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Development of Safflower Germplasm Core Collection Based on Quantitative Descriptors

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The large size of germplasm collection presents problems in its management and accessibility for breeding purposes. The use of collections is limited by lack of knowledge of genetic diversity in the collection. To overcome these problems the core was developed for better utilization and accessibility to vast collection of germplasm material. Safflower germplasm consists of 6374 accessions belonging to 57 countries. The data on 13 qualitative traits was standardized each variable to eliminate scale differences. A total of 6201 safflower germplasm accessions were used for development of core after elimination of missing and blank values from 6374 accessions. A core was developed based on 13 quantitative descriptors. The total accessions arrayed into 20 distinct clusters using Wards minimum variance method. From each cluster stratified sampling has been carried out to establish core subset of 620 (10%) accessions. Differences among means of the entire collection and core subset for the 13 quantitative descriptors used in developing the core subset were not significant, and the variances of the entire collection and core subset were homogeneous for all the traits. The zero mean difference per cent and more than 80 coincidence rate per cent indicated the representativeness of core with total collection.

Biography

K.Alivelu has completed her Ph.D from JNTU, Hyderabad. She is working as Senior Scientist in DOR, Hyderabad. She has a total of 48 publications (research papers, poster presentations, presented in conferences articles and book chapters). She has been associated in the coordination of research work of All India Coordinated Research Project on safflower at 21 centres spread all over India.

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