



Multivariate analysis of some important quantitative traits in rapeseed (*Brassica napus*) advanced lines

V Rameeh

Agriculture and Natural Resources Research Center of Mazandran, Sari, Iran

Corresponding author: vrameeh@yahoo.com

(Received: 12 March 2014; Revised: 19 April 2014; Accepted: 25 June 2014)

Abstract

Development of new rapeseed (*Brassica napus* L.) cultivars requires efficient tools to monitor traits relationship in a breeding program. Twenty four rapeseed genotypes including 2 cultivars and 22 advanced lines were evaluated based on randomized complete block design with three replications. Significant genotypes effects were exhibited for phenological traits, plant height, yield components and seed yield, indicating significant genetic differences among the genotypes. High broad sense heritability were estimated for phenological traits, pods on main axis and seed yield signifying selection gain for improving these traits will be high. Duration of flowering and pods on main axis had high value of genetic coefficient of variation. The results of factor analysis exhibited four factors including sink factor (pod per plant, pods length and seed yield), fixed capital factor (phenological traits), secondary fixed capital factor (duration of flowering) and metric factor (plant height). The results of stepwise regression analysis revealed that plant height and pods per plant had more decreasing and increasing effects on seed yield, respectively. On the basis of cluster analysis, the genotypes were classified in four groups and the group with high seed yield had high mean value of pods per plant.

Key words: Cluster analysis, rapeseed, stepwise regression

Introduction

Rapeseed is grown as a high quality source of vegetable oil for the food industry and supplies protein to the animal feed market (Khachatourians *et al.*, 2001; Mahasi and Kamundia, 2007). It is also becoming a popular oilseed crop in Iran, including north provinces, due to its high oil and protein contents. Improvement of seed yield in rapeseed (*Brassica napus* L.) has been the primary objective of rapeseed breeders for many years. To increase the yield, study of direct and indirect effects of yield components provides the basis for its successful breeding program and hence the problem of yield increase can be more effectively tackled on the basis of performance of yield components and selection for closely related characters (Aytac *et al.*, 2008; Marjanovic-Jeromela *et al.*, 2009). The multivariate analysis particularly factor and cluster analyses are utilized for evaluation of germplasm when studying various

traits and a large number of accessions. Cluster analysis assigns genotypes into qualitative homogenous groups based on response similarities and also assists to classify genotypes. The method among group means and produces a dendrogram showing successive fusion of individuals. Greater heterotic effect is generated when clusters are divergent. Genetic diversity among the Brassica genotypes was assessed by Choudhary and Joshi (2001) using cluster analysis. The morphological characters viz., days to flowering, plant height, secondary branches per plant and 1000-seed weight contributed maximum towards genetic divergence (Leilah and Al-Khatee 2005; Aytac *et al.*, 2009). 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 (Khan *et al.*, 2006; Ivanovska *et al.*, 2007; Basalma, 2008; Hashemi *et al.*, 2010; Semahegn Belete, 2011). Zang and Zhou (2006) reported that pods per plant,

seeds per plant and 1000-seed weight traits were positively correlated with seed yield. On the other hand, Length of pod was negatively correlated with seed yield. Jeromela *et al.* (2007) studied 30 rapeseed varieties and demonstrated that pods per plant have the highest correlation with seed yield. Khan *et al.* (2008) also reported the positive significance correlation between seed yield and plant height, pods per plant, seeds per pod and pod length. Sheikh *et al.* (1999) found high heritability estimates coupled with high genetic advanced for seed yield per plant, pods per plant and seed weight in rapeseed (*B. rapa*) genotypes. They also reported positive correlation of all the yield components with seed yield. Genetic variability is pre requisite for improving any crop plant.

The main applications of factor analytic techniques are to reduce the number of variables, and to detect structure in the relationship between variables, that is to classify variable (Sharma, 1996). 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 (2010) and also it was used for detecting factors relating to environmental stress including drought resistance in *B. napus* (Naderi and Emam, 2010).

