Systems and Synthetic Biology

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Recently developed Open Tools and Resources for Arabidopsis Researchers


A library of synthetic transcriptional regulators (activators, repressors and promoters) that modulate expression strength in planta.


A species-independent, web-based platform that integrates genome-wide stdies of TF-target binding, TF-target regulation and other TF-centric omic datasets and uses these to build and refine validated or inferred gene regulatory networks.


Phytobricks are standardized DNA parts for plants that can be assembled hierarchically into transcriptional units and multigene constructs. This protocol describes Phytobrick design and construction and their assembly in manual and nanoscale automated one-step reactions as well as high-throughput sequence verification of assembled plasmids.


The authors generated and validated 18 promoter::luciferase and suggest an experimental setup for high-throughput analysis. They recommended novel markers for the analysis of auxin, abscisic acid, cytokinin, salicylic acid and jasmonic acid responses.


Prediction of causal gene regulatory relationships based on time series data as well as known network edges and steady-state data. The method across different species has improved predictive accuracy over other state-of-the-art methods.
**Recent or Future activities of Subcommittee members**

(i) (Plant session at) 4th German Conference on Synthetic Biology, 24 & 25 September 2020, Virtual

(ii) 4th International Conference on Plant Synthetic Biology, Bioengineering, and Biotechnology October 30 - November 1, 2020, Virtual

(iii) Cold Spring Harbor Network Biology Meeting; March 16-19, 2021; Virtual; Organizers included Pascal Falter-Braun, a member of this subcommittee

(iv) Second iPSB: EMBO Workshop on International Plant Systems Biology: April 26-27, 2021; Main Organizers: Katherine Denby and Miriam Gifford

(v) 31st March 2021 Plantae SynBio, Virtual

**Selected Publications**


A systems-level map of the Arabidopsis phytohormone signalling network.

Capture of stable and transient TF-target interactions of NLP7, a master regulator of the nitrogen signaling pathway, using time-series ChIPseq and DamID-seq. These approaches can be applied to validate dynamic GRN models for any pathway of interest.


Design of a suite of synthetic promoters of different strengths that can regulate the relative expression of output genes in simple genetic devices.


Identification of gene networks activated by two immunity elicitors (flg22 and Pep1) in epidermis cortex and pericycle cells of Arabidopsis. A tool to analyze paired transcription factor binding motifs was also developed.


A PXY-mediated transcriptional network was mapped which revealed a feedforward loop incorporating WOX14, TMO6 and LBD4. These integrate both auxin and PXY signaling to determine the phloem-procambium boundary in vascular tissue.

Planning for Fourth Decadal Roadmap.

(i) Translation of Arabidopsis research to crop plants – including close relatives like other Brassicas, and other relatives like tomato and more distantly related dicots

(ii) Model-guided predictable engineering of complex traits.

(iii) Spatial and temporal dynamics in plant biology.