Heritability and path coefficient analysis for quantitative traits of rapeseed advanced lines

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Abstract

This study was undertaken to examine phenotypic, and genetic variability, broad-sense heritability, genetic gain under selection, and interrelationships of some agronomic traits of rapeseed genotypes. Genotypes showed significant variation for all studied characters. High heritability, and genetic advance estimates were recorded for days to flowering, and seeds per pod indicating the existence of additive gene action for the expression of these traits. High value of heritability, and moderate value of genetic advance were observed for days to end of flowering, and days to maturity suggesting the involvement of non-additive(dominance or epistatic) gene effect for these traits. For all traits, genetic variances were lower as compared to phenotypic ones, demonstrating the environmental influence in their expression. The direct effect of days to flowering (0.35*), pods on main raceme (0.36*), pods per plant (0.56**), and seed yield were positive, and significant, therefore these traits can be used as indirect selection criteria for improving seed yield. The positive association between oil content, and seed yield per plant indicate the possibility of improving these most important traits in rapeseed simultaneously. Among the genotypes, G6, G7, G5, G14, G19, and G21 with seed yield of 3053, 3070, 3094, 3113, 3338, and 3415 kg ha^{-1}, respectively were higher yielding than other genotypes.

Key words: *genetic correlations, genetic path coefficient, heritability, rapeseed, yield*

Introduction

Rapeseed (*Brassica napus* L.) is the second most important oilseed crop in the international oilseed market followed by soybean. The seeds of modern varieties typically have 40% to 45% oil, which supplies a raw material for many other products ranging from rapeseed methyl ester (biodiesel) to industrial lubricants, and hydraulic oils for detergent and soap production and biodegradable plastics (Friedt *et al.,* 2007). It is a main crop in Iran for more than a decade, and has major role in providing self-sufficiency in edible oil to the country. Therefore, it is essential to develop new varieties of rapeseed with high seed yield. Optimizing yield is one of the most important objectives for most rapeseed breeders. Seed yield is a complex character determined by several components reflecting positive or negative effects upon this trait, while it is important to examine the role 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). Therefore, the estimation of heritability of desired traits needs to be performed in order to apply an efficient breeding strategy. Heritability represents the ratio between genotypic, and phenotypic variance, and expresses individual's phenotypes determined by their genotypes (Engqvist and Becker, 1993; Giessen *et al.,* 2003; Akbar *et al.,* 2007). Heritability along with genetic gain is more valuable than heritability alone in the precise prediction of the effects of selection. The phenotypic values of different traits in the same individual are often found to be correlated (Lynch and Walsh, 1988). A trait having the wider range of genetic variability, relatively high heritability, and moderate to high genetic advance would be an effective means to get better seed yield (Aytaç and Kinaci, 2009). When the selection is simultaneous for various traits, the correlation between them may

restrict the response to selection. 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). Keeping in view the importance of rapeseed as an oil crop, this study was conducted to estimate genetic, and phenotypic variability, broad-sense heritability, and interrelationships between seed yield and some related traits.

Materials and Methods

The material under study consisted of 24 rapeseed (*Brassica napus* L.) genotypes including three cultivars, and 21 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 ($13^o53^{'}$ E; $43^o36^{'}$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 applied to make the crop free from insect-pests. The pods on main raceme, and pods per plant were recorded based on 10 randomly tagged plants in each plot. The pod length, and seeds per pod were recorded based on five randomly tagged pods on the main raceme of 10 plants in each plot. Seed yield (adjusted to kg ha^{-1}) 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). The component of variance including error variance (V_E), genotypic variance (V_G) and phenotypic variance (V_P) were estimated according to the following formula :

$$V_E = MS_E$$

$$V_G = (MS_G - MS_E)/r$$

$$V_P = V_G + V_E$$

Broad sense heritability (h^2_B) was estimated as : h^2_B=VG/VE (Falconer, 1989). The coefficient of variation was estimated as CV=$(\sqrt{V_G})/\mu$ in which μ is the mean of genotypes for each trait. Expected genetic advance (GA) and GA as percent of the mean assuming selection of the superior 10% of the genotypes were estimated in accordance to Falconer, (1989) as:

$$GA = k. \sqrt{V_P}. h^2_B$$

$$GA(\text{as \% of the mean}) = (G_A/\bar{x}) \text{ x } 100$$

where *k* is a standardized selection differential (with 10% selection intensity it is 1.755), is the phenotypic standard deviation, h^2_B is the broad sense heritability, and refers to the mean of the character. Genetic correlation coefficients were calculated from the analysis of covariance (Singh and Chaudhary, 1979). Direct and indirect path coefficients were calculated as described by previous studies (Lynch and Walsh, 1988; Williams *et al.,* 1990) as:

