Universität Basel

Research Project

Investigating the tissue specific epigenetic code in plants

Third-party funded project

Project title Investigating the tissue specific epigenetic code in plants
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Organisation / Research unit
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Department
Project start 01.02.2011
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Status Completed
Aims of this project: Epigenetics describes mechanisms by which gene expression patterns can be inherited through cell division (mitosis or meiosis) independently of the underlying DNA sequence. The aim of this project is to learn what are the different epigenetic states of different organs and tissues and more importantly, what are the molecular mechanisms that are controlling it.

Context and significance of the project: Epigenetics encompasses a variety of highly conserved molecular mechanisms that provide an additional layer of information superimposed on the genetic code. Epigenetic repression of transcription also plays an essential role in suppressing the activity of transposable elements, which could have deleterious effects on the host organism. This transcriptional repression can bring endogenous genes under epigenetic control when transposons integrate in their vicinity. This type of regulation of gene expression is very general and has been observed in prokaryotes and eukaryotes. While there are some reports proposing a tissue specific epigenetic code in plants this has so far not been investigated systematically. This research project will give fundamental insights into the mechanisms of epigenetic coordination of development and the role of transposons in this process.

Scientific context and methodology: The aim of this project is to gain understanding on how epigenetic states are set up and maintained in differentiated plant organs (such as roots, leafs, flowers and stems), individual tissues and cell lineages. In order to address this, Arabidopsis will be used as an established model system. The project will be based on an epigenetically controlled and highly tissue specific reporter transgene gene in Arabidopsis. This transgene leads to the expression of a green fluorescent protein (GFP) in specific tissues. In order to identify novel epigenetic factors that control tissue specific gene expression, plants have now been mutagenized and are currently being screened for new expression patterns. So far, more than 100 putative mutant plants with 7 different expression patterns have been identified. The project will now focus on mapping mutations to identify the genes involved using classical mapping approaches and whole genome sequencing. Developmental and molecular characterization of mutants will be carried out using state of the art technologies such as transcription profiling based on tiling arrays, genome wide DNA methylation analysis of individual tissues and biochemical approaches.

Keywords epigenetics, arabidopsis, tissue specific gene expression, DNA methylation, transposons, RNA silencing
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