

Variance, Heritability, Genetic Advance and Correlation of Some Phenological, Morphological and Productivity Traits in Some Safflower (*Carthamus tinctorius* L.) Genotypes

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Abstract

In this study some of the phenological, morphological and productivity characteristics of six safflower (*Carthamus tinctorius* L.) genotypes (local, Thick orange 480, Acar 6, Syrian-1, Gila and Son 11), were assessed using some genetic indicators (genetic and phenotypic variances, genotypic and phenotypic correlation coefficients, broad- sense heritability and genetic advance between seeds yield and its components) at Dmsrkho site in Latakia governorate, during two seasons (2014/2015) and (2015/2016). Completely Randomized Design (CRD) was used with three replicates, to detect the genetic potentiality to be exploited to a maximum extent therefor, to determine the appropriate selectorial indices to improve safflower crop. Analysis of variance indicated that the genotypes differed significantly ($P < 0.05$) for all studied characters, moreover, years effect and genotype by years interaction were significant for all studied traits. The values of mean and range revealed that there is wide variability among genotypes for most of the characters. The biological yield per plant, seed yield per plant, number of seeds per capitulum, number of capitulum per plant, number of branches per plant and harvest index exhibited wide range and high PCV and GCV giving an opportunity for improvement through election. Besides, these characters also had narrow differences between the values of PCV and GCV showing least influence of environment. High heritability coupled with high genetic advance observed for seed yield per plant, biological yield per plant, 100 seed weight, plant height and number of seeds per capitulum indicated that these traits are governed by additive gene action. Hence, there are good chances of improvement of these traits through direct selection. The highest phenotypic correlations were observed between seed yield with some traits such as: biological yield/plant and No. of capitula/plant, thus these traits, may be used for selecting high yielding genotypes.

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

Introduction:

Safflower (*Carthamus tinctorius* L.) is an oilseed crop that belongs to *Asteraceae* family. The genus *Carthamus* has 25 species, of which *C. tinctorius* is the only cultivated one, and has $2n = 24$ chromosomes (Helm *et al.*, 1991).

It is dicotyledonous, herbaceous, and annual plant. It has colorful flower heads, a deep taproot, and the production of white, oil-bearing seeds. It is adapted to grow in hot, dry climates, and well-drained soil (Maryam *et al.*, 2011).

Currently, it is grown as an oilseed crop in over 60 countries worldwide, and India is the largest producer of safflower (Weiss, 2009). Safflower is mainly cultivated for its seed, which is used primarily for edible oil. In the past, the crop is grown for its flowers used for coloring and flavoring foods, making dyes and medicine (Yang *et al.*, 2007). Study of yield components and detecting suitable selection indexes has a very important role in safflower breeding programs.

(Choulwar *et al.*, 2005) observed that the estimates of phenotypic coefficient of variation (PCV) was higher in comparison to genotypic coefficient of variation (GCV) for yield and yield contributing characters. Also, they found that the estimate of heritability for plant height was highest and lowest for weight. High heritability with high expected genetic advance was observed for number of secondary branches, number of seeds per capitulum, seed yield per plant, number of capitula per plant and plant height.

(Lakshyadeep and Shanna, 2005) recorded significant variances among genotypes for all traits except for number of leaves on main axis after branching, 100-seed weight and oil content. Also, they reported high heritability for number of capitula per plant and seed yield per plant. Biradar *et al.*, (2012) reported high genotypic and phenotypic coefficient of variations for number of capitula per plant, number of seeds per capitulum, 100 seed weight and oil content. Reddy *et al.*, (2003) reported high genetic advance for weight, seed yield per plant, and number of seeds per capitulum. Moderate to high genetic advance was recorded for number of capitula per plant. Low genetic advance was observed for plant height. Sarang *et al.*, (2004) observed high expected genetic advance for yield per plant followed by number of secondary branches and number of capitula per plant.

Lande and Deshmukh, (2012) recorded high expected genetic advance for seed yield per plant. Dalvi *et al.*, (2013) observed that the number of primary branches, number of secondary branches, number of capitula per plant and number of effective capitula per plant showed significant and positive correlations with seed yield at both phenotypic and genotypic levels, while weight showed positive significant correlation with seed yield at the genotypic level.

