

Genetic Variability, Correlation and Path Coefficient Analysis of Yield and Some Yield Components in Landraces of Lentil (*Lens culinaris* Medik)

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ABSTRACT

The critical assessment of the nature and magnitude of variability in the available germplasm and finding out associations among yield and its contributing characters are the pre-requisites to any breeding program. Keeping these points in view, genetic variability and interrelationship among 10 quantitative characters were studied in a set of 27 lentil genotypes during two growing seasons 2010-2011 and 2011-2012. The field experiments were laid out in a randomized complete block design and conducted at the research farm, Scientific Agricultural Research Center of Dara'a, GCSAR, Syria. The results showed that sufficient variability was present among the genotypes for all the characters studied. The component of genotypic variance of characters like number of primary branches per plant, number of pods per plant, 100-seed weight, biological yield, harvest index, and seed yield was higher than the environmental variance component; indicating that the genotypic component was the major contributor to total or phenotypic variance. Generally, the values of PCV were higher than the corresponding ones of GCV for all the characters, but in many cases, both values differed only slightly. Characters like number of primary branches per plant, number of pods per plant, biological yield and seed yield have recorded accompanied high estimates of GCV, heritability and genetic advance over character mean. The seed yield showed positive and highly significant associations with number of primary branches per plant and biological yield at the both genotypic and phenotypic levels. The highest positive direct effects have belonged to number of primary branches per plant followed by plant height and days to 50 % flowering; suggesting the importance of these characters and necessity of adoption them as selection criteria for seed yield improvement.

Keywords: Lentil, Variability, Heritability, Genetic Advance, Path Analysis.

INTRODUCTION

Lentil (*Lens culinaris* Medik) is the fourth most important pulse crop in the world after bean, pea and chickpea. Yield per unit area generally less than one-half those of the major cereal grains. There are several reasons why grain legumes yield in general and those of

lentil in particular have lagged behind: relegation of these crops to poorer soils, minimal research efforts until very recently, and various biotic and abiotic limitations (Lizica *et al.*, 2011).

In Syria, lentil is at the first rank among the grain legumes in respect of sowing area and production, being 139903 hectares and 112470 tons, respectively (FAO, 2011). Despite the progress made in cultivar development in lentil, the released varieties could not make the way to boost up the yield *per se* and the average lentil yield in Syria is still low as compared to other countries around the world such as China, Turkey and USA.

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One of the primary objectives of lentil breeders in any breeding program is to increase the seed yield. Generally, yield represents the final character resulting from many developmental and biochemical processes which occur between germination and maturity (Abdipur *et al.*, 2011).

Although, range can provide a preliminary idea about the variability, coefficient of variation is more reliable as it is the independent unit of measurement. The extent of variability as measured by GCV and PCV also provides information regarding the relative magnitude of variation in different populations. Absolute variability values of different characters do not reveal, which of the characters are showing the high variability. This could be assessed through the estimates of genotypic and phenotypic variance by obtaining the coefficients of variation. Hanson *et al.* (1956) proposed heritability as the ratio of genotypic variance to the total variance in a non-segregating population and which represents an indication for effectiveness of selection. The magnitude of heritability helps in predicting the behavior of succeeding generations by devising the appropriate selection criteria and assessing the level of genetic improvement (Ajmal *et al.*, 2009). Estimation of heritability is vital for boosting confidence during selection procedures and characters with high heritability can easily be fixed with simple selection resulting quick progress (Saleem *et al.*, 2002). Genetic advance is the measure of improvement that can be achieved by practicing selection in a population and it represents, for a character, the product of its heritability, phenotypic standard deviation and selection differential (Burton & Devane, 1953).

Estimation of genetic parameters of lentil genotypes can act as a useful guide to suggest effective breeding procedures for improvement of quantitatively inherited characters. Hence, the information on the relative magnitude of genotypic and phenotypic coefficients of

variability and character associations is of immense value in starting a scientific breeding program. Further, knowledge of relative contribution of different characters towards seed yield, directly as well as indirectly is also important in formulating suitable breeding procedures. Very little is known about genetic parameters of available germplasm of lentil and in the present investigation, an attempt has been made to assess the nature and magnitude of genetic variability, to determine the extent of interrelationship among various characters, and to identify selection criteria in Syrian landraces of lentil for further exploitation.

