

Variance, Heritability, Genetic Advance and Correlation Coefficient of Some Phenological, Morphological and Productivity Traits in Some Lentils (*Lens culinaris* M.) Genotypes

Mohammad Nael Khattab^{*(1)}

(1). Crops Field Department, Faculty of Agriculture, Tishreen University, Latakia, Syria.

(*Corresponding author: Dr. Mohammad Nael Khattab. E-Mail: aboalabd876@gmail.com).

Received: 20/09/2017

Accepted: 08/11/2017

Abstract

The phenological, morphological and productivity characteristics of six lentil genotypes (Idlib 1, Idlib 2, Idlib 3, Idlib 4, Balade and Kurdi) were assessed, using some genetic indicators (genetic and phenotypic variance, genotypic and phenotypic correlation coefficients, broad- sense heritability, and the genetic advance between seeds yield and its components at Dmsrkho area, in Latakia during two seasons (2014/2015) and (2015/2016). Randomized complete block design with three replicates was used, in order to investigate as much as possible, the genetic power of the genotypes to exploit them to the fullest extent and determine the appropriate selectorial evidence to improve lentils crop. Analysis of variance indicated that the genotypes differ significantly ($P < 0.05$) for all studied characters. Moreover, years, genotype and years by genotypes interaction were significant for all studied traits. Phenotypic coefficient of variation was slightly higher than genetic coefficient of variation, and heritability values were high for most traits, this indicates the dominance of genetic factors and the low impact of environmental factors. Seed yield/plant (g) had a significant, positive genotypic and phenotypic correlation on number of pods/plant ($r_g = 0.905^{**}$ and $r_{ph} = 0.907^{**}$), while hundred seed weight ($r_g = 0.294^{**}$ and $r_{ph} = 0.294^{**}$) and biological yield ($r_g = 0.76^{**}$ and $r_{ph} = 0.78^{**}$). Biological yield had significant positive genotypic and phenotypic correlation with hundred seed weight ($r_g = 0.62^*$ and $r_{ph} = 0.59^*$) and seed yield ($r_g = 0.93^*$ and $r_{ph} = 0.95^{**}$). This indicates the possibility of selection for the biological yield through the selection of hundred seed weight and seed yield.

Keywords: Lentil, Heritability, Genetic advance, Genetic variance, Phenotypic variance, Correlation coefficient.

Introduction:

Lentil (*Lens culinaris* Medik. subsp.culinaris, $2n = 14$), belongs to the Leguminosae family (Bond *et al.*, 1983), which is considered the fourth most important pulse (legume) crop in the world, after beans, peas and chickpeas, according to FAO statistical office (FAOSTAT, 2009). This crop is originated in Eastern Mediterranean region, which is the center of genetic diversity (Ladizinsky, 1979). Lentils are a major source of human nutrition, containing a group of essential amino acids which are essential for the human body, especially lysine (Anonymous, 2008). The seeds had the importance as fodder because it contains a percentage of minerals (2%) and carbohydrates (59%) (Frederick *et al.*, 2006). In addition to the lentils role in crop rotation, it has the ability to fix the atmospheric nitrogen by *Rhizobium leguminosorum*, this provides the amounts of nitrogen fertilizers to be added to the soil (Dixit *et al.*, 2011).

The study and evaluation of genetic material is a key step in improving any crop of importance in the development of genetic and agricultural characteristics (Meena and Baha, 2013). The genetic

variation between and within populations of crop species is a major interest of plant breeders and geneticists (Edossa *et al.*, 2007).

Genotypic and phenotypic coefficients of variations are the amount of genotypic and phenotypic variability that exists in a species, that is essential in developing better varieties and in initiating a breeding program. Also, genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given population (Gemetchu *et al.*, 2005). The information provided by the genetic variance (additive variation, dominance variation and epistasis variation) is very important in improving crop yields through breeding processes (Rahul *et al.*, 2007). This could be achieved through a better understanding of the yield components. However, these components vary from year to year and from location to location, even for the same lentil genotype (Frederick *et al.*, 2006).

