Genetic variability among sunflower (*Helianthus annuus* L.) accessions for relative growth and seedling traits

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Abstract: Sunflower (*Helianthus annuus* L.) is an important oilseed crop that can contribute a big share in enhancing Pakistan's local edible oil production due to its short duration, more oil contents, better fitting in the cropping pattern, tolerance to drought and its high yield potential. Twenty sunflower accessions were used to estimate the genetic variability for relative growth rate, emergence and seedling traits. Seeds were sown in polythene bags following completely randomized design with three replications per genotype. Five seedlings of each accession per replication were uprooted and data were recorded on emergence percentage, emergence index, root length, shoot length, fresh root weight, fresh shoot weight, dried root weight, dried shoot weight, root/ shoot ratio and relative growth rate. The data were subjected to analysis of variance and broad sense heritability. Highly significant differences among the genotype were found for root length, shoot length, dry root weight and dry shoot weight. Fresh root weight, fresh shoot weight, dry root weight and root/shoot ratio was significant. Highest heritability was recorded for seedling emergence percentage (0.97) for pooled data analysis while 0.94 for fresh shoot weight, 0.94 root/shoot ratio, 0.76 shoot length on first harvest, 0.89 for shoot length 0.61 for dry shoot weight on 2nd harvest and 0.87 for shoot length on 3rd harvest. The higher broad sense heritability suggested that the germplasm may be used for the development of hybrid sunflower. It was concluded form present study that the selection of drought resistant sunflower genotypes on the basis of shoot length may be helpful to improve grain and oil yield.
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Abbreviations
DF = Degree of freedom, **E%** = Emergence percentage, **EI** = Emergence index, **RL** = Root length, **SL =** Shoot length, **FRW** = Fresh root weight, **FSW =** Fresh shoot weight, **DRW** = Dry root weight, **DSW** = Dry Shoot weight, **RSR** = Root/shoot ratio

Introduction

Sunflower (Helianthus annuus L.) can contribute a big share in improving Pakistan's local edible oil production due to its short duration, more oil contents, better fitting in the cropping pattern, tolerance to drought and its high yield potential. It is high yielding, non-conventional short duration (90-110 days) crop that can be grown twice a year. The seed of sunflower contains 40% oil while some varieties have up to 50% (Skoric and Marinkovic, 1986) with good adaptability under different agro climatic conditions. High level of unsaturated fatty acids, light color, and high smoke point make sunflower oil more attractive (Reddy, 2006). Sunflower oil is considered to be of supreme quality as it contains soluble vitamin A, D, E and K (George, 2002). Due to high percentage of linoleic acid and low percentage of linolenic acid which is most desirable character and lacked in other oilseeds its quality is better.

Sunflower is grown mostly as a source of vegetable oil and proteins in many countries (Leon *et al*., 1995; Hu *et al*., 2010) and is the second most important oilseed crop after soybean worldwide (Paniego *et al*., 2002). Sunflower is the 2nd major oilseed crop in Pakistan cultivated on 0.7 million hectares producing 0.144 million tons of oil which is 22% of the local edible oil production (Pakistan economic survey, 2013-14). Unfortunately its yield per hectare (1345 kg ha-1) is less than that of other countries like Turkey (2036 Kg ha-1), China (1752 Kg ha-1) and USA (2036 kg ha-1) (FAO, 2013). Therefore, there is a need to evolve hybrids and varieties of sunflower with improved genetic potential for high achene yield and oil contents. Seed yield in sunflower is combination of many traits, which are polygenic in nature and it is difficult to make direct selection for these traits. Therefore, indirect selection through associated component traits is possible to improve the yield. Sunflower breeder

reported different types of characters associations (Ashok *et al.,* 2000).

As the demand of sunflower utilization is increasing day by day, it is necessary to make efforts for the development of high yielding sunflower cultivar. Genetic variability shows the differences among individuals of breeding material. It is a measure of the tendency of individual genotypes in a population to vary from one another. Genetic variability shows the differences in the breeding material and is important because it is helpful for plant breeder to adopt proper breeding procedure. Information on the nature and level of genetic variability present in a crop species is important in crop improvement and development programs and also in the improvement of the desired character (Dabholkar, 1999). Correlation of particular character with other characters is important in indirect selection of genotypes for higher seed yield. Correlation analysis explains interactions of morphological characters with seed yield, but it only determine the relationships.

