

## Towards a programming code of circadian clock in plants

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Transcriptomics offers the opportunity for comprehensive analysis of clock mediated processes. However, the ability to identify circadian genes with confidence remains elusive and this has been limited by the lack of a non-biased method suitable for identification of circadian genes from relatively short time course transcriptomic data. We have developed a non-biased principal component analysis pipeline for exploration of high-dimensional genome-wide data and for extraction of time dependent patterns of expression change. This is achieved through representation of the cycles through global optimization, which preserves the topology of the patterns present in a highly dimensional Euclidian space. Circadian gene expression rhythms were analyzed across plant species and consistent conserved dominant profiles of circadian gene expression were detected presumed to be, global properties of the circadian system in plants. Mining circadian microarray time course data in this way carries the potential to decipher the higher order structure of cis regulatory modules in plants. We present a novel model for learning from expression data that allows for classification of circadian genes, based on combinatorial combinations of promoter motifs. Conserved dominant profiles of circadian gene expression were detected corresponding to 4 cohesive, regulatory modules that are consistent across plant species. The study, therefore, breaks new ground in the way the circadian clock is perceived in plants and how the dynamic code results in a stable phenotype.