



Correlation and path analysis in advanced lines of rapeseed (*Brassica napus*) for yield components

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Abstract

Thirty-six rapeseed genotypes including four cultivars and 32 advanced lines were evaluated in randomized complete block design with three replications. Analysis of variance indicated significant genetic variation for different seed yield contributing characters. Most variations among the genotypes were in seeds per siliqua and siliquae on main raceme with 18.0 and 25.3 per cent coefficient of variation, respectively. Heritability (bs) estimates were high for siliquae on main raceme, seeds per siliqua and siliquae per plant (0.70, 0.77 and 0.81, respectively). Siliquae per plant had significant positive correlation (0.80**) with seed yield and also it had significant positive direct effect (0.85**) on seed yield. So any change for this trait will have considerable effect on seed yield.

Key words : Coefficient of variation, heritability, *Brassica napus*

Introduction

Rapeseed is an important species from *Brassica* genus and a high value crop for oil production. It is an important crop in Iran for more than a decade and has major role in providing self-sufficiency in edible oil to the country. Hence, it is necessary to develop new varieties of rapeseed with high seed yield. Optimizing yield is one of the most important goals for most rapeseed breeders. Seed yield is a complex character that can be determined by several components reflecting positive or negative effects upon this trait, whereas it is important to examine the contribution of each of the various components in order to give more attention to those having the greatest influence on seed yield (Marjanovic-Jeromela *et al.*, 2007). Determination of correlation coefficients is an important statistical procedure to evaluate breeding programs for high yield, as well as to examine direct and indirect contributions to yield variables (Ali *et al.*, 2003). Path-coefficient technique splits the correlation coefficients into direct and indirect effects via alternative characters or pathways and thus permits a critical examination of components that influence a given correlation and can be helpful in formulating an efficient selection strategy

(Sabaghnia *et al.*, 2010). With this background, the present study aimed to estimate the coefficient of variation, broad sense heritability, relationship among yield components for improving seed yield in spring type of rapeseed advanced lines and cultivars.

Materials and Methods

The material under study consisted of 36 rapeseed (*Brassica napus* L.) genotypes including four cultivars and 32 advanced lines, which were selected on the basis of different agronomic characters. The genotypes were evaluated in randomized complete block design with three replications at Biekol Agriculture Research Station, located in Neka, Iran (13°53' E; 43°36' N latitude, 15 m above sea level) during 2010-11. Each plot consisted of four rows of 5 m length spaced 30 cm apart. The plant to plant spacing was maintained at 5 cm. Crop management factors like land preparation, crop rotation, fertilizer, and weed control were followed as recommended for local area. All the plant protection measures were adopted to make the crop free from insect-pests. The siliquae per main raceme and siliquae per plant were recorded based on 10 randomly tagged plants in each plot. The siliqua length and seeds per siliqua were recorded based on five randomly tagged

siliquae on the main raceme of 10 plants in each plot. Seed yield (adjusted to kg/ha) was recorded based on two middle rows of each plot.

Variance components were estimated from the mean squares in the analysis of variance (Singh *et al.*, 1993). Broad sense heritability (h^2) was estimated according to Singh *et al.* (1993). Direct and indirect path coefficients were calculated as described by Williams *et al.* (1990), Lynch and Walsh (1998). All the analyses were performed using MS-Excel and SAS software version 9.

Results and Discussion

Significant mean square due to genotypes were observed for yield components including branches/plant, siliquae/main raceme, siliquae/plant, siliqua length, seeds/siliqua, 1000-seed weight and seed

yield indicating significant genetic variation for these traits. These results are the same as those reported by Ali *et al.* (2002) and Sabaghnia *et al.* (2010). Broad sense heritability estimates varied from 0.42 (1000-seed weight) to 0.81 (siliquae/plant). High estimates of heritability (bs) were found for siliquae on main raceme, seeds per siliqua and siliquae per plant (0.70, 0.77 and 0.81, respectively), indicating high selection gain for improving these traits in breeding programme. In earlier studies, Marjanovic-Jeromela *et al.* (2007) and Sabaghnia *et al.* (2010) reported high heritability estimates for yield components. Coefficient of variation of the studied traits varied from 11.4 to 25.3 related to 1000-seed weight and siliquae on main raceme, respectively (Table 1). High genotypic variations were noted for seeds per siliqua and siliquae on main raceme with 18.0 per cent and 25.3 per cent coefficient of variation, respectively.

