



Genetic variability and inter-relation of seed yield with contributing traits in Indian mustard (*Brassica juncea*)

HS Meena*, Arun Kumar, VV Singh, PD Meena, Bhagirath Ram and Swarnim Kulshrestha

ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur-321303 (Raj) India

*Corresponding author: singh_hari2006@yahoo.co.in

(Received: 19 Dec 2016; Revised: 26 June 2017; Accepted: 29 June 2017)

Abstract

The experiments were conducted involving thirty nine genotypes of Indian mustard including 28 F₁ crosses and 11 parental genotypes during Rabi 2014-15 to 2015-16 at ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur, India. Analysis of variance on 12 quantitative characters was carried out which revealed considerable amount of genetic variability in genotypes for all the traits. The mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance were calculated. High genetic advance (GA %) coupled with high heritability for seed yield, 1000-seed weight, siliqua length, plant height and number of primary branches/ plant indicated the effectiveness of selection for these traits. 1000-seed weight, siliqua length, plant height, main shoot length and days to maturity were positively associated with seed yield; hence the selection for these traits would help in improving the seed yield. The crosses NRCHB 101 x NPJ 112, (NPJ 112 x RRN 727) x RH 406 and NPJ 112 x RRN 727 revealed high mean performance for seed yield can be advanced for yield improvement and selection of superior genotypes.

Key words: Genetic variability, GCV, PCV, heritability, character association, genetic advance

Introduction

Indian mustard [*Brassica juncea* (L.) Czern & Coss.] is an important oilseed crop accounts for more than 80% of the total acreage under rapeseed-mustard crops in India (Meena *et al.*, 2015). It contributes nearly 27% of edible oil pool in India and more than 13% of the global edible oil production (Singh *et al.*, 2013a; Meena *et al.*, 2014a). During last one and half decade, the average productivity in India oscillating between 1.0 to 1.2 tonnes/ha which is much lower than the world average of 1.98 tonnes/ha. The mustard crop faces numerous adverse conditions like high temperature at crop establishment and maturity stage, unpredictable cold spells, frost damage, fog and intermittent rains during crop growth, incidence of various pests and diseases that causes considerable yield losses. The extent of yield reduction depends upon the degree, duration and timing of adverse conditions. Moreover, there is wider yield gaps when productivity of India is compared with countries like Germany (4.3 tonnes/ha), France (3.8 tonnes/ha) and UK (3.4 tonnes/ha)

(Yadava *et al.*, 2012). Thus, there is compelling need to increase and stabilize the productivity of Indian mustard to meet the growing demands for edible oil. This can be achieved through effective utilization of germplasm resources to impart efficiency and pace of breeding processes. Hence, the research strategies to overcome the constraints are highly needed to harness the full potential of the crop.

The genetic variability has been the central dogma of plant breeding. An understanding of the genetic behaviour of various agro-morphological and yield contributing traits is required for efficient selection of genotypes and breeding for trait specific genotypes. It is highly desirable to study the genetic variability for desirable traits among available promising genotypes and test genotypes to select suitable genotypes and crosses. Since, exploitation of genetic differences in traits contributing to yield may be a means of improving the crop for these traits. The extent of diversity available in the crop decides the success of any crop improvement programme with manifested objectives. Creation and

assessment of divergence in Indian mustard is highly needed to develop high yielding genotypes with desirable traits.

The traits for which variability present should be highly heritable as the progress through selection depend on heritability, selection intensity and genetic advance of the trait. An estimate of genetic advance along with heritability is helpful in assessing the reliability of character for selection. Yield is complexly inherited character and it is dependent on several contributing traits, generally inherited quantitatively (Yadava *et al.*, 2011). The relationship between two traits plays an important role in breeding programme, as changes brought about by natural or artificial selection in a trait, especially in one of the major adaptive traits, are associated with changes in other trait (Meena *et al.*, 2014b). Knowledge of inter-relationships between different traits is of great significance to plant breeders. This is highly useful in selecting characters which are neither easily observed nor genotypic values of which are modified by the environmental effects. Thus, any morphological character, which is associated with seed yield or makes a significant contribution to yielding ability, would be useful in the improvement of seed yield. Inter-relationships between characters help the breeder to assess the nature, extent and direction of selection pressure on characters. The improvement of yield components and the understanding of their association with its main component are helpful in formulating the breeding programme. It is therefore, essential to know the components of genetic variation and association of various yield contributing traits. Keeping this in view, the present study was undertaken to ascertain the extent of genetic variability, heritability, genetic advance and inter-relationship of seed yield components to establish their implications in the selection of better genotypes of Indian mustard.

