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Genetic diversity and relationship of oil palm germplasm as revealed by microsatellite (SSR) markers

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Oil palm (*Elaeis guineensis* Jacq), the highest oil yielding crop accounted for 34.7% of world production of vegetable oils from an area of 4.8% of the total area cultivated with oil seeds. With the increase in area of the crop under diverse environments, it has become essential to develop oil palm varieties with high yield, compactness/dwarfness, high oil extraction ratio and tolerance to low moisture regimes. Evaluation and characterization of diversity in the available germplasm is essential for both utilization as well as maintenance of the traits of interest. Compared to conventional/morphological characterization, molecular methods of diversity estimation are fast and reliable. Molecular markers have the uniqueness that they are not influenced by the environment and the potential to reduce time needed for breeding new crop varieties. Also, problems of germplasm management arise as to the availability of land to ensure that we conserve as much as possible, the total genetic diversity of the species without duplication. In this context, the present study was taken up to estimate genetic variability and relationship of different accessions available at Palode using SSR markers. Thirty one genotypes including 29 germplasm accessions and two reference genotypes have been evaluated for the extent of diversity and relatedness. Among the 9 primer pairs used for SSR analysis, mEgCIR3399 gave the highest number of alleles (17) and sMo00129 produced the lowest number (6) of alleles. Cluster analysis, based on UPGMA was performed in order to realize the extent of similarity/dissimilarity between the oil palms. Based on the dendrogram, the germplasm accessions were divided into two main groups. Cluster I consisted of four genotypes belonging to *Elaeis oleifera*. The cluster two included the remaining accessions and had six sub-clusters. Diversity was confirmed through 2-D and 3-D PCA plots. The study revealed significant variability among the accessions studied as well as classified similar ones to same category. It has helped to identify unique ones for introgression into breeding lines for development of improved variety as well as widening the genetic base and helped to avoid similar ones.

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