Full Length Research Paper

Genetic variability of some rapeseed (*Brassica napus* L.) cultivars in Southern Iran

Mahdi Zare* and Shahram Sharafzadeh

Department of Agriculture, Firoozabad Branch, Islamic Azad University, Firoozabad, Iran.

Eight rapeseed cultivars were studied for variability, heritability and correlation analysis of seed yield and yield components in Southern Iran for two years (2009 and 2010). These genotypes were planted in field arranged on randomized completely blocks design with three replications at the Research Centre of Islamic Azad University of Firoozabad, 95 km of Shiraz. The studied traits were days from emergence to flowering, days from emergence to physiological maturity, plant height, pod length, pods number on main stem, pods per plant, seeds per pod, 1000-seed weight, harvest index and grain yield. Results showed that genetic variability of genotypes was significant for all traits except for pod length and seeds per pod. Interaction between year and genotype was highly significant for seeds per pod. Based on broad sense heritability of traits and correlation between grain yields and other traits, pods per plant, 1000-grain weight and pods on main stem had high direct effect on grain yield in both years. Therefore, selection for increasing grain yield through these traits might be more successful. Selection of desirable varieties to increase grain yield is based on yield component. Based on the results of cluster analysis, the genotypes were grouped into four clusters irrespective of the geographical divergence. Therefore, Modena and Sarigol cultivars were the best resources to increase grain yield during both years and Okapi cultivar was the worst.

Key words: Rapeseed, heritability, correlation, grain yield.

INTRODUCTION

Rapeseed (*Brassica napus* L.) oil ranks third behind soybean (*Glycine max* L.) and oil palm (*Guineensis elaeis*) showing the importance of this product. Apart from direct human and animal consumption, industrial uses include the manufacture of rapeseed oil and convert biomass to bioenergy have been developed in the recent years in world (Ofori and Becker, 2008). Iran has had an important rapeseed breeding program in recent years, supported by the Seed and Plant Improvement Institute (Sabaghnia et al., 2010). Seed yield is 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. Therefore, information on the association of plant characters with seed yield is of great importance to a breeder in selecting a desirable genotype (Hakan, 1999).

Identification of superior cultivars requires variation in the population (Murtaza, 2005). Large genotype × environment effects tend to be viewed as problematic in breeding because the lack of a predictable response hinders progress from selection (Dudley and Moll, 1969). Dudley (1997) have emphasized that information on the inheritance of quantitative traits have application to planning breeding strategies for cultivar development. Cluster analysis is a useful technique for describing differential yield responses of breeding cultivars grown across environments (Yau and Oritz-Ferrara, 1994). Cultivar identification and discrimination has become an important issue in rapeseed breeding programs (Mailer et al., 1997).

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,

_____

*Corresponding author. E-mail: zaremahdi@hotmail.com. Tel: + 989173064147. Fax: +987126224402.

Table 1. Bartlett's test for homogeneity of variances based on χ^2 distribution.

Trait	χ^2
days from emergence to flowering	2.23581 [ns]
days from emergence to physiological maturity	1.70677 [ns]
plant height (cm)	0.34265 [ns]
pod length	1.50246 [ns]
pods on main stem	0.05065 [ns]
pods per plant	0.022942 [ns]
seeds per pod	0.00007 [ns]
1000-seed weight (g)	15.04488 [ns]
harvest index	0.52213 [ns]
grain yield (g plant^{-1})	1.36013 [ns]

$\chi^2_{0.05}$ (14) = 23.68. ns: not significant.

length of pod was negatively correlated with seed yield. Singh and Singh (1997) reported greatest positive direct of pods per plant, seeds per plant and seed weight on 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. 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.

The objective of this study was to evaluate the performance of eight rapeseed cultivars during two different years, estimate the heritability and relationship between seed yield and related traits in rapeseed for potential use as selection criteria.

