

## GENETIC DIVERGENCE IN SUNFLOWER ACCESSIONS

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### **Importance of sunflower-**

Sunflower (*Helianthus annuus* L.), belonging to the family 'Asteraceae' (Compositae) and genus 'Helianthus', is a diploid species ( $2n = 2x = 34$ ) and native to southern parts of USA and Mexico. Sunflower is an important oilseed crop and is the preferred source of oil for domestic consumption and cooking worldwide (Hu *et al.*, 2010). Sunflower was introduced to India during 1969 and gained popularity during 1980's with the development of first sunflower hybrid BSH-1 (Seetharam, 1980). In the oilseed scenario, sunflower competes with other three major oilseeds, *i.e.* soyabean, groundnut and rapeseed mustard at global level. Sunflower has a great potential in bridging the gap between the demand and supply of edible oil in future. Sunflower holds great promise because of its short duration, wider adaptability, photo-insensitivity, drought tolerance and higher amount of superior quality oil. The oil and protein content in sunflower ranges from 35-45 per cent and 18-20 per cent, respectively. Higher oil yield is an ultimate objective of sunflower researchers as this oil is considered as a good quality oil from health point of view, due to presence of polyunsaturated fatty acids which are known to reduce the risk of cardiac related problems (Monotti, 2004). Additionally, due to the possibility of using its oil as raw material for manufacturing biodiesel, it is arousing the interest of farmers, agriculture professionals and companies in the world.

### **Importance of genetic divergence in crop improvement-**

In plant breeding, genetic diversity in parental lines is a pre-requisite for developing genetically superior hybrids. More diverse the parents, greater are the chances of obtaining heterotic expression in F<sub>1</sub> with possibility of broad spectrum of variability in segregating generations. Yield is the combination of numerous components which are influenced by environmental instabilities. It is highly recommended to explore configuration of yield via breeding approaches. Sunflower being a highly cross-pollinated crop has a great scope for increasing productivity by diversifying hybrid base. In downsizing the breeding lines to be maintained, assessment of genetic divergence also helps a lot. The concept of D<sup>2</sup> statistics, based on measurements of morphological characters is frequently used as a tool for estimating genetic divergence by the plant breeders (Mahalanobis, 1936; Rao, 1952). Tracing D<sup>2</sup> as a generalized statistical distance, genotypes are grouped on the basis of minimum genetic distance using Tocher's method as described by Rao (1952). Varieties from different localities are generally included in the hybridization programmes assuming genetic diversity and greater likelihood of recovering promising segregants. However, Murthy and Anand (1966) noted that there is no parallelism between geographical and genetical diversity. Genetic diversity existing within and between groups of germplasm is important, and particularly, useful in proper choice of parents for realising higher heterosis and obtaining useful recombinants. D<sup>2</sup> statistic is a useful tool for estimating the genetic divergence in plant breeding experiments.

The knowledge about the magnitude and nature of variability present in a population due to the genetic and non-genetic causes is an important prerequisite for a breeding programme to improve the yield potential of genotypes, as greater variability among the genotypes leads to better chance for further improvement in the crop.

### Methods to measure genetic divergence-

Evaluation of genetic divergence is performed through methods based on agronomic, morphology and molecular characteristics. Mahalanobis (1936) outlined a statistical procedure 'D<sup>2</sup> statistic' to measure the genetic divergence among the test genotypes involving quantitative characters in a given population. This concept is based on the technique of utilising measurement in respect of an aggregate of characters. Clustering methods objectify to separate a group of original observations on different subgroups in order to obtain homogeneity within and heterogeneity between subgroups. Among these methods, optimization and hierarchical ones are employed on a large scale by plant breeders. Visualization and interpretation of distances may be facilitated by the use of a clustering method and/or graphical dispersion. Multivariate analysis has been considered as an important tool in quantifying the degree of genetic divergence in different crops (Rao, 1952).

### Genetic divergence in sunflower-

Genetic divergence is a process of one species diverging over time into more than one species, *i.e.*, passing small random changes over time, from one generation to next generation. Varieties from different localities are generally included in the hybridization programmes assuming genetic diversity and greater likelihood of recovering promising segregants. However, Murthy and Anand (1966) noted that there is no parallelism between geographical and genetical diversity. Several investigations that evaluated the genetic divergence in sunflower crop were conducted by using morphoagronomic characters (Arshad *et al.*, 2007). Genetic divergence estimation between different sunflower genotypes has been studied, aiming to develop parents for hybrids constitution or even the formation of new segregating populations, from the intercross of divergent genotypes with complementary agronomic characteristics.

