

Original Research Article

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## Evaluation of Selected Segregating Populations of Indian Rapeseed (*Brassica rapa* L.) for Yield and Yield Related Traits

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### ABSTRACT

#### Keywords

Toria, Yellow sarson, Seed yield/plant, Genetic variation, Heritability, Genetic advance

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Toria is the predominant oilseed crop of Assam, but productivity is very low compared to all India average. Therefore, continued efforts are necessary to achieve high seed yield through breeding high yielding varieties. The present study was conducted to evaluate the segregating populations of some toria x yellow sarson crosses for yield and related traits. During Rabi 2015-16, 21 populations consisting of 5 parents, 3 F<sub>1</sub>s and 13 F<sub>3</sub>s were grown. Highly significant differences were observed among the populations for different yield attributing characters. High genotypic variation was observed for number of secondary branches per plant, seed yield/plant, biological yield/plant and harvest index. High heritability was observed for days to 50% flowering, seed yield per plant and plant height. High genetic advance was recorded for number of secondary branches, seed yield/ plant, biological yield/ plant, harvest index and days to 50% flowering. Jeuti was early maturing genotype. The genetic variation present in toria and yellow sarson populations could be utilized in breeding useful varieties of toria and yellow sarson types.

### Introduction

Rapeseed (*Brassica napus* L. and *B. rapa* L.) and mustard (*B. juncea*) are the major oilseed Brassica species in India. Crop Brassicas are of great importance as vegetables, oilseeds and fodder throughout the world. The oleiferous Brassica species play an important role for vegetable oil production worldwide. From nutritional point of view, fats and oils in our diet are needed for calories and translocation of fat soluble vitamins. At present, rapeseed-mustard is the third most important source of edible oils in the world after palm oil and soybean, and it is used for

both nutritional and industrial purposes (FAO, 2014). Brassica oilseed production has increased over the last 50 years (FAO, 2014). The largest acreage of Brassica oilseeds is found in India, followed by China and Canada. The highest seed yields are reported from Europe (France, Germany and the UK) with average yields of about 3.0 tonnes/ha, more than twice the seed yields obtained in Canada and Australia (Rakow, 2004).

In India, rapeseed-mustard is the second most important oilseed crop after soybean. It is an important source of edible oil in Indian diet especially in Eastern and North-Western India.

Toria and to a lesser extent Yellow sarson (*Brassica rapa* L.) are grown in Assam. It is the most important oilseed in Assam with acreage of 2.57 lakh hectares producing 1.45 lakh tonnes resulting in average yield of 564 kg/ha. Assam accounts for 3.9 percent and 1.9 percent of the total Indian acreage and production, respectively (DRMR, 2016). Toria is characterized by hollow and weak stem, shallow roots, low biological yield, but high harvest index and short crop duration. On the other hand Yellow sarson has erect growth habit, deeper roots, solid stems, high biological yield but low harvest index (Barua, 1992). Attempts have been made to recombine the desirable yield component characters of Toria and Yellow sarson towards development of high yielding varieties of Toria and Yellow sarson which are highly cross compatible. However, continued efforts are necessary to achieve high seed yield through recombination breeding. The present study was to evaluate some segregating populations of Toria-Yellow sarson crosses for yield and related characters.

### **Materials and Methods**

The investigation was carried out at the experimental area of the Department of Plant Breeding and Genetics, Assam Agricultural University, Jorhat. The site is located at 26<sup>o</sup>44' north latitude and 94<sup>o</sup>10' east longitude having an elevation of 91 m above the mean sea level ([www.aau.ac.in](http://www.aau.ac.in)). Temperature recorded during period of experiment was between 9.4-28.8<sup>o</sup>c with relative humidity 55-99% with low rainfall and bright sunshine hours. Twenty one entries were sown on 5<sup>th</sup> November 2015 in randomized block design with three replications during *rabi* season 2015-16. Each plot contained 4 rows measuring 4 m in length. Row to row spacing was 30 cm and plant spacing within row was adjusted to 10-15 cm by thinning at seedling stage. The experimental material comprised of five varieties and three F<sub>1</sub> and thirteen F<sub>3</sub>

populations, as given in Table 1. Well decomposed cow dung was applied @ 2 t/ha along with N: P<sub>2</sub>O<sub>5</sub>: K<sub>2</sub>O @ 60:40:40 kg/ha in the form of urea, single super phosphate and muriate of potash. Irrigation of the experimental fields was done by sprinkling water manually six times, twice at sowing-seedling stage, twice at active vegetative, and twice during flowering and pod filling stages. Manual weeding and thinning were done during vegetative growth period, 15-20 days after sowing. Malathion 5 percent dust was applied by mixing with cow dung one week after germination to protect the seedlings from ants. At siliqua formation stage of the crop Rogor 30 EC was sprayed once to keep aphid population under control. No other serious pest and diseases were observed.

