



VARIABILITY TRAIT ASSOCIATION AND PATH ANALYSIS STUDIES IN LOCAL GERMPASM OF YELLOW SARSON (*BRASSICA RAPA* VAR. YELLOW SARSON PRAIN)

Sanchika Snehi*, Usha Pant, Ram Bhajan, A.K. Singh and N.K. Singh

Department of Genetics and Plant Breeding, GBPUA & T, Pantnagar, U.S. Nagar (Uttarakhand), India.

Abstract

Genetic variability, trait association and path coefficient analysis were carried out using 59 genotypes of *Brassica rapa* var. yellow sarson. The genotypes were evaluated in randomised block design for twelve yield and contributing trait. The ANOVA for design of experiment confirmed substantial variability in the material studied. Higher estimates of phenotypic and genotypic coefficient of variation were recorded for number of primary branches, siliqua on main raceme, number of seeds per siliqua, 1000-seed weight and seed yield. High heritability coupled with high genetic advance were observed for number of primary branches, length of main raceme, siliqua on main raceme, siliqua density, siliqua length, number of seeds per siliqua, test weight and seed yield. The seed yield per plant manifested significant positive correlation with length of main raceme, siliqua on main raceme and siliqua density. Length of main raceme exhibited maximum direct effect on seed yield per plant followed by siliqua density, number of seeds per siliqua, test weight and number of primary branches.

Key words: *Brassica rapa* var. yellow sarson, phenotypic coefficient of variation, genotypic coefficient of variation, heritability, genetic advance, correlation, path analysis.

Introduction

Oilseeds play a significant role in the agricultural economy of India. The country being global leader account for nearly 7 percent of edible oil production and 14 percent share in area. Despite being leading producer of vegetable oils, country is heavily dependent on import need to meet domestic demand. Low and unstable yields of most oilseed crops and uncertainty in return to investment, resulting from prolonged cultivation of oilseeds in rainfed, high risk production environment are the key factors in creating a huge demand-supply gap. Rapeseed-mustard is one of the important *rabi* oilseeds accounting for about one-fourth (24.6%) of total (nine) oilseeds production and 22 percent of the total acreage, plays a pivotal role towards self-sufficiency in vegetable oils. The production of rapeseed-mustard in the country was 7.9 million tonnes (Mt) with an acreage of 6.1 million hectare and productivity of 1303 kg/hac in 2016-17 (Directorate of Economics & Statistics GOI. 2016). Botanically, the genus *Brassica* contains six economically important species *viz.*, *B. campestris*, *B. oleracea*, *B. nigra*, *B. juncea*, *B. napus* and *B. carinata*). The first three

species being elementary and diploid species with $2n=20$, 18 and 16 chromosomes and next three being tetraploids with chromosome number $2n=36$, 38 and 34 respectively.

Among Brassicas, *Brassica juncea* (Indian mustard) and *B. rapa* occupies authoritative position. Further, *B. rapa* is divided into three ecotypes, *viz.*, toria, brown sarson and yellow sarson which are grown in India. Amongst the three ecotypes of *B. rapa*, yellow sarson occupies key position owing to high oil content (up to 46%), high seed yield and early maturity (around 100 days as compared to 130-150 days Indian mustard). In addition, its yellow seed coat colour imparts light coloured clearer oil which is preferred over brown seeded toria and brown sarson. The yellow sarson are autogamous in nature and is chiefly grown in Assam, Bihar, Uttar Pradesh, Sikkim, Meghalaya and West Bengal. The oil is mainly used for edible purposes and in addition to this, the yellow sarson is most preferred choice as leafy vegetables among the entire cultivated oilseed brassicas in India (Chatterjee, 1992).

Success of breeding programmes largely depends on the extent and nature of genetic variability, heritable variation and genetic advance present in the breeding

*Author for correspondence : E-mail: sanchikasnehi26@gmail.com

population. Greater the variability, greater is the probability of recovering of desired plant types. In general, direct selection for yield alone may not be rewarding, on account of yield being a complex trait. Association studies presents an idea about relative contribution of different traits towards seed yield and magnitude of correlation between yield component and yield and among themselves. Consequently, an insight into interrelationships existing amidst yield components is needed, for selection to be effective. Correlation studies alone fails to depict the clear picture with respect to the association between different traits. Path analysis determine the yield components, directly or indirectly influencing the yield. Hence, the present investigation was carried out to study the genetic variability, trait association and path coefficients in order to devise selection criteria for identifying high yielding genotypes in yellow sarson.

