

## Abstract

The conventional method for development of microsatellite makers have been time consuming and expensive. Currently, the discovery of simple sequence repeat (SSR) marker in expressed sequence tags (ESTs) provided the opportunity to develop microsatellites in a simple and direct way, by data mining of EST database. In the present study 5,610 and 75,948 oil palm ESTs generated by the PalmGenes and National center of genetic engineering and biotechnology, respectively, were investigated for identification and development of simple sequence repeat markers derived from expressed sequence tags (EST-SSR). All sequence data were clustered and assembled into 47,256 clusters. Based on the minimum repeat unit defined as 10, 5, 5, 3, 3 and 3 for mono-, di-, tri-, tetra-, penta- and hexa nucleotides, respectively, 1,570 EST containing SSRs were identified. Homology searching revealed that EST-SSRs represented 120, 5 and 1,445 clusters of known gene products, hypothetical proteins and unknown proteins, respectively. The 374 EST-SSRs based on high repeat unit were selected for primer designed. Three hundred and two primer pairs successfully amplified and 284 of them showed polymorphism among 57 oil palm accessions with an average allele number of 2.68 per locus, average Polymorphism Information Content of 0.34 and average Discrimination Power of 0.48. Two hundred and fifty-four and 195 primer pairs successfully cross-amplified in *E. oleifera* and *Cocos nucifera* (coconut), respectively. Sixty-five markers putatively fitted Mendelian segregation evaluated in 10 F1 randomly selected progenies and their two parents. Comparing EST-SSRs and genomic SSRs (gSSR) for their informativeness indicated the lower Polymorphism Information Content in EST-SSRs. Linkage disequilibrium between pairs of linked EST-SSR and gSSR markers mapped in the other study was investigated. None of linked SSR markers showed linkage disequilibrium suggesting that the large number of markers may be used for whole genome scan association mapping in diverse germplasm of highly heterozygous oil palm.