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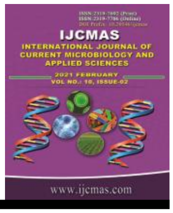

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Genetic Variability Studies for Yield and Yield Attributing Traits in Brown Sarson (*Brassica rapa* L.) Genotypes under Temperate Conditions of Kashmir

Tahmeena Bano[1], Shahina A. Nagoo[2*], M. Asif Iqbal Qureshi[3], M. Altaf Wani[1], Sanjay Kumar[1], F. A Sheikh[1], M. Ashraf Bhat[1], M. Ashraf Rather[1], Z. A. Dar[4], Z. I. Buhroo[2] and Sabiha Ashraf[2]

[1]Faculty of Agriculture-Wadura, [2]College of Temperate Sericulture-Mirgund, [3]Saffron Research Station-Pampore, [4]Dryland Agriculture Research Station-Budgam, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir Srinagar, J&K, India-190025

**Corresponding author*

ABSTRACT

Keywords

Brown sarson (*Brassica rapa* L.), Genetic, Genotypes, Kashmir, Temperate, Variability, Yield

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The present study was carried out with 57 genotypes of brown sarson (*Brassica rapa* L.) during rabi 2019-2020. Estimationof the genetic variability, heritability, genetic advance and correlation analysis in the set of 57 *B. rapa* lines revealed that all the characters exhibited large amount of variability. The high amount of PCV and GCV along with high values of broad sense of heritability and genetic advance was found, no. of seeds per siliqua, no. of siliqua per plant followed by seed weight. The association analysis showed that the no. of seeds per siliqua, Siliqua length, no. of siliqua per plant and seed weight had significant positive correlation with seed yield plot^{-1}. The difference between PCV and GCV were observed low for all the traits. The genetic variability present in the set of breeding material shall not only provide a basis for selection but also provided some valuable information regarding selection of diverse parents to be used in the hybridization programme. Hence, In the present study, significant amount of differences were observed in the studied genotypes for all characteristics which give an insight into the existence of genetic variation in the available genotypes and thus there is a great scope for selection and further improvement of *Brassica rapa* L in terms of quality and quantity.

Introduction

Brassica species have been exploited by man, among all the different oilseed groups, domesticated and modified to meet the altering needs as a source of vegetable oil for centuries. India ranks second area wise and third in production for oilseed brassica crops. Among the rapeseed–mustard group *B. juncea* is grown on more than 80 per cent of the total cultivated area under rapeseed mustard in the country as it suits perfectly in cropping system of rainfed areas. Globally, rapeseed-mustard is cultivated over an area of 33.64 mha with production of 72.37 million tonnes (FAO, 2019). During 2018-19, India produced 9.33 million tonnes of Rapeseed-mustard from a stretch of 6.23 mha with a productivity of 15.0q/ha (Economic Survey, 2020). In the Rapeseed-mustard group, *B. rapa* L. var. brown sarson is cultivated on a larger scale in rabi season in the Kashmir valley. The rapeseed mustard crop occupied an extent of 53000 hectare with the production of 34 thousand quintals and an average productivity of 6.97 q/ha during 2017-18 in J&K state (Anonymous, 2018c). The crop suits perfectly in the oilseed– paddy rotation prevalent in the valley and has a great buffering capacity to tolerate the frost conditions. But temperatures below 25°F will likely kill stands. The small and round seeds of *Brassica* contains carbohydrate (14-16 percent), fiber (10-15 percent), moisture (6-8 percent), ash (4-6 percent), mineral (3-4 percent), vitamins (0.7-0.9 percent) glucosinolate (2-3 percent), phytic acid (3-6 percent), sinapine (1-1.5percent) and 1.6-3.1 percent of tannin (Agnihotri and Kumar 2004) and about 40 to 44 % oil (dry weight basis) and 38 to 41 % protein, high percentage of oleic acid (60.2 %), linolenic acid (10.9%), linoleic acid (21.3 %), eicosenoic acid (1.3%) and low erucic acid (0.5%). Much effort has been made to improve methods for recognizing varieties because of its economic value (Cooke 1999). The success of any breeding system, in particular the improvement of specific characteristics through selection, depends entirely on the genetic variation in that crop's germplasm (Yadava et al., 2011). Thus, it becomes necessary for a plant breeder to assess the variability with the assistance of parameters like PCV, GCV, heritability and genetic advance. To achieve higher produce, and thus shift the state's edible oilseed scenario, it is imperative to develop early maturing improved varieties of Brown Sarson with high yielding ability, high oil content, better oil quality. In view of the above fact the study was aimed to evaluate the Brown Sarson (*B. rapa* L.) genotypes through genetic variability, heritability and genetic advance estimation and correlation analysis.