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

Materials and Methods

The material under study consisted of 24 *B. napus* genotypes which were selected based on different agronomic characters. The genotypes were evaluated based on 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 2011-12. 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 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 insects. Phenological traits including days to flowering, days to end of flowering, duration of flowering and days to maturity were determined based of phenological stages of the genotypes in each plot. Pods per main axis, pods length and pods per plant were recorded based on 10 randomly plants of 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.*, 2010). The component of variance including error variance (VE), genotypic variance (VG) and phenotypic variance (VP) were estimated according to the following formula:

$$E = \text{MSE}$$

$$VG = (\text{MSG} - \text{MSE})/r$$

$$VP = VG + VE$$

Broad sense heritability (h^2) was estimated according to Singh *et al.*, (1993) as: $h^2 = VG/VE$. The coefficient of variation was estimated as $CV = (\sqrt{VG})/\mu$ in which μ is the mean of genotypes for each trait.

The correlation coefficients between the traits were estimated and then factor analysis on the base of major factors analysis and varimax rotations was done on the data. Principal components method analysis was used to extract factorial load of matrix and also to estimate the number of factors (Sharma, 1996). Therefore, the factors which had a root bigger than one were selected and were used to form factorial coefficients matrix. By means of varimax rotation, rotation was done on the major factorial loads matrix and the matrix of rotated factorial loads was obtained (Sharma, 1996; Rameeh, 2010). The average-linkage-between-groups method of cluster analysis, often aptly called

UPGMA (un weighted pair-group method using arithmetic averages) was used, in which defines the distance between two clusters as the average of the distances between all pairs of cases in which one member of the pair is from each of the clusters.. All the analyses were performed using MS-Excel and SAS software version 9 (SAS INSTITUTE INC, 2004).

Results and Discussion

Analysis of variance

Significant mean square of genotypes were determined for the traits including days to flowering, days to end of flowering, duration of flowering, days to maturity, plant height, pods per main axis, pods per plant, pods length, 1000-seed weight and seed yield indicating significant genetic variation for these traits (Table 1). These results are the same as those reported by Aytac and Kinaci (2009) and Sabaghnia *et al.* (2010). Broad sense heritability estimates ranged from 0.21 to 0.94 related to pods per plant and days to flowering, respectively. High broad sense heritability estimates for phenological traits and seed yield indicating selection gain for improving these traits will be high. In earlier study (Aytaç *et al.*, 2008) was reported high broad sense heritability estimates for yield components. Genetic coefficient of variation which is indicating the genetic diversity of the genotypes, was varied from 0.05 to 43.66 related to pods per plant and duration of flowering, respectively (Table 2). The high value of genetic variations of the genotypes was detected for pods length, pods on main axis and duration of flowering.

Correlation among the traits and means of the genotypes

Means value of days to flowering ranged from 151 to 178 days in G1 and G6, respectively (Table 2). Significant positive correlation was detected between days to flowering and days to maturity (Table 3), therefore selection for low means value of this trait is early and direct selection for early maturity genotypes. The genotypes including G2, G20, G9, G13, G14, G19, G22 and G24 with low means value of days to end of flowering preferable. The genotypes G2, G9, G13, G22 and G24 with low mean value of days to maturity were detected as

Table 1- Randomize complete block (RCBD) analysis of variance for the studied traits

S.O.V.	df	MS									
		Days to flowering	Days to end of flowering	Duration of flowering	Days to maturity	Plant height	Pods per main axis	Pods per plant	Pods length	1000 seed weight	Seed yield
Replication	2	0.10	3.4*	2.6	1.8	935.5***	20.4	4560.6**	0.45	2.31**	2474595**
Treatments	23	107.7**	69.1**	79.1**	57.4**	420.6**	263.7**	584.9**	1.13**	0.11**	460219**
Error	46	2.40	0.75	3.2	3.5	140.1	68.13	324.43	0.39	0.05	70560
Broad-sense heritability	0.94	0.97	0.89	0.84	0.40	0.49	0.21	0.39	0.2+9	0.65	

*, **, Significant at p=0.50 and 0.01, respectively.