Observations were recorded on ten random plants per plot for 13 quantitative different characters (as in Table 4) related to growth and yield. Days to 50 percent flowering and maturity were observed on plot basis. Stem solidness/ hollowness was recorded by pressing between fingers at the stage of maturity. The plot mean data were subjected to analysis of variance for each character following standard statistical procedure in the fixed model (Gomez and Gomez, 1984). Mean performance was compared by critical differences at 5 and 1 percent level of significance. Genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance were estimated by standard biometrical procedures (Dabholkar, 1999). All calculations were done by using MS Excel 2007.

### **Results and Discussion**

The presence of variability is prerequisite for any breeding programme. In the present study, significant variation was observed among the populations for all yield and component traits recorded (Table 2). High genotypic and

phenotypic coefficients of variation were recorded for number of secondary branches, seed yield per plant, biological yield per plant and harvest index (Table 3). From the ranges of mean values, it was observed that there were large variations for all the characters, though coefficients of variation were not large. High broad sense heritability was observed for days to 50% flowering, seed yield per plant, plant height, secondary branches per plant, harvest index and biological yield per plant. High genetic advance was recorded for number of secondary branch, seed yield per plant, biological yield per plant, harvest index and days to 50% flowering. Thus for days to 50% flowering, seed yield per plant, plant height, secondary branches per plant, harvest index and biological yield per plant high heritability as well as high genetic advance were observed. High heritability and high genetic advance are indication of additive gene effects for such traits (Panse, 1957). Similar findings were reported in the inheritance of these traits in rapeseed (Kahrizi and Allahvarand, 2012; Khan *et al.*, 2013; Halder *et al.*, 2014). Therefore additive genetic effects were important in the inheritance of these characters. Non-additive gene effects were probably more influential in the inheritance of the other traits. Less difference between GCV and PCV for days to 50% flowering indicated that the genotypes have relatively less adaptive variation for flowering, as also inferred by Jahan (2014).

From the present investigation high heritability with moderate genetic advance was recorded for plant height. Similar result was observed by Saifullah (2012), whereas Naznin (2013) found high heritability with low genetic advance and Halder *et al.*, (2014) observed moderate heritability with low genetic advance for this trait. For number of primary branches per plant low heritability with low genetic advance was observed.

However, for number of secondary branches per plant moderate heritability with high genetic advance was recorded. High GCV was also observed for this trait. Jahan *et al.*, (2014) reported similar results in their study. Low heritability with moderate genetic advance was recorded for main shoot length and moderate heritability with moderate genetic advance for number of siliquae on main shoot. Moderate heritability was also recorded by Khan *et al.*, (2008) for main shoot length. Ghosh and Gulati (2001) reported high heritability for number of pods per main shoot in Indian mustard. For number of seeds per siliqua moderate heritability with moderate genetic advance and moderate GCV was recorded. Similar results were reported by Jahan *et al.*, (2014). Halder *et al.*, (2014) observed moderate heritability with moderate genetic advance for number of seeds per siliqua and thousand seed weight. In the present investigation also similar results were recorded for thousand seed weight. On the other hand, low heritability with low genetic advance was observed for maximum root length.

For seed yield per plant, high heritability with high genetic advance was recorded. High heritability was also recorded by Ullah *et al.*, (2015) for seed yield per plant. High broad sense heritability for seed yield per plant indicated more genetic control and less environmental influence on this trait. Similar findings were reported by Ali *et al.*, (2003), Tahira *et al.*, (2006), Aytac and Kinaci (2009) and Singh and Singh (2012) and they also observed high heritability for seed yield per plant. Similarly, relatively high heritability with high genetic advance was recorded for biological yield per plant and harvest index. The results from present investigation showed considerable variations among the rapeseed populations for yield and yield attributing characters revealing good scope for breeding a high yielding variety of rapeseed.

