Asian Journal of
Biological
Sciences

Estimation and Interrelationships of Genetic Variability Parameters of Some Morpho-phenological Traits in Spring Rapeseed (*Brassica napus* L.)

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ABSTRACT

Oilseed rape (*Brassica napus* L.) is one of the most important oil seed crops. The present study was carried out to (1) study of some agro-phenological traits and (2) to estimate genetic variability parameters for the studied traits in 17 spring rapeseed genotypes (SW Highly, Olga, Eagle, Cracker Jack, Sarigol, Mozart, SW 3497, RGS003, Amica, Calimar, Hyola 330, Hyola 401, Hyola 308, Goliath, Zarfam, Profit and Option 500). The experiment was conducted based on Randomized Complete Blocks Design (RCBD) with three replications. The characters studied were grain yield, some phenological, morphological and physiological traits. Statistical analysis showed significantly differences among the genotypes based on the most studied traits. This indicated that there was sufficient variability available to have an effective selection. Genotypic and phenotypic coefficients of variations were high for grain yield, crown to first node distance (CND), Harvest Index (HI). High genetic gain was observed for HI (42.91%) and CND (39.25%). Correlation analysis showed the grain yield was significantly and negatively correlated with phenological traits include days to flowering initiation (-0.57), days to 10% flowering (-0.57), days to 50% flowering (-0.59), days to complete flowering (-0.57), days to complete ripening (-0.55) and was significantly and positively correlated with HI (0.80) and chlorophyll content (-0.32). High heritability estimates in characters i.e., all phonological traits (from 84.38 to 93.18) and chlorophyll content (65.35), whereas low heritability was observed for the grain yield (32.49), CND (33.15) and HI (30.25).

Key words: Genetic advance, genetic gain, heritability, rapeseed

INTRODUCTION

Rapeseed (*Brassica napus* L.) is an important oilseed crop because of the high quality of its oil and meal for nutritional approaches (Qian *et al.*, 2007). The development of high yielding rapeseed cultivars is the main objective of any breeding programs in the world. In spite of high genetic potential of rapeseed, average yield of it is very low (Ali *et al.*, 2003). The genetic variation for the trait under selection and a higher heritability are necessary to have response to selection (Falconer and Mackay, 1996; Moghaddam *et al.*, 1997; Shukla *et al.*, 2006). Identification of key traits, genetic systems controlling their inheritance and genetic and environmental factors that influence their expression is essential for breeding programs. To access a well-developed program,

understanding of the breeding systems and statistical analysis of inheritance together is a necessary issue (Srivastava and Dhamania, 1989; Yap and Harvey, 1972).

Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to yield of a crop would be great importance in planning a successful breeding program (Mary and Gopalan, 2006). Existence of genetic variation for yield and its components is a prerequisite to progress in high-yielding varieties. Among the observed variability that is a combined estimate of genetic and environmental factors, genetic causes is heritable only. Estimates of heritability have to be considered in conjunction with estimates of genetic advance, because do not provide a clear idea about the expected gain in the next generation alone (Shukla *et al.*, 2006). many studies in different crops shown that the magnitude of genetic variability is prerequisite to being success in crop breeding programs (Ehdaie and Waines, 1989; Moghaddam *et al.*, 1997; Sumathi *et al.*, 2005; Baye and Becker, 2005; Vanaja and Babu, 2006; Mary and Gopalan, 2006; Shukla *et al.*, 2006; Maniee *et al.*, 2009) but very limited on spring rapeseed. An awareness of the genetic association between grain yield and its components can improve the efficiency of selection in breeding programs. Therefore, it is important to study the relationships among the characters (Ehdaie and Waines, 1989).

The objective of this research was to study genetic variability of some agro-phenological characters in spring rapeseed genotypes to estimate genetic variability parameters for the studied traits.

MATERIALS AND METHODS

Plant materials, experimental lay out and cultural practice: This study was carried out with 17 genotypes based on Randomized Complete Blocks Design (RCBD) with three replications at the research farm of the Agricultural College, Razi University, Kermanshah, Iran, in 2005-2006 cropping season. The genotypes used in this study are given in Table 1. The plot sizes were 3.0×1.2 m. Standard cultural practices were followed for raising the crop.

