



RESEARCH PAPER

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Assessment of broad sense heritability and genetic advance in safflower

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Abstract

Broad sense heritability and genetic advance are the important parameters in breeding programs. In this study broad-sense heritability and genetic advance of seed yield and yield components were evaluated in 20 safflower genotypes. This experiment was conducted in randomized complete block design with three replications. Days to flowering, days to maturity, plant height, number of capitol per plant, number of seeds per capitol, main capitol diameter, 1000 seeds weight and seed yield per plant were measured and recorded. Genotypic effect was significant for the studied traits. The results of broad-sense heritability indicated that main capitol diameter, number of seeds per capitol, 1000 seed weight and plant height traits had the highest value. The main capitol diameter and plant height revealed higher values of genetic advance. High genetic advance coupled with heritability was observed for main capitol diameter and plant height traits. Thus selection based on these traits will be useful in safflower breeding programs. Cluster analysis based on characters of main capitol diameter, number of seeds per capitol, 1000 seed weight and plant height suggested that genotypes of Soviet1, IL111, Goldasht and Tajikistan can be considered as genotypes with high broad-sense heritability and genetic advance and so can be used for breeding purposes.

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Introduction

Safflower (*Carthamus tinctorius* L.) is an annual plant belonging to Compositeae family which is diploid and has $2n = 2x = 24$ chromosomes (Bowles, 2010; Jaradat and Shahid, 2006). The origins of Safflower are Mediterranean, the Middle East and Iran (Bowles, 2010, Golkar *et al.*, 2011). The basic application of safflower is the production of edible oil which its oil is rich in unsaturated fatty acids (Bahmankar *et al.*, 2014; Jaradat and Shahid, 2006). In breeding programs, having information regarding the heritability and genetic advance of traits is useful (Mohamed *et al.* 2012; Sardar *et al.*, 2006). Heritability represents genetic variations out of total variations and is a criterion which determines the type of breeding method and power of heritability each trait for plant (Hassani *et al.*, 2012). Traits with high heritability have much more efficiency in screening programs and in the opposite, in traits with low heritability, it is difficult to select and selection based on that trait will not be useful. Genetic advance is also very important in breeding programs because they show the amount of expected genetic gains from a selection period (Hamdi *et al.*, 2003). Estimating heritability by itself cannot provide a reliable idea regarding the prediction of functioning in the next generation and to attain more reliability it should be studied along with genetic advance so as to study variations in generations' means (Chaghakaboodi *et al.*, 2012). Thus, heritability along with phenotypic variance and the severity of selection provide estimableness of genetic advance or responding to the selection which is very useful in the selection of promising lines (Johnson *et al.*, 1995; Roham *et al.*, 2003). Parameters of heritability and genetic advance have been successfully employed in the breeding programs to reform traits in different crop plant. These include sorghum (Ali *et al.*, 2012), cow (Idahosa *et al.*, 2010), Maize (Bello *et al.*, 2012) and Rapeseed (Ahmad *et al.*, 2013). Therefore, having information regarding the heritability and genetic advance of traits is useful in the breeding programs and traits with high heritability and genetic advance have much more efficiency in screening programs. This study was designed with the purpose assessment

of broad heritability and the genetic advance of morpho-phonologic traits in the genotypes of safflower to be used in breeding programs.

Material and methods

Plant materials and growth condition

This study was conducted in a Research Center for Agriculture and Natural Resources in Yasuj, Iran in 2012. In this experiment, 20 safflower genotypes (table 1) including 6 genotypes from Iran along with 14 genotypes from the Institute of Plant Genetics and Crop Plant Research (IPK) in Germany was planted in the trail study of randomized completed blocks design with three replications in spring 2012. During growth periods, required cares were taken.

Studied traits and its measuring method

Eight plants were selected randomly from each plot and all phonologic and morphologic traits including days to flowering, days to maturity, plant height, number of capitol per plant, number of seeds per capitol, main capitol diameter, 1000 seeds weight and yield per plant were measured and written down.

Statistical analysis

Genetic parameters including variance (genetic and environmental components), heritability and genetic advance were calculated based on mathematical expectation (table 2). In order to grouping similar genotypes based on measured traits used Wards' clustering analysis and Squared Euclidean Distance. Statistical analyses of the data were conducted using the SPSS ver 19. In the table 2, δ^2_p stands for phenotypic variance, δ^2_g stands for genotypic variance, δ^2_e for environmental variance, h^2_b for general heritability, GA for genetic advance and i for standardized selection differential. A standardized selection differential value for the selection severity 1 % is equal to 2/64, the selection intensity of 5% is equal to 2 / 06 and a selection intensity of 10 % equals 1/75.

