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Research Note

Genetic variability and genetic diversity in sunflower

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Abstract
One hundred and seventy four accessions of sunflower were evaluated in a randomized block design with two replications during Kharif 2010-11 at Regional Agricultural Research Station, Nandyal, Andhra Pradesh to investigate the extent of genetic variability and genetic diversity. The Analysis of variance revealed significant differences among the genotypes for all the traits indicating considerable magnitude of genetic variability of the material used for the study. Low heritability coupled with high GAM was observed for seed yield per plant due to high environmental effects and selection is effective. The genetic divergence study infers the grouping of 174 accessions in 13 clusters which indicates prevalence of good extent of diversity in the material. Cluster I had more no. of genotypes followed by clusters IV, VII and VIII. Cluster X had higher mean value for plant height and head diameter, cluster XII had higher test weight and cluster XI had high seed yield per plant. The maximum inter cluster distance was recorded between cluster XI and XII followed by cluster X and XII and clusters V and XII. Hence, it is suggested that if the diverse accessions from these diverse groups are used in the breeding programme, it is expected to produce a wide range of genetic variability in the population. The traits, 100 seed weight, plant height and days to maturity were the major causing genetic divergence among the accessions.

Keywords
Sunflower, variability, genetic divergence

India is among the largest vegetable oil economies in the world after USA and China and enjoys a distinct position in terms of diversity in annual oilseed crops. Oilseeds form the second largest agricultural commodity after cereals in India accounting for 14 per cent of the country's gross cropped area and contributes for nearly five per cent of the gross national product and 10 per cent of the value of all agricultural products. Sunflower is the second major oilseed crop having a potential source for vegetable oil and protein. Exploitation of genetic variability is the foremost important for further genetic up gradation of the crop as genetic variation is the base for effective plant improvement programme. Information on nature and magnitude of variability presents in a population due to genetic and non-genetic causes is an important prerequisite for a systematic breeding programme. As so, involvement of genetically divergent parents in hybridization will result in enhanced vigour or heterosis in the resultant hybrid. 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, Sankarpandian *et al*., 1996 and Teklewold *et al*., 2000). In this context the present study was attempted to investigate the extent of genetic variability and genetic diversity in 174 accessions of sunflower.

The material under investigation consisted of one hundred and seventy four genotypes of sunflower which were grown during *Kharif* 2010-11 and evaluated in a randomized block design with two replications at Regional Agricultural Research Centre, Nandyal, Andhra Pradesh. All the recommended package of practices were followed for raising healthy crop. Observations were recorded on, plot as well as on single plant basis. Observations on plot basis were recorded for days to 50% flowering and days to maturity. For recording single plant observations, five competitive plants from each plot were randomly selected. Average of these five plants was taken for plant height, head diameter, 100 seed weight and seed yield per plant. After computing means, the data were subjected to Mahalanobis (1936) D^2 analysis as described by Rao (1952). The genotypes were grouped into different clusters according to Toucher's method (Rao, 1952) and inter and intra cluster distances were calculated as per Singh and Chaudhary (1977).

The analysis of variance for randomized block design revealed highly significant differences among the accessions for all the characters under investigation thereby indicating the presence of a considerable magnitude of genetic variability among 174 accessions of sunflower for these characters (Table1).

The range of variation (Table 2) was found to be maximum for plant height (75.3-111.0) followed by seed yield per plant (18.02-39.80) which infers better scope for selection of these traits. A wide range of variation was also reported for seed yield and its

components by Sutar *et al*., 2010 and Patil *et al*., 1996. A close correspondence of PCV and GCV values indicates stable expression of all the traits and least influence of environment. The same result was noticed in the findings of Sutar *et al*., 2010 and Janamma *et al*., 2008. Higher amount of variability was noticed for seed yield per plant (18.36 % PCV and 14.8 % GCV), head diameter (16.04 % PCV and 12.10 % GCV) and 100 seed weight (14.43 % PCV and 13.62 % GCV) supporting the presence of substantial magnitude of genetic variability in the experimental material of sunflower and better scope for improvement of these traits (Fatima sultana *et al*., 2005 and Sujatha *et al*., 2002). Days to 50 % flowering and days to maturity had lower PCV and GCV values and hence less scope existed for improvement of these traits.

