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HERITABILITY, GENETIC VARIABILITY AND CORRELATION ANALYSIS OF SOME IMPORTANT AGRONOMIC TRAITS IN RAPESEED ADVANCED LINES

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ABSTRACT. 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.Twenty one rapeseed genotypes were evaluated based on randomized complete block design with three replications. Significant genotypes effects were exhibited for phenological traits, plant height, yield components except pod length and seed yield, indicating significant genetic differences among the genotypes. High broad sense heritability were determined for phenological traits, plant height and seed yield demonstrating selection gain for improving these traits will be high. Pods on main axis and pods per plant had high value of genetic coefficient of variation and also were significant correlated with seed yield. The results of factor analysis exhibited three factors including first yield components (plant height, pods on main axis and seed yield), second yield components (pods per plant, seeds per pod and 1000-seed weight) and fixed capital factor (phenological traits). On the basis of cluster analysis, the genotypes were classified in three groups and the group with high seed yield had high mean values of plant height, days to maturity and pods per plant.

Key words: Coefficient of variation; Cluster analysis; Factor analysis; Seed yield.

INTRODUCTION

Rapeseed is the most important plant oil source and the second most important oil plant in the world after soybean (FAO, 2007). Response to selection is resulted from significant genetic variation and high heritability (Singh and Chowdhury, 1985). Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance and genetic and environmental factors that influence their expression. To plan an efficient developmental program, it is necessary to have an understanding of the breeding systems

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coupled with statistical analysis of inheritance data (Falconer and Mackay, 1996). Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to the yield of a crop would be great objectives of plant breeders (Mary and Gopalan, 2006). Determination of correlation coefficients is an important statistical procedure to evaluate traits contributions to seed yield (Khan *et al.,* 2006; Ivanovska *et al.,* 2007; Basalma, 2008; Hashemi *et al.,* 2010; 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 (*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 multivariate analysis particularly factor and cluster analyses are utilized for evaluation of germplasm when studying various traits and a large number of accessions. 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 and also it was used for detecting factors relating to environmental stress including drought resistance in *Brassica napus* (Naderi and Emam, 2010). Cluster analysis assigns genotypes into qualitative homogenous groups based on response similarities and also assists to classify genotypes. Greater heterotic effect is generated when clusters are divergent (Mahasi and Kamundia, 2007). 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 (Khachatourians *et al.*, 2001; Leilah and Al-Khatee 2005; Aytaç and Kınacı, 2009).

The present investigation is aimed to evaluate variability, 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 cluster analysis.

MATERIALS AND METHODS

The experimental material for the present investigation comprised of 21 rapeseed (*Brassica napus* L.) genotypes which were selected based on diversity of 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 2013-14. 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, and days to maturity were determined based of phenological stages of the genotypes in each plot. Plant height, pods per main axis, pods length and pods per plant, seeds per pod were recorded based on 10 randomly plants of 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 (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 (h^2) was estimated according to Singh *et al.* (1993) as: $h^2 = VG/VE$. The coefficient of variation was estimated as CV=($\sqrt{VG}$)/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 (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. 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 and Broad sense heritability

Genotypes had significant variance for the traits including days to flowering, days to end of flowering, days to maturity, plant height, pods per main axis, pods per plant, seeds per pod, 1000-seed weight and seed yield indicating significant genetic variation for these traits (*Table 1*). Similar results were reported by Aytaç and Kınacı (2009) and Sabaghnia *et al.* (2010). Broad sense heritability estimates varied from 0.18 to 0.98 for pods length and days to end of flowering, respectively. High broad sense heritability estimates for phenological traits indicating that selection gain for improving these traits will be high. Aytaç *et al.* (2008) reported high broad sense heritability estimates for yield components. Genetic coefficient of variation, which is indicating the genetic diversity of the genotypes, varied from 1.93 to 18.95 for days to maturity and seed yield, respectively (*Table 2*). The high value of genetic variations of the genotypes were detected for pods per main axis, pods per plant.