Table 1: The mean of seed yield and its components in 36 rapeseed spring genotypes

Genotypes	Traits	Branches /plant	Siliquae on main raceme	Siliquae /plant	Siliqua length (cm)	Seeds /siliqua	1000 seed weight (g)	Seed yield (kg/ha)
1-RW38		6.1	30.7	158.8	4.9	19.3	3.9	2861
2-RW41		8.2	45.7	172.7	5.3	23.9	4.1	3315
3-SAR38		6.9	42.3	157.3	6.2	25.2	3.7	3475
4-RG341		8.1	32.6	136.0	4.7	19.3	4.8	2448
5-RG641		4.7	25.9	156.3	4.8	21.3	3.7	3186
6-RG638		6.1	58.7	163.7	5.6	23.2	4.5	3413
7-19R41		5.3	36.9	142.7	6.2	24.9	3.9	3137
8-19R38		8.1	57.8	125.7	5.4	21.6	3.7	2955
9-RG338		5.4	49.4	157.7	6.3	26.1	3.2	3327
10-19SAR1		4.8	61.2	180.7	6.3	20.6	4.7	3466
11-SAR38		5.9	37.7	122.3	5.2	18.3	3.0	2275
12-POT38		7.3	27.8	132.3	4.9	20.9	3.9	2777
13-OPT41		5.6	39.7	177.3	5.5	21.5	4.0	3008
14-RWRG3		5.3	32.4	133.3	5.7	15.4	4.8	2873
15-19OPT		6.2	32.7	135.2	5.6	23.2	4.4	2733
16-RG3OPT		6.3	34.3	120.7	5.1	16.1	3.6	2673
17-RWOPT		5.9	31.2	122.3	5.3	21.3	4.6	2500
18-SAR41		8.2	43.9	180.3	5.5	20.1	3.5	3182

19-RG3SAR	6.7	65.9	150.7	5.8	18.0	4.5	2933
20-RWSAR	6.3	35.2	118.3	4.9	17.9	4.1	2144
21-RAS19	6.3	47.0	183.5	6.4	23.4	3.8	3072
22-19RG3	6.0	54.7	128.3	5.5	21.9	4.2	2800
23-RWRG3	5.3	42.8	157.3	7.5	30.0	4.9	3182
24-RASRW	6.8	63.1	139.7	5.3	17.5	3.2	2888
25-RASSAR	6.6	32.2	188.7	5.4	24.5	4.1	3200
26-RASRG3	6.7	40.8	150.0	6.6	20.6	4.3	2867
27-RASOPT	6.8	30.0	132.0	4.5	14.5	4.4	2378
28-RASRG3	6.7	33.8	168.3	6.2	27.1	4.6	3370
29-ZAR41	6.8	46.3	173.3	6.3	26.7	4.0	3269
30-RW19	7.8	52.8	166.7	6.7	27.4	4.5	3256
31-19SAR2	7.1	54.3	178.3	6.9	29.7	4.1	3493
32-19SAR3	7.0	33.0	183.4	6.8	30.0	4.3	3649
33-Sarigol	8.9	47.0	177.2	5.8	23.9	3.6	3102
34-RGS003	6.8	40.6	172.3	5.1	20.9	4.0	3245
35-Hyola401	6.5	41.6	178.3	6.3	27.0	4.2	3716
36-Zarfam	6.0	50.1	152.0	6.0	24.5	4.0	2707
Broad sense heritability	0.6	0.4	0.8	0.5	0.8	0.70	0.7
LSD(p=0.01)	0.9	9.3	14.3	0.9	2.9	0.6	374.8
Genetic variation	15.1	25.3	14.0	12.3	18.0	11.4	12.6

Table 2: Pearson correlation coefficients of seed yield and its components

Traits	1	2	3	4	5	6	7
1- Branches/plant	1						
2- Siliquae on main raceme	0.13	1					
3- Siliquae/ plant	0.14	0.21	1				
4- siliqua length	-0.10	0.37*	0.49**	1			
5- Seeds/ siliqua	0.06	0.14	0.59**	0.77**	1		
6-1000-Seed weight	-0.12	-0.08	0.04	0.19	0.09	1	
7- Seed yield	0.03	0.30	0.80**	0.62**	0.70**	0.04	1

