

Research Article

Multivariate Regression Analyses of Yield Associated Traits in Rapeseed (*Brassica napus* L.) Genotypes

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Received 5 April 2014; Revised 26 July 2014; Accepted 14 August 2014; Published 24 August 2014

Academic Editor: Nnadozie Oraguzie

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The efficiency of a breeding program depends mainly on the direction of the correlation between yield and its components and the relative importance of each component involved in contributing to seed yield. The interrelationships of nine quantitative traits in 28 genotypes of spring oilseed rape (days to flowering, days to end of flowering, duration of flowering, days to maturity, pods per main raceme, pods length and pods per plant, and seed yield) were computed. Significant genotypic effects were found for phenological traits, yield components, and seed yield, indicating significant genetic differences among the genotypes. High broad sense heritability was estimated for phenological traits, seeds per pod, and seed yield, signifying high selection gain for improving these traits. Path coefficient analysis revealed that days to flowering and number of pods per plant had the highest direct effects on seed yield. Duration of flowering, number of branches, pods on main raceme, pods per plant, and seed yield had high genetic coefficient of variation. The results of factor analysis showed three factors including factor 1 (phenological traits), factor 2 (primary yield components), and factor 3 (secondary yield components). The results of stepwise regression analysis revealed that pods per plant, number of branches, and duration of flowering had considerable effects on seed yield.

1. Introduction

Improvement of seed yield in canola (*Brassica napus* L.) has been the main objective of canola breeders for many years [1, 2]. Seed yield is a quantitative trait, which is principally influenced by the environment and consequently has a low heritability [3, 4]. As a result, the response to direct selection for seed yield may be unpredictable, unless there is good control of environmental variation. Plant breeders are seldom interested in a single trait and therefore, there is the need to examine the relationships among different traits, especially between seed yield and other traits. As the number of independent variables influencing a particular dependent variable increases, a certain amount of interdependence is expected. In such situations, correlations may be inadequate to explain the associations in a way that will enable breeders to decide on a direct or indirect selection strategy [5]. The multivariate analyses, particularly factor and cluster analyses, are utilized for evaluation of a large number of accessions for different traits in a germplasm collection. Cluster analysis assigns genotypes into qualitative homogenous groups based on

response similarities and also assists in classifying genotypes. The method produces a dendrogram showing successive fusion of individuals. Greater heterotic effect is generated when clusters are divergent. Genetic diversity among the *Brassica* genotypes has been assessed by Choudhary and Joshi [6] using cluster analysis. The morphological characters, namely, days to flowering, plant height, secondary branches per plant, and 1000-seed weight, had a major contribution to genetic divergence [7, 8]. 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 [9–13].

The main applications of factor analytic techniques are to reduce the number of variables and to detect structure in the relationship between variables [14]. In plant breeding factor analysis is mainly applied as structure detection method, and sometimes it can be used as index selection for improving more than one trait. Factor analysis was used to determine structural factors related to growth trait and yield components and also to detect factors relating to environmental stress including drought resistance in *B. napus* [15].

The objectives of the present study were to estimate the genetic coefficient of variation, broad sense heritability, and the relationship among yield associated traits for improving seed yield in spring type rapeseed advanced lines.

2. Materials and Methods

The material under study consisted of 28 rapeseed (*B. napus* L.) genotypes which were selected based on different agronomic characters. The genotypes were planted in a randomized complete block design with three replications at Baykola Agriculture Research Station, located in Neka, Iran (53°13' E longitude and 36°43' N latitude, 15 m above sea level) during 2012-13. The plots consisted of four rows 5 m long and 30 cm apart. The distance between plants on each row was 5 cm resulting in approximately 400 plants per plot, which were sufficient for statistical analysis. Crop management including land preparation, crop rotation, fertilizer, and weed control followed standard practices in the local area. All plant protection measures were adopted to make the crop free from insects. Phenological traits including days to flowering, days to end of flowering, duration of flowering, and days to maturity were determined based on phenological stages of the genotypes in each plot. Pods per main raceme, pods length, and pods per plant were recorded using 10 randomly selected plants in each plot. Seed yield of two middle rows of each plot was adjusted to kg/ha.