MATERIALS AND METHODS

Twenty seven genotypes of lentil including twenty five landraces obtained from Bank of Genetic Resources, GCSAR were collected from 9 sites in Syria (Table 1); for utilizing the variability in their characters and for their adaptation to local environments. As well as two improved released varieties as checks *viz.*, Idlib-1 and Idlib-2 and evaluated in a randomized complete block design with three replications during two growing seasons 2010-2011 and 2011-2012 under rainfed conditions (Table 2) at the research farm of Scientific Agricultural Research Center of Dara'a [32° 25' N, 36° 50' E, altitude 421 m], GCSAR, Syria. The soil of site is classified as clay-silt texture, pH is neutral 7.35, lightly alkali, poor of organic matter content 0.45 %. Each genotype was assigned in paired rows of 4 m length in each replication. The row to row and seed to seed distance was kept 30 cm and 10 cm, respectively. The observations were recorded on ten randomly selected competitive plants from each plot per replication on the following metric characters:

- 1- Plant height: At the end of flowering period from ground to the highest part of plant in centimeter.
- 2- Height of first pod: At the end of maturity period from ground to the first pod in centimeter.

3- Number of primary branches per plant: Average of actual count of primary branches on the main stem per plant.

4- Number of pods per plant: Average of actual count of both fertile and non-fertile pods per plant.

5- 100-seed weight: Weight of randomly selected hundred seeds weighted on a sensitive balance in gram.

6- Days to 50 % flowering: Days from sowing date to the stage when 50 % of the plants have started flowering per pot.

7- Days to maturity: Days from sowing date to the stage when 90 % of the pods mature per pot.

8- Biological yield: Weight in gram of all above ground plant part per pot at harvest then the weight was converted to kilogram and calculated on 0.1 hectare basis.

9- Seed yield: the weight of seeds harvested from the pot in gram then the weight was converted to kilogram and calculated on 0.1 hectare basis.

10- Harvest index: the percentage ratio of seed yield to biological yield per pot.

Table 1. Eco-geographical information about 9 collection sites of 25 lentil landraces.

Landraces	District	Site	Latitude (N)	Longitude (E)	Altitude (m)	Long-term average seasonal rainfall (mm)
55505-55506-55507-55508	Homos	El-Norah	34.69	36.37	270	290
55517-55514	Hama	Betateek	34.91	36.32	720	340
55498-55504-55500	Damascus	Zabadani	33.72	36.11	1110	480
55495-55527-55526	Sewdaa	Nadealremaiah	32.42	36.60	1100	466
55509-55510-55511-55512	Homos	Telkelakh	34.67	36.23	300	281
55519	Idleb	Harm	36.22	36.60	380	372
55524-55523-55522-55520	Sewdaa	Sahwataalkheder	32.60	36.72	1450	490
55518-55513	Idleb	Kelbaloz	36.14	36.57	660	344
55516-55515	Damascus	Zabadani	33.68	36.10	1300	425

Standard statistical procedures of average data over two growing seasons were used for the analysis of variance according to Steel *et al.* (1997) by MSTAT-C statistical computer package software (Michigan State University, 1991):

1- Genotypic (GCV) and phenotypic coefficients of variation (PCV) were estimated according to (Burton, 1952):

$$GCV = \frac{\sqrt{V_g}}{\bar{X}} \times 100 \quad PCV = \frac{\sqrt{V_{ph}}}{\bar{X}} \times 100$$

Where:

V_g , V_{ph} , \bar{X} : is genotypic variance, phenotypic variance, and the general mean of character mentioned, respectively.

2- Heritability in broad sense was calculated according to (Hanson *et al.*, 1956):

$$H = \frac{V_g}{V_{ph}} \times 100$$

3- Genetic advance as percent of mean (RGA) was estimated according to (Johnson *et al.*, 1955):

$$RGA = \frac{K \times \sqrt{V_{ph}} \times H}{\bar{X}} \times 100$$

Where:

K , V_{ph} , H , \bar{X} : is selection differential equals 1.76, phenotypic variance, heritability, and the general mean of character mentioned, respectively.