Means values of the genotypes and correlation analysis

Mean values of days to flowering ranged from 102 to 126 days in G11 and G21, 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 G11, G3, G8, G16, G4, G14 and G10 with low means value of days to flowering:102, 104, 104, 104, 105, 105 and 106, respectively were preferable. Days to end of flowering was varied from 165 to 184 days in G6 and G21, respectively. For reducing some of pests damages and also having enough opportunity for second crop cultivation after rapeseed, early maturity is ideotype trait for breeding *Brassica napus* L. and other related brassica specious. The genotypes G3, G4, G8, G11, G13 and G17 with low means value of days to maturity were detected as suitable genotypes for improving this trait. Due to low mean value of genetic coefficient of variation for days to maturity, selection gain for improving this trait will be low. Plant height ranged from 107 to 158 cm in G4 and G21, respectively. For ideotype breeding of rapeseed low mean value of plant height is favored, therefore G4, G1, G16, G6 and G2 with 107, 117, 123, 125 and 126 cm of plant height were merit genotypes. Pods per main axis was significant correlated with seed yield, therefore the genotypes G7, G14, G9, G16 and G21 with 49, 49, 48, 44 and 43 pods on main axis were suitable genotypes for improving this trait. The mean values of pods per plant as the main important yield component were high in the genotypes G6, G7, G9, G10 and G14. The genotypes including G6, G7, G12, G19, G20 and G21had high means value of pods length and seeds per pod. High 1000-seed weight was belonged to the genotypes including G5, G10, G12, G13, G15, G16 and G21. Zhang and Zhou (2006) reported that pods per plant, seeds per plant and 1000-seed weight traits were positively correlated with seed yield.

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

S.O.V	df	MS									
		Days to flowering	Days to end of flowering	Days to maturity	Plant height	Pods per main axis	Pods per plant	Pods length	Seeds per pod	1000-seed weight	Seed yield
Replication	2	0.3	1.3*	7.3**	45.0	929.4**	6423**	0.48	6.1	0.04	1402563**
Treatments	20	141.0**	54.9**	49.1**	467.3**	119.5**	1384**	0.56	16.6**	0.33*	607206**
Error	40	2.4	0.3	0.9	117.6	41.2	558	0.34	5.8	0.18	120474
Broad-sense heritability		0.95	0.98	0.95	0.50	0.39	0.33	0.18	0.38	0.20	0.57

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

Table 3 - 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 per main axis	6-Pods per plant	7- Pods length	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	0.48*	1								
3-Days to maturity	0.80**	0.45*	1							
4-Plant height	0.41	0.26	0.56**	1						
5-Pods per main axis	0.48*	0.13	0.48*	0.41	1					
6-Pods per plant	0.24	-0.09	0.39	0.24	0.59**	1				
7- Pods length	0.39	-0.26	0.35	0.44*	0.37	0.23	1			
8-Seeds per pod	0.36	0.17	0.31	-0.11	0.18	0.40	-0.05	1		
9-1000-seed weight	-0.07	0.02	0.11	0.35	-0.22	-0.45*	0.27	-0.36	1	
10-Seed yield	0.53*	0.33	0.67**	0.71**	0.62**	0.48*	0.24	0.13	0.04	1

*, ** 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	Days to end of flowering	Days to maturity	Plant height (cm)	Pods per main axis	Pods per plant	Pods length (cm)	Seeds per pod	1000-seed weight (g)	Seed yield (kg/ha)
1-SR4200 (G1)	108	173	209	117	32	132	5.33	26	3.36	1590
2-PH101(G2)	108	175	212	126	39	133	5.52	25	3.22	2729
3-SOPT1(G3)	104	174	206	140	31	118	5.77	19	3.38	2412
4-SR3080(G4)	105	171	202	107	29	118	5.20	25	3.01	1501
5-OPT401(G5)	111	169	212	137	33	96	6.67	22	4.39	2101
6-Hyola401(G6)	107	165	210	125	37	170	6.83	26	3.14	1818
7-Zafar(G7)	120	171	212	153	49	166	6.63	27	3.17	3064
8- SR4201(G8)	104	171	206	140	42	117	5.87	25	3.52	1873
9-PH23(G9)	115	167	214	143	48	159	6.23	21	3.41	2829
10-RAS(G10)	106	174	213	158	35	163	5.70	25	3.80	2773
11-PH11(G11)	102	169	205	137	32	113	5.80	21	3.39	1979
12-N892(G12)	107	168	209	135	29	102	5.90	27	3.77	2296
13-RGS3006(G13)	107	171	206	138	33	114	6.13	22	3.74	2223
14- N492(G14)	105	171	210	142	49	159	6.03	25	3.21	2857
15- N392(G15)	110	173	210	144	37	147	6.27	23	3.85	2657
16-PH16(G16)	104	174	205	123	44	131	5.80	24	3.76	2323
17-N792(G17)	109	166	206	138	41	127	6.57	21	3.59	2118
18-N1292(G18)	121	172	214	139	41	148	5.80	26	3.35	2923
19-PH4(G19)	123	179	214	132	42	139	6.17	27	3.07	2462
20-RGS003(G20)	111	172	210	137	36	132	6.17	26	3.49	2565
21-Sarigol(G21)	126	184	219	158	43	120	6.27	24	3.72	2768
Genetic coefficient of variation	6.22	2.49	1.93	9.13	16.57	16.11	7.15	9.77	9.42	18.95
$LSD_{(\alpha=0.05)}$	2.56	0.90	1.56	17.89	10.59	38.97	-	3.97	0.72	572.47
$LSD_{(\alpha=0.01)}$	3.42	1.21	2.09	23.91	14.15	52.09	-	5.31	0.96	765.18