Variance components were estimated from the mean squares (MS) in the analysis of variance [16]. The components of variance including error variance (VE), genotypic variance (VG), and phenotypic variance (VP) were estimated according to the following formula:

$$\begin{aligned} \text{VE} &= \text{MSE}, \\ \text{VG} &= \frac{(\text{MSG} - \text{MSE})}{r}, \\ \text{VP} &= \text{VG} + \text{VE}. \end{aligned} \quad (1)$$

Broad sense heritability (h^2) was estimated according to Khan et al. [17] as $h^2 = \text{VG}/\text{VE}$. The coefficient of variation was estimated as $\text{CV} = (\sqrt{\text{VG}})/\mu$ where μ is the mean of genotypes for each trait.

Pearson's correlation coefficients between the traits, path coefficient analysis, and factor analysis based on Varimax rotation matrix were done on the data. Principal components method analysis was used to extract factorial load of matrix and also to estimate the number of factors [14, 18]. The factors which had a root bigger than one were selected and were used to build the factorial coefficients matrix. All the calculations were performed using MS-Excel and SAS software version 9 [19].

3. Results and Discussions

3.1. Analysis of Variance. Significant mean square of genotypes were determined for the traits including days to flowering, duration of flowering, days to maturity, number of

branches, pods per main raceme, pods per plant, seeds per pod, and seed yield indicating significant genetic variation for these traits (Table 1). Generally these results are similar to those reported by Aytaç and Kinaci [8] and Sabaghnia et al. [20]. Broad sense heritability estimates ranged from 0.12 to 0.98 for plant height and days to flowering, respectively. High values of broad sense heritability estimates for the phenological traits, seeds per pod, and seed yield indicate that selection gain for improving these traits will be high. Aytac et al. [3] also reported high broad sense heritability estimates for yield components. Genetic coefficient of variation, an indicator of the genetic diversity of the genotypes, varied from 18.7 to 26.8 for days to maturity and seed yield, respectively (Table 2). A high value for genetic variation was detected for duration of flowering, pods per main raceme, pods per plant, and seed yield.

3.2. Genotypic Means. Days to flowering ranged from 79 to 119 days (Table 2). A significant positive correlation was detected between days to flowering and days to maturity (Table 3), which suggests that selection for this trait could be done for early maturity genotypes. The genotypes including genotype 3 (G3), G16, G18, G25, and G27 with low mean values would be preferred for improving days to flowering (Table 2). These genotypes had low mean values of days for maturity. In rapeseed, since flowering and seed formation occurred about the same time, genotypes showing high mean values for duration of flowering will be preferable. High mean value for duration of flowering suggests that the plant gets enough time and opportunity for seed formation, and genotypes G3, G8, G18, and G25 with high mean values would be considered suitable for improving this trait. For reducing pest damage and also facilitate second crop cultivation after rapeseed, early maturity would be an ideal trait for breeding *B. napus* L. and other related Brassica species. Plant height ranged from 150 to 181 cm. For ideotype breeding of rapeseed, low mean value of plant height is favored, and genotypes G6, G10, G12, and G19 would be suitable parents for this trait. Number of branches varied from 3.2 to 5.6. Since pods per plant were found significantly correlated with seed yield, the genotypes including G5, G14, G15, G19, and G21 would be suitable for improving this trait. Sharma [14] reported that pods per plant, seeds per plant, and 1000-seed weight traits were positively correlated with seed yield. Khan et al. [17] also reported a positive significant correlation between seed yield and plant height, pods per plant, seeds per pod, and pod length. The genotypes G14, G19, G21, G22, G23, and G24 with high mean values for seed yield also had high mean values for some other yield components.

3.3. Multivariate Analyses. Path coefficient analysis revealed that days to flowering and number of pods per plant had the highest positive effects on seed yield but duration of flowering and pods on main raceme had a significant negative effect on seed yield (Table 4). Marjanović-Jeromela et al. [21] studied 30 rapeseed varieties and demonstrated that pods per plant have the highest correlation with seed yield. Sheikh et al. [22] found high heritability estimates coupled with high genetic

TABLE 1: Analyses of variance (ANOVA) and broad sense heritability estimates for the traits studied.