Result and discussion

Broad sense heritability

Findings obtained from the study of broad heritability

suggest that the traits of main capitulum diameter, 1000 seeds weight, plant height and number of seeds per capitulum have the most parameters (table 3). High heritability of the mentioned traits showed that they can be reformed using selection (Reddy *et al.* 2013).

Camas and Esendal also reported high general heritability for studied traits in safflower and recommended the use of selection to reform traits (Camas and Esendal, 2006).

Table 1. List of names and origin of safflower genotypes.

Genotype	Origin	Genotype	Origin
Khatam Yazd	Iran	C130	Morocco
Goldasht	Iran	C132	Germany
Sina411	Iran	C161	Soviet Union
Local Isfahan	Iran	C24	Morocco
Isfahan 14	Iran	C151	Pakistan
IL111	Iran	C83	Tajikistan
C19	Polish	C9	Republic of Czech
C160	Soviet Union	C56	USA
C173	Indian	C55	Polish
C124	Pakistan	C159	Germany

Table 2. The methods of estimate genetic parameters.

Parameter	Formula	Formula
Phenotypic variance		$\delta^2_p = \delta^2_g + \delta^2_e$
Genotypic variance		$\delta^2_g = \frac{MSt - MSe}{r}$
Environmental variance		$MS_e = \delta^2_e$
Genetic advances		$GA = i * h^2_b * \sqrt{\delta^2_p}$
Broad sense heritability		$h^2_b = \frac{\delta^2_g}{\delta^2_p}$

Genetic advance

The results from the study of genetic advance of traits to be evaluated showed that the two traits of main capitulum diameter and plant height have the most frequencies (table 3). Generally, heritability and high genetic advance in the traits of main capitulum diameter,

plant height, number of seeds per capitulum and 1000 seeds weight indicated that genetic factors in comparison with environmental conditions are more effective and thus using selection in breeding programs to reform the mentioned traits will be useful.

Table 3. The estimate of genetic parameters for evaluated traits in safflower.

Trait	Mean	MS _t	MS _e	V _G	V _P	H ² _b	GA
DF	63.195	93.5**	5.06	29.48	34.54	0.85	8.74
DM	116.62	113.1**	3.74	36.82	40.56	0.91	10.15
HP	11.025	8.1**	2.95	3.88	6.83	0.57	2.60
PH	72.72	262.1**	1.41	86.87	88.28	0.98	16.11
MHD	233.41	5650**	12.15	1879.8	1891.95	0.99	75.35
SH	33.68	79.9**	0.69	46.21	46.9	0.98	11.74
SYP	12.52	47.5**	7.4	13.34	20.74	0.64	5.10
SW	35.03	118.3**	0.19	39.36	39.55	0.99	10.90

*and**significant at the 0.05 and 0.01 level respectively

DF: Days to flowering; DM: Days to maturity; HP: heads per plant; PH: plant height; MHD: Main head diameter; SH: seeds per head; SY: seed yield per plant; SW: 1000-seed weight.

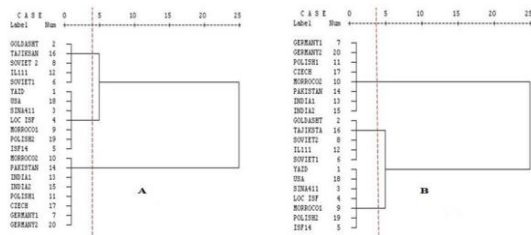


Fig. 1. Dendrogram of different genotypes of safflower based on broad-sense heritability (A) and genetic advance (B).

Cluster analysis

The results of clustering analysis of superior traits from the standpoint of general heritability parameters and genetic advance indicated that genotypes were placed in three separate groups (figure 1- A and B). Regarding the results, from the perspective of genetic advance and general heritability Soviet Union 1, IL111, Goldasht and Tajikstan genotypes can be used as superior genotypes for breeding purposes. Hassani *et al.* and Hosseini *et al.* used general heritability and genetic advance in rapeseed and rice respectively and reported that genetic factors in comparison with environmental conditions are more effective and thus suggested that which selection in breeding programs to reform the evaluated traits will be useful (Hassani *et al.*, 2012 ;Hosseini *et al.*, 2011). Generally in breeding programs, having information regarding the heritability and genetic advance of traits is useful and traits with high heritability and genetic advance have much more efficiency in screening programs. Thus, heritability along with genetic advance is important parameter that which provides information about responding to the selection which is very useful in the selection of promising lines.

