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Correlation and factor analyses of quantitative traits in rapeseed (*Brassica napus* L.)

V. Rameeh

Correspondence address to: Valiollah Rameeh, Agriculture and Natural Resources Research Center of Mazandran, Sari, Iran.
E-mail: valvandi225@yahoo.com

***Abstract* – Improvement of new rapeseed (*Brassica napus* L.) cultivars requires efficient tools to monitor trait relationship in a breeding program. Twenty rapeseed genotypes including 4 cultivars and 16 advanced lines were evaluated based on randomized complete block design with three replications. Significant genotypes effect were exhibited for phenological traits, plant height, seed yield and yield components except seeds per pod. High broad sense heritability estimates for phenological traits, plant height, pods per plant, 1000-seed weight and seed indicating selection gain for improving these traits will be high. 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. The results of factor analysis revealed three factors including fixed capital factor (phenological traits), sink factor (pod per plant, seeds per pod and seed yield) and secondary yield components (pods per main axis and 1000-seed weight) for 10 studied traits. On the basis of scattering of the genotypes based on their scores for three factors, the genotypes G19, G18, G15, G10, G8 and G4 were classified as the same group and all of these had high seed yield. Scattering of genotypes based on their scores for related factors can be used as suitable method for grouping and classifying the genotypes for more important yield associated traits.**

Keywords – Breeding program, Coefficient of variation, Factor analysis and Heritability.

INTRODUCTION

Oilseed rape, from *Brassica* genus, provides a convenient alternative in cereal-based agricultural systems, for its broad leaves and capacity to be a break crop in continuous run of cereals [11]. 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 canola (*Brassica napus* L.) has been the primary objective of canola breeders for many years. Average yield of rapeseed is very low compared to its genetic potential. 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 [1, 2, 3]. Different statistical techniques have been used in modeling crops yield, including correlation, regression, path analysis, factor analysis, principal components and cluster analysis [3, 14]. 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 [1, 5, 7, 9, 12, 15,1 6, 23]. Seed yield is also a complex character that can be determined by several components reflective 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. Zang and Zhou [27] 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. [10] studied 30 rapeseed varieties and demonstrated that pods per plant have the highest correlation with seed yield. Khan et al. [12] also reported the positive significance correlation between seed yield and plant height, pods per plant, seeds per pod and pod length. Sheikh et al. [25] found high heritability estimates coupled with high genetic advanced for seed yield per plant, pods per plant and seed weight in rapeseed (*Brassica campestris*) 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 information about the nature and extent of variation coupled with the knowledge of character association are help full for improving the seed yield through selection. Heritability and genetic advance of seed yield and its components help to assess the genetic gain that can be obtained by selection.

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 [24]. 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 [20] and also it was used for detecting factors relating to environmental stress including drought resistance in *Brassica napus* [18].

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 analysis.

MATERIALS AND METHODS

The material under study consisted of 20 rapeseed (*Brassica napus* L.) 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 2010-11. 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 raceme 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 [26]. The component of variance including error variance (VE), genotypic variance (VG) and phenotypic variance (VP) were estimated according to the following formula:

VE= MSE
VG= (MSG-MSE)/r
VP= VG+VE

Broad sense heritability (h2) was estimated according to Singh *et al.*, (1993) as: h2=VG/VE. The coefficient of variation was estimated as CV=($\sqrt{VG}$)/μ 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 [24]. 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 [20, 24]. Also Eigen values, percent variance, variance and cumulative percentage share of each of the extracted factors were calculated. All the analyses were performed using MS-Excel and SAS software version 9 [22].

