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Estimation of Genetic Variability Parameters for Seed Yield and its Component Traits among Accessions of *Brassica rapa* Var. Yellow Sarson

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Abstract

Brassicas being one of the commercially important species worldwide is an important player in the world oilseed market. Genetic variability assessment thus, becomes important for the crop improvement programme. The present investigation aimed at assessment of variability parameters among 41 accessions of *Brassica rapa* var. yellow sarson including 5 checks i.e., PPS-1, Pant Sweta, YSH-0401, Pitambari, and B-9. The accessions were evaluated for eleven yield and yield attributing traits and wasanalysed using appropriate statistical techniques. Results of ANOVA revealed the presence of highly significant mean sum of squares among all the accessions in all the environments. The estimates of PCV were found to be more than the corresponding GCV estimates in all the environments and seed yield (GCV: 20.10; 20.14; 18.14 & PCV: 21.62; 20.94; 20.01) was found to be administering highest GCV and PCV values followed by number of primary branches per plant (GCV: 23.41; 19.01; 19.05 & PCV: 19.03; 16.89; 15.87), in all the environments respectively. Seed yield (h^2_b : 86.46%; 92.53%; 82.19% & GA as % of mean: 38.50%; 39.91%; 33.88%) and thousand seed weight (h^2_b : 76.79%; 85.52%; 83.4% & GA as % of mean: 25.17%; 23.78%; 25.30%) were found to be the winners of the race in case of high heritability along with high genetic advance as percent of mean, whereas, oil content (h^2_b : 63.70%; 62.79%; 66.92% & GA as % of mean: 4.50%; 4.45%; 4.79%) showed high estimates of heritability along with low genetic advance as percent of mean in E-1, E-2 and E-3. Selection for thousand seed weight, number of primary branches per plant, number of seeds per siliqua and seed yield seems to be effective for the crop improvement program whereas as selection for oil content may not be rewarding in this case.

Key words : *Brassica rapa, accessions, genetic variability, GCV, PCV*

Introduction

Oilseeds make a good fraction of the economically important crops and we all are very well aware about the importance of oilseeds in our day-to-day life as an individual and their economic importance at global level. Taking into consideration the Indian context, the demand for oilseed is ever increasing and is expected to be increasing at even higher rates in future (1). India occupies a prominent place in global oilseed scenario with 12-15% of area, 6-7 % of vegetable oil production and 9-10% of the total edible oil consumption and 13.6% of vegetable oil imports (2). India is the 5th largest vegetable oil economy in the world after USA, China, Brazil and Argentina accounting for 5-8% of vegetable oil production (3)**.** The production of oilseeds is hampered due to lack of suitable conservation methods and other environmental related problems like salinity, drought, susceptible to different biotic and abiotic stress etc. So, it becomes the need of the hour to boost the production of oilseeds by using suitable crop improvement techniques. Ingeneral, also, the plant breeding programs aiming at improvement of oilseed crops are focused on increasing production and quality of the crop. After years of efforts, we successfully increased the production, but still are not able to meet the demands and depend on imports, and thus, it becomes important to lead the research in that direction. Many oilseed crops are grown across the world including edible and non-edible ones viz., brassica, soybean, peanut, sunflower, safflower etc. Among these crops *Brassica* is one of the commercially important oilseed crops. Out of all the species of Brassica six are of major importance and among these six also four species are widely cultivated for oilseeds and vegetables are *Brassica rapa*L, *Brassica juncea*(L) Czern&Coss, *Brassica napus* L. and *Brassica carinata* A. Braun. (4,5,6)**.**

In the present study our crop of concern is *Brassica rapa* var. yellow sarson. *Brassica rapa* is the second most grown oilseed brassica in the northern and north-eastern parts of the country (7) and among the three ecotypes of it viz., brown sarson, yellow sarson and toria, yellow sarson is of prime economic importance due to quality and quantity of its oil. The yellow seed color of this crop adds on to its economic importance and is one of the component traits that is desirable to breeders. Because of the clear oil texture of yellow sarson plant breeders try to transfer the yellow seed cost trait to *B. napus* as well **(**8**).** Despite of being a very desirable crop, it faces issues when it comes to the productivity and for that strict measure in the direction of crop improvement of the crop needs to be taken. For the purpose the genetic variability