Despite the development of agriculture and safflower production in Syria, researchers still have a wide range of potential to improve the yield of this crop, because it has large genetic potential that can be found in the use of various methods of farming and agricultural operations. 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 safflower cultivated in Syria, to explore potentials oh these varieties to define the selectorial indexes in order to obtain an additive and fast development method for this crop.

Materials and Methods:

This experiment was carried out during two seasons (2014 /2015) and (2015/2016). Randomized complete block design was used with three replications. Six safflower varieties (local, Thick orange 480, Acar 6, Syrian-1, Gila and Son 11), which were selected on the basis of phenotypic diversity, and used to study of the quantitative characters.

The genotypes were planted on 4 m × 4 m (16 m²) plot area. The spacing was 75 cm between rows and 15cm between plants in each row. There were six rows per plot and 18 experimental units. All agricultural practices were carried out in accordance to the instructions of the Ministry of Agriculture for safflower crop. This study took place at Dmsrkho, in Latakia Governorate, this site rises 15 meters above sea level, and locates at 35 longitude and 35 latitude, which is characterized

by medium soil, has a neutral reaction to light acidity, and rich in organic matter and phosphorus which is suitable for safflower cultivation.

Table 1. Precipitation (mm) and temperature (°C) distribution during growing seasons at Dmsrkho, Latakia Governorate

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

Source: Dmsrkho meteorological station.

Table (1) shows that the lowest temperature value (12 °C) which was recorded in January and February of 2015 and (9 °C) in January of 2016, and annual precipitation amounted to (360 and 673 mm) respectively during the two-agriculture seasons respectively, according to the meteorological station in Latakia. The soil is clay, with moderate acidity, and suitable for growing safflower.

Investigated traits:

The following observations were recorded:

- 1- Days to 50% of flowering: number of days taken from the date of sowing to the date when 50% of plants flowered in each plot.
- 2- Days to maturity: number of days taken from sowing to physiological maturity.
- 3- Plant height (cm): it was measured in cm, from the ground level to the tip of the main shoot at the time of maturity.
- 4- Number of branches per plant: number of branches emerged from main stem at the time of maturity.
- 5- Number of capitula per plant: total number of capitula of the selected plants at the time of maturity and averaged.
- 6- Number of seeds per capitulum: A random sample of 25 capitula was picked from each plot.
- 7- 100-seed weight (g): 100-seed from a mixture of 5 selected plants were counted randomly.
- 8- Biological yield per plant (g): weight of total biomass of a single plant was recorded in grams.
- 9- Harvest index (%): it was calculated by the following equation:
Harvest index (%) = (Economic yield/Biological yield) x100
- 10- Seed yield per plant (g): seeds were obtained from each single plant and were weighed and measured in grams.

Statistical analysis:

The results were analyzed using the statistical program Genstat V. 12.

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

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

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

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 parent to the progeny (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:

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

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

$$\delta^2_e = Mse$$

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 was 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 to estimate phenotypic and genotypic correlation coefficients between all pairs of characters, were computed following the same as variance analysis.

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

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

Where, $\text{COV}_g(xy)$ and $\text{COV}_{ph}(xy)$ are the genotypic and phenotypic covariances 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 variance:

The data for all the ten traits were analyzed and presented in Table (2). 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 of genotypes, years and its interaction for all traits, indicating relatively high magnitude of genetic diversity in these genotypes under study.

Table 2. Analysis of genotypic variance for different quantitative characters of six safflower (*Carthamus tinctorius* L.) genotypes in 2014/2015

SOV	df (n-1)	Mean of squares									
		Days to %50 flowering	Days to maturity	Plant height (cm)	No. of branches/plant	No. of capitula / plant	No. of seeds per capitulum	100-seed weight	Biological yield per plant (gm)	Harvest index	Seed yield / plant (gm)
Genotype	5	108.77*	33.85**	315.95**	54.62**	135.46**	96.15**	95.80*	463.75**	112.03**	1014.27**
Year	1	7.9*	1.8*	108.77**	0.8*	2.78*	1.19*	5.5*	113.3*	6.2*	31.62*
Genotype x year	5	1.3*	0.9*	17.22*	0.33*	6.92*	1.04*	0.76*	6.7*	0.9*	3.5*
Error	5	1.97	2.12	5.73	0.79	5.08	6.1	3.67	2.23	2.86	5.87

* Significant at 0.05 probability level, ** Significant at 0.01 probability level

The data in Table (3) shows that mean, range, phenotypic and genotypic coefficients of variation, heritability and genetic advance as percentage of mean which were estimated for all the studied traits. The high values of the genetic variation coefficient indicate that the environmental factors are less likely to be affected, and the selection of that characteristic is feasible. While the high values of the phenotypic difference coefficient indicate that the effect is influenced by environmental factors as well as by genetic factors. The selection of these traits may be effective (depending on the highest value).

