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INTERRELATIONSHIPS AMONG GRAIN YIELD AND RELATED TRAITS OF CANDIDATE RESTORER LINES OF *BRASSICA NAPUS* L.

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Abstract

Forty-three candidate restorer lines of *Brassica napus* were evaluated for 11 agronomic traits for genetic variability and interrelationships among yield traits to find out yield contributing traits. A wide range of variability and character association was observed among the lines. The line BNR-017 took the lowest time for first (26.67 days) and 100% flowering (41.00 days) whereas BNR-031 (74.33 days) and BNR-034 (74.00 days) matured earlier. The lines BNR-022 (1.07m) and BNR-026 (1.02m) were found with the shortest plant stature and all other lines were in average plant height of around 1.35m. The lines BNR-039, BNR-011, BNR-001, BNR-013 and BNR-014 were found the best performer for number of pods per plant, seeds per pod and seed yield per plant. Estimates of genotypic and phenotypic coefficient of variation were high (≥30%) for seed yield per plant (30.52 and 33.13, respectively). High broad sense heritability was recorded for 1000-seed weight (97.69%), days to ripening (97.12%), days to first flowering (96.80%), days to 100% flowering (95.50%) and pod length (92.74%). Significant and negative correlation was observed between seed yield per plant and number of seeds per pod, -0.217* and -0.192*, respectively both at genotypic and phenotypic level, while the highest positive and significant genotypic (0.786**) and phenotypic (0.795**) correlation were found with pod length. Path co-efficient analysis showed the highest positive and direct phenotypic effect of number of seeds per pod (1.221) on seed yield per plant while days to first flowering had the maximum negative direct effect (-0.039). The results of genotypic and phenotypic coefficient of variation, heritability and genetic advance in percent of mean, correlation co-efficient and path co-efficient revealed that pods per plant, pod length, seeds per pod and 1000-seed weight could be used as selection criteria to increase seed yield in rapeseed.

Keywords: Mustard, genetic variability, heritability, male sterility, hybrid, seed yield.

Introduction

Rapeseed (*Brassica napus*) is a cross pollinated crop belongs to the family Brassicaceae. It is one of the most important oilseed crop's throughout the world after soybean and palm (FAO, 2014). The centre of origin of *Brassica* spp. is not clearly understood. But it is the most important oil seed crop growing in the northern Europe, Canada, and China. The *Brassica* spp. (*Brassica napus, Brassica campestris, Brassica juncea*) are now the world's third most important source of edible vegetable oils. Mustard commonly known as Sarisha is a widely grown oilseed crops of Bangladesh occupying 0.532 million ha of land with the yield of 2.26 MT (metric ton)/ ha in 2017-18

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(BBS, 2019). It is now ranked as the second largest oilseed crop among oilseed crops of the world as well as first in the Bangladesh after soybean (BBS, 2019). Domestic need of edible oil in Bangladesh mainly derives from mustard and sesame. Mustard and rapeseed seeds contain 42% oil and 25% protein (Kaul, 2006). Moreover, its meal has a complete profile of amino acids (38-40% protein) including lysine, methionine and cysteine. Oil cake is a nutritious food item for cattle and fish as well as a good source of organic fertilizer. The seed meal of rapeseed contains about 40% protein with excellent amino acid composition. Brassica seed generally contain more than 40% erucic fatty acid in oil, and more than 100 μmol glucosinolates g^{-1} dry matter which is considered as undesirable for human nutrition (Bell, 1993). The discovery of zero erucic acid and low glucosinolate genetic variations in the natural population of *B. napus* open the door for its improvement and called as “double low rapeseed” or “canola” (Stefansson and Downey, 1995). However, intensive breeding efforts in the past few decades increased seed yield, agronomic traits as well as oil quality and currently become one of the most important oilseed crops in the world.