Materials and Methods

The experiments were carried out at ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur during 2014-15 and 2015-16. The experimental material for the study consisted of 39 genotypes including 28 F_1 s (19 single crosses & 9

three way crosses) and 11 parental genotypes namely RH-749 (RH-781/RH-9617), RH-406 (RH-6908/RH-8812), Rohini (Pure line selection from Varuna), NRC DR-2 (MDOC-43/NBPGR-36), NRCHB-101 (BL-4/Pusa Bold), SEJ-2 (Synthetic amphiploid from *B. campestris*/*B. nigra*), DRMRIJ-31 (HB-9908/HB-9916), DRMR 2019 (EC-399288/BEC-107), DRMR 2035 (PHR-1/BEC-107), NPJ-112 (SEJ-8/Pusa Jagannath), RRN 727 (RW-01-02/Patan 67) of Indian mustard (*Brassica juncea*). The parental genotypes were selected on the basis of their wider range of adaptability and diversity for various yield contributing attributes. The main objective of the present study was to determine the genetic variability parameters and selection of better combinations.

All 39 treatments were planted in randomized complete block design with three replications during *Rabi* 2015–16. The treatments were raised in rows of 5m length with a distance of 30cm between rows and 15cm between plants, where each treatment was represented by two rows. Standard agronomic practices were followed to raise the good crop. Recommended doses of fertilizers *viz.*, 80:40:40:40 kg/ha of N: P: K: S, respectively, were applied and irrigated thrice including pre-sowing irrigation. Observations were recorded on twelve quantitative traits, *viz.*, days to flowering, days to maturity, plant height (cm), number of primary branches / plant, number of secondary branches / plant, main shoot length (cm), number of siliquae on main shoot, siliqua length (cm), number of seeds per siliqua, 1,000-seed weight (g), oil content (%) and seed yield / hectare (kg). Observations on days to flowering and maturity were recorded on per plot basis, seed yield was converted & expressed in kg per hectare and the observations on remaining traits were recorded on randomly selected ten competitive plants in each replication. Standard procedures were followed for analysis of variance. The phenotypic and genotypic coefficients of variation (PCV, GCV) were calculated as per method suggested by Burton (1954). The correlation coefficients at genotypic and phenotypic level were computed as per Johnson *et al.* (1955). The calculations were performed through computer generated programme WINDOW STAT version 8.6 from INDOSTAT Services, Hyderabad, India.

Results and Discussion

Analysis of variance revealed that mean sum of squares due to genotypes (treatments) was significant for all the twelve traits studied (Table 1). It indicated significant differences among different treatments for all characters. Therefore, a general conclusion can be that there is considerable amount

of genetic variability for various traits among different parental genotypes and crosses. High magnitude of variability has been earlier reported in Indian mustard for various characters by many workers for days to 50% flowering, days to maturity, plant height, total siliquae/plant, 1000-seed weight and seed yield (Kumar and Misra, 2007; Yadava *et al.*, 2011; Meena *et al.*, 2015).

Table 1: Mean sum of squares for various sources of variation in RBD analysis for 12 traits

Source of Var.	Replication	Treatment	Error
D.F.	2	38	76
Days to flowering	13.41	158.09**	17.07
Days to maturity	105.24	295.86**	40.96
Plant height (cm)	158.96	2817.91**	113.01
Number of primary branches/plant	0.11	5.22**	0.71
Number of secondary branches/plant	2.37	43.12**	9.84
Number of siliquae on main shoot	29.27	188.64**	40.25
Main shoot length (cm)	63.96	283.69**	45.06
Silique length (cm)	0.19	1.58**	0.07
Number of seeds/silique	0.32	7.32**	1.53
1000-Seed weight (gm)	0.03	3.17**	0.12
Oil content (%)	1.75	2.07**	0.93
Seed yield/ha (kg)	13513.95	1064598.26**	13654.73

