

Heritability and genetic advance in rapeseed (*Brassica napus* L.)

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Abstract

The present study was carried out to estimate genetic variability parameters for some traits such as pods per plant, cell membrane stability, one thousand kernel weight, flowering period, grain filling period, chlorophyll content, relative water content, leaf excised water content, seed per pod and pod length, in 16 winter rapeseed genotypes. Statistical analysis showed significant differences between the tested genotypes. Genotypic and phenotypic coefficients of variations were high for yield, pods per plant and cell membrane stability. Heritability estimates were high for pods per plant, cell membrane stability, one thousand kernel weight and flowering period. A high genetic gain was observed for pods per plant and cell membrane stability. Correlation analysis showed a significant and negative relationship between the flowering and grain filling period (-0.883) and between cell membrane stability and chlorophyll content (SPAD) (-0.587). A positive and significant correlation was found between the grain yield and relative water content (0.603).

Keywords: Genetic variability, Heritability, Genetic gain, Rapeseed (*Brassica napus* L.).

ABBREVIATIONS

PPP: pods per plant; CMS: cell membrane stability; TKW: thousand kernel weight; FP: flowering period; GFP: grain filling period; SPAD: soil plant analysis

development; RWC: relative water content; LEWC: leaf excised water content; SP: seed per pod; PL: pod length; GCV: genotypic coefficient of variation; PVC: phenotypic coefficient of variation; GG: genetic gain.

INTRODUCTION

Rapeseed (*Brassica napus* L.) is one of the important agricultural crops especially for its edible oil. The meal remains after oil extraction is valuable as a source of protein for the livestock feed industries. In Iran, the production of rapeseed is mainly limited by drought and soil salinity.

Response to selection is resulted from significant genetic variation and high heritability (Falconer and Mackay, 1996; Shukla *et al.*, 2006). In plants, genetic variability and parameters are calculated for many crops (Kahrizi and Mohammadi, 2009; Maniee *et al.*, 2009; Kahrizi *et al.*, 2010 a, b; Garavandi *et al.*, 2011; Safavi *et al.*, 2011).

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 coupled with statistical analysis of inheritance data (Srivastava and Dhamania, 1986). 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 of a great importance in planning a successful breeding program

(Mary and Gopalan, 2006). The observed variability is a combined estimate of genetic and environmental causes, of which only the former is heritable. However, the estimates of heritability alone do not provide an idea about the expected gain in the next generation, but it has to be considered in conjugation with the estimates of genetic advance, the change in mean value between generations (Shukla *et al.*, 2006).

According to Raje and Rao (2000) genetic variability is essential in order to realize response to the selection. The estimates of genetic parameters of variation are specific for a particular population and the phenotypic expression of the quantitative characters may be altered by environmental stresses that affect plant growth and development. Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection (Hamdi *et al.*, 2003).

In a population under selection for a quantitative character, genotypic frequencies and hence gene frequencies are altered and these changes are further modified by the mating systems that may be employed to advance the selected individuals to the next generation (Chopra, 2000).

Generally, the success of any crop improvement program largely depends on nature, magnitude of genetic variability, genetic advance, characters association, direct and indirect effect on yield and yield attri-

butes. Correlation studies are useful in most breeding programs. Genetic diversity is important for selecting parents to recover transgressive segregates (Kiran and Ravisankar, 2004).

Heritability is a measure of the expression of a character. The estimates of heritability alone give no indication of the associating genetic progress that would result from selecting the best plants. Heritability along with phenotypic variance and the selection intensity, however, promise the estimation of genetic advance or response to selection, which is more useful in the selection of promising lines (Johnson *et al.*, 1955; Iqbal *et al.*, 2003; Rohman *et al.*, 2003).

The progress of a breeding program is conditioned by the degree and the nature of the genotypic and non-genotypic variation in various characters. Since most of the economic characters (e.g. yield) are complex in inheritance and are 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. Heritability levels show the reliability with which the genotype will be recognized by its phenotype expression (Chandrababu and Sharma, 1999).