Materials and Methods

The experiment was conducted with 57 genotypes of Brown Sarson (*Brassica rapa* L.) in the experimental farm of the Department of Genetics and Plant Breeding, Sheri-Kashmir University of Agricultural Sciences and Technology, FoA, Wadura-Kashmir (Table 1). The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Ten plants were selected randomly from each plot for collection of data for various yield contributing characters viz. plant height, Plant main Shoot length, siliqua per plant, siliqua length, seeds per siliqua, 1000 seed weight, and yield/plot and average of these ten plants were worked out, however except 50% days to flowering, maturity and yield data, the data were recorded on whole plot basis. The average values of all of the observations were used for statistical analysis. Genotypic and phenotypic coefficients of variation were calculated according to the formula given by Burton and De-Vane (1953). Heritability was calculated according to the formula given by Hanson *et al.,* (1956). From the heritability estimates the genetic advance was estimated as per Johnson *et al.,* (1955). Correlation coefficients were estimated using the formula given by Miller *et al.,* (1958).

Results and Discussion

The presence of variability in any crop population is essential for improvement in breeding program of a crop (Hasan *et al.*, 2006). The analysis of variance for 11 yield and yield attributing traits of 57 *B. rapa* L. germplasm genotypes presented in Table-2 depict that the mean total of squares due to genotypes was found to be highly significant in all the traits viz., flowering period, plant height, primary branches per plant, Plant main shoot length, siliqua per plant, seeds per siliqua, length of siliqua, 80 % maturity period, seed weight, oil content and yield per plot. This suggests a significant amount of genetic variation among the genotypes for all the characters under investigation and offers an opportunity for further study and assessment of variability parameters. Rameeh (2014) observed significant differences for the traits including days to flowering, duration of flowering, days to maturity, number of branches, pods main raceme^{-1}, pods plant^{-1}, seeds pod^{-1}, and seed yield and Chaurasiya *et al.,* (2018) recorded highly significant differences for all characters namely, days to 50% flowering, days to maturity, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of siliqua plant^{-1}, number of seed siliqua^{-1}, 1000- seed weight, biological yield plant^{-1}, harvest index, oil content and seed yield plant^{-1}.

The coefficient of variation was measured at genotypic and phenotypic rates. Usually, the phenotypic coefficient of variation was greater in magnitude than the coefficient of variation in the genotypes signifying that the variability is not only due to genotypes but also due to the influence of climate. In the current study (Table 3 and 4).

the moderate value of genotypic coefficient of variation (14 to 4%) was shown by siliqua number per plant (19.9%) followed by Primary branches number per plant (16.8%), plant length (14.2%), Plant main shoot length (13.4%) followed by siliqua length (13.2%), seed weight (13.0), number of seeds per siliqua (11.0). Moderate magnitude of phenotypic coefficient of variation (PCV) was recorded for number of Siliqua per plant (21.8%) followed by number of primary branches per plant (19.8%), siliqua length (16.66%), plant main shoot length (16.6%), number of seeds per siliqua (16.4%), plant height (15.8%), seed weight (14.9%) Similarly, Rouf *et al.,* (2018) reported moderate PCV and GCV no. of seed per siliqua, 1000 seed weight; Mahendra *et al.,* (2020) in *Brassica rapa* L. reported moderate GCV and PCV for no of seed per siliqua , plant height. High estimate of heritability broad sense (Ã60%) was recorded for 50 per cent flowering period (96.6%) then for 80 per cent maturity period (95.1%), seeds per siliqua (91.6%), siliqua no. per plant (84.3%), plant height (81.5%) and seed weight (80.8%). Maximum broad sense heritability value for the mentioned traits indicates that selection gain to improve this trait would be higher. Similar results of high heritability for 50 % flowering period are in agreement with the observations of Mahendra *et al.,* (2020) in *Brassica rapa.* Rout *et al*., (2019) also reported high heritability number of siliqua per plant, Seeds per siliquain *Brassica juncea* L. The results of high heritability for number of siliqua per plant are in conformity with the findings of MariaIslam *et al.,* 2020 in *B. rapa*. For the traits namely seeds per siliqua (31.2%), siliqua per plant (30.8%), thousand seed weight (27.3%), siliqua length (20.5 %), the magnitude of genetic advance as a percentage of mean was reported high. High estimates of genetic advance for characters no. of seeds per siliqua and number of siliqua per plant were also stated by Aktar*et al.,* (2019) in Brassica genotypes. All characteristics with high genetic advance values suggest that these traits are regulated by additive genes, and selection will be beneficial for the enhancement of these characteristics. The characters that demonstrated strong heritability correlated with strong genetic advance in the present study are no. of seeds per siliqua, no. of siliqua per plant, seed weight. Similar outcomes were described by Rout *et al.*, (2019) in *B. juncea*, Gupta *et al.*, (2019) in *B. juncea* for siliqua/ plant, seeds/ siliqua and thousand seed weight in *B. juncea*; Lodhi *et al.*, (2014) in *B. juncea* for no. of seeds per siliqua, seed weight.