4- Genotypic (r_g) and phenotypic correlation coefficients (r_{ph}) were computed using genotypic and phenotypic variances and co-variances according to (Al-Jibouri *et al.*, 1958):

$$r_g = \frac{Cov_{g_{xy}}}{\sqrt{V_{g_x} \cdot V_{g_y}}} \quad r_{ph} = \frac{Cov_{ph_{xy}}}{\sqrt{V_{ph_x} \cdot V_{ph_y}}}$$

Where:

$Cov_{g_{xy}}$, $Cov_{ph_{xy}}$, V_{g_x} , V_{g_y} , V_{ph_x} , V_{ph_y} : is genotypic co-variance of the two characters x and y, phenotypic co-variance of the two characters x and y, genotypic variance of the character x, genotypic variance of the character y, phenotypic variance of the character x, phenotypic variance of the character y, respectively.

5- The path coefficient analysis was done according to the method of Dewey & Lu (1959).

Table 2. Some monthly meteorological data of the two seasons of study

Seasons	Meteorology	Months							
		Nov.	Dec.	Jan.	Feb.	March	April	May	June
2010/2011	T max. (° C)	13	9	11	12	24	26	28	29
	T min. (° C)	7	6	6	6.5	9	11	18	19
	RH (%)	51	74	81	81	70	61	47	50
	W (m.s ⁻¹)	2.9	3.1	1.7	1.6	2.0	2.2	2.3	3.6
	R (mm)	5	156	44.5	105	41.8	75	25.5	0
2011/2012	T max. (° C)	16	14	11	13.5	22	25.4	26.8	28
	T min. (° C)	5	4	2.4	3.9	7.6	10.4	14	15.7
	RH (%)	55	77	74	78	67	56	49	44
	W (m.s ⁻¹)	2.0	13	1.9	2.2	2.4	3.0	2.8	3.4
	R (mm)	32	28	90	133.5	82	0	5	0

T max.: Maximum temperature, T min. : Minimum temperature, RH: Relative humidity, W: Winds speed, R: Rainfall

RESULTS AND DISCUSSION

Analysis of variance:

Table 3 showed that the mean squares (F values) due to genotypes were significant ($P < 0.05$) for days to 50 % flowering and plant height, whereas they were highly significant ($P < 0.01$) for the other characters studied, indicating the presence of sufficient variability among the genotypes for each of 10 characters assessed and offering ample chances for the genetic improvement of the crop. The range of values reflects the amount of phenotypic variability, which is not very reliable since it includes genotypic, environmental and genotype-environment interaction components and does not reveal as to which character showing higher degree of variability (Kaushik *et al.*, 1996). The range of variation was the highest for biological yield (28.75-166.50 kg/0.1 ha) followed by number of pods per plant (17.50-73.50) and seed yield (11.00-52.25 kg/0.1 ha), whereas the lowest was for 100-seed weight (2.13-5.05) followed by number of primary branches per plant (2-7). The characters showing wide range of variation provide ample scope for selection of the desirable types.

Data regarding mean performance of the lentil genotypes for the ten characters studied over the study seasons was exhibited through Table 4. The landraces 55505, 55519, and 55520 were the earliest ones in flowering (103 days) with significant variations from all the rest landraces. For maturity, the landraces 55517, 55515, 55526, 55516, and 55527 were the earliest where they took (145, 148, 148, 149, 149 days), respectively. Two genotypes *viz.*, 55512 and *Idleb-2* had the tallest plants (35.17, 35.00 cm), respectively and differed