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among the genotypes needs to be assessed to get an idea of the amount of diversity present among the genotypes. Genetic variability can be simply said as the diversity in the array of genes present in a crop plant. Genetic variability is a play of alleles differing at a loci and different combinations of such genes among the genotypes in a population. Furthermore, for leading a successful crop improvement program, the assessment of genetic variability becomes important and is fundamental for the purpose to identify the most important traits and genotypes in crop improvement program. Presence of genetic variability helps in selection of desirable genotypes, by giving more options to choose upon. The variability among genotypes can be seen through their phenotypes, which again is a result of genotype and the environment. Here, it becomes important to estimate the amount of variability that is actually due to the genetic component, more precisely heritable variability. Genetic advance on the other hand is another important factor, which estimated the effectiveness of the selection for the trait under study. The estimates of heritability along with genetic advance gives more precise insights in predicting the gain under effective selection (9). High heritability with high genetic advance is the requirement for selection to be more effective. Knowledge of the magnitude of genetic variability, heritability and genetic gain under selection of desirable characters could assist the plant breeder in ascertaining criteria to be used for the breeding programmes (10).

Materials and Methods

The present investigation was conducted in the rabi season of year 2018-19, 2019-20 and 2020-21, with an objective of estimating the genetic diversity among forty-one accessions (Table-1) of Yellow sarson (*Brassica rapa* var. yellow sarson) including five checks viz., PPS-1, Pant Sweta, YSH-0401, Pitambari, and B-9, at Oilseed Breeding Block of N.E. Borlaug Crop Research Centre, GBPUA&T, Pantnagar, Uttarakhand, India. Each year was considered as a different environment and so, we evaluated the material for 3 environments i.e., three consecutive years. Recommended package of practices and intercultural operations were taken care of as per the requirement of the crop, during the study. The experiments were laid in Randomized Block design with three replications and the steps involved in analysis of RBD were as per (11).In total eleven characters were used for the study viz., days to maturity (DM), plant height (PH), length of main raceme (LMR), siliquae on main raceme (SMR), siliqua density (SD), number of primary branches per plant (NPB), siliqua length (SL), number of seeds per siliqua (NSPS), oil content (OC), thousand seeds weight (TSW) and seed yield (SY). The analysis of variance (ANOVA) was performed for each trait under each environmental condition and the genetic variability parameters *viz.*, GCV, PCV, heritability and genetic advance were estimated using Variability (0.1.0 version) package of R Studio 4.2.2 version.

Results and Discussion

In the present investigation the data was collected and analysed for eleven variability traits, grown in RBD with three replications, for three consecutive years. The results of ANOVA revealed the presence of highly significant mean sum of squares among all the accessions and for all the traits taken into consideration and for all the years, presence of sufficient amount of genetic variability for these traits, for carrying out crop improvement program further. Presence of sufficient amount of variability among yellow sarson gene pool was reported in a study (12). The estimates of genetic parameters are presented in Table 2 for all the characters studied under different environments i.e. 2018-19, 2019-20 and 2020-21. In general, the magnitude of PCV was slightly higher than the corresponding GCV estimates, for all the traits and all the environments, indicating the presence of sufficient environmental variation, as depicted in Fig.-1. The estimates of PCV and GCV were found to be moderately high for almost all the traits except for days to maturity and oil content, for all the environments implying the significant contribution of these traits for the crop improvement program. Moreover, the PCV and GCV estimates were differing very slightly, suggesting the prevalence of additive genetic effects for these traits. The selection for these traits will be helpful. The prevalence of additive genetic effects was also reported by (13), while studying genetic variability in mustard. Though the estimates of PCV were slightly higher than GCV for days to maturity and oil content, the individual values of PCV and GCV were found to be almost same for these traits, in all the environments, indicating less influence of environment on these traits.

In case of Environment-1 the magnitude of PCV was found to be highest for number of primary branches per plant (23.412%) followed by seed yield (21.617%) and siliquae on main raceme (18.447%), whereas, the estimates of GCV were reported highest for seed yield (20.1001) followed by number of primary branches per plant (19.0273) and siliquae on main raceme (14.7891). Moreover, the values of PCV (3.4301) and GCV (2.7377) were both reported high for seed yield followed by siliquae on main racemeand were found to be lowest for oil content. The findings of (14) corresponded with the results where they also reported higher estimates of PCV and GCV for seed yield per plant, number of primary branches, and number of siliquae on main raceme.

Table-1 : List of germplasm accessions of yellow sarson alongwith checks included in the study.