Brassica hybrids with high yield, early maturity, disease/insect resistance and acceptable oil quality have very good prospects in future. Thus, hybrids breeding in *Brassica* would be an effective strategy to increase edible oil production. Effective genetic mechanisms for commercial hybrids seed production include cytoplasmic male sterility (CMS), genetic male sterility (GMS), self-incompatibility (SI) and fertility restoration. CMS-based hybrid seed technology requires three lines - A line or CMS line, B line or maintainer line and R line or Restorer line. However, lack of stable fertility restorer has hampered the exploitation of these CMS systems for producing commercial hybrid seed. Development of new CMS lines and identification of maintainers and fertility restoration lines have brightened the prospects of the development of commercial hybrids in brassica (Thakur and Sagwal, 1997). The CMS lines having the male-sterile cytoplasm with a CMS triggering gene (hereafter termed a CMS gene) and lacks a functional nuclear restorer of fertility (Rf or restorer) gene or genes (Sarmah and Sarla, 1998), and is used as the female parent. The maintainer line has normal fertile cytoplasm but contains the same nuclear genome as the CMS line, and thus serves as the male parent in crosses for the propagation of the CMS line (Saha *et al.*, 2011). The restorer line possesses a functional Rf gene or genes, and thus serves as the male parent to cross with the CMS line to produce F_1 hybrid seeds. In the F_1 lines, the Rf gene restores male fertility, and the combination of nuclear genomes from the CMS line and the restorer line produces hybrid vigor (Chen and Liu, 2014). Complete fertility restorers could be developed for polima, tournefortii and lyratus CMS sources in *B. napus*. The major difficulty in finding restorer in natural accessions is the multilocus control of incompatibility between the mitochondrial and nuclear genome (Downey and Chopra, 1996). Lack of restorers has hindered the exploitation of several other CMS systems for producing commercial hybrid seed (Singh and Verma, 1997). It is essential to have effective restorer lines in order to develop commercial brassica hybrids. On the other hand, an understanding of the mature and magnitude of variability among the genetic materials is of prime importance to the breeder. To identify elite material, it is required to evaluate the existing materials through the estimate of genetic variance components. The variation is occurred due to genetical and environmental effects whereas genetical effect is heritable. However, the estimate of genetic advance should be considered also along with heritability that provide an idea of the expected gain in the next generation. Correlation and path analysis establishes the association between yield and yield contributing traits and also find out the relative importance of their direct and indirect effects that gives a clear understanding of their association with yield (Vijaya et al. 2014). Therefore, the present research was undertaken to develop and identify restorer lines from the segregating population of exotic hybrids. The objectives of the present research are (i) to identify elite restorer lines from the segregating populations of exotic *Brassica napus* hybrid, and (ii) to characterize the selected restorer lines for agronomic traits.

Materials and Methods

The seeds of 43 candidate restorer lines obtain from segregating populations (F_6 and later) of exotic hybrids including three check (BARI sharisha-8, BARI sharisha-13 and Tori-7) were used as plant materials**.** present research work was conducted at the experimental farm, Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur. The location of the experimental site was at the center of Madhupur Tract (24.05'N latitude and 90.25'E longitude) with an elevation of 8.4m from the sea level. The soil type of experimental field belongs to the Shallow Red Brown Terrace type under Salna series of Madhupur Tract (Brammer, 1971; Saheed, 1984) of Agro Ecological Zone (AEZ) 28. The land was prepared thoroughly by 3-4 time ploughing and cross ploughing followed by laddering. Land was finally prepared by addition of basal dose of fertilizers. Adequate soil fertility was ensured by applying additional quantities of N-P-K-S-Zn-B @ 120-35-65-20-5-1.5 kg/ha, respectively. Total TSP, MP and Gypsum, Zink Sulphate and Boric Acid were applied in final land preparation (Halder et al., 2007). Cow dung was also applied during final land preparation @ 10 MT/ha. Total urea was applied in three installments at 15, 30 and 50 days after sowing (DAS). Seeds of 43 lines were sown in the row spacing of 30 cm and plant spacing of 15 cm within the row using randomized complete block design with three replications. The seedlings were emerged out within four days after sowing. Necessary intercultural operations were taken during cropping period for proper growth and development of the plants. Irrigation was given at 15 days interval and when necessary. Malathion 57 EC was applied three times as foliar spray at an interval of 10-15 days after seedling emergence to control aphid. Ten randomly selected competitive plants from each of the entries were used for recording the data on days to 1st flowering, days to 100% flowering, days to 1st ripening, plant height, number of branches per plant, number of pods per plant, pod length, no. of seeds per pods, number of seeds per plant, 1000-seed weight and seed yield per plant. The recorded data for different characters were analyzed statistically using SAS (SAS, 2010). Genotypic and phenotypic variances were estimated according to the formula given by Johnson *et al.* (1955). Genotypic, phenotypic and environmental co-efficient of variation were estimated by the formula suggested by Burton (1952). Genotypic and phenotypic correlation co-efficient for all possible combinations was calculated by the formula suggested by Miller *et al.* (1958), Johnson *et al.* (1955) and Hanson *et al.* (1956). OPSTAT software was used for analyzing genotypic and phenotypic correlation co-efficient. Genotypic correlation co-efficient was further partitioned into components of direct and indirect effects by path co-efficient analysis originally developed by Dewey and Lu (1959) and worked example by Sheoran *et al.* (1998).