$$r_{yi} = P_{yi} + \quad \text{For i}'''\text{i}' \text{ and i}'''1$$

where r_{yi} is the simple correlation coefficient between the *i*-th causal variable (*Xi*), and effect variable (*y*), $r_{ii'}$ is the simple correlation coefficient between the *i*-th and *i'*-th causal variables, *Pyi* is the path coefficient (direct effect) of the *i*-th causal variable (*Xi*), $r_{ii'} P_{yi'}$ is the indirect effect of the *i*-th causal variable via the *i'*-th causal variable. To determine P_{yi} values, square matrics of the correlation coefficient between independent traits in all possible pairs were inverted and then multiplied by the correlation coefficients between the independent and dependent traits.All the analyses were performed using MS-Excel, and SAS software version 9 (SAS Institute INC., 2004).

Results and Discussions

Genotypes differed significantly (p < 0.01) for all investigated traits (Table1), verifying the possibility of improving these traits through selection.These results are the same as those reported in earlier studies (Ali *et al.,* 2003; Sabaghnia *et al.,* 2010). To compare the variation among various traits,

Table 1. Randomize complete block (RCBD) analysis of variance, broad-sense heritability, and genetic advance estimates for the traits studied

S.O.V	Df	M.S								
		Days to flowering	Days to end of flowering	Days to maturity	Plant height	Pods on main raceme	Pods per plant	Pods length	Seeds per pod	Seed yield
Replication	2	2.2	7.9	4.2	1071**	878***	3690**	4.95**	225.3**	1013675*
Treatments	23	96.9**	82.5**	44.3**	168*	105*	563***	0.55*	15.8**	622533**
Error	46	1.1	13.5	4.0	96	33	196	0.26	3.6	231549

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

Table 2. Genetic parameters of some quantitative traits of advance rapeseed lines

Traits	Parameters					
	Vp	VG	PCV	GCV	h^2_B	GA (%)
Days to flowering	361877	130328	23.46	14.08	0.97	9.22
Days to end of flowering	7.7	4.1	13.22	9.63	0.63	3.98
Days to maturity	0.4	0.1	10.43	5.43	0.77	2.68
Plant height (cm)	318.3	122.3	19.65	12.18	0.20	2.35
Pods on main raceme	57.0	24.0	19.04	12.35	0.42	14.03
Pods per plant	120.0	24.0	6.69	2.99	0.38	13.11
Pods length (cm)	17.4	13.4	1.98	1.74	0.27	4.94
Seeds per pod	36.5	23.0	3.60	2.86	0.53	12.29
Seed yield (kg ha^{-1})	33.0	31.9	5.41	5.32	0.36	14.82

Vp: phenotypic variance; V_G: genotypic variance); PCV: phenotypic coefficient of variation; GCV: genotypic coefficient of variation; h^2_B: broad-sense heritability, GA(%): genetic advance.

descriptive statistics including phenotypic (PCV), and genetic coefficient of variability (GCV), broad sense heritability (h^2_B), genetic advance, and genetic advance (GA) as a percentage of mean are given in Table 2. For all traits, genetic variances were lower as compared to phenotypic ones, demonstrating the environmental influence in their expression.

Flowering is the most critical stage having great influence on the yield of oilseed *Brassica*. The onset of flower initiation can have strong influence on flower, pod, and seed related parameters (Baye and Becker, 2005).Various studies on oilseed rape have shown flowering period to be a highly heritable character. Days to flowering ranged from 97 days

(G3 and G18) to 117 days (G13) (Table 3). It is in conformity with the findings of some already reported research regarding the traits (Holland *et al.,* 2002; Ivanovska *et al.,* 2007; Sajid and Farhatullah Khalil, 2008), which strengthened our results. High value of broad-sense heritability (90.3), and moderate value of genetic advance (16.88) were observed for days to flowering (Table 2), suggesting non-additive (dominance or epistatic) gene effect for this trait. High heritability also reported for days to flowering (Khan *et al.,* 2008). This indicated that a trait having high heritability did not essentially produce high genetic advance. Non-significant positive correlation was determined between days to flowering, and seed yield (Table 4). Decisions solely based on correlation coefficients may not always be effective since they provide only limited information, disregarding interrelations among traits. Thus, information obtained from correlation coefficient can be enhanced by partitioning them into direct, and indirect effects for a set of prior cause, and interrelation-ship.Path diagram, and the result of path coefficient analysis for studied traits are presented in Fig. 1 and Table 5, respectively. Days to flowering had significant positive direct effect on seed yield. This trait can be used as selection criterion for seed yield in the early generations.