Table 1: The genotypes of spring *B. napus* that used in this study

Genotype	Descriptive	Place of supplying
SW Highly	Spring oilseed cultivar	SPII, Karaj, Iran
Olga	Spring oilseed cultivar	SPII, Karaj, Iran
Eagle	Spring oilseed cultivar	SPII, Karaj, Iran
Cracker Jack	Spring oilseed cultivar	SPII, Karaj, Iran
Sarigol	Spring oilseed cultivar	SPII, Karaj, Iran
Mozart	Spring oilseed cultivar	SPII, Karaj, Iran
SW 3497	Spring oilseed cultivar	SPII, Karaj, Iran
RGS003	Spring oilseed cultivar	SPII, Karaj, Iran
Amica	Spring oilseed cultivar	SPII, Karaj, Iran
Calimar	Spring oilseed cultivar	SPII, Karaj, Iran
Hyola 330	Spring oilseed cultivar	SPII, Karaj, Iran
Hyola 401	Spring oilseed cultivar	SPII, Karaj, Iran
Hyola 308	Spring oilseed cultivar	SPII, Karaj, Iran
Goliath	Spring oilseed cultivar	SPII, Karaj, Iran
Zarfam	Spring oilseed cultivar	SPII, Karaj, Iran
Option 500	Spring oilseed cultivar	SPII, Karaj, Iran
Profit	Spring oilseed cultivar	SPII, Karaj, Iran

SPII: Seed and Plant Improvement Institute

Traits: The characters studied were grain yield, phenologic traits include Days to Flowering Initiation (DFI), Days to 10% Flowering (DTF), Days to 50% Flowering (DFF), Days to Complete Flowering (DCR) and complete ripening, morphologic traits include Plant Height (PH), Stem Diameter (SDI), Crown to First Node Distance (CND), Pod Number per Plant (PPP), Pod Length (PL), Seed Number per Pod (SPP), Thousand Seeds Weight (TSW), Harvest Index (HI) and Chlorophyll Content (CLC).

Statistical analysis: Data were statistically analyzed for each character separately. The analysis of variance for different characters were measured followed by Duncan's New Multiple Range Test (DMRT) (Steel and Torrie, 1960) to test the significance difference between means. The mean squares were used to estimate genotypic and phenotypic variance according to Johnson *et al.* (1955). The coefficient of variation was calculated based on the formula suggested by Burton (1952). The genotypic and phenotypic coefficient of variation and heritability were calculated as suggested the formula used by Singh and Chowdhury (1985) and genetic advance by Allard (1960) as well as correlation coefficient by Zaman *et al.* (1982).

RESULTS AND DISCUSSION

The results of analysis of variance (ANOVA) for each trait are given in Table 2. The genotypes showed significant differences for grain yield, DFI, DTF, DFF, DCF, DCR, PH, CND, HI and CLC, indicating the presence of adequate variability among the genotypes.

Mean values for the genotypes based on each character is also shown in Table 3. From this table, genotype SW Highly showed the highest mean yield performance (393.55 g m^{-2}).

The estimations of variability parameters for phonological, morphological and yield were presented in Tables 4 and 5. In case of DFI, genotypes ranged from 64.30-84.00 days and the mean was 70.20 (Table 4). Low genotypic and phenotypic co-efficient of variations were observed for DFI (Table 5). The high heritability and moderate genetic gain was observed for the DFI. This trait showed a significant and positive correlation with all phonological traits and had a significant and negative correlation with grain yield, CND and HI (Table 6). To predict the selection effects precisely, heritability accompanied with genetic gain is more useful than heritability alone (Johnson *et al.*, 1955).

The Days to 10% Flowering (DTF) varied from 66.00-88.30 days with mean value 74.70 (Table 4). The high heritability and moderate genetic gain was observed for the DTF, indicating the major part of phenotypic variations is belonging to genotypic variations (Table 5). The DTF was significantly and negatively correlated with grain yield, CND and HI and positively correlated with all phonological traits.