*, **: Significant at 5% and 1% levels, respectively

The mean performance, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation GCV, heritability (H^2) and genetic advance (GA) of treatments for 12 characters are presented in Table 2. The magnitude of PCV was higher than the GCV for all the characters under study. Both PCV and GCV were high for seed yield/ha, 1000-seed weight, number of primary & secondary branches / plant, silique length, plant height, days to flowering and number of silique on main shoot. These are the major yield contributing traits in Indian mustard. The high GCV and PCV have been reported earlier by Kardam and Singh (2005) and Yadava *et al.* (2011) for different yield contributing traits in Indian mustard. Similar findings pertaining to occurrence of high genetic variability has also been reported by Singh (2004) for different traits including seed yield. The results indicated the presence of high amount of genetic variability in the evaluated treatments for the major yield contributing traits along with seed yield which showed possibility of further improvement for these traits.

Seed yield/ha, 1000-seed weight, silique length and plant height exhibited high heritability. High heritability was also observed for days to flowering, days to maturity, number of primary & secondary branches, number of silique on main shoot, main shoot length and number of seeds / silique. High heritability for various traits has also been reported earlier (Mahla *et al.*, 2003; Singh, 2004; Kumar and Misra, 2007; Yadava *et al.*, 2011). Genetic advance as per cent of mean was higher for 1000-seed weight, silique length, plant height and number of primary branches indicating that selection for these traits would be effective for the improvement. Similar findings related to high genetic advance as per cent of mean have been reported by earlier workers for various traits (Mahla *et al.*, 2003; Yadava *et al.*, 2011). High heritability with high genetic advance for seed yield/plant has also been reported (Kumar and Misra, 2007 and Yadava *et al.*, 2011) which supports the results of the present investigation.

Table 2: Estimates of different genetic parameters of variation for 12 traits among parents and crosses

Character	Mean	Range		PCV (%)	GCV (%)	H ² (%)	GA as % of Mean
		Min.	Max.				
Days to flowering	45.61	31.33	63.33	17.55	15.03	73.36	26.52
Days to maturity	125.98	105.33	142.33	8.91	7.32	67.47	12.38
Plant height (cm)	182.65	99.13	235.67	17.44	16.44	88.86	31.92
Number of primary branches/plant	7.05	4.93	10.07	21.11	17.39	67.87	29.51
Number of secondary branches/plant	21.16	14.13	28.8	21.62	15.74	52.99	23.6
Number of siliquae on main shoot	56.91	44.0	76.13	16.64	12.36	55.14	18.9
Main shoot length (cm)	82.19	55.07	102.33	13.58	10.85	63.84	17.86
Silique length (cm)	4.17	2.7	6.08	18.18	17.03	87.79	32.87
Number of seeds/silique	16.1	12.93	19.73	11.54	8.63	55.88	13.29
1000-Seed weight (gm)	3.82	1.42	6.07	27.96	26.43	89.35	51.46
Oil content (%)	41.13	38.6	42.33	2.79	1.5	29.05	1.66
Seed yield/ha (kg)	2090.25	829.63	3293.01	28.86	28.32	96.25	57.23

PCV: Phenotypic coefficients of variation; GCV: Genotypic coefficients of variation; H²: Heritability; GA: Genetic advance

An individual mean performance of treatments for various traits is presented in Table 3. With regards to mean performance, the cross NRCHB 101 x NPJ 112 showed the highest seed yield (3293.0 kg/ha) followed by (NPJ 112 x RRN 727) x RH 406 (3077.4 kg/ha) and NPJ 112 x RRN 727 (2975.3 kg/ha) among all test genotypes. Genotype RRN 727 revealed lowest seed yield (829.6 kg/ha). Hence, the parental genotype RRN 727 was not included for seed yield but it has many desirable traits like short height, early maturity and more branches. It has reduced plant height and duration of maturity in all the crosses where it was one of the parent and resulted into many heterotic crosses *viz.*, RH 406 x RRN 727 and NPJ 112 x RRN 727, (NPJ 112 x RRN 727) x RH 406, (NPJ 112 x RRN 727) x NRCDR 2 directly or indirectly. Mean oil content was 41.1 % and it was ranged from 38.6% (RRN 727) to 42.3% (DRMR 2019 x RRN 727) amongst the treatments. A heterotic cross with desirable traits has been earlier reported by many workers (Verma *et al.*, 2011; Yadava *et al.*, 2012; Meena *et al.*, 2015).