MATERIALS AND METHODS

Eight rapeseed genotypes Modena (G1), Okapi (G2), Sarigol (G3), Licord (G4), Hyola308 (G5), Zarfam (G6), RGS003 (G7) and SLM046 (G8) of winter rapeseed were planted in field at the Research centre of Islamic Azad University of Firoozabad (28.35°N, 52.40°E and 1327 m above sea level). The experiment was conducted as randomly completed blocks design with three replications. Seeds were hand-sewn on December 24 and 21 in 2008 to 2009 and 2009 to 2010 growing seasons respectively. Each plot consisted of 6 rows with 3 m long and spacing of 10 cm between plants within row and 30 cm between rows (180 plant plot^{-1}).

Fertilizer broadcast were 150 kg/ha of ammonium phosphate, 150 kg/ha of potassium sulphate and 60 kg/ha N applied prior to planting plus an additional 60 kg/ha N topdressed at 7 to 9-leaf stage. Hand-weeding was carried out four times during the growth period. Eight plant samples were chosen from middle part of each row and were signed by labels and the border parts were left out. Then, the labeled plant samples were measured for the following traits: days from emergence to flowering, days from emergence to physiological maturity, plant height, pod length, pods on main stem, pods per plant, seeds per pod, 1000-seed weight, harvest index and grain yield. Seed yield was measured at physiological maturity and yield was adjusted to 12.5% seed moisture content.

The data were tested for skewness, kurtosis, homogeneity of variance and normality by MINITAB (1998) statistical software. Then, combined analysis of variance based on Random Complete Block Design (RCBD), phenotypic correlation and comparison of quantitative traits means based on Duncan's new multiple range test (DNMRT), were performed in SAS (2001). Interaction analysis was carried out by MSTATC software. Minitab software was used for cluster analysis and its dendrogram draw. Broad sense heritability (h^2_{bs}) was calculated based on Singh and Ceccarelli (1996) formula as follows:

$$h^2_{bs} = \frac{V_G}{V_G + V_E + V_{GE}}$$

Where, V_G = genotypic variance; V_E = environmental variance and V_{GE} = interaction between genotype and environment.

The phenotypic correlation between variable x and y (r_{xy}) was also estimated following Kwon and Torrie (1964):

$$r_{xy} = \frac{Cov_{xy}}{\sqrt{(Var_x . Var_y)}}$$

Where, Cov_{xy} = covariance between variable x and y, Var_x = variance of x and Var_y = variance of y.

RESULTS AND DISCUSSION

The results of Bartlett's test are given in Table 2. The χ^2 values were not significant ($P > 0.05$) for all traits, indicating homogeneity of variances for them (Table 1). Therefore, allowed the use of combined analysis of variance for all traits.

The combined analysis of variance (ANOVA) for all traits during two years showed significant differences between the years for days from crop emergence to flowering, days from crop emergence to physiological maturity, plant height, seeds per pod and harvest index (Table 2). Genetic variability of genotypes was significant for all traits except for pod length and seeds per pod.

Table 2. Combined analysis of variance for traits in rapeseed.

S.O.V.	df	Mean of squares									
		Days from crop emergence to flowering	Days from emergence to physiological maturity	Plant height (cm)	Pod length	Pods on main stem	Pods per plant	Seeds per pod	1000-seed weight (g)	Harvest index	Grain yield (g plant-1)
Year	1	136.68**	243*	27.65*	0.023 ns	14.63 ns	128.31 ns	153.9*	0.203 ns	0.1418**	87185.18 ns
Rep (year)	4	6.35	20.42	1.98	0.612	41.52	177.63	4.17	0.243	0.0004	256518.65
Genotype	7	468.78**	348.32**	1190.99**	0.448 ns	331.0**	705.89**	8.41 ns	2.60**	0.005**	3542765**
Year* genotype	7	2.78 ns	3.43 ns	2.40 ns	0.005 ns	5.82 ns	0.48 ns	22.81**	0.02 ns	0.0006 ns	84510.57 ns
Error	28	5.57	8.61	62.79	0.445	18.62	54.28	1.58	0.134	0.0005	108059.22
%CV		2.25	1.5	5.79	10.37	13.7	8.81	6.41	10.79	4.98	11.63
%h^2_{bs}		93.3	87	75.9	14.3	74.4	68.4	-	76.2	20.2	74.2
Correlation [a]	2009	-0.15 ns	-0.36*	-0.29 ns	0.03 ns	0.38*	0.57**	0.30 ns	0.45*	0.58**	-
	2010	-0.28 ns	-0.37*	-0.34*	0.04 ns	0.34*	0.54**	0.32*	0.52**	0.32*	-