Results and Discussion

Analysis of variance (ANOVA)

Analysis of variance was calculated for 11 agronomic characters of 43 candidate restorer lines of *Brassica napus* (Table 1). The results showed large range of variation among the lines that indicates the presence of highly significant genetic variability among them except number branches per plant. This variability can be demonstrated by observing genetic variability, genotypic correlation and phenotypic correlation coefficient, and path analysis. Significant means square due to replication was also found for days to pod ripening, number of branches per plant and pod length indicates presence of experimental error for these traits. Replication provides good estimate of experimental error which increases the accuracy of estimated means. It might occur due to difference in plant growth or management over replication.

Table 1. Analysis of variance (ANOVA) for 11 yield contributing traits of 43 candidate restorer line (pollen parents) of *B. napus*

Sources of variation	df	DFF	DHF	DPR	NBP	PHT	NPP	PLT	NSP	TSW	NSPl	SYP
Replication	2	2.52	1.15	18.26**	1.15**	0.004	397.22	0.23*	5.12	0	988216.69	10.36
Genotype	42	180.38**	107.33**	163.61**	0.2	0.13**	18507.59**	1.84**	27.82**	0.47**	10300745.16**	138.14**
Error	84	1.85	1.68	1.58	0.18	0.01	1252.93	0.05	4.28	0.004	902601.99	10.3

* and ** indicate significance at 5% and 1% levels, respectively DFF - Days to first flowering, DHF - Days to 100% flowering, DPR - Days to pod ripening, NBP - Number of branches per plant, PHT - Plant height (m), NPP - Number of pods per plant, PLT - Pod length (cm), NSP - Number of seeds per pod, TSW - Thousand seed weight (g), NSPl - Number of seeds per plant, SYP – Seed yield per plant (g)

Days to flowering

BNR-017, which took the minimum days to first flowering (26.67) which was statistically similar with the check BARI-8 (Table 2). BNR-017 also took the least days (41.00) to reach 100% flowering but the check variety took more than 45 days to reach 100% flowering. The performance of BNR-009 and BNR-010 lines was near to the BNR-017 and the lines took minimum days (28.33) to first flowering. On the other hand, BNR-039 took the maximum days for first flower (64.67) and 100% flowering (73.00) which was much higher than the other check variety BARI-13 (35.00). Days to first flowering exhibited 3.88% coefficient of variation whereas 100% flowering showed 2.61% coefficient of variation (Table 2).

Days to ripening

In case of ripening BNR-034, which took the least days (74) to begin was followed by BNR-031 (74.33), BNR -020 (74.67), BNR-021(75.00), BNR -023 (75.33) and BNR-018 (75.67) lines. In case of BARI-8 and TORI-7 also found same days to be reached at ripening. BNR-042 required the highest days (101.33) for ripening. The mean days for ripening was 81.18 (Table 2). Hasan *et al.* (2014) also reported significant differences for days to maturity among *Brassica napus* genotypes.

Number of branches per plant

There was minimum variation among the genotypes for number of branches. BNR-025 had four branches per plant which was higher than three check cultivars. The mean number of branches per plant was 3.24 and minimum number was produced by BNR-017 (2.67). Hossain *et al.* (2013) reported the highest and the lowest number of branches per plant 8.41 and 7.84, respectively in mustard. Maximum number of branches per plant (6.43) was reported by Ali *et al*. (2003) from the genotype PF-7045/91 in winter rapeseed.

Plant height (m)

The check cultivar TORI-7 produced the shortest (0.99 m) plant among the lines. Plant height of BNR-022 (1.02 m), BNR-026 (1.07 m) and BNR-002 (1.2 m) were near to the shortest check TORI-7. The tallest plant was observed in the lines BNR-039 and BNR-42 (1.81 m) followed by BNR-030 (1.80 m). Majority lines were short enough in height and similar to check cultivars. Muhammad *et al.* (2014) also reported significant differences for plant height in brassica genotypes with a mean value of 166 cm. Plant height should be lower for *Brassica napus* to avoid lodging. The growth behavior and lodging tolerance of a crop depends on the final plant height which was supported by Alam *et al.* (2014). Azam *et al.* (2013) had also found the plant height at the range of 81- 198 cm in *Brassica napus* L.