Table 2: Mean squares for different characters of 17 cultivars of spring *Brassica napus*

Sources	df	yield	DFI	DTF	DFF	DCF	DCR	PH	SDI	CND	PPP	PL	SPP	TSW	HI	CLC
Block	2	1744	6.73	20.8	4.4	1.87	11.87	333.3	0.44	388.4	13.5	1.33	30.3	0.49	90.9	27.29
Genotypes	16	837.4*	84.80**	117**	139.2**	154.6*	154.6**	489.7*	0.20^{ns}	519.9*	31.9^{ns}	1.38^{ns}	26.0^{ns}	0.25^{ns}	240.2*	105.9**
Error	32	342.6	4.7	6.8	4.5	3.72	3.72	212.8	0.22	209	65.1	2.45	33.3	0.57	92	15.9

*,**Significant at 5 and 1% level of probability, respectively; ns: Non-significant, DFI: Days to flowering initiation, DTF: Days to 10% flowering, DFF: Days to 50% flowering, DCF: Days to complete flowering, DCR: Days to complete ripening, PH: Plant height, SDI: Stem diameter, CND: Crown to first node distance, PPP: Pod number per plant, PL: Pod length, SPP: Seed number per pod, TSW: Thousand seeds weight, HI: Harvest index and CLC: Chlorophyll content

Table 3: Mean performance of 17 cultivars of spring *B. napus* for different characters

