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STUDY ON GENETIC DIVERSITY IN SUNFLOWER (*HELIANTHUS ANNUUS* L.) 33 ELITE GENOTYPES

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ABSTRACT

In the present investigation, thirty three sunflower (*Helianthus annuus* L.) genotypes including three checks were evaluated to study genetic divergence. The experiment was laid out at Research Farm, School of Agriculture, ITM University, Gwalior during *rabi* 2020-2022. Data were recorded on ten quantitative characters. The thirty three genotypes of sunflower were grouped into seven cluster using Tocher method of the seven clusters formed, cluster I and III were the largest groups comprising of eleven and eight genotypes, respectively, followed by cluster V with six genotypes, cluster II with five genotypes. The 3 monogenic clusters *i.e.* IV, VI and VII showed zero intra-cluster. Based on cluster mean values for a given character, we can select highly divergent genotypes from the respective clusters to be used in crossing work.

Key words : Sunflower, Genotypes, Diversity.

Introduction

Sunflower (*Helianthus annuus* L.) emerged as an admirable crop for its quality oil in the oilseed scenario of India. The introduction of sunflower "a crop of all seasons" in India was taken up in view of its various advantages *viz*., photo and thermo insensitivity, short duration, high yield and better quality of oil with low cholesterol content. Sunflower belongs to family Compositeae (Asteraceae). It is diploid with chromosome number 2n = 34 and protandrous in nature where in pollen and stigma mature at different time, therefore it has been essentially categories as a cross pollinated crop. Sunflower has great potential in bridging gap between demand and supply of edible oil to a significant extent. Selection of suitable parents with high genetic diversity is a basic requirement in any successful hybridization to produce desirable character combination for selection of high yielding genotypes. Presently, it is cultivated in an area of 20.00 million hectares globally with production of 30.00 million tonnes and productivity of 1,500 kg ha-1. Asia accounts for nearly 20-22 per cent of the total sunflower area in the world, contributing 18 per cent of the total production. Mahalanobis's 'D^2' technique is one of the efficient tools for estimating genetic divergence and for identifying the desirable parents for any crossing programme. Therefore, there is a need to study the genetic divergence among various genotypes

In order to evaluate their usefulness as progenitors in hybridization programme. The D^2 analysis has been successfully utilized in sunflower to classify genotypes and determine their inter relationships by many workers (Marinkovic *et al.*, 1992 and Teklewold *et al.*, 2000). The studies on genetic divergence based on the evaluation of 33 genotypes of sunflower for 10 characters pertaining to yield, yield components and early seedling vigour related traits were analysed by adopting Mahalanobis D^2 statistic. The results of the study are presented below under the following heads in this context; an attempt was

made to study the genetic diversity among thirty three genotype. Selection of divergent parental material in hybridization program is an important breeding strategy for the development of superior hybrid /cultivar (Madhavi Latha, 2017). By the help of Mahalanobis D^2 statistical techniques the parental lines can be identified with presence of high variability and heritability.

Materials and Methods

Thirty three germplasm accessions were collected from the ICAR-Indian Institute Oilseeds Research (IIOR) Rajendranagar, Hyderabad, India which included 30 sunflower germplasms accessions and three checks (DRSF-113, DRSF-108 (National checks) and Phule Bhaskar (Local check grown in Maharashtra) (Table 1). The field experiment was carried out at the crop research centre of department of Genetics and Plant Breeding, ITM University, Gwalior, Madhya Pradesh, India, geographically located at 26.22^0N, 78.18^0E and at an average elevation of about 197 m above the mean sea level. All the accessions were evaluated during *rabi* seasons of 2021-22 in a Randomized Block Design (RBD) with three replications, with spacing of 60 × 30 cm with a plot size of 3m × 3m. For each genotype seed was seeded by dribbling and 2 seed seachhill were sown to ensure the germination. The experimental was subjected to standard agronomic practices. The following ten characters were observed for statistical analysis namely, days to 50% flowering, days to maturity, plant height, head diameter, volume of seed weight (100ml/g), seed filling %, 100g test weight, seed yield per plant, hull content %, oil content %. To record observations, five plants were picked at random from each progeny and five plants from the check in each replication. Separate observations were conducted on each plant. For each genotype of these plants, the average value for each character was determined individually. On ten yield component characters, the following observations were made. The data were analysed using package

Table 1 : List of sunflower genotypes used in the study and their attributes.