It is more useful to estimate heritability value together with genetic advance in predicting the expected progress to be achieved through selection. Germplasm serves as the most valuable natural reservoir in providing needed attributes for developing successful varieties (Hawkes, 1981; Burton, 1952; Johnson *et al.*; 1955).

Seed yield is a complex character and is the ultimate expression of different yield components. The study of different genetic parameters like phenotypic and genotypic variances, heritability and genetic advance of various developmental and economic traits is helpful to determine genetic behavior which ultimately plays an important role in formulating an effective breeding programme. It is more advantageous to select of different yield related traits, which are well recognized (Johnson *et al.*, 1955; Kwon and Torrie, 1964; Panse, 1957). The positive correlation of pairs of characters shows the possibility of simultaneous selection as any improvement in one of the character will be positively reflected in the increase of the other, while the negative correlation prevents the simultaneous improvement of those character side by side. It has been noticed from the fact that lentil cultivation in Syria has decreased, and its productivity in the unit area fluctuated during the successive seasons. There was a need to find new and improved genes to increase the productivity and stability of the area unit, through the estimation of genetic, phenotypic variance, genotypic and phenotypic correlation coefficients, broad sense heritability, and the genetic advance for seeds yield and its components for the most important varieties of lentils cultivated in Syria, that's to explore potentials in the studied genotypes in region, in order to obtain an additive and fast way to improve it.

Materials and Methods:

This experiment was carried out during (2014/2015) and (2015/2016) seasons. Randomized complete block design (RCBD) with three replications was used. Six lentil genotypes i.e. Idlib 1, Idlib 2, Idlib 3, Idlib 4, balade and Kurdi were collected from the Agricultural Research Center in Idlib. The genotypes were planted on 1.5 m × 2 m (3 m²) plot area. The spacing was 30 cm between rows and 8 cm between plants. Six rows per plot and 18 experimental units. All agricultural service operations were carried out in accordance of the instructions of the Ministry of Agriculture for the cultivation of lentils. This study took place at Dmsrkho in Latakia, which is characterized by medium soil, a neutral reaction to the light base, rich in organic matter and phosphorus, and suitable for lentil cultivation. Table (1) shows the climatic data of the location.

Table 1. Precipitation (mm) and temperature (°C) distribution during the growing seasons at Dmsrkho in Lattakia*

Months	Precipitation (mm),	Temperature (°C)	Precipitation (mm),	Temperature (°C)
	2014		2015	
Oct.	16	18	37	21
Nov.	19	16	45	15
Dec.	26	14	85	13
	2015		2016	
Jan.	62	12	113	9
Feb.	45	12	118	11
March	117	15	120	14
April	33	18	75	16
May	42	21	80	22

*According to Dmsrkho weather station

Table (1) shows that the temperature was sufficient for cultivation and growth, while rainfall did not reach its limits at Dmsrkho station during the two growing seasons of lentils.

Investigated traits:

Phenological traits:

1. Days to 50 % of flowering: It was determined from planting until flowering of 50% of the studied plants (day).
2. Days to 95 % of maturity: It was determined from planting until maturity of 95% of the pods of the studied plants (day).

Growth Parameters: Five plants were selected randomly from each plot to measure:

1. Plant height (cm): It was measured from the ground level to the tip of the plant, at physiological maturity stage.
2. Number of primary branches per plant.

Yield Components:

1. Number of pods per plant: It is the average number of pods per plant for five randomly selected plants per plot at harvest.
2. Number of seeds per plant: The average number of seeds per plant, which was recorded from ten randomly taken plants from each plot.
- 3- Seed weight/plant (g): It was obtained by weighing the seeds of each plant.
- 4- 100 seed weight (g): It was measured for 100 seeds that were taken from each plot by counting 100 seeds.
5. Seed yield (kg/ha): It was obtained by weighing the seeds from each experimental plot at standard moisture level.
6. Biomass yield (kg/ha): It was recorded by weighing the total above ground biomass, which harvested from each experimental plot at harvest.

