

# Engineering with auxin: characterization of a synthetic signal processing toolbox

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**Short Abstract** — Auxin is a small signaling molecule involved in almost every aspect of plant growth and development. A network composed of three core components initiates translation of this hormone signal into different cellular responses. These components belong to large gene families and the specific combination of components expressed in a given plant cell is thought to determine the auxin response of that cell. We have successfully ported the core components of the auxin network into yeast to study their dynamic responses in isolation. We identified a mathematical model able to quantitatively describe the interaction between two of the components with a single parameter. By characterizing additional interactions, we can create a design framework for more complex synthetic networks, with the aim of engineering multi-cellular behavior in yeast.

**Keywords** — auxin gene network, orthogonal organism, synthetic biology, model discrimination, parameter reduction.

## I. INTRODUCTION

AUXIN is a small signaling molecule that directs many aspects of plant development as well as responses to environmental cues, yet it remains unresolved how specificity is encoded. Specificity is hypothesized to be generated by expression of different combinations of the three core signaling components: ARF transcription factors (23 variants in *A. thaliana*), which bind to and regulate downstream promoters; Aux/IAA co-receptors (29 variants), which inhibit ARF activity [1,2,3]; and the F-box receptors (AFBs, 6 variants), which bind Aux/IAs in the presence of auxin, targeting them for destruction through ubiquitination, and relieving inhibition on the ARF proteins [4, 5].

Because of the difficulty of characterizing auxin signal transduction in plants, previous studies focused on characterizing individual interactions. However, these results do not illuminate the full pathway dynamics. Using a synthetic approach, we ported the pathway into an orthogonal organism (*S. cerevisiae*) to study the dynamic output of components. This synthetic system has several

advantages such as precise control of auxin input levels, the ability to study IAA|AFB pairs in isolation, and the absence of extraneous factors that affect the auxin signaling pathway.

## II. RESULTS

Experimental data qualitatively showed a wide range of degradation among the IAA|AFB pairs. Specifically, we observed that the choice of receptor protein has the biggest impact on degradation rates. To quantify our observations, we evaluated a variety of models to identify the one that best captures the dynamic auxin response in both time-course and dose-response experimental data. The resulting model, a second-order nonlinear set of ODEs, distills the degradation dynamics into a single parameter. This parameter, the degradation rate, is consistent with the qualitative behaviors observed in experimental data. For example, the fastest degrading IAA|AFB pair had the highest parameter value.

## III. CONCLUSION

This simple description of a complex interaction, combined with previously defined protein interaction kinetics [6], revealed that binding affinity alone does not determine the degradation dynamics. Additionally, the collection of degradation rates provides us with a useful data-sheet describing the tunability of the IAA|AFB module. Using this data-sheet, we can rationally design, test, and build synthetic auxin signaling pathways that can give rise to novel behaviors in yeast.

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Acknowledgements: This work was funded by the Paul G. Allen Family Foundation, NIH Training Grant T32HD007183, NSF Graduate Fellowship, the ARCS Foundation, and National Science Foundation grants CISE-0832773 and IOS-0919021.

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