RESULTS AND DISCUSSIONS

1-*Analysis of variance*

Significant mean square of genotypes 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, 1000-seed weight and seed yield indicating significant genetic variation for these traits (Table 1). These results are the same as those reported by Ali, et. al., [2] and Sabaghnia, et. al., [21]. Broad sense heritability estimates ranged from 0.05 to 0.99 related to seeds per pod and days to flowering, respectively. High broad sense heritability estimates for phenological traits, plant height, pods per plant, 1000-seed weight and seed indicating selection gain for improving these traits will be high. In earlier studies [2, 3, 4, 21] were 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 2.20 to 19.9 related to days to maturity and pods per main axis, respectively (Table 2). The high value of genetic variations of the genotypes were detected for days to flowering, duration of flowering and pods per main axis.

[Place of Table 1]
[Place of Table 2]

2- *Mean performances of the genotypes*

Means value of days to flowering ranged from 72 to 144 days in G5 and G12, 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 has reduction effect on days to maturity as ideotype form. The genotypes including G5, G17 and G15 with low means value of days to maturity are preferable. The genotypes G5, G6 and G15 with low means value of days to end of flowering were detected as 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. 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 G5, G14, G16 and G17 with high mean value of duration of flowering (84.33, 82.67, 80.33 and 84.67 days, respectively) were considered as suitable genotypes for improving this trait. For reducing some of pests damages and also having enough opportunity for second crop after rapeseed cultivation, early maturity is the main goal of ideotype breeding of *Brassica napus* L. and other related brassica specious. The genotypes G5, G10 and G15 with the low value of days to maturity were favorable for early maturity. Plant height ranged from 127.87 to 214.33 cm in G7 and G12, respectively. For ideotype breeding of rapeseed low mean value of plant height is favored, therefore merit G6, G7 and G17 were merit genotypes for this trait. Pods per main axis was significant correlated with seed yield, therefore the genotypes G3, G10, G17, G19 and G20 were suitable for improving this trait. The means value of pods per plant as the main important yield component were high in the genotypes G4, G10, G15, G18 and G19. The genotypes including G2, G5, G9 and G10 had high means value of seeds per pod and 1000-seed weight. Zhou [27] 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. [10] studied 30 rapeseed varieties and demonstrated that pods per plant have the highest correlation with seed yield. Khan et al. [12] also reported the positive significance correlation between seed yield and plant height, pods per plant, seeds per pod and pod length. The genotypes G8, G10, G15 and G19 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.

3-*Factor analysis*

The results of factor analysis based on minimum eigenvalue revealed three factors for 10 studied traits (Table 4). The eigenvalues for factor one to three were 4.55, 2.09 and 1.37, respectively. The cumulative variation for these factors was 0.81 and also it's portions for factor one to three were 0.46, 0.21 and 0.14, respectively. Factor one was detected as fixed capital factor in which, days to flowering, duration of flowering and days to maturity had high coefficients for factor loading. The second factor and third factor were named sink factor (pod per plant, seeds per pod and seed yield) and secondary yield components (pods per main axis and 1000-seed weight).

Scattering of the genotypes based on their scores for factor 1 is presented in Fig 1.

The genotypes G19, G18, G15, G10, G8 and G4 were classified as the same group and all of these had high seed yield. The genotypes G5 and G17 with low distance from circle origin had low means value of seed yield and also low means value of days to flowering, days to end of flowering and duration of flowering (Fig 1). The same clustering based on the genotypes distances from circle origin can be concluded from Fig 2 and Fig 3.Therefore scattering of genotypes based on their scores for related factors can be used as suitable method for grouping and classifying the genotypes. In earlier studies [18, 20] 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 *Brassica napus* L.

In general the phenological traits, pods per plant and 1000-seed weight were more heritable than the other traits. Due to significant positive correlation of pods per plant and seeds per pod 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. Scattering of genotypes based on their scores for related factors can be used as suitable method for grouping and classifying the genotypes.

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AUTHOR PROFILE

Valiollah Rameeh
Asistant Professor and Faculty member of Agriculture and Natural
Resources Research Center of Mazandran,
Sari, Iran.
E-mail: valvandi225@yahoo.com

Table 1: Combined analysis of variance for phenologlical traits, plant height, yield components, seed yield and oil content.