S.No.	Genotype	S.No.	Genotype	S.No.	Genotype	S.No.	Genotype
1.	PYSC-2011-41	12.	PYS-2015-5	23.	PYS-2018-2	34.	PYS-2020-6
2.	PYSC-2011-43	13.	PYS-2016-7	24.	PYS-2018-3	35.	PYS-2020-7
3.	PYSC-2011-48	14.	PYS-2016-8	25.	PYS-2018-4	36.	PYS-2020-12
4.	PYS-2013-3	15.	PYS-2016-10	26.	PYS-2018-7	37.	PPS-1
5.	PYS-2013-4	16.	PYS-2016-13	27.	PYS-2018-8	38.	Pant Sweta
6.	PYS-2013-6	17.	PYS-2016-15	28.	PYS-2018-9	39.	YSH-0401
7.	PYS-2013-8	18.	PYS-2017-6	29.	PYS-2018-10	40.	Pitambari
8.	PYS-2015-1	19.	PYS-2017-8	30.	PYS-2019-1	41.	B-9
9.	PYS-2015-2	20.	PYS-2017-11	31.	PYS-2019-2		
10.	PYS-2015-3	21.	PYS-2017-13	32.	PYS-2020-2		
11.	PYS-2015-4	22.	PYS-2018-1	33.	PYS-2020-3		

Table-2 : Genetic parameters for different characters among the accessions of yellow sarson under different environments.

S.No.	Character	Year	ECV	GCV	PCV	h^2 (b)%	GA as % of mean
1.	Days to maturity	E1	2.897	3.365	4.44	57.43	5.252
		E2	2.475	3.577	4.35	67.64	6.061
		E3	3.117	3.152	4.433	50.57	4.618
2.	Plant height	E1	4.374	9.15	10.142	81.40	17.006
		E2	3.672	7.466	8.32	80.52	13.802
		E3	5.067	9.709	10.952	78.59	17.732
3.	Length of main raceme	E1	8.188	11.007	13.719	64.38	18.193
		E2	6.972	9.2	11.543	63.52	15.105
		E3	6.417	9.078	11.117	66.68	15.271
4.	Siliquae on main raceme	E1	11.026	14.789	18.447	64.27	24.424
		E2	9.111	12.475	15.448	65.22	20.753
		E3	9.227	9.364	13.146	50.74	13.741
5.	Siliqua density	E1	10.993	9.635	14.636	43.33	13.067
		E2	10.584	9.363	14.155	43.75	12.756
		E3	11.305	6.481	13.064	24.62	6.627
6.	Number of primary branches per plant	E1	13.642	19.027	23.412	66.05	31.856
		E2	8.735	16.889	19.014	78.90	30.904
		E3	10.529	15.87	19.046	69.43	27.243
7.	Siliqua length	E1	6.849	7.336	10.037	53.42	11.045
		E2	5.944	5.774	8.288	48.53	8.285
		E3	5.077	6.908	8.572	64.95	11.468
8.	Number of seeds per siliqua	E1	11.42	12.992	17.297	56.41	20.1
		E2	10.705	14.412	17.953	64.44	23.833
		E3	10.94	15.195	18.724	65.86	25.402
9.	Oil content	E1	2.067	2.738	3.43	63.70	4.501
		E2	2.098	2.725	3.439	62.79	4.448
		E3	1.997	2.841	3.473	66.92	4.787
10.	Thousand seeds weight	E1	7.665	13.944	15.912	76.79	25.17
		E2	5.139	12.48	13.495	85.52	23.775
		E3	5.999	13.449	14.727	83.40	25.303
11.	Seed yield	E1	7.954	20.1	21.617	86.46	38.501
		E2	5.72	20.138	20.935	92.53	39.906
		E3	8.443	18.139	20.007	82.19	33.877

Taking Environment-2 into consideration the estimates of PCV and GCV together and in particular were found highest for seed yield (20.934; 20.138) followed by number of primary branches per plant (19.014; 16.889) and number of seeds per siliquae (17.95; 14.412). PCV and GCV values for environment-3 were found to be oriented in similar fashion as that of environment-2. The estimates were reported to be highest for seed yield (20.007; 18.139) at both, together and in particular, followed by number of primary branches per plant (19.046; 15.870) and number of seeds per siliquae (18.725; 15.195).