The present investigation is aimed to evaluate variability, heritability and genetic advance of grain yield and its component characters in sixteen rapeseed genotypes to provide necessary information that could be

Table 1. The genotypes used in this study.

Number	Genotype	Source and origin	Type
1	Geronimo	Rosticafrance (European=Winter)-(Mexican-China-Canadian=Spring)	Winter
2	Celecious	Sralof	Winter
3	Milena	Germany	Winter
4	Sahra	Danisco	Winter
5	Sunday	Danisco	Winter
6	Zarfam	Iran	Winter
7	Dante	Germany	Winter
8	SLM-046	Germany	Winter
9	Talaye	Iran	Winter
10	Talent	Germany	Winter
11	ARC2	U. S. A.	Winter
12	Opera	SW-sweden	Winter
13	ARC5	U. S. A.	Winter
14	Licord	Germany	Winter-Spring
15	Elite	Rosticafrance (European=Winter)-(Mexican-China-Canadian=Spring)	Winter
16	Ebonite	Rosticafrance (European=Winter)-(Mexican-China-Canadian=Spring)	Winter

useful in rapeseed improvement programs aimed to improve yield character.

MATERIALS AND METHODS

This study was carried out with 16 genotypes based on complete randomized blocks design (CRBD) with three replications at the research farm of Razi University, Kermanshah, Iran. The names of genotypes, their origin and types are given in (Table 1). The size of plots was

4 m. Standard cultural practices were followed for raising the crop. The characters studied were yield, pods per plant (PPP), leaf excised water content (LEWC), relative water content (RWC), cell membrane stability (CMS), chlorophyll content (SPAD), seed per pod (SP), pod length (PL), thousand kernel weight (TKW), grain filling period (GFP) and flowering period (FP). Data were statistically analyzed for each character, separately. The analysis of variance for different characters was measured followed by the Duncan's new

Table 2. Mean squares for different characters of 16 genotypes of *B. napus*.

Source	df	Mean square										
		Yield	PPP	SP	PL	TKW	GFP	FP	SPAD	CMS	LEWC	RWC
Block	2	10058	1954.1	1.75	0.10	0.00	0.75	5.08	30.94	8.18	2.237	30.25
Geno- type	15	1519828**	16249**	17.83**	0.56**	0.44**	9.51**	49.8**	184.8**	253.26**	78.85**	189.10**
Error	30	8486	827.16	1.77	0.06	0.021	0.76	1.39	32.22	15.77	7.36	19.21

** : Significant at 1% level of probability.

Where PPP: pods per plant; CMS: cell membrane stability; TKW: thousand kernel weight; FP: flowering period; GFP: grain filling period; SPAD: soil plant analysis development (chlorophyll content); RWC: relative water content; LEWC: leaf excised water content; SP: seed per pod; PL: pod length.

Table 3. Mean performance of 16 genotypes of *B. napus* for different characters.