Genotypes	Characters									
	Yield (g m⁻²)	DFI (days)	DTF (days)	DFF (days)	DCF (days)	DCR (days)	PH (cm)	CND (cm)	HI	CLC (%)
SW Highly	393.55ᵃ	69.6ᵈᶠᵉ	73.0ᵉᶠᵍ	77.0ᵈᵉ	82.3ᵉ	107.3ᶜᵈ	79.8ᵉ	10.3ᵈ	41.6ᵃ	36.9ᵈ
Olga	129.50ᵇᶜᵈ	75.6ᶜ	80.3ᵇᶜ	83.3ᶜ	78.3ᶜᵈ	109.0ᵇᶜᵈ	88.3ᶜᵈᵉ	17.5ᶜᵈ	13.9ᵇᶜᵈᵉ	52.5ᵃᵇᶜ
Eagle	186.50ᵇᶜᵈ	67.0ᵉᶠᵍʰ	74.3ᵈᵉᶠ	81.4ᶜ	85.0ᵈᵉ	107.3ᵇᶜᵈ	84.3ᵈᵉ	23.7ᵃᵇᶜᵈ	17.9ᵇᶜᵈᵉ	54.9ᵃᵇ
Cracker Jack	116.00ᵇᶜᵈ	70.3ᵇᶜᵈ	78.0ᶜᵈ	81.7ᶜ	85.3ᶜᵈᵉ	107.7ᵇᶜᵈ	92.6ᵇᶜᵈᵉ	20.3ᵇᶜᵈ	12.9ᶜᵈᵉ	55.8ᵃᵇ
Sarigol	121.00ᵇᶜᵈ	72.0ᵈ	79.3ᵇᶜ	83.7ᶜ	87.7ᶜ	111.0ᵇᶜᵈ	93.1ᵇᶜᵈᵉ	33.3ᵃᵇᶜᵈ	15.0ᵇᶜᵈᵉ	53.7ᵃᵇᶜ
Mozart	50.00ᶜᵈ	79.3ᵇ	83.3ᵇ	87.7ᵇ	96.7ᵇ	118.3ᵃᵇ	106.8ᵇᶜᵈᵉ	23.6ᵃᵇᶜᵈ	10.5ᵈᵉ	48.3ᵇᶜ
SW 3497	102.50ᵇᶜᵈ	65.3ᵍʰ	68.6ᵍʰⁱ	72.7ᶠ	75.7ᶠᵍ	107.3ᶜᵈ	115.3ᵃᵇᶜ	46.9ᵃᵇ	23.1ᵇᶜᵈ	39.6ᵈ
RGS003	207.50ᵇᶜᵈ	66.0ᵍʰ	68.6ᵍʰⁱ	72.7ᶠ	78.3ᶠ	111.3ᵇᶜ	108.0ᵃᵇᶜᵈᵉ	47.8ᵃᵇ	32.7ᵃᵇ	47.0ᶜ
Amica	189.50ᵇᶜᵈ	71.0ᵈᵉ	76.6ᶜᵈᵉ	80.7ᶜᵈ	84.7ᵈᵉ	111.3ᵇᶜ	119.0ᵃᵇ	39.8ᵃᵇᶜ	16.4ᵇᶜᵈᵉ	55.0ᵃᵇ
Calimar	208.50ᵇᶜᵈ	69.0ᵈᵉᶠᵍ	71.0ᵍʰ	73.7ᵉᶠ	78.3ᶠ	102.0ᵈ	124.5ᵃ	50.8ᵃ	21.1ᵇᶜᵈᵉ	56.1ᵃᵇ
Hyola 330	147.00ᵇᶜᵈ	66.0ᶠᵍʰ	68.0ʰⁱ	73.0ᶠ	76.3ᶠᵍ	103.3ᶜᵈ	115.6ᵃᵇᶜ	40.9ᵃᵇᶜ	19.3ᵇᶜᵈᵉ	46.6ᶜ
Hyola 401	218.50ᵇᶜ	64.3ʰ	66.7ʰⁱ	68.3ᵍ	75.3ᶠᵍ	91.0ᵉ	114.6ᵃᵇᶜ	36.1ᵃᵇᶜᵈ	19.6ᵇᶜᵈᵉ	54.7ᵃᵇ
Hyola 308	251.00ᵃᵇ	64.3ʰ	66.0ⁱ	68.0ᵍ	74.3ᵍ	104.7ᶜᵈ	109.9ᵃᵇᶜᵈ	44.3ᵃᵇᶜ	29.7ᵃᵇᶜ	53.5ᵃᵇᶜ
Goliath	173.00ᵇᶜᵈ	69.0ᵈᵉᶠᵍ	75.0ᶜᵈᵉᶠ	80.0ᶜᵈ	83.7ᵉ	107.7ᶜᵈ	100.0ᵃᵇᶜᵈᵉ	26.5ᵃᵇᶜᵈ	16.2ᵇᶜᵈᵉ	55.7ᵃᵇ
Zarfam	27.60ᵈ	84.0ᵃ	88.3ᵃ	94.0ᵃ	100.3ᵃ	126.7ᵃ	98.8ᵃᵇᶜᵈᵉ	31.6ᵃᵇᶜᵈ	3.0ᵉ	57.9ᵃ
Option 500	212.50ᵇᶜ	72.0ᵈ	78.6ᵇᶜᵈ	79.7ᶜᵈ	83.7ᵉ	102.3ᵈ	97.3ᵃᵇᶜᵈᵉ	8.36ᵈ	24.7ᵃᵇᶜᵈ	55.2ᵃᵇ
Profit	197.00ᵇᶜᵈ	69.0ᵈᵉᶠᵍ	74.0ᵈᵉᶠ	80.3ᶜᵈ	84.7ᵈᵉ	105.0ᶜᵈ	101.0ᵃᵇᶜᵈᵉ	21.1ᵇᶜᵈ	21.9ᵇᶜᵈ	52.8ᵃᵇᶜ

In each column similar letters show that there is no significant difference at 5% level, DFI: Days to flowering initiation, DTF: Days to 10% flowering, DFF: Days to 50% flowering, DCF: Days to complete flowering, DCR: Days to complete ripening, PH: Plant height, SDI: Stem diameter, CND: Crown to first node distance, PPP: Pod number per plant, PL: Pod length, SPP: Seed number per pod, TSW: Thousand seeds weight, HI: Harvest index and CLC: Chlorophyll content

Table 4: Range, mean, standard error of mean and coefficient of variation for different characters in spring *B. napus*