ns, * and **: Not significant, significant at the 5% and 1% levels of probability, respectively; a: coefficient of phenotypic correlation between grain yield and other traits.

Interaction between year and genotype was highly significant for seeds per pod, indicating that genotypes did not respond to the environments similarly (Table 2). Y1*G1 and Y2*G3 interactions had the highest and lowest seeds per pod, respectively (Figure 1). Non-significant year × genotype interaction indicated that selection for days from crop emergence to flowering, days from crop emergence to physiological maturity, plant height, pod length, pods on main stem, pods per plant, 1000-seed weight, harvest index and grain yield at one environment might be effective for a broad range of environments.

Broad sense heritability varied from low (14.3%) for pod length to very high (93.3%) for days from crop emergence to flowering. Days from crop emergence to physiological maturity, 1000-seed weight, plant height and grain yield also had high broad sense heritability (87, 76.2, 75.9 and 74.2%, respectively). The relatively high values indicate the possibility of genetic gain in selection for these traits based on selection. The broad

sense heritability estimate for these traits was consistent with the estimates given by Sabaghnia et al. (2010) for 1000-seed weight of rapeseed.

Comparison between means showed that Okapi and Licord cultivars had the highest days from crop emergence to flowering and days from crop emergence to physiological maturity (Table 3). Hyola308 and Zarfam cultivars had the lowest days from emergence to flowering and days from emergence to physiological maturity, respectively. In plant breeding, decreasing days from emergence to flowering and physiological maturity traits are suitable for grain yield improvement (Yadava and Singh, 1999). Therefore, these cultivars seem to be suitable. Both Okapi and Licord cultivars also had the highest plant height and Zarfam had the lowest plant height. Since high plant height can decrease grain yield via lodging and breaking, Zarfam can be used for decreasing plant height (Table 3).

Licord and Okapi cultivars had the highest and lowest pods on main stem and pods per plant.

Modena cultivar had the highest 1000-grain weight and Okapi and Zarfam cultivars had the lowest 1000- grain weight. Modena and Sarigol cultivars had the highest grain yield and Hyola308 and RGS003 cultivars had the lowest grain yield (Table 3).

Based on the dendrogram of cluster analysis, the genotypes were grouped into four clusters irrespective of the geographical divergence (Figure 2). Based on the results, Modena and Sarigol, which had the highest grain yield, were located in a major cluster and Okapi, which had the lowest grain yield, was located in a single cluster else. SLM046, RGS003 and Hyola308 cultivars, which had lower grain yield, were placed in the third cluster that was partitioned into two small clusters. The fourth cluster included Licord and Zarfam cultivars also had high grain yield (Figure 2).