Material and Methods

The experimental materials for the present investigation consisted of 11 local germplasm lines collected from Uttarakhand hills, Eastern UP and Bihar *viz.* PYSC-13-12, PYSC-11-3, PYSC11-31, PYSC-11-36, PYSC-13-1, PYSC-11-44, PYSC-1146, IC-338742, PYSC-13-14-2, NDYS-117, PYSC-12-1 used as females and 4 released popular varieties used as males *viz.* Pant Sweta, YSH-401, PPS-1, B-9 . All the crosses were produced by hand emasculating and pollination to avoid chances of mixing. The parents were crossed in line × tester mating design. A set of experimental material consisting of 11 lines, 4 testers and 44 F1 were evaluated in a randomized block design with three replications in single environments during *rabi* season of 2016-17 for 12 traits including days to 50 percent flowering, days to maturity, plant height (cm), number of primary branches per plant, number of siliquae on main raceme, length of main raceme (cm), siliqua density, siliqua length (cm), seeds per siliqua, 1000-seed weight (g), seed yield per plant (g), oil content (%). Oil content was determined from NIR facility available at DRMR, Bharatpur. Each plot in a replication comprised of a single row of 3 m length spaced at 30cm and plant to plant distance of 10cm was maintained by thinning. In order to debar border effect, experimental plots were encircled by one row of B-9. Standard variety Pant Sweta was treated as check in the experiments. Recommended package of practise was followed equally for all the entries in order to raise a good crop. The analysis of variance for the design of experiment was carried out according to the procedure defined by Panse and Sukhatme, (1967). The significance of difference among treatments means were tested by ‘F’ test. Phenotypic, genotypic and environmental

coefficients of variation were calculated according to Burton (1952). The heritability in broad sense $h^2(b)$ was estimated for each character as the ratio of genotypic variance to phenotypic variance by the formula:

$$h^2(b) = (\sigma^2g / \sigma^2p) \times 100$$

Where,

$h^2(b)$ = Heritability in broad sense

σ^2g = Genotypic variance

σ^2p = Phenotypic variance

The expected genetic advance under selection for the different characters was estimated as suggested by Allard, (1960). Genetic advance as percent of mean for each character was estimated as defined by Johnson, Robinson and Comstock, (1955). The correlation coefficients were calculated to determine the degree of association of characters with yield as suggested by Searle, S.R., (1961). The significance of correlation coefficients was tested against ‘r’ values given by Fisher and Yates, (1963). The path coefficients were obtained according to Dewey and Lu, (1959). Seed yield was considered to be dependent variable (effect) which is affected by independent variable (cause) all the (eleven characters), directly as well as indirectly through other characters. The variation in seed yield unexplained by the traits under consideration was supposed to be contributed by a residual factor which is uncorrelated with other factors.

Results and Discussions

Analysis of variance for the design of experiment was implied for all the 12 traits studied for appraising 59 treatments *viz.* 44 F₁s, 11 lines and 4 testers and a standard variety Pant Sweta. The mean of squares due to treatments were found to be significant for all the 12 traits studied (Table 1). Existence of genetic variability is of paramount significance for improvement of any crop. A perusal of PCV, GCV and ECV showed that in general the magnitude of PCV was observed greater than GCV and ECV for all the traits studied (Table 2) this result was in agreement with the results of Patel and Patel, (2005); Kumar and Mishra, (2006) in *Brassica*. Higher estimates (>20%) of PCV and GCV were observed for number of primary branches, siliqua on main raceme, number of seeds per siliqua, 1000-seed weight, seed yield. The characters *viz.*, length of main raceme, siliqua density and siliqua length manifested moderate estimates (10-20%) for PCV and GCV while the characters *viz.*, days to 50% flowering, days to maturity, plant height and oil content exhibited low estimates for PCV and GCV (<10%). These results are in agreement with those of

Table 1: Analysis of variance for different characters in yellow sarson.

