

Investigating the epigenetic regulation of reproductive development in the oil palm



F. Richaud¹, S. Adler², T. Beulé¹, P. Ilbert¹, A. Rival¹, E. Jaligot¹
 1 – CIRAD, UMR DIADE (IRD, UMSF) – Montpellier, France



2 – current address: UMR PVBMT (CIRAD, U. La Réunion) – St Pierre, La Réunion, France

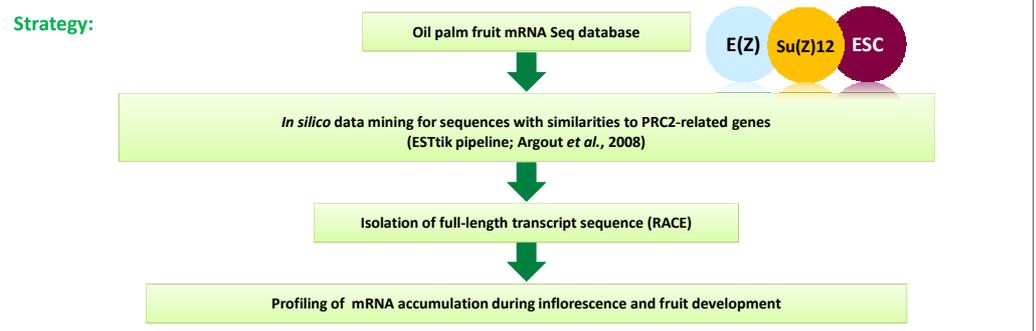
Context :
 The “mantled” somaclonal variation of oil palm alters flower and fruit morphogenesis in approximately 5% of the clonal regenerants and therefore leads to a decrease in oil production. This abnormality has been associated with a perturbation of epigenetic mechanisms characterized by a significant genome-wide hypomethylation (Jaligot *et al.*, 2000). In animals as well as in plants, Polycomb Group (PcG) proteins are essential actors of the epigenetic machinery regulating cell fate and transitions between developmental phases (Hennig and Derkacheva, 2009). Among PcG proteins, those involved in the Polycomb Repressive Complex 2 (PRC2) are known to target some of the MADS-box genes controlling floral organogenesis. Moreover, a functional analysis of the tomato genes encoding the components of the PRC2 has recently confirmed that this complex plays an important role in the development of the reproductive organs (How Kit *et al.*, 2010).



Figure 1: The « mantled » somaclonal phenotype of oil palm, as observed on fruits from somatic embryo-derived palms. From left to right: normal, (N) lightly « mantled » (LM) and severely « mantled » (SM) fruits.

Objectives:

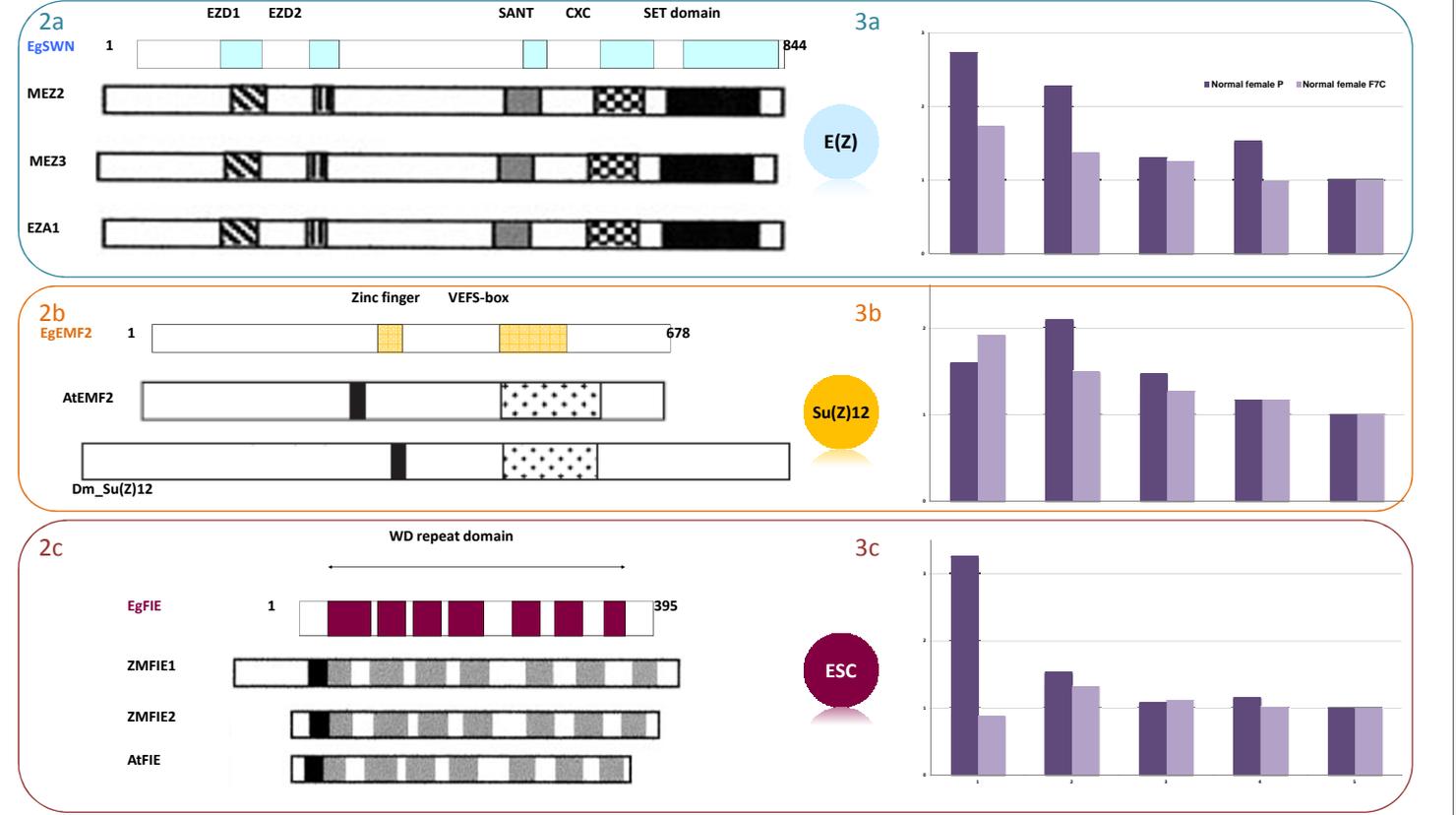
- to identify the oil palm orthologues of the PRC2 genes belonging to each of the three superfamilies: ENHANCER OF ZESTE [E(Z)], SUPPRESSOR OF ZESTE 12 [SU(Z)12] and EXTRA SEX COMBS [ESC];
- to characterize their expression during the course of inflorescence and fruit development.



Results:

Figure 2: Structural analysis of three oil palm putative PcG proteins (modified from Birve *et al.*, 2001 and Springer *et al.*, 2002). Sizes of the putative oil palm translation products are indicated in aminoacids, the structural domains have been identified through InterProScan analysis.

Figure 3: qPCR quantification of the PRC2-type transcripts during the development of the female oil palm inflorescence. Experiments performed in technical triplicates on inflorescences series sampled on two palms with different genotypes. The developmental stages of the inflorescence are labeled from 1 to 5 according to Adam *et al.*, 2005.



References:
 Adam *et al.*, 2005. American Journal of Botany 92:1836.
 Argout *et al.*, 2008. BMC Genomics 9:512. Birve *et al.*, 2001. Development 128,3371-3379. Hennig and Derkacheva, 2009. Trends in Genetics 25, 414-423. How Kit *et al.*, 2010. Plant Molecular Biology 74:201-213. Jaligot *et al.*, 2000. Plant Cell Reports 19,684-690. Springer *et al.*, 2002. Plant Physiology 128:1332-1345.

Conclusions & Perspectives :
 This study allowed us to identify putative members of PRC2 in oil palm. We have isolated putative orthologous genes for each family E(z), SUZ (12) and ESC displaying sequence similarities with the *Arabidopsis* genes SWN, EMF2 and FIE, respectively. The expression patterns of all three transcripts have been analyzed during the female oil palm inflorescence development and they all show stage-dependent accumulation. A similar study is currently being performed on the developing male inflorescence. This work provides a first step towards the elucidation of the role of the PcG genes in the reproductive development of the oil palm.