The estimates of heritability along with genetic advance as a percent of mean in environment-1 were found to be high for seed yield (86.46%; 38.5%), thousand seed weight (87.97%; 25.14%), number of primary branches per plant (66.1%; 31.86%) and siliquae on main raceme (64.5%; 24.42%), whereas, high heritability with low genetic advance was administered for oil content (63.7%; 4.501%). The heritability in particular was

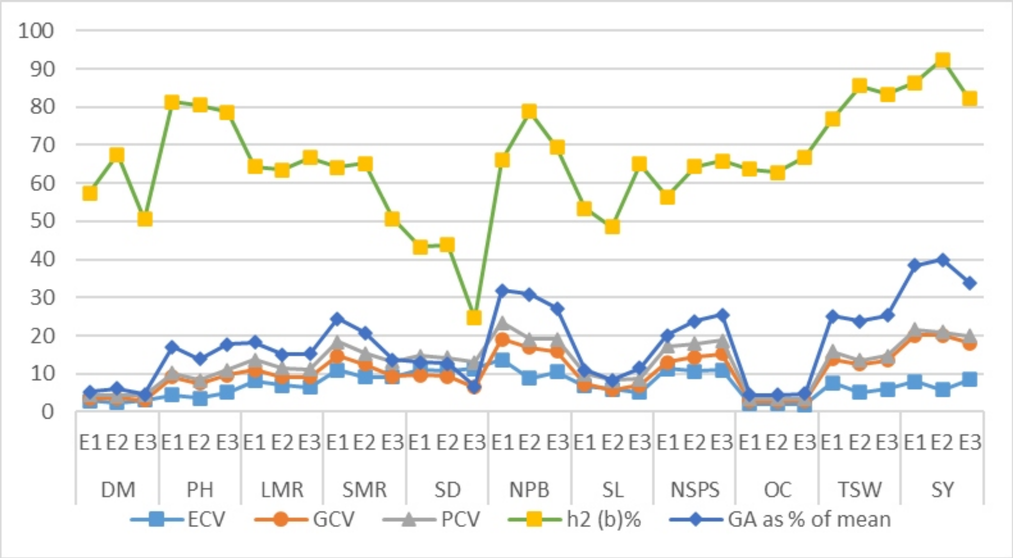

Fig.-1 : Graphical representation of genetic parameters in different environment (i.e. E1, E2 and E3).

observed high for traits viz., seed yield (86.46%) followed by plant height (81.4%) and thousand seed weight (76.79%) and was recorded lowest for siliqua length (53.42%). Genetic advance as a percent of mean in case of environment-1 was found highest for seed yield (38.5011) and lowest for oil content (4.501).In case of Environment-2, high heritability coupled with high genetic advance was observed for seed yield (92.53%; 39.9%), thousand seed weight (85.5%; 23.775%), number of primary branches per plant (78.9%; 30.9%) and number of seeds per siliqua (64.44%;33.83%) andthe characters viz., oil content (62.8%; 4.45%) and days to maturity (67.6%; 6.061%) showed high heritability along with low genetic advance as a percent of mean. The estimates of heritability alone, were found to be highest for seed yield (92.53%), thousand seed weight (85.52%) and plant height (80.52%) and lowest for siliqua density (43.75%). Seed yield (39.9056) showed highest value of genetic advance as a percent of mean whereas, it was lowest for oil content (4.4478), following the trend of environment-1. In environment-3 however, high heritability along with high genetic advance was administered by thousand seed weight (83.4%; 25.30%), seed yield (82.2%; 33.88%), number of seeds per siliqua (65.9%; 25.402%) and number of primary branches per plant (69.4%; 27.2%). Oil content (66.9%; 4.79%) showed high heritability paired with low genetic advance as percent of mean, and siliqua density (24.6%; 6.63%) showed low heritability with low genetic advance as percent of mean. Heritability specifically was found highest for thousand seed weight (83.4%) followed by seed yield (82.2%) and plant height (78.6%) and was lowest for siliquae density (24.6%). Genetic advance as a percent of mean was highest for seed yield per plant (33.88%), like environment-1 and -2 and was lowest for days to maturity (4.618%).

High heritability along with high genetic advance as percent of mean as well as high GCV and PCV values were recorded for characters viz., Seed yield, number of primary branches per plant and number of seeds per siliqua commonly for all the environments implying that the heritability of these traits is due to additive gene effects and selection will be effective for these traits, whereas, oil content showed high heritability with low genetic advance as percent of mean and low GCV and PCV values.The traits viz., seed yield, thousand seed weight, number of primary branches per plant and number of seeds per siliquawere found to be administering high heritability along with high genetic advance in all the environments, as presented in the Fig. 1, implying that the selection program needs to be taken out for these traits, on the other hand selection for oil content,selection may not be rewarding. Overall, the traits viz., seed yield, number of primary branches per plant, number of seeds per siliqua, thousand seed weight and siliquae on main raceme were found to be contributing more towards variability and are suggested to be explored in further crop improvement programs.

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