The results of correlation coefficient among the traits studied during 2009 and 2010 are shown in Table 2. Highly significant and positive correlation
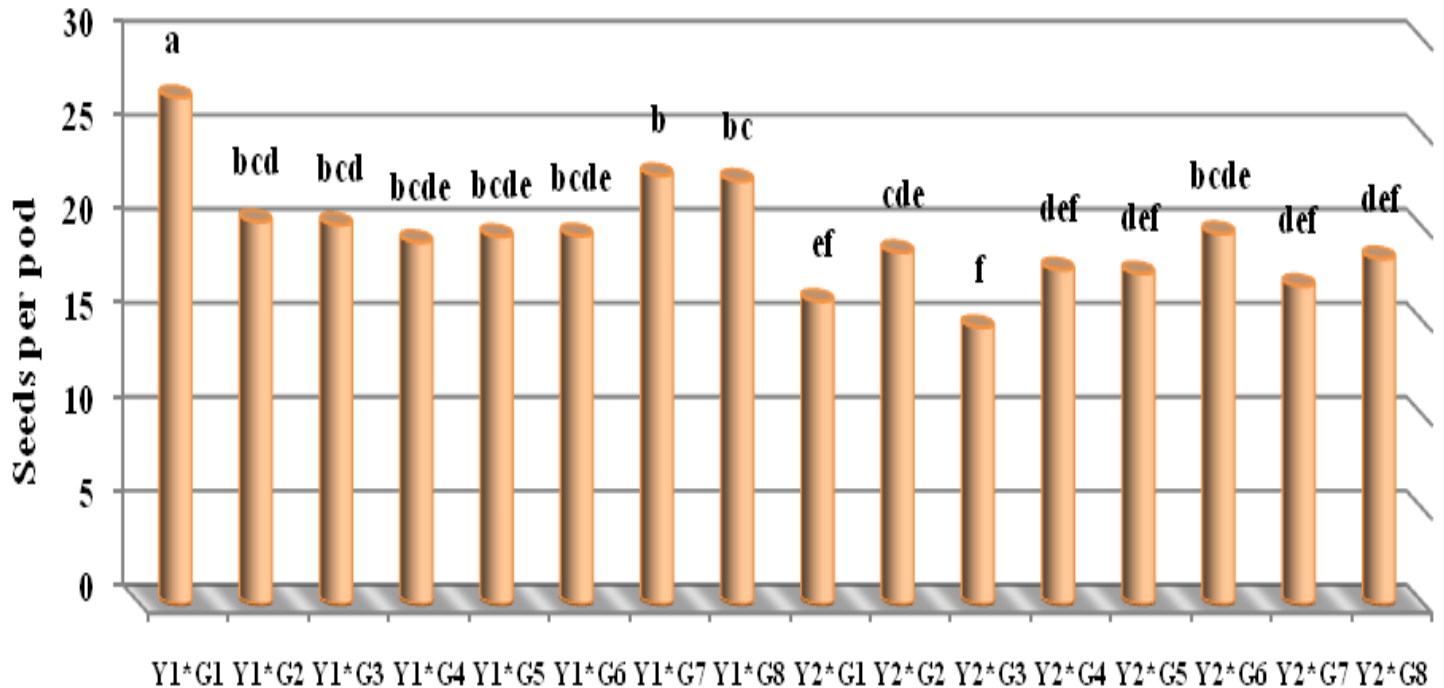
Figure 1. Interaction between years (Y) and genotypes (G) on seeds per pod in rapeseed (combined analysis of 2008 t0 2009 and 2009 to 2010 sasons).

(p < 0.01) was observed between pods per plant and grain yield in both years (r = 0.57 in 2009 and r = 0.54 in 2010,respectively). Ivanovska et al. (2007) also found highly significant and positive correlation of seed yield with pods per plant. On the other hand, negative significant correlations were recorded between days from emergence to physiological maturity and grain yield in both years (r = -0.36 in 2009 and r = -0.37 in 2010, respectively). Ali et al. (2003) also reported the same results for these two traits. Correlations between days from emergence to flowering and grain yield were not significant and negative during both years (r = -0.15 in 2009 and r = -0.28 in 2010, respectively). Sabaghnia et al. (2010) reported non-significant negative correlation between days from emergence to flowering with grain yield.