Table 4 - Factor analysis for 10 studied traits in rapeseed genotypes

Traits	Factor loadings		
	1	2	3
1-Days to flowering	0.17	0.18	0.61
2-Days to end of flowering	-0.01	-0.01	**0.93**
3-Days to maturity	0.28	0.10	**0.58**
4-Plant height	**0.77**	-0.31	0.27
5-Pods per main axis	**0.73**	0.39	0.06
6-Pods per plant	**0.57**	**0.68**	-0.14
7- Pods length	**0.75**	-0.20	-0.29
8-Seeds per pod	0.03	**0.68**	0.32
9-1000-seed weight	0.17	**-0.87**	0.06
10-Seed yield	**0.75**	0.11	0.38
Eigen value	4.03	1.91	1.48
Portion	0.40	0.19	0.15
Cumulative	0.40	0.59	0.74

Table 5 - The means of clustering groups for 10 studied traits

Clustering groups	Traits									
	Days to flowering	Days to end of flowering	Days to maturity	Plant height (cm)	Pods per main axis	Pods per plant	Pods length (cm)	Seeds per pod	1000-seed weight (g)	Seed yield (kg/ha)
C1	106.17	172.00	205.33	111.97	30.63	124.80	5.27	25.20	3.19	1545.56
C2	107.90	170.63	207.87	134.47	36.14	122.47	6.15	23.34	3.57	2160.55
C3	113.59	173.19	212.59	144.52	41.91	147.40	6.07	24.71	3.47	2796.02

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 G5, G13, G17 and G6 with high means value of seed yield (3064, 2923, 2857 and 2829 kg ha^{-1}, respectively) had high mean value of yield components.

Factor and cluster analyses

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 4.03, 1.91 and 1.48, respectively. The cumulative variation for these factors was 0.74 and also it's portions for factor one to four were 0.40, 0.19 and 0.15, respectively. Factor one, two and three were detected: first yield components (plant height, pods on main axis and seed yield), second yield components (pods per plant, seeds per pod and 1000-seed weight) and fixed capital factor (phenological traits), 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 *Brassica napus* L.

The results of cluster analysis for 10 studied traits in 21 genotypes are presented in *Fig. 1* and *Table 5*. All the genotypes were classified in three groups with different mean values of the traits. The high seed yield genotypes with high mean value of pods on main axis and pods per plant were classified in group1(C1). Group 1 (C1) and group 2(C2) had 1545.56 and 2160.55 kg ha^{-1}of seed yield, respectively. Genetic diversity among the Brassica genotypes was assessed by Choudhary and Joshi (2001) using cluster analysis.

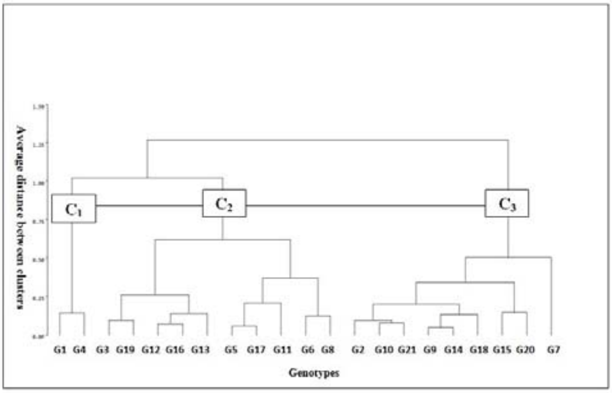

Figure 1 - Clustering dendrogram of 21 rapeseed genotypes (the genotypes code as in *Table 2*) based on 10 studied traits

CONCLUSION

In general, the phenological traits 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 trait including days to flowering can be used. Cluster analysis can be used as suitable method for classifying the high yield genotypes with high component characters.

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REFERENCES

Aytac Z., Kınacı, G., Kınacı E., 2008 - Genetic variation, heritability and path analysis of summer rapeseed cultivars, J. Appl. Biol. Sci., 2(3): 35-39.

Aytaç Z., Kınacı, G. 2009 - Genetic variability and association studies of some quantitative characters in winter rapeseed (*Brassica napus* L.). Afr. J. Biotechnol., 8 (15): 3547-3554.