Statistical analysis:

Estimation of genetic parameters: The genotypic and phenotypic coefficients of variability were undertaken according to the formulae of Singh and Chaundary (1991).

$$\text{Genotypic Coefficient of Variation } G CV\% = \frac{\sqrt{\sigma^2_g}}{\bar{x}} \times 100$$

$$\text{Phenotypic Coefficient of Variation } Ph CV\% = \frac{\sqrt{\sigma^2_p}}{\bar{x}} \times 100$$

Where, σ_g and σ_{ph} are genotypic and phenotypic standard deviations, respectively.

Broad-sense Heritability and Genetic Advance:

From breeding point of view, usefulness of heritability is related to its onward transmission from the parents to the progenies (Raiz and Chowdhury, 2003).

-Broad sense heritability (h^2) expressed as the percentage of the ratio of the genotypic variance (σ^2_g) to the phenotypic variance (σ^2_p) and was estimated on genotype mean basis as follows:

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p} = \frac{\sigma^2_g}{\sigma^2_g + \sigma^2_e}$$

$$\sigma^2_g = \frac{MSt - MSe}{r}$$

$$\sigma^2_e = Mse$$

MSt :Mean square due to genotypes /accessions.

MSe: Mean square of error.

r: Number of replications.

Genetic advance in absolute unit (GA):

Assuming selection of superior 5% of the genotypes, Genetic advance was estimated as:

$$GA = K. \sigma_p. h^2. 100 / \bar{x}$$

Where, K = The standardized selection differential at 5% selection intensity and (K = 2.063), σ_{ph} = Phenotypic standard deviation, h^2 = heritability and \bar{x} = grand mean

Analysis of Phenotypic and Genotypic Correlation Coefficients: The estimation of phenotypic and genotypic correlation coefficients between all pairs of characters was computed following the same formulas:

Genotypic correlation coefficient, $r_g = COV_g(xy) / \sqrt{\sigma^2_g(x) * \sigma^2_g(y)}$

Phenotypic correlation coefficient, $r_{ph} = COV_{ph}(xy) / \sqrt{\sigma^2_{ph}(x) * \sigma^2_{ph}(y)}$

Where, $COV_g(xy)$ and $COV_{ph}(xy)$ are the genotypic and phenotypic covariance of two variables (X and Y), respectively. $\sigma_g(x)$ and $\sigma_g(y)$ are the genotypic standard deviations for variables, X and Y, respectively.

$\sigma_{ph}(x)$ and $\sigma_{ph}(y)$ are the phenotypic standard deviations of variables, X and Y, respectively. The calculated phenotypic correlation value was tested for its significance using t-test: $t = r_{ph} / SE(r_{ph})$

Where: r_{ph} = Phenotypic correlation; $SE(r_{ph})$ = Standard error of phenotypic correlation (Sarker *et al.*, 2003).

Results and Discussion:

Analysis of genotypic variance for different quantitative characters in lentil:

Estimation of variability is one of the most important factors in any crop for identification of lines, which can generate further variability, so that artificial selection of desirable genotype could be made. Combined analysis of variance of two years data revealed significant differences for genotypes, and years and genotype x year interaction for all the characteristics, indicating relatively high magnitude of genetic diversity in these genotypes under study, as reported earlier by Rahul *et al.*, (2007) (Table 2).

Table 2. Analysis of genotypic variance for different quantitative characters in 6 lentil genotypes during 2014/2015

SOV	df	Mean of squares
-----	----	-----------------

Genotype	5	31.378*	245.911*	5.778*	3.004*	8.628*	1.119*	8.828*	27.417*	287870.76*	1645443.4*
Year	1	25*	455.11*	25*	1.778*	30.25*	2.85*	0.08*	330.209*	45014.694*	252171.36*
Genotype * Year	5	7.263*	47.178*	1.667*	0.111*	1.117*	0.027*	0.002*	2.246*	4486.094*	20272.628*
Error	5	5.278	8.056	2.389	0.472	2.472	0.093	0.02	7.005	11407.306	39085.611
Total	16	8576.11	18029.611	1166.88	20.55	1036.75	3.81	20.23	1630.94	1326674.3	23074554.42

* Significant at 0.05 probability level

The data in Table (3) shows that in general the values of phenotypic coefficients of variation were greater than their respective genotypic coefficients of variation for all traits. This implies more contribution of environment to the expression of traits (Sarwar *et al.*, 2010).