Number of pods per plant

Wide range of variation in mean number of pods per plant was observed among 43 lines of *Brassica napus* (Table 2). The highest number of pods per plant was observed in the line BNR-39 (282.17) followed by BNR-013 (267.33) and BNR-014 (259.33) which was significantly higher than the mean value (184.36), but lower than the check TORI-7 (596.83). The number of pods per plant showed 19.2% coefficient of variation (Table 2). Alam *et al.* (2014) found maximum number of 136 pods per plant in their study. Sadat *et al.* (2010) also reported significant difference among rape seed genotypes for pods plant.

Sadia *et al.* (2015*)* reported that pods per plant ranged from 487 to 994 with the mean value of 668 *Brassica napus* L.

Pod length

The longest pod was observed in the genotype BNR-005 (9.93cm) which exceeds the pod length of check cultivars (Table 2). All the lines had considerable length of pod except the genotype BNR-019 (5.7 cm) which was the lowest one followed by BNR-022 (5.9cm). The pod length showed 2.92% coefficient of variation with the grand mean of 7.40cm (Table 2). Aytac and Kinaci (2009) also reported significant difference among rapeseed genotypes for pod length. Hossain *et al.* (2013) reported the longest pod length as 5.29 cm whereas Sadia *et. al.* (2015) revealed an average pod length was 7.00 in *Brassica napus* L.

Number of seeds per pod

The line BNR-008 yielded the highest (33.33) number of seeds per pod and the lowest (22.33) in BNR-006 (Table 2). The lines BNR-11(32.33), BNR-001 (32.00), BNR-024 (31.33), BNR-041 (31.33), BNR-014 (31.00), BNR-.040 (31.00), BNR-034 (31.00) had higher number of seeds per pod than the check cultivars. Jahan and Zakaria (1997) reported the lowest number of seeds per pod in improved Tori (18.0). Khan and Khan (2005) also reported significant difference among rape seed genotypes for seeds per pod. Azam *et al*. (2013) reported average number of seeds per pod (20.50) in *Brassica napus* L.

Number of seeds per plant

The highest number of seeds per plant was found in BNR-013 (8133.33). The lines BNR-014 (8065.45), BNR-001 (6900.13), BNR-039 (6683.5), BNR-033(6425.33) and BNR-025 (6026.38) were produced number of seeds per plant similar to the checks, BARI-8 (7800.00) and BARI-13 (6178.93).

Thousand seed weight

Thousand seed weight was ranged from 3.07g (BNR-030) to 4.47 g (BNR-022) that beat the highest value of the check cultivars (3.09 to 3.62 g). Nine lines produced 1000-seed weight more than 4.0g and these lines were designated as bold seeded lines. Line (BNR-030) and the check cultivar BARI-13 produced minimum 1000-seed weight and was around 3.0g. Sadia *et al.* (2015) confirmed the result with the findings of average 3.71g from their experiment. Hossain *et al.* (2013) reported a range of 2.50 to 3.49g for 1000-seed weight.

Seed yield per plant

Seed yield per plant is a very significant trait for selection of a novel genotype for further utilization. In this study, seed yield per plant was ranged from 8.98g (BNR-029) to 32.02g (BNR-014). The line BNR-014 exceeded the seed yield per plant of three checks (Table 2). The lines BNR-013 (28.79), BNR-040 (25.52), BNR-001 (24.61), BNR-041 (23.64), BNR-011 (22.91), BNR-039 (22.45), BNR-033 (22.19) were also found for better seed yield per plant. Coefficient of variation was 17.4% for seed yield per plant with the grand mean 18.44g (Table 2). Aytac and Kinaci (2009) also reported significant difference among rapeseed genotypes for seed yield per plant. Sadia *et al*. (2015) reported the average seed yield per plant was 58.6g in their study *Brassica napus* L.

