

## 139. Systems Level Regulation of Rhythmic Growth Rate and Biomass Accumulation in Grasses

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**Project Goals: The overall goal of this project is to understand the transcriptional regulation of biomass accumulation, which occurs during a specific time of day. Our aims are to (1) Identify growth-associated genes by temporal transcriptome analysis of developing *Brachypodium distachyon*. (2) Ascertain the time of maximum plant growth and cues that determine that timing through real-time imaging of *Brachypodium* growth. (3) Identify molecular regulatory circuits for biomass accumulation by screening for transcription factor interactions with promoters of growth-associated genes. (4) Determine the functional role of genes that modulate biomass accumulation.**

Plant growth is commonly regulated by external cues such as light, temperature, water availability, and internal cues generated by the circadian clock. Changes in the rate of growth within the course of a day have been observed in the leaves, stems, and roots of numerous species. We examined the influence of diurnal temperature and light changes, and that of the circadian clock on leaf length growth patterns in *Brachypodium distachyon* using high-resolution time-lapse imaging. Pronounced changes in growth rate were observed under combined photocycles and thermocycles or with thermocycles alone. A considerably more rapid growth rate was observed at 28°C than 12°C, irrespective of the presence or absence of light. Despite evidence of circadian clock regulated gene expression, plants exhibited no change in growth rate under conditions of constant light and temperature or under photocycles alone. Therefore, temperature primarily drives oscillations in growth rate, which is not impacted by the circadian clock or by photoreceptor activity. Furthermore, temperature did not affect leaf meristem size or final cell length. Therefore, the nearly five-fold difference in growth rate observed across thermocycles can be attributed to proportionate changes in the rates of cell division and expansion. To better understand relative contributions of diurnal and circadian factors on gene expression changes, we analyzed the *B. distachyon* transcriptome in three conditions: photocycles and thermocycles, thermocycles alone, and constant light and temperature. Overall, we found ~9,000 genes exhibit cyclic expression in any one condition. Furthermore, far fewer genes are cyclic in free-running conditions in *B. distachyon* in comparison to *Arabidopsis thaliana*. Circadian clock regulated genes cycled with lower amplitude and longer periodicity, indicating a looser control of the clock on gene expression. Together, these data suggest fundamental differences between diurnal control of gene expression between cereals and dicots, especially with regard to temperature. Interestingly, the expression of cellulose and lignin genes was lowest in warm conditions; thus, negatively correlated with leaf elongation. Based on coexpression, we have identified candidate genes for the transcriptional regulation of temperature specific growth and biomass accumulation. A better understanding of the growth cues in *B. distachyon* will further our ability to model metabolism and biomass accumulation in grasses.

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