**Table.1** Experimental populations grown during *Rabi* 2015-16

SN		Population	Ecotype	Source
1.		YSH401	Yellow sarson	CCS HAU, Hisar
2.		NRCYS05-03	Yellow sarson	DRMR, Bharatpur
3.		TS38	Toria	RARS, Shillongani, AAU
4.		Jeuti	Toria	Dept of PBG, AAU
5.		B9	Yellow sarson	ICR Farm, AAU
6.	JT 12-1	TS38 x Jeuti F <sub>3</sub>	Toria	Dept of PBG, AAU
7.	JT 12-2-1	TS67 x YSH401 F <sub>3</sub> Sel-1	Toria x yellow	Dept of PBG, AAU
8.	JT 12-3	TS67 x NRCYS05-03 F <sub>3</sub>	Toria x yellow	Dept of PBG, AAU
9.	JT 12-2-2	TS67 x YSH401F <sub>3</sub> Sel-2 (early)	Toria x yellow	Dept of PBG, AAU
10.	JT 14-1	Jeuti x YSH401 F <sub>1</sub>	Toria x yellow	Dept of PBG, AAU
11.	JT 14-1	Jeuti x B9 F <sub>1</sub>	Toria x yellow	Dept of PBG, AAU
12.	JT 12-5	NRCYS05-03 x Jeuti F <sub>3</sub>	Yellow sarson x toria	Dept of PBG, AAU
13.	JT 12-6	NRCYS05-03 x TS38 F <sub>3</sub>	Yellow sarson x toria	Dept of PBG, AAU
14.	JYS 12-1	NRCYS05-03 x B9 F <sub>3</sub>	Yellow sarson x yellow sarson	Dept of PBG, AAU
15.	JT 12-7	YSH401 x TS38 F <sub>3</sub>	Yellow sarson x toria	Dept of PBG, AAU
16.	JT 12-8	YSH401 x Jeuti F <sub>3</sub>	Yellow sarson x toria	Dept of PBG, AAU
17.	JYS 12-2-1	YSH401 x B9 F <sub>3</sub> Sel-1 (brown seeds)	Yellow sarson x yellow sarson	Dept of PBG, AAU
18.	JYS 12-2-2	YSH401 x B9 F <sub>3</sub> Sel-2 (erect pods)	Yellow sarson x yellow sarson	Dept of PBG, AAU
19.	JYS 14-1	YSH401 x B9 F <sub>1</sub>	Yellow sarson x yellow sarson	Dept of PBG, AAU
20.	JYS 12-2-3	YSH401 x B9 F <sub>3</sub> Sel-3 (yellow seed)	Yellow sarson x yellow sarson	Dept of PBG, AAU
21.	JYS 12-2-4	YSH401 x B9 F <sub>3</sub> Sel-4 (brown seed, early)	Yellow sarson x yellow sarson	Dept of PBG, AAU

SN	Designation of population	Pedigree
1.	YSH401	Selection from local germplasm
2.	NRCYS 05-03	Selection from local germplasm IC 355419
3.	TS38	Recurrent selection in M27
4.	Jeuti	M27 x B9
5.	B9	Selection from local germplasm of Assam
6.	JT 12-1	TS38 x Jeuti (F <sub>3</sub> )
7.	JT 12-2-1	TS67 x YSH401 (F <sub>3</sub> ) sel-1
8.	JT 12-3	TS67 x NRCYS05-03(F <sub>3</sub> )
9.	JT 12-2-2	TS67 x YSH401(F <sub>3</sub> ) sel-2 (early)
10.	JT 14-1	Jeuti x YSH401(F <sub>1</sub> )
11.	JT 14-2	Jeuti x B9 (F <sub>1</sub> )
12.	JT 12-4	NRCYS05-03 x Jeuti (F <sub>3</sub> )
13.	JT 12-5	NRCYS05-03 x TS38 (F <sub>3</sub> )
14.	JYS 12-1	NRCYS05-03 x B9 (F <sub>3</sub> )
15.	JT 12-6	YSH401 x TS38 (F <sub>3</sub> )
16.	JT 12-7	YSH401 x Jeuti (F <sub>3</sub> )
17.	JYS 12-2-1	YSH401 x B9 (F <sub>3</sub> ) Sel-1 (brown seeds)
18.	JYS 12-2-2	YSH401 x B9 (F <sub>3</sub> ) sel-2 (erect pods)
19.	JYS 14-1	YSH401 x B9 (F <sub>1</sub> )
20.	JYS 12-2-3	YSH401 x B9 (F <sub>3</sub> ) sel-3 (yellow seed)
21.	JYS 12-2-4	YSH401 x B9 (F <sub>3</sub> ) sel-4 (brown seed, early)