References

- Ahmad B, Mohammad S, Azam FI, Ali I, Ali J and Rehman SU.** 2013. Studies of Genetic Variability, Heritability and Phenotypic Correlations of Some Qualitative Traits in Advance Mutant Lines of Winter Rapeseed (*Brassica napus* L.). American-Eurasian Journal Agriculture and Environmental Science **13**, 531-538.
- Ali HI, Mahmoud KM, Amir AA.** 2012. Estimation of Genetic Variability, Heritability and

Genetic Advance in Grain Sorghum Population, American-Eurasian Journal Agriculture and Environmental Science **12**, 414-422.

Bahmankar M, Nabati Ahmadi D, Dehdrai M. 2014. Correlation, multiple regression and path analysis for some yield-related traits in safflower, Journal of Biodiversity and Environmental Sciences **4**, 111-118.

Bello OB, Ige SA, Azeez MA, Afolabi MS, Abdulmalik SY, Mahamood J. 2012. Heritability and Genetic Advance for Grain Yield and its Component Characters in Maize (*Zea Mays* L.), International Journal of Plant Research **2**, 138-145.

Bowles V. 2010. Relationshipship and introgression within *Carthamus* (Asteraceae), with an emphasis on safflower (*Carthamus tinctorious* L.).A Thesis of M.S, University of Alberta.

Camas N, Esendal E. 2006. Estimates of broad-sense heritability for seed yield and yield components of safflower (*Carthamus tinctorius* L.), Hereditas **143**, 55-57.
<http://dx.doi.org/10.1111/j.2006.0018-0661.01914.x>

Chaghakaboodi Z, Kahrizi D, Zebarjadi A. 2012. Heritability and genetic advance in rapeseed (*Brassica napus* L.), Iranian journal of genetics and plant breeding **1**, 16-21.

Golkar P, Arzani A, Rezaei AM. 2011. Genetic Variation in Safflower (*Carthamus tinctorious* L.) for Seed Quality-Related Traits and Inter-Simple Sequence Repeat (ISSR) Markers, International Journal of Molecular Sciences **12**, 2664-2677.
<http://dx.doi.org/10.3390/ijms12042664>

Hamdi A, Ghareib EI, Shafey A, Ibrahim SA. 2003. Genetic variability, heritability and expected genetic advance for earliness and seed yield from selection in lentil. Egypt Journal Agricultural Research **81**, 125-137.

- Hassani Z, Pirdashti H, Fotokiyani M, Hosseini SJ, Abasiyan A.** 2012. Evaluation of general heritability and genetic advance in different canola (*Brassica napus* L.) genotypes. 12th Congress of Agronomy and Plant Breeding, Azad University of Karaj, Tehran.
- Hosseini SJ.** 2011. Effect of salt stress in different rice genotypes. M Sc Thesis, Tarbiat Modares University, 127 pages.
- Idahosa DO, Alike JE, Omoregie AU.** 2010. Genetic Variability, Heritability and Expected Genetic Advance as Indices for Yield and Yield Components Selection in Cowpea (*Vigna unguiculata* (L.) Walp. *Academia Arena* **2**, 22-26.
- Jaradat A and Shahid M.** 2006. Pattern of phenotypic variation in a germplasm collection of *Carthamus tinctorious* From the Middle East. *Genetic Resources and Crop Evolution* **53**, 225-244.
- Johnson HW, Robinson HF, Comstock RE.** 1955. Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* **47**, 314-318.
- Mohamed SM, Ali EE, Mohamed TY.** 2012. Study of Heritability and Genetic Variability among Different Plant and Fruit Characters of Tomato (*Solanum lycopersicum* L.), *International Journal of Scientific & Technology Research* **1**, 55-58.
- Reddy BR, Reddy DS, Reddaiah K, Sunil N.** 2013. Studies on genetic variability, heritability and genetic advance for yield and quality traits in Tomato (*Solanum lycopersicum* L.). *International Journal of Current Microbiology and Applied Sciences* **2**, 238-244.
- Roham MM, Iqbal ASM, Arifin MS, Akhtar Z, Husanuzzaman M.** 2003. Genetic variability, correlation and path analysis in mungbean, *Asian Journal of Plant Science* **2**, 1209-1211.
<http://dx.doi.org/10.3923/ajps.2003.1209.1211>
- Sardar A, Hidayat UR, Raziuddin S, Salim S, Hassan G.** 2006. Estimates of Variability, Heritability and Genetic Advance for Fodder Traits in Two Maize Populations. *Pakistan Journal of Biological Sciences* **9**, 2618-2623.
<http://dx.doi.org/10.3923/pjbs.2006.2618.2623>