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To study on genetic variability for yield and its contributing traits in yellow mustard under sodic soil

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Abstract

The experiment was conducted at Research Farm of Department of Genetics & Plant Breeding, ANDUAT, Narendra Nagar, Ayodhya (U.P.) during *rabi*, 2018 with 28 yellow mustard genotypes for assessment of genetic variability. The analysis of variance (ANOVA) was found significant for all the characters under study. The genotype NDYS-2 followed by YSCN16-3, NDYS16-6, YSCN-2 and YSCN16-5 producing higher seed yield per plant. The highest estimates of PCV and GCV was observed in case of seed yield per plant (g) (PCV 29.193%, GCV = 25.546%) followed by primary branches per plant (PCV = 25.407%, GCV = 21.573%), and number of seed per silique (PCV = 21.645%, GCV = 20.891%) recorded higher for GCV and PCV. The heritability in broad sense was recorded higher of character length of main raceme (94.00%) followed by number of seed per silique (93.10%), oil content (%) (90.10%), silique on main raceme (30.97%), and length of main raceme (27.87%). The high estimate of heritability coupled with high genetic advance for seed yield per plant (g), number of seed per silique, silique on main raceme, and length of main raceme.

Keywords: Variability, phenotypic coefficient, genotypic coefficient

Introduction

Field mustard (Brassica rapa L. synonym: B. campestris L.) are originated from the highlands near the Mediterranean Sea rather than from the Mediterranean coastal areas. Field mustard are the world's third most important sources of vegetable edible oil. Rapeseed crops are cultivated in 53 countries spreading over the six continents across the globe covered area. It is also known as Turnip rape/Yellow sarson/Bird rape/Keblock/Colza. Yellow sarson is the major Rabi season, self-compatible and largely self-pollinated crop (85-90%). Mustard is the most important oilseed crops of rapeseed mustard group and it is the most dominating *Rabi*, oilseed crop of U.P. India is the largest agrarian subcontinent supporting 26% world's agricultural population on 12% arable land. Despite being the third largest producer (11.3%) of oilseed brassica after Canada and China in the world. China, India, Canada, Japan and Germany are the major rapeseed-mustard growing countries. India meets 57% of the domestic edible oil requirements through imports and ranked 7th largest importer of edible oils in the world. India has area 6.23 million hector, production 9.34 million tons, and productivity 1499 kg/hector and also Uttar Pradesh has area 0.75 million hector, production 1.12 million tons and productivity 1483 kg/hector (2018-19). The largest mustard seed producing states in India are Rajasthan (45%), Haryana (13%), Madhya Pradesh (13%) and Uttar Pradesh (11%). It is also grown under some nontraditional areas of South India including Karnataka, Tamil Nadu, and Andhra Pradesh. It comprises of several economically important species which yield edible roots, stems, leaves, buds, flowers and seed condiment.

The Indian mustard have nutritional value *viz.*, carbohydrates 4.51g, sugar 1.41g, dietary fiber 2g, fat 0.47g and protein 2.56g per 100g seeds. Indian cultivars have high glucosinolate (18-120 μ moles (g) in seed meal) and contains adequate amount of two essential fatty acids, linoleic and linolenic. The oil of mustard possesses a sizable amount of erucic acid (38-57%), together with linolenic acid (4.7 to13.0%). The protein content in rapeseed and mustard normally ranges between 24- 30% on the basis of whole seed basis and between 35-40% on meal basis. But the presence of toxic glucosinolates in the mustard cake renders it unsuitable as a source of human protein. 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.

Material and Methods

The investigation was conducted at Research Farm of Department of Genetics & Plant Breeding, Acharya, Narendra Deva University of agriculture and Technology, Narendra Nagar, Ayodhya (U.P.) during rabi, 2017-18. The materials 26 yellow mustard genotypes viz. - NDYS08-1, NDYS08-4, NDYS-125, NDYS11-3, NDYS116-1, NDYS-128, NDYS11-2, NDYS116-1, NDYS16-12, NDYS16-1, NDYS16-7, NDYS16-9, NDYS16-10, NDYS16-4, NDYS16-8, NDYS16-NDYS16-6, YSCN16-1, YSCN16-2, YSCN16-3, 5. YSCN16-4, YSCN16-5, YSCN16-6, along with 2 check variety Jagriti, and NDYS-2 was grown in Randomized Block Design with three replication. These 4 lines were growing in single row of 3 meter spaced at 30cm apart. The distance between plant to plant 15 cm was maintained by thinning. All the recommended dose of fertilizers and cultural practices