Therefore, the aims of this study were:

1) To work out genetic variability among sunflower accessions for seedling and relative growth rate parameters.

2) To estimate broad sense heritability of traits to find out the contribution of genotype to the expression of the traits.

Material and methods

The present investigation was carried out in wire house of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan during the year 2014. Faisalabad lies between 31˚ - 26˚ N and 73˚ - 60˚ E longitude with an elevation of 184 meters above sea level. In Faisalabad usually arid climate conditions exist. The plant material for research consisted of 20 sunflower genotypes (Table 1) developed and maintained by the Oilseeds Research Program (ORP), Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad.

Table 1. Sunflower accessions used as research material

Sr. No.	Accessions	Sr. No.	Accessions
1	A.7.4	11	A.2.19
2	C.2.26	12	A.1.17
3	C.3.1	13	A.2.23
4	A.13.11	14	A.6.1
5	A.10.1	15	A.2.10
6	B.2.21	16	A.1.2
7	C.2.27	17	C.3.3
8	A.12.1	18	B.3.1
9	A.2.18	19	B.2.23
10	B.1.1	20	A.2.14

The experiment was laid out following complete randomized design (CRD) with three replications. The sunflower seeds were planted in polythene begs filled with sand and soil. Four seeds of one accession were sown in the polythene bags at the depth of 1.5 cm and six bags of each accession per replication were prepared. Data were recorded on seedling emergence percentage (G %), emergence index (EI), root length (cm), shoot length (cm), fresh root weight (mg), fresh shoot weight (mg), dried shoot weight (mg), dried root weight (mg), root/shoot ratio and relative growth rate.

The data recorded was subjected to analysis of variance (Steel *et al*., 1997) and coefficients of variability, and broad sense heritability were determined using following expressions

The coefficients of variability of each character were calculated.

$CV\% = (SD/x) \times 100$

Where,

CV $\qquad$ = Coefficient of variability (%)

SD $\qquad$ = Standard deviation

$\overline{X}$ $\quad$ = grand mean for the trait

Correlation Coefficients$_p$ $\quad$ = $\quad$ COVpij $\quad$ /√ (VARpi) (VARpj)

Heritability in broad sense was estimated according to Burton and De Vane (1953) which is given as under:

$h^2 (B.S.) = (Vg/Vp) \times 100$

Where,

V_g $\quad$ = the genotypic variance

V_p $\quad$ = the phenotypic variance

$h^2 (B.S.)$ = heritability (Broad sense)

Results and discussion

Analysis of variance was performed for emergence for nine characters including emergence percentage, emergence index (EI), fresh root weight, fresh shoot weight, dry root weight, dry shoot weight, root length, shoot length, and root/shoot ratio. Accessions showed significant differences for root length shoot length, fresh root weight, fresh shoot weight and dry root weight and non-significant differences for dry shoot weight and root shoot ratio. Harvests were significant for all the traits under study. Accessions × harvest interactions was significant for shoot length and fresh shoot weight whereas, non-significant for root length, fresh root weight, dry root weight dry shoot weight and root/shoot ratio (Table 2). Accessions showed significant differences for root length, shoot length, and fresh shoot weight whereas, differences among the accessions were non-significant for fresh root weight, dry root weight, dry shoot weight and root/shoot ratio for first harvest (Table 3). While, the

differences among accessions were significant for shoot length, dry root weight, and dry shoot weight and root/shoot ratio. However, differences among the accessions were non- significant for root length, fresh root weight, and fresh shoot weight during second harvest (Table 4). Whereas, root length, fresh root weight, dry root weight, dry shoot weight and root/shoot ratios were non- significant and shoot length showed significant result for third harvest (Table 5).

