

Genetic Variability, Heritability and Genetic Advance Studies in Yellow Sarson (*Brassica rapa* var. Yellow Sarson)

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Abstract – An experiment was carried out during Rabi season of 2014-15 at Research farm College of Agriculture, Gwalior, Madhya Pradesh to assess the genetic variability, heritability and genetic advance in 21 diverse genotypes of yellow sarson (*Brassica rapa* var. yellow sarson) for ten yield and its contributing characters. Analysis of variance for the design of the experiment indicated highly significant differences for all the characters. High Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) were observed for number of secondary branches per plant followed by seed yield per plant, number of primary branches per plant and number of siliqua on main raceme. Hence, direct selection of these traits will prove effective. Days to flowering, plant height and length of siliqua showed low PCV and GCV. Higher estimates of broad sense heritability were observed for all the characters. High heritability coupled with high genetic advance was observed for number of secondary branches per plant, seed yield per plant, length of main raceme, number of siliqua on main raceme, number of seeds per siliqua and number of primary branches per plant. High heritability with moderate genetic advance in case of length of siliqua and 1000 seed weight whereas, High heritability and low genetic advance was observed for days to flowering and plant height. This study revealed that variations in the extent of genetic variability, heritability and genetic advance in traits under study can facilitate selection for further improvement of important traits of *Brassica rapa* var. yellow sarson.

Keywords – Variability, Heritability, Genetic Advance, Yellow Sarson.

I. INTRODUCTION

In India, rapeseed-mustard is the second most important edible oilseed after groundnut sharing 27.8% in the India's oilseed economy. Oleiferous *Brassica* species can be classified into three groups viz the cole, the rapeseed and the mustard. The coles are consumed as vegetables and the other two are the valuable sources of edible oils and proteins. The mustard groups include species like *Brassica juncea* (Indian mustard/ Rai/ Raya/ Laha), *Brassica nigra* (Black mustard/ Banarsi rai) and *Brassica carinata* (Ethiopian mustard); whereas the rapeseed groups include *Brassica rapa* Syn. *B. campestris* (Turnip rape/ Yellow sarson/ Field mustard/ Bird rape/ Keblock/ Colza) and *Brassica napus* (Oilseed rape/ Canola) [16] and [1]. In India, these crops had production of 6.31 million tonnes from an area of 5.79 million hectares with an average productivity of 1089 kg ha⁻¹. Madhya Pradesh has second rank in area and production after Rajasthan. In Madhya Pradesh the total area of rapeseed-mustard is 0.71 million hectares with production of 0.72 million tonnes and total average productivity is 1006 kg ha⁻¹ [2].

The genomic constitutions of the three diploid elemental species of *Brassica* are AA for *Brassica rapa*, BB for *Brassica nigra* and CC for *Brassica oleracea* having haploid chromosome number of 10, 8 and 9 respectively. On the other hand, the species *Brassica juncea* (AABB), *Brassica carinata* (BBCC) and *Brassica napus* (AACC) are the amphidiploids and originated by combinations of the diploid elemental species [4] and [5]. Among rapeseed-mustard, yellow sarson endowed with higher oil content, early maturity and produce pale yellow coloured oil, which has consumer preference. The meal cake from yellow sarson is preferred in blending in feeds but the productivity is comparatively low than mustard varieties and there are several reasons responsible for it. The use of higher productive genotypes is the most important measure for increasing the productivity in a sustainable manner. Development of high yielding cultivars requires excellent knowledge of the existing genetic variations for yield and its components. However, estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in mean value among successive generations [12]. Thus, in the present investigation, attempt has been made to identify the extent of genetic variability, heritability and genetic advance among the 21 diverse genotypes of *Brassica rapa* var. yellow sarson.

II. MATERIALS AND METHODS

The experiment was carried out at the Research farm, College of Agriculture Gwalior, Madhya Pradesh, using 21 diverse genotypes of yellow sarson (Table-I) obtained from the Directorate of Rapeseed-Mustard Research, Bharatpur, Rajasthan. The experiment was laid out in Randomized Block Design with three replications during Rabi season of 2014-15. Each treatment was grown in 3m long single row plot spaced 45cm apart. The plant to plant distance was maintained 15cm. Five competitive plants from each plot were selected randomly for recording the data on ten characters viz. days to flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, length of main raceme (cm), number of siliqua on main raceme, siliqua length (cm), number of seeds per siliqua, 1000-seed weight (g) and seed yield per plant (g).

The mean data were subjected to analysis of variance as per standard procedure outlined by [9]. The Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV) and heritability in broad sense were

calculated using the formula suggested by [3]. Genetic advance was calculated by the method suggested by [6].

III. RESULTS AND DISCUSSION

Analysis of variance for the design of the experiment indicated highly significant differences for all the characters which indicated the presence of considerable genetic variation among the genotypes for all the traits (Table-II). In general, PCV (Phenotypic Coefficients of Variation) were higher than GCV (Genotypic Coefficients of Variation) for all the characters (Table-III). High PCV and GCV were observed for number of secondary branches per plant followed by seed yield per plant, number of primary branches per plant and number of siliqua on main raceme. Number of seeds per siliqua showed high PCV (23.11) with moderate GCV (19.81). Higher magnitude of genetic variability indicated better scope of phenotypic selection through traits for improvement in yellow sarson. High estimates of phenotypic and genotypic coefficient of variability for these characters were also reported by [11] and [16]. Moderate PCV & GCV was recorded for length of main raceme, whereas 1000 seed weight showed moderate PCV (10.82) with low GCV (9.19). Days to 50% flowering, plant height and length of siliqua showed low PCV and GCV. Low values of genotypic coefficient of variation indicated the need to create variability either by hybridization or mutation followed by selection. Similar trend was also reported by [10], [13] and [8]. The difference between PCV and GCV was relatively high for number of secondary branches per plant, number of siliqua on main raceme, number of seeds per siliqua and seed yield per plant indicated these traits were highly influenced by the environment. A close proximity in the estimates of GCV and PCV was observed for days to flowering, plant height and length of siliqua indicated a low influence of environment in the expression of these traits and ample scope for improvement.

