Journal of Biodiversity and Environmental Sciences (JBES)
ISSN: 2220-6663 (Print) 2222-3045 (Online)
Vol. 6, No. 1, p. 152-159, 2015
http://www.innspub.net

RESEARCH PAPER OPEN ACCESS

Assessment of genetic diversity in sunflower (*Helianthus annus* L.) genotypes using agro-morphological traits

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Article published on January 05, 2015

Key words: Diversity, Genetic parameters, heritability, genetic advance, genetic gain, sunflower lines.

Abstract

Selection of genotypes based on high value of heritability and forecasted genetic conditions would be an effective method for improvement of sunflower lines.The present investigation was carried out to (i) study of some agro-morphologic traits and (ii) to estimate genetic variability parameters for the studied traits in 36 lines of sunflower. Analysis of variance showed that genotypes significantly differed for two studied traits. Genotypic and phenotypic coefficients of variations were high for Thousand Kernal Weight (TKW), Head Diameter (HD) and Leaf Number (LN). Heritability estimates were LN, Days to physiological Maturity (DM) and Seed yield (SY). High genetic gain was observed for TKW, HD and LN. Correlation analysis showed HD was significantly correlated with a trait TKW. High heritability estimates associated with high genetic advance as percent mean (GG) were obtained in characters i.e., TKW, SY, HD and LN.

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Introduction

The objectives of a plant breeder embrace selection from a natural population or from an indigenous population for one or several attributes. Yield is a complex character and is a function of several component traits and their interaction with environment. It is more appropriate if the structure of yield is probed through breeding techniques. It is important to measure the mutual relationship between various plant attributes and determine the component characters, on which selection procedure can be based for direct and indirect genetic improvement of crop yield. Sunflower (*Helianthus annuus* L.) has become an important oil crop in the world with annual production of 20 to 25 million hectares worldwide in present decade (Machikowa and Saetang, 2008).Sunflower (*Helianthus annus* L.) is an important oilseed crop (Pourdad and Beg, 2008). It ranks third after Soybean and palm oil in worldwide vegetable oil production (Iqbal *et al*., 2009). Turkey, Morocco, Pakistan, Iran, Iraq and Sudan were the leading producers in WANA (Beg *et al*., 2007).The understanding and knowledge of genetic variation and genetic similarities present within individuals or populations are useful for the efficient use of genetic resources in breeding program (Safavi *et al*., 2010).

The development of an effective plant breeding program is dependent upon the existence of genetic variability. The efficiency of selection largely depense upon the magnitude of genetic variability present in the plant population. Thus the success of genetic improvement in any character depends on the nature of variability present in the gene pool for that character. Hence an insight into the magnitude of variability present in the gene pool of a crop species is of utmost importance to a plant breeder for starting a judicious plant breeding program. In earlier years the visual observations used to be the measure of variability in a plant population. Now biometrical methods are available for systematic assessment of variability (Singh and Narayanan, 1993).

Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance, and genetic and environmental factors that influence their expression. To plan an efficient development program, it is necessary to have an understanding of the breeding systems coupled with statistical analysis of inheritance data (Yap and Harvey 1972, Srivastava and Dhamania, 1989).

Genetic parameters have been estimated in many crops (Maniee *et al*., 2009; Kahrizi *et al*., 2010a; Kahrizi *et al*., 2010b; Garavandi *et al*., 2011).

Quantitative traits with high genetic gain and high heritability are very important in selection of genotype at early stages of breeding programs (Memon *et al*, 2005). Using family selection method may led us to success in the case of selection for traits with low heritability and high interactions between genotypes and environment (Aycicek and Yildirim, 2006). The aims of this study were (i) study of some agro-morphologic traits and (ii) estimate genetic variability parameters for the studied traits in 36 lines of sunflower.

Material and methods

Current study was carried out with 36 genotypes based on Randomized Complete Blocks Design (RCBD) with two replication at the research in Sararood station, Kermanshah, Iran, 2010 cropping season. The genotypes used in this study are given in Table 1. The plot sizes were 6.0×6.0 m. Standard cultural practices were followed for raising the crop. The characters studied were Days to Start of Flowering (DSF), Days to Finish of Flowering (DFF), Days to physiological Maturity (DM), Leaf Number (LN), Head Diameter (HD), Seed yield (SY) and Thousand Kernal Weight (TKW). Data were statistically analyzed for each character separately. Plant growth analysis was done based on Bullock *et al*. (1993). The analysis of variance for different characters were measured followed by Duncan's New Multiple Range Test (DMRT) (Steel and Torrie, 1960), to test the significance difference between

means. The mean squares were used to estimate genotypic and phenotypic variance according to Johnson *et al.* (1955). The coefficient of variation was calculated based on the formula suggested by Burton (1952). The genotypic and phenotypic coefficient of variation and heritability were calculated as suggested the formula used by Singh and Choudhury (1985) and genetic advance by Allard (1960) as well as correlation coefficient by Zaman *et al.* (1982). The goal of this research was to study some morphological traits of sunflower lines (ii) to estimate genetic variability parameters for the studied traits.