Source of variation	d.f.	Mean squares											
		DF	DM	PH	NPB	LMR	SMR	SD	SL	NSS	TW	SY	OC
Replications	2	135.62	7.20	4.38	3.69	12.71	7.91	0.004	0.05	3.96	0.03	21.19	6.54
Genotypes	58	30.46**	97.16**	358.38**	5.70**	175.18**	218.24**	0.04**	1.15**	131**	1.34**	8.79**	1.57
Error	116	1.44	1.55	6.29	0.87	7.84	7.41	0.003	0.05	213	0.03	0.91	0.24
CD at 5%		1.94	2.02	4.06	1.51	4.53	4.40	0.08	0.35	2.36	0.28	1.54	0.79
CD at 1%		2.57	2.67	5.36	1.99	5.99	5.82	0.11	0.47	3.12	0.37	2.04	1.04
CV (%)		3.28	1.11	2.16	12.15	6.09	9.50	8.64	4.63	5.43	5.28	12.42	1.11

* and ** Significant at 5% and 1% level, respectively; *Note DF= days to 50% flowering, DM= days to maturity, PH= plant height, NPB= number of primary branches, LMR= Length of main raceme, SMR= Siliqua on main raceme, SD= siliqua density, SL=siliqua length, NSS= number of seeds per siliqua, TW= Test weight, SY= seed yield/plant, OC= oil content.

Mishra *et al.*, (2007); Misra *et al.*, (2012) and Hasan *et al.*, (2015).

Since mere existence of variability doesn't guarantee the transmission to the progeny, hence estimates of heritability were also worked out for the traits (Table 2). This parameter reflects the prospects of selection based on phenotype. In the set of materials studied, the highest estimate for broad sense heritability was observed for number of seeds per siliqua closely followed by days to maturity and 1000-seed weight. However, Sikarwar *et al.*, (2000) found high heritability for all the characters studied. On the other side number of primary branches and oil content exhibited low estimate of broad sense heritability as also reported by Prakash *et al.*, (2013) in yellow sarson.

Higher heritability need not necessarily ensure higher genetic advance. The estimates of heritability in conjunction with genetic advance are considered more accurate in predicting the gains via selection (Johnson, 1955). Results showed that genetic advance expressed as percent of mean (Gs %) depicted a wide range in its estimates (Table 2). In general, high Gs % was accompanied by high heritability for most of the traits.

The traits which manifested high broad sense heritability together with high genetic advance expressed as percent of mean are number of primary branches, length of main raceme, siliqua on main raceme, siliqua density, siliqua length, number of seeds per siliqua, test weight and seed yield in yellow sarson. These findings are in consonance with that of Singh and Mishra, (2001). The traits *viz.*, days to flower, days to maturity and oil content manifested high heritability coupled with low genetic advance revealing the role of non-additive gene effects in the expression of these traits which connote that selection for such traits might not be rewarding.

Trait association studies between yield and yield component are advantageous in selection of desirable plant type for effective breeding programme. Yield being complex trait is resultant of multiplicative interaction of different traits referred to as yield components. Hence, genetic architect of seed yield in yellow sarson and other crops is resultant of the balance or overall net effect manifested by various yield components directly or in interaction with one to other. Consequently, identification of significant yield components and information about their association with yield and also with each other is

Table 2: General mean ± SE, coefficient of variation (phenotypic, genotypic, environmental) heritability (broad sense), genetic advance and genetic advance as percent mean for different traits in yellow sarson.