Characters	Range	Mean	Standard error (±)	Coefficient of variation (%)
Yield (g m⁻²)	27.60-393.55	172.42	20.26	10.73
Days to flowering initiation (days)	64.30-84.00	70.20	1.29	3.08
Days to 10% flowering (days)	66.00-88.30	74.70	1.50	3.49
Days to 50% flowering (days)	68.00-94.00	78.70	1.65	2.69
Days to complete flowering (days)	74.33-100.33	82.98	1.74	2.32
Days to complete ripening (days)	91.00-126.70	107.83	1.81	1.78
Crown to first node distance	8.36-47.80	30.75	3.19	47.00
Plant height (cm)	79.80-124.50	102.85	3.10	14.16
Harvest index	2.97-41.56	19.97	2.17	48.00
Chlorophyll content (%)	36.90-57-93	51.54	1.44	7.73

The range and mean values for Days to 50% flowering (DFF) were 68 to 94 and 78.7 days and low genotypic and phenotypic coefficient of variation (GCV and PCV) were also observed (Table 4, 5) showing high environment effect on the expression of DFF. This trait was significantly and positively correlated with all phonological traits and negatively correlated with grain yield, CND and HI.

High heritability and moderate genetic gain were observed for Days to Complete Flowering (DCF) (Table 5). This variable is negatively correlated with grain yield.

It was worthy of mention that all phonological traits are negatively correlated with grain yield. The reason returns to encounter of grain filling period with warm weather and pollen beetle in Kermanshah city conditions.

Table 5: Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance in percentage of mean for different characters

Characters	Genotypic variances	Phenotypic variances	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (%)	Genetic gain (%)
Yield	164.93	507.53	37.25	65.30	32.49	14.85	8.61
Days to flowering initiation (days)	26.70	31.40	3.10	7.98	85.03	9.80	13.96
Days to 10% flowering (days)	36.73	43.53	8.16	8.82	84.38	11.40	15.26
Days to 50% flowering (days)	44.90	49.40	8.51	8.93	90.89	13.03	0.16
Days to complete flowering (days)	50.29	54.01	5.56	8.86	93.18	14.08	15.70
Days to complete ripening (days)	48.19	76.51	6.38	8.10	62.98	11.35	10.50
Crown to first node distance	103.63	312.63	33.10	57.49	33.15	12.07	39.25
Plant height	92.30	305.10	9.33	16.98	30.25	10.89	10.59
Harvest index	49.40	141.40	35.20	59.54	34.94	8.57	42.91
Chlorophyll content	29.99	45.89	10.63	13.13	65.35	9.06	17.58

Table 6: Correlation coefficients among different morpho-phenological characters

	1	2	3	4	5	6	7	8	9	10
1: Yield	1									
2: Days to flowering initiation	-0.57*	1								
3: Days to 10% flowering	-0.57*	0.90**	1							
4: Days to 50% flowering	-0.59*	0.91**	0.97**	1						
5: Days to complete flowering	-0.57*	0.94**	0.96**	0.97**	1					
6: Days to complete ripening	-0.55*	0.75**	0.71**	0.76**	0.70**	1				
7: Crown to first branch distance	-0.1^{ns}	-0.57*	-0.49*	-0.45^{ns}	-0.39^{ns}	-0.01^{ns}	1			
8: Plant height	-0.16^{ns}	-0.28^{ns}	-0.43^{ns}	-0.46^{ns}	-0.41^{ns}	-0.2^{ns}	0.80**	1		
9: Harvest index	0.80**	-0.60**	-0.60**	-0.60**	-0.60**	-0.40^{ns}	-0.01^{ns}	-0.60**	1	
10: Chlorophyll content	-0.32*	0.25^{ns}	0.35^{ns}	0.30^{ns}	0.29^{ns}	-0.01^{ns}	-0.05^{ns}	-0.07^{ns}	-0.60^{ns}	1

**Significant at 1% level of probability, *Significant at 5% level of probability, ns: Non-significant probability

Mean range in the genotypes for Crown to First Node Distance (CND) was 8.36 to 47.80 cm. The difference between GCV and PCV for CND was high, showing the significant effects of the environment on its expression. The high values genetic gain (39.25%) was observed for CND (Table 5) showed this character was governed by additive genes in studied rapeseed genotypes.

