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Character Association and Genetic Divergence in Germplasm Lines of Sunflower (*Helianthus annuus* L.)

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ABSTRACT: Genetic variability is an important tool for the improvement of seed yield in sunflower. The analysis of variance of 33 sunflower genotypes revealed significant differences for all 12 characters studied. The phenotypic and genotypic coefficients of variation were high for seed yield per plant, hulling%, number of leaves per plant and 100 achene weights indicating the scope for improvement by selection for these characters. Correspondence between phenotypic and genotypic coefficients of variation (PCV & GCV) indicated that all characters studied were least affected by environment. High heritability coupled with the high genetic advance were recorded for plant height, number of leaves/plants, hulling percentage and 100 achene weight indicating the presence of additive gene action in controlling these traits. At the phenotypic level, plant height and head diameter were positively and significantly correlated with seed yield. Character such as head diameter had the highest direct effect on the yield/plant both at genotypic and phenotypic level. Genetic divergence using Mahalanobis D^2 statistic was worked out in 33 genotypes including two checks. These 33 genotypes were grouped into seven clusters. Cluster I was the largest cluster including 15 genotypes followed by cluster II and cluster III with seven and five genotypes respectively. Highest inter-cluster distance was found between cluster IV and cluster VII, thus suggesting that the genotypes of these clusters may be exploited to explore the entire range of variability for the character (s) to realize good recombinant lines.

Keywords: PCV, GCV, Heritability, Genetic Advance, Correlation, Genetic divergence.

INTRODUCTION

Sunflower is the third major oilseed crop in the world after soybean and rapeseed & mustard. It has been recognized as a major source of high-quality edible oil primarily used for culinary purposes (Pal et al., 2015). It also occupies fourth position in India after groundnut, rapeseed & mustard and soybean (Zia et al., 2013). Sunflower contains 40 to 44% of good quality oil and 45% and 50% of quality protein in cake (Malik & Saini 2018). The oil of sunflower is light yellow in color and possesses a good odour which can be used for cooking. The oil is also used in the manufacture of hydrogenated oil. High level of linoleic acid and low oleic acid content in sunflower oil reduces the level of blood cholesterol, a factor which is responsible for the incidence of coronary heart disease in human beings. It also contains phenolic antioxidants and phytosterols, which help in the alteration of cholesterol synthesis, thereby reducing the cholesterol level in the serum through cholesterol excretion (Zoumpoulakis et al., 2017). At present, it is also catching the interest of

farmers and companies day by day because of its possibility of using its oil as raw material for manufacturing biodiesel (Backes et al., 2008). Yield stagnation is the vital concern for making sunflower a competitive and efficient oil seed crop in the country. The limited genetic variability for desirable agronomic traits in the cultivars and germplasm is one of the major limitations in realizing higher productivity in sunflower. The large-scale replacement of hand races by modern high yielding cultivars and hybrids has brought about a dramatic reduction in genetic variability. In order to improve the crop production of sunflower, different aspects of research through plant breeding are being carried out for obtaining desirable genotypes (Messetti and Padovani 2004). On the other hand breeding programmes with an objective of evolving cultivars and hybrids with varying maturity durations coupled with high yield as well as high oil content require basic information on the event of variability present in the germplasm available. In quantitative traits, these variations are partly

attributable to the environmental factors and to a certain extent contributed by the genetic influence (Nehru and Manjunath 2003). It is also essential to measure the interrelationship between various plant attributes and determine the component characters, on which the selection procedure can be based for the genetic improvement of crop yield (Hassan et al., 2013). Correlation coefficient analysis measures the mutual relationship among various plant traits and determines the component traits on which selection can be based for improvement in yield. Similarly, path coefficient analysis is a powerful statistical technique that provides means to quantify the interrelationship of different yield components and indicates whether the influence is directly or indirectly on seed yield (Tyagi et al., 2013). Mahalakshmi et al. (2019) concluded that hybrid vigor depends upon parental divergence. With this background the present investigation was carried out to study the genetic variability, character association, direct and indirect effect of yield attributing characters on seed yield and genetic divergence among 33 germplasm lines of sunflower.