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

Traits/ Genotypes	Days to flowering	Days to end of flowering	Duration of flowering	Days to maturity	Plant height (cm)	Pods per main axis	Pods per plant	Pods length	1000 seed weight (g)	Seed yield (kg/ha)
1-Fornex/401(G1)	151	206	55	238	147	68	155	6.97	3.88	3056
2-Zarfam/401(G2)	159	197	39	224	141	45	116	5.03	3.39	2110
3-Zarfam/308(G3)	162	199	37	228	143	70	124	5.17	3.87	2128
4-Fornex/401(G4)	164	206	42	237	126	56	142	6.08	3.93	2928
5-Fornex/308(G5)	166	204	38	233	111	40	134	6.03	3.64	2956
6-Folesta/308(G6)	178	211	33	239	142	51	138	5.04	3.37	2805
7-Modena/308(G7)	166	207	41	233	143	52	153	6.10	3.81	2978
8-Opera/308(G8)	176	208	32	238	129	39	121	5.20	3.60	1906
9-Slm046/401(G9)	166	198	32	227	143	59	135	5.29	3.57	2478
10-Zarfam/401(G10)	166	200	34	231	154	41	133	4.84	3.68	2217
11-Zarfam/401(G11)	168	204	36	232	149	59	148	5.53	3.75	2733
12-Slm046/401(G12)	168	206	38	231	138	38	138	5.45	3.57	2333
13-Okapi/308(G13)	169	198	29	226	122	50	125	4.88	3.78	2278
14-Okapi/308(G14)	169	198	29	230	115	50	115	4.59	3.70	2370
15-Okapi/308(G15)	170	206	36	232	127	37	114	5.27	3.53	1767
16-Slm046/308(G16)	168	204	36	232	124	47	124	5.92	3.84	2206
17-Folesta/401(G17)	177	211	33	240	139	44	116	4.71	3.44	2333
18-Sarigol(G18)	172	208	36	235	134	42	125	4.92	3.74	2247
19-Hsari(G19)	165	198	33	230	133	59	155	6.00	3.93	2924
20-Hyola401(G20)	160	196	36	227	121	40	132	5.53	3.62	2839
21-RGS003(G21)	161	199	38	231	136	49	119	5.24	4.07	2586
22-Zodras22(G22)	165	198	34	228	147	63	152	6.32	3.65	2956
23-Zodras13(G23)	170	208	38	236	156	45	127	4.81	3.66	2117
24-Zafar(G24)	165	198	33	229	134	52	155	6.25	4.10	3015
Genetic coefficient of variation	5.94	2.90	43.66	2.74	6.35	22.22	0.05	9.24	4.19	1.16
LSD _(df=0.05)	2.53	1.41	2.92	3.06	19.33	13.48	29.4	1.02	0.37	433.8
LSD _(df=0.01)	3.36	1.88	3.89	4.06	25.71	17.93	39.1	1.36	0.49	576.9

suitable genotypes for improving this trait. Due to low mean value of genetic coefficient of variation for days to end of flowering, selection gain for improving this trait will be low. In rapeseed, flowering and seed formation are to some extent the same time, therefore high means value of duration of flowering will be preferable. High mean value of duration of flowering make possible for plant to have enough opportunity for seed formation, therefore correlation between duration of flowering and 1000-seed weight was positive. The genotypes G1, G4 and G7 with high mean value of duration of flowering were considered as suitable genotypes for improving this trait. For reducing some of pests damages and also having enough opportunity for second crop cultivation after rapeseed, early maturity is ideotype trait for breeding *B. napus* and other related *Brassica* species. Plant height ranged from 111 to 156 cm in G5 and G23, respectively. For ideotype breeding of rapeseed low mean value of plant height is favored, therefore G5, G14 and G20 were merit genotypes for this trait. Pods per main axis was significant correlated with seed yield, therefore the genotypes G1, G3, G4, G11 and G19 were suitable for improving this trait. The means value of pods per plant as the main important yield component were high in the genotypes G1, G7, G19 and G24. The genotypes including G1, G7, G19 and G24 had high means value of pods length and 1000-seed weight. Zhang and Zhou (2006) reported that pods per plant, seeds per plant and 1000-seed weight traits were positively correlated with seed yield. Jeromela *et al.* (2007) studied 30 rapeseed varieties and demonstrated that pods per plant have the highest correlation with seed yield. Khan *et al.* (2006) also reported the positive significance correlation between seed yield and plant height, pods per plant, seeds per pod and pod length. The genotypes G1, G4, G7, G19 and G24 with high means value of seed yield (4089, 4117, 4094 and 4289 kg/ha, respectively) had high mean value of the some of yield components.

