



# CDB SEMINAR

## Vincent Colot

Centre National de la Recherche Scientifique (CNRS), France

Tuesday, December 15, 2009

15:00~16:00 C1F CDB Auditorium

## RNAi-dependent DNA methylation of repeat elements and gene expression homeostasis in Arabidopsis

### Summary

DNA methylation is essential for silencing repeat elements and some genes in mammals and plants. While methylation is restricted to cytosines belonging to CG dinucleotides in mammals, it occurs also at CHG and CHH sites in plants (where H=A, T or C). Genetic studies have identified many of the factors involved in DNA methylation in the reference plant Arabidopsis. These factors include "maintenance" and "de novo" DNA methyltransferases (MTases), DNA demethylases, histone-modifying or remodeling enzymes, and RNA interference (RNAi) components. Epigenomic mapping has revealed two major patterns of methylation in the Arabidopsis genome. One is specific to most repeat elements and is defined by co-extensive CG, CHG and CHH methylation. The second is specific to part of the transcribed region of approximately 30% of genes, and is defined by CG methylation only. We have shown that although RNAi contributes little to the overall methylation of repeat elements in Arabidopsis, it plays an essential role in enabling their faithful remethylation after accidental methylation loss [1]. Following on from this study, we have uncovered an important function of RNAi in maintaining proper expression of a small number of genes located near methylated repeat elements. These findings will be presented and their implications for epigenetic regulation will be discussed.

### Host:

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### Reference

1. Teixeira FK, Heredia F, Sarazin A, Roudier F, Boccara M, et al. (2009) A Role for RNAi in the Selective Correction of DNA Methylation Defects. *Science* 323: 1600-1604.

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