significantly from majority of the other landraces. Two landraces *viz.*, 55520 and 55495 recorded the maximum number for primary branches per plant (5.50, 5.50) which varied statistically from most of the other landraces. For number of pods per plant, four genotypes *viz.*, *Idleb-1*, 55506, 55510, and 55495 possessed the highest values (64.17, 56.00, 56.00, 56.00), respectively. The maximum values for 100-seed weight have been showed by the two landraces 55506 and 55523 (4.57, 4.08 g), respectively with significant variations from majority of the other landraces. Two landraces 55527 and 55495 recorded the highest biological yield (163.50, 160.33 kg/0.1 ha) with statistically variations from all the rest ones. For harvest index, three landraces *viz.*, 55510, 55516, and 55507 showed the highest magnitude (41.49, 40.85, 40.25 %), respectively. The highest values for seed yield were recorded by the landraces 55495, 55527, and 55526 (50.53, 40.73, 40.13 kg/0.1 ha), respectively, which differed significantly from all the other genotypes. In general, all the genotypes studied exhibited low seed yield; which may be attributed to the sudden increase in temperature in March and April when instance flowering and pod elongation occurred. This may force the plant to maturity and prevent flower setting and pod formation. In addition, the undesirable late precipitation in May increases the effect of drought stress and causes considerably increased spread of wilt diseases (Table 2). Similar variability among lentil genotypes was reported by Rahul *et al.* (2007); Bicer & Sakar (2008); Bicer & Sakar (2010); Abdipur *et al.* (2011).

Table 3. Phenotypic variation in 10 quantitative characters of 27 different genotypes of lentil (average data over two study seasons).

Characters	Range	Mean \pm S.E.	Coefficient of variation (%)	F value for genotypes
Days to 50 % flowering	101-109	105 \pm 1.19	1.35	1.72*
Days to maturity	144-160	152 \pm 1.56	1.59	3.92**
Plant height (cm)	26-37	35.51 \pm 1.48	6.72	1.75*
Height of first pod (cm)	17-24	20.38 \pm 1.12	6.14	3.30**
No. of primary branches per plant	2-7	3.47 \pm 0.77	17.01	6.74**
No. of pods per plant	17.50-73.50	41.80 \pm 2.27	12.28	13.00**
100-seed weight (g)	2.13-5.05	3.17 \pm 0.61	11.73	5.38**
Biological yield (kg / 0.1 ha.)	28.75-166.50	83.39 \pm 2.38	6.80	107.51**
Harvest index (%)	24.65-43.94	33.30 \pm 1.58	7.49	8.58**
Seed yield (kg / 0.1 ha.)	11.00-52.25	25.58 \pm 1.48	8.60	42.95**

*, ** : significant at 5 % and 1 % probability level, respectively

Genetic variability:

Data on the different variances and genetic parameters estimated are presented in Table 5. Generally, the phenotypic variance was higher than the genotypic variance in all the characters studied. The magnitude of the genotypic variance was higher than the environmental variance for all the characters except days to 50 % flowering (0.48 , 2.00), days to maturity (5.65 , 5.80), plant height (1.19 , 4.77), and height of first pod (1.20 , 1.57), respectively; indicating that the genotypic component was the major contributor to the total variance for most of the characters under study.

Absolute variation values of different characters do not reveal which of the characters are showing the high variation. This could only be assessed through

standardizing the genotypic and phenotypic variance estimates by obtaining the coefficients of variation. The genotypic (GCV) and phenotypic coefficients of variation (PCV) were high for number of primary branches per plant, (23.63 , 29.11 %), number of pods per plant (24.57 , 27.46 %), biological yield (40.53 , 41.10 %) and seed yield (32.13 , 33.27 %), respectively, which suggested greater genotypic and phenotypic variability among the genotypes and sensitiveness of these characters for making further improvement by selection. The PCV has greater values than the corresponding ones of GCV for all the characters; denoting environmental factors influencing their expression to some degree or other. Wide difference between GCV and PCV for days to 50 % flowering

(0.66 , 1.51), days to maturity (1.57 , 2.22), plant height (3.35 , 7.51), and height of first pod (5.40 , 8.15), respectively, implied its susceptibility to environmental fluctuation and they were the same characters possessing high values of environmental variance, whereas narrow difference between GCV and PCV for the other characters suggested their relative resistance to environmental alteration.

The effectiveness of a selection program depends not only the total available variability but also on the extent of heritability and genetic advance. The heritability in broad sense was high for number of primary branches per plant (0.66), number of pods per plant (0.80), biological yield (0.97), harvest index (0.72), and seed yield (0.93). Such high values of heritability for these characters clarified that they were least affected by environmental modification and selection based on phenotypic performance would be reliable.