Multivariate analyses

The results of stepwise regression analysis indicated that plant height and pods per plant had important effects on seed yield (Table 4). Plant height and pods per plant had decreasing and increasing effects on seed yield, respectively and final

Table 3: Correlation among the traits in rapeseed

Traits	1-Days to flowering	2-Days to end of flowering	3-Duration of flowering	4-Days to maturity	5-Plant height (cm)	6-Pods per main axis	7-Pods per plant	8- Pods length	9-1000 seed weight (g)	10-Seed yield (kg/ha)
1-Days to flowering	1									
2-Days to end of flowering	0.57**	1								
3-Duration of flowering	-0.64**	0.27	1							
4-Days to maturity	0.45*	0.89**	0.31	1						
5-Plant height	-0.06	0.18	0.24	0.12	1					
6-Pods per main axis	-0.44*	-0.28	0.26	-0.13	0.34	1				
7-Pods per plant	-0.21	-0.05	0.32	0.04	0.31	0.52**	1			
8- Pods length	-0.56**	-0.06	0.59**	0.04	-0.01	0.45*	0.78**	1		
9-1000-seed weight	-0.44*	-0.31	0.22	-0.11	-0.09	0.44*	0.40	0.47*	1	
10-Seed yield	-0.38	-0.14	0.31	0.05	-0.02	0.46*	0.81**	0.72**	0.39	1

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

regression model detected as $Y = 449.89 + 9X_5 - 25.41X_7$ in which X_5 and X_7 were plant height and pods per plant, respectively.

The results of factor analysis based on minimum

eigenvalue revealed four factors for 10 studied traits (Table 5). The eigenvalues for factor one to four were 3.99, 3.32, 1.17 and 1.06, respectively. The cumulative variation for these factors was 0.86 and

Table 4: The results of stepwise regression analysis of 10 studied traits.

Step	Variable entered	Partial R-square	Model R-square	F-test
1	X_5 :plant height	0.66	0.66	43.77**
2	X_7 :pods per plant	0.08	0.74	6.46*

Final regression model: $Y(\text{seed yield}) = 449.87 - 9X_5 + 25.41X_7$

Table 5: Factor analysis for 10 studied traits in rapeseed genotypes.

Traits	Factor loadings			
	1	2	3	4
Days to flowering	-0.30	0.54	-0.78	-0.07
Days to end of flowering	-0.13	0.97	0.01	0.07
Duration of flowering	0.22	0.29	0.91	0.15
Days to maturity	0.06	0.95	0.05	0.01
Plant height	-0.01	0.13	0.08	0.95
Pods per main axis	0.57	-0.28	0.15	0.52
Pods per plant	0.90	0.05	0.06	0.29
Pods length	0.80	0.04	0.47	-0.06
1000-seed weight	0.58	-0.28	0.24	-0.13
Seed yield	0.91	0.01	0.09	-0.02
Eigen value	3.99	2.32	1.17	1.06
Portion	0.39	0.23	0.12	0.11
Cumulative	0.40	0.63	0.75	0.86