Genotypic coefficient of variation was maximum for seeds weight (41.8%), biological weight (34.8%), 100-seed weight/g (26.84%), and seed weight/plant (21.7%) (Table 3). However, phenotypic coefficient of variation was greater for seeds weight (55.9%), biological weight (44.1%), 100-seed weight/g (27.92%), and seed weight/plant (26.89%). This shows the presence of genetic variability for these traits. Similar results were also obtained by (Younis *et al.*, 2008). Higher values of phenotypic coefficients of variation for seed yield and biological yield have also been reported by (Sadiq *et al.*, 2005) and only for seed yield by (Idrees *et al.*, 2006).

Heritability was found to be maximum for days to maturity and 100-seed weight/g ($h^2 = 0.91$) followed by days to 50% of flowering ($h^2 = 0.81$) (Table 3). Such heritable variation for these traits is useful in making selection among lentil genotypes. For other traits, the heritability estimates were low to moderate.

Days to maturity had the highest heritability ($h^2 = 0.91$ with 1.16 percent of genetic advance. Higher estimates of genetic advance for seed yield were also reported by (Younis *et al.*, 2008). Seeds weight had the highest heritability ($h^2 = 0.55$) with 10.16 percent of genetic advance. The traits like days to maturity and biomass may be considered, while making selections directly to improve seed yield because characters having high heritability combined with high values of genetic advance are governed by additive types of genes as reported earlier (Johnson *et al.*, 1955; Sarwar *et al.*, 2004; Sarwar *et al.*, 2010).

Table 3. Coefficient of variability, heritability, genetic advance and rang for different characters in lentil genotypes

Characters	SOV	Days to	Days to	Plant	Number	Number	Seed	100	Number of	Seed	Total
		50%	Maturity	height/cm	of main	of	weight/plant	seed			
		flowering			branches	pods/plant	(g)	weight		yield/g	yield
								(g)			(g)
GCV%		7.5	4.7	10.3	14.9	3.7	21.7	26.84	7.3	41.8	34.8
Ph CV%		8.9	4.9	13.7	18.01	4.4	26.89	27.92	11.81	55.9	44.1
Heritability (h^2)		0.81	0.91	0.61	0.68	0.54	0.76	0.91	0.39	0.55	0.63
Genetic advance %		0.54	1.16	0.11	7.97	1.75	5.91	3.76	2.55	10.16	3.99
Range	L	89.6	122.83	32.66	3.67	30.83	1.575	3.4	40.445	865.83	3995.17
	H	95.84	142.17	35.17	5.67	33.835	1.85	6.75	46.175	1418.2	5448

* Significant at 0.05 probability level.

Study of genetic and phenotypic correlations between traits is important in genetic programs because they provide information about the genetic structure of the two correlated characters and make it

possible to determine the most appropriate selectorial indices that can be used in subsequent breeding to improve Syrian lentil productivity.

The estimates of correlation coefficient between seed yield and yield related traits indicated that in general, genotypic correlation coefficients were higher than their corresponding phenotypic correlation coefficients, indicating that the environmental effect reduces the value of the phenotypic correlation coefficient of the studied characters (Table 4). Similar results were also obtained by Sharma (1999).

Days to flower had positive and significant genotypic and phenotypic correlation with days to maturity ($r_g=0.894^{**}$ and $r_{ph} 0.906^{**}$ respectively) and with 100-seed weight ($r_g=0.163^{**}$ and $r_{ph} 0.164^{**}$ respectively), and negative correlation with plant height, pods per plant, seed yield/plant, seed yield and total biological yield (Table 4).

Days to mature had positive and significant genotypic and phenotypic correlation with all the traits including seed yield. Hence the results revealed that long duration genotypes have all the desirable traits. The results are in line with Arshad *et al.*, (2004).

Plant height had positive correlation with biological yield ($r_g=0.54$ and $r_{ph} 0.30^{**}$) and seed yield ($r_g=0.34$ and $r_{ph} 0.26^{**}$), indicating the possibility of selection for the plant height through the selection of the characteristics of the biological yield and seed yield. Positive correlation of plant height with seed yield has also been reported by Kumar *et al.*, (2004).