Genetic variability in *Brassica napus* lines

Variability confirms selection of superior genotypes in crop improvement program. Notable variation among the breeding

Table 2. Mean performance of 43 candidate restorer lines (pollen parents) of *B. napus* hybrid for 11 yield contributing traits

Genotype	DFF	DHF	DPR	NBP	PHT	NPP	PLT	NSP	TSW	NSPl	SYP
BNR-001	36.00	48.67	81.33	3.33	1.31	215.70	7.37	32.00	3.57	6900.13	24.61
BNR-002	34.00	52.67	79.33	3.33	1.21	182.33	7.27	29.67	3.42	5391.50	18.42
BNR-003	31.00	46.33	83.00	3.00	1.43	190.53	7.03	27.67	3.43	5266.73	18.08
BNR-004	31.67	54.67	80.67	4.00	1.20	140.67	8.33	28.00	4.06	3925.33	15.92
BNR-005	31.00	49.67	83.67	3.00	1.25	188.50	9.93	22.67	3.60	4274.00	15.41
BNR-006	30.33	49.33	81.33	3.00	1.18	241.89	7.40	22.33	3.47	5402.67	18.74
BNR-007	32.00	46.33	83.67	3.33	1.28	188.27	7.20	29.67	3.51	5573.42	19.61
BNR-008	34.67	54.67	81.33	3.00	1.36	164.67	7.90	33.33	3.45	5511.33	19.02
BNR-009	28.33	47.67	80.00	3.00	1.27	180.13	6.80	26.67	4.21	4808.87	20.24
BNR-010	28.33	44.33	85.33	3.00	1.34	163.67	7.17	26.33	3.43	4305.67	14.77
BNR-011	32.00	48.67	77.33	3.67	1.29	170.44	7.13	32.33	4.16	5511.85	22.91
BNR-012	35.67	47.67	80.00	3.33	1.31	162.33	6.83	24.33	3.68	3949.00	14.55
BNR-013	35.67	48.33	76.00	3.33	1.30	267.33	6.60	30.33	3.54	8133.33	28.79
BNR-014	34.67	48.00	76.67	3.33	1.33	259.33	6.47	31.00	3.97	8065.45	32.02
BNR-015	34.67	48.00	76.33	3.00	1.24	139.55	7.57	27.33	3.21	3826.27	12.28
BNR-016	32.67	47.67	79.33	3.33	1.25	171.11	7.40	25.67	3.27	4385.31	14.36
BNR-017	26.67	41.00	80.00	2.67	1.28	213.67	7.27	25.33	3.24	5407.00	17.50
BNR-018	33.00	48.00	75.67	3.00	1.45	167.11	8.50	26.67	3.21	4465.19	14.33
BNR-019	32.00	47.67	76.33	3.33	1.22	132.44	5.70	29.33	3.74	3889.52	14.51
BNR-020	35.00	47.33	74.67	3.33	1.54	120.33	7.23	26.00	3.79	3131.58	11.88
BNR-021	31.00	47.00	75.00	3.00	1.12	145.44	7.20	29.67	3.75	4317.19	16.19
BNR-022	32.33	46.67	80.67	3.33	1.02	121.00	5.90	30.00	4.47	3627.68	16.23
BNR-023	29.33	45.67	75.33	3.33	1.16	86.22	6.90	30.33	3.64	2613.93	9.51
BNR-024	31.00	47.33	80.00	3.33	1.12	106.33	6.73	31.33	3.44	3328.00	11.45
BNR-025	36.00	47.33	80.00	4.00	1.16	210.22	7.20	28.67	3.20	6026.38	19.28
BNR-026	32.67	47.33	79.00	3.33	1.07	114.75	7.10	31.00	4.26	3558.67	15.17
BNR-027	31.00	49.00	76.33	3.00	1.50	156.11	7.10	30.33	4.22	4735.20	19.99
BNR-029	31.00	47.67	77.33	3.33	1.25	110.55	7.93	25.33	3.21	2802.05	8.98
BNR-030	34.00	47.67	77.33	3.33	1.80	129.00	7.60	23.67	3.07	3059.33	9.41
BNR-031	35.00	52.67	74.33	3.00	1.61	158.11	8.23	26.00	3.21	4127.08	13.26
BNR-032	32.67	47.67	76.67	3.33	1.24	176.21	6.23	25.33	3.65	4453.23	16.24
BNR-033	31.33	47.00	76.33	3.33	1.48	246.83	7.50	26.00	3.45	6425.33	22.19
BNR-034	32.00	46.33	74.00	3.00	1.49	161.33	8.93	31.00	3.23	5004.56	16.15
BNR-035	33.00	45.33	84.67	3.33	1.43	167.17	8.37	24.33	3.75	4062.67	15.22
BNR-037	51.00	61.67	94.67	3.33	1.45	148.83	8.10	24.67	3.64	3663.33	13.32
BNR-039	64.67	73.00	96.00	3.00	1.81	282.17	7.77	23.67	3.36	6683.50	22.45

Table 2. Continued.

