GENETIC DIVERGENCE STUDIES IN SUNFLOWER (HELIANTHUS ANNUUS L.)

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Abstract

Thirty-six diverse strains of sunflower (Helianthus annuus L.), representing the broad spectrum of variation from various agro-climatic conditions of the world, were assessed for genetic divergence using Mahalanobis D^2 technique. The genetic material exhibited wide genetic diversity for almost all the characters investigated. With the help of multivariate analysis strains were grouped into eight clusters. Cluster III consisted of maximum genotypes. In general, there was no relationship between the geographical origin and genetic divergence. Statistical distances revealed that clusters II and I were most compact. Clustering pattern of the strains has suggested the use of D^2 technique for judging the genetic diversity of the parents to be used in hybridization programme. The inter-cluster distance between cluster IV and VII was the highest followed by that between cluster IV and V. The present findings suggested crossing between the strains of these distant groups.

Introduction

The selection of parents or lines based on individual attributes may not be as fruitful as that based on a number of important characters collectively and this is more important when the aim is to seek improvement in a complex quantitative trait such as grain yield. The D^2 statistic which is based on several characters is one of the powerful tool to assess the relative contribution of different component traits to the total diversity to quantify the degree of divergence between populations, to understand the trend of evolution and to choose genetically diverse parents for obtaining desirable recombinations. The present study was, therefore, undertaken to assess the genetic distances between 36 populations of sunflower (Helianthus annuus L.).

Materials and Methods

The experimental material consisted of 36 diverse populations of sunflower, representing the broad spectrum of variation from various agroclimatic regions of the world. The detail of the 36 populations including their place of origin is given in Table 1. These genotypes were sown in randomized block design with three replications in 6 m long single row plots. The spacing between plant and rows was kept at 10 and 60 cm respectively. The observations on 10 randomly selected competitive plants were recorded for head diameter, percentage of filled seeds, days to maturity, 100-seed weight (g), oil per cent and seed yield/plant (g). Transformation of original measurements to standardize variables was done by piotal condensation method (Rao, 1952). The D^2 values of divergence between any two genotypes were obtained as sum of squares of differences in the values of their corresponding transformed values. Based on these D^2 values, the 36 genotypes were grouped into clusters by Toucher's method (Rao, 1952).

Results

The analysis of variance revealed significant differences among the populations for each of the six characters. An examination of cluster means revealed that the genotype grouped in I, VI and VII all were low yielder for grain yield. The varieties included in clusters IV, III and II were characterised by highest seed yield/plant (g), percentage of filled seeds and relatively higher oil per cent (g), percentage of filled seeds and relatively higher oil per cent (Table 2). The 36 sunflower populations studied could

be grouped into 8 clusters (Table 3). The highest inter-cluster distance was between IV and VII (D = 1105.27) while the lowest was between II and VIII (D = 121.62). The intra-cluster distance of cluster II was minimum followed by Cluster I indicating their compactness (Table 4). In general, there was no relationship between the geographical origin and genetic divergence except Cluster I, where four strains from Canada fall in one and the same group.

Discussion

The material for the present study was a set of highly selected strains of sunflower from different eco-geographical regions. The nature of selection forces operating under the eco-geographical region seem to be similar to that of other region, since varieties from distant places were grouped together. Strains from one eco-geographical region were grouped in different clusters indicating substantial variability within themselves. The analysis of variance indicated highly significant differences among genotypes revealing thereby that material under study involved enough variability. The pattern of grouping of clusters showed a pattern of diversity in all the clusters except in cluster I where all the four genotypes of Canada fall in the same group. So more logical presumption that genotypes derived from different places would genetically be the most diverse, may not always be true. The results of the present study have clearly indicated that D^2 statistic is an adequate technique to identify and quantify the genetic distance between the strains. Therefore, for any hybridization programme, the selection of parents must be based on D^2 analysis of the available germplasm and breeding objection of the crop for the region. Theoretically speaking, the maximum amount of heterosis will be manifested in cross combination involving the parents belonging to most divergent clusters. However, for a practical plant breeder, the objective is not only to get high heterosis but also to achieve high level of production and reducing life span of the varieties so that it can be fitted in the relay cropping pattern. In the present study, the maximum distance (D = 1105.27) existed between cluster IV and VII. The mean seed yield of cluster VII was very low and therefore, even if the crosses involving the parent from this cluster may exhibit high heterosis, the actual yield may not be very high. Keeping this in view, for getting high heterosis, the crossing between cluster IV and VII and between cluster IV and V is suggested and for getting high heterosis as well as high level of production the crossing between cluster III and IV is recommended.