The genetic advance as percent of mean ranged from (0.51 %) for days to 50 % flowering to (70.16 %) for biological yield. High estimates of genetic advance were obtained for number of primary branches per plant (33.27 %), number of pods per plant (38.66 %), biological yield (70.16 %) and seed yield (54.46 %) which portrayed that they could be improved to a large extent through selection.

Burton (1952); Johnson *et al.* (1955) found that it was more useful to estimate heritability value together with genetic advance in predicting the expected progress to be achieved through selection. High heritability along with high GCV and genetic advance as percent of mean were noticed for number of primary branches per plant (0.66 , 23.63 % , 33.72 %), number of pods per plant (0.80 , 24.57 % , 38.66 %), biological yield (0.97 , 40.53 % , 70.16 %), and seed yield (0.93 , 32.13 % , 54.46 %), respectively, which might be assigned to additive gene effects governing their inheritance and their improvement could be achieved by simple selection procedures in the early generations. Low to moderate estimates of heritability coupled with low GCV and genetic advance were observed for days to 50 % flowering (0.18 , 0.66 % , 0.51 %), days to maturity (0.49 , 1.57 % , 1.92 %), plant height (0.20 , 3.35 % , 2.65 %), and height of first pod (0.43 , 5.40 % , 6.18 %), respectively; indicating that these characters were highly influenced by environmental factors and selection would be ineffective. These results agreed with Ashraf *et al.* (2008) and Younis *et al.* (2008) for number of pods per plant and seed yield; Tyagi & Khan (2010) for days to maturity, plant height and number of primary branches per plant.

Table 4. Mean performance of 10 quantitative characters in 27 lentil genotypes (average data over two study seasons).

Sr. No.	Genotypes	Days to 50 % flower.	Days to maturity	Plant height (cm)	Height of first pod (cm)	No. of primary branches per plant	No. of pods per plant	100-seed weight (g)	Biological yield (kg/0.1 ha)	Harvest index (%)	Seed yield (kg/0.1 ha)
1	55505	103	152	33.67	20.17	3.00	26.83	3.93	60.42	38.16	23.00
2	55506	104	152	30.83	18.83	2.83	56.00	4.57	45.97	37.13	18.68
3	55507	106	153	33.00	20.17	2.50	34.17	2.89	50.75	40.25	20.17
4	55508	106	156	30.83	19.50	3.33	41.33	3.73	51.83	31.78	16.00
5	55509	106	156	32.33	20.17	2.33	43.67	2.67	59.42	30.42	17.53
6	55510	106	155	31.67	20.00	3.33	56.00	2.71	58.00	41.49	24.17
7	55511	104	156	31.83	19.67	3.67	31.83	3.73	72.67	30.27	20.28
8	55512	106	156	35.17	20.50	3.67	49.00	2.87	89.42	37.89	34.15
9	55513	104	154	31.50	20.00	2.83	28.17	2.49	52.67	38.07	20.63
10	55514	105	153	32.83	19.83	3.33	35.00	2.87	67.00	32.33	20.75
11	55515	105	148	34.67	20.50	2.83	30.67	3.19	60.83	35.29	20.77
12	55516	104	149	33.83	20.33	2.67	33.83	3.60	61.33	40.85	25.93
13	55517	104	145	33.50	20.17	3.50	49.50	3.55	89.00	29.70	24.32
14	55518	104	152	34.50	20.83	3.17	32.17	2.46	128.67	27.31	30.17
15	55519	103	153	30.00	17.50	4.83	48.83	2.93	85.58	31.07	25.70
16	55520	103	152	32.67	18.17	5.50	47.67	2.82	120.67	28.03	31.72
17	55522	106	150	33.50	21.00	2.33	54.67	2.84	60.08	35.90	21.67
18	55523	104	153	32.67	20.00	4.33	44.00	4.08	120.75	30.32	29.63
19	55524	105	150	32.83	19.83	3.83	37.50	3.18	100.33	27.97	23.17
20	55526	104	148	32.33	21.67	4.00	37.33	3.00	118.17	35.17	40.13
21	55527	106	149	32.33	20.17	3.17	30.17	2.87	163.50	28.94	40.73
22	55495	105	150	32.33	20.83	5.50	56.00	3.19	160.33	33.99	50.53
23	55500	106	152	28.33	22.67	2.83	50.83	3.16	34.25	34.71	12.97
24	55504	106	152	29.50	23.67	4.67	48.83	3.15	71.17	29.63	20.45
25	55498	106	150	31.67	23.00	4.00	26.50	3.14	94.67	31.12	26.45
26	Idelb-1	106	151	34.33	21.33	2.50	64.17	3.40	101.92	31.09	29.83
27	Idleb-2	106	153	35.00	19.83	3.17	33.83	3.02	72.00	30.21	21.13
L.S.D_{0.05}		2.32	3.95	3.58	2.05	0.97	8.41	0.61	9.29	4.09	3.60