Genotype	DFF	DHF	DPR	NBP	PHT	NPP	PLT	NSP	TSW	NSPl	SYP
BNR-040	45.33	52.67	95.33	3.33	1.70	198.17	7.90	31.00	4.16	6147.50	25.52
BNR-041	50.67	52.33	98.33	3.33	1.81	178.83	8.13	31.33	4.22	5603.00	23.64
BNR-042	51.00	62.67	101.33	3.33	1.71	152.83	7.47	30.33	3.32	4623.50	15.28
BNR-043	51.67	64.67	100.33	3.33	1.63	169.83	7.27	30.67	3.48	5209.00	18.15
BARI -8	26.67	45.33	74.33	3.00	1.21	251.50	6.57	31.00	4.58	7800.50	35.72
TORI-7	29.67	42.67	75.67	3.33	0.99	596.83	7.07	23.00	3.23	13248.50	31.01
BARI-13	35.00	46.33	75.67	3.00	1.17	199.33	8.03	31.00	3.09	6178.93	19.07
Mean	35.05	49.6	81.18	3.24	1.35	184.36	7.4	28.05	3.62	5102.87	18.44
SE	1.11	1.06	1.03	0.35	0.08	28.9	0.18	1.69	0.05	775.72	2.62
LSD (0.05)	2.21	2.11	2.05	0.70	0.16	57.57	0.36	3.37	0.10	1545.23	5.22
CV (%)	3.88	2.61	1.55	13.06	6.88	19.2	2.92	7.38	1.66	18.62	17.4

DFF - Days to first flowering, DHF - Days to 100% flowering, DPR - Days to pod ripening, NBP - Number of branches per plant, PHT - Plant height (m), NPP - Number of pods per plant, PLT - Pod length (cm), NSP - Number of seeds per pod, TSW - Thousand seed weight (g), NSPl - Number of seeds per plant, SYP – Seed yield per plant (g)

materials is one of the most important prerequisites for development of varieties through selection. Genetic variability, heritability as well as genetic gain in selection contribute to success of any crop improvement program (Khan *et al.*, 2006). The range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2_b), genetic advance (GA) and genetic advance in % mean are presented in Table 3. The PCV was higher than the GCV for all the traits which indicates that the small environmental influence on the expression of these traits and considerable amount of variation was controlled by the genotypes *per se* (Table 3). Khan *et al.* (2006) found significant variation for yield and yield contributing characters for eleven accessions of *Brassica napus* L. Naazar *et al.* (2003) reported that genotypic and phenotypic variances in rapeseed were high for pods per plant followed by plant height. The estimates of GCV and PCV were high (≥30%) for seed yield per plant (30.52 and 33.13, respectively) indicating the existence of wide range of genetic variability among the lines for the traits. Chattopadhyay *et al.* (2011) reported broad genetic base of the traits and less environmental influence under the control of additive gene effects ensuring enormous scope for further improvement through selection. In the present study, high h^2b was recorded for the traits of 1000-seed weight (97.69%), days to ripening (97.12%), days to first flowering (96.80%), days to 100% flowering (95.50%) and pod length (92.74%). High heritability estimates associated with high genetic advance for plant height, pods per plant and seed yield were reported by Singh and Singh (1997). Higher genetic advance in percent of mean were observed for number of seeds per plant, days to flowering, number of pods per plant (48.83, 48.69 and 48.68, respectively). Heritability estimates together with genetic

Table 3. Genetic variability parameters for 11 traits of 43 restorer lines of *B. napus*

Traits	Range	GM	GCV	PCV	h^2_b (%)	GA	GA (% of mean)
DFF	26.67-64.67	35.05	22.05	22.41	96.80	15.67	44.69
DHF	41 -73	49.60	11.95	12.23	95.50	11.93	24.06
DPR	74.33-101.33	81.18	9.12	9.26	97.12	15.04	18.52
NBP	2.67-4.00	3.24	2.97	13.14	5.11	0.04	1.38
PHT	0.99-1.81	1.35	15.19	16.69	82.87	0.38	28.50
NPP	86.22-596.83	184.36	25.51	27.53	85.81	85.67	48.68
PLT	5.7-9.93	7.40	10.45	10.85	92.74	1.53	20.73
NSP	23-32.33	28.05	9.86	11.87	68.99	4.75	16.88
TSW	3.07-4.58	3.62	10.85	10.98	97.69	0.80	22.10
NSPl	2613.93-13248.5	5102.87	26.50	29.63	80.00	2412.09	48.83
SYP	8.98-35.72	18.44	30.52	33.13	84.84	10.37	57.92

DFF - Days to first flowering, DHF - Days to 100% flowering, DPR - Days to pod ripening, NBP - Number of branches per plant, PHT - Plant height (m), NPP - Number of pods per plant, PLT - Pod length (cm), NSP - Number of seeds per pod, TSW - Thousand seed weight (g), NSPl - Number of seeds per plant, SYP – Seed yield per plant (g); GM= General mean, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, hb^2= Heritability in broad sense (%), and GA= Genetic advance

advance work better for effective selection than either of the parameters alone (Johnson *et al.* 1955).