Reddy and Devasenamma (2004) studied 61 genotypes of sunflower and grouped them into 19 clusters based on their genetic diversity. Based on inter cluster distance value and *per se* performance of genotypes, the genotypes namely, EC-376211, EC-399318, RHA-344 and BLC-P6 were selected which could be intercrossed to obtain high heterotic expression and also to recover desirable transgressive segregants.

Reddy *et al.* (2005) assessed genetic divergence among 102 genotypes and grouped them into 12 clusters. Based on the inter cluster distances and *per se* performance, the genotypes namely, GMU-4, GMU-11, GMU-14, GMU-16, GMU-25, GMU-40 and GMU-70 were selected which could be intercrossed to obtain high heterosis and also to recover desirable transgressive segregants. Seed yield/plant contributed maximum to divergence (40.2%) which was followed by number of leaves/plant (25.8%) and 100-seed weight (17.0%).

Loganathan *et al.* (2006) conducted multivariate analysis of divergence among 50 genotypes of sunflower which led to their grouping into 14 clusters. Seed yield contributed maximum towards genetic divergence, followed by 100-seed weight and plant height.

Mahalakshmi *et al.* (2006) studied 29 genotypes of sunflower for their genetic divergence by D<sup>2</sup> analysis. The genotypes were grouped into 7 clusters. The character, days to first flowering contributed more towards genetic divergence.

Sridhar *et al.* (2006) assessed genetic divergence using D<sup>2</sup> statistics among 44 sunflower genotypes and grouped them into 9 clusters. Plant height and oil content contributed more towards genetic divergence.

Binodh *et al.* (2007) studied genetic divergence of 24 breeding lines for 8 traits in sunflower. The genotypes were grouped into 10 clusters where cluster I was the largest containing 13 genotypes, followed by cluster IV with 3 genotypes. The inter-cluster distance was the maximum between cluster VI and cluster VIII, followed by cluster IV and cluster VI and cluster VI and cluster IX. The study revealed that plant height contributed maximum towards divergence (45.29%),

followed by seed yield per plant (25.72%) and oil content (15.94%). Based on the inter-cluster distance and *per se* performance, the genotypes *viz.*, 17A, 47A, CSFI 5325, CSFI 5415, CSFI 5436 and CSFI 5013 were identified as suitable parents which could be intercrossed to obtain high heterosis.

Camarano *et al.* (2010) investigated genotypic divergence among 10 sunflower populations using Mahalanobis'  $D^2$  statistics and canonic variables to identify more similar and/or divergent groups. The results of the individual variance analyses pointed out significant differences for the initial flowering, final flowering, plant height, oil content, moisture content and yield in all the experiments. Very high genetic variability was noted among the populations for these traits. The traits, stem diameter, head diameter, 1000-seed weight and number of seeds per head presented differences, which were sometimes significant and sometimes not, indicating that these traits show genotype-environment interaction.

Punitha *et al.* (2010) assessed genetic diversity among 17 sunflower genotypes using 9 agronomic characters and indicated the presence of substantial genetic diversity. The genotypes were grouped into 4 clusters. Among the investigated characters, seed yield, plant height, oil content and oil yield exhibited high contribution towards genetic divergence. It was observed that the inclusion of CSFI 5076, CSFI 5162, CMS 47A, CSFI 5005, CMS 17A, CMS 47A, CSFI 5069, CSFI 5422, CSFI 5109, CSFI 5155, CSFI 5002, COSF 1A, CSFI 5161 and CSFI 5015 in future breeding programs could result in the development of superior sunflower cultivars.

Mandel *et al.* (2011) conducted population genetic analysis of the primary gene pool of sunflower based on a broad sampling of 433 cultivated accessions and 24 wild sunflower populations. Gene diversity across the cultivars was 0.47, as compared with 0.70 in the wilds, indicating that cultivated sunflower harbours roughly two-thirds of the total genetic diversity present in wild sunflower.

Kumari and Sheoran (2012) evaluated 80 sunflower genotypes for genetic divergence using  $D^2$  analysis. The genotypes were grouped into 10 clusters. Cluster I was the largest one with 22 genotypes, followed by cluster II (18), IV (17), VI (11), III (7) and V, VII, VIII, IX and X with one genotype each. The genotypes, DRSF-120 R, P70R, Nandyal-1 and RHA-586 were identified as divergent and superior performers. Likewise, genotypes from different sources were grouped in the same cluster, thus, suggesting that geographical diversity does not necessarily represent genetic diversity.