Trait	General mean ± SE	Coefficient of variation (%)			Heritability in broad sense (%)	Genetic advances	GS %
		Phenotypic	Genotypic	Environmental			
DF	37.63±0.24	6.979	6.889	1.119	97.43	5.272	14.01
DM	113.67±0.63	5.706	5.626	0.953	97.21	12.99	11.43
PH	115.98±2.18	10.822	10.322	3.252	90.97	23.52	20.27
NPB	8.85±0.63	29.63	26.95	12.30	82.76	4.47	50.51
LMR	45.94±1.62	17.36	16.26	6.09	87.68	14.41	31.36
SMR	28.64±1.57	30.77	29.26	9.50	90.47	16.43	57.34
SD	0.61±0.03	19.93	17.96	8.64	81.19	0.204	33.33
SL	4.73±0.13	13.64	12.83	1.01	88.50	1.176	24.86
NSS	26.02±1.05	31.37	30.65	6.99	95.44	16.05	61.67
TW	3.28±0.10	21.32	20.64	5.32	93.78	1.35	41.18
SY	7.83±0.52	35.55	33.65	11.44	89.64	5.14	65.64
OC	43.66±0.28	1.89	1.53	1.11	65.32	1.11	2.54

Table 3: Phenotypic correlation coefficient for different character in yellow sarson.

Traits	DF	DM	PHT	NPB	LMR	SMR	SD	SL	NSS	TW	SYP	OC
DF	1											
DM	.493**	1										
PHT	.286*	.104	1									
NPB	-.070	.085	.294*	1								
LMR	.097	-.110	.661**	.136	1							
SMR	.234	0.009	.724**	.204	.801**	1						
SD	.263*	.123	.540**	.250	.367**	.823**	1					
SL	-.086	-.062	-.250	-.278*	-.362**	-.322*	-.251	1				
NSS	.377**	.134	.037	-.336**	-.106	.052	.094	.514**	1			
TW	.268*	.100	.248	-.028	.350**	.347**	.191	-.254	.049	1		
SYP	-.072	-.168	.209	.073	.373**	.368**	.268*	-.033	.113	.181	1	
OC	-.098	-.030	-.135	-.194	.196	.042	-.106	-.074	-.036	.100	.144	1

** . Correlation is significant at the 0.01 level (2-tailed); * . Correlation is significant at the 0.05 level (2-tailed).

crucial for designing efficient breeding program in order to breed high yielding varieties. Henceforth, correlation coefficient which bestow symmetrical measurement regarding degree of association between two variables or traits assist in elucidating the nature and magnitude of association among yield and yield components. The correlation coefficients with seed yield vis-a-vis other yield components and their all possible interrelationships are presented in table 3. The seed yield per plant manifested significant positive correlation with length of main raceme (0.373**), siliqua on main raceme (0.368**) and siliqua density (0.268**) while plant height (0.209), test wight (0.181), oil content (0.144), number of seeds per siliqua (0.113) and number of primary branches (0.073) exhibited positive but non-significant correlation.

Oil content showed negative but non-significant correlation for most of the traits except length of main raceme (0.196), siliqua on main raceme (0.042) and test weight which showed positive but non-significant correlation.

Test weight expressed significant positive correlation

with length of main raceme (0.350**), siliqua on main raceme (0.347**) and days to flower (0.268**) while, other traits showed positive but non-significant correlation with test weight

Number of seeds per siliqua showed significant positive correlation with siliqua length (0.514**) and days to flower (0.377**), while, days to maturity (0.134), siliqua density (0.094), siliqua on main raceme (0.052) and plant height (0.049) exhibited positive non-significant correlation.

Length of siliqua correlated significantly and positively with number of seeds per siliqua (0.514**) on contrary, significant negative correlation were observed for number of primary branch (-0.278*), length of main raceme (-0.362**) and siliqua on main raceme (-0.322**). Siliqua density manifested a strong significant correlation with siliqua on main raceme (0.823**), plant height (0.540**) length of main raceme (0.367**) and days to flower (0.263*). Siliqua on main raceme exhibited positive significant correlation with length of main raceme (0.801**)

Table 4: Direct (bold and diagonal) and indirect effects of different yield components and oil content at genotypic level on seed yield in yellow sarson.