However, the coefficients of variation indicated only the extent of variability existed for different characters and did not indicate heritable portion of a character. Hence, heritability was estimated which is a good index of transmission of characters to off spring (Falconer, 1981). Heritability estimates were found to be high for all the traits ranging from 56.90 to 95.30. The highest heritability was noticed for days to maturity (95.30) followed by 100 seed weight (89.10) and days to 50 % flowering (77.50).

Johnson *et al*., (1955) suggested that heritability considered together with genetic advance is more reliable in predicting the effect of selection than heritability alone. High heritability coupled with low GAM was observed for days to maturity suggesting that role of favourable environment rather than genotype and selection is not rewarding. High heritability coupled with high GAM was noticed for 100 seed weight infering that this trait was governed by additive gene action and directional selection for this trait was more effective. Low heritability coupled with high GAM was observed for seed yield per plant indicating that yield is governed by additive gene effects and was highly influenced by environments as so in case of range and PCV and GCV and selection is effective. However, Sutar *et al*., 2010 and Ashok *et al*., 2000 reported high heritability and high genetic advance as per cent of mean for seed yield.

Existence of wider range, high PCV and GCV, low heritability and high GAM were noticed for seed yield per plant implying that existence of better scope for variability, high influence of environment, additive gene action and effectiveness of selection procedure.

All the 174 genotypes were grouped into 13 clusters (Table 1.) Among the clusters, cluster I was the largest comprised of 138 genotypes followed by cluster IV which had 15 genotypes. The cluster VII possessed 8 genotypes and cluster VIII had 5 genotypes and the rest of the clusters had one genotype each. Therefore, 174 genotypes falling as many as 13 clusters is an indication of prevalence of good extent of diversity in the materials. The genotypes grouped within a cluster exhibited a narrow range of genetic variability, whereas in different clusters indicated wider variability, however, depending on their inter cluster distances. The average inter and intra cluster distances for the present study are presented in the Table 5. Maximum intra cluster distance was noticed in cluster VII (5.59) followed by cluster I (5.51) and cluster VIII (5.41) indicating that they incorporated genotypes with greater intra cluster distances and infered more genetic divergence among them. The least intra cluster distance was noticed among the genotypes belonging to clusters II, III, V, VI, IX, X, XI, XII and XIII indicating the accessions of these clusters were genetically less diverse and were almost with same genetic makeup. Such type of narrow range of genetic variability among the genotypes within the clusters was also reported by many authors (Chandirakala and Manivannan, 2014; Srinivas *et al*., 2006 and Ramasubrhamanyam *et al*., 2003).

The maximum inter-cluster distance was recorded between cluster XI and XII (18.67) followed by cluster X and XII (16.99) and clusters V and XII (16.60). Hence, it is suggested that if the diverse accessions from these diverse groups are used in breeding programme, it is expected to produce a wide range of genetic variability in the population. The above findings involving parents from divergent clusters to obtain superior heterosis is in accordance with the reports of Chandirakala and Manivannan, 2014 and Anandakumar *et al*., 2008.

Cluster means for the 6 traits of all the 13 clusters were worked out (Table 4). Contrasting genotypes for days to flowering and maturity were being grouped in II & VI and XIII, for plant height in VIII and X, for head diameter in XI and X, for test weight in III and XII, for seed yield in VI and XI. The genotype GMU 447 belonging to XI cluster had higher seed yield per plant with medium maturity and medium head diameter indicated higher no. of filled seeds per head. This genotype could be used in crossing programmes for producing heterotic hybrids and for generating variability. To get early maturing hybrids, the genotypes *viz.*, GMU 433 (II), GMU 445 (II), and for developing late maturing hybrids, GMU 325 (XIII) can be involved. The genotypes belonging to cluster I could be used for developing medium duration, short

stature, medium head diameter and optimum seed yield hybrids.