Table 2 Mean square values from analysis of variance of across the of sunflower accessions

Sources of Variation	Accessions	Harvests	Gen × Har	Error
Df	19	2	38	120
RL	10.22*	8625.96**	5.62	4.613
SL	44.00**	6640.88**	22.91**	4.26
FRW	7496.39	6565589.18**	6421.56	5420.88
FSW	36777.24**	3221348.78**	22522.58**	601763
DRW	4599.93*	3505736.53**	3772.12	2781.87
DSW	3040.2	3569576.96**	4468.98	3799.39
RSR	1.24	5.90*	1.09	1.83

Table 3 Mean square values from analysis of variance for the first harvest of sunflower accessions

Sources of Variation	Df	RL	SL	FRW	FSW	DRW	DSW	RSR
Accessions	19	9.73**	16.87**	8791.34	70002.19**	1203.54	890.77	2.64
Error	156	549.73	3.993	6978.79	3919.53	1991.80	901.66	5.11

Table 4 Mean square values from analysis for the second harvest the of sunflower accessions

Sources of Variation	Df	RL	SL	FRW	FSW	DRW	DSW	RSR
Accessions	19	10.51	44.29**	5127.79	5511.50	5228.48*	5122.68*	0.74*
Error	156	8.84	5.02	3460.1641	4269.67	2159.70	1981.69	0.31

Table 5 Mean square values from analysis for the third harvest the of sunflower accessions

Sources of Variation	Df	RL	SL	FRW	FSW	DRW	DSW	RSR
Accessions	19	1.28	28.37**	6420.36	6308.71	5712.15	5964.71	0.044
Error	156	1.39	3.75	5823.69	6860.75	4194.12	8514.82	0.05

* = Significant 5% probability Level;   ** = significant 1% probability Level

Coefficient of variation

For various traits studied (Table 6) ranged from 7.84% to 121.83% across the harvests. The maximum variation was observed for root shoot ratio followed by dry shoot weight and dry root weight respectively. Fresh shoot weight exhibited minimum variation across the harvests. In first harvest coefficient of variation for various traits studied ranged from 8.70% to 154.16%. The maximum variation was observed for root shoot ratio followed by dry root weight and dry shoot weight. Fresh shoot weight showed minimum variation in first harvest. In the second harvest various traits studied ranged from 7.09% to 64.25% for coefficient of variation. The maximum variation was observed for root shoot ratio followed by dry root weight and dry shoot weight. Fresh shoot weight exhibited minimum variation in second harvest. In third harvest coefficient of variation for various traits studied ranged from 4.25% to 24.48%. The maximum variation was observed for root shoot ratio followed by dry root weight and dry shoot

weight. Root length weight showed minimum variation in third harvest.

The results indicated that maximum variability in the accessions was present for root/shoot ratio. Dry root weight and dry shoot weight ranked 2nd and 3rd respectively for presence of variability across the harvests and third harvest. Whereas, dry root weight stood 2nd and dry shoot weight 3rd in second third harvest. This suggests probability of improvement of these traits through breeding which may result in the better establishment of crop stand (Ali *et al*., 2013; Ali *et al*., 2014abcd, Awan *et al*., 2015, Waseem *et al*., 2014; Bibi *et al*., 2015).

Broad sense heritability

Heritability for various traits studied ranged from 25% to 97% across the harvests (Table 7). Emergence percentage showed high heritability, whereas all the other traits had medium heritability. Dry shoot weight exhibited minimum heritability across the harvests. Heritability for various traits ranged from 1% to 94% in the first harvest.

Emergence percentage showed high heritability, whereas all the other traits had medium heritability. Dry shoot weight exhibited minimum heritability in the first harvests. In the second harvest various traits studied ranged from 16% to 89% for heritability. The maximum heritability was observed for shoot length followed by dry root weight and root/shoot ratio. Root length exhibited minimum heritability in second harvest. In third harvest heritability for various traits studied ranged from 9% to 87%. Root length and fresh shoot weight had low heritability, fresh root weight showed medium estimates of heritability, whereas, shoot length, dry root weight, dry shoot weight and root/shoot ratio exhibited high heritability. The results indicate that genotype has an important role in the expression of these traits and selection may be effective for the improvement of these traits for improvement of sunflower (Javed *et al*., 2014; Khan *et al*., 2014; Masood *et al*., 2015ab; Naseem *et al*., 2015; Saeed *et al*., 2014; Zameer *et al*., 2015ab).