Genotypic and phenotypic correlation coefficients among seed yield and contributing traits are presented in Table 4. In general, the magnitude of genotypic correlation coefficients were higher than

their corresponding phenotypic coefficients indicating the strong inherent association between different traits and the phenotypic expression of these traits was less under the influence of environment. Seed yield per hectare was found to be positively correlated with 1000-seed weight, silique length, plant height, main shoot length and days to maturity. Similar findings were earlier reported by many workers (Kumar *et al.*, 1984; Kardam and Singh, 2005; Verma *et al.*, 2008; Yadava *et al.*, 2011; Singh *et al.*, 2013b). Hence, the selection for these traits would also help in improving the seed yield in this crop.

Days to flowering showed significant positive correlations with days to maturity, plant height, number of primary & secondary branches, silique on main shoot, silique length and 1000-seed weight and negative with oil content. Days to maturity was positively correlated with plant height, primary branches, silique length, 1000-seed weight and seed yield; plant height with primary & secondary branches, siliquae on main shoot, main shoot length, silique length, 1000-seed weight and seed yield. Number of primary branches were positively correlated with secondary branches, silique length and 1000-seed weight and negatively with number of seeds per silique and oil content. Number of silique

Table 3: Mean performance of parents and crosses related parameters for 12 traits in Indian mustard