Table 1. 36 lines of sunflower that used in current study.

Lines	
SIL-20	SIL-210
SIL-42	SIL-215
SIL-53	SIL-217
SIL-54	SIL-222
SIL-75	SIL-224
SIL-80	SIL-226
SIL-82	SIL-227
SIL-94	SIL-237
SIL-96	SIL-238
SIL-97	SIL-254
SIL-99	SIL-259
SIL-114	SIL-260
SIL-140	SIL-280
SIL-162	SIL-196
SIL-200	SIL-218
SIL-203	SIL-231
SIL-205	SIL-240
SIL-206	SIL-211

Biometrical genetic analysis

The recorded data were subjected to analysis of variance using SAS V9.1 software to ascertain existence of variability among the genotypes.

The phenotypic and genotypic coefficient of variation (PCV and GCV), broad sense heritability (h^2_{bs}), genetic gain and co-heritability were estimated according to (Farshadfar, 2013) from the components of variance and covariance as follows:

$$V_E = MS_e$$

$$V_G = \frac{MS_g - MS_e}{r}$$

$V_P = V_G + V_E$

$$PCV = 100\sqrt{\sigma_p^2}/\bar{x}$$

$$GCV = 100\sqrt{\sigma_g^2}/\bar{x}$$

$$ECV = 100\sqrt{\sigma_E^2}/\bar{x}$$

$$h^2_{bs} = \sigma_g^2/\sigma_p^2$$

$$GG = (i.\sigma_g^2/\sqrt{\sigma_p^2})100/\bar{x}$$

$$r_p = \frac{PCOV_{XY}}{\sqrt{(PV_X.PV_Y)}}$$

$$r_g = \frac{GCOV_{XY}}{\sqrt{(GV_X.GV_Y)}}$$

$$r_e = \frac{ECOV_{XY}}{\sqrt{EV_X.EV_Y}}$$

Ve = environmental variation, MSE = error mean square, Vg = genotypic variation, r = number of replication, Vp = phenotypic variation $\bar{x}$ is the mean, σ^2_g is genetic variance, σ^2_p is phenotypic variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, ECV = environmental coefficient of variation, h^2_{bs} = broadsense heritability, GG = genetec gain, r_p= phenotypic correlation, r_g= genetic correlation, re= environmental correlation.

Results and discussion

Descriptive statistics and variability

The genotypes showed significant differences for DM and SY, indicating the presence of adequate variability among the genotypes (Table 2). Genotype *SIL-237* showed the highest SY (Table 3). In case of DSF genotypes ranged from 80.50-85.50 day and the mean was 83.43 (Table 4). Moderate genotypic and phenotypic co-efficient of variations were observed for HD (Table 5). This trait showed a significant and positive correlation with TKW (Table6).

Days to Finish of Flowering (DFF) varied from 92.00 to 93.50 with mean value 92.62 (Table 4).

Table 2. Mean squares for different characters of 36 lines of sunflower.

Sources	Mean square							
	Df	DSF	DFF	DM	LN	HD	SY	TKW
Block	1	1.125	42.014	0.889	0.823	117.635	145323.41	859.134
Genotypes	35	5.787^{ns}	0.767^{ns}	1.187*	29.016^{ns}	114.353^{ns}	826114.58*	1299.54^{ns}
Error	35	2.954	0.385	0.403	14.301	57.198	683988.72	606.226

**significant at 1% level of probability, *significant at 5% level of probability,

Table 3. Mean performance of 36 lines of sunflower for different characters.