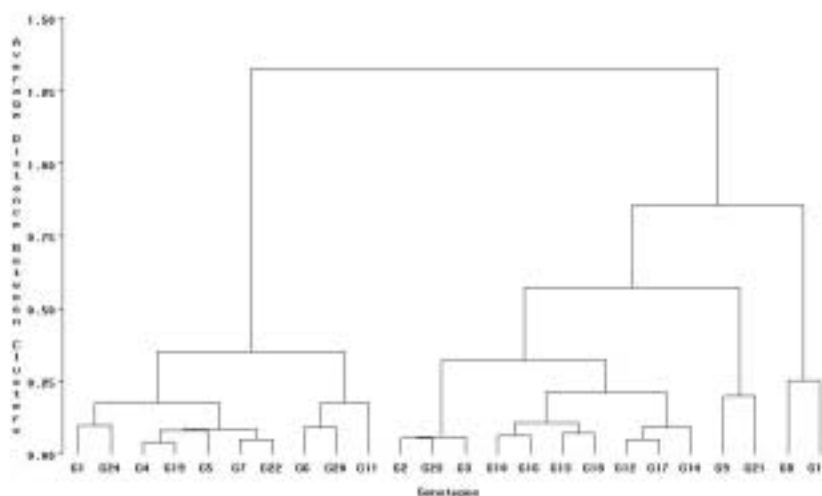


Fig 1: Clustering dendrogram of 24 rapeseed genotypes (the genotypes code as in Table 2) based on 10 studied traits.

Table 6: The means of clustering groups for 10 studied traits.

Traits Clustering groups	Days to flowering	Days to end of flowering	Duration of flowering	Days to maturity	Plant height (cm)	Pods per main axis	Pods per plant	Pods length (cm)	1000 seed weight (g)	Seed yield (kg/ha)
C1	163	202	39	232	134	54	147	6.09	3.81	2931
C2	168	203	35	231	137	47	124	5.03	3.67	2234
C3	164	199	35	229	139	54	127	5.27	3.82	2532
C4	173	207	34	235	128	38	118	5.23	3.57	1836

also its portions for factor one to four were 0.39, 0.23, 0.12 and 0.11, respectively. Factor one was detected as sink factor in which, pod per plant, pods length and seed yield had high coefficients for factor loading. The second, third and fourth factors were named fixed capital factor (phenological traits), secondary fixed capital factor (duration of flowering) and metric factor (plant height), respectively. In earlier studies (Naderi and Emam, 2010; Rameeh, 2010) factor analysis were used to determine structural factors related to growth trait and yield components and also it was used for detecting factors relating to environmental stress including drought resistance in *B. napus*.

The results of cluster analysis for 10 studied traits in 24 genotypes are presented in Figure 1 and Table 6. All the genotypes were classified in four groups with different means value of the traits. The high seed yield genotypes with high mean value of pods per plant were classified in group1 (C1). Group 2 (C2) and group 4(C4) had 2234 and 1836 kg ha⁻¹ of seed yield, respectively. Genetic diversity among the Brassica genotypes was assessed by Choudhary and Joshi (2001) using cluster analysis.

In general the phenological traits, pods on main axis and seed yield were more heritable than the other traits. Due to significant positive correlation of yield components with seed yield these traits can be used as indirect selection for improving seed yield. Days to maturity had low value of genetic coefficient of variation and therefore for improving this trait, the correlated traits viz. days to flowering and days to end of flowering can be used. Cluster analysis can be used as suitable method for classifying the high yield genotypes.

Acknowledgements

The authors wish to thanks Agricultural and Natural Resources Research Center of Mazandaran and Seed and Plant Improvement Institute (SPII) for providing genetic materials and facility for conducting the experiment.

References

- Aytac Z, Kinaci G and Kinaci E. 2008. Genetic variation, heritability and path analysis of summer rapeseed cultivars. *J Appl Biol Sci* 2: 35-39.

