

## **A synthetic approach to parse gene regulatory logic in plant development**

Edith Pierre-Jerome and Philip N. Benfey

Department of Biology, Duke University, Durham, NC 27708, USA;  
Howard Hughes Medical Institute, Duke University, Durham, NC 27708, USA  
[edith.pierre.jerome@duke.edu](mailto:edith.pierre.jerome@duke.edu)

Transcription factors form intricate regulatory networks to execute coordinated programs of gene expression. These programs of gene expression shape cell identity by modulating a cell's capacity to perceive and respond to intrinsic and external cues. Recurring patterns of interactions between transcription factors and the genes they regulate, known as network motifs, have been posited to perform information processing functions that translate a signal into specific changes in gene expression.

One of the most prevalent motifs in gene regulatory networks is the feed-forward loop (FFL). In a coherent FFL, one transcription factor activates a second transcription factor, and both activate a third target gene. In *Arabidopsis*, the transcription factors *SHORTROOT* and *SCARECROW* regulate numerous targets in a feed-forward manner. One key target is *CYCLIN D6*, a cell cycle gene that drives asymmetric cell division to form the two distinct layers of the ground tissue. However, the feed-forward circuit that regulates *CYCLIN D6* is embedded within the elaborate *SHORTROOT-SCARECROW* gene regulatory network.

To directly test the function of a transcriptional FFL in early plant development, I am building a synthetic FFL to regulate *CYCLIN D6* independent of the endogenous network. I am characterizing how promoter architecture and physical interactions between two synthetic transcription factors can be used to modulate gene regulatory logic to generate FFL variants and simpler derivatives. By integrating these synthetic circuits in the multicellular context of a developing seedling, direct connections between molecular circuit form and function can be elucidated and enhance our fundamental understanding of complex gene regulation.