S. no.	Accessions number	Remark
1	GMU-78	Early, dwarf
2	GMU-55	High yield
3	GMU-1073	High yield
4	GMU-463	High yield, medium maturity
5	GMU-190	High yield, medium maturity
6	GMU-1020	High yield
7	GMU-934	High yield
8	GMU-1021	High yield
9	GMU-787	High yield
10	GMU-59	Early, medium maturity
11	GMU-1079	High yield
12	GMU-1096	High yield
13	GMU-1026	High yield
14	GMU-356	High yield
15	GMU-177	High yield
16	GMU-468	High yield
17	GMU-231	High yield
18	GMU-127	High yield
19	GMU-1147	High yield, medium to high oil
20	GMU-249	High yield
21	GMU-1041	High yield
22	GMU-486	High yield
23	GMU-837	High Yield
24	GMU-495	Early, medium maturity
25	GMU-383	Early
26	GMU-1031	High Yield
27	GMU-1037	High Yield
28	GMU-687	Medium to high yield
29	GMU-1058	High yield
30	TNAU COSFV5	Released variety
31	PHULEBHASKAR	Local check©
32	DRSF-108	National check©
33	DRSF-113	National check©

Results and Discussion

Plant breeders must select suitable parents for use in crop improvement programmes, which is an important but difficult task. Genetic diversity is thought to be important for achieving heterotic response in F_1 as well as a wide range of variability in segregating generations. Diversity analysis aids in determining the nature of diversity and identifying genetically diverse genotypes for use in breeding programmes. The diversity of parents is always emphasized in heterosis breeding programmes. The more diverse the parent within a reasonable range, the better the chances of improving economic characteristics under consideration in the resulting offspring. Mahalnobis' D^2 statistic is a one-of-a-kind tool for classifying genetically diverse parents based on quantitative traits that could be useful in hybridization programmes.

Genetic diversity is the total number of genetic characteristics in the genetic makeup of a species. Genetic diversity serves as a way for populations to adapt to changing environments. With more variation, it is more likely that some individuals in a population will possess variations of alleles that are suited for the environment.