- Aytac Z and Kýnaci G. 2009. Genetic variability and association studies of some quantitative characters in winter rapeseed (*B. napus* L.). *Afric J Biotechnol* **8**: 3547-3554.
- Basalma D. 2008. The correlation and path analysis of yield and yield components of different winter Rapeseed (*B. napus* ssp. *oleifera* L) cultivars. *Res J Agri Biol Sci* **4**: 120-125.
- Choudhary BR and Joshi P. 2001. Genetic diversity in advanced derivatives of *Brassica* interspecific hybrids. *Euphytica* **121**: 1-7.
- Friedt W, Snowdon R, Ordon F and Ahlemeyer V. 2007. Plant Breeding: assessment of genetic diversity in crop plants and its exploitation in Breeding. *Progress in Bot* **168**: 152-177.
- Hashemi AS, Nematzadeh GA, Babaeian JN and Ghasemi CO. 2010. Genetic evaluation of yield and yield components at advanced generations in rapeseed (*B. napus* L). *Afric J Agric Res* **5**: 1958-1964.
- Ivanovska S, Stojkovski C, Dimov Z, Marjanovic-Jeromela A, Jankulovska M and Jankuloski LJ. 2007. Interrelationship between yield and yield related traits of spring Canola (*B. napus* L) genotypes. *Genetika* **39**: 325-332.
- Jeromela A, Marinkovic R, Mijic A, Jankulovska M and Zdunic Z. 2007. Interrelationship between oil yield and other quantitative traits in rapeseed (*B. napus* L). *J Central Eur Agric* **8**: 165-170.
- Khachatourians GG, Summer AK and Phillips PWB. 2001. An introduction to the history of canola and the scientific basis for innovation. CABI, London.
- Khan FA, Ali S, Shakeel A, Saeed A and Abbas G. 2006. Correlation analysis of some quantitative characters in *B. napus*. *J Agric Res* **44**: 7-14.
- Khan S, Farhatullah I and Khallil H. 2008. Phenotypic correlation analysis of elite F3:4 *Brassica* populations for quantitative and qualitative traits. *ARPN J Agric Biol Sci* **3**: 38-42.
- Leilah AA and Al-Khateeb SA. 2005. Yield analysis of canola (*B. napus* L) using some statistical procedures. *Saudi J Bio Sci* **12**: 103-113.
- Mahasi MJ and Kamundia JW. 2007. Cluster analysis in rapeseed (*B. napus* L). *Afric J Agri Res* **2**: 409-411.
- Marjanovic-Jeromela A, Kondic-Spika A, Saftic-Pankovic D, Marinkovic R and Hristov N. 2009. Phenotypic and molecular evaluation of genetic diversity of rapeseed (*B. napus*) genotypes. *Afric J Biotechnol* **8**: 4835-4844.
- Naderi R and Emam Y. 2010. Interrelationships among grain yield and related characters of four oilseed rape (*B. napus* L) cultivars under drought stress conditions. *Desert* **15**: 133-138.
- Rameeh V. 2010. Combining ability and factor analysis in F₂ diallel crosses of rapeseed varieties. *Plant Breed Seed Sci* **62**: 73-83.
- Sabaghnia N, Dehghani H, Alizadeh B and Mohghaddam M. 2010. Interrelationships between seed yield and 20 related traits of 49 canola (*B. napus* L) genotypes in non-stressed and water-stressed environments. *Spanish J Agril Res* **8**: 356-370.
- SAS Institute INC. 2004. SAS/STAT user's guide. Version 9. Fourth Edition. Statistical Analysis Institute Inc., Cary North Carolina.
- Semahegn Belete Y. 2011. Genetic variability, correlation and path analysis studies in Ethiopian mustard (*B. carinata* A Brun) Genotypes. *Int J Plant Breed Genet* **5**: 328-338.
- Sharma S. 1996. Applied multivariate techniques. 1st ed. John Wiley and Sons, New York, pp. 493.
- Sheikh FA, Rather AG and Wani SA. 1999. Genetic variability and inter-relationship in toria (*B. campestris* L var. Toria). *Adv Plant Sci* **12**: 139-143.
- Singh M, Ceccarelli S and Hamblin J. 1993. Estimation of heritability from varietal trials data. *Theor Appl Genet* **86**: 437-441.
- Zhang G and Zhou W. 2006. Genetic analysis of agronomic and seed quality traits of synthetic oilseed *B. napus* produced from interspecific hybridization of *B. campestris* and *B. oleracea*. *J Genet* **85**: 45-51.