Days to end of flowering ranged from 157 to 176 days in G23 and G11, respectively (Table 3). High mean values of this trait will follow high mean values of pod formation, therefore the genotypes including G1, G9, G7, G3, and G11 with 174, 174, 174, 175, and 176 days to end of flowering were superior for improving this trait. Phenotypic, and genotypic coefficient of variations for Days to end of flowering were 7.7, and 4.1 respectively, Days to end of flowering also displayed high broad-sense heritability (0.63), and low genetic advance (3.98) for the genotypes (Table 2).

Days to maturity varied from 204 to 221 days in G18, and G22, respectively. Due to non-significant correlation between days to maturity, and seed yield, selection of high-yield potential genotypes with negligible losses of seed yield is possible. Phenotypic, and genotypic variances of genotypes for days to maturity were 0.4, and 0.1, respectively. Phenotypic
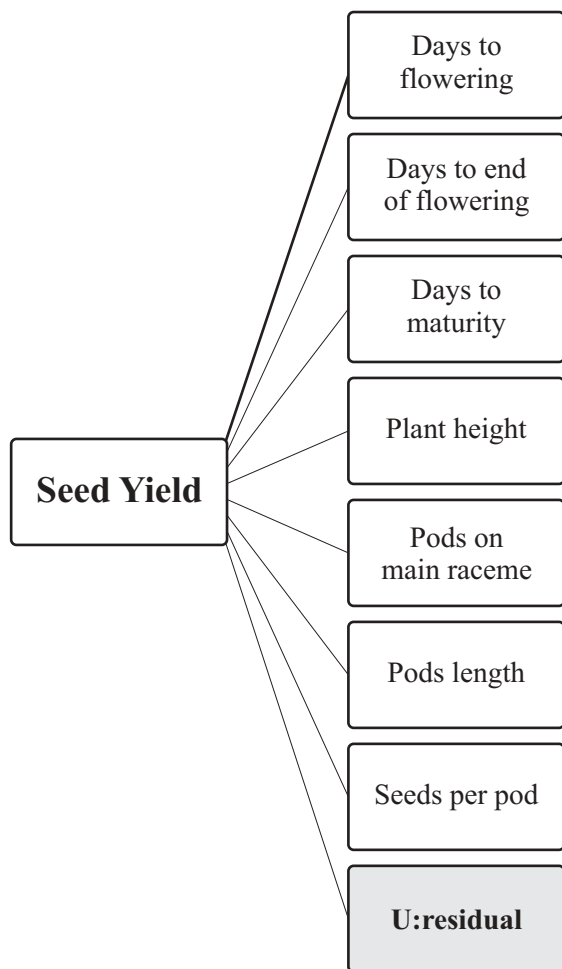

Fig. 1: Path diagram for seed yield and other eight related characteristics

Table 3. Mean comparison of the rapeseed genotypes for phenological traits, plant height, yield components, and seed yield

