



Mendel Centre Seminar



The Syntenic Network Pipeline (SynNets) Provides Insights into the Evolution of Plant MADS-Box Transcription Factors

03/11/2015

TUESDAY

start 16:00

delivered by

Seminar room 252, building A29

University Campus Bohunice

Kamenice 5, Brno

Prof. Dr. M. Eric Schranz

Department of Plant Sciences - Biosystematics, Wageningen University, The Netherlands

Hosted by doc. Mgr. Martin Lysák, Ph.D.

Abstract:

Conserved genomic context (synteny) can provide valuable information about the evolution of genes and genomes. However, frequent polyploidy and chromosomal rearrangements in plants complicate such analyses, particularly when analyzing large multi-gene families across broad phylogenetic groups. We have developed a pipeline, named Synet (synteny network pipeline), based on genomic gene collinearity between and within genomes. We use the completed genomes of fifty-one plant species to visualize genes by syntenic links allowing us to infer gene duplications resulting from polyploidy, transpositions and ancient tandem-arrangements. We present our analysis of the key transcriptional regulators of plants, the MADS-box gene family. By doing so, we can identify patterns not detected by phylogenetic analyses including several very ancient Type II tandem-gene clusters (e.g. SEP-SQUA/TM8/FLC) that predate the diversification of angiosperms, lineage specific gene transpositions (such as AP3, PI and FLC in Brassicales) and highly conserved Type I and MIKC* clusters involved in embryo and pollen development. These new insights provide new hypotheses about the function and evolution of these key developmental regulators and the of plant phenotypes.