

Studying the epigenetic regulations of floral morphogenesis: the case of oil palm

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Plant development is controlled by a network of epigenetic regulations which are highly sensitive to environmental parameters, and it is thus susceptible to changes occurring during micropropagation and regeneration processes. As a case study, we found that approximatively 5% of somatic embryo-derived oil palms (*Elaeis guineensis* Jacq.) are affected by the 'mantled' somaclonal variation, involving a male-to-female conversion of floral organs. The epigenetic origin of this phenotype is now well established and we are now focusing on regulations occurring around candidate target sequences showing a varying expression pattern between normal and variant palms, and which putative functions point to a role in developmental regulation pathways. We propose to build upon the previous isolation of MADS-box floral homeotic genes and to undertake a comprehensive investigation of the epigenetic mechanisms controlling their expression and of their role in the onset and in the maintenance of the 'mantled' somaclonal phenotype. We will investigate modifications in DNA methylation patterns in regulating and coding sequences, chromatin conformation changes of surrounding genomic domains as well as the possible involvement of small non-coding RNA species. The proposed strategy will be, to our knowledge, the first attempt to address in vitro-generated epigenetic dysfunctions in a global way, from the cell culture to the field. Moreover, by providing a set of molecular tools derived from cutting-edge technologies, we will implement a monitoring/diagnostic approach to the crucial issue of phenotypic stability of micropropagated and transformed plants.

Keywords: epigenetics, flower development, DNA methylation, chromatin, small RNAs.