Genetic diversity analysis for agro-morphological traits in sunflower (*Helianthus annuus* L.)

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SUMMARY : Genetic diversity analysis was performed on 70 genotypes of sunflower through Mahalanobis D^2 statistics. Based on the results, the genotypes were categorized into 10 clusters connoting the existence of ample genetic diversity in the material evaluated. Cluster I was the largest with 56 genotypes. This was followed by cluster IV with four genotypes; cluster VII with three genotypes and the remaining were monogenotypic clusters. Maximum inter-cluster distance was observed between cluster VI and VIII (19.02) implying that utilization of the genotypes in those clusters might result in desired F_1's upon hybridization. The study also revealed that the traits in the genotypes *viz.,* SCMR (30.31%) followed by hull content (24.39%) contributed more to the total genetic divergence. Five genotypes belonging to monogenotypic clusters *viz.*, DRM-342, R-45, CPI-1, NDI-16 and CMS-17B can be utilized in future breeding programme to harness desired heterotic F_1s.

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