The coefficient of variation does not offer the full scope of heritable variation. It can be determined with greater degree of accuracy when heritability in conjunction with genetic advance is studied. Hence, heritability and genetic advance are important parameters to study the scope of improvement in various characters through selection. Heritability estimates in association with genetic advance are much useful for selection than heritability alone is also suggested by [6]. In the present study higher estimates of broad sense heritability were observed for all the characters (Table-IV). High heritability coupled with high genetic advance was observed for number of secondary branches per plant, seed yield per plant, length of main raceme, number of siliqua on main raceme, number of seeds per siliqua and number of primary branches per plant. This indicated the preponderance of additive gene action with less influence of environment in the inheritance of these traits and selection would be more effective. These results are in conformity with [7] and [15]. High heritability with moderate genetic advance in case of length of siliqua and 1000 seed weight indicated

the importance of both additive and non-additive gene action. High heritability and low genetic advance was observed for plant height and days to flowering rendering them unsuitable for improvement through simple selection due to prevalence of non-additive gene action. Similar result was reported by [8].

IV. CONCLUSIONS

From this study it is concluded that Seed yield per plant, Number of siliqua on main raceme, Number of primary branches per plant and Number of secondary branches per plant showed maximum potential for effectiveness of selection, because these traits show high PCV, GCV, heritability and genetic advance. Therefore it can be used in further improvement in yield of yellow sarson.

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Table I. Name of strains/varieties

S. No.	strains/varieties	Sr. No.	strains/varieties	Sr. No.	strains/varieties
1	YST-151	8	Anmol gold	15	YS-19
2	Pitambari	9	YS-16	16	YS-34
3	YS-24	10	YS-30	17	YS-22
4	Ulhas	11	YS-2	18	YS-13
5	Gold-10	12	YS-23	19	YS-7
6	Firangi	13	YS-33	20	YS-36
7	YS-1	14	YS-35	21	K-Local

Table II. Analysis of variance for 10 quantitative characters in yellow sarson

Source of variation	Degrees of freedom	Mean squares									
		DF	PH (cm)	NPB	NSB	LMR (cm)	NSMR	LS (cm)	NSS	1000-SW (g)	SYP (g)
Replication	2	5.86	0.12	0.29	0.23	9.22	16.89	0.004	4.91	0.004	1.02
Treatments	20	15.88**	86.91**	19.58**	17.03**	190.69**	304.15**	0.88**	112.08**	0.41**	69.04**
Error	40	6.21	8.67	1.75	0.21	13.14	22.03	0.04	9.13	0.04	3.81

* =Significant at 5% probability level, **= Significant at 1% probability level, DF= days to flowering, PH= plant height, NPB= Number of primary branches per plant, NSB= Number of secondary branches per plant, LMR= Length of main raceme, NSMR= Number of siliqua on main raceme, LS= Siliqua length, NSS= Number of seeds per siliqua, 1000-SW= 1000-seed weight, SYP= Seed yield per plant

Table III. Mean, range, genotypic, phenotypic and error variance and coefficient of variation for 10 quantitative characters in yellow sarson.

S.N.	Characters	Grand mean X±SE	Range		σ^2_p	σ^2_g	GCV	PCV	σ^2_e	CV (%)
			Min.	Max.						
1	DF	50.75±0.78	48.53	54.43	6.55	4.72	4.28	5.03	6.45	2.67
2	PH	101.54±1.70	93.40	115.83	34.94	26.28	5.05	5.82	8.67	2.90
3	NPB	7.39±0.76	2.53	12.53	7.65	5.94	32.97	37.45	1.72	17.76
4	NSB	3.30±0.26	0.00	8.53	5.57	5.38	70.33	71.59	0.19	13.37
5	LMR	50.52±2.09	39.53	67.93	72.32	59.18	15.32	16.91	13.14	7.18
6	NSMR	32.92±2.67	18.00	62.13	115.51	94.09	29.47	32.64	21.41	14.06
7	LS	5.83±0.12	4.37	6.67	0.32	0.28	9.11	9.77	0.04	3.52
8	NSS	30.54±1.74	18.27	39.60	45.71	36.69	19.81	23.11	9.03	9.84
9	1000-SW	3.97±0.12	3.10	4.27	0.17	0.13	9.19	10.82	0.04	5.23
10	SYP	12.01±1.02	4.70	26.37	24.37	21.23	38.37	41.11	3.14	14.75

σ^2_p = Phenotypic variance, σ^2_g = Genotypic variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, σ^2_e = Error variance, CV= Coefficient of variation

Table IV. Heritability (%) in broad sense, genetic advance and genetic advance in percent of mean for 10 quantitative characters in yellow sarson

S.N.	Characters	Heritability (%)	Genetic advance	Genetic advance in percent of mean
1	Days to flowering	72.13	3.82	7.47
2	Plant height	75.20	9.16	9.02
3	Number of primary branches per plant	77.50	4.42	59.79
4	Number of secondary branches per plant	95.30	4.62	132.18
5	Length of main raceme	81.60	14.24	28.26
6	Number of siliqua on main raceme	81.56	18.02	54.71
7	Length of siliqua	87.00	1.02	17.50
8	Number of seeds per siliqua	80.30	11.18	36.60
9	1000-seed weight	74.30	0.63	15.79
10	Seed yield per plant	87.15	8.88	73.79