MATERIALS AND METHODS

The present experiment was carried out in Randomized Complete Block Design with three replications during Rabi, 2018-2019 to elicit information on 31 exotic and indigenous germplasm lines and two checks. Each genotype was sown in two rows of three meters length with a spacing of 60x30 cm. Observations on 12 quantitative characters like days to 50% flowering, plant height, stem diameter, number of leaves/plants, number of ray florets/head, days to maturity, head diameter, seed filling%, hulling%, volume weight, 100 achene weight, yield/plant were recorded from five random plants from each replication for all the entries. Analysis of variance (ANOVA) was carried out on mean values of different characters separately following standard analysis of variance technique for RBD design (Panse and Sukhatme 1954). The phenotypic, genotypic and environmental variance components for different characters were estimated from ANOVA using the expectation of mean square following Al-Jibouri et al. (1958). Heritability (in broad sense) for different traits was estimated using the components of variance as suggested by Hanson et al. (1956). Estimation of correlation coefficient and its significance test is done by using the variance and covariance components, the genotypic and phenotypic correlations between two characters (X and Y) were computed following Al-Jibouri et al. (1958). The path coefficient was obtained by solving using the method given by Dewey and Lu (1959). Mahalanobis (1936) D² statistics was used for assessing genetic divergence among all the genotypes. The clustering of D² values was done using Tocher's method as described by Rao (1952), while the intra- and inter- cluster distances were calculated using the formula given by Singh and Choudhary (1985). The

relative contribution (%) of each character to total divergence was assessed in two ways: (i) Average D2 for individual character as suggested by Singh (1981).

RESULTS AND DISCUSSION

Development of an effective plant breeding program largely depends upon the existence of genetic variability in the population. Hence, the magnitude of variability present in a gene pool of a crop species is most important to plant breeders for planning a judicious plant breeding program. The coefficients of variation expressed at phenotypic and genotypic levels were used to compare the variability observed among different characters. Analysis of variance (Table 1) showed significant differences among the genotypes with respect to all 12 characters studied. This result was in agreement with the findings of Tyagi et al. (2010); Serheed & Hussein (2019). The variation of different characters under study showed exactly the same trend in case of both PCV and GCV for all the quantitative characters. Even though PCV was higher than the GCV, the difference in the magnitude was smaller, indicating a smaller degree of environmental factors on the expression of the characters. These results corroborated with the result of Riaz et al. (2019). Phenotypic and genotypic coefficients of variations were high (>20%)for characters like plant height, no. of leaves /plant, no. of ray florets/head, hulling%, 100 achene weight and yield/plant (Fig. 1). Hence these characters were reliable for simple selection for further improvement of the traits. The above results were attested by Reddy and Nadaf (2014); Supriya et al. (2016); Rani et al. (2017); Divya et al. (2019). Moderate PCV and GCV (10-20%) were recorded for stem diameter, head diameter and volume weight. This finding was supported by Riaz et al. (2019) for head diameter and Supriya et al. (2016)) for volume weight. Lower magnitude of PCV and GCV was observed for characters like days to 50% flowering. days to maturity and seed filling % which was parallel with the findings of Nenny et al. (2019) for days to 50% flowering and Dudhe et al. (2019); Varalakshmi et al. (2020); Reavanth et al. (2022). Lower magnitude of variation warrants search for variation in other materials for improvement of these characters.