Lines	Characters						
	DSF (day)	DFF (day)	DM (day)	LN	HD (cm)	SY (kg/ha)	TKW(gr)
SIL-20	83.5	92	103.5bc	18.35	10.44	2777abcdefgh	25.18
SIL-42	84.5	93.5	105ab	25.3	11.4	2313bcdefgh	32.3
SIL-53	83	92	104.5abc	25.9	8.8	1424fgh	38.1
SIL-54	84.5	93.5	103.5bc	23.5	12.79	1586defgh	35.6
SIL-75	83	92	104abc	20.3	12.7	1888cdefgh	33.95
SIL-80	83.5	92	105ab	27.9	7.345	1792defgh	20.28
SIL-82	83	93	104abc	22.35	10.43	2421abcdefgh	29.16
SIL-94	82.5	93	105ab	18.1	7.348	1379fgh	24.76
SIL-96	85.5	92.5	104.5abc	26.75	10.67	2680abcdefgh	30.22
SIL-97	85.5	92.5	103.5bc	23.7	9.2	1966cdefgh	37.05
SIL-99	83	92	104abc	23	14.2	2886abcdefgh	43.22
SIL-114	84.5	93	104abc	23.1	10.8	2546abcdefgh	36.7
SIL-140	82	92.5	104.5abc	24.1	15.88	2302bcdefgh	103.9
SIL-162	82	92.5	104.5abc	16.8	11.9	1534efgh	46.35
SIL-200	83	93	103.5bc	20.7	7.097	1489efgh	20.99
SIL-203	83	93	103c	21.1	11.31	2042cdefgh	29.33
SIL-205	83	93	103.5bc	18.65	9.044	1874cdefgh	21.91
SIL-206	81.5	93	103c	21.15	11.6	2679abcdefgh	29.35
SIL-210	84.5	93	104abc	20.55	12.51	2813abcdefgh	35.3
SIL-215	82	93	105ab	24.45	9.242	3409abcdef	27.64
SIL-217	80.5	93	105.5a	25.8	33.6	3127abcdefg	30.45
SIL-222	85.5	92.5	105ab	22.4	9.802	3852abc	27.5
SIL-224	84.5	92.5	105ab	24.1	13.9	3498abcde	30.95
SIL-226	84.5	93	105ab	16.9	10.06	1734defgh	22.06
SIL-227	82	93	104abc	22.1	27.18	2856abcdefgh	97.08
SIL-237	83.5	92.5	104.5abc	25.7	16.14	4347a	51.2
SIL-238	84	92	104.5abc	22.5	12.02	2419abcdefgh	39.93
SIL-254	84.5	92.5	104abc	21.75	15.57	1334gh	29.42
SIL-259	83.5	92.5	104abc	24.1	13.9	1868cdefgh	36.15
SIL-260	84.5	92.5	103.5bc	20.45	14.8	1034h	34.65
SIL-280	82	92.5	104abc	18.7	11.83	1365gh	36.77
SIL-196	84.5	92.5	104.5abc	20.7	11.06	2855abcdefgh	32.84
SIL-218	83.5	92	104.5abc	23.1	22.84	3614abcd	70.75
SIL-231	82.5	93	103.5bc	20.9	7.646	4222ab	21.12
SIL-240	83	92.5	104.5abc	21	13.42	2492abcdefgh	57.19
SIL-211	84	92	104.5abc	21.6	13.9	2357abcdefgh	30.25

Table4. Range, mean, standard error of mean and co-efficient of different characters of 36 lines of sunflower.

Characters	Range	Mean	SE(±)	Coefficient of variation (%)
DSF	80.50-85.50	83.43	0.19	2.06
DFF	92.00-93.50	92.62	0.07	0.66
DM	103.00-105.50	104.22	0.10	0.609
LN	16.80-27.90	22.15	0.45	17.06
HD	7.10-33.60	12.84	0.89	58.88
SY	1034.00-4347.00	2410.38	0.14	34.31
TKW	20.28-103.90	37.4	0.31	65.67

Table5. Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), heritability and genetic advance in percentage of mean for different characters of 36 lines of sunflower.

Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic advance (%)	Genetic gain (%)
DSF	1.42	3.53	16.13	0.97	1.16
DFF	0.464	1.155	17.85	0.37	0.39
DM	0.594	1.20	24.65	0.62	0.59
LN	12.24	29.70	41.21	5.55	25.05
HD	41.58	101.94	16.65	4.31	33.56
SY	11.05	50.98	21.69	531.60	22.05
TKW	49.65	116.46	18.18	16.18	43.16

Table 6. Correlation coefficient among different characters of 36 lines of sunflower.

Characters	DSF	DFF	DM	LN	HD	SY	TKW
DSF	1						
DFF	-0.106	1					
DM	0.002	-0.130	1				
LN	0.133	-0.103	0.325	1			
HD	-0.356*	-0.10	0.227	0.220	1		
SY	-0.19	-0.18	0.227	0.308	0.261	1	
TKW	-0.248	-0.136	0.061	0.142	0.537**	0.152	1

Genetic variability

The high heritability and genetic gain was observed for the LN, indicating the major part of phenotypic variations is belonging to genotypic variations (Table 5). The HD high genotypic and phenotypic coefficient of variation (GCV and PCV) were also observed (Table 4, 5) showing little environment effect on the expression of HD. Low heritability and genetic gain were observed for Days to Start of Flowering (DSF) (Table 5).