The highest PVC and GVC were shown for seed yield/plant (43.98 and 34.81 gm respectively), biological yield/plant (34.62 and 34.15 gm respectively) and No. of seeds per capitulum (29.33 and 28.74 respectively). The lack of variation between the phenotypic and genetic differences, reflecting the effect of genetic factors and the low impact of environmental factors on the expression of traits, giving a greater chance of selection for desirable traits.

High variability has been reported for seed yield/plant (Sarang *et al.*, 2004), No. of branches/plant (Reddy *et al.*, 2003), No. of seeds/capitulum (Reddy *et al.*, 2003; Lakshyadeep *et al.*, 2005), and No. of capitula/plant (Pandya *et al.*, 1996; Reddy- *et al.*, 2003; Lakshyadeep *et al.*, 2005).

Heritability provides information about the degree of inheritance of a particular trait. Broad sense heritability, which is the proportion of genotypic variance to the phenotypic variance, is an important parameter for selection of parents because selection has to be made on the basis of phenotypic values of the characters, which are the result of breeding values and their interplay with the environment.

The broad sense heritability values ranged from 0.60 for days to maturity – 0.95 for 100-seed weight (gm). Wakjira, (2011) reported high heritability (0.91) for days to flowering, and such high heritability estimate has been reported for seed yield/plant by Sarang *et al.*, (2004).

The highest genetic advance as percent of mean (77.54) was recorded for seed yield/plant (gm), while the lowest value for this parameter (4.07) was recorded for days to maturity. High heritability value along with high genetic advance was shown by seed yield plant (gm), biological yield/plant and no. of seeds per capitulum. Otti *et al.*, (2012) and Kandil *et al.*, (2012) reported similar results for capsules/plant. The highest genetic advance as percent of mean coupled with the high

heritability value implies selection for the trait considered would be effective in early generation due to the likely additive gene action.

Apart from showing high heritability estimates, the characters viz., harvest index, seed yield/plant, no. of seeds/capitulum, and no. of capitula/plant showed high GCV estimates, thereby pointing to the improvement of these characters through simple mass selection. Such a high heritability coupled with high genetic advance has been reported for seed yield/plant by Reddy *et al.*, (2003); Sarang *et al.*, (2004); and Choulwar *et al.*, (2005).

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

Characters	Mean	Range		PCV (%)	GCV (%)	Heritability (BS) (%)	Genetic Advance	Genetic advance as % of mean
		Min.	Max					
Days to 50% flowering	102.85	93.12	115.67	6.97	6.79	0.92	12.34	11.99
Days to maturity	142.95	135.89	154.33	3.59	3.28	0.69	5.83	4.07
Plant height (cm)	109.80	84.08	132.00	11.85	11.69	0.93	23.21	21.13
No. of branches/ plant	6.73	5.24	10.67	25.28	23.37	0.81	2.79	41.45
No. of capitula/ plant	11.64	7.33	19.56	24.69	23.47	0.93	6.61	56.78
No. of seeds per capitulum	15.12	7.33	23.43	29.33	2874	0.92	9.84	65.07
100-seed weight (gm)	5.45	3.43	6.28	9.91	9.68	0.95	1.12	20.55
Biological yield p/plant	33.63	15.00	65.68	34.62	34.15	0.94	24.13	71.75
Harvest index	30.34	19.13	37.62	22.21	21.19	0.90	12.17	40.11
Seed yield / plant (gm)	9.62	4.57	16.71	34.98	34.81	0.93	7.46	77.54

Study of genetic and phenotypic correlations between traits is important in genetic programs because they provide information on 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 safflower productivity.

The genotypic correlation of seed yield/plant and its components are shown in Table (4). The results of genotypic correlations indicated that seed yield/ plant is correlated with some traits such as: the biological yield/plant, no. of capitula/plant, no. of branches/plant and 100-seed weight. The highest genotypic correlation was observed between days to 50% flowering and days to maturity (gm) ($r=0.85^*$), and plant height (cm) ($r=0.85^*$).