Table.1 List of genotypes used in the experiment.

S .No.	Genotype/Germplasm line	Source
01	KBSG-10	IPK, Germany
02	KBSG-92	IPK, Germany
03	KBSG-146	IPK, Germany
04	KBSG-1	IPK, Germany
05	KBSG-45	IPK, Germany
06	KBSG-18	IPK, Germany
07	KBSG-33	IPK, Germany
08	KBSG-2	IPK, Germany
09	KBSG-80	IPK, Germany
10	KBSG-128	IPK, Germany
11	KBSG-8	IPK, Germany
12	KBSG-123	IPK, Germany
13	KBSG-15	IPK, Germany
14	KBSG-147	IPK, Germany
15	KBSG-79	IPK, Germany
16	KBSG-124	IPK, Germany
17	KBSG-19	IPK, Germany
18	KBSG-29	IPK, Germany
19	KBSG-17	IPK, Germany
20	KBSG-74	IPK ,Germany
21	KBSG-5	IPK, Germany
22	KBSG-63	IPK, Germany
23	KBSG-68	IPK, Germany
24	KBSG-38	IPK, Germany
25	KBSG-112	IPK, Germany

26	KBSG-39	IPK, Germany
27	KBSG-102	IPK, Germany
28	KBSG-119	IPK, Germany
29	KBSG-141	IPK, Germany
30	KBSG-14	IPK, Germany
31	KBSG-18	IPK, Germany
32	KBSG-140	IPK, Germany
33	KBSG-120	IPK, Germany
34	KBSG-34	IPK, Germany
35	KBSG-151	IPK, Germany
36	KBSG-51	IPK, Germany
37	KBSG-111	IPK, Germany
38	KBSG-66	IPK, Germany
39	KBSG-85	IPK, Germany
40	KBSG-56	IPK, Germany
41	KBSG-64	IPK, Germany
42	KBSG-139	IPK, Germany
43	KBSG-134	IPK, Germany
44	KBSG-130	IPK, Germany
45	KBSG-127	IPK, Germany
46	KBSG-122	IPK, Germany
47	KBSG-118	IPK, Germany
48	KBSG-116	IPK, Germany
49	KBSG-114	IPK, Germany
50	KBSG-110	IPK, Germany
51	KBSG-107	IPK, Germany
52	KBSG-105	IPK, Germany
53	KBSG-103	IPK, Germany
54	KBSG-109	IPK, Germany
55	SS-1 (Check)	SKUAST-K
56	SS-2 (Check)	SKUAST-K
57	SS-3 (Check)	SKUAST-K

Table.2 Analysis of variances for yield and yield attributing traits in *Brassica rapa* L. genotypes

Source	**Degree of freedom**	**PMSL (cm)**	**PH (cm)**	**NPBPP**	**NSPP**	**SL(cm)**	**NSS**	**SW (g)**	**Df (day)**	**DM (day)**	**Seed yield plot^{-1}**	**Oil content (%)**
Replication	2	465.71	0.24	3.23	0.08	3.69	4.21	1.58	1.61	2.74	0.05	0.01
Treatment	56	1101.64*	1561.42*	2710.26*	12815.38*	23.61*	229.91*	0.65*	58.18*	179.0*	4.43*	18.20*
Error	112	244.84	18.93	0.54	0.37	0.19	0.70	0.11	0.96	0.87	0.21	0.30

*Significant at 0.05 level of significance

PMSL = Plant main shoot length, PH= Plant height, NPBPP=Number of primary branches plant^{-1}, NSPP= Number of siliqua plant^{-1}, SL= Siliqua length, NSS= Number of seeds siliqua^{-1}, SW= 1000 seed weight, DF= Days to 50% flowering, DM=Days to 80%maturity, seed yield Plot^{-1}(kg), Oil content(%).