Table 5. Components of variation, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (H) and genetic advance (GA) in 10 characters of 27 genotypes of lentil (average data over two study seasons).

Characters	Components of variance			GCV (%)	PCV (%)	H	GA *	GA (%)
	V _e	V _g	V _{ph}					
Days to 50 % flowering	2.00	0.48	2.48	0.66	1.51	0.19	0.53	0.51
Days to maturity	5.80	5.65	11.45	1.57	2.22	0.49	2.92	1.92
Plant height (cm)	4.77	1.19	5.96	3.35	7.51	0.20	0.86	2.65
Height of first pod (cm)	1.57	1.20	2.77	5.40	8.15	0.43	1.26	6.18
No. of primary branches/plant	0.35	0.67	1.02	23.63	29.11	0.66	1.17	33.72
No. of pods per plant	26.36	105.47	131.83	24.57	27.46	0.80	16.16	38.66
100-seed weight (g)	0.14	0.20	0.34	14.20	18.30	0.59	0.60	18.93
Biological yield (kg / 0.1 ha.)	32.18	1142.41	1174.59	40.53	41.10	0.97	58.51	70.16
Harvest index (%)	6.22	15.70	21.92	11.89	14.05	0.72	5.93	17.81
Seed yield (kg / 0.1 ha.)	4.84	67.64	72.48	32.13	33.27	0.93	13.93	54.46

* : the selection differential used was 1.76 at 10 % selection intensity

Character association:

Correlation analysis provides information on nature and magnitude of the association of different component characters with seed yield which is regarded as a highly complex character in which the breeder is ultimately interested. A lot of research has been done to increase the present yield of grain legumes including lentil, but so far, no breakthrough has occurred in the yield ceiling of these crops and yield of this crop remain low. However, component characters of yield are independent from each other, while one character may express at the expense of the other (Anjam *et al.*, 2005).

The estimates of genotypic (r_g) and phenotypic correlation coefficients (r_p) are shown in Table 6. In general, magnitude of the genotypic correlations were higher than the corresponding phenotypic ones in most of the character pairs showing that masking effects of the environment was little and suggesting that a strong inherent association existing for the characters studied and thus phenotypic selection may be rewarding. The genotypic and phenotypic associations of seed yield

were positive and highly significant with number of primary branches per plant (0.56^{**}, 0.47^{**}) and biological yield (0.90^{**}, 0.88^{**}), respectively; suggesting thereby that selection, if focused on either of these both characters is likely to bring about improvement in the seed yield, but negative and highly significant with days to maturity (-0.35^{**}, -0.32^{**}), which might be due to that the latter part of the reproductive growth phase in lentil often coincides with increasing temperature and dry conditions and this exaggerates the indeterminate nature of the crop, leading to immature pod/seed development, and subsequently resulting enforced maturity with low seed yield. Number of primary branches/plant had positive and highly significant correlation with biological yield (0.61, 0.50), but negative and highly significant correlation with harvest index (-0.46^{**}, -0.31^{**}) at both genotypic and phenotypic levels, respectively.

Negative correlations are often found between morphological components of yield in crop plants and they probably arise primarily from developmentally-

induced relationships (Tambal *et al.*, 2000). According to Tullu *et al.* (2001), high seed yield has been obtained through developing of cultivars with shorter vegetative

and generative growth periods. These findings were in agreement with the studies reported earlier by Hamdi *et al.* (2003); Kumar *et al.* (2009); Tyagi & Khan (2010).

