



Genetic variability studies for yield and yield attributing traits in Gobhi Sarson (*Brassica napus* L.) genotypes under temperate ecology of Kashmir

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Abstract

The present study was carried out with fifty genotypes of gobhi sarson (*Brassica napus* L.) to estimate the genetic variability, heritability, genetic advance and correlation analysis in the set of 50 *B. napus* lines grown during Rabi 2019-2020. The analysis of variance revealed that all the characters exhibited a large amount of variability. For siliqua no. per plant, the high amount of PCV and GCV along with high values of broad sense heritability and genetic advance was found followed by number of seeds per siliqua and number of siliqua on main raceme length. The association analysis showed that the plant height, siliqua number on main raceme length, number of seeds per siliqua, no. of siliqua plant⁻¹ had significant positive correlation with seed yield plot⁻¹. The difference between the values of GCV and PCV 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.

Keywords: *Brassica napus*, genetic variability, heritability, genetic advance

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 currently the brown sarson productivity levels in the valley are not satisfactory mostly due to non-availability of high yielding genotypes besides the crop has to

overwinter under snow and frost for more than 90 days. During this period the growth of the crop is restricted to rosette stage. However, it is worthwhile to mention that the Gobhi sarson genotypes have similar buffering capacity and are genetically better yielders in comparison to Brown sarson genotypes. Further–more the oil extracted from Gobhi sarson are high quality oil rich in fatty acid profiling. *Brassica napus* L. is second most important oilseed crop in the international oilseed market after soybean and important source of vegetable oil (Verma *et al.*, 2016). 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 Gobhi Sarson with high yielding ability, high oil content, better oil quality. In view of the above fact the study was aimed to evaluate the Gobhi Sarson (*B. napus* L.) genotypes through genetic variability, heritability and genetic advance estimation and correlation analysis.

Materials and Methods

The experiment was conducted with 50 genotypes of Gobhi Sarson (*Brassica napus* L.) in the experimental farm of the Department of Genetics and Plant Breeding, Sheri-Kashmir University of Agricultural Sciences and Technology, FoA, Wadura. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Five plants were selected randomly from each plot for collection of data for various yield contributing characters viz. plant height, raceme length, siliqua per raceme, siliqua length, seeds per siliqua, 1000 seed weight, and yield/plot and average of these five 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

Variability analysis

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 12 yield and yield attributing traits of 50 *B. napus* L. germplasm genotypes displayed in Table-1 showed 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, main raceme length, siliqua no. on main raceme length, siliqua per plant, seeds per siliqua, length of siliqua, 80 per cent 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. Laghari *et al.* (2020), registered similar form of results in *B. napus*, Rout *et al.* (2019) in *B. juncea*, Gupta *et al.* (2019) in *B. juncea* & *B. napus*, Nur-E-Nabi *et al.* (2019) in *B. napus*, Dobrzycka *et al.* (2016) and Joya *et al.* (2016) in *B. napus*.

The coefficient of variation was measured at genotypical 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-2),

Table 1: Analysis of variance for yield and yield attributing traits in *Brassica napus* genotypes

Source	df	DF	PH	NPBP	MRL	SMRL	NSPP	NSPS	SL	DM	SW	OC	YP
Replication	2	88.45**	885.70	9.006	243.50**	189.47*	6046.00**	3.235**	1.239	85.81**	0.6629	5.88**	0.00507
Treatment	49	74.96**	65.90**	1.032**	608.80**	178.780**	15385**	18.69**	0.439**	56.890**	0.0082**	8.602**	0.011**
Error	98	0.45	96.10	1.882	44.60	33.77	564	0.06	0.2812	0.45	0.0161	0.73	0.00029

DF= days to 50% flowering, PH= plant height (cm), NPBP=Number of primary branches per plant, MRL= main raceme length (cm), SMRL= siliqua number on main raceme length, 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). *, ** = significant at 0.05 and 0.01 levels.

Table 2: Estimation of genetic parameters for yield and yield attributing traits in *Brassica napus* L. genotypes

Trait	Mean	Range	CV (%)	GCV	PCV	h ² (bs)	GA (5%)
DF	189.50	179.3-199.3	0.35	2.63	2.65	98.22	5.36
PH	161.031	113.06-118.6	6.08	10.07	11.77	73.25	17.76
NPBPP	20.20	16.6-24.5	6.7	7.62	10.21	55.78	11.73
MSL	75.59	59.8-93.6	8.8	10.77	13.93	59.78	17.16
SMSL	47.17	35.1-60.8	12.3	15.27	19.61	60.58	24.48
NSPP	264.35	205.8-353.7	8.9	16.17	18.49	76.41	29.11
NSPS	6.60	4.9-8.2	3.6	15.57	16.01	94.63	31.23
SL	4.13	2.9-15.5	12.8	13.60	18.69	52.95	20.38
DM	234.40	225-240.3	0.28	1.85	1.87	97.66	3.76
SW	3.66	2.9-4.9	3.4	12.67	13.14	93.05	25.19
OC	40.30	37.0-43.6	2.1	4.01	4.53	78.23	7.31
YP	0.73	0.64-0.787	6.2	4.29	7.54	38.46	5.04