Genotype/Cross	Days to flowering	Days to maturity	Plant height (cm)	No. of primary branches /plant	No. of secondary branches /plant	No. of siliquae on main shoot	Main shoot length (cm)	Silique length (cm)	No. of seeds /siliqua	1000-Seed weight (gm)	Oil content (%)	Seed yield /ha (kg)
RH-749 × NPJ-112	52.3	133.6	235.7	9.8	25.2	60.5	81.3	4.69	14.67	4.60	40.29	2716.9
[NPJ-112 × RRN 727] × RH-749	49.7	131.3	174.2	8.2	26.0	65.9	67.0	4.33	16.13	3.75	41.61	1763.9
RH-749 × RRN 727	44.3	124.0	152.3	6.3	22.2	46.1	63.2	3.16	15.40	2.52	41.24	1497.9
RH-406 × NPJ-112	49.7	132.6	208.0	10.1	24.2	59.8	75.0	4.27	14.93	4.31	41.55	2534.2
[NPJ-112 × RRN 727] × RH-406	42.3	130.0	196.3	6.6	26.1	62.8	91.4	3.71	17.33	4.02	40.92	3077.4
RH-406 × RRN 727	49.3	134.3	229.6	9.2	21.9	55.3	82.6	5.00	13.80	6.07	40.41	2609.0
ROHINI × NPJ-112	48.3	124.3	216.2	7.4	21.4	66.9	88.0	4.47	15.13	4.67	40.63	2588.5
[NPJ-112 × RRN 727] × ROHINI	44.7	127.7	180.0	4.9	20.0	59.8	94.0	3.84	15.60	3.27	40.88	1576.1
ROHINI × RRN 727	41.3	121.7	161.2	5.6	19.4	44.0	70.6	3.55	17.40	2.71	42.12	1809.0
NRCDR-02 × NPJ-112	51.3	131.3	224.3	8.2	24.5	60.8	89.0	4.20	16.07	4.23	40.67	2455.1
[NPJ-112 × RRN 727] × NRCDR-02	43.7	126.0	193.0	6.7	22.3	54.2	85.6	4.19	16.67	3.53	42.23	2946.5
NRCDR-02 × RRN 727	44.7	126.7	186.6	7.6	25.3	64.8	80.4	3.87	17.00	2.77	42.03	1707.0
NRCRB-101 × NPJ-112	44.0	137.0	190.0	6.3	19.1	49.1	85.2	5.16	19.73	4.61	41.47	3293.0
[NPJ-112 × RRN 727] × NRCRB-101	36.3	105.3	181.6	5.9	18.2	50.6	86.1	4.22	16.87	3.93	41.05	2156.4
NRCRB-101 × RRN 727	31.3	119.3	136.6	6.5	21.5	51.3	78.6	3.25	13.60	2.68	42.04	1896.3
SEJ-2 × NPJ-112	47.3	107.3	202.6	7.7	24.2	63.5	92.0	4.50	17.27	4.65	41.02	2197.5
[NPJ-112 × RRN 727] × SEJ-2	44.0	107.3	160.3	6.4	16.4	76.1	96.0	3.89	16.53	3.05	41.17	1701.2
SEJ-2 × RRN 727	36.6	118.6	143.3	6.2	22.3	61.3	83.0	3.21	15.27	2.22	40.99	1023.9
DRMRJ-31 × NPJ-112	44.0	128.3	170.0	7.3	17.5	49.6	78.3	5.02	16.93	4.62	42.01	1997.5
[NPJ-112 × RRN 727] × DRMRJ-31	38.0	121.6	171.6	5.2	21.6	62.6	102.3	3.85	18.13	3.69	41.85	2258.4
DRMR J-31 × RRN 727	41.7	121.7	134.3	5.5	19.0	60.7	77.3	3.82	17.53	2.51	41.42	1506.2
WR-2019 × NPJ-112	42.6	128.0	184.6	7.5	16.3	44.1	87.3	4.87	18.67	4.27	41.32	2215.6
[NPJ-112 × RRN 727] × WR-2019	42.3	127.6	172.0	5.5	16.8	52.4	85.3	4.73	16.53	3.13	42.05	1804.1
WR-2019 × RRN 727	38.3	122.6	140.6	5.5	14.1	51.8	82.6	3.61	16.60	2.41	42.33	1069.1
WR-2035 × NPJ-112	53.6	132.0	204.6	8.2	25.2	65.4	94.6	4.25	18.87	3.35	39.85	1818.1
[NPJ-112 × RRN 727] × WR-2035	48.3	130.3	177.3	7.4	21.7	51.1	78.0	3.61	14.07	3.31	40.50	1665.8
WR-2035 × RRN 727	47.3	126.6	156.0	5.9	19.5	53.3	70.6	3.34	14.67	2.24	40.79	1013.9
NPJ-112 × RRN 727	35.0	105.6	151.0	6.4	27.2	46.7	71.0	3.49	17.00	3.54	41.43	2975.3
RH-749	62.7	142.3	231.0	8.7	22.9	69.0	85.6	5.13	14.80	4.85	39.66	2360.5
RH-406	59.3	140.7	218.0	8.6	18.6	55.4	77.3	4.35	15.53	5.16	40.26	2026.3
ROHINI	54.3	135.6	230.6	9.2	28.8	55.2	72.3	4.09	13.33	4.51	41.43	1970.3
NRCDR-02	51.6	135.7	206.6	7.8	28.1	63.7	94.8	5.82	16.13	4.47	41.66	2434.5
NRCRB-101	47.6	132.7	196.3	6.6	19.2	46.0	82.6	6.08	18.13	5.24	41.15	2886.1
SEJ-2	44.0	108.3	177.7	5.8	15.0	62.7	78.8	3.21	12.93	3.80	40.92	1687.2
DRMRJ-31	45.6	133.0	183.6	6.6	16.4	69.4	88.3	4.40	16.53	5.25	41.96	2212.3
DRMR-2019	45.7	133.6	179.0	5.4	14.8	53.6	95.0	4.52	15.73	4.78	42.30	2159.6
DRMR-2035	63.3	138.6	197.3	7.8	21.3	56.2	80.2	3.92	15.20	4.36	40.09	2724.2
NPJ-112	39.3	119.6	169.3	6.1	19.0	49.8	78.2	4.35	16.60	4.37	40.02	2354.7
RRN 727	32.7	109.6	99.13	7.6	20.8	46.6	55.0	2.70	14.73	1.42	38.60	829.6
Mean	45.6	125.9	182.6	7.0	21.2	56.9	82.1	4.17	16.10	3.82	41.13	2090.2
S.E.	2.38	3.69	6.14	0.5	1.8	3.66	3.87	0.15	0.71	0.20	0.56	67.46
C.D. 5%	6.7	10.41	17.29	1.5	5.1	10.3	10.9	0.43	2.01	0.57	1.57	190.0
Range	31.3	105.3	99.13	4.9	14.1	44.0	55.0	2.70	12.93	1.42	38.60	829.6
	63.3	142.3	235.6	10.1	28.8	76.1	102.3	6.08	19.73	6.07	42.33	3293.0

(min.)
(max.)

