

Differentially expressed transcripts related to height in oil palm

ABSTRACT

A subtractive cDNA library was constructed using MPOB Planting Series 1 (PS1) population to isolate differentially expressed transcripts associated with height increment in oil palm. After differential screening, 98 clones were identified to be potentially positive with cDNA inserts ranging from 250 to 1000 bp. A total of 123 sequences generated and low quality sequences ≤ 20 were eliminated using Phred program to assess the sequence quality and determine the accurate consensus sequence. Contig assembly by CAP3 program generated 51 contigs and four singletons (55 unigenes). Blast search showed 49 unique sequences had significant match to various plant species in the GeneBank database with E-value $\leq 1e-5$, and four sequences showed no significant similarity. Gene ontology analysis output from Blast2 GO program revealed that the sequences encoding for auxin responsive protein, circadian clock-associated protein1, zinc-finger protein and basic leucine zipper protein were potentially associated to dwarfism. The genes were identified based on their putative functions in regulating height in plants, particularly in growth hormone biosynthesis such as auxin (Aux/IAA), gibberellins (GA) and brassinosteroids (BR).

Keyword: Auxin; Brassinosteroids; Differentially expressed transcripts; Dwarfism; Gibberellins; Suppression subtractive hybridisation (SSH)