Heritability estimates are used to determine the amount of variation present in the population. Heritability combined with genetic advance will bring out the genetic gain expected from selection. High estimates of heritability (>80%) were observed for all 12 quantitative characters. This was in broad agreement with the findings of Baloch *et al.* (2016) excepting head diameter (Fig. 1). Hulling% showed the highest heritability (99.91%) followed by plant height (99.68%) and days to 50% flowering (99.44%). Genetic advance as percentage of mean (GAM) gives an expected progress for a trait under selection. The estimates were low (0-10%) for days to maturity and seed filling percentage, moderate (10-20%) for days to 50% flowering, and 100ml volume weight. High genetic advance (>20%) was recorded for characters like plant height, stem diameter, no. of leaves/plant, number of ray florets/head, head diameter, hulling percentage, 100 achene weight and yield/plant. Similar result was obtained by Fahmy et al. (2019) in segregating generation of sunflower. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone (Johnson et al., 1955). High heritability accompanied with high genetic advance as percentage of mean was recorded for characters like plant height, stem diameter, no. of leaves/plant, number of ray florets/head, head diameter, hulling percentage, 100 achene weight and vield/plant. This suggested that heritability is due to additive gene effect. Therefore, early generation selection could be effective for these traits for improvement of yield due to reliability on additive gene action. This result is in agreement with the findings of Hassan et al. (2020); Lakshman et al.(2021); Farooq et al. (2021). High heritability and moderate genetic advance (10-20%) were recorded for days to 50% flowering, and 100ml volume weight, which indicated the influence of additive as well as non-additive gene action on expression of these characters. This was in broad agreement with the findings of Fahmy et al. (2019). High heritability but low GAM was observed for days to maturity and seedfilling%. Hence selection for these traits should be practiced in later generations to utilize maximum gain from selection.

Yield is a complex character governed by several contributing traits. Estimates of genetic association of different characters along with phenotypic correlation show the inherent association as well as indicate the level of environmental influence on phenotypic expression of the character. Correlation between different character may arise due to linkage and can be broken down through recombination but it is impossible to overcome the correlation due to pleiotropy. Understanding the nature and extent of association of different yield components with yield and interrelationship among themselves is an essential prerequisite for planning of breeding procedure for effective improvement of yield.

The efficiency of selection mainly depends on direction and magnitude of association between yield and its component traits. In the present study, yield/plant exhibited positive correlation with plant height, disc diameter, no. of leaves/plant, seed filling %, stem diameter, number of ray florets/head, days to maturity and volume weight, out of which plant height and head diameter were significant both at genotypic and phenotypic level (Table 2). This result is in broad agreement with reports of Kalukhe *et al.* (2010); Deengra *et al.* (2013); Neny *et al.* (2021). The magnitude of genotypic correlation was higher than phenotypic correlation for a no. paired of charactersstudied suggesting the presence of strong inherent association between the characters at genotypic level and low environmental influence on expression of these characters as suggested by Riaz et al. (2019). In almost all cases the direction of phenotypic as well as genotypic correlation between different characters followed a similar trend. This creates a greater opportunity for a breeder to practice selection on the basis of phenotype for the improvement of yield. It was interesting to note that 100 achene weight exhibited negative association with almost all the component traits including yield/plant. Therefore, the utility of this trait in improving yield potential is doubtful. This result was highly supported by Jacovic et al. (2012). Days to 50% flowering was significantly and positively correlated with days to maturity (0.429, 0.436) and seed filling percentage (0.368, 0.370), while it was and significantly and negatively associated with 100 achene weight (-0.408,-0.422) both at phenotypic and genotypic level. Plant height was in significant and positive association with stem diameter (0.420, 0.446), no. of leaves/plant (0.598 0.604), days to maturity (0.481, 0.488), disc diameter (0.564, 0.621) including yield/ plant (0.494, 0.517) at 1% probability and with seed filling percentage (0.369, 0.373) at 5% probability both at genotypic and phenotypic level. There was significant and positive association between number of leaves/ plant, days to maturity (0.415, 0.427) and disc diameter (0.469, 0.529) both phenotypically and genotypically.

The correlation coefficient between two characters would not give a complete picture of a complex character like yield which is jointly determined by number of traits. In such a situation path analysis is useful. The associations between yield and its component traits were further subjected to path analysis to find out the direct and indirect effects of the component traits on grain yield. Character like head diameter (0.522) had highest direct positive effect on yield /plant followed by hulling percentage (0.220), filled grain percentage (0,205), no. of leaves /plant (0.177) no. of ray florets/head (0.112), plant height (0.102), 100 ml volume weight (0.080) and days to maturity (0.069) at phenotypic level (Table 3).

