

A transcriptome approach to study epigenetic somaclonal variation in oil palm (*Elaeis guineensis* Jacq.).

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Micropropagation by somatic embryogenesis in oil palm produces a small but significant proportion of individuals displaying homeotic floral modifications known as the "*mantled*" phenotype. The identification of molecular markers has been undertaken in order to discriminate as early as possible during the *in vitro* process those cell lines which are variant and also to better understand the mechanism leading to abnormal flower development. Since a DNA sequence mutation does not appear to be involved, but rather an epigenetic alteration, we chose to analyse differential gene expression patterns at the transcriptome level between variant and normal material. Four SSH libraries were constructed from oil palm cell suspensions and male inflorescences. Studies of transcript abundance by macroarray hybridization allowed the identification of a range of genes altered in their expression in abnormal tissues, several of which were subsequently validated by RT-PCR analysis. The relevance of the genes identified and the biological processes in which they may be involved will be discussed.