Number of primary branches, had positive genotypic and phenotypic correlation with all the traits, including seed yield. Positive and significant correlation of pods per plant with biological and seed yield was observed, indicating the possibility of selection for the biological yield and seed yield through the selection of pods per plant. Similar results were observed by Om-Vir *et al.*, (2001).

Seed yield/plant (g) had significant positive genotypic and phenotypic correlation with number of pods/plant ($r_g=0.905^{**}$ and $r_{ph} 0.907^{**}$), hundred seed weight ($r_g=0.294^{**}$ - $r_{ph} 0.294^{**}$) and biological yield ($r_g=0.76^{**}$ and $r_{ph} 0.78^{**}$).

Biological yield had significant positive genotypic and phenotypic correlation with hundred seed weight ($r_g=0.62^*$ and $r_{ph} 0.59^*$), and seed yield ($r_g=0.93^*$ and $r_{ph} 0.95^{**}$), indicating the possibility of selection for the biological yield through the selection of hundred seed weight and seed yield.

Table 4. The genotypic and phenotypic correlations between different traits of lentil genotypes

Characters	correlation coefficients	Days to maturity (no.)	Plant height (cm)	branches/ plant (no.)	Pods/ plant (no.)	Seed yield/ plant (g)	100-seed weight (g)	Seed yield	Total biological yield
Days to 50% of Flowering	Rg	0.894**	-0.035	0.076	-0.052	-0.045	0.163**	-0.50	-0.48
	Rp	0.906**	-0.037	0.126	-0.052	-0.045	0.164**	-0.49	-0.52
Days to Maturity	Rg	-	0.032	0.138*	0.014	0.039	0.224**	0.31	0.14
	Rp	-	0.033	0.192**	0.017	0.037	0.228**	0.19**	0.08
Plant height (cm)	Rg		-	0.047	-0.073	-0.078	0.045	0.34	0.54
	Rp		-	0.071	-0.077	-0.080	0.049	0.26**	0.30**
branches/ plant	Rg			-	0.475**	0.407**	0.079	0.57*	0.61*
	Rp			-	0.544**	0.462**	0.083	0.34	0.54*
No of pods/plant	Rg				-	0.905**	-0.025	0.54	0.52
	Rp				-	0.907**	-0.024	0.18	0.17**
Seed yield/ plant (g)	Rg					-	0.294**	0.88*	0.76**
	Rp					-	0.294**	0.89**	0.78**
100-seed weight (g)	Rg						-	0.76**	0.62*
	Rp						-	0.73**	0.59*
number of seeds/plant	Rg							0.79**	0.75*
	Rp							0.84**	0.68**
Seed yield	Rg							-	0.93*
	Rp							-	0.95**

Conclusion:

This study showed a genetic diversity for morphological and productivity characteristics, and thoughtful importance of lentils, and therefore the possibility of using the items considered in civic education programs in the future through the selection.

Analysis of variance indicates that the genotypes differ significantly for all studied characters, moreover, years effect and genotype by years interaction were significant for all studied traits.

Phenotypic coefficient of variation was slightly higher than genetic coefficient of variation, and heritability values were high and associated with high genetic advance for most traits, and this has a positive effect on breeding and genetic improvement processes.

Seed yield/plant (g) had significant positive genotypic and phenotypic correlation with number of pods/plant ($r_g=0.905^{**}$ and $r_{ph}=0.907^{**}$), hundred seed weight ($r_g=0.294^{**}$ - $r_{ph}=0.294^{**}$), and biological yield ($r_g=0.76^{**}$ and $r_{ph}=0.78^{**}$).

Biological yield had significant positive genotypic and phenotypic correlation with hundred seed weight ($r_g=0.62^*$ and $r_{ph}=0.59^*$) and seed yield ($r_g=0.93^*$ and $r_{ph}=0.95^{**}$), this indicates the genetic relationship between each of two characteristics. Indicating the possibility of selection for the biological yield through the selection of hundred seed weight and seed yield.

In addition, the correlation coefficient analysis revealed that the above qualities are important that contribute directly to production, thus can be used as selectorial evidence in improving lentil yield.