In present study, head diameter recorded significant positive correlation with yield and direct effect of later is also high both at genotypic and phenotypic level (Table 3 & 4). Plant height is significantly and positively associated with yield, but its direct effect is low. Indirect effect of this character via head diameter was high. This result corroborated with the findings of Kang and Ahmad (2014). On the contrary Follmann *et al.* (2019) concluded that head diameter did not have any direct effect on achene yield but it had direct effect on the number of achene per head. So based on correlation and path analysis head diameter was identified as the most important yield attributing characters. As both at phenotypic and genotypic level P(R) was 0.673 and 0.566, so characters studied are not sufficient and more no. of characters are to be included in the study.

Genetic diversity is the basis of crop improvement and is produced due to inherent genetic differences among the genotypes. It plays an important role in choice of parents because hybrids between the lines of diverged origin generally show a greater heterosis than those between closely related parents. Mahalakshmi et al. (2019) concluded that hybrid vigor depends upon parental divergence. In the present investigation of 33 genotypes, which were grouped into as many as seven clusters (Table 5). Cluster I was the largest cluster including 15 genotypes followed by cluster II and cluster III with seven and five genotypes respectively. Cluster IV and V included two genotypes each whereas cluster VI & VII were mono-genotypic clusters and were more divergent than the rest of the genotypes justifying their individual identity. Intra-cluster and inter- cluster distances among seven clusters (Table 6) indicated that, Cluster IV and cluster VII were more diverged from each other with an inter cluster distance

of (11182.770) followed by cluster III and VII (7226. 546) and cluster VI and VII (5883.610). The clusters I and II were least diverged from each other with an inter cluster distance of (873.424). Intra-cluster distance was highest in case of cluster VI (965.554).

In the present study the highest contribution towards genetic divergence (Table 7) was made by hulling percentage (54.85%), followed by plant height (13.46%), days to 50% flowering (7.86%), 100 achene weight (7.83%). No. of ray florets/head, no. of leaves/plant, yield/plant, stem diameter and head diameter had very less contribution towards divergence (<5%). Dhillon et al. (2017) suggested the genotypes selected from different clusters based on inter-cluster distance and mean performance can be utilized in further breeding program. Cluster mean for different characters (Table 8) were of higher productivity in sunflower. Over all observations revealed that the genotypes under study differ with respect to quantitative characters providing ample scope for selection and utilization in further breeding programs.

| Sr. No. | Changetong | M | Mean sum of squares (d.f.) | | | | | |
|---------|-----------------------------|-----------------|----------------------------|------------|--|--|--|--|
| | Characters | Replication (2) | Genotypes (31) | Error (64) | | | | |
| 1. | Days to 50% flowering | 1.296 | 80.912* | 0.449 | | | | |
| 2. | Plant height (cm.) | 6.705 | 3017.417** | 9.766 | | | | |
| 3. | Stem diameter (mm.) | 4.353 | 28.402** | 3.160 | | | | |
| 4. | No. of leaves/plant | 1.117 | 91.303** | 2.069 | | | | |
| 5. | No. of ray florets /head | 3.749 | 324.424** | 13.668 | | | | |
| 6. | Days to maturity | 4.659 | 29.411* | 0.563 | | | | |
| 7. | Head Diameter (cm.) | 13.434 | 18.602** | 3.090 | | | | |
| 8. | Seed Filling Percentage (%) | 1.336 | 79.120** | 1.542 | | | | |
| 9. | Hulling Percentage (%) | 0.165 | 446.843* | 0.407 | | | | |
| 10. | Volume Weight (g/100ml.) | 1.396 | 31.116** | 1.961 | | | | |
| 11. | 100 Achene Weight (g) | 0.103 | 6.150* | 0.078 | | | | |
| 12. | Achene Yield/ plant (g) | 19.873 | 163.488** | 13.271 | | | | |

