Y1H Services Core's Approach for Authorships/Collaborations for Publications

The purpose of the Yeast One-Hybrid (Y1H) Services Core facility is to carry out high-throughput mating-based yeast assays to screen for protein (transcription factor)—DNA (promoter or regulatory region) interactions. The core currently provides a screening service between promoters and collections of Arabidopsis, maize, and sorghum transcription factors. Each screening takes months of research and requires special technical expertise. Furthermore, we have developed expertise in this field of research and established the inhouse transcription factor collections over many years of hard work (using our own lab's research grant money and start-up).

This service was initially developed due to the request for collaboration from the plant biology community internationally. In the beginning, over the period of several years, the Brady Lab collaborated with these groups, but the cost of materials, service contract support for the Singer ROTOR robot and labor became overwhelming and far beyond our research budget. To the best of our knowledge, this Yeast One-Hybrid Services Core facility is the only such facility in the world. Thus, instead of ceasing these collaborations, we began a service core, asking our collaborators to cover, at-cost, these supplies and associated labor. Despite this arrangement, we still work with our customers to design experiments, guidance on promoter cloning and prey choice, as well as interpretation of results.

We are very excited and proud that research produced directly from this facility has been published in multiple publications. Find a list of these manuscripts below.

In the great majority of screens we have carried out for customers, we have been included as authors on these manuscripts. We have contributed to the writing of the manuscript, not just in terms of methods, but also in placing results in the context of current systems biology/network analysis literature. This has been particularly advantageous when considering common criticisms that reviewers make when considering network manuscripts/analyses, particularly using this methodology. Furthermore, we have been actively involved in each of these cases with the review process for all these manuscripts by answering comments about methodology or network analyses.

We acknowledge that there are differences in how one views authorship contribution. As a customer you have the right to choose if you prefer to proceed independently without shared authorship, and forego our group's contribution in terms of writing. If you prefer to go this route, we ask you to mention our services and the work performed in the acknowledgements of your publications. This will support our work and ensures that we may continue to provide and improve our services offered. Please add a sentence like this to your acknowledgements: "The Yeast one-hybrid screening was carried out by the Yeast One-Hybrid Services Core at the UC Davis Genome Center, at the University of California, Davis."

However, if you feel the work and results provided were essential in bringing your manuscript to fruition, please recognize our contributions by including us as an authors. We greatly enjoy working with our customers to place results in the context of the literature and sharing our knowledge and ideas amassed over the last decade. For a more detailed discussion of authorships when using a core facilities, please have a look at the ABRF Authorship Guidelines: https://abrf.org/authorship-guidelines. These are the community standards most core facilities follow when there are questions about authorship.

Research produced directly from the Yeast One-Hybrid Services Core facility has been published in several journals:

Antoine Nicolas, Aude Maugarny-Calès, Bernard Adroher, Liudmila Chelysheva, Yu Li, Jasmine Burguet, Anne-Maarit Bågman, Margot E Smit, Siobhan M Brady, Yunhai Li, Patrick Laufs. (2022). De novo stem cell establishment in meristems requires repression of organ boundary cell fate. *The Plant Cell*. Volume 34, Issue 12, Pages 4738-4759, https://doi.org/10.1093/plcell/koac269.

Tang M, Li B, Zhou X, Bolt T, Li JJ, Cruz N, Gaudinier A, Ngo R, Clark-Wiest C, Kliebenstein DJ, Brady SM. (2021). A genome-scale TF-DNA interaction network of transcriptional regulation of Arabidopsis primary and specialized metabolism. *Molecular Systems Biology*. 17(11):e10625.

Truskina et al. (2021). A network of transcriptional repressors modulates auxin responses. *Nature*.

Smit ME, Llavata-Peris CI, Roosjen M, van Beijnum H, Novikova D, Levitsky V, Sevilem I, Roszak P, Slane D, Jurgens G, Mironova V, Brady SM, Weijers D. (2020). Specification and regulation of vascular tissue identity in the *Arabidopsis* embryo. *Development.* 147(8): dev186130.

Li B, Tang M, Caseys C, Nelson A, Zhou M, Zhou X, Brady SM, Kliebenstein DJ. (2020). Epistatic Transcription Factor Networks Differentially Modulate *Arabidopsis* Growth and Defense. *Genetics.* 214(2):529-541.

Dickinson et al. (2020). A bipartite transcription factor module controlling expression in the bundle sheath of *Arabidopsis thaliana*. *Nature Plants*.

Smit et al. (2019). A PXY-Mediated Transcriptional Network Integrates Signaling Mechanisms to Control Vascular Development in Arabidopsis. *The Plant Cell*.

Gaudinier et al. (2018). Transcriptional regulation of nitrogen-associated metabolism and growth. *Nature*.

Sakamoto et al. (2018). Complete substitution of a secondary cell wall with a primary cell wall in Arabidopsis. *Nature Plants*.

Ikeuchi et al. (2018). A Gene Regulatory Network for Cellular Reprogramming in Plant Regeneration. *Plant and Cell Physiology*.

Gaudinier A., Tang M, Bågman AM, Brady SM. (2017). Identification of Protein-DNA Interactions Using Enhanced Yeast One-Hybrid Assays and a Semiautomated Approach. *Methods in Molecular Biology* 1610:187-215.

Gaudinier A. and Brady SM. (2016) Mapping Transcriptional Networks in Plants: DataDriven Discovery of Novel Biological Mechanisms. *Annual Reviews of Plant Biology* 67:575-594.

Sparks et al. (2016). Establishment of Expression in the SHORTROOT-SCARECROW Transcriptional Cascade through Opposing Activities of Both Activators and Repressors. *Developmental Cell*.

Murphy et al. (2016). RALFL34 regulates formative cell divisions in Arabidopsis pericycle during lateral root initiation. *Journal of Experimental Biology*.

Porco et al. (2016). Lateral root emergence in Arabidopsis is dependent on transcription factor LBD29 regulation of auxin influx carrier LAX3. *Development*.

Taylor-Teeples et al. (2015). An Arabidopsis gene regulatory network for secondary cell wall synthesis. *Nature*.

Koryacho et al. (2015). Clustering and Differential Alignment Algorithm: Identification of Early Stage Regulators in the *Arabidopsis thaliana* Iron Deficiency Response. *PLoS ONE*.

Li et al. (2014). Promoter-based integration in plant defense regulation. *Plant Physiology*.