S.O.V	Df	Mean squares								
		Days to flowering	Duration of flowering	Days to maturity	Plant height	Number of branches	Pods per main raceme	Pods per plant	Seeds per pod	Seed yield
Replication	2	2.3	16.9	3.0	938.9**	7.72**	1074**	4005**	216.3**	973157*
Treatments	27	161.1**	219.9**	51.6**	156.1	1.03**	98**	561**	16.0**	810934**
Error	54	1.0	13.9	3.7	111.2	0.31	32.2	175.1	3.6	202709
Broad sense heritability		0.98	0.83	0.81	0.12	0.44	0.41	0.42	0.53	0.50

SOV: source of variation.

*,** Significant at $P < 0.05$ and 0.01, respectively.

TABLE 2: Mean comparison of the rapeseed genotypes for phenological traits, plant height, yield components, and seed yield.

Genotypes	Traits								
	Days to flowering	Duration of flowering	Days to maturity	Plant height (cm)	Number of branches	Pods per main raceme	Pods per plant	Seeds per pod	Seed yield (kg/ha)
1-Zar08-1	106	68	213	168	4.9	52	90	24	1952
2-Zar01-3	106	64	213	176	4.9	41	72	22	2171
3-Zar01-7	97	77	206	169	5.3	37	77	24	1893
4-Zar01-8	104	61	206	160	4.6	47	72	23	2493
5-22B01-14	108	61	212	163	5.1	38	110	24	3094
6-22B01-15	111	54	211	154	4.3	31	87	18	3053
7-22B01-16	109	65	211	168	3.9	39	102	19	3070
8-Forn08-1	103	69	206	157	4.1	35	101	18	2194
9-Forn01-7	106	68	208	165	4.3	36	70	19	1846
10-Forn08	111	51	215	150	4.6	42	103	18	2704
11-Mod04	108	68	213	160	3.8	34	71	19	2445
12-Mod05	106	58	209	154	3.9	35	82	19	2484
13-Mod06	117	51	214	181	5.6	47	81	22	2322
14-Mod08	102	68	208	172	4.6	41	109	22	3113
15-Mod09	104	68	212	158	5.2	34	107	22	2859
16-Mod010	99	67	205	167	4.7	40	93	22	2274
17-Mod011	103	67	209	163	5.1	34	83	19	2126
18-Mod014	97	68	204	165	5.1	42	90	20	2195
19-Mod01	109	50	210	152	4.6	32	107	21	3338
20-Mod02	110	54	211	166	3.2	32	82	20	2830
21-Zar01	110	54	212	163	4.8	40	114	20	3415
22-Zar03	105	61	209	161	3.3	32	69	18	3104
23-Zar025	103	61	213	167	4.5	43	102	21	3664
24-Zar029	109	58	215	170	4.8	36	101	19	3582
25-OKP08	79	82	201	172	4.9	39	84	17	2152
26-Sarigol	119	49	221	171	4.4	45	100	19	2427
27-Hyola401	97	60	210	167	5.2	47	91	26	2764
28-RGS003	104	47	213	163	4.6	49	85	24	2487
LSD _(α=0.05)	0.94	3.52	1.81	9.94	0.52	5.35	12.48	1.79	424.48
LSD _(α=0.01)	1.25	4.68	2.41	13.22	0.70	7.12	16.59	2.38	564.56
Genetic coefficient of variation	19.8	23.0	18.7	19.1	22.4	23.4	23.8	21.6	26.8

TABLE 3: Pearson's correlations between pairs of traits in rapeseed.

Traits	(1) Days to flowering	(2) Duration of flowering	(3) Days to maturity	(4) Plant height	(5) Number of branches	(6) Pods per main raceme	(7) Pods per plant	(8) Seeds per pod	(9) Seed yield
(1) Days to flowering	1								
(2) Duration of flowering	-0.75**	1							
(3) Days to maturity	0.80**	-0.68**	1						
(4) Plant height	-0.11	0.23	0.06	1					
(5) Number of branches	-0.21	0.16	-0.04	0.35	1				
(6) Pods per main raceme	-0.02	-0.14	0.21	0.44*	0.46*	1			
(7) Pods per plant	0.16	-0.22	0.25	-0.16	0.23	0.04	1		
(8) Seeds per pod	-0.07	-0.04	0.05	0.28	0.52**	0.56**	0.04	1	
(9) Seed yield	0.29	-0.45*	0.33	-0.21	-0.21	-0.23	0.58**	-0.08	1

*,** Significant at $P < 0.05$ and 0.01 , respectively.