Table 6. genotypic (r_g) and phenotypic correlation coefficients (r_p) among various pairs of the characters under study of 27 genotypes of lentil (average data over two study seasons).

Characters	r	Days to mat.	Plant height	Height of first pod	No. of prim. Bran/plant	No. of pods/plant	100-seed weight	Biological yield	Harvest index	Seed yield
Days to 50 % flowering	G	0.33**	0.15	0.98**	-0.63**	0.32*	-0.26*	-0.27*	0.16	-0.27*
	P	0.18	-0.02	0.21	-0.21	0.02	-0.09	-0.12	-0.06	-0.14
Days to mat.	G		-0.33**	-0.37**	-0.05	0.12	-0.14	-0.39**	0.18	-0.35**
	P		-0.07	-0.14	-0.10	-0.02	-0.08	-0.30**	0.04	-0.32**
Plant height	G			-0.66**	-0.39**	-0.43**	-0.16	0.40**	0.11	0.51**
	P			0.15	-0.17	-0.04	-0.10	0.14	-0.007	0.14
Height of first pod	G				-0.12	-0.06	-0.16	0.002	0.03	0.06
	P				-0.08	0.05	-0.07	-0.009	0.001	-0.01
No. of prim. bran. /plant	G					0.18	0.02	0.61**	-0.46**	0.56**
	P					0.13	-0.03	0.50**	-0.31**	0.47**
No. of pods per plant	G						0.14	0.01	0.05	0.11
	P						0.11	0.02	0.02	0.11
100-seed weight	G							-0.17	0.09	-0.18
	P							-0.14	0.06	-0.13
Biological yield	G								-0.54**	0.90**
	P								-0.47**	0.88**
Harvest index	G									-0.09
	P									0.01

*, ** : significant at 5 % and 1 % probability level, respectively

Path coefficient analysis:

Knowledge of correlation alone is often misleading as the correlation observed may not be always true. Two characters may show correlation just because they are correlated with a common third one. Partitioning of the total correlation into direct and indirect effects would provide actual information on the contribution of characters and thus form the basis for selection to improve grain yield (Manggoel *et al.*, 2012). Singh (1977) suggested, from correlation and path analysis

studies on lentil, that either phenotypic or genotypic correlations might be used in path analysis with equal efficiency.

The genotypic path coefficient analysis (Table 7) explained that number of primary branches per plant had the maximum positive direct effect (1.512) followed by plant height (0.774) and days to 50 % flowering (0.691). Number of primary branches per plant exhibited high positive direct effect (1.512) on seed yield which in

conjunction with its positive indirect effects via days to maturity (0.019) and height of first pod (0.010) and after dilution by its negative indirect effects through days to 50 % flowering (-0.435), plant height (-0.302), and harvest index (-0.211) resulting in its strong positive association with seed yield.

Data of Table 6 revealed that biological yield correlated positively and significantly with seed yield (0.90^{**}, 0.88^{**}), whereas the direct effect was negative and negligible at the genotypic level (-0.043). Therefore, the positive indirect effects via days to maturity (0.145), plant height (0.310), and number of primary branches per plant (0.922) seem to be cause of this correlation. In such situations, these indirect causal factors are to be considered simultaneously for

selection. Days to 50 % flowering had a negative and significant correlation with seed yield (-0.27^{*}), but its direct effect was high and positive (0.691). So, a restricted simultaneous selection model is to be followed to nullify the undesirable indirect effects in order to make use of the direct effect (Singh & Kakar, 1977).

The unexplained variation in genotypic paths was (31.54 %) which might be due to many reasons such as other characters not considered here, environmental factors and sampling errors (Sengupta & Karatia, 1971). The trend of these results was in accordance with Rasheed *et al.* (2008); Younis *et al.* (2008) and Kumar *et al.* (2009), but contradicted Hamdi *et al.* (2003) and Punia *et al.* (2011).

Table 7. Direct (bold diagonal) and indirect genetic effects of various component characters on seed yield of lentil.