Correlation among yield contributing traits

Seed yield in rapeseed is a complex character and consequences from the interaction of a number of traits. Hence, improvement of seed yield would be done based on degree of association of these traits with the yield. The study of correlation co-efficient of nine different characters with seed yield has been performed for 43 restorer lines of *Brassica napus*. Results revealed that genotypic correlation co-efficient was higher than phenotypic correlation co-efficient that indicates a strong inherent association among these characters. Seed yield per plant showed significant negative correlation with number of seeds per pod (-0.217* and -0.192*, respectively) both at genotypic and phenotypic levels (Table 4). On the other hand, seed yield has significant positive correlation with pod length (0.786** and 0.795**, respectively), thousand seed weight (0.397** and 0.411**, respectively) and number of seeds per plant (0.455** and 0.412**, respectively) both at genotypic and phenotypic levels. Other characters have no significant correlation with seed yield per plant. A positive and highly significant character association between pods per plant and yield per plant was also found by Tuncturk and Ciftci (2007). Highly positive correlation found between plant height and yield per plant, pods per plant and yield per plant by Khayat *et al.* (2012). Result of positive correlation of days to flowering with days to maturity as well as negative correlation of these two traits with seed and oil yield are in agreement with the results of Delesa (2006).

Table 4. Genotypic correlation coefficient (G) and phenotypic correlation coefficient (P) among yield and yield contributing traits of 43 restorer lines of *B. napus*

Traits		DHF	DPR	NBP	PHT	NPP	PLT	NSP	TSW	NSPl	SYP
DHF	r_g	0.895**	0.822**	0.199*	0.699**	0.178*	0.202*	0.029^{ns}	-0.056^{ns}	0.166^{ns}	0.113^{ns}
	r_p	0.860**	0.800**	0.034^{ns}	0.623**	0.153^{ns}	0.197*	0.025^{ns}	-0.052^{ns}	0.135^{ns}	0.093^{ns}
DPR	r_g		0.729**	0.189*	0.580**	0.113^{ns}	0.234**	-0.014^{ns}	-0.051^{ns}	0.075^{ns}	0.037^{ns}
	r_p		0.697**	0.060^{ns}	0.520**	0.105^{ns}	0.214*	-0.013^{ns}	-0.046^{ns}	0.068^{ns}	0.036^{ns}
NBP	r_g			0.044^{ns}	0.602**	0.089^{ns}	0.220*	0.037^{ns}	0.070^{ns}	0.079^{ns}	0.085^{ns}
	r_p			0.020^{ns}	0.528**	0.073^{ns}	0.210*	0.014^{ns}	0.074^{ns}	0.053^{ns}	0.065^{ns}
PHT	r_g				-0.447**	-0.392**	-0.483**	0.378**	0.327**	-0.188*	-0.099^{ns}
	r_p				-0.114^{ns}	-0.124^{ns}	-0.081^{n}	0.084^{ns}	0.081^{ns}	-0.076^{ns}	-0.051^{n}
NPP	r_g					0.092^{ns}	0.369**	-0.091^{ns}	-0.104^{ns}	0.067^{ns}	0.047^{ns}
	r_p					0.089^{ns}	0.337**	-0.077^{ns}	-0.091^{ns}	0.063^{ns}	0.047^{ns}
PLT	r_g						-0.014^{n}	-0.109^{ns}	-0.060^{ns}	0.915**	0.786**
	r_p						0.016^{ns}	-0.084^{ns}	-0.060^{ns}	0.901**	0.795**
NSP	r_g							-0.283**	-0.318**	-0.120^{ns}	-0.217*
	r_p							-0.215*	-0.305**	-0.103^{ns}	-0.192*
TSW	r_g								0.390**	0.289**	0.397**
	r_p								0.310**	0.342**	0.411**
NSPl	r_g									0.098^{ns}	0.455**
	r_p									0.075^{ns}	0.412**
SYP	r_g										0.924**
	r_p										0.934**