DF= days to 50% flowering, PH= plant height (cm), NPBPP=Number of primary branches per plant, MRL= main raceme length (cm) SMRL= siliqua number on main raceme length, 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 3: Correlation analysis of yield and various yield attributing traits in *Brassica napus* genotypes

	NPBPP	MRL	SMRL	NSP	NSPS	SL	SW	DF	DM	OC	YPP
PH	0.46	0.11	0.83**	0.80	0.77**	0.45	0.40	0.33	0.57	0.33	0.80**
NPBPP		-0.03	0.43	0.32	0.32	0.77**	0.56**	0.18	0.23	0.12	0.34
MRL			-0.052*	0.11	0.12*	0.058	-0.07*	0.29	0.18	-0.12*	0.003
SMRL				0.82**	0.81**	0.48	0.45	0.23	0.44	0.34	0.77**
NSP					0.81**	0.29	0.37	0.30	0.44	0.32	0.64**
NSPS						0.24	0.27	0.31	0.55	0.30	0.73**
SL							0.67**	0.19	0.21	0.21	0.45
SW								0.10	0.10	0.15	0.37
DF									0.85**	0.74*	0.32
DM										0.06	0.63
OC											0.34

the moderate value of genotypic coefficient of variation (10 to 2%) was shown by siliqua number per plant (16.2%) followed by number of seeds per siliqua (15.6%), siliqua number on main raceme length (15.3%), siliqua length (13.6%) followed by seed weight (12.7%), main raceme length (10.8%) and plant height (10.07%). Moderate magnitude of phenotypic coefficient of variation (PCV) was recorded for siliqua number on main raceme length (19.6%) followed by siliqua length (18.7%), siliqua per plant (18.5%), seeds per siliqua (16.0%), main raceme length (13.9%), thousand seed weight (13.1%), plant length (11.8%) and primary branches per plant (10.2%). Similarly, Rouf *et al.* (2018) reported moderate PCV and GCV for main raceme length, no. of siliqua per plant, no. of seed per siliqua, 1000 seed weight; Sandhu *et al.* (2017) in *Brassica napus* L. reported moderate GCV and PCV for siliqua no. on main raceme length, seed weight and plant

height. High estimate of heritability broad sense (\bar{A} 60%) was recorded for 50 per cent flowering period (98.2%) then for 80 per cent maturity period (97.7%), seeds per siliqua (94.6%), thousand seed weight (93.1%), oil content (78.23%), siliqua per plant (76.4%), plant height (73.3%) and siliqua number on main raceme length (60.6%). 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 Aftab *et al.* (2020) in *Brassica napus* L. Gupta *et al.* (2019) in *Brassica juncea* L. and *Brassica napus* L. also reported high heritability for days to 80 per cent maturity, number of siliqua per plant and seeds per siliqua. The results of high heritability for number of siliqua on the main raceme length are in conformity with the findings of Devi (2018) in *Brassica juncea* L., Shaukat *et al.* 2015 in

B. napus. For the traits namely seeds per siliqua (31.2%), siliqua per plant (29.1%), thousand seed weight (25.2%), number of siliqua on the main raceme length (24.5 %) and siliqua length (20.4 %), 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, seed weight, no. of siliqua per plant and siliqua number on main raceme length. 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 and siliqua number on main raceme length.

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 plant height (0.8), siliqua number on main raceme length (0.77), seeds per siliqua (0.73), siliquae per plant (0.64). Oil content showed negative and significant association with days to flowering (-0.74), main raceme length (-0.12). Days to 80 per cent maturity showed positive and highly significant association with days to 50 percent flowering (0.85). Similarly, seed weight displayed positive and highly significant association with siliqua length (0.67), no. of primary branches per plant (0.56) and presented negative and significant association with main raceme length (-0.07). The siliqua length exhibited positive highly significant association with primary branch no. per plant (0.77), whileas, seed no. per siliqua presented positive and highly significant association with siliqua no. per plant (0.81), siliqua number on main raceme length (0.81), plant height (0.77) and showed positive and significant association with main raceme length (0.12). The siliqua no. per plant exhibited positive and highly significant association with siliqua on main raceme length (0.82) and plant height (0.80). The results revealed by Laghari *et al.* (2020) in *Brassica napus* L., and Kumar *et al.* (2019) in *Brassica juncea* L. stated positive correlation between plant height and yield in their study. Laghari *et al.* (2020) and Ahmadzadeh *et al.* (2019) in *Brassica napus* 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.

Conclusion

It is clear from the results that significant amount of differences in the studied genotypes for all characteristics under investigation give an insight into the existence of genetic variation in the available genotypes and thus there is a great scope for selection. Traits like no. of seeds per siliqua, seed weight, no. of siliqua per plant and siliqua number on main raceme length 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. Traits like plant height, siliqua number on main raceme length, seeds per siliqua, siliquae per plant 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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