were done. All the observation are recorded based on five competitive plants from each plot selected randomly except day to 50% flowering and days to maturity which were recorded on plot basis. Geographical, this place is located at 26.56° N latitude, and 81.83° E longitudes and at an altitude of 113 m above from mean sea level in the gangetic plains of eastern U.P. this area falls in sub-tropical climatic zone. The annual rainfall is about 1270 mm. Analysis of variance for design of experiment was carried out for each character separately following Panse and Sukhatme (1967). Variability for different characters was estimated as suggested by Burton and de Vane (1953). Heritability in broad sense (h² b) was suggested by Burton and de Vane (1953). Genetic advance (\overline{Ga}) was estimated by the method suggested by Johnson *et al.* (1955).

Result and Discussion

The mean squares due to treatments in ANOVA were highly significant for all the characters except plant height are significant under study presented in Table 1.

S. N.	Traits	Replicate (2)	Treatments (25)	Error (50)
1	Day to flowering 50%	3.17	12.43**	2.17
2	Days to maturity 50%	4.65	12.09**	2.05
3	Plant height (cm)	577.71	839.19*	492.45
4	Primary branches/plant.	1.13	6.04**	0.69
5	Silique on main raceme	19.21	129.69**	10.40
6	Lengh of main Raceme	11.33	159.26**	3.33
7	No. of seed/silique	0.74	189.47**	4.53
8	Oil content (%)	0.36	5.73**	0.20
9	Yield/plant (gm)	2.60	14.69**	1.36

Table 1: Analysis of variance

*, ** Significant at 5% & 1% respectively.

The mean performance of 26 genotypes including checks for 9 characters are given in Table 2. The NDYS-2 genotype produced highest seed yield per plant (12.7333) followed by YSCN16-3 (12.00), NDYS16-6 (12.00), YSCN-2 (10.73), YSCN16-5 (10.40) the remaining genotypes their by

constituting top non- significant group for higher seed yield in the Graph 1. In addition to the genotypes mentioned above, some other genotype showing very high mean performance for other characters can be used for improving these characters.

S. N.	Genotypes	Day to flowering 50%	Days to maturity 50%	Plant height (cm)	Primary branches /plant	Silique on main raceme	Length of main raceme	No. of seed /silique	Oil content (%)	Yield /plant (gm)
1	NDYS08-1	71.00	105.00	93.27	5.07	26.73	40.80	27.60	40.52	6.53
2	NDYS08-4	71.00	106.00	93.07	4.80	28.33	37.60	25.33	40.99	5.00
3	NDYS-125	66.33	102.33	106.13	7.07	35.27	47.60	38.53	41.06	6.80
4	NDYS11-3	69.00	105.00	107.40	4.87	30.47	49.80	36.33	43.50	5.87
5	NDYS116-1	69.33	106.33	115.00	5.00	36.13	51.40	20.20	43.10	5.87
6	NDYS-128	66.33	107.33	110.93	5.00	29.53	41.20	41.83	44.53	6.27
7	NDYS11-2	71.67	106.67	108.27	4.87	34.53	47.27	39.40	43.60	6.40
8	NDYS116-1	70.67	105.67	168.20	5.40	27.93	57.93	39.40	43.25	6.39
9	NDYS16-12	68.67	104.67	131.87	6.73	41.47	57.93	36.60	44.15	8.60
10	NDYS16-1	69.67	106.67	108.73	4.33	31.93	46.40	18.47	42.13	5.67
11	NDYS16-7	70.67	106.67	100.27	4.73	30.20	47.27	38.53	44.04	7.80
12	NDYS16-9	63.67	108.67	122.47	6.73	42.67	52.53	38.20	45.04	9.40
13	NDYS16-10	71.67	107.67	122.40	7.73	38.00	54.20	39.33	45.13	8.33
14	NDYS16-4	67.67	104.67	105.73	4.33	30.80	46.53	42.07	44.98	8.07
15	NDYS16-8	70.67	108.67	133.73	5.93	41.13	55.20	38.73	43.61	6.00
16	NDYS16-8	71.00	109.00	130.13	5.00	45.87	58.80	44.73	42.59	6.73
17	NDYS16-5	67.33	108.33	141.73	5.47	43.07	67.13	35.87	43.42	9.00
18	NDYS16-6	69.67	106.67	137.80	7.93	40.40	59.20	48.40	45.22	12.00
19	YSCN16-1	70.67	108.67	127.13	8.00	38.87	55.33	43.33	45.05	10.33
20	YSCN16-2	71.33	109.33	111.40	7.20	39.87	50.00	40.07	44.80	10.73