Table.3 Estimation of genetic parameters for yield and yield attributing traits in *Brassica rapa* L. genotypes

S. No.	Trait	Mean	Range	CV (%)	PCV	GCV	h^2(bs)	GA (5%)
1	Plant main shoot length (cm)	48.42	11.4-98.7	22.31	16.64	13.38	53.73	16.27
2	Plant height (cm)	145.64	97.5- 206. 5	5.98	15.85	14. 22	81.52	18.03
3	No. of primary branches plant^{-1}	36.74	4.1-95	2.00	19.81	16.77	58.88	12.95
4	No. of siliqua plant $^{-1}$	142.55	245.9-29.4	5.42	21.84	19.84	84.32	30.81
5	Siliqua length (cm)	4.75	1.66-11.7	9.38	16.66	13.21	55.18	20.57
6	No. of seeds siliqua^{-1}	17.07	4-36	4.9	16.49	11.03	91.18	32.81
7	1000- seed weight (g)	2.51	1-3.9	13.42	14.93	12.94	80.82	27.37
8	Days to 50% flowering	17.24	162.182	0.57	2.63	2.50	96.63	6.41
9	Days to 80% maturity	209.61	196-228	0.44	1.71	1.66	95.11	4.59
10	Seed Yield plot^{-1} (kg)	0.69	0.10-0.99	20.28	8.30	5.82	44.75	6.00
11	Oil content (%)	34.57	28-32.8	13	4.32	4.01	67.9	7.29

DF= days to 50% flowering, PH= plant height (cm), NPBPP=Number of primary branches per plant, PMSL=Plant main Shoot length (cm), NSPP= number of siliqua per plant, NSPS= number of seeds per siliqua, S.L= siliqua length (cm), DM= days to 80% maturity, SW= seed weight (g), OC= oil content (%), YP= yield per plot (kg).

Table.4 Correlation analysis of yield and various yield attributing traits in *Brassica rapa* genotypes.

	PMSL	**PH**	**NPBPP**	**NSPP**	**SL**	**NSS**	**1000SW**	**DF**	**DM**	**Yield**	**Oc(%)**
PMSL	-	0.94	0.76**	0.90	0.86	0.91	0.41	0.033*	0.036	0.55	0.034*
PH		-	0.684**	0.878	0.792	0.874	0.497	0.079*	0.068	0.525	-0.039
NPBPP			-	0.901	0.953	0.918	0.607	0.025**	0.192**	0.827	0.431
NSPP				-	0.919	0.962	0.617	0.064**	0.120**	0.214**	0.733
SL					-	0.966	0.594	0.072*	0.180**	0.748**	0.295
NSS						-	0.586	0.074**	0.154**	0.744**	0.224
SW							-	0.337	0.327	0.584**	0.291
DF								-	0.832	0.124*	-0.047
DM									-	0.301	0.175
Yield										-	0.509

Association studies between yield and yield contributing characters

The yield coefficients for correlation and various character attributes are given in Table 3. The yield per plot (kg) displayed positive and highly significant association with number of siliqua plant^{-1} (0.21), siliqua length (0.748), number of seeds siliqua^{-1} (0.74), 1000 seed weight (0.58). Oil content showed negative and significant association with days to flowering (-0.04) and plant height (0.03). Days to 80 per cent maturity showed positive and highly significant association with days to number of primary branches per plant, number of siliqua per plant, siliqua length, and number of seeds per siliqua. Similarly, plant main shoot length displayed positive and highly significant association with no. of primary branches per plant (0.76) and Oil content (0.034). The plant length exhibited positive highly significant association with no. of primary branch per plant (0.68), while as, seed no. per siliqua presented positive and highly significant association with days to 50 % flowering (0.74), and days to 80% maturity (0.15). The siliqua no. per plant exhibited positive and highly significant association with days to 50% flowering (0.064) and days to 80 % maturity (0.12). Siliqua length exhibited positive and significant association with days to 50% flowering (0.072)and days to 80% maturity (0.18).The results revealed by Tabassum *et al.*, (2021) in *Brassica rapa* L., and Mudha Aggarwal *et al.*, (2019) in *Brassica juncea* L. stated positive correlation between no. of primary branches per plant and yield in their study. Maria Islam *et al.*, (2020) and Nitesh kumar *et al.*, (2019) in *Brassica rapa* L., reported a significant and positive genotypic correlation of number of siliqua per plant, with yield. Positive association between desirable characteristics is beneficial as it allows all characters to develop simultaneously. Negative correlation, by contrast, would impede the simultaneous expression of both high value characters. In such a case there has to be some economic compromise.

In conclusion, study with 57 genotypes of brown sarson (*Brassica rapa* L.) revealed significant amount of differences among the genotypes for all characteristics which gives an insight into the existence of genetic variation in the available genotypes reflecting that there is a great scope for selection. Traits like, no. of seeds per siliqua, Siliqua length, seed weight, and no. of siliqua per plant have high heritability as well as high genetic advance and selection can be based on these traits. Correlation analysis furnishes a basis in determining the relative contribution of each character to seed yield. Trait Number of seeds per siliqua, siliqua length, no of seeds per siliqua and seed weight displayed positive and highly significant association with yield per plot. Therefore, selection of these characters would be more effective for the improvement of the crop.

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