The low heritability and genetic gain were observed in Plant Height (PH) (Table 4) due to larger phenotypic variances indicating great environmental influence. These results indicated that selection for this character would not be effective due to predominant effects of non additive gene in this population. In addition to this subject, PH had significantly correlation with CND variable only. Then this was not a suitable variable for selection.

The range of variation for Harvest Index (HI) was 2.97 to 41.56 with mean value 19.97. Genotypic and phenotypic co-efficient of variations were 35.20 to 59.54 (Table 5). This trait was positively and significantly correlated with grain yield. According to the results of this study, the positive direct effect of HI on yield supports the statement of breeding for increased HI remains the most effective method of breeding for high yield (Ali *et al.*, 2003).

Moderate heritability coupled with high genetic gain indicates the presence of additive gene effects; hence their improvement can be done through mass selection (Ali *et al.*, 2003).

The range of Chlorophyll Content (CLC) varied from 36.9-75.93. Genotypic and phenotypic co-efficient of variation were moderate (10.63-13.13).

The progress of a breeding program is conditioned by the magnitude and the nature of the genotypic and non-genotypic variation in the various characters. Since most of the economic characters (e.g., yield) are complex in inheritance and were greatly influenced by various environmental conditions, the study of heritability and genetic advance is very useful in order to estimate the scope for improvement by selection. Importance of heritability reveals the reliability with which the genotype will be identified by its phenotype expression (Chandrababu and Sharma, 1999).

The heritability estimates were high (>60%) for characters the all phenological traits and chlorophyll content. These traits were significantly and negatively correlation with grain yield. A comparatively low value of heritability was observed for the character grain yield, CND, PH and HI (<40%) (Table 5). The heritability estimates for different characters depend upon the genetic make up of the breeding materials studied. Therefore, understanding mentioned values in the materials in which breeders are interested is of great significance. High heritability estimates indicate that the selection for these characters will be effective being less influenced by environmental effects. Heritability estimates are useful to indicate relative value of selection based on phenotypic expression of different traits. Johnson *et al.* (1955) reported heritability values plus estimates of Genetic Gain (GG) were better than heritability alone in predicting the effect of selection. High heritability estimates associated with moderate genetic advance as percent mean (GG) were obtained in the characters i.e., DFI, DFF, DCF and CLC which indicated that selection for these characters would be more effective because these characters have high heritability and genetic advance. High heritability values followed by high genetic advance indicated the presence of additive gene action (Johnson *et al.*, 1955; Kashif *et al.*, 2003).

Grain yield among rapeseed genotypes range were from 27.60 to 393.55 g m^{-2} with mean value of 172.42 g m^{-2}. Low heritability and moderate genetic advance was observed for the grain yield as has been already reported by Ali *et al.* (2003). The results of correlation coefficient analysis showed that the all phonological traits, HI and CNC contributed significantly towards grain yield (Table 6). Among these traits, HI has correlated positively with grain yield only. It can be concluded on the basis of the results obtained in the present investigation that the range of variability was quite appreciable for almost all the characters studied among different genotypes.

By comparing the correlation coefficients values of nine independent variables against the yield per plant, significant differences became evident. Harvest index had highly significant association with grain yield. The harvest index was the only characteristics that exhibited the highest direct effect on yield per plant. Therefore, both these traits seem to be a good selection criterion to improve seed yield of winter type rapeseed. Similar results were also observed by Ali *et al.* (2003).

CONCLUSION

This indicated that there is sufficient variability available to have an effective selection. Genotypic and phenotypic coefficients of variations were high for grain yield, crown to first node distance, harvest index. High genetic gain was observed for HI and CND. Correlation analysis showed the grain yield was significantly and negatively correlated with phenological traits.

ACKNOWLEDGMENTS

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