Table 1: Analysis of variance for 12 qualitative traits of 33 sunflower genotypes.





| Characters | | DF (50%) | PH (cm.) | NLP | NRFD | DM | HD (cm.) | SF% | HULL% | 100ml VW (g) | 100AW (g) | ҮРР |
|-------------|----------------|-------------|-------------|---------|---------|---------|-------------|--------|--------|-----------------|--------------|---------|
| | r _p | 0.227 | 0.068 | 0.111 | -0.071 | 0.429* | 0.123 | 0.368* | 0.239 | -0.075 | -0.408* | -0.064 |
| DF (50%) | rg | 0.227 | 0.071 | 0.112 | -0.073 | 0.436* | 0.137 | 0.370* | 0.240 | -0.079 | -0.422* | -0.066 |
| PH | r _p | | 0.420* | 0.598** | 0.190 | 0.481** | 0.564** | 0.369* | 0.078 | 0.281 | -0.252 | 0.494** |
| (cm.) | rg | | 0.446** | 0.604** | 0.195 | 0.488** | 0.621** | 0.373* | 0.078 | 0.291 | -0.255 | 0.517** |
| SD | rp | | | 0.660** | 0.496** | 0.608** | 0.531** | 0.146 | 0.039 | -0.085 | -0.079 | 0.209 |
| (mm.) | rg | | | 0.713** | 0.541** | 0.643** | 0.614** | 0.151 | 0.043 | -0.116 | -0.089 | 0.228 |
| NI D | rp | | | | 0.343 | 0.415* | 0.469** | 0.128 | -0.124 | 0.013 | -0.103 | 0.300 |
| INLF | rg | | | | 0.358* | 0.427* | 0.529** | 0.131 | -0.125 | 0.008 | -0.107 | 0.319 |
| NRED | rp | | | | | 0.333 | 0.463** | 0.052 | -0.145 | -0.223 | 0.268 | 0.214 |
| INKED | rg | | | | | 0.343 | 0.516** | 0.061 | -0.148 | -0.232 | 0.281 | 0.216 |
| DM | r _p | | | | | | 0.541** | 0.347* | 0.131 | -0.227 | -0.144 | 0.250 |
| DIVI | rg | | | | | | 0.589** | 0.353 | 0.133 | -0.247 | -0.150 | 0.262 |
| HD | rp | | | | | | | 0.309 | 0.012 | -0.020 | -0.010 | 0.587** |
| (cm.) | rg | | | | | | | 0.331 | 0.013 | -0.011 | -0.015 | 0.655** |
| SE(0/-) | rp | | | | | | | | 0.097 | 0.148 | -0.012 | 0.302 |
| 31(%) | rg | | | | | | | | 0.098 | 0.158 | -0.014 | 0.323 |
| | r _p | | | | | | | | | 0.084 | -0.219 | 0.175 |
| HULL(%) | rg | | | | | | | | | 0.087 | -0.220 | 0.182 |
| VW(g/100ml | r _p | | | | | | | | | | -0.169 | 0.203 |
|) | rg | | | | | | | | | | -0.183 | 0.223 |
| 100 AW(a) | r _p | | | | | | | | | | | -0.126 |
| 100 AW(g) | rg | | | | | | | | | | | -0.136 |

Table 2: Phenotypic(r_p) and genotypic correlation coefficient(r_g) among 12 characters in 33 sunflower genotypes.