S.O.V	df	F-test									
		Days to flowering	Days to end of flowering	Duration of flowering	Days to maturity	Plant height	Pods per main axis	Pods per plant	Seeds per pod	1000-seed weight	Seed yield
Replication	1	0.86	8.33**	5.11*	1.33	1.56	0.73	3.41*	0.06	13.46**	8.92**
Treatments	6	346**	22.03**	32.20**	14.28**	10.08**	2.75**	3.98**	1.16	4.19**	4.65**
Error	84	-	-	-	-	-	-	-	-	-	-
Brad-sense heritabilit		0.99	0.88	0.91	0.82	0.75	0.37	0.50	0.05	0.51	0.55

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

Table 2: Mean comparison of the rapeseed genotypes for phenologlical 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	Seeds per pod	1000-seed weight (g)	Seed yield (kg/ha)
1- ZR401(G1)	113.00	180.33	67.33	217.33	185.47	49.70	145.00	20.63	3.06	3072
2- FORNR308(G2)	138.67	186.00	47.33	221.00	154.00	26.08	200.00	26.00	3.06	3500
3- ZR308(G3)	98.67	169.67	71.00	214.33	159.87	52.42	174.10	22.03	4.28	3229
4- SLR308(G4)	99.00	166.00	67.00	216.67	162.07	44.27	218.73	21.00	3.94	3783
5-Opti308(G5)	72.00	156.33	84.33	204.00	156.93	40.47	140.00	18.60	4.13	2506
6-306-308(G6)	86.00	161.67	75.67	214.67	138.77	32.10	165.00	19.33	3.85	3133
7- RG3308(G7)	88.67	167.67	79.00	213.67	127.87	38.80	176.07	20.20	3.27	3444
8- RWRG3(G8)	121.33	179.33	58.00	217.33	155.80	51.00	198.43	23.07	3.55	4089
9-19HRG3(G9)	115.00	174.00	59.00	218.67	153.00	45.27	198.87	20.73	4.06	3344
10-19HSAR(G10)	123.67	176.67	53.00	213.00	178.40	68.40	207.67	25.33	3.84	4117

11-Ok308(G11)	113.00	168.00	55.00	215.67	160.93	45.87	191.40	24.80	3.49	3122
12-Zarfam(G12)	144.00	189.00	45.00	228.33	214.33	40.33	177.00	20.03	3.71	3116
13-Sarigol(G13)	133.33	183.33	50.00	219.33	173.87	37.47	175.10	22.23	3.12	3233
14-RW19H(G14)	88.33	171.00	82.67	216.00	160.07	40.13	171.47	19.20	4.51	3411
15-Hyola401(G15)	87.00	161.67	74.67	209.67	151.33	39.87	206.50	21.40	4.07	4094
16-RG003(G16)	90.00	170.33	80.33	216.67	166.13	52.67	176.50	16.90	3.62	3500
17-RWOPT(G17)	85.00	169.67	84.67	215.33	147.80	41.80	141.67	20.73	3.41	2650
18-MOD308(G18)	125.00	174.67	49.67	220.00	152.27	49.13	210.80	25.83	3.67	3922
19-FOL308(G19)	103.33	176.00	72.67	217.67	157.67	53.07	212.00	24.00	2.93	4289
20-RG3OPT(G20)	112.00	179.00	67.00	219.67	167.07	55.60	178.90	18.00	4.23	3250
Genetic coefficient of variation	18.84	4.89	19.90	2.20	11.10	20.52	12.91	12.26	12.30	14.07
LSD$_{(\alpha=0.05)}$	3.09	5.15	6.63	3.60	16.10	13.19	33.87	6.98	0.64	641.08
LSD$_{(\alpha=0.01)}$	4.13	6.89	8.87	4.82	21.54	17.65	45.32	9.34	0.86	857.74