TABLE 4: Direct (along the diagonal) and indirect (above and below the diagonal) effects of yield components on seed yield.

Traits	1	2	3	4	5	6	7	8
(1) Days to flowering	0.40*	0.41	0.16	-0.02	0.06	0.01	0.09	-0.01
(2) Duration of flowering	0.30	-0.54**	-0.14	0.04	-0.05	0.06	-0.13	-0.01
(3) Days to maturity	-0.32	0.36	0.20	0.01	0.01	-0.09	0.15	0.01
(4) Plant height	0.04	-0.12	0.01	0.18	-0.11	-0.19	-0.09	0.05
(5) Number of branches	0.08	-0.09	-0.01	0.06	-0.29	-0.19	0.13	0.09
(6) Pods per main raceme	0.01	0.07	0.04	0.08	-0.14	-0.42*	0.02	0.11
(7) Pods per plant	-0.06	0.12	0.05	-0.03	-0.07	0.02	0.58**	0.01
(8) Seeds per pod	0.03	0.02	0.01	0.05	0.05	0.08	0.11	0.17

*,** Significant at $P < 0.05$ and 0.01 , respectively.

TABLE 5: The results of stepwise regression analysis in which 3 out of 9 studied traits were selected.

Step	Variable entered	Partial R-square	Model R-square	F-test
1	X7: pods per plant	0.34	0.34	13.4**
2	X5: number of branches	0.12	0.46	5.7*
3	X2: duration of flowering	0.07	0.56	3.3

Final regression model: Y (seed yield) = $2835.9 - 16.4X7 - 269.6X5 + 22.5X2$.

*,** Significant at $P < 0.05$ and 0.01 , respectively.

advance for seed yield per plant, pods per plant, and seed weight in rapeseed (*B. campestris*) genotypes.

The results of stepwise regression analysis indicated that pods per plant, number of branches, and duration of flowering had considerable effects on seed yield (Table 5).

The results of factor analysis revealed three factors for the nine traits studied (Table 6). The eigenvalues for factors 1, 2, and 3 were 2.96, 2.35, and 1.33, respectively. The cumulative variation for these factors was 0.74 while the proportion of variation contributed by each factor was 0.32, 0.26, and 0.15, respectively. Factor 1 "could be regarded as the main factor (phenological traits)" and include days to flowering, duration of flowering, and days to maturity which had high coefficients on the factor loading. The second factor includes yield components such as number of branches, pods on

main raceme, and seeds per pod. The third factor includes second yield components such as pods per plant and seed yield. In earlier studies [15, 18] factor analyses were used to determine structural factors related to growth trait and yield components and also for detecting factors relating to environmental stress including drought resistance in *B. napus* L.

In general, phenological traits, seeds per pod, and seed yield were more heritable than the other traits. Due to the significant positive correlation of yield components with seed yield these traits can be used as indirect selection criteria for improving seed yield. The low value of genetic coefficient of variation for days to maturity suggests that for improving this trait the correlated trait including days to flowering can be used as indirect selection criterion.

TABLE 6: Factor analysis of all traits studied in rapeseed genotypes.

Traits	Factor loadings		
	1	2	3
(1) Days to flowering	0.92	-0.11	0.05
(2) Duration of flowering	-0.86	0.04	-0.23
(3) Days to maturity	0.90	0.13	0.13
(4) Plant height	-0.03	0.62	-0.32
(5) Number of branches	-0.23	0.79	0.19
(6) Pods per main raceme	0.18	0.83	-0.13
(7) Pods per plant	0.09	0.13	0.91
(8) Seeds per pod	0.01	0.78	0.07
(9) Seed yield	0.31	-0.23	0.77
Eigen value	2.96	2.35	1.33
Portion	0.32	0.26	0.15
Cumulative	0.32	0.59	0.74

Conflict of Interests

The author declares that there is no conflict of interests regarding the publication of this paper.

Acknowledgments

The author wishes to thank Agricultural and Natural Resources Research Center of Mazandaran and Seed and Plant Improvement Institute (SPII) for providing genetic materials and facility for conducting this experiment.

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