Geno- type	Yield (kg/ha)	PPP	SP	PL (cm)	TKW (g)	GFP	FP	SPAD (%)	CMS (%)	LEWC (%)	RWC (%)
1	3474 ^c	319.6 ^{b-d}	27.83 ^{c-f}	8.6 ^a	4.5 ^{ab}	48.00 ^{b-e}	20.7 ^c	52.0 ^{ab}	47.80 ^{c-e}	76.5 ^a	83.3 ^{ab}
2	3609 ^c	203.3 ^{fg}	27.47 ^{d-f}	7.1 ^{cd}	4.2 ^{bc}	33.47 ^{c-g}	67.3 ^b	28.2 ^{b-f}	64.90 ^{c-e}	73.5 ^{a-c}	81.2 ^{ab}
3	2235 ^f	358.6 ^{a-c}	28.27 ^{c-f}	7.5 ^{bc}	3.8 ^{de}	46.00 ^{e-g}	20.7 ^c	50.6 ^{a-c}	15.02 ^{b-d}	78.1 ^a	63.7 ^d
4	2649 ^e	398.1 ^a	25.88 ^{ef}	7.7 ^{bc}	4.7 ^a	47.67 ^{b-f}	29.0 ^{ab}	47.3 ^{a-e}	37.90 ^{ef}	76.1 ^a	68.5 ^{cd}
5	3161 ^d	254.8 ^{d-g}	28.42 ^{c-f}	7.6 ^{bc}	3.8 ^{de}	48.33 ^{b-d}	19.7 ^c	59.6 ^a	35.35 ^f	68.6 ^{bc}	74.6 ^{bc}
6	4276 ^a	388.8 ^{ab}	34.46 ^a	7.8 ^{bc}	3.9 ^{cd}	45.67 ^{fg}	30.3 ^a	45.0 ^{b-f}	52.20 ^{bc}	74.0 ^{ab}	81.8 ^{ab}
7	4042 ^b	321.9 ^{b-d}	29.04 ^{b-e}	6.6 ^d	4.3 ^{bc}	45.67 ^{fg}	20.3 ^c	32.1 ^f	55.30 ^{bc}	76.8 ^a	81.1 ^{ab}
8	3665 ^c	263.2 ^{d-f}	27.93 ^{c-f}	7.9 ^b	3.6 ^{d-f}	49.33 ^{bc}	20.7 ^c	35.6 ^{d-f}	32.08 ^f	76.5 ^a	87.2 ^a
9	3213 ^d	186.2 ^{gh}	27.73 ^{d-f}	7.5 ^{bc}	3.6 ^{d-f}	45.33 ^g	30.7 ^a	48.6 ^{a-e}	38.40 ^{ef}	73.5 ^{a-c}	86.0 ^a
10	2357 ^f	281.9 ^{de}	28.14 ^{c-f}	7.5 ^{bc}	3.3 ^f	47.67 ^{b-f}	19.3 ^c	58.0 ^{ab}	41.02 ^{d-f}	57.3 ^d	86.4 ^a
11	3695 ^c	275.5 ^{d-f}	32.31 ^{ab}	7.4 ^{bc}	3.9 ^{de}	49.67 ^b	26.7 ^b	38.0 ^{b-f}	53.50 ^{bc}	67.0 ^c	83.9 ^{ab}
12	2794 ^e	258.0 ^{d-f}	29.56 ^{b-d}	7.9 ^b	3.8 ^{de}	47.00 ^{d-g}	21.3 ^c	49.9 ^{a-d}	45.80 ^{c-e}	73.7 ^{a-c}	88.4 ^a
13	2264 ^f	242.9 ^{e-g}	31.22 ^{bc}	7.4 ^{bc}	3.5 ^{ef}	46.67 ^{d-g}	20.3 ^c	38.8 ^{b-f}	65.50 ^a	75.0 ^{ab}	67.4 ^{cd}
14	4179 ^{ab}	126.8 ^h	28.08 ^{c-f}	7.8 ^b	3.7 ^{de}	51.67 ^a	22.3 ^c	34.7 ^{ef}	45.34 ^{c-e}	74.5 ^{ab}	86.9 ^a
15	2261 ^f	207.4 ^{fg}	32.12 ^{ab}	7.9 ^b	3.7 ^{de}	49.33 ^{bc}	19.3 ^c	42.8 ^{b-f}	38.90 ^{ef}	73.5 ^{a-c}	74.0 ^{b-d}
16	3655 ^c	297.5 ^{c-e}	25.16 ^f	7.8 ^b	3.7 ^f	49.67 ^b	21.7 ^c	35.9 ^{c-f}	59.30 ^{ab}	76.2 ^a	86.9 ^a

Note: Means followed by the same letter (s) in each column are not significantly different according to the Duncan's multiple range test (probability level of 5%).