In both years, correlation between 1000-grain weight and grain yield was statistically significant (p < 0.05 and p < 0.01, respectively) and positive (r = 0.45 in 2009 and r = 0.52 in 2010, respectively). Marjanovich et al. (2008) also reached similar inferences regarding correlations between 1000- grain weight and grain yield. We obtained that there was a statistically significant (p < 0.05) and negative correlation (r = -0.34) between plant height and grain yield only in 2009. Results indicated that negative and non-significant statistically correlation between plant height and grain yield was lower in second year than first year. There was non-significant (p > 0.05) and positive

correlation between pod length and grain yield during two years (r = 0.03 in 2009 and r = 0.04 in 2010, respectively). The results of our study were in agreement with Azadgoleh et al. (2009) who reported non-significant positive correlation between pod length and grain yield in rapeseed. Pods on main stem positively correlated with grain yield at 5% probability level in both years (r = 0.38 in 2009 and r = 0.34 in 2010, respectively), which was in agreement with the results of Sabaghnia et al. (2010). Seeds per pod was significantly positively correlated with grain yield (r = 0.32) in 2010. The correlation between these two traits was positive and non-significant (r = 0.3) in 2009. Correlations between harvest index and grain yield were statistically significant (p < 0.01 and p < 0.05, respectively) and positive (r = 0.58 in 2009 and r = 0.32 in 2010, respectively). Sabaghnia et al. (2010) reported similar results for these traits.

Based on broad sense heritability of traits and correlation between grain yields and other traits, pods per plant, 1000-grain weight and pods on main stem had high direct effect on grain yield in both years. Therefore, selection for increasing grain yield through these traits might be more successful. Selection of desirable varieties to increase grain yield is based on yield component. Based on the results of cluster analysis, Modena and Sarigol cultivars were the best resources to increase grain yield during both years and okapi cultivar was the worst.

Table 3. Effect of genotypes on traits in rapeseed (combined analysis of 2008 to 2009 and 2009 to 2010 seasons).

Treatment		Mean									
		Days from crop emergence to flowering	Days from emergence to physiological maturity	Plant height (cm)	Pod length	Pods on main stem	Pods per plant	Seeds per pod	1000-seed weight (g)	Harvest index	Grain yield (g plant^{-1})
Year	2009	106.71^a	196.54^a	136.19^b	6.46^a	30.94^a	85.28^a	21.42^a	3.34^a	0.410^b	2782.9^a
	2010	103.33^b	192.04^b	137.71^a	6.41^a	32.05^a	82.01^a	17.84^b	3.47^a	0.519^a	2868.1^a
Genotype	Modena	105.83^c	191.5b^c	138.62^b	6.45^a	32.97^{bc}	82.06^{cd}	21.01^a	4.61^a	0.4996^a	3732.9^a
	Okapi	113.5^a	205.17^a	161^a	6.62^a	21.28^e	70.2^e	19.9^a	2.69^d	0.4263^d	1429.1^e
	Sarigol	100.83^d	190^c	125.67^{de}	6.06^a	26.38^{de}	91.67^b	17.47^a	3.77^b	0.4705^{abc}	3738.1^a
	Licord	115.83^a	206^a	119.93^a	6.44^a	45.03^a	104.8^a	19.07^a	3.07^{cd}	0.4543^c	3182.2^b
	Hyola308	88.67^e	188.67^c	128.35^{cde}	6.17^a	31.72^{cd}	73.82^{de}	19.09^a	3.39^{bc}	0.4244^d	2452.9^d
	Zarfam	98.33^d	184.67^d	119.93^e	6.22^a	26.23^{de}	82.9^{bcd}	19.17^a	2.63^d	0.4933^a	3000.6^{bc}
	RGS003	109.67^b	193.67^b	130.63^{bcd}	6.66^a	37.93^b	85.36^{bc}	20.37^a	3.84^b	0.459^{bc}	2360.5^d
	SLM046	107.5b^c	194.67^b	137.85^{bc}	6.86^a	30.4^{cd}	78.3^{cde}	20.97^a	3.2^c	0.4864^{ab}	2707.6^{cd}

