Porting the Auxin Signaling Pathway to Yeast

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AUXIN is involved in many aspects of plant growth, development, and behavior. Different cell types in the plant respond to the same auxin signals in different ways, but use essentially the same machinery: auxin-activated F-box receptors (AFBs) that facilitate degradation of transcriptional co-repressors (IAAs) to relieve repression of transcription factors (ARFs). By combining different AFBs, IAAs, and ARFs, the plant seems to create cell specific signal processing circuits that may account for the diversity of auxin responses observed. How exactly these circuits work is not known, however, primarily because most of what *is* known about the above families of genes is via indirect assays that estimate protein interactions and/or affinities but not dynamic quantities such as frequency response or signal-to-noise ratios. In joint work with Prof. Jennifer Nemhauser's group, we have begun the process of porting the auxin signaling pathway from *A. thaliana* to *S. cerevisiae* (yeast), which provides a compatible ubiquitin pathway required by the AFBs, but which is otherwise a "blank slate" it terms of auxin signaling. In yeast we can isolate individual parts and small combinations of parts to obtain high-resolution, single-cell time-series of their responses to auxin signals. In my talk, I will describe our work in reconstructing several functioning circuits consisting of one or more AFBs, IAAs, and/or ARFs that shed light on how such a diversity of behaviors can be produced from such a small set of components, and which provide new parts and methods for synthetic biology.