21	YSCN16-3	70.33	107.00	112.07	7.40	39.40	52.20	45.40	45.39	12.00
22	YSCN16-4	72.33	110.33	110.40	8.47	42.33	47.60	40.13	44.24	10.00
23	YSCN16-5	69.67	111.67	121.20	6.87	35.60	44.73	40.60	43.44	10.40
24	YSCN16-6	67.00	107.00	121.00	6.87	41.33	55.27	36.53	42.51	8.00
25	Jagriti (ch)	70.00	109.00	127.40	5.73	45.60	51.60	28.53	44.25	9.60
26	NDYS-2(ch)	69.00	107.00	138.73	9.40	53.27	67.47	53.00	45.16	12.73
	Mean	69.47	107.15	119.48	6.19	37.34	51.65	37.58	43.68	8.25
	C.V.	2.12	1.34	18.57	13.42	8.64	3.53	5.67	1.03	14.13
	S.E.	0.85	0.83	12.81	0.48	1.86	1.05	1.23	0.26	0.67
	C.D. 5%	2.41	2.35	36.39	1.36	5.29	2.99	3.49	0.74	1.91
	C.D. 1%	3.22	3.13	48.52	1.82	7.05	3.99	4.66	0.98	2.55
	Min	63.67	102.33	93.07	4.33	26.73	37.60	18.47	40.52	5.00
	Max	72.33	111.67	168.20	9.40	53.27	67.47	53.00	45.39	12.73
	Range	8.67	9.33	75.13	5.07	26.53	29.87	34.53	4.88	7.73

In this regard, the most desirable genotypes were NDYS16-9, NDYS-125, NDYS-128, NDYS16-4 and NDYS16-112 for early flowering and for early maturity NDYS-125, NDYS16-4, NDYS08-1, NDYS11-3 and NDYS116-1; for plant height NDYS08-4, NDYS08-1, NDYS16-7, NDYS16-4 and NDYS-125 have short stature. For maximum primary branches per plant NDYS-2, YSCN-4, YSCN-1,NDYS-16-6, and YSCN-3; For maximum length of main raceme NDYS-2, NDYS16-5,NDYS16-6, and NDYS16-8; and others; For silique on

main raceme NDYS-2, NDYS16-8, Jagriti, NDYS16-5 and NDYS16-9, For number of seeds per silique NDYS-2, NDYS16-6, YSCN-3 and NDYS16-8; for oil content (%) YSCN16-3, NDYS16-6, NDYS16-10, NDYS-2 and YSCN16-1. Similarly, the genotypes showing very high mean performance in desirable direction for various characters may also be used for improving the characters for which they have high mean performance.



Fig 1: Mean performance of seed yield per plant

The estimates of genotypic coefficients of variation (GCV), phenotypic coefficients of variation (PCV), heritability and genetic advance for nine characters of mustard genotypes evaluated are presented in Table-3 & Graph-2. The highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed in case of seed yield per plant (g) (PCV 29.193%, GCV = 25.546%) followed by primary branches per plant (PCV = 25.407%, GCV = 21.573%), and number of seed per silique (PCV = 21.645%, GCV = 20.891%) can be considered as higher because these value are >20%. Moderate estimates (>10% to <20%) of PCV as well as GCV were recorded for, Silique on main raceme (PCV = 18.97 %, GCV = 16.89 %), and length of main raceme (PCV = 14.398 %, GCV = 13.957%). Four characters exhibited low estimates (< 10%) of PCV as well as GCV. The lowest estimates of PCV and GCV were observed for days to maturity (PCV = 2.168%, GCV = 1.707%) followed by oil content (%) (PCV = 3.273%, GCV = 3.107%) and day to 50% flowering (PCV = 3.403%, GCV = 3.403%). The character Plant height (cm) has higher PCV

(20.64) and low GCV (9.00) it may be due to higher environmental effects on plant height (cm). The existence of genetic variation is a basic necessity for evolution of any species. The variability for yield, its components that we can see, measure and study is the ultimate result of the variability in the genetic constitution of the individuals. The information on the amount of genetic variability present in the genotype with respect to important traits is considered a priority for directed improvement in the concerned species. The fundamental principle involved in plant breeding is the application of the genetic variability available in the breeding material for various characters to change the genetic architecture of plant in order to develop improved genotype possessing higher economic yield and value than existing one. Obviously, genetic variability is the raw material on which selection acts to bring out improvement in genetic architecture of plant. The phenotypic and genotypic coefficients of variation were computed to assess the nature and magnitude of existing variability in the genotype. For seed yield and its components, PCV and GCV were higher for seed yield per

plant (g), primary branches per plant, and number of seed per silique. Similar results were observed by Roy *et al.* (2011) ^[8],

Ullah *et al.* (2015) ^[13], Salam *et al.* (2017) ^[9], Sikarwar *et al.* (2017) ^[11], and Raliya *et al.* (2018) ^[7].

