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Title : EVALUATION OF THE SIMPLE SEQUENCE REPEAT (SSR) GENOTYPING OF *Elaeis oleifera* GERMPLASM

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Special attention has been given to the second species of oil palm, Elaeis oleifera as it possess several interesting agronomic traits such as slow growth, higher oil unsaturation and disease resistance. Studying the variability of E. oleifera germplasm is therefore very important as it serves as a tool to select source of genetic diversity for the oil palm conservation programme. The objectives of this study were 1) to identify the polymorphic E. oleifera gSSRs for E. oleifera, 2) to measure the information content of E. oleifera gSSRs, 3) to unravel the genetic diversity of E. oleifera germplasm, 4) to determine the genetic differentiation of E. oleifera germplasm and 5) to assess the genetic structure of E. oleifera germplasm. MPOB has developed a collection of simple sequence repeats (SSRs) from E. oleifera genome. Initially, optimization of PCR conditions for analysis of the oleifera samples using E. oleifera gSSRs was carried out. A total of 316 E. oleifera gSSRs were tested to evaluate their usefulness to assess the genetic diversity and population structure of E. oleifera populations. The PCR conditions were optimized while keeping the original DNA concentration, annealing temperature (TA) and other reagent constant. Out of 316 E. oleifera gSSRs screened, 270 produced amplicons and of these numbers, 140 were polymorphic and potentially useful for diversity analysis. The modified PCR condition increases the success of amplifying E. oleifera gSSRs in the E. oleifera DNA samples analyzed. The PCR methods together with the polymorphic E. oleifera gSSRs were applied in genotyping the entire E. oleifera populations. A set of 21 polymorphic E. oleifera gSSRs was analyzed on a total of 214 E. oleifera genomic DNA belonging to eight germplasm originated from four countries in Central and South America (Columbia, Panama, Costa Rica and Honduras). The analysis covered on genetic diversity and genetic structure of eight E. oleifera populations, inferences from 21 polymorphic E. oleifera gSSRs. The average observed heterozygosity across population (Ho=0.249) was less than the expected heterozygosity (He=0.363). The highest population diversity was obtained in population 08 from Columbia (He=0.460±0.055, I=0.870±0.121. Eight of 21 polymorphic E. oleifera gSSRs were informative with PIC>0.5, where sMo00131 is the most informative (PIC=0.853). The populations analysed showed great genetic differentiation (FST=0.223). The Nei genetic distance showed the highest genetic distance was between population 01 from Columbia and population 02 from Costa Rica (0.555) while the lowest was between population 02 and population 03 from Honduras (0.019). The eigenvalues of PCoA plot showed that the first two components explained 38.70% of the total variation, which roughly ordinated the E. oleifera individuals into three major groups. Construction of neighbour-joining (NJ) tree separated E. oleifera individuals into two clusters. Model based clustering revealed that E. oleifera population has the highest ΔK when K was set to 7. The present study provides a diverse pattern of genetic diversity and the existence of genetic differentiation among E. oleifera germplasm. This study highlights the potential contribution of genetic variation of the E. oleifera collection analyzed using E. oleifera gSSRs for germplasm conservation and for utilization in breeding programs. Further conservation should focus on more populations with less number of palms per population development of core collection.