*and** indicate significance at 5% and 1% levels, respectively

DFF - Days to first flowering, DHF - Days to 100% flowering, DPR - Days to pod ripening, NBP - Number of branches per plant, PHT - Plant height (m), NPP - Number of pods per plant, PLT - Pod length (cm), NSP - Number of seeds per pod, TSW - Thousand seed weight (g), NSPl - Number of seeds per plant, SYP – Seed yield per plant (g)

Path co-efficient analysis

Significant genetic correlation co-efficient between two characters does not always prove that the traits are linked together (Majumder *et al*., 2012). Path analysis partitions correlation co-efficient into their direct and indirect effects. The highest positive direct effect (1.221) was found in number of seeds per pod towards seed yield per plant. Thousand seed weight also contributed a significant effect (0.345) on seed yield per plant. All other traits had negative direct effects except days to 100% flowering (0.013), days to ripening (0.005) and plant height (0.005). Sinha *et al.* (2001) and Rauf and Rahim (2018) reported that plant height had negative direct effect on yield per plant. Days to flowering revealed the maximum negative direct effect (-0.039) on seed yield per plant. The highest positive and significant indirect effects were observed in number of seeds per pod (0.934) followed by number of pods per plant (0.795). Among the other traits, thousand seed weight and

Table 5. Partitioning of phenotypic correlation into direct (bold) and indirect component of 43 restorer lines of *B. napus*

Traits	DFF	DHF	DPR	NBP	PHT	NPP	PLT	NSP	TSW	NSPl	SYP
DFF	-0.039	0.011	0.004	-0.0003	0.019	-0.045	-0.0004	-0.003	-0.017	0.164	0.093^{ns}
DHF	-0.033	0.013	0.003	-0.0004	0.016	-0.031	-0.0005	0.002	-0.015	0.083	0.036^{ns}
DPR	-0.031	0.008	0.005	-0.0002	0.016	-0.021	-0.0005	-0.002	0.025	0.064	0.065^{ns}
NBP	-0.001	0.001	0.0001	-0.007	-0.004	0.036	0.0002	-0.011	0.027	-0.092	-0.051^{ns}
PHT	-0.024	0.006	0.002	0.001	0.032	-0.026	-0.001	0.010	-0.031	0.077	0.047^{ns}
NPP	-0.005	0.001	0.0003	0.001	0.003	-0.295	0.000	0.011	-0.021	1.10	0.795**
PLT	-0.007	0.002	0.0001	0.001	0.011	0.004	-0.002	0.029	-0.105	-0.125	-0.192*
NSP	0.001	-0.0002	0.0001	-0.001	-0.002	0.024	0.001	-0.135	0.106	0.417	0.411**
TSW	0.002	-0.001	0.0003	-0.001	-0.003	0.017	0.001	-0.042	0.345	0.091	0.412**
NSPl	-0.005	0.001	0.0002	0.001	0.002	-0.265	0.0002	-0.046	0.025	1.221	0.934**

*and** indicate significance at 5% and 1% levels, respectively, Residual effect= 0.008. DFF - Days to first flowering, DHF - Days to 100% flowering, DPR - Days to pod ripening, NBP - Number of branches per plant, PHT - Plant height (m), NPP - Number of pods per plant, PLT - Pod length (cm), NSP - Number of seeds per pod, TSW - Thousand seed weight (g), NSPl - Number of seeds per plant, SYP – Seed yield per plant (g)

number of seeds per pod showed significant positive (0.412** and 0.411*, respectively) and pod length showed significant negative (-0.192) indirect effects towards seed yield per plant. Khayat *et al.* (2012) reported that thousand seed weight had the highest positive direct effect on seed yield per plant. These results are partially agreeing with the earlier findings of Tahira *et al.* (2011). Basalma (2011) confirmed that direct effects of plant height and branches per plant on yield were negative. The path co-efficient analysis indicated that days to flowering, days to ripening, number of pods per plant, number of seeds per pod, and 1000-seed weight were the most important contributors to seed yield per plant which could be taken in consideration for future hybridization program. The value of residual effect was 0.008. It indicated that beside the component traits, there was little contribution of other traits (approx. 0.8%) on seed yield per plant.

Conclusions

For rapeseed breeding the variables pods per plant, seeds per pod and 1000-seed weight were found with maximum potential of selection for yield improvement because these traits possessed high h^2b, highly significant positive correlation and maximum positive direct effects with seed yield per plant.

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