

Functional characterization of genes with daily expression patterns in common wheat

Kiseleva A.A.^{1, 2*}, Salina E.A.^{1, 2}

¹ Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

² Kurchatov Genomic Center of the Institute of Cytology and Genetics, SB RAS, Novosibirsk, Russia

* antkiseleva@bionet.nsc.ru

Key words: common wheat; RNA-seq; daily expression pattern; circadian rhythms

Motivation and Aim: Plant circadian rhythms represent daily changes in the activity of various processes, which are based on changes in the levels of gene expression and protein synthesis. In wheat, some key components of plant circadian clock have been identified, but there is little data on the daily expression and interactions of these genes.

Methods and Algorithms: Common wheat cultivar Chinese Spring (CS) plants were cultivated for 21 days post-germination in controlled conditions with short days. Samples were harvested at 0, 3, 9, and 16-hour intervals over 24 hours, reflecting various stages of the light cycle. RNA was extracted and sequenced using a NextSeq 550 sequencer, resulting in over 420 million sequences deposited in the Sequence Read Archive NCBI database. Transcript mapping to the reference bread wheat genome and assembly were performed, followed by expression level assessment and normalization. Rhythmic gene expression analysis was conducted using JTK-CYCLE and Cosinor algorithms, with subsequent module separation using the R CemiTool package. Functional enrichment analysis was carried out using AgriGOv2.0 and g:Profiler, with visualization provided by the REViGO web server.

Results: In this work, for the first time, a comprehensive analysis of the daily transcriptome of common wheat was performed. There were 1421 genes with daily expression pattern divided into 5 modules according to their expression peak. The largest number of genes was expressed at the evening time point. GO enrichment analysis revealed biological processes in each module. The results indicated that plants prepare for sensing signals from the environment (predominantly light stimuli) at the end of the night before the light is turned on. During the day and in the evening, plants actively synthesize and accumulate different metabolites, including carbohydrates, lipids and a number of secondary metabolites. These processes are aimed at the active growth and development of plants. During the night period, all processes decrease; plants have a “rest”. A comparison of daily expression patterns of genes of the central oscillator of common wheat with homologous genes of *Arabidopsis* demonstrated that wheat has homologs for most key circadian genes of *Arabidopsis*. Most of them were represented by three homoeologous genes. The expression patterns of core loop genes coincided, indicating a similar functional role of these genes in wheat. Although the expression patterns of some accessory genes were different compared to *Arabidopsis*, the whole mechanism of the central oscillator was uniform while changing the individual parts.

Conclusion: Thus, one can assume a high level of conservatism of the system of circadian clock in different plant species.

Funding: The study is supported RNA sequencing was funded by the RSF (Russian Science Foundation) project No. 21-76-30003.