References:

- Anonymous. (2008). Agricultural statistics of Pakistan (2007-08). Government of Pakistan, Ministry of Food, Agriculture and Livestock (Economic Wing), Islamabad, Pakistan. Pp.50-51.
- Arshad, M.; A. Bakhsh; and A. Ghafoor (2004). Path coefficient analysis in chickpea (*Cicer arietinum* L.) under field conditions. Pak. J. Bot., 36(1): 75-81.
- Bond, D.A. (1983). Stability of faba beans and peas in EEC-joint trials 1980- 1982. In: ViciaFaba: Agronomy, Physiology and Breeding. 177-184.

- Burton, G.W. (1952). Quantitative inheritance in grasses. Proceedings of 6th International Grassland Congress. 1: 227-283.
- Dixit, G.P.; P.K. Katiya; and BB. Singh (2011). Characterization of lentil (*Lens culinaris* Medik.) varieties based on morphological traits. Journal of Food Legumes. 24: 194-197.
- Edossa, F.; T. Kassahun; and B. Endashaw (2007). Genetic diversity and population structure of Ethiopian lentil (*Lens culinaris* Medikus) landraces as revealed by ISSR marker. African Journal of Biotechnology. 6(12): 1460-1468.
- FAOSTAT (2009). Distribution of global lentil production among India, Canada and Turkey (the "big three" producers) and by continent. FAOSTAT. <http://faostat.fao.org/>.
- Frederick, M.; S. Sarker; A. McPhee; C. Coyne; P. Rajesh; and P. Ford (2006). Application of biotechnology in breeding lentil for resistance to biotic and abiotic stress. Euphytica. 147:149-165
- Gemechu, K.; J. Mussa; W. Tezera; and D. Getinet (2005). Extent and pattern of genetic diversity for morpho-agronomic traits in Ethiopian highland pulse landraces. 1. Field pea (*Pisum sativum* L.). Genetic Resource Crop Evolution. 52: 801-808
- Idress, A.; M.S. Sadiq; M. Hanif; G. Abbas; and S. Haider (2006). Genetic parameters and path coefficient analysis in mutated generation of mungbean (*Vigna radiata* L. Wilczek). J. Agric. Res., 44(3): 181-189.
- Johnson, H.W.; H.E.; Robinson; and R. E. Comstock. (1955). Estimates of genetic and environmental variability in soybean. Agron. J., 47: 314-318.
- Hawkes, J.G. (1981). Germplasm collection, evaluation and use. In: KJ Frey (Ed), Plant Breeding (2nd Ed), Iowa State University Press, Iowa, USA. Pp 57-84.
- Kumar, A.; D.P. Singh; and B.B. Singh (2004). Association analysis in lentil. Indian Journal of Pulses Research. (8)1: 20-24.
- Ladizinsky G. (1979). The origin of lentil and wild gene pool. Euphytica **28**:179-187.
- Meena, O.; and V. Baha (2013). Assessment of breeding potential of tomato germplasm using D2 analysis. The Bioscan. 8(4): 1145-1148.
- Muehlbauer, F.J.; W.J. Kaiser; and R.S. Clementand (1994). Production and breeding of lentil. Advances Agronomy. 54:315-316.
- Rahul, S.P. Sharma; and J.S. Brar (2007). Genetic studies for physiological traits and their relationship with seed yield in lentil. Journal of Food Legumes. 20: 29-32.
- Raiz, R.; and A. Chowdhry (2003). Estimation of variation and heritability of some physio70 morphic traits of wheat under drought condition. Asian Journal of Plant Science. 2(10): 748-755.
- Sadiq, M.S.; S. Haider; and G. Abbas (2005). Genetic parameters for economic traits in exotic germplasm of mungbean (*Vigna radiata* Wilczek). J. Agric. Res., 43(2):103-109.
- Sarker, A.; W. Erskine; and M. Singh (2003). Variation in shoot and root characteristics and their association with drought tolerance in lentil landraces. Genetic Resources Crop Evolution. 52:87-95.
- Sharma, S.K. (1999). Studies on genetic variability and correlation of grain yield and other quantitative characters in lentil (*Lens culinaris* Medik). Annals of Agric. Bioresearch. 4(1): 121-124.
- Sarwar, G.; M.S. Sadiq; M. Saleem; and G. Abbas (2004). Selection criteria in F3 and F4 population of mungbean. Pak. J. Bot. 36:297-310.
- Sarwar, G., G. Abbas; and M.J. Asghar (2010). Genetic study of quantitative traits in F5 generation of lentil (*Lens culinaris* Medik). J. Agric. Res., 48 (3): 279-288.