P(R) = 0.673

*Significant at P=0.05; **Significant at P=0.01

Table 3: Phenotypic path coefficient (pp) analysis showing direct and indirect effect of different traits on seed yield per plant.

| Characters | DF (50%) | PH (cm) | SD (mm.) | NLP | NRFD | DM | HD (cm.) | FG% | HULL% | 100ml VW (g.) | 100 AW (g.) | Corr. with YPP |
|-----------------|-------------|------------|-------------|--------|--------|--------|-------------|--------|--------|---------------------|-------------------|----------------------|
| DF (50%) | -0.379 | 0.023 | -0.024 | 0.020 | -0.008 | 0.030 | 0.064 | 0.075 | 0.053 | -0.006 | 0.088 | -0,064 |
| PH (in cm) | -0.086 | 0.102 | -0.146 | 0.106 | 0.021 | 0.033 | 0.295 | 0.076 | 0.017 | 0.022 | 0.054 | 0.494** |
| SD (in mm.) | -0.026 | 0.043 | -0.348 | 0.117 | 0.055 | 0.042 | 0.277 | 0.030 | 0.009 | -0.007 | 0.017 | 0.209 |
| NLP | -0.042 | 0.061 | -0.230 | 0.177 | 0.038 | 0.029 | 0.245 | 0.026 | -0.027 | 0.001 | 0.022 | 0.300 |
| NRFD | 0.027 | 0.019 | -0.173 | 0.061 | 0.112 | 0.023 | 0.242 | 0.011 | -0.032 | -0.018 | -0.058 | 0.214 |
| DM | -0.163 | 0.049 | -0.212 | 0.073 | 0.037 | 0.069 | 0.283 | 0.071 | 0.029 | -0.018 | 0.031 | 0.250 |
| HD (in cm.) | -0.047 | 0.057 | -0.185 | 0.083 | 0.052 | 0.038 | 0.522 | 0.063 | 0.003 | -0.002 | 0.002 | 0,587** |
| FG % | -0.139 | 0.038 | -0.051 | 0.023 | 0.006 | 0.024 | 0.161 | 0.205 | 0.021 | 0.012 | 0.003 | 0.302 |
| HULL% | -0.091 | 0.008 | -0.014 | -0.022 | -0.016 | 0.009 | 0.006 | 0.020 | 0.220 | 0.007 | 0.047 | 0.175 |
| 100ml VW (g) | 0.028 | 0.029 | 0.030 | 0.002 | -0.025 | -0.016 | -0.010 | 0.030 | 0.019 | 0.080 | 0.036 | 0.203 |
| 100 AW (g) | 0.155 | -0.026 | 0.028 | -0.018 | 0.030 | -0.010 | -0.005 | -0.002 | -0.048 | -0.014 | -0.215 | -0.126 |

P(R) = 0.673

*Significant at P=0.05; **Significant at P=0.01

Table 4: Genotypic path coefficient (pp) analysis showing direct and indirect effects of different traits on seed yield per plant.

| Characters | DF (50%) | PH (cm.) | SD (mm.) | NLP | NRFD | DM | HD (cm.) | FG % | HULL % | 100ml VW (g) | 100 AW (g) | Corr. with YPP |
|--------------|-------------|-------------|-------------|--------|--------|--------|-------------|--------|-----------|-----------------|------------------|----------------------|
| DF (50%) | -0.440 | -0.007 | -0.041 | 0.033 | -0.007 | 0.051 | 0.101 | 0.079 | 0.061 | -0.006 | 0.110 | -0.066 |
| PH (in cm) | -0.100 | -0.030 | -0.256 | 0.180 | 0.018 | 0.057 | 0.456 | 0.079 | 0.020 | 0.024 | 0.068 | 0.517** |
| SD (in mm.) | -0.031 | -0.013 | -0.574 | 0.213 | 0.050 | 0.075 | 0.451 | 0.032 | 0.011 | -0.009 | 0.024 | 0.228 |
| NLP | -0.049 | -0.018 | -0.409 | 0.298 | 0.033 | 0.050 | 0.389 | 0.028 | -0.032 | 0.001 | 0.029 | 0.319 |
| NRFD | 0.032 | -0.006 | -0.311 | 0.107 | 0.093 | 0.040 | 0.379 | 0.013 | -0.038 | -0.019 | -0.075 | 0.216 |
| DM | -0.192 | -0.015 | -0.369 | 0.127 | 0.032 | 0.117 | 0.433 | 0.075 | 0.034 | -0.020 | 0.040 | 0.262 |
| HD (in cm.) | -0.060 | -0.019 | -0.353 | 0.158 | 0.048 | 0.069 | 0.735 | 0.071 | 0.003 | -0.001 | 0.004 | 0.655** |
| FG % | -0.163 | -0.011 | -0.087 | 0.039 | 0.006 | 0.041 | 0.243 | 0.213 | 0.025 | 0.013 | 0.004 | 0.323 |
| HULL % | -0.106 | -0.002 | -0.025 | -0.037 | -0.014 | 0.015 | 0.010 | 0.021 | 0.254 | 0.007 | 0.059 | 0.182 |
| VW (g/100ml) | 0.035 | -0.009 | 0.067 | 0.002 | -0.022 | -0.029 | -0.008 | 0.034 | 0.022 | 0.082 | 0.049 | 0.223 |
| 100 AW (g) | 0.181 | 0.008 | 0.051 | -0.032 | 0.026 | -0.017 | -0.011 | -0.003 | -0.056 | -0.015 | -0.268 | -0.136 |