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-Seeds per pod	9-1000-seed weight (g)	10-Seed yield (kg/ha)
1-Days to flowering	1									
2-Days to end of flowering	0.89**	1								
3-Duration of flowering	0.95**	-0.72**	1							
4-Days to maturity	0.77**	0.84**	-0.64**	1						
5-Plant height	0.57**	0.61**	-0.48*	0.51*	1					
6-Pods per main axis	0.07	0.09	-0.05	-0.06	0.28	1				
7-Pods per plant	0.40	0.18	-0.49*	0.24	-0.05	0.23	1			
8-Seeds per pod	0.55*	0.33	-0.64**	0.16	-0.04	0.11	0.58**	1		
9-1000-seed weight	-0.37	-0.44*	0.28	-0.29	-0.02	0.16	-0.03	-0.41	1	
10-Seed yield	0.25	0.17	-0.27	0.12	-0.07	0.38	0.86**	0.48*	-0.11	1

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

Table 1: Factor analysis for 10 studied traits in rapeseed genotypes.

	Factor loadings		
Traits	1	2	3
Days to flowering	**0.911**	0.331	-0.146
Days to end of flowering	**0.929**	0.120	-0.113
Duration of flowering	**-0.798**	-0.429	0.150
Days to maturity	**0.855**	0.057	-0.127
Plant height	**0.794**	-0.214	0.395
Pods per main axis	0.110	0.319	**0.766**
Pods per plant	0.127	**0.915**	0.102
Seeds per pod	0.259	**0.757**	-0.339
1000-seed weight	-0.317	-0.179	**0.669**
Seed yield	0.026	**0.899**	0.191
Eigen value	4.55	2.09	1.37
Portion	0.46	0.21	0.14
Cumulative	0.46	0.67	0.81

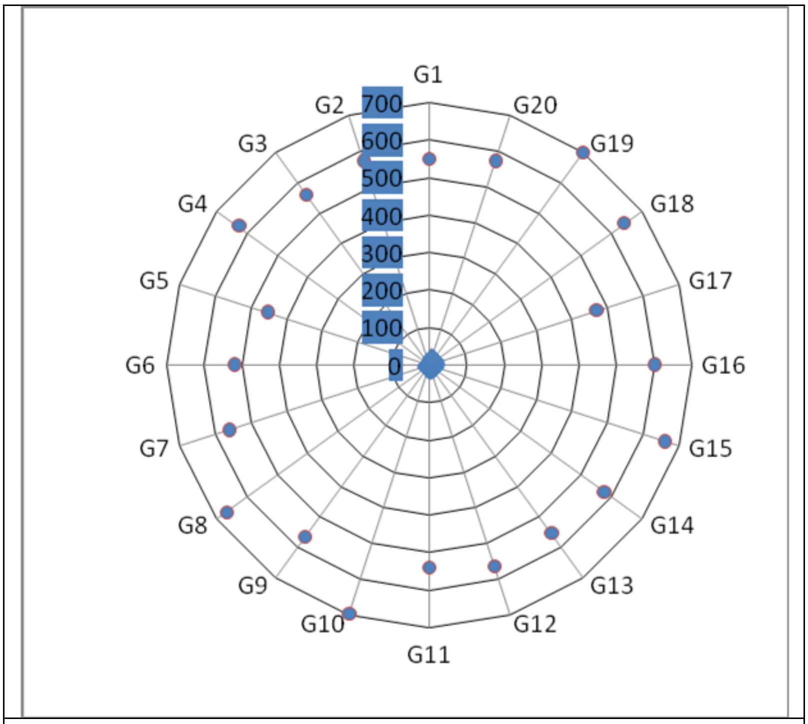

Fig 1. Scattering of the genotypes based on theirs scores for factor 1.