The progress of a breeding program is conditioned by the magnitude and the nature of the genotypic and non-genotypic variation in the various characters Since, most of the economic characters (e.g., yield) are complex in inheritance and are greatly influenced by various environmental conditions, the study of heritability and genetic advance is very useful in order to estimate the scope for improvement by selection. Heritability magnitude indicates the reliability with which the genotype will be recognized by its phenotype expression (Chandraba and Sharma, 1999).

The character LN showed heritability values ranging that is, between 40 to 60%. A comparatively low value of heritability was observed for the character produced, DM, SY, TKW, DFF, HD and DSF (<40%) (Table 5). The heritability estimates for different characters depend upon the genetic make up of the breeding materials studied. Therefore, knowledge about these values in the materials in which breeders are interested is of great significance. High heritability estimates indicate that the selection for these characters will be effective being less influenced by environmental effects. Heritability estimates have been found to be useful in indicating the relative value of selection based on phenotypic expression of different characters. The results of correlation coefficient analysis showed that the HD contributed significantly towards TKW (table 6). It can be

conclude on the basis of the results obtained in the present investigation that the range of variability was quite appreciable for almost all the characters studied among different genotypes.

Primarily, biological variation present in the plant population is of three types, viz., phenotypic, genotypic and environmental. It is the total variability which is observable. It includes both genotypic and environmental variation and hence changes under different environmental conditions. Such variation is measured in terms of phenotypic variance. It is the inherent or genetic variability which remains unaltered by environmental conditions.

This type of variability is more useful to a plant breeder for exploitation in selection or hybridization. Such variation is measured in terms of genotypic variance. The genotypic variance consists of additive, dominance and epistatic components. Environmental variation refers to non-heritable variation which is entirely due to environmental effects and varies under different environmental conditions. This uncontrolled variation is measured in terms of error mean variance. The variation in true breeding parental lines and their F1 is non-heritable. Fisher was the first to divide in 1918, the genetic variance into additive, dominance and epistatic components (Mather and Jinks, 1985).

Evolution by natural selection requires heritable variation. The most common way to represent the pattern and magnitude of the genetic basis of a series of traits is the genetic variance –covariance matrix, also known as the G-matrix. G-matrix is extremely useful for predicting the response to selection over the short term. A population will evolve most rapidly along axes that have the most genetic variation, and more slowly in directions with little genetic variance. Because G accounts for genetic covariance as well, G can also help in predicting the indirect response to selection on one character from selection on another trait. If the genetic covariance between two traits is different from zero, selection on one trait will affect response to selection on the other (Guillaume and Whitlock, 2007).

Covariance matrix

According to the results of Table 7, the highest phenotypic covariance observed between SY and DM (0.310), the highest phenotypic covariance observed between DFF and TKW (0.723) and the highest environmental covariance observed between HD and SY (0.541) traits, respectively.

Table 7. Genotypic (A) and phenotypic (B) and environmental (C) correlations covariance matrix among different characters of 36 lines of sunflower.

(A)

Characters	DSF	DFF	DM	LN	HD	SY	TKW
DSF	1	0.004	0.014	0.013	-0.0036	-0.100	-1.33
DFF		1	-0.033	-0.013	-0.020	-0.430	-3.41
DM			1	0.022	-0.069	0.310	0.120
LN				1	0.098	0.010	-0.730
HD					1	-0.730	-0.18
SY						1	0.124
TKW							1

(B)

Characters	DSF	DFF	DM	LN	HD	SY	TKW
DSF	1	0.039	0.045	0.044	-0.016	0.043	0.623
DFF		1	-0.015	-0.084	-0.0250	-0.435	0.723
DM			1	0.0858	-0.0145	-0.119	-0.321
LN				1	0.0645	0.154	-0.167
HD					1	-0.386	-0.207
SY						1	0.678
TKW							1

(C)

Characters	DSF	DFF	DM	LN	HD	SY	TKW
DSF	1	-0.017	0.0144	0.002	-0.0012	0.043	-0.113
DFF		1	-0.023	-0.0277	-0.0032	-0.435	0.033
DM			1	0.0055	0.00829	-0.119	0.385
LN				1	0.0066	0.032	-0.198
HD					1	0.541	0.004
SY						1	0.108
TKW							1

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