Epigenetic analysis of somaclonal variation in higher plants: Oil palm as a case study

Alain Rival¹, Estelle Jaligot², Thierry Beulé³, James Tregear⁴ and Jean Finnegam¹

1. CSIRO Plant Industry. GPO Box 1600. Canberra, Australia.
2. INRA, Université Montpellier II. 34000 Montpellier, France.

Background

Epigenetics is the study of heritable changes in gene expression that occur without a change in DNA sequence. In higher plants, these phenomena have economic relevance in the case of somaclonal variation: a genetic and phenotypic variation among clonally propagated plants from a single donor genotype.

In oil palm (Elaeis guineensis Jacq), approximately 5% of somatic embryo-derived palms show abnormalities in their floral development. This variant phenotype offers a very interesting model, because somaclonal variation alters the expression of genes coding, directly or indirectly, for the flower structure.

Studies on genomic DNA methylation changes induced by tissue culture together with results from long term field studies have suggested that epigenetic mechanisms play an important role in the determination of somaclonal variation in oil palm.

Aims

1. To use complementary approaches for the development of methylation-sensitive markers of epigenetic instability in regenerant palms,
2. To integrate these markers in a strategy aimed at the identification of in vitro treatments which are prone to generate epigenetic variability in somatic embryogenesis-based micropropagation processes

Results

Using MSAP (Methylation Sensitive Amplified Polymorphism) the methylation status of CCGG sites was studied in four distinct genotypes. Overall, 64 selective primer combinations were used and they have amplified 23 markers exhibiting a differential methylation pattern. Each of the 23 markers isolated in the present study could discriminate between the two phenotypes only when they were from the same genetic origin. Valuable information on putative target sequences will be obtained from the further characterization of these markers.

We are presently studying expression profiles of DNA Methyltransferases in normal and mantled material, in order to explore their part in the previously observed differences in global methylation rates.

Three different families of METases are being analyzed, namely: MET (maintenance of methylation at CG sites), CMT (methylation of heterochromatin DNA at CNG motifs) and DRM (methylation of isolated Cytosine).

Differences in global DNA methylation rates between normal and variant callus material could not be attributed to changes in MET or CMT expression. The isolation of full-length cDNAs of oil palm Methyltranferases from the three families is under way together with the study of DRM expression.

Conclusions

✓ The mantled somaclonal variation is oil palm is characterised by a sizeable hypomethylation of genomic DNA
✓ Methylation-sensitive DNA markers such as MS-RFLPs and MSAPs were found to provide genotype-dependant profiles which hampered their use in the early detection of somaclonal variation.
✓ Analysis of DNA-MTase expression suggest the presence of a post-transcriptional regulation of MET and CMT activities.