Genotypes	Days to flowering	Days to end of flowering	Days to maturity	Plant height (cm)	Pods on main raceme	Pods per plant	Pods length (cm)	Seeds per pod	Seed yield (kg ha^{-1})
G1: Zar08-1	106	174	213	168.0	52.0	90.2	5.8	23.9	1952
G2: Zar01-3	106	170	213	175.7	40.5	71.7	5.7	21.8	2171
G3: Zar01-7	97	175	206	169.4	36.7	77.2	5.9	23.5	1893
G4: Zar01-8	104	165	206	160.1	47.1	72.0	5.7	23.2	2493
G5:22B01-14	108	169	212	162.6	37.5	109.7	5.6	24.0	3094
G6: 22B01-15	111	165	211	154.3	31.0	86.7	5.1	18.5	3053
G7: 22B01-16	109	174	211	168.4	39.5	102.3	6.1	19.3	3070
G8: Forn08-1	103	172	206	156.8	34.9	101.3	5.7	17.6	2194
G9: Forn01-7	106	174	208	165.1	36.5	69.7	5.6	18.8	1846
G10: Forn01-8	111	162	215	150.4	42.3	103.3	5.2	17.9	2704
G11:Mod08-2-4	108	176	213	160.1	34.4	71.1	5.5	18.7	2445
G12: Mod08-2-5	106	165	209	154.0	34.7	82.1	5.5	19.4	2484
G13: Mod08-2-6	117	168	214	181.3	46.7	80.8	6.0	22.2	2322
G14: Mod08-2-8	102	171	208	172.2	41.5	108.6	5.7	21.9	3113
G15: Mod08-2-9	104	172	212	157.7	34.4	106.8	5.4	22.1	2859
G16: Mod08-2-0	99	166	205	166.8	40.3	92.9	5.3	22.1	2274
G17: Mod08-2-1	103	169	209	162.5	34.5	83.3	5.2	19.0	2126
G18: Mod08-2-14	97	164	204	164.7	41.7	90.0	5.9	19.9	2195
G19: Mod08-6-1	109	159	210	152.1	31.8	106.7	6.6	21.3	3338
G20: Mod08-6-2	110	164	211	166.3	31.9	81.5	5.7	19.7	2830
G21: Zar01-2-1	110	164	212	162.8	40.1	114.0	5.4	20.2	3415
G22: Sarigol	119	169	221	171.0	45.5	100.4	6.7	18.6	2427
G23: Hyola401	97	157	210	167.1	47.2	91.2	6.5	25.8	2764
G24: RGS003	104	161	213	162.5	49.3	85.3	5.6	23.6	2487
LSD$_{(á=0.05)}$	1.7	6.1	3.3	16.2	9.5	23.1	0.8	3.1	793.7
LSD$_{(á=0.01)}$	2.3	8.1	4.4	21.6	12.7	30.9	1.1	4.2	1060.8

and genotypic coefficient of variations for days to maturity were 10.4, and 5.4, respectively, Days to maturity displayed high broad-sense heritability (0.77), and low genetic advance (2.35) for the tested genotypes. High heritability does not necessarily mean high genetic gain. The utility of heritability estimates is, therefore, increased when they are used to estimate genetic advance (Scheiner *et al.,* 2000), which indicates the degree of gain in a character obtained under a particular selection pressure. The expected genetic advance is a function of selection intensity, phenotypic variance, and heritability. Thus, the genetic advance has an added edge over heritability as a guiding factor to breeders in a selection program (Semahegn Belete, 2011).

Both genetic, and environmental factors play a vital role in determining the plant height of a plant. The data revealed that the plant height of different rapeseed genotypes under study was significant (Table 1). Plant height varied from 150.4 to 181.3 cm in G10, and G13, respectively. For plant height Vp (318.3) was higher than the VG (122.3), and similarly PCV (19.65) was higher compared to GCV (12.18), and as well as the mentioned traits according to Table 2 exhibited low heritability (0.20), and moderate genetic advance (2.35). This suggests the involvement of non-additive (dominance or epistatic) gene effects for this trait. High genotypic and phenotypic variances also reported for plant height, and pods per plant in *B. juncea* (Basalma, 2008).

Non-significant positive correlation was detected between pods on main raceme, and seed yield (Table 4). Pods on main raceme ranged from 31 to 52 in G6, and G1, respectively. The phenotypic, and the genotypic coefficient of variations for pods on main raceme were 19.0, and 12.35, respectively, this trait displayed moderate heritability (0.42), and high genetic advance (14.03) for the tested genotypes. Pods per plant varied from 69.7, and 114 in G9, and G21, respectively. High average mean value of this trait was observed in G19 (106.7), G15 (106.8), G14 (108.6), G5 (109.7), and G21 (114). For this trait phenotypic variance was 120, and genotypic variance was 24, and the phenotypic and the genotypic coefficient of variations were 6.69, and 2.99, respectively (Table 2). Significant positive

correlation was detected between pods per plant and seed yield; therefore, this trait can be used as selection criterion for improving seed yield. High direct effect of pods per plant, and 1000 seed weight on yield per plant were stressed. Pods per plant are decisive for seed yield (Baye and Becker, 2005). Pods per plant had significant positive correlation (0.67**) with seed yield (Table 4), and it also had significant positive direct effect (0.56**) on seed yield (Table 5). So any change for this trait will have considerable effect on seed yield. Pods per plant had also positive indirect effect on seed yield through pod length, and seeds/pod. There are several reports on correlation and path-coefficient analysis in canola (Ali *et al.,* 2003; Khan *et al.,* 2008; Hashemi *et al.,* 2010 and other *Brassica* species (Semahegn Belete, 2011). In most of these studies pods/plant, and pods on main raceme had significant positive correlation with seed yield.