Seed yield/plant was positively and significantly correlated with biological yield/plant (gm) ($r=0.69^*$). Rafiei, (2002) found negative but Abulhasani, (2003) reported a positive correlation between seed yield and 100-seed weight.

Genetic correlation is due to two reasons for the multiple effects of genes, as well as a link between genes and low environmental vulnerability, which gives full confidence in the direct selection of these traits (Maryam *et al.*, 2012).

Table 4. Estimates of genotypic correlation coefficients for some quantitative characters in of six safflower varieties

Characters	Days to maturity	Plant height (cm)	No. of branches/ plant	No. of capitula / plant	Number of seeds per capitulum	100-seed weight (gm)	Biological yield p/plant (gm)	Harvest index	Seed yield/ plant (gm)
Days to 50% flowering	0.85*	0.84*	-0.46	-0.49	0.04	0.29	-0.26	0.12	-0.12
Days to maturity	-	0.85*	-0.49	-0.59	0.11	0.24	-0.20	0.02	-0.28
Plant height	-	-	-0.60	-0.56	0.11	0.32	0.13	0.03	-0.24
No. of branches/ plant (cm)	-	-	-	0.76	-0.32	-0.01	0.42	-0.02	0.53
No. of capitula / plant	-	-	-	-	-0.25	0.04	0.58	-0.20	0.62*
Number of seeds per capitulum	-	-	-	-	-	0.16	0.04	-0.05	-0.052
100-seed weight (gm)	-	-	-	-	-	-	-0.14	0.43	0.39
Biological yield p/plant (gm)	-	-	-	-	-	-	-	-0.72	0.69*
Harvest index	-	-	-	-	-	-	-	-	0.12

** Correlation is significant at the 0.01 level (1-tailed).

* Correlation is significant at the 0.05 level (1-tailed).

The phenotypic correlation of seed yield/plant and its components are shown in Table (5). The results of phenotypic correlations indicated that seed yield/ plant is correlated with some traits such as: the biological yield p/plant, no. of capitula/plant, no. of branches/plant and 100-seed weight.

The highest phenotypic correlation was observed between days to 50% flowering with days to maturity (gm) and plant height (cm) ($r=0.67^{**}$).

Seed yield/plant was positively and significantly correlated with biological yield/plant (gm) ($r=0.54^{**}$).

Mukta *et al.*, (2008) reported similar findings for seed yield per plant, lower branch height, number of capitula per plant, number of branches per plant, biological yield per plant, harvest index, seed yield per plant, number of seeds per capitulum and 100 seed weight in safflower.

The phenotypic correlation between traits is due to the association between the additive genes and non-additive action of the genes responsible for the two properties and the effects of the environment. This includes the effect of genetic and environmental factors (Yazdi and Abd-mishani, 1989)

Table 5. Estimates of phenotypic correlation coefficients for some quantitative characters of six safflower varieties

Characters	Days to maturity	Plant height (cm)	No. of branches/plant	No. of capitula / plant	Number of seeds per capitulum	100-seed weight (gm)	Biological yield p/plant (gm)	Harvest index	Seed yield/plant (gm)
Days to 50% flowering	0.67**	0.67**	-0.32**	-0.34**	-0.07	0.17*	-0.18*	0.08	-0.16
Days to maturity	-	0.63**	-0.42**	-0.35**	0.05	0.22*	-0.21*	0.08	-0.23*
Plant height(cm)	-	-	-0.45**	-0.34**	-0.01	-0.27**	-0.02	-0.03	-0.15
No. of branches/plant	-	-	-	0.49**	-0.23**	-0.01	0.31**	-0.10	0.32**
No. of capitula / plant	-	-	-	-	-0.11	0.04	0.47**	-0.09	0.46**
Number of seeds per capitulum	-	-	-	-	-	-0.09	-0.01	-0.02	-0.05
100-seed weight (gm)	-	-	-	-	-	-	-0.09	0.31**	0.28**
Biological yield p/plant(gm)	-	-	-	-	-	-	-	-0.52**	0.54**
Harvest index	-	-	-	-	-	-	-	-	0.16

** Correlation is significant at the 0.01 level (1-tailed).

* Correlation is significant at the 0.05 level (1-tailed).

Conclusion:

The discussion pertaining to the various relevant topics of the present investigation has been furnished *viz.*, genetic variability, heritability, genetic advance and correlation analysis.

-The value of mean sum of squares due to genotypes was significant for all the traits, which indicated that the experimental material differed significantly amongst them.