Where PPP: pods per plant; CMS: cell membrane stability; TKW: thousand kernel weight; FP: flowering period; GFP: grain filling period; SPAD: soil plant analysis development (chlorophyll content); RWC: relative water content; LEWC: leaf excised water content; SP: seed per pod; PL: pod length.

Table 4. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance in percentage of mean for different characters of 16 genotypes of *B. napus*.

Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (%)	Genetic gain (%)
PPP	26	28	86.14	136.86	49.94
SP	8	9	75.14	3.85	13.15
PL	5	6	65.38	0.59	07.74
TKW	10	10	87.50	0.66	16.95
GFP	7	8	79.35	3.16	13.42
FP	8	9	92.06	7.76	16.23
SPAD	15	20	61.22	11.27	24.29
CMS	19	21	83.39	16.06	34.55
LEWC	7	8	76.40	8.05	11.01
RWC	9	11	74.67	12.56	15.68

Where PPP: pods per plant; CMS: cell membrane stability; TKW: thousand kernel weight; FP: flowering period; GFP: grain filling period; SPAD: soil plant analysis development (chlorophyll content); RWC: relative water content; LEWC: leaf excised water content; SP: seed per pod; PL: pod length.

multiple range test (DMRT) (Steel and Torrie, 1960), to test the significant differences 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 coefficients of variation and heritability were calculated as suggested by Singh and Chowdhury, (1985) and genetic advance by Allard (1960) as well as correlation coefficient by Zaman *et al.*, (1982).

RESULTS

The analysis of variance and mean comparison results are shown in (Tables 2 and 3), respectively. The genotypes showed significant differences for all traits in this study, indicating the presence of an adequate variability among the genotypes for effective selection to identify the superior genotypes (Table 2). These results are in agreement with those of Ali (1985) and Ali *et al.*, (2002).

Among these genotypes, seed yield ranged from 2357 to 4276 kg/ha and the highest yield (4276 kg/ha) was obtained from the Zarfam genotype with the highest seed per plant (34.46).

The high heritability (86.14) and genetic gain (46.94) was observed for PPP, indicating the major part of phenotypic variations belonging to genotypic variation (Table 4). Also, high genotypic and phenotypic coefficients of variation (GCV and PCV) were observed (Table 4).

In the case of SP, genotypes ranged from 25.88 to

35.5 and the mean was 29.28 (Table 5). Average genotypic and phenotypic coefficients of variations (GCV and PCV), heritability and genetic gain were observed for SP (Table 4). The SP showed a non-significant correlation with other traits (Table 6).

The PL varied from 6.64 to 8.70 cm with a mean value of 7.66 cm (Table 5). Heritability (h^2) was moderate (65.38) and genetic gain (GG) was low (7.74) for the above trait, indicating that the phenotypic variations belonged to genotypic and environmental variations (Table 4). The TKW varied from 3.37 to 4.75 (gr) with a mean value of 3.89 (gr) (Table 5). Heritability (h^2) and genetic gain were high and moderate for this trait, re-

Table 5. Range, mean, standard error of mean and coefficient of different characters of 16 genotypes of *B. napus*.

Characters	Range	Mean	Coefficient of variation (%)
Yield	2357-4276	3220.64	2.83
PPP	126.8-398.1	274.03	10.50
SP	25.88-35.5	29.28	4.59
PL	6.64-8.70	7.66	3.24
TKW	3.3-4.75	3.89	3.71
GFP	20-31	23.56	1.76
FP	45.33-51.67	47.81	5.11
SPAD	26.96-84.07	46.39	12.97
CMS	32.08-65.52	46.47	8.51
LEWC	57.3-78.1	73.16	3.71
RWC	63.74-88.37	80.10	5.47

Where PPP: pods per plant; CMS: cell membrane stability; TKW: thousand kernel weight; FP: flowering period; GFP: grain filling period; SPAD: soil plant analysis development (chlorophyll content); RWC: relative water content; LEWC: leaf excised water content; SP: seed per pod; PL: pod length.