Basalma D., 2008 - The correlation and path analysis of yield and yield components of different winter rapeseed *(Brassica napus* ssp. *oleifera* L.) cultivars. Res. J. Agric. Biol. Sci., 4 (2): 120-125.

Belete Y.S., 2011 - Genetic variability, correlation and path analysis studies in Ethiopian Mustard (*Brassica carinata* A. Brun) Genotypes. Int. J. Plant Breed. Genet., 5: (4):328-338.

Choudhary BR, Joshi P., 2001 - Genetic diversity in advanced derivatives of *Brassica* interspecific hybrids. Euphytica, 121: 1-7.

Falconer D.S., Mackay T.F.C., 1996 - Introduction to quantitative genetics. 4th Ed., Benjamin Cummings, England, ISBN-10: 0582243025.

F.A.O., 2007 - http:// faostat. fao. org/.

Friedt W., Snowdon R., Ordon F., Ahlemeyer J., 2007 - Plant breeding: assessment of genetic diversity in crop plants and its exploitation in breeding. Progress in Botany, 168:152-177.

Hashemi Ameneh S., Nematzadeh G.A., Babaeian Jelodar N., Ghasemi Chapi O., 2010 - Genetic evaluation of yield and yield components at advanced generations in rapeseed (*Brassica napus* L.). Afr. J. Agric. Res., 5(15): 1958-1964.

Ivanovska S., Stojkovski C., Dimov Z., Marjanovic-Jeromela A., Jankulovska M., Jankuloski L.J., 2007 - Interrelationship between yield and yield related traits of spring canola (*Brassica napus L.*) genotypes. Genetika, 39, (3): 325-332.

Jeromela A., Marinkovic R., Mijic A., Jankulovska M., Zdunic Z., 2007 - Interrelationship between oil yield and other quantitative traits in rapeseed (*Brassica napus* L.). J. Central Eur. Agric., 8: 165-170.

Khachatourians G.G., Summer A.K., Phillips P.W.B., 2001 - An introduction to the history of canola and the scientific basis for innovation. CABI, London.

Khan F.A., Ali S., Shakeel A., Saeed A., Abbas G., 2006 - Correlation analysis of some quantitative characters in *Brassica napus* L. J Agric Res., 44: 7-14.

Khan S., Farhatullah I., 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 A.A., and Al-Khateeb S.A., 2005 - Yield analysis of canola (*Brassica napus* L.) using some statistical procedures. Saudi J. Bio. Sci. 2005, 12; 103-113.

Mahasi M.J., Kamundia J.W., 2007 - Cluster analysis in rapeseed (*Brassica napus* L.). African J. Agric. Res. Vol. 2 (9), pp. 409-411.

Mary S.S., Goplan A., 2006 - Dissection of genetic attributes yield traits of folder cowpea in F3 and F4. Journal of Applied Science, 2: 805-808.

Naderi R., Emam Y., 2010 - Interrelationships among grain yield and related characters of four oilseed rape (*Brassica napus* L.) cultivars under drought stress conditions. DESERT, 15: 133-138.

Rameeh V., 2010 - Combining ability and factor analysis in F_2 diallel crosses of rapeseed varieties. Plant. Breed. Seed Sci., 62: 73-83.

Sabaghnia N., Dehghani H., Alizadeh B., Mohghaddam M., 2010 - Interrelationships between seed yield and 20 related traits of 49 canola (*Brassica napus* L.) genotypes in non-stressed and water-stressed environments. Spanish J. Agric. Res. 8(2): 356-370.

SAS INSTITUTE INC., 2004 - SAS/STAT user's guide. Version 9 Fourth Ed., Statistical Analysis Institute Inc., Cary North Carolina.

Sharma S., 1996 - Applied multivariate techniques. 1st Ed., John Wiley and Sons, New York, p. 493.

Sheikh F.A., Rather A.G., Wani S.A., 1999 - Genetic variability and inter-relationship in toria (*Brassica campestris* L. var. Tori). Adv. Plant Sci., 12(1): 139-143.

Singh M., Ceccarelli S., Hamblin J., 1993 - Estimation of heritability from varietal trials data. Theor. Appl. Genet., 86: 437-441.

Singh R.K., Chowdhury B.D., 1985 - Biometrical method in quantitative genetic analysis 2nd Ed., Kalyani Publishers, Ludhiana, New Dehli, India, pp: 54-57.

Zhang G., Zhou W., 2006 - Genetic analysis of agronomic and seed quality traits of synthetic oilseed Brassica napus producted from interspecific hybridization of *B. campestris* and *B. oleracea*. J. Gen., 85(1): 45-51.