



Mendel Centre Seminar



Alternative splicing in the cold temperature response of Arabidopsis: an RNA-seq approach

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start 16:00

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Seminar room 252, building A29
University Campus Bohunice
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Abstract:

Alternative splicing (AS) has been implicated in a wide range of developmental and physiological processes. We have shown that AS is important in regulating expression of key circadian clock genes and mediating the response of the clock to changes in temperature. The circadian clock is a cellular mechanism able to organize many physiological processes in anticipation/preparation to daily and seasonal changes. AS may therefore have roles in temperature perception, entrainment, compensation, regulation of downstream physiological responses and acclimation to exposure to low temperature. We have generated data to build transcription and splicing networks to identify genes that may regulate alternative splicing of core clock genes at low temperature. It also represents a high resolution time-course of the response of plants to cold. We are using Salmon to analyse the RNA-seq data and quantify transcripts. To use Salmon, we have developed a comprehensive, non-redundant Reference Transcript Dataset (AtRTD) covering more than 33,000 genes and 75,000 transcripts and we are currently improving this by incorporating transcripts from the assembly of nearly 9 Bn reads. The AtRTD allows us to analyse expression at the level of individual transcripts. We have very good correlation between the individual transcript abundances and experimental data from our high resolution RT-PCR system (Spearman's correlation coefficient = 0.902). The dynamic time-course data of individual transcripts has allowed the identification of genes which are regulated only by transcription, genes which are regulated only by AS and genes which are regulated by both. We have identified genes with major changes in AS in response to cold, including isoform switches that occur rapidly after transfer to cold.