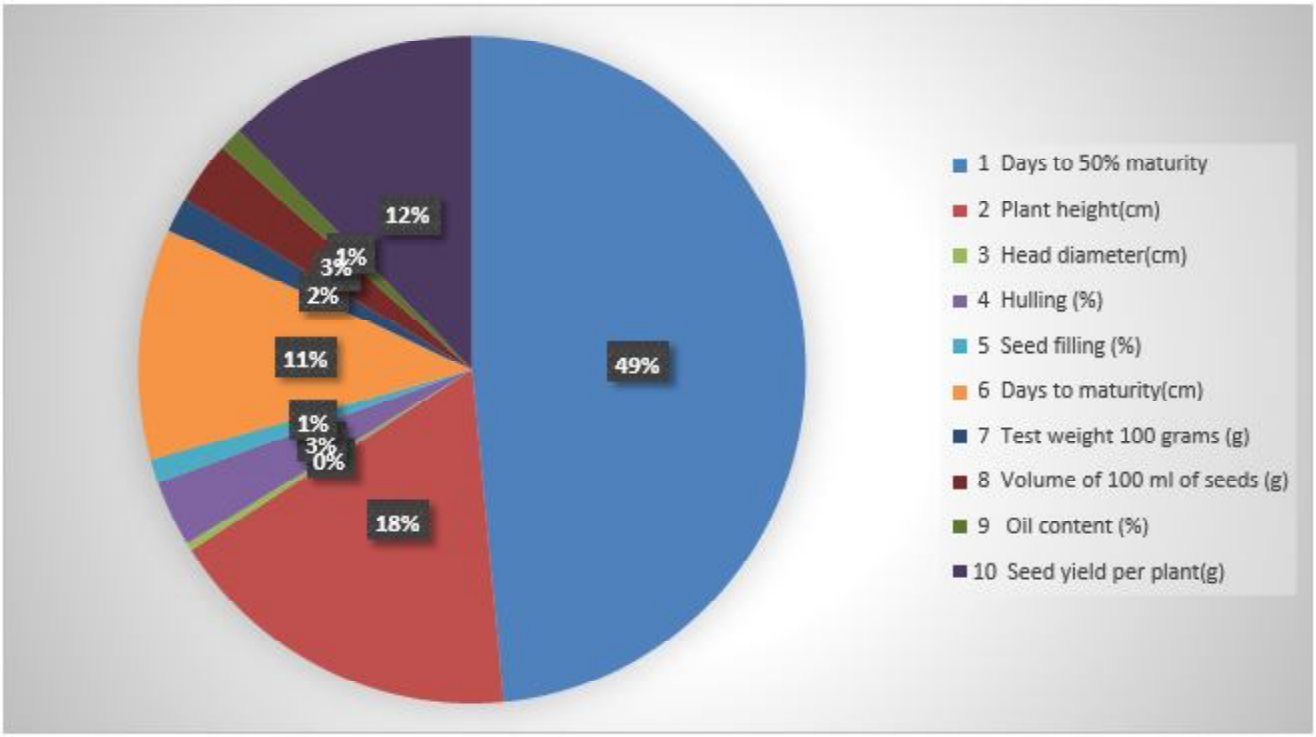

Fig. 1 : Percent contribution of 10 characters for divergence in sunflower.

Table 2 : Distribution of thirty three genotypes of sunflower in different cluster.

Clusters	No. of genotypes included	Genotypes
I	11	GMU-468, GMU-1058, GMU-59, DRSF-108, GMU-356, GMU- 127, GMU-55, GMU-1073, GMU-1021, GMU-177, GMU-934.
II	5	GMU-1037, GMU-687, GMU-383, TNAUCOSFV5, GMU-1031
III	8	GMU-1026, GMU-1041, PULEBHASKAR, GMU-231, GMU-1096, GMU- 1079, GMU-190, GMU-495
IV	1	GMU-1147
V	6	GMU-463, GMU-1020, GMU-239, DRSF-113, GMU-837, GMU-78
VI	1	GMU-787
VII	1	GMU-486

Those individuals are more likely to survive to produce offspring bearing that allele. The population will continue for more generations because of the success of these individuals.

All the genotypes were grouped into different clusters on the basis of genetic distance among the genotypes. The distribution pattern of genotypes, cluster mean for different clusters, intra and inter cluster divergence (D^2) value and contribution percentage of various traits towards genetic divergence were presented in the table

Clustering pattern

In the present investigation, all the thirty three genotypes taken for genetic divergence analysis differed significantly with regard to the characters studied and displayed marked divergence. They were grouped in to seven clusters on the basis of Tocher's method of clustering utilizing D^2 values (Table 2). Cluster I comprised eleven genotypes namely GMU-468, GMU-1058, GMU-59, DRSF- 108, GMU-356, GMU-127, GMU-55, GMU-1073, GMU-1021, GMU-177, GMU-934. Cluster II comprised five genotyes namely GMU-1037, GMU-687, GMU-383, GMU-1031, TNAUCOSFV5. Cluster III comprised eight genotypes namely GMU-1026, PULEBHASKAR, GMU-1041, GMU- 231, GMU-1096, GMU-1079, GMU-190, GMU-495. Cluster IV comprised one genotypes namely GMU-1147. Cluster V comprised six genotypes namely GMU-463, GMU-1020, DRSF-113,