The important character contributing to the total divergence observed was 100 seed weight (43.31 %). The traits like plant height and days to maturity had been next in the order. The above findings are in accordance with the earlier reports by Anandakumar *et al*., 2008 wherein, seed yield per plant, days to maturity, plant height and head diameter had shown contribution towards genetic divergence. The present finding implied that in order to select genetically diverse parents, one has to classify material on the basis of traits like test weight, plant height, days to maturity and seed yield per plant.

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Table 1. General ANOVA for yield and yield components in sunflower

Character	Mean sum of squares		
	Replications (1 df)	Genotypes (173 df)	Error (173 df)
Days to 50 % flowering	65.52	22.96**	2.907
Plant height (cm)	581.37	207.62**	43.80
Head diameter (cm)	20.85	2.83**	0.77
100 Seed weight (g)	0.161	1.352**	0.078
Days to maturity	42.07	18.36**	0.442
Seed yield per plant (g)	389.02	29.97**	6.48

** - Significant at 1% level

Table 2. Genetic variability for different parameters in sunflower

Character	Mean	Range		PCV (%)	GCV (%)	Heritability (%)	GAM
		Min.	Max.				
Days to 50 % flowering	54.00	48.0	60.0	6.63	5.84	77.50	10.60
Plant height (cm)	97.89	75.30	111.0	10.63	10.17	91.65	20.05
Head diameter (cm)	8.40	7.20	10.5	16.04	12.10	56.90	18.80
100 Seed weight (g)	5.87	4.90	7.4	14.43	13.62	89.10	26.49
Days to maturity	84.00	78.0	90.0	3.64	3.60	95.30	7.15
Seed yield per plant (g)	23.25	18.02	39.8	18.36	14.80	64.50	24.38

Table 3. Clusters with germplasm accessions in sunflower (*Helianthus annuus* L.)

Cluster	Number of genotypes clustered	Germplasm lines
I	138	All other accessions except the following
II	1	GMU 433
III	1	GMU531
IV	15	GMU,429, 441, 413, 420, 463, 1131-1, 1064, 334, 448, 1057, 1045, 509, 397, 404, 1058
V	1	GMU 475
VI	1	GMU 445
VII	8	GMU 455, 470, 378, 548, 469, 485, 559, 439
VIII	5	GMU 497, 1189, 442, 549, 1032
IX	1	GMU 389
X	1	GMU 423
XI	1	GMU 447
XII	1	GMU 401
XIII	1	GMU 325

Table 4. Average intra and inter cluster D^2 values for thirteen clusters formed with six characters in sunflower

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	**5.51**	7.28	6.96	7.75	7.42	7.38	7.52	9.50	7.23	9.95	9.85	11.82	10.26
II		**0.00**	10.59	12.02	1.60	1.74	4.01	10.78	7.58	5.63	5.79	15.87	14.23
III			**0.00**	5.19	10.03	10.75	10.73	13.41	5.70	11.83	13.01	12.65	7.76
IV				**5.68**	11.91	12.02	11.94	12.13	8.45	13.80	14.17	10.48	8.02
V					**0.00**	2.94	4.43	11.92	6.80	5.37	5.67	16.60	13.99
VI						**0.00**	4.35	10.34	8.00	5.14	7.38	15.14	14.43
VII							**5.59**	10.42	8.72	7.37	7.21	15.46	14.10
VIII								**5.41**	14.02	14.03	13.05	9.94	14.47
IX									**0.00**	8.48	9.47	15.02	10.49
X										**0.00**	9.79	16.99	15.75
XI											**0.00**	18.67	15.56
XII												**0.00**	12.49
XIII													**0.00**