-The values of mean and range revealed that there was a wide variability among genotypes for most of the characters.

-The characters namely, biological yield per plant, followed by seed yield per plant, number of seeds per capitulum, number of capitulum per plant, number of branches per plant and harvest index exhibited wide range and high PCV and GCV give an opportunity for improvement through selection. Besides, these characters also had narrow differences between the values of PCV and GCV showing least influence of environment.

-High heritability coupled with high genetic advance observed for seed yield per plant, biological yield per plant, 100 seed weight, plant height and number of seeds per capitulum indicated that these traits are governed by additive gene action. Hence, there are good chances of improvement of these traits through direct selection.

-The highest phenotypic correlations were observed between seed yield with some traits such as: biological yield/plant and no. of capitula/ plant, thus, these traits may be used as selectorial indices in improving safflower yield.

References:

- Abulhasani, K. (2003). Evaluation of selected lines from Al-Jibouri, H.A., Miller, P.A. and Robinson, H.F. 1958. Genotypic and environmental variance and covariance in an upland cotton cross of interspecific origin. *Agronomy Journal*. 50: 633- 637.
- Ashri, A. (1975). Evaluation of the germplasm collection of safflowers (*Carthamus tinctorius* L.), Distribution and regional divergence for morphological characters. *Euphytica*. 24:651–659.
- Biradar, S.; V. Rudra; S.A. Desai; G. Parameshwarappa; P.M. Salimath; L. Nanumantharaya; G. soumanagouda; M.P. Bhasavaraj; and Babu Harish (2012). Assessing genetic variability parameters for yield and yield components in f3 segregating generation of safflower (*Carthamus tinctorius* L.). *J. Oilseed Res.*, (29): 61-64.
- Choulwar, S.B.; R.R. Dhutmal; I. Madrap; and B.M. Joshi (2005). Genetic variability for yield and yields related traits in F2 population of safflower. *Journal of Maharashtra Agricultural Universities*. 30(1): 114-116.
- Dalvi, V.A.; L.A. Madrap; and D.S. Phad (2013). Correlation and path analysis study in safflower. *J. Maharashtra Agril. Univ*. 30(2): 232-234.
- Helm, J.L.; A.A. Schneiter; N. Riveland; and J. Bergman (1991). *Safflower Production*. North Dakota State University, Fargo, USA.
- Kandil, A.A.; A.E. Sharief; T.A. Abo-Zaied and A.G.T. Moussa (2012). Multivariate analysis of some economic characters in flex, *Pak. J. Biol. Sci.*, 15:85-91.
- Knowles, P.F. (1969). Centers of plant diversity and conservation of crop germplasm: Safflower. *Econ. Bot.*, 23:324.329.
- Lakshyadeep, S.P.; and S.S. Shanna (2005). Genetic variability and correlation studies in safflower, *Carthamus tinctorius* L. *Journal/Oilseeds Research*. 22(1): 180-182.
- Lande, S.S.; and S.N. Deshmukh (2012). Population improvement in safflower (*Carthamus tinctorius* L.). *J. Oilseed Res.*, 29 (Spl. Issue):
- Maryam, S.; Z. Hossein; and Y. Ehdi (2011). Investigation of genetic variation in *Carthamus Tinctorius* L. genotypes using agro-morphological traits. *Journal of Research in Agricultural Science*. 2: 101- 108.
- Maryam, H.R.; Z.M. Ali; and A. Fashat (2012) seed yield and yield component of safflower (*Carthamus tinctorius* L.), grown in north of Iran conditions. *J. Oilseed Res.*, 29: 36-39.
- Mukta, N.; V.V. Gopinath; and N. Sreedhar (2008). Studies on genetic divergence in safflower (*Carthamus tinctorius* L.). *Indian J. Genet.*, 21(2): 120-122.
- Ottai, M.E.S.; M.A.A. Al-Kordy; R.M. Hussein; and M.S. Hassanein (2012). Genetic diversity among Romanian fiber flax varieties under Egyptian conditions. *Aust. J. Basic, Applied Sci.*, 6: 162-168.
- Pandya, N.K.; S.S. Gupta; and A.K. Nagda (1996). Path analysis of some yield contributing traits in safflower. *Crop Research*. 11: 313-318.
- Rafiei, F. (2002). Investigation of genetic variations of agronomic traits of safflower in Isfahan. M.Sc. Thesis. Collage of Agriculture, Isfahan University of Technology.
- 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.