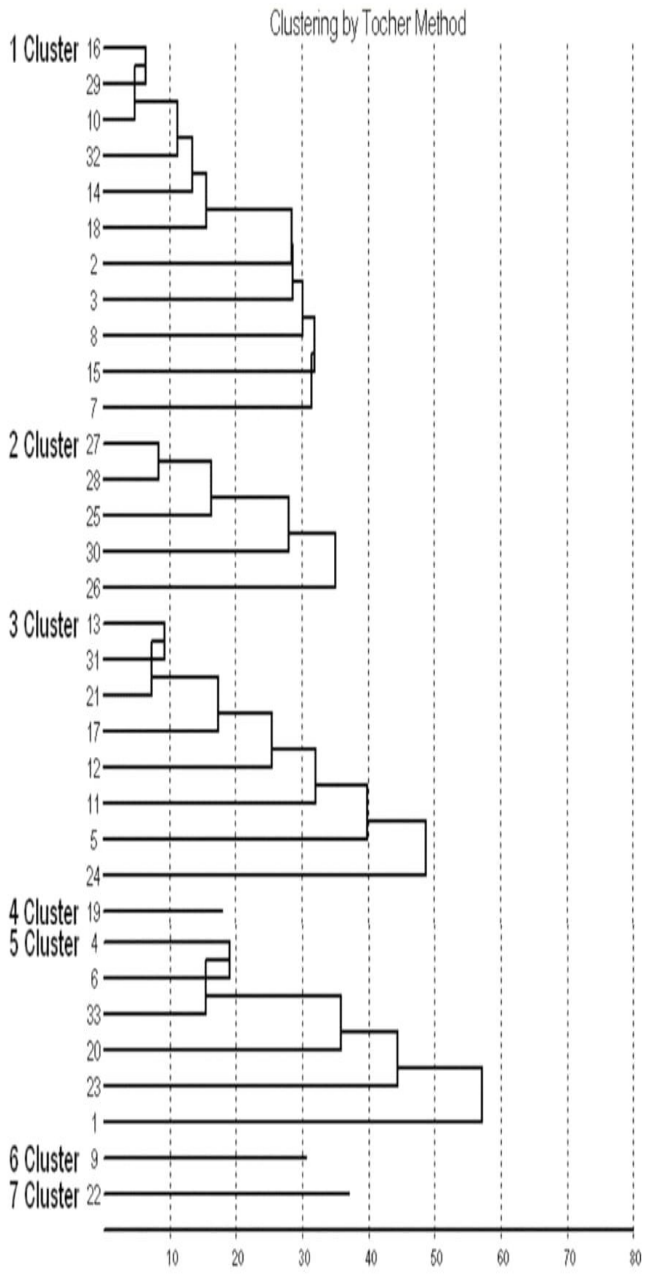

Fig. 2 : Clustering by Tocher method.

DRSF- 249, GMU-837, GMU-78. Cluster VI comprised one genotypes namely GMU-787. Cluster VII comprised one genotypes namely GMU-486. The distribution of different clusters is shown in Table 3. Out of seven clusters formed, cluster I and III were the largest groups comprising of eleven and eight genotypes, respectively, followed by cluster V with six genotypes, cluster II with five genotypes, IV, VI and cluster VII with one genotype each. The 3 monogenic clusters *i.e.* IV, VI and VII showed zero intra-cluster confirming to the result of Mohan and Seetharam (2015) also observed similar clustering pattern of genotypes among cluster as some cluster were unique having only single genotypes (Mohmad Shamshad *et al*., 2014 and Pandya *et al*., 2014). These results are in conformity with the observations made by Anand Kumar *et al*. (2018), Kumar *et al*. (2018), Sujatha *et al*. (2012) and Dudhe (2013).

Cluster mean for characters in sunflower

The mean performances of cluster values of ten characters are presented in Table 3. A considerable inter cluster variation in respect of cluster was observed among the various clusters for ten characters studied. Cluster VI recorded highest plant height (161.27cm), seed filling % (79.36%), volume of seeds (100ml/g) (53.92g), oil content (36.81%). Clusters II and IV ranked next. Clusters II excellent in days to 50% flowering (50%) and head diameter (21.87cm). Cluster IV excellent in hulling % (21.17%) and days to maturity (79.66 days). However, cluster III recorded outstanding values with recorded to seed yield (37.64 g). Cluster II, which recorded earlier in flowering lagged behind in days to maturity. However, clusters VII AND III which also ranked second and third respectively in flowering lagged much in days to maturity. Similar results were reported by Riaz *et al*. (2019) and Dudhe *et al*. (2019).

Table 3 : Cluster mean for characters in sunflower.

Cluster	DF	PH	HD	H	SF	DM	TW	VS	OL	SY
I	61.30	151.37	21.65	27.52	73.45	91.22	4.38	49.26	31.51	34.05
II	50	145.11	21.87	28.82	73.72	88.91	4.42	48.17	30.68	32.41
III	57.72	151.52	21.53	26.61	74.52	90.63	4.37	49.15	30.14	37.64
IV	62.88	136.95	20.34	21.17	71.41	79.66	4.25	43.59	34.24	25.20
V	61.87	132.04	21.56	31.51	74.49	94.11	4.52	51.44	32.46	32.72
VI	59.66	161.27	17.26	25.55	79.36	81.55	3.53	53.92	36.81	31.83
VII	53.11	153.7	19.9	32.90	72.80	99.33	3.84	50.83	30.08	17.63