Traits	DF	DM	PHT	NPB	LMR	SMR	SD	SL	NSS	TW	OC
DF	-0.171	-0.0845	-0.049	0.01203	-0.0167	-0.04016	-0.04508	0.01469	-0.06465	-0.04602	0.01671
DM	-0.05402	-0.11	-0.01137	-0.00929	0.01209	-0.001	-0.01344	0.0068	-0.01468	-0.01081	0.00327
PHT	-0.0314	-0.01139	-0.11	-0.0323	-0.0726	-0.0795	-0.05926	0.0275	-0.00403	-0.02802	0.01477
NPB	-.007	0.00891	0.03092	0.105	0.01431	0.02145	0.02627	-0.02926	-0.03531	-0.00213	-0.02038
LMR	.07094	-0.08031	0.48116	0.09906	0.728	0.58288	0.26708	-0.26342	-0.0773	0.25799	0.14272
SMR	-0.15397	-0.00602	-0.47566	-0.13408	-0.52619	-0.657	-0.54081	0.21186	-0.03442	-0.23304	-0.02758
SD	0.15988	0.07457	0.32799	0.15188	0.22303	0.50025	0.608	-0.15241	0.05701	0.12325	-0.06445
SL	-0.00492	-0.00356	-0.01436	-0.01597	-0.02076	-0.0185	-0.01439	0.057	0.02947	-0.01456	-0.00425
NSS	0.09593	0.03408	0.00934	-0.08544	-0.02701	0.01332	0.02385	0.13061	0.254	0.01084	-0.00921
TW	0.03269	0.01201	0.03106	-0.00247	0.04315	0.04318	0.02469	-0.0309	0.00519	0.122	0.01158
OC	-0.00791	-0.00242	-0.01091	-0.01572	0.0159	0.0034	-0.0086	-0.006	-0.00294	0.00772	0.08111

Residual Effect : 0.73098

and plant height (0.724**). A strong positive correlation of length of main raceme was observed with plant height (0.661**). Number of primary branches manifested positive correlation for plant height (0.294*). Plant height seem to correlate positively with days to flower (0.286*) while days to maturity recorded significant positive correlation with days to flower (0.493**). This is in consonant to the earlier findings on Brassica (Kumari *et al.*, 2017; Mishra *et al.*, 2007; Patel and Patel, 2005; Yadav *et al.*, 2001; Kumar *et al.*, 2001).

Correlation alone frequently depicts misleading results when more characters are accounted in the correlation study. It may be possible that many of the traits can correlate by virtue of mutual association, positive or negative, with other traits. Inclusion of more variables in the correlation studies further complicate their indirect association, thus, perplexing the selections. Under such situations, the path coefficient analysis proves to be an empathic tool for separating direct and indirect cause of association, thus allowing critical analysis of the specific forces operating to produce a given correlation and to appraise the relative proportion of each casual factor. The path coefficient analysis was carried out by using simple correlations between twelve characters to resolve direct and indirect effects of different characters on seed yield. The direct and indirect effects on seed yield per plant (g) is presented in (Table 4). Length of main raceme (0.728) exhibited maximum direct effect on seed yield per plant followed by siliqua density (0.608), number of seeds per siliqua (0.254), test weight (0.122) and number of primary branches (0.105). The result clearly gestures towards importance of these traits in direct selection for improvement of seed yield per plant in yellow sarson. The above finding is in agreement with Singh *et al.*, 2013; Srivastava and Singh, (2002); Panth *et al.*, (2002). Kumari *et al.*, 2017; reported maximum direct effect of harvest index and 1000-seed weight while siliqua length (-0.1363) and oil content (-0.0558) exerted negative direct effect on seed yield in yellow sarson. Siliqua length (0.057) and oil content (0.081) recorded positive but negligible magnitude of direct effect. Islam *et al.*, 2016; reported high direct effect of 1000 seed weight on seed yield in yellow sarson. On the contrary, siliqua on main raceme (-0.657), days to flower (-0.171), days to maturity (-0.11) and plant height (-0.11) manifested negative values of direct effect on yield. Maximum indirect positive effect was exhibited by siliqua on main raceme followed by plant height, siliqua density, test weight siliqua length and oil content which implies that these traits should also be given due consideration while selecting for seed yield per plant. The residual effect of 0.731 is high since the trait contribute only 26.9% to the variability in the seed

yield per plant. The result calls for inclusion of some other traits which have not been studied, to account fully for the variation in seed yield per plant.

Conclusion

Thus, the material studied is of diverse nature and information emanated would help in designing the selection methodology which can further be used in the breeding programme for improvement of seed yield in yellow sarson.

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