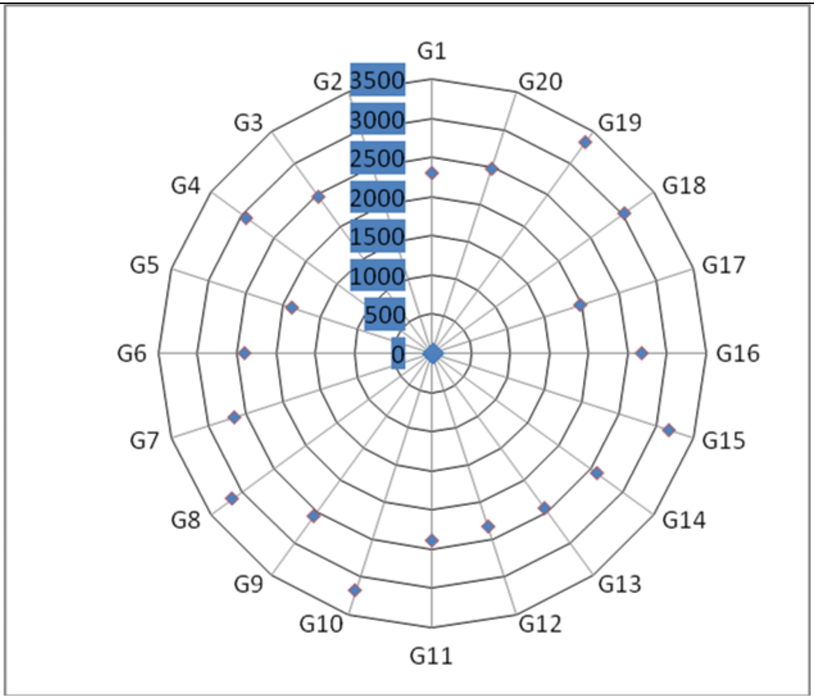

Fig 2. Scattering of the genotypes based on theirs scores for factor 2.

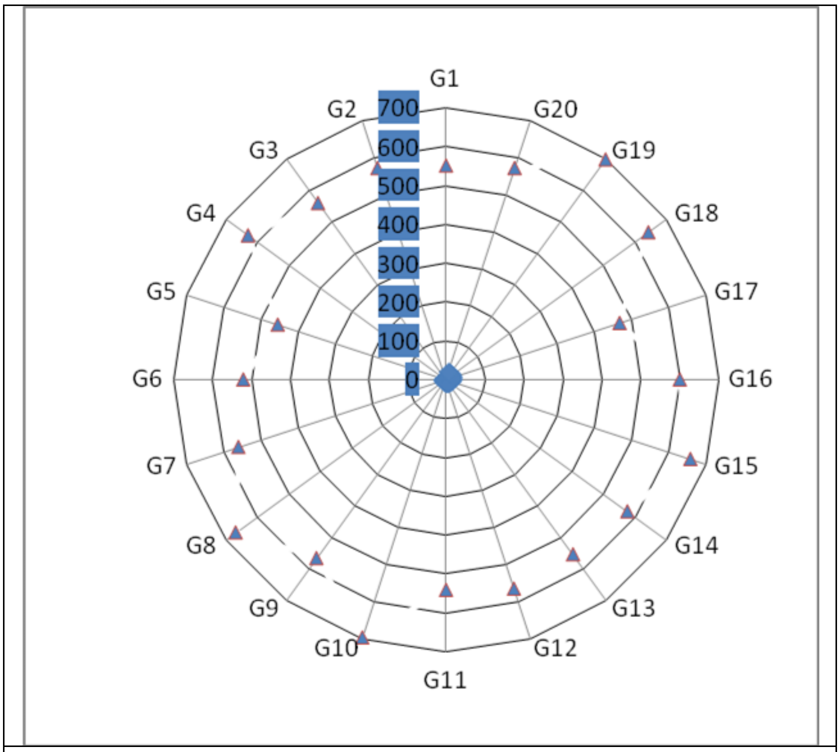

Fig 3. Scattering of the genotypes based on theirs scores for factor 3.