Table 4: Genotypic and phenotypic correlation coefficients for twelve characters

Character		X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
X1	G	0.854**	0.833**	0.699**	0.325*	0.443**	0.172	0.504**	-0.19	0.568**	-0.431**	0.298
	P	0.532**	0.663**	0.521**	0.206	0.266	0.069	0.359**	-0.185	0.521**	-0.227	0.252
X2	G		0.642**	0.512**	0.222	0.078	0.135	0.573**	-0.049	0.548**	-0.115	0.351*
	P		0.534**	0.372**	0.135	0.082	0.101	0.454**	-0.007	0.406*	0.051	0.273
X3	G			0.698**	0.421**	0.381*	0.415*	0.642**	-0.11	0.828**	-0.201	0.632**
	P			0.566**	0.322	0.293	0.366*	0.592**	-0.052	0.732**	-0.099	0.590**
X4	G				0.589**	0.259	-0.19	0.337*	-0.382*	0.499**	-0.501**	0.292
	P				0.537**	0.178	-0.168	0.267	-0.237	0.387*	-0.324	0.276
X5	G					0.216	-0.156	0.033	-0.201	0.064	-0.203	0.318
	P					0.227	-0.048	0.038	-0.011	0.055	-0.166	0.24
X6	G						0.470**	0.098	-0.098	0.178	-0.05	0.006
	P						0.524**	0.038	-0.101	0.122	-0.099	0.009
X7	G							0.474**	0.464**	0.415*	0.317	0.374*
	P							0.354*	0.256	0.317	0.129	0.305
X8	G								0.350*	0.803**	0.119	0.603**
	P								0.328*	0.686**	0.094	0.557**
X9	G									0.034	0.387*	0.324
	P									0.021	0.169	0.236
X10	G										-0.106	0.741**
	P										0.022	0.693**
X11	G											0.119
	P											0.014

G: Genotypic correlation coefficients, P: Phenotypic correlation coefficients, X1: Days to flowering, X2: Days to maturity, X3: Plant height, X4: Number of primary branches, X5: Number of secondary branches, X6: Number of siliquae on main shoot, X7: Main shoot length, X8: Siliqua length, X9: Number of seeds/siliqua, X10: 1000-Seed weight, X11: Oil content, X12: Seed yield/hectare; *, **: Significant at 5% and 1% levels, respectively

on main shoot was positively correlated with main shoot length; main shoot length with siliqua length, seeds / siliqua, 1000-seed weight and seed yield; siliqua length with number of seeds / siliqua, 1000-seed weight and seed yield; while number of seeds / siliqua was correlated with oil content. Similar results for different traits were earlier reported (Kumar *et al.*, 1984; Srivastava and Singh, 2002; Verma *et al.*, 2008; Gangapur *et al.*, 2009; Singh *et al.*, 2010; Misra, 2012; Singh *et al.*, 2013b) in rapeseed-mustard.

The correlation coefficients clearly indicated that amongst the yield and yield components 1000-seed weight, siliqua length, plant height, main shoot length and days to maturity had high significant positive correlations with seed yield. Therefore, it may be concluded that among the yield and yield components these traits were most important contributed to seed yield. A number of genotypes / crosses under present study showed the same trends. Hence, indirect selection for these traits would be effective in

improving the grain yield. Thus, the material studied is of diverse nature and information emanated would help in designing the selection methodology which can further be used in the breeding programme for improvement of seed yield.

Acknowledgement

Authors are thankful to the Director, ICAR-Directorate of Rapeseed-Mustard Research, Bharatpur for providing experimental facilities.

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