P(R) = 0.566

*Significant at P=0.05; **Significant at P=0.01

| Cluster | No. of genotypes | Genotypes included in the cluster |
|---------|------------------|---|
| | | IC 296478, EC 494385, EC 180886, IC 502038, EC 198101, EC 276266, |
| I | 15 | EC 494382, EC 201851, EC 178170, EC 601615, EC 116212, EC 399490, |
| | | EC 276294, DRSH-1, EC 620190 |
| II | 7 | IC 75693, GMU-520-I IC 502032 EC 399512, EC 198068, KBSH-44, EC75268-III-S3 |
| III | 5 | EC 640320, IC 75642, EC 279370, EC 399286, EC 289514-I |
| IV | 2 | IC 585833, IC 75638 |
| V | 2 | EC 276532, EC 276161 |
| VI | 1 | EC 279309 |
| VII | 1 | EC 279520 |

Table 5: Cluster composition of 33 genotypes based on D² value.

Table 6: Average intra-cluster (diagonal) and inter-cluster distance (D2 values).

| Cluster | I(15) | II(7) | III(5) | IV(2) | V(2) | VI (1) | VII(1) |
|---------|---------|---------|----------|----------|----------|---------------|----------|
| Ι | 619.210 | 873.424 | 1449.121 | 2187.078 | 1643.871 | 1291.119 | 4536.432 |
| II | | 463.452 | 1367.865 | 2972.211 | 1903.926 | 1478.183 | 3606.930 |
| III | | | 564.938 | 1184.743 | 4201.712 | 2832.930 | 7226.546 |
| IV | | | | 348.588 | 5882.584 | 3199.969 | 11182.77 |
| V | | | | | 965.554 | 2315.533 | 2076.998 |
| VI | | | | | | 0.000000 | 5883.610 |
| VII | | | | | | | 0.000000 |

Table 7: Relative contribution of different characters to genetic divergence.

| Sr. No. | Characters | Average D ² | Percentage of total D ² |
|---------|-----------------------------|------------------------|------------------------------------|
| 1. | Days to 50% flowering | 120.15(3) | 7.86 (3) |
| 2. | Plant Height (cm.) | 205.76(2) | 13.46 (2) |
| 3. | Stem Diameter (mm.) | 7.15(11) | 0.47 (11) |
| 4. | No. of Leaves /Plant | 22.07(8) | 1.44 (8) |
| 5. | No. of Ray Florets/ head | 20.78(9) | 1.36 (9) |
| 6. | Days to maturity | 79.19(5) | 5.18 (5) |
| 7. | Head Diameter (cm.) | 5.94(12) | 0.39 (12) |
| 8. | Filled Grain Percentage (%) | 36.22 (7) | 2.37 (7) |
| 9. | Hulling Percentage (%) | 838.70(1) | 54.85 (1) |
| 10. | Volume Weight (g/100ml.) | 53.91(6) | 3.53 (6) |
| 11. | 100 Achene Weight (g) | 119.76 (4) | 7.83 (4) |
| 12. | Yield/ Plant (g) | 19.40 (10) | 1.27 (10) |
| | TOTAL | 1529.03 | 100 |