**Table.2** Analysis of variance (mean square) for seed yield and related traits in rapeseed

Sources of variation	df	Days to 50% flower	Days to maturity	Plant height	Primary branches per plant	Secondary branches per plant	Main shoot length	Siliquae on main shoot	Seeds per siliqua	Maximum root length	1000 seed weight	Seed yield per plant	Biological yield per plant	Harvest index
Replications	2	20.63**	26.05**	71.84**	0.44	0.38	17.62**	5.80**	17.20**	27.13**	0.13	0.09	0.06	16.55
Genotypes	20	82.05**	40.45**	306.69**	2.92**	7.01**	38.74**	45.74**	39.33**	6.83**	1.15**	10.47**	27.51**	308.85**
Error	40	3.23	6.06	22.81	0.89	0.42	8.42	5.29	6.74	2.14	0.21	0.69	2.38	24.51
CV %		5.17	2.72	4.20	16.10	21.18	6.10	6.33	12.92	6.70	10.98	15.25	13.14	10.56

\*significant at P=0.05

\*\*significant at P=0.01

**Table.4** Mean performance of different populations for seed yield and related traits in rapeseed

Population	ST*	DF	DM	PH	PB	SB	MSL	SMS	SSQ	MRL	TSW	SYP	BYP	HI
YSH401	S	43.7	91.7	123.0	5.67	0.83	51.17	35.90	21.27	23.33	4.67	5.38	10.81	44.89
NRCYS 05-03	S	35.3	96.3	124.4	6.00	0.83	46.12	39.37	31.27	24.20	4.13	5.17	13.23	34.50
TS38	H	33.0	88.7	91.1	6.00	6.70	46.67	35.30	18.60	22.77	3.30	7.03	14.38	44.46
Jeuti	H	30.3	86.0	96.3	4.00	1.33	44.23	29.50	18.93	21.03	4.17	4.59	9.99	41.59
B9	S	34.0	94.7	119.4	5.33	0.83	42.45	26.10	24.00	20.07	3.90	4.53	8.49	47.62
JT 12-1	H	31.3	90.0	107.1	5.67	1.77	43.00	36.80	21.47	22.87	3.33	5.24	9.45	50.19
JT 12-2-1	H	42.7	93.7	120.9	8.00	4.57	52.60	34.40	18.53	22.00	4.73	7.74	15.13	45.98
JT 12-3	H	31.7	89.0	97.9	4.33	2.50	43.03	31.40	16.73	17.93	4.37	2.86	6.49	39.19
JT 12-2-2	H	34.0	88.7	108.6	5.00	1.40	47.27	33.00	20.53	21.67	3.50	5.46	10.68	46.48
JT 14-1	H	32.0	89.7	110.3	5.00	1.17	47.30	35.77	16.13	20.67	4.30	4.24	8.43	45.80
JT 14-2	H	40.3	89.0	118.1	4.67	2.00	53.63	38.10	18.00	23.53	4.70	6.32	11.24	51.27
JT 12-4	H	32.3	88.3	107.8	6.00	0.90	46.82	40.07	19.60	22.27	4.13	5.09	8.76	53.12
JT 12-5	H	43.0	95.3	118.1	6.67	3.33	52.85	41.33	18.93	20.33	4.70	10.43	17.83	53.51
JYS 12-1	S	30.7	89.7	129.0	7.00	0.87	49.57	38.57	17.93	21.60	4.60	3.33	13.66	19.58
JT 12-6	H	33.0	92.0	117.5	7.00	1.37	45.63	36.33	18.07	21.27	4.97	2.88	12.86	17.36
JT 12-7	H	32.7	88.3	113.5	6.00	0.83	47.53	37.63	17.87	22.67	4.63	4.30	13.03	28.08
JYS 12-2-1	S	32.7	94.3	125.6	6.67	3.53	54.55	40.83	20.33	21.27	3.50	5.85	12.63	41.22
JYS 12-2-2	S	30.7	87.3	110.8	5.00	1.53	45.37	36.43	19.60	20.80	3.43	4.62	11.68	34.96
JYS 14-1	S	47.0	100.0	118.3	6.33	0.60	44.80	35.33	27.67	23.33	5.47	8.29	15.00	50.35
JYS 12-2-3	S	37.3	90.3	123.6	6.33	1.37	48.83	41.37	19.27	20.87	4.73	7.12	15.94	39.69
JYS 12-2-4	S	34.3	87.3	109.3	6.67	3.13	46.03	39.17	17.33	23.93	3.43	3.90	7.11	49.79
Mean		34.8	90.6	113.8	5.87	1.97	47.59	36.32	20.10	21.83	4.22	5.45	11.75	41.89
SE (m)		1.0	1.4	2.8	0.37	0.32	1.67	1.33	1.50	0.84	0.27	0.48	0.89	2.86
CD (P=0.05)		3.0	4.1	7.9	1.56	0.91	4.79	3.80	4.29	2.41	0.77	1.37	2.55	8.17
CD (P=0.01)		4.0	5.4	10.5	2.09	1.22	6.40	5.08	5.73	3.23	1.02	1.83	3.41	10.93