Table 6. Correlation coefficient among different characters of *B. napus*.

Charac- ters	Yield	pH	PPP	SP	PL	TKW	GFP	FP	SPAD	CMS	LEWC	RWC
Yield	1.00											
pH	-0.31	1.00										
PPP	-0.06	-0.10	1.00									
SP	0.06	0.07	0.04	1.00								
PL	0.08	0.30	0.08	-0.06	1.00							
TKW	0.07	-0.24	0.36	0.10	0.23	1.00						
GFP	-0.02	0.08	0.06	0.11	0.33	-0.11	1.00					
FP	0.25	-0.12	-0.16	-0.14	-0.15	0.23	-0.89**	1.00				
SPAD	-0.47	0.08	0.28	0.00	0.19	-0.10	0.27	-0.43	1.00			
CMS	0.38	0.48	-0.17	0.15	-0.08	-0.04	-0.30	0.39	-0.59*	1.00		
LEWC	0.20	-0.09	0.18	-0.12	0.26	0.34	-0.07	0.04	-0.29	-0.01	1.00	
RWC	0.60*	0.14	-0.35	-0.08	0.21	-0.27	0.10	0.06	-0.24	0.28	-0.26	1.00

*, **: Significant at 1% and 5% levels of probability, respectively.

Where PPP: pods per plant; CMS: cell membrane stability; TKW: thousand kernel weight; FP: flowering period; GFP: grain filling period; SPAD: soil plant analysis development (chlorophyll content); RWC: relative water content; LEWC: leaf excised water content; SP: seed per pod; PL: pod length.

spectively that indicates this trait is influenced by both additive and dominant effects.

The range of variation for GFP was 20 to 31 with a mean value of 23.56. GCV and PCV values for this trait were 7 and 8, respectively (Table 4). Heritability (79.35) and genetic gain (13.42) were moderate for this trait. The GFP showed a significant and negative correlation (-0.883) with FP. This indicates that with decreasing flowering period (FP) grain filling period will increase.

The FP varied from 45.33 to 51.67 with a mean value of 47.81 (Table 5). Heritability (h^2) and genetic gain (GG) were high and moderate for this trait, respectively. As mentioned above, a reduction in this period increased grain filling period.

The range of variation for SPAD was 26.96 to 84.07 with a mean value of 46.39. Heritability (h^2) and genetic gain (GG) were moderate for this trait. The SPAD showed a significant and negative correlation (-0.587) with CMS.

CMS varied from 32.08 to 65.52 with a mean value of 46.47 (Table 5). Heritability (h^2) and genetic gain (GG) were high for this trait (Table 4). These results indicated that environment had a little effect on the expression of CMS. It further shows that the genotypes of *B. napus* were governed by additive genes.

The range of variation for LEWC was 57.3 to 78.1 with a mean value of 73.16. The heritability (h^2) and

genetic gain (GG) were moderate for this trait.

RWC varied from 63.74 to 88.37 with a mean value of 80.10 (Table 5). Heritability (h^2) and genetic gain (GG) were moderate. RWC showed a significant and positive correlation (0.63) with grain yield. This indicates that genotypes with a higher relative water content can produce a higher grain yield.

DISCUSSION

A low GG was observed for PL indicating that selection for this character would not be effective due to the predominant effects of non additive genes in this population. Then, this is not a suitable variable for selection. This result is in agreement with those found by Maniee *et al.*, (2009).

The basic objective of any breeding and bio-engineering program is the improvement of crop yield. The measurement and evaluation of variability are essential steps in drawing meaningful conclusions from a given set of observations (Mehdi and Khan, 1994; Marwede *et al.*, 2004). Genetic variability of a metric trait can be studied by the use of various statistical parameters such as mean, range, variance components and coefficients of variation.

The heritability estimates for different characters depend upon the genetic make up of the breeding materials studied. Therefore, the knowledge about the materials values 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 have been found to be useful in indicating the relative values of selection based on phenotypic expression of different characters.

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