*, ** Significant at p=0.05 and 0.01, respectively

Maximum and minimum number of branches was 4.7 (RG 641) and 8.9 (Sarigol). The correlation between this trait and seed yield was not significant, so selection based on number of branches may not be effective for improving seed yield (Table 2). Significant positive correlation was observed between siliquae on main raceme and siliqua length. So the genotypes with higher number of siliquae on main raceme had longer siliqua. Positive correlation between siliquae on main raceme and seed yield indicated that genotypes having higher number of siliquae on main raceme should be

selected for maximizing seed yield. Siliquae per plant varied from 120.7 (RG3OPT) to 188.9 (RASSAR) and genotypes 19SAR1, RAS19, 19SAR3 and RASSAR with higher number of siliquae per plant were selected as promising genotypes. Path diagram and the result of path coefficient analysis for studied traits are presented in fig. 1 and Table 3, respectively. Siliquae per plant had significant positive correlation (0.80**) with seed yield and it also had significant positive direct effect (0.85**) on seed yield. So any change for this trait will have considerable effect on seed yield. Siliquae per plant

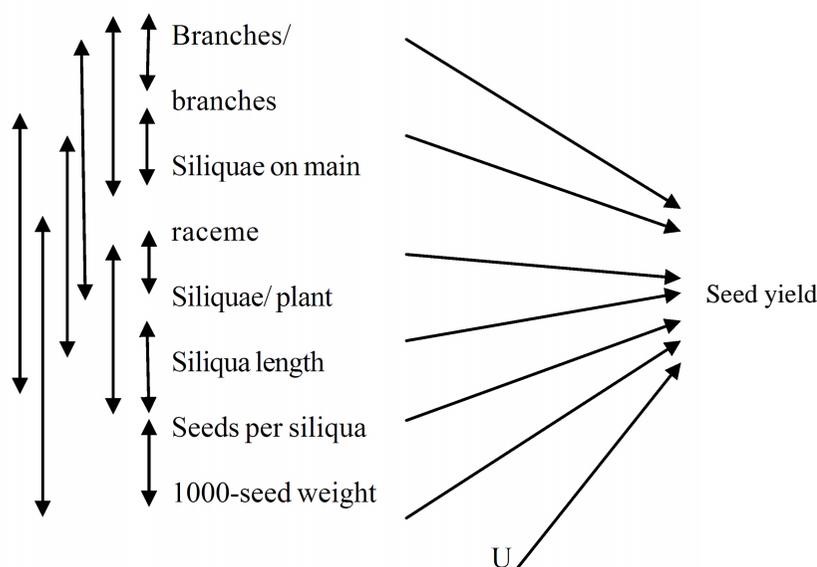


Fig 1 : Path diagram for direct and indirect effects of yield components on seed yield.

Table 3: Direct (on diagonal) and indirect (out of diagonal) effects of yield components on seed yield.

Traits	1	2	3	4	5	6
1- Branches /plant	-0.08	0.15	0.08	-0.01	0.02	0.01
2- Siliquae on main raceme	-0.11	0.12	0.12	0.02	0.04	0.01
3- Siliquae / plant	-0.01	0.03	0.58**	0.03	0.18	-0.1
4- Siliqua length	0.01	0.05	0.28	0.06	0.23	-0.01
5- Seeds/ siliqua	-0.01	0.02	0.34	0.05	0.30*	-0.01
6-1000-seed weight	0.01	-0.01	0.03	0.01	0.03	-0.02

*, ** Significant at p=0.05 and 0.01, respectively

also had positive indirect effect on seed yield through siliqua length and seeds per siliqua. There are several reports on correlation and path-coefficient analysis in canola (Ali *et al.*, 2003; Khan *et al.*, 2008; Basalma, 2008; Hashemi Ameneh, 2010) and other *Brassica* species (Semahegn Belete, 2011). In most of these studies siliquae per plant and siliquae on main raceme had significant positive correlation with seed yield.

Although significant positive correlation was observed between siliqua length and seed yield, but its direct effect on seed yield was not significant. Seeds per siliqua ranged from 14.5 to 30.0 and the genotypes 19SAR2, 19SAR3 and RWRG3 were selected as promising based on higher seeds per siliqua. Seeds per siliqua had significant positive correlation with seed yield and also it had significant positive direct effect on seed yield. Due to compensative yield components, 1000-seed weight had no significant correlation with seed yield. Seed yield ranged from 2144 to 3716 kg/ha and the genotypes Hyola 401 and 19SAR3 with high seed yield were considered as suitable genotypes.

In general, siliquae per plant and siliquae on main raceme were more heritable than other yield components. Due to significant positive correlation of siliquae per plant and seeds per siliqua with seed yield and also their significant positive direct effect on seed yield, these two yield components can be used for indirect selection for seed yield improvement.

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