

Molecular basis and regulation of circadian rhythms in plants

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Dr. C. Robertson McClung and his colleagues are investigating the genetic basis and molecular mechanisms of circadian cycling and regulation in plants. Dr. McClung, of the Department of Biological Sciences, Dartmouth College, will be presenting this work at the President's symposium of the annual meeting of the American Society of Plant Biologists in Mérida, Mexico.

Clock genes have been identified in mammals, *Drosophila*, fungi, and cyanobacteria and their oscillatory mechanisms analyzed with studies of mutants. Many of these genes are conserved across taxa, but plants appear to have a novel mechanism.

McClung and other scientists have shown that, in the model organism *Arabidopsis*, members of the PRR (pseudo-response regulator) gene family are integral parts of several oscillatory loops that may affect carbon fixation, stem elongation, biomass, flowering time, and survival. In particular, McClung and his co-workers showed that PRR7 and PRR9 are critical for responses to temperature, although they appear to function in other circadian cycles as well.

It is not accidental that the members of the PRR family are transcribed from DNA to RNA at different times of day, suggesting that the protein products function in processes that are coordinated with diurnal events. Thus, one of the mechanisms of clock gene regulation is the control of transcription and accumulation of RNA transcripts. Other forms of regulation are post-translational—after the clock gene proteins have

been made. These proteins are translocated to different compartments to perform their functions, have phosphate groups attached to them to change their activity, or are marked for degradation—all precisely timed for optimal function.

With mutant analyses, McClung and his coworkers have shown that the PRR genes do not act in isolation, but rather are integrated and overlapping in function. Double and triple mutants have effects that are not simply additive but are much larger than those of single mutants. This suggests that it is adaptive for plants to have a group of genes, each with a small effect, but when functionally linked with other genes, part of a precise mechanism capable of subtle and specific responses, like the interlocking wheels of a clock.

McClung and his colleagues are studying how such mechanisms could have evolved. Through sequence analysis of PRR7 in over 100 different cultivars of *Arabidopsis*, they have shown that the nucleotides in the gene's DNA are replaced at a significant rate, resulting in greater genetic variation at this locus (chromosomal region). If plants have to respond to different conditions of light and temperature at different locations, then it makes sense for different varieties of the same plant to have slightly different forms (alleles) of the gene. Similar mutations in other clock genes will then result in the evolution of many clocks and circadian rhythms keyed to local conditions—the plant equivalent of time zones.

The scientists are now also examining the clock genes in other plants and have found quantitative trait loci (QTLs) for these genes in the model crop species *Brassica rapa* (rapeseed). QTLs are chromosomal regions containing closely related genes that all influence a trait, resulting in, for example, a range of heights or eye color. Such loci are consistent with multiple interlocking genes in the clock mechanisms of circadian rhythms.

The knowledge of circadian rhythms in animals is being used in medicine to facilitate drug delivery and cancer treatments. Understanding the clock genes through which plants interact with their environments can aid in engineering crops and cultivars for higher productivity, as well as adaptation of foreign plants to new environmental conditions.

Source: American Society of Plant Biologists

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