945.70**	1995.72**	5486.48**	26.55	299.53
	E_2	1991.81	657.16**	723.89**	497.95**	29.12	52.57
	E_3	5249.09	724.76**	950.98**	1312.27**	83.08	144.54
	Pooled	7815.97	446.17**	814.66**	1953.99**	13.74	110.75
PB	E_1	336.54	6.64	23.13**	84.13**	7.04	10.89
	E_2	10.25	11.51**	11.45**	2.56	3.55	3.50
	E_3	4.06	9.69**	9.41*	1.01	2.57	2.49
	Pooled	61.68	3.10	6.03**	15.42**	1.84	2.52
SP	E_1	3467.12	1648.00**	1738.95	866.78**	51.28	92.05
	E_2	90.04	622.57**	595.94	22.51	22.35	22.35
	E_3	2352.51	1589.04**	1627.21	588.13**	86.81	111.88
	Pooled	43.85	353.17**	337.71**	10.96	20.19	19.73
SS	E_1	373.00	50.14	66.29	93.25**	18.51	22.25
	E_2	8.14	60.00	57.41	2.03	48.38	46.06
	E_3	121.84	29.96	34.56	30.46	22.20	22.61
	Pooled	84.02*	19.63	22.85	21.01	13.06	13.45
TW	E_1	0.44	1.46	1.41	0.11	1.43	1.36
	E_2	9.35*	3.01	3.33	2.34	1.34	1.39
	E_3	0.25	1.63	1.56	6.37*	1.87	1.78
	Pooled	1.15	0.64	0.67	0.29	0.42	0.41
BY	E_1	1440.01	633.18**	673.53**	360.00**	16.62	33.79
	E_2	636.84	268.10**	286.34**	158.21**	33.45	39.69
	E_3	71.50*	364.76**	350.10**	17.88	18.94	18.89
	Pooled	2.09	164.59**	156.66**	0.52	7.12	6.79
SY	E_1	64.85	20.55**	22.76**	16.21**	1.67	2.40
	E_2	6.81	10.17**	10.00	1.70	3.74	3.64
	E_3	0.88	13.52**	12.89	0.22	2.17	2.07
	Pooled	2.25	6.42**	6.21**	0.56	0.87	0.85
HI	E_1	27.73**	35.46**	35.07**	6.93	4.96	5.01
	E_2	44.25*	48.37**	48.16**	11.06	11.86	11.82
	E_3	22.56	61.29**	59.35**	5.64	7.39	7.31
	Pooled	4.18	14.36*	13.85**	1.05	2.71	2.63
OC	E_1	77.42	23.57**	26.26**	19.35**	0.40	1.34
	E_2	5.40	19.81**	19.09**	1.35**	0.19	0.25
	E_3	4.13**	25.35**	24.29**	1.03	0.57	0.54
	Pooled	19.23	12.78**	13.11**	4.81**	0.15	0.38

*,** Significant at 5% and 1% probability levels, respectively

The significant mean squares due to testers, P_1 *vs* P_2 and $P_1 + P_2$ *vs* F_1 for all characters except SS and TW revealed the existence of significant genetic variability between L_1 and L_2. High genetic divergence between these testers culminated into manifestation of high amount of heterosis in their F_1 (L_3), which is also evident from significant mean squares due to $P_1 + P_2$ *vs* F_1.

Test of epistasis based on pooled analysis of variance showed significant mean squares due to epistasis ($L_{1i} + L_{2i} - 2L_{3i}$) for all characters except SS and TW indicating the importance of epistasis for these characters (Table 2). Further partitioning of total epistasis showed that [j + 1] component was significant for all characters exhibiting epistasis, whereas [i] type of epistasis was detected only for SS and PB. Environment-wise estimates of epistasis under irrigated (E1) and rainfed (E3) conditions at CRS Masodha showed that [i] type epistasis was significant for OC and BY under rainfed condition while HI showed importance of this component in irrigated as well as rainfed situations. The estimates of [i] type epistasis were non-significant for remaining characters. The [j + 1] type of epistasis was significant for SY and its key components -BY, HI, PH, SP and OC in E1 as well as in E3. However, this component of epistasis emerged important for DF and DM under irrigated conditions and for PB under rainfed conditions only.

Although significant epistasis was detected in the present study, the additive (D) and dominance (H) components were nevertheless computed in order to assess their relative contribution in the inheritance of various characters studied. Mean squares due to both sums ($L_{1i} + L_{2i}$) and differences ($L_{1i}- L_{2i}$) were significant for all the characters except SS, for which only additive variance was present. The relative magnitude of D and H components indicated the predominance of the later component for two characters namely HI and OC, and that of former for remaining 9 characters. These results confirmed the earlier findings [2, 3].

The interaction between [i] type epistasis and environments was significant for PH in all the environments, for DF in E2, DM in E2 and E3, SP in E1 and E3, TW in E3, PB, SS and SY in E1, BY and OC in E1 and E2. The interaction of [j + 1] with environment was non-significant for all the characters. This indicated that [i] type epistasis was more sensitive to changes in environments than [j + 1] type epistasis. The correlation coefficient between sums and differences was non-significant for all the characters, which indicated that dominant alleles were dispersed between the testers.

In the present study, epistatic effects have been detected for all the characters with conspicuous presence of non-fixable type of epistasis, [j +1]. These results are in agreement with those of [4, 5] in toria, and [6] in brown *sarson.* It is, thus, evident that epistasis was an integral component of genetic architecture of various characters in the pool of material studied in yellow *sarson,* an ecotype of *B. rapa* L. Hence detection, estimation and consideration of this component is important for the formulation of breeding programmes and to determine the genetic cause of heterosis with greater reliance.

It is thus obvious that besides additive and dominance genetic components with former being predominant, epistasis effects, mostly of non-fixable types have also been found to be significant for majority of the traits. Under such a situation, breeding method, as suggested earlier [7] should be followed where out-crossing concurrent with selection is advocated.

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