The data revealed significant differences for pod length among the genotypes (Table 1). This trait ranged from 5.1 to 6.7 in G6, and G22, respectively. High mean value of pod length was determined for G13, G7, G23, G19, and G22 (6, 6.1, 6.5, 6.6 and 6.7cm, respectively). Significant differences were observed for seeds per pod among 23 tested genotypes (Table 2). For this trait phenotypic variance was 36.5, and genotypic variance was 23, and the phenotypic and the genotypic coefficient of variations were 3.6, and 2.7, respectively (Table 3). Moreover, the traits exhibited high heritability (0.53), and genetic advance (12.3).

Seed yield of the genotypes varied from 1846 to 3415 kg ha⁻¹ in G9, and G21, respectively. High mean value of seed yield was determined for G6, G7, G5, G14, G19, and G21 (3053, 3070, 3094, 3113, 3338 and 3415 kg ha⁻¹, respectively). Phenotypic, and genotypic variances of genotypes for seed yield were 33, and 31.9, respectively. Phenotypic, and genotypic coefficient of variations for seed yield were 5.4, and 5.3 respectively, the seed yield also displayed low broad-sense heritability (0.36), and high genetic advance (14.8) for the tested genotypes (Table 2). High GCV, PCV were stated for seed yield, and number of pods per plant (Engqvist and Becker, 1993; Akbar *et al.,* 2007). Seed yield per

Table 4. Correlation among the traits in rapeseed

Traits	1 Days to flowering	2 Days to end of flowering	3 Days to maturity	4 Plant height (cm)	5 Pods on main raceme	6 Pods per plant	7 Pods length (cm)	8 Seeds per pod	9 Seed yield (kg ha^{-1})
Days to flowering	1								
Days to end of flowering	0.03	1							
Days to maturity	0.79**	-0.03	1						
Plant height	0.05	0.31	0.13	1					
Pods on main raceme	-0.11	-0.14	0.25	0.47*	1				
Pods per plant	0.13	-0.19	0.18	-0.22	-0.02	1			
Pods length	0.14	-0.16	0.22	0.34	0.29	0.13	1		
Seeds per pod	0.40*	-0.18	-0.11	0.36	0.52**	-0.02	0.26	1	
Seed yield (kg ha^{-1})	0.29	-0.41*	0.21	-0.31	0.24	0.67**	0.06	0.01	1

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

Table 5: Path coefficient analysis between yield and related traits in rapeseed genotypes.

Traits	Direct effect on seed yield	Indirect effect on seed yield via							
		Days to flowering	Days to end of flowering	Days to maturity	Plant height (cm)	Pods on main raceme	Pods per plant	Pods length (cm)	Seeds per pod
Days to flowering	0.35*	-	-0.01	-0.03	-0.01	-0.04	-0.07	-0.11	-0.13
Days to end of flowering	-0.31	0.01	-	0.01	-0.06	0.05	-0.11	0.02	-0.06
Days to maturity	-0.04	0.28	0.01	-	-0.03	-0.09	0.12	-0.08	-0.04
Plant height	-0.02	0.02	-0.09	-0.06	-	-0.17	-0.13	-0.07	0.13
Pods on main raceme	0.36*	0.04	-0.05	-0.11	-0.09	-	-0.02	-0.03	0.16
Pods per plant	0.56**	0.05	0.06	-0.08	0.04	0.07	-	-0.01	-0.07
Pods length	-0.08	0.06	0.05	-0.01	-0.07	-0.11	0.08	-	0.08
Seeds per pod	0.32	-0.15	0.06	0.04	-0.07	-0.19	-0.02	-0.02	-

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

plant had significant positive genetic correlations with pods per plant. The other traits exhibited positive non significant or negative associations with seed yield. The direct effect of pods per plant on seed yield per plant was positive, and highly significant.

Conclusions

In conclusion, the divergence of the studied material represents solid basis for starting effective breeding program for increasing seed yield. Seed yield per plant had significant positive genetic correlations with pods per plant. The other traits exhibited positive non significant or negative associations with seed yield. The direct effect of pods per plant on seed yield per plant was positive, and highly significant. According to the present study, the positive association between oil content, and seed yield per plant indicate the possibility of improving these most important traits in rapeseed simultaneously.

Acknowledgements

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