Characters	Days to 50 % flowering	Days to mat.	Plant height	Height of first pod	No. of prim. bran. /plant	No. of pods per plant	100-seed weight	Biological yield	Harvest index	r _g with seed yield
Days to 50 % flowering	0.691	-0.123	0.116	-0.077	-0.953	-0.001	0.000	0.012	0.073	-0.27
Days to mat.	0.228	-0.371	-0.225	0.029	-0.076	0.000	0.000	0.017	0.082	-0.35
Plant height	0.104	0.123	0.774	0.052	-0.590	0.001	0.000	-0.017	0.050	0.51
Height of first pod	0.677	0.137	-0.511	-0.079	-0.182	0.000	0.000	0.000	0.014	0.06
No. of prim. bran. /plant	-0.435	0.019	-0.302	0.010	1.512	-0.001	0.000	-0.026	-0.211	0.56
No. of pods per plant	0.221	-0.045	-0.333	0.005	0.272	-0.003	0.000	-0.001	0.023	0.11
100-seed weight	-0.180	0.052	-0.124	0.013	0.030	-0.001	0.003	0.006	0.028	-0.18
Biological yield	-0.187	0.145	0.310	0.000	0.922	0.000	0.000	-0.043	-0.247	0.90
Harvest index	0.111	-0.067	0.085	-0.003	-0.696	0.000	0.000	0.023	0.458	-0.09

Residual effect = 0.3154

CONCLUSION

On the basis of genetic parameters estimated, the most important attention should be given to characters like number of primary branches per plant, number of pod per plant, biological yield and seed yield, because the maximum advance could be achieved by simple selection procedures. Whereas, on the basis of

correlation and path analysis studies. It can be concluded that number of primary branches per plant and plant height exerted a high influence on seed yield resulting in a strong positive correlation and this should be taken into consideration while selecting of desirable genotypes for higher seed yield in lentil.

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التباين الوراثي، الارتباط وتحليل معامل المسار للغلّة وبعض مكوناتها في سلالات محلية من العدس

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ملخص

يُعدّ تقييم طبيعة ومقدار التباين المتاح في المواد الأولية واكتشاف علاقات الارتباط القائمة بين الغلّة والصفات المكوّنة لها متطلبات رئيسية في أي برنامج تربية. انطلاقاً من ذلك، تم دراسة التباين وعلاقات التداخل بين عشر صفات كمية في مجموعة مكوّنة من سبعة وعشرين طراز وراثي من العدس خلال موسمي الزراعة 2010-2011 و 2011-2012، بتصميم قطاعات عشوائية كاملة بثلاثة مكررات وذلك في الحقل التجريبي لمركز بحوث درعا التابع للهيئة العامة للبحوث العلمية الزراعية في سورية. أوضحت النتائج أن تبايناً كافياً وجد بين طرز الدراسة لجميع الصفات المختبرة، وكان التباين الوراثي المكوّن الرئيس للتباينات المشاهدة لدى صفات عدد الفروع الأولية/نبات، عدد القرون/نبات، وزن الـ 100 بذرة، المحصول البيولوجي، دليل الحصاد وغلّة البذور. كانت القيم العائدة لمعامل التباين المظهري - إجمالاً - أكبر من مقابلاتها لمعامل التباين الوراثي لجميع صفات الدراسة. سجّلت صفات عدد الفروع الأولية/نبات، عدد القرون/نبات، المحصول البيولوجي وغلّة البذور قيماً عالية متلازمة لكل من معامل التباين الوراثي، درجة التوريث بالمفهوم الواسع والتقدم الوراثي محسوباً كنسبة مئوية من متوسط الصفة المعنية. أظهرت غلّة البذور ارتباطاً موجباً ذا دلالة إحصائية مع كل من عدد الفروع الأولية/نبات والمحصول البيولوجي، كما سجّلت صفات عدد الفروع الأولية/نبات، ارتفاع النبات وعدد الأيام حتى 50% من الإزهار التأثيرات المباشرة الموجبة الأعلى على غلّة البذور؛ مما يؤكد أهمية تبنيتها كمعايير انتخاب مهمة لتحسين غلّة البذور في العدس.

الكلمات الدالة: عدس، تباين، درجة التوريث، التقدم الوراثي، تحليل المسار.

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