Table 8: Cluster means in 12 different quantitative characters of sunflower.

| Sr. No. | Characters | I(15) | II (7) | III(5) | IV(2) | V(2) | VI (1) | VII (1) | Grand Mean |
|---------|-----------------------------|--------|---------------|--------|--------|--------|---------------|------------|---------------|
| 1. | Days to 50% flowering | 63.58 | 70.71 | 62.80 | 58.83 | 63.83 | 79.00 | 65.00 | 65.21 |
| 2. | Plant Height (cm.) | 124.49 | 164.70 | 164.14 | 111.68 | 124.91 | 80.33 | 192.38 | 139.00 |
| 3. | Stem Diameter (mm.) | 15.39 | 16.63 | 19.62 | 15.31 | 17.30 | 15.62 | 21.68 | 16.60 |
| 4. | No. of Leaves /Plant | 18.84 | 22.26 | 28.88 | 15.81 | 20.25 | 16.81 | 22.67 | 21.01 |
| 5. | No. of Ray Florets/ Disc | 48.16 | 45.82 | 55.89 | 37.62 | 47.10 | 34.10 | 42.97 | 47.55 |
| 6. | Days to Maturity | 92.33 | 95.72 | 95.13 | 92.17 | 92.33 | 91.67 | 101.00 | 93.71 |
| 7. | Disc Diameter (cm.) | 14.27 | 15.35 | 16.78 | 12.97 | 13.01 | 11.87 | 16.92 | 14.73 |
| 8. | Filled Grain Percentage (%) | 91.07 | 91.81 | 92.13 | 91.17 | 88.00 | 97.00 | 99.00 | 91.63 |
| 9. | Hulling Percentage (%) | 31.45 | 30.89 | 15.67 | 7.22 | 49.83 | 30.88 | 62.78 | 29.52 |
| 10. | 100ml Volume Weight (g) | 30.36 | 31.86 | 31.02 | 28.86 | 31.93 | 25.28 | 29.57 | 30.60 |
| 11. | 100 Achene Weight (g) | 5.59 | 4.88 | 5.54 | 7.01 | 6.91 | 4.46 | 4.31 | 5.52 |
| 12. | Yield/ Plant (g) | 18.43 | 20.03 | 26.84 | 12.31 | 20.07 | 10.80 | 33.79 | 20.00 |

CONCLUSIONS

High estimate of heritability coupled with high genetic advance for characters like plant height, stem diameter, no. of leaves/plant, number of ray florets/head, head diameter, hulling percentage, 100 achene weight and yield/plant attributed to the preponderance of additive gene action and these traits possessed high selective value. Head diameter showed significant positive correlation with yield/plant with high direct effect. So, emphasis should be given on direct selection for this trait while attempting yield improvement in sunflower Thirty- three genotypes were grouped into seven clusters out of which two are monogenotypic. Hulling percentage and plant height contributed maximum to genetic divergence. Hulling percentage and plant height contributed maximum to genetic divergence. Based on maximum genetic distance and cluster mean it is desirable to make crosses between the genotypes of cluster, cluster IV and cluster VI and with the genotype of cluster VII for creation of genetic variability to isolate transgressive segregants for earliness and enhancement of yield of sunflower.

FUTURE SCOPE

Based on maximum genetic distance and cluster mean it is desirable to make crosses between the genotypes of cluster IV and cluster VI and with the genotypes of cluster VII for creation of genetic variability to isolate transgressive segregants for earliness and enhancement of yield of sunflower. Yield related traits like head diameter with high heritability as well as high genetic advance and having significant positive correlation with vield can be used as selection criterion for yield improvement in sunflower.

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