DF-Days to 50% flowering
DM-Days to maturity
PH-Plant height (cm)
TW-Test weight 100 (g)
HD- Head diameter (cm)
VS-Volume of seeds (100ml/g)
H-Hulling (%)
OL- Oil content (%)
SF-Seed filling (%)
SY-Seed yield per plant (g)

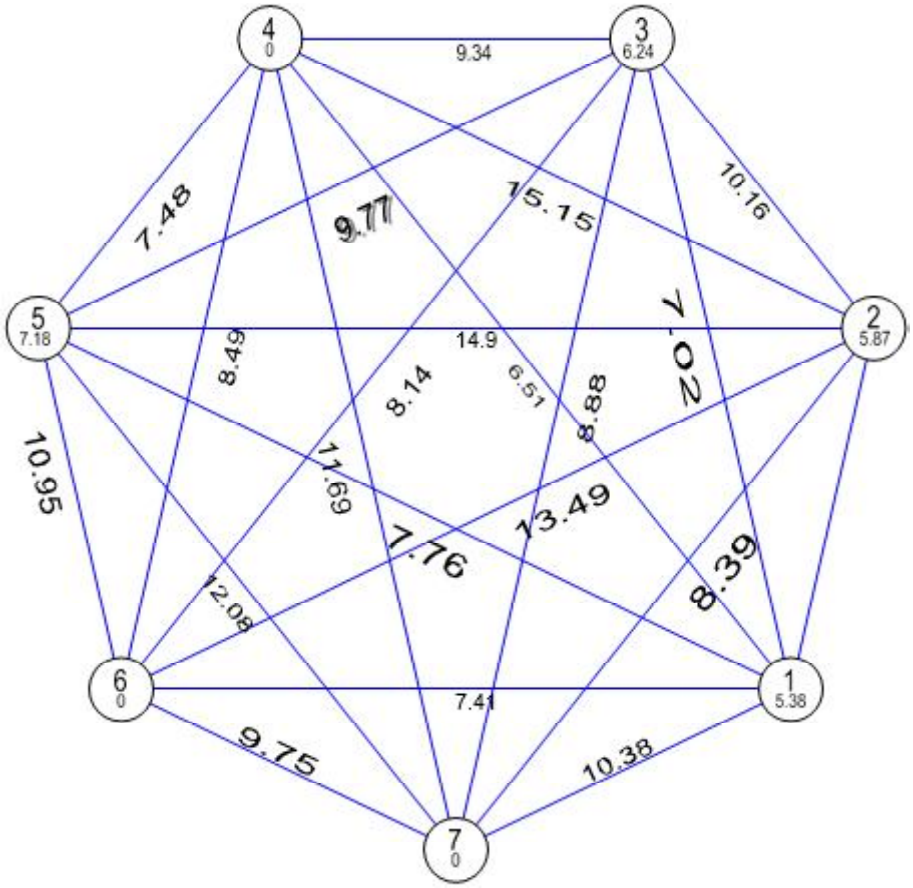

Fig. 3 : Mahalnobis Euclidean Distance Nottothe Scale).

Table 4 : Cluster distances.

	I	II	III	IV	V	VI	VII
I	**5.383**						
II	13.47	**5.874**					
III	7.02	10.167	**6.24**				
IV	6.513	15.152	9.234	**0**			
V	7.765	14.966	9.771	7.489	**7.18**		
VI	7.411	13.494	8.14	8.49	10.95	**0**	
VII	10.338	8.397	8.888	11.697	12.086	9.75	**0**

Intra and inter cluster distance

The intra-cluster distance is highest for cluster v (7.18) followed by cluster III (6.24), while it is minimum for the mono-genotypic cluster IV, cluster VI and cluster VII. The inter cluster distance is maximum between the cluster IV and II followed by the clusters V and II, while it is minimum between the cluster IV and I.