- Singh, R. and S. Chowdhury (1991). Induced co-dominant mutation for dwarfness in lentil. *Indian Journal of Genetics and Plant Breeding* 51: 370-372.
- Vir, O., V.P. Gupta; and O.P. Vir (2001). Association among yield and yield contributing characters in macrosperma and microsperma erivatives of lentil. *Crop Improvement*. 28(1): 75-80.
- Younis, N.; M. Hanif; M.S. Sadiq; G. Abbas, M.J. Asghar; and M.A. Haq (2008). Estimates of genetic parameters and path analysis in lentil. *Pak. J. Agri. Sci.*, 45 (3): 44-48.

التباين، درجة التوريث، التقدم الوراثي ومعامل الارتباط لبعض الصفات التطورية والشكلية والإنتاجية في عدة طرز من العدس (*Lens culinaris M.*)

محمد نائل خطاب*⁽¹⁾

(1). قسم المحاصيل الحقلية، كلية الزراعة، جامعة تشرين، اللاذقية، سورية.
*للمراسلة: د. محمد نائل خطاب. البريد الإلكتروني: aboalabd876@gmail.com.

تاريخ القبول: 2017/11/08

تاريخ الاستلام: 2017/09/20

الملخص

نفذ البحث لتقييم بعض الصفات الفينولوجية والمورفولوجية والإنتاجية لسته طرز وراثية من العدس هي: إدلب1، وإدلب2، وإدلب3، وإدلب4، وبلدي، وكردبي، باستخدام بعض المؤشرات الوراثية (معامل التباين الوراثي والمظهري، معامل التوريث بالمفهوم الواسع، التقدم الوراثي، معامل الارتباط الوراثي والمظهري) في منطقة دمسخو التابعة لمدينة اللاذقية خلال موسمي الزراعة (2014 / 2015) و(2015/2016) بتصميم القطاعات العشوائية الكاملة وبثلاث مكررات، بهدف التحقق من الطاقة الوراثية التي تتمتع بها تلك الطرز لاستغلالها إلى أقصى حد وتحديد الأدلة الانتخابية المناسبة لتحسين محصول العدس. أظهر تحليل التباين التجميحي وجود معنوية ($P \leq 0.05$) لتأثير التراكيب الوراثية والسنوات والتفاعل بين التراكيب الوراثية والسنوات عند كل الصفات المدروسة. أيضاً كان معامل الاختلاف المظهري أعلى من الوراثي ولكن بشكل طفيف، ودرجة التوريث كانت عالية عند معظم الصفات المدروسة وهذا يشير إلى سيطرة العوامل الوراثية وقلة تأثير العوامل البيئية عليها. كان معامل الارتباط المظهري والوراثي لإنتاجية النبات الواحد/غ معنوياً في صفات عدد القرون في النبات ($r_g = 0.905^{**} - r_{ph} 0.907^{**}$) ووزن 100 بذرة ($r_g = 0.294^{**} - r_{ph} 0.294^{**}$) والوزن البيولوجي ($r_g = 0.76^{**} - r_{ph} 0.78^{**}$). معامل الارتباط المظهري والوراثي للوزن البيولوجي كان معنوياً في صفات وزن 100 بذرة ($r_g = 0.62^* - r_{ph} 0.59^*$) ووزن البذور ($r_g = 0.93^* - r_{ph} 0.95^{**}$). وهذا يعطي إمكانية الانتخاب للوزن البيولوجي من خلال الانتخاب لصفات وزن 100 بذرة، ووزن البذور في النبات.

الكلمات المفتاحية: العدس، درجة التوريث، التقدم الوراثي، معامل التباين الوراثي، معامل التباين المظهري، معامل الارتباط.