Table 6. Co-efficient of variation for various seedling traits of sunflower in different

CV	Across the Harvest	Harvest 1	Harvest 2	Harvest 3
E%	11.380			
ERI	13.606			
RL	9.968	31.895	12.954	4.275
SL	12.864	19.197	14.831	8.609
FRW	15.080	50.353	12.466	9.228
FSW	7.844	8.702	7.907	7.122
DRW	24.990	88.963	49.453	13.243
DSW	26.637	53.034	34.907	18.091
R/S ratio	121.830	154.16	64.259	24.487

Table 7. Heritability for various seedling traits of sunflower in different

Heritability	Pooled	Harvest 1	Harvest 2	Harvest 3
G%	0.97			
ERI	0.33			
RL	0.55	0.55	0.16	0.09
SL	0.45	0.76	0.89	0.87
FRW	0.28	0.21	0.33	0.09
FSW	0.36	0.94	0.23	0.09
DRW	0.40	0.65	0.59	0.27
DSW	0.25	0.01	0.61	0.43
R/S ratio	0.48	0.94	0.58	0.14

Conclusion:

The studied breeding material had enough genetic variability for all the traits. This variability can be exploited in the breeding programmes aimed at the improvement of seedling establishment and growth rate to obtain a good crop stand. The accessions C.3.1, A.7.4, A.2.26, B.3.1, and A.13.11 could be used as parents in hybridization program to converge desirable traits.

References
1. Ali Q, Ahsan M, Ali F, Aslam M, Khan NH, Munzoor M, Mustafa HSB, Muhammad S. 2013. Heritability, heterosis and heterobeltiosis studies for morphological traits of maize (Zea mays L.) seedlings. Adv. life sci., 1(1): 52-63.
2. Ali Q, Ali A, Ahsan M, Ali S, Khan NH, Muhammad S, Abbas HG, Nasir IA, Husnain T. 2014c. Line × Tester analysis for morpho-physiological traits of Zea mays L. seedlings. Adv. life sci., 1(4): 242-253.
3. Ali Q, Ali A, Awan MF, Tariq M, Ali S, Samiullah TR, Azam S, Din S, Ahmad M, Sharif NM, Muhammad S, Khan NH, Ahsan M, Nasir IA and Hussain T. 2014b. Combining ability analysis for various physiological, grain yield and quality traits of *Zea mays* L. Life Sci J 11(8s):540-551.
4. Ali Q, Ali A, Waseem M, Muzaffar A, Ahmad S, Ali S, Awan MF, Samiullah TR, Nasir IA, and Tayyab H. Correlation analysis for morpho-physiological traits of maize (*Zea mays* L.). Life Sci J 2014d;11(12s):9-13.
5. Ali, Q., A. Ali, M. Tariq, M.A. abbas, B. Sarwar, M. Ahmad, M.F. Awaan, S. Ahmad, Z.A. Nazar, F. Akram, A. Shahzad, T.R.

Samiullah, I.A. Nasir, and T. Husnain 2014a. Gene Action for Various Grain and Fodder Quality Traits in *Zea Mays*. *Journal of Food and Nutrition Research*, 2(10): 704-717.

6. Ashok, S., S.N. Mohamed and S.L. Narayanan. 2000. Character association and path coefficient analysis in sunflower. Crop Res. Hisar 20(3): 453-456.

7. Awan ZK, Naseem Z, Masood SA, Nasir B, Sarwar F, Amin E and Qurban Ali. How to improve *Sorghum bicolor* (L.) Moench production: An Overview. *Life Sci J* 2015; 12(3s):99-103.

8. Bibi T, Mustafa HSB, Hasan EU, Rauf S, Mahmood T and Ali Q. Analysis of genetic diversity in linseed using molecular markers. *Life Sci J* 2015;12(4s): 28-37

9. Burton, G.W. and E.H. DeVane. 1953. Estimating heritability in tall fescue (*Fescuea arundinancea*) from replicated clonal material. Agron. J. 45(10): 478-481.