\*Stem texture: S=Solid, H=Hollow



**Table.3** Estimates of genetic parameters for various characters for seed yield and Related traits in rapeseed

Characters	Range	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (%)
Days to 50% flowering	30.3 – 47.0	15.96	16.78	90.50	31.29
Days to maturity	86.0 - 100.0	4.33	5.11	71.77	7.56
Plant height (cm)	91.1 - 129.0	8.54	9.52	80.58	15.80
No. of primary branches per plant	4.0 - 8.0	13.98	21.32	42.97	18.87
No. of secondary branches per plant	0.6 – 6.7	35.23	39.74	78.58	64.33
Main shoot length (cm)	42.5 - 54.5	6.68	9.04	54.57	10.17
No. of siliquae on main shoot	26.1 - 41.4	10.11	11.93	71.83	17.65
No. of seeds per siliqua	16.1 - 31.3	16.40	20.88	61.69	26.53
Maximum root length (cm)	17.9 - 24.2	5.73	8.82	42.20	7.67
1000 seed wt (g)	3.30 - 4.70	13.22	17.18	59.20	20.95
Seed yield per plant (g)	2.86 - 10.43	33.15	36.49	82.54	62.05
Biological yield per plant (g)	6.49 - 17.83	24.62	27.91	77.83	44.75
Harvest index (%)	17.4 - 53.5	20.76	23.29	79.45	38.13

The mean performances of the twenty one populations are presented in (Table 4). Jeuti was the earliest flowering and maturing population. TS38, JT 12-1, JT 12-3, JT 12- JT 12-7, JYS 12-2-2 and JYS 12-2-4 are other early flowering and maturing populations. On the other hand JYS 14-1 was the late in flowering and maturity. TS 38 was a short statured genotype followed by Jeuti and JT 12-3. All other genotypes are taller and JYS 12-1 was the tallest with a height of 129 cm. All the Yellow sarson varieties and their derivatives were characterized with solid stem and the Toria genotypes with hollow stem (Table 4). NRCYS 05-03 produced the longest roots (24.2 cm) followed by JYS 12-2-4, JT 14-2, JYS 14-1, YSH 401, JT 12-1, JT 12-7, TS 38, which were at par with NRCYS 05-03.

More number of primary branches was observed for the populations JT 12-2-1, JYS 12-1 and JT 12-6. The highest number of secondary branches was observed for TS38 (6.7) followed by JT 12-2-1, JYS 12-2-1 and JYS 12-2-4 were other populations with more

secondary branches. In case of main shoots, among the populations JYS 12-2-1, JT 14-2, JT 12-5, JT 12-2-1 and YSH401 had long main shoots (51.17 to 54.55 cm) and JYS 12-2-3 produced the highest number of siliqua on main shoot (41.37) followed by JT 12-5, JYS 12-2-1, JT 12-4, NRCYS05-03, and JYS 12-2-4. JYS 12-2-1 possess long main shoot as well as more siliqua on main shoot, which ultimately contribute to increase yield. On the other hand B9 produced the least number of siliqua on main shoot. The highest number of seeds (31.27) per siliqua was recorded for the population NRCYS05-03 followed by JYS 14-1. The highest 1000 seed weight was recorded as for the population JYS 14-1 (5.47 g) followed by JT 12-6, JYS 12-2-3, JT 12-2-1, JT 14-2. The highest seed yield per plant was recorded for the population JT 12-5 (10.43 g), followed by JYS 14-1, JT 12-2-1 and JYS 12-2-3 and highest Biological yield per plant was (17.83 g) for the population JT 12-5 and JYS 12-2-3 and JYS 14-1 which were at par. Harvest index was maximum (53.51%) for JT 12-5 followed by JT 12-4, JT 14-2, JYS 14-1, JT 12-1. On view of above

the result, we can select JT 12-2-1, JT 12-5, JYS 14-1 and JYS 12-2-3 are superior than the other entries based on yield related characters. Also TS38 and their cross derivatives can use in future breeding line for seed production purpose as produce more seed yield as well as biological yield.

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