Traits	Variance genotypical	Variance phenotypical	GCV	PCV	h ² (Broad sense)	Gen. adv as % of mean 5%
Day to flowering 50%	3.42	5.59	2.66	3.40	61.20	4.29
Days to maturity 50%	3.34	5.40	1.71	2.17	62.00	2.77
Plant height (cm)	115.58	608.03	9.00	20.64	19.00	8.08
Primary branches/plant.	1.78	2.47	21.57	25.41	72.10	37.73
Silique on main raceme	39.76	50.16	16.89	18.97	79.30	30.98
Length of main Raceme	51.98	55.31	13.96	14.40	94.00	27.87
No. of seed/silique	61.65	66.18	20.89	21.65	93.10	41.53
Oil content (%)	1.84	2.04	3.11	3.27	90.10	6.08
Yield/plant (gm)	4.44	5.80	25.55	29.19	76.60	46.05





Fig 2: Genetic parameters

The highest estimate of heritability in broad sense was recorded by length of main raceme (94.00%) followed by number of seed per siliqua (93.10%), oil content (%) (90.10%), siliquae on main raceme (79.30%), yield per plant (g) (76.60%), exhibited high estimates of heritability (>75%), while the lowest value by plant height (cm) (19.00%). The characters exhibiting high estimates (>20%) of genetic advance in per cent of mean were number of seed per silique (41.534%), primary branches per plant. (37.734%), silique on main raceme (30.977%), length of main raceme (27.872%). The characters exhibiting moderate estimates (>10%) of genetic advance in per cent of mean were not found in any lines. The lower estimates of genetic advance (<10) resulted in case of plant height (cm) (8.082%), oil content (%) (6.075%), day to 50 % flowering (4.292%) and days to (2.767%). Heritability estimation provides maturity information on transmission of character from the parent to the progeny. Selection programme depends primarily upon the magnitude of heritable portion of variability. Heritability (h²_(bs)) and genetic advance in per cent of mean as direct selection parameters provide index of transmissibility of traits which gives indication about the effectiveness of selection in improving the characters. Johnson et al. (1955) have suggested that heritability estimates in association with genetic advance are much useful for selection program than heritability alone. The high estimate of heritability coupled with high genetic advance for seed yield per plant (g), number of seed per silique, silique on main raceme, and length of

main raceme, that's reason the selection of genotypes based on these characters are more useful for genetic improvement of genotypes and similar results were observed by Bind *et al.* (2013) ^[3], Kumar *et al.* (2013) ^[4], Tesfaye *et al.* (2014) ^[12].

Conclusion

The analysis of variance were found highly significant for all the characters except plant height are found significant under study. The genotype NDYS-2 followed by YSCN16-3, NDYS16-6, YSCN-2 and YSCN16-5 produced higher seed yield per plant. Most desirable genotypes for other characters than seed yield per plant were NDYS16-9 for early flowering; for early maturity NDYS-125; for plant height (cm) NDYS08-4; for primary branches per plant NDYS-2; for length of main raceme (cm) NDYS-2; for siliquae on main raceme NDYS-2; for number of seeds per siliqua NDYS-2 and for oil content (%) YSCN16-3, these genotypes showed very high mean performance in different characters. The highest estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) was observed in case of seed yield per plant (g) followed by primary branches per plant and number of seed per silique are found higher, that's reason these characters have higher phenotypic variability and genetic variability. The highest estimated of heritability in broad sense was recorded by length of main raceme followed by number of seed per silique, oil content (%), silique on main raceme, and seed yield per plant (g) are found higher. The characters exhibiting high estimates of genetic advance in

per cent of mean were number of seed per silique, primary branches per plant, silique on main raceme, and length of main raceme. The high estimate of heritability coupled with high genetic advance for seed yield per plant (g), number of seed per silique, silique on main raceme, and length of main raceme, that's reason the selection of genotypes based on these characters are more useful for genetic improvement of genotypes.

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