10. Dabholkar, A.R. 1999. Elements of Biometrical Genetics. Concept Publishing Company, New Delhi, India.

11. FAO. 2013. Food and Agriculture Oraganization of the United Nations, Rome, Italy.

12. George, M. 2002. The world's healthiest foods. The George Mateljan Foundation [http://www.ijab.org].

13. Hu, Y.M., W.C. Ye, Z.Q. Yin and S.X. Zhao. 2007. Acta Pharm. Sin. 42(3): 286-291.

14. Javed I, Ahmad HM, Ahsan M, Ali Q, Ghani UM, Iqbal MS, Rashid M and Akram HN. Induced genetic variability by gamma radiation and traits association study in mungbean (*Vigna radiata* L.). Life Sci J 2014;11(8s):530-539.

15. Khan NH, Ahsan M, Saleem, M and Ali A. Genetic association among various morpho-physiological traits of *Zea mays* under drought. Life Sci J 2014;11(10s):112-122.

16. Leon, A.J., G.K. Rufener, S.T. Berry and R.P. Mowers. 1995. Use of RFLP markers for genetic linkage analysis of oil percentage in sunflower seed. Crop Sci. 35: 558-564.

17. Masood SA, Sofia J, Madiha A, Zain N, Anum J and Q Ali. Genetic Association of transcriptional factors (OsAP2 gene family) to incorporate drought tolerance in rice (*Oryza sativa* L. ssp. indica): An overview. Life Sci J 2015;12(3s):71-76.

18. Masood SA, Zain N, Madiha A, Arshad S, Anum J, Samad A and Q Ali. An overview of genetic improvement for drought tolerance in rice (*Oryza sativa*). Life Sci J 2015;12(3s):63-70.

19. Naseem Z, Masood SA, Ali Q, Ali A and Kanwal N. Study of genetic variability in *Helianthus annuus* for seedling traits: An Overview. *Life Sci J* 2015;12(3s):109-114

20. Naseem Z, SA Masood, S Irshad, N Annum, MK Bashir, R Anum, Qurban A, Arfan A, Naila K. Critical study of gene action and combining ability for varietal development in wheat: An Overview. *Life Sci J* 2015;12(3s):104-108.

21. Pakistan economic survey. 2013-13. Ministry of Finance, Economic Advisor's Wing, Islamabad.

22. Peniego, N., M. Echaide, M. Munoz, L. Fernandez, S. Torales, P. Faccio, I. Fuxan, M. Carrera, R. Zandomeni, E.Y. Suarez, and H.E. Hopp. 2002. Microsatellite isolation and characterization in sunflower (*Helianthus annuus L.)*. Genome 4: 34-43.

23. Reddy, S.R. 2006. Agronomy of Field Crops (2nd ed.). Kalyani Publishers, New Dehli, India.

24. Saeed A, Nadeem H, Amir S, Muhammad FS, Nazar HK, Khurram Z, Rana AMK, and Nadeem S. Genetic analysis to find suitable parents for development of tomato hybrids. Life Sci J 2014;11(12s):30-35.

25. Skoric, D. and R. Marinkovic. 1986. Most recent results in sunflower breeding. Int. Symposium on Sunflower, Budapest, Hungry.

26. Steel, R.G.D., J.H. Torrie and D.A. Dickey. 1997. Principles and Procedures of Statistics: A biometrical approach (3rd ed.). McGraw-Hill, New York.

27. Waseem M, Ali Q, Ali A, Samiullah TR, Ahmad S, Baloch DM, Khan MA, Ali S, Muzaffar A, Abbas MA, Bajwa KS.Genetic analysis for various traits of *Cicer arietinum* under different spacing. Life Sci J 2014;11(12s):14-21.

28. Zameer, M, B Tabassum, Q Ali, M Tariq, H Zahid, IA Nasir, W Akram and M Baqir. Role of PGPR to improve potential growth of tomato under saline condition: An overview. *Life Sci J* 2015; 12(3s):54-62.

29. Zameer, M, S Munawar, B Tabassum, Q Ali, N Shahid, HB Saadat and S Sana. Appraisal of various floral species biodiversity from Iskandarabad, Pakistan. Life Sci J 2015; 12(3s):77-87.

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