Reddy *et al.* (2012) studied genetic divergence in 64 genotypes of sunflower and grouped the genotypes into 9 clusters. The pattern of distribution of genotypes into various clusters was random and indicated that the geographical and genetic diversity were not related. Plant height contributed maximum towards genetic divergence, followed by stem diameter and head diameter.

Ayaz *et al.* (2014) evaluated seventeen sunflower hybrids and fifteen inbred lines including ten Cytoplasmic male sterile lines and five restorer lines for flower initiation days, full flowering days, full developmental days, height of plant, disk diameter, stem thickness, leaves per plant, hundred achenes weight, achenes yield and oil content percentage. The maximum achenes yield was contributed by Hysun-33 2119 kg/h followed by SMH-0924 and SMH-0925. SMH-1028 and SMH-0926 were suggested as potential significant hybrids for future breeding plans to incorporate maximum achenes yield and oil content percentage. The CMS-11, CMS-25 and CMS-10 were long statured with vigorous stem and all the restorers were early maturing recommended for including in hybridization program to generate high heterotic factions.

Chandirakala *et al.* (2014) assessed genetic divergence of 38 sunflower genotypes using Mahalanobis  $D^2$  statistics. These genotypes were grouped into 13 clusters, among which the cluster IX with 9 genotypes was the largest. Maximum inter cluster distance was recorded between cluster XII and XIII (39.58) followed by clusters II and XII (38.18). Hence hybridizing between these

divergent groups may lead to higher variation in segregating population. In this study, the genotypes viz., GMU 322, COSF3B and COSF4B in the cluster II, the genotypes viz., GMU 503, GMU 1074, GMU 1108 in the cluster XII and the genotype COSF1B in the cluster XIII are widely divergent and crosses may be effected among the genotypes of these clusters to get more heterosis among the hybrids.

Pandya *et al.* (2014) evaluated forty genotypes of sunflower [*Helianthus annuus* (L.)] for seed yield and its components and grouped them in 5 clusters. The clustering pattern of genotypes was independent of their geographical distribution. Taking into account cluster mean for important seed yield components, the various clusters which can provide the desired parents like GMU-1033, GMU-411 for hybridization for improvement of characters.

Masvodza *et al.* (2015) used 16 cytoplasmic male sterile (CMS) lines and 10 male restorer (R) lines and characterised them for ten morphological variables namely, days to 50% flowering, head diameter, leaf length, leaf width, petiole length, nodding, lodging, number of leaves, plant height, stem diameter and uniformity. The genetic base of the collection was observed as narrow and would need more diversification.

### **Sunflower improvement in relation to genetic divergence-**

Genetic diversity existing within and between groups of germplasm is important, and particularly, useful in proper choice of parents for realising higher heterosis and obtaining useful recombinants. D<sup>2</sup> statistic is a useful tool for estimating the genetic divergence in plant breeding experiments. To get more heterotic F<sub>1</sub>'s and large number of desirable transgressive segregants, selection of parents for hybridization should be properly based on genetic diversity rather than geographic diversity. The mating systems in any field crop determine the gene flow and hence the propensity with which reference population can be improved through genetic amelioration. Sunflower is predominately a cross- pollinated crop and the pollination is by and large insect-mediated, though some degree of self pollination cannot be ruled out in some genotypes for the reasons of hermaphroditism and some homogamy. This necessitates that heterozygosity *per se* be maintained in sunflower populations.

Sunflower improvement strategies include; development of heterotic hybrids, elite composites and/ or improved open-pollinated populations developed through random mating (hand pollination or male sterility mediated), followed by selection (various recurrent selection procedures). All these methods would necessarily entail in their objectives for accumulation of gene constellations for intra and inter allelic interactions in genotypic background(s) of agronomic significance. In hybrids, dominance deviation of alleles, and in improved populations, accumulation of additive genes with greater complimentary effects are harnessed for better trait expression and hence higher economic yield.

The success of any chosen breeding programme would depend upon the extent of heritable genetic variation, response of selection pressure exerted, the magnitude and direction of associations among various yield contributing traits and selection indices used in reference population(s). Hence , analysis of genetic diversity among inbred accessions is of vital importance in Sunflower breeding.

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