References

RAO, C.R. 1952. **Advanced Statistical Methods in Biometrical Research. Edn.1. Johnwiley and Sons, New Yord,** p.390.

Table 1

Identification and source of different genotypes of sunflower (**Helianthus annuus L.**)

Sl. No.	Genotype	Source	Sl. No.	Genotype	Source
1.	EC 16751	USSR	19.	EC 85818	Argentina
2.	EC 21991	-do-	20.	EC 85820	-do-
3.	EC 21992	-do-	21.	EC 85820-M	-do-
4.	EC 21993	-do-	22.	EC 89093-1	Bulgaria
5.	EC 27290	Canada	23.	EC 89100	-do-
6.	EC 27424	Hungary	24.	EC 97916	Hungary
7.	EC 27621	Australia	25.	EC 100103	USSR
8.	EC 27628	-do-	26.	EC 101492	-do-
9.	EC 27993	-do-	27.	EC 101495	-do-
10.	EC 66002	USA	28.	EC 101497	-do-
11.	EC 68414	USSR	29.	EC 61039	-do-
12.	EC 75229	-do-	30.	Cm-312	Canada
13.	EC 75273	Polland	31.	Cm-338	-do-
14.	EC 77194	USA	32.	Cm-361	-do-
15.	EC 89150	UK	33.	Romsun Record	Rumania
16.	EC 82819-1	Hungary	34.	EC 68415	USSR
17.	EC 83096	-do-	35.	EC 93613	Argentina
18.	EC 85815	-do-	36.	EC 69874	USSR

Table 2

Intra-cluster group means for six characters in sunflower

Cluster	Head diameter (cm)	Percentage of filled seeds	Days to maturity	100-seed weight (g)	Oil per cent	Seed yield/ plant (g)
I	15.52	69.32	79.33	7.26	37.04	34.14
II	16.65	66.86	78.66	7.51	33.50	45.77
III	17.41	71.68	80.19	7.14	30.83	47.08
IV	16.96	71.85	79.33	7.35	38.19	51.85
V	18.00	45.54	77.33	9.40	28.76	42.29
VI	17.60	34.55	75.33	9.46	31.22	27.37
VII	10.80	60.34	80.33	4.70	29.47	18.45
VIII	18.53	43.85	85.00	9.00	35.45	45.61

Table 3

Grouping of 36 populations of sunflower into eight clusters

Cluster	Populations included	Number of populations
I	EC 89100, EC 68415, CM-361, EC 27628, EC 68414, EC 27424, EC 93613, EC 85818, EC 27290, CM-312 and CM-338	11
II	EC 77194, EC 97916, EC 69874, EC 75273, Romsun Record, EC 101497, EC 21993	7
III	EC 101492, EC 101495, EC 27993, EC 66002, EC 89150, EC 83096, EC 85820, EC 85820-M, EC 27621, EC 100103, EC 82819-1, EC 75229, EC 89093-1	12
IV	EC 75229, EC 61039	2
V	EC 16751	1
VI	EC 21991	1
VII	EC 85815	1
VIII	EC 89093-1	1

Table 4

Intra and Inter-cluster D^2 values among 36 genotypes of sunflower

Clusters	I	II	III	IV	V	VI	VII	VIII
I	62.88	234.09	673.13	131.91	688.21	508.20	764.35	169.60
II		46.51	193.02	286.63	313.15	215.39	387.06	121.62
III			84.27	790.52	128.94	253.22	253.74	441.27
IV				81.00	1060.24	722.68	1105.27	171.36
V					0.00	132.20	244.68	528.19
VI						0.00	244.23	286.44
VII							0.00	669.48
VIII								0.00