ns, * and **: Not significant, significant at the 5% and 1% levels of probability, respectively..
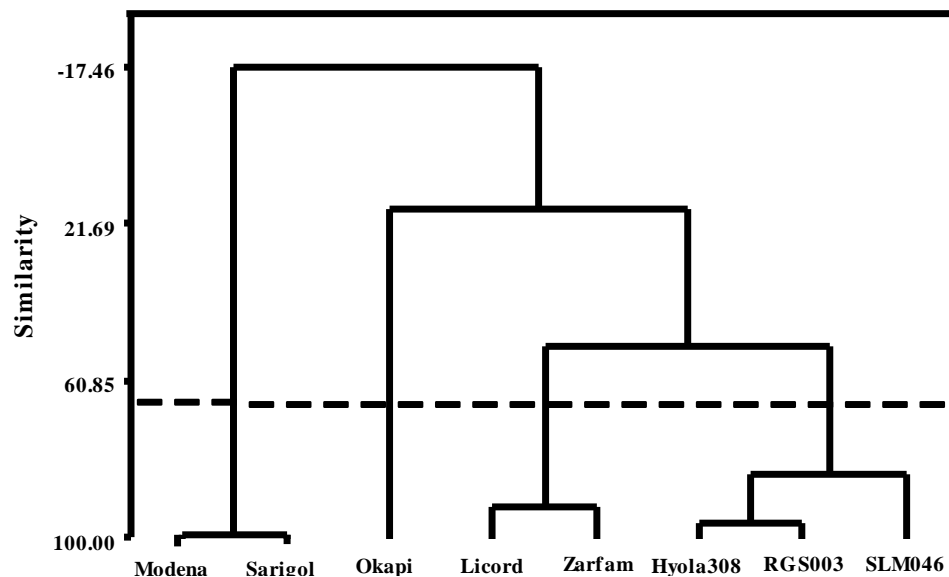

Figure 2. Cluster analysis of eight rapeseed cultivars using Ward method.

REFERENCES

Ali N, Javidfar F, Elmira JY, Mirza MY (2003). Relationship among yield components and selection criteria for yield improvement in winter rapeseed (*Brassica napus* L.). Pak. J. Bot., 35: 167-174.

Dudley JW (1997). Quantitative genetics and plant breeding. Adv. Agron., 59: 1-23.

Dudley JW, Moll RH (1969). Interpretation and use of estimates of heritability and genetic variances in plant brreding. Crop Sci., 9: 257-262.

Azadgoleh EMA, Zamani M, Yasari E (2009). Agronomical important traits correlation in rapeseed (*Brassica napus* L.) genotypes. Res. J. Agric. Biol. Sci., 5(5): 798-802.

Hakan Z (1999). Relations between yield and yield components on currently improved spring rapeseed cultivars. Tr. J. Agric. For., 23: 603-607.

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

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

Marjanovic-Jeromela A, Marinkovi R, Mijic A, Zdunic Z, Ivanovska S, Jankulovska M (2008). Correlation and path analysis of quantitative traits in winter rapeseed (*Brassica napus* L.). Agric. Consp. Sci., 73: 13-18.

Minitab (1998). MINITAB 12. Minitab, State College, PA.

Murtaza N (2005). Study of gene effects for boll number, boll weight, and seed index in cotton. J. Central Eur. Agric., 6(3): 255-262.

Ofori A, Becker HC (2008). Breeding of brassica rapa for biogas production: heterosis and combining ability of biomass yield. Bioenergy Res., 1: 98-104.

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 (2001). SAS user's guide. Version 8. SAS Institute Inc Cary, NC.

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

Singh M, Ceccarelli S (1996). Estimation of heritability of crop trial data. Technical Manual International Center for Agricultural Research in the Dry Areas, Aleppo, Syria, p. 21.

Singh M, Singh G (1997). Correlation and path analysis in Indian mustard (*Brassica juncea* L.) under mid hills of Sikkim. J. Hill Res. (India), 10(1): 557-585.

Yadava JS, Singh NB (1999). Strategies to enhance yield potential of rapeseed-mustard in India. Proceedings of 10th International Rapeseed Congress, Conbbera, Australia, www.regional.org.au/au/gcirc/6/634.htm-34k.

Yau SK, Ortiz-Ferrara G (1994). Regression and cluster analysis of elite wheat lines grown in rainfed environment. J. Genet. Breed., 48: 183-190.

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.