- Reddy M.V.; P. Chand; and V. Band (2003). Analysis of variability parameters for yield and its components in the F3 generation of safflower (*Carthamus tinctorius* L.). *Progressive Agriculture*. 3(1/2): 143-144.
- Sarang, D.H.; A.A. Chavan; A.S. Gunjkar; V.N. Chinchane; and S.P. Pole (2004). Study of genetic variability following hybridization in Samower. *Annals Plant Physiology*. 18(1): 68-70.
- Sarker, A.; W. Erskine; and M. Singh (2003). Variation in shoot and root characteristics and their association with drought tolerance in lentil landraces. *Genetic Recourses Crop Evolution*. 52:87-95.
- Singh, R.; and S. Chowdhury (1991). Induced co-dominant mutation for dwarfness in lentil. *Indian Journal of Genetics and Plant Breeding*. 51: 370-372.
- Vavilov, N.I. (1951). *The origin, variation, immunity and breeding of cultivated plants*. The Ronald Press Co., New York.
- Wakjira, A., (2011). Genetic variability among linseed collections. In: *Oilseeds- Engine for economic development*, Terefe, G., A, Wakjira and D. Gorfu (Eds.). Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia. pp: 61-72.
- Weiss, E.A. (2009). *Oil seed crops*. Blackwell Science Ltd, Oxford, UK.
- Yang, Y.X.; W.Wu; Y.L. Zheng; L. Chen; R.J. Liu; and C.Y. Huang (2007). Genetic diversity and relationships among safflower (*Carthamus tinctorius* L.) analyzed by inter-simple sequence repeats (ISSRs). *Genet. Resour. Crop. Evol.*, 54:1043.1051.
- Yazdi Samadi, U.; and B.C. Abd-mishani (1989). Cluster analysis in safflower. *Second International Safflower Conference INDIA*, 9-13 Jan., pp: 119-126.

التباين، درجة التوريث، التقدم الوراثي ومعامل الارتباط لبعض الصفات التطورية والشكلية والإنتاجية في عدة طرز من القرطم (*Carthamus tinctorius*)

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الملخص

نفذ البحث لتقييم بعض الصفات الفينولوجية والمورفولوجية والإنتاجية لستة طرز وراثية من القرطم (*Carthamus tinctorius*) وهي (Gila، Syrian-1، Acar 6، Thick orange 480، local) باستخدام بعض المؤشرات الوراثية (معامل التباين الوراثي والمظهري، معامل التوريث بالمفهوم الواسع، التقدم الوراثي، معامل الارتباط الوراثي والمظهري) في منطقة دمسرخو 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 القرطم. أظهر تحليل التباين التجمعي وجود فروقات معنوية ($P < 0.05$) لتأثير التراكيب الوراثية والسنوات والتفاعل بين التراكيب الوراثية والسنوات عند كل الصفات المدروسة. وكشفت قيم المتوسط والمدى أن هناك تبايناً واسعاً بين الأنماط الجينية لمعظم الصفات. كما أبدت صفات الوزن البيولوجي/نبات، يليه وزن البذور/نبات، عدد البذور/القرص، عدد الأقراص/نبات، عدد الفروع/نبات ومؤشر دليل الحصاد مدى واسع ومرتفع من التباين الوراثي والمظهري، وهذا التباين يوفر مجالاً واسعاً للتحسين من خلال الانتخاب. بالإضافة إلى ذلك، كان لهذه الصفات أيضاً اختلافات ضيقة بين قيم معامل الاختلاف الوراثي والمظهري وهذا يدل على قلة التأثير بالبيئة. أيضاً لوحظ ارتفاع درجة التوريث بالمفهوم الواسع مقترنة بالتقدم الوراثي العالي في وزن البذور/نبات، الوزن البيولوجي/نبات، وزن 100 بذرة، ارتفاع النبات وعدد البذور/القرص، وهذا يشير إلى أن هذه الصفات تحكمها الجينات الإضافية. وبالتالي، هناك فرص جيدة لتحسين هذه الصفات من خلال الانتخاب المباشر. كما كان معامل الارتباط المظهري عالي بين وزن البذور/النبات وكل من الوزن البيولوجي/النبات وعدد الأقراص/النبات، وبالتالي يمكن استخدام هذه الصفات لانتخاب المورثات عالية الغلة.

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