Percent contribution of 10 characters for divergence in sunflower

Out of 10 characters studied, the maximum contribution to divergence was reported in characters Days to 50% flowering (48.48%), plant height (17.42%), and seed yield per plant (12.31%). It was followed by Days to maturity (11.17%) remaining characters followed the divergence. Similar results were reported by Varalakshmi *et al*. (2020), Radic *et al*. (2021)

Conclusion

Genetic diversity is of major interest to plant breeders, more diverse the parents, greater are the chances of obtaining heterotic expression in F_1 with possibility of broad spectrum of variability in segregating generations. While selecting appropriate sunflower germplasm, the breeder looks for genetically diverse and superior genotypes, which could be utilized in population and heterosis breeding. The present study exhibited very high differences among the genotypes for seed yield and almost all the yield component characters which may favour the selection and its further utilization in recombination breeding programmes. The genetically diverse sunflower germplasm identified from the present study could be utilized in development of diverse inbreds which may be utilized in future heterosis breeding. Promising trait specific superior sunflower germplasm accessions identified will serve as donors for the development of trait specific heterotic gene pools, which can be further exploited in sunflower improvement

References

Anandkumar, B.V., Parameshwarappa K.G. and Lingaraju B.S. (2018). Genetic divergence in parental and inbred lines of sunflower (*Helianthus annuus* L.). *Karnataka J. Agric. Sci*., **21(3)**, 339.

Dudhe, M.Y., Ranganatha A.R.G. and Vishnuvardhan Reddy A. (2010). Identification of restorers and maintainers from newly developed inbreds. *Biosci. Discov*., **10(1)**, 21–24.

Mahalanobis, P.C. (1936). On the generalized distance in statistics. *Proc. Nat. Inst. Sci*., **2(1)**, 49-55.

Marnikovic, R. (1992). Path coefficient analysis of some yield components of sunflower. *Euphytica*, **60**, 201-205.

Mohan, G.S. and Seetharam A. (2015). Genetic divergence in lines of sunflower derived from inter specific hybridization. *Sabrao J*., **37**, 77-84.

Muppidathi, N., Sankarapandian R. and Rajarathinam S. (1995). Genetic divergence, correlation and path analysis in sunflower. *Crop Improv*., **22(2)**, 221-224.

Pandya, M.M., Patel P.B., Narwade A.V. and Vaidya G.B. (2014). Genetic divergence studies in Sunflower (*Helianthus annus* L.). *Trends Biosci*., **7(3)**, 167-169.

Radiæ, V., Balaliæ I., Jaæimoviæ G., Krstiæ M., Jockoviæ M. and Jociæ S. (2021). A study of correlations and path analyses of some traits in sunflower parental lines. *Ratarstvoipovrtarstvo*., **58(1)**, 7-13.

Ramesh, M., Arunakumari J., Prashanth Y., Ranganatha A.R.G. and Dudhe M.Y. (2013). Population improvement for seed yield and oil content by using working germplasm in sunflower (*Helianthus annuus* L.). *SABRAO J Breed Genet*., **45(2)**, 291–295.

Rao, C.R. (1952). *Advanced statistical methods in Biometrical Research*. John Willey and Sons. Inc., New York.

Reddy, S.M., Reddy T.D. and Dudhe M.Y. (2012). Analysis of genetic diversity in germplasm accessions of sunflower (*Helianthus annuus* L.). *Madras Agri. J.*, **99**, 457–460.

Riaz, A., Tahir M.H.N., Rizwan M., Fiaz S., Chachar S., Razzaq K., Riaz B. and Sadia H. (2019). Developing a selection criterion using correlation and path coefficient analysis in sunflower (*Helianthus annuus* L.). *Helia*, **42(70)**, 85-99.

Singh, R.K. and Choudhary B.D. (1977). Variance and covariance analysis. "*Biometrical methods in quantitative genetic analysis*". Kalyani publication, New Delhi, pp. 39-68

Sujatha, H.L., Chikkadevaiah and Nandini (2012). Assessment of Genetic Diversity among 51 Inbred Sunflower Lines. *Helia*, **25(37)**, 101-108.

Teklewold, A., Jayaramaiah H. and Jayaramegowda (2000). Genetic divergence studies in sunflower (*Helianthus annuus* L.). *Helia*, **23**, 93-104.

Varalakshmi, K., Neelima S., Reddy R.N. and Sreenivasulu K.N. (2020). Genetic variability studies for yield and its component traits in newly developed sunflower (*Helianthus annuus* L.) hybrids. *Electron. J. Plant Breed.*, **11(01)**, 301-305.