

Gene discovery via expressed sequence tags from oil palm (*Elaeis guineensis* Jacq.) mesocarp.

ABSTRACT

Expressed sequence tags (ESTs) have been used for many applications such as to reveal gene expression patterns, gene regulation and sequence diversity. A total of 1011 unique transcripts corresponding to 1463 genes have been identified from the ESTs generated from 17-week oil palm mesocarp cDNA library. This approach was found to be successful in the discovery of new and important genes expressed in the mesocarp tissue which are associated with the various cellular processes of the tissue. It was observed that 12.9% of the total genes expressed in the 17-week mesocarp cDNA library can be categorized under metabolism. This is in agreement with the function of the tissue which is involved in many biochemical processes including amino acid and fatty acid metabolism. Most importantly are the discoveries of genes playing important roles in the fatty acid and wax biosynthesis pathway such as acetyl-CoA carboxylase, stearyl-ACP desaturase, acyl carrier protein (ACP), lysophosphatidic acid acyltransferase, γ -6-palmitoyl-ACP desaturase and lipase. These genes can serve as targets for genetic manipulation where such endeavours have been extensively carried out in other plants such as *Brassica napus* and *Olea europaea* to help increase the economic value of the oil. Genes and protein associated with ethylene synthesis and signal transduction pathway were also identified from the 17-week mesocarp ESTs. Dot blot analysis was carried out to help in identifying potential tissuespecific genes, which can lead to the isolation of the tissue-specific promoters for manipulation of the mesocarp tissue. This is in particular to direct accumulation of transgenic products, such as new specialty oils and value-added products like pharmaceuticals and nutraceuticals to the mesocarp.

Keyword: Expressed sequence tags (EST); Mesocarp; Oil palm; *Elaeis guineensis*; Tissue-specific genes.