LOF1 and Interacting Transcription Factors in Plant Development and Crop Yield

Zoe Yeoh  
*Gettysburg College*

Elizabeth Luscher  
*University of California, Riverside*

Patricia Springer  
*University of California, Riverside*

Follow this and additional works at: [https://cupola.gettysburg.edu/student_scholarship](https://cupola.gettysburg.edu/student_scholarship)

Part of the [Biology Commons](https://cupola.gettysburg.edu/biology), [Cell Biology Commons](https://cupola.gettysburg.edu/cell-biology), and the [Plant Biology Commons](https://cupola.gettysburg.edu/plant-biology)

*Share feedback about the accessibility of this item.*

Yeoh, Zoe; Luscher, Elizabeth; and Springer, Patricia, "LOF1 and Interacting Transcription Factors in Plant Development and Crop Yield" (2016). *Student Publications*. 506.  
[https://cupola.gettysburg.edu/student_scholarship/506](https://cupola.gettysburg.edu/student_scholarship/506)

This is the author's version of the work. This publication appears in Gettysburg College's institutional repository by permission of the copyright owner for personal use, not for redistribution. Cupola permanent link: [https://cupola.gettysburg.edu/student_scholarship/506](https://cupola.gettysburg.edu/student_scholarship/506)

This open access poster is brought to you by The Cupola: Scholarship at Gettysburg College. It has been accepted for inclusion by an authorized administrator of The Cupola. For more information, please contact cupola@gettysburg.edu.
LOF1 and Interacting Transcription Factors in Plant Development and Crop Yield

Abstract
Transcription factors (TFs) help ensure proper gene expression in developing tissues, and thus play a role in plant development and plant architecture. LATERAL ORGAN FUSION1, or LOF1, is a TF expressed in the organ boundaries of Arabidopsis thaliana. lof1 mutants have fused axillary branches and cauline leaves, which indicates importance in boundary development. Because transcription factors are known to act in complexes, we wanted to discover what other proteins interact with LOF1. We executed a yeast-2-hybrid (Y2H) screen that identified several TFs as potential interactors: WHIRLY 3 (WHY3), MYB DOMAIN PROTEIN32 (MYB32), HOMEOBOX-LEUCINE ZIPPER PROTEIN4 (HB4), and LIGHT RESPONSE BTB2 (LRB2). WHIRLY1 (WHY1) and HOMEOBOX ARABIDOPSIS THALIANA3 (HAT3) are thought to be redundant with WHY3 and HB4, respectively, and are included in our study. To gain evidence that the interactions between the potential protein interactors and LOF1 is biologically relevant in planta, we will characterize T-DNA insertion lines in which the genes that encode these interactors are disrupted. Our goal is three-fold: genotype the T-DNA lines to identify homozygous mutants; characterize the phenotypes of these mutants and compare to known phenotypes; and create double- and triple-mutants between lof1 and the other TFs. Because the boundary region is involved in determining leaf angle and leaf angle affects planting density, changes in leaf angle have the potential to impact crop yield. In the future, we may be able to apply the knowledge we obtain in the model plant Arabidopsis thaliana to crop species in order to improve crop yield.

Keywords
molecular biology, plant research, PCR, LOF1, transcription factors

Disciplines
Biology | Cell Biology | Plant Biology

Comments
Research funded by the National Science Foundation REU Program. Presented at the 2017 Emerging Researchers National Conference in Washington, D.C., the 2016 University of California-Riverside Center for Plant Cell Biology Research Experience for Undergraduates Symposium, and at the Undergraduate Research on the Cycle (UROC) during Gettysburg College’s Year of Food (2016-2017).
LOF1 and Interacting Transcription Factors in Plant Development and Crop Yield

Zoe C. Yeoh¹, Elizabeth Luscher², Patricia Springer²
¹Department of Biology, Gettysburg College, Gettysburg, PA
²Center for Plant and Cell Biology, University of California, Riverside, CA

Introduction

Transcription factors (TFs) help ensure proper gene expression in developing tissues, playing a role in plant development and plant architecture. LATERAL ORGAN FUSION1, or LOF1, is a TF expressed in organ boundaries of Arabidopsis thaliana. Because TFs are known to act in complexes, we want to discover what other proteins interact with LOF1. A yeast-2-hybrid (Y2H) screen identified several potential protein interactors (listed below). To explore the role of these proteins in LOF1-related processes in planta, we obtained T-DNA insertion lines of the genes that encode these proteins. Because the boundary region is involved in determining leaf angle and leaf angle affects planting density, understanding how boundary proteins interact to affect leaf angle has the potential to improve crop yield.

**lof1 mutant phenotype**

*lof1* mutants have fusion between the axillary branch and cauline leaf and abnormal boundary cell division and growth.

**Genotyping T-DNA Insertion Lines**

Plants were genotyped using Polymerase Chain Reaction (PCR) to identify homozygous mutants.

1. Gene-specific primers amplify wild-type product if wild-type allele is present; T-DNA primer and one gene-specific primer amplify T-DNA product if insertion allele is present.

2. Comparison of amplified PCR products from both reactions indicates the genotype of the plants tested (example).

**T-DNA Insertion Site Identification**

- Insertions sites were confirmed via sequencing of PCR products containing genomic DNA flanking left border.

**HOMEOBOX ARABIDOPSIS THALIANA 3 (HAT3)**

**HOMEOBOX-LEUCINE ZIPPER PROTEIN 4 (HB4)**

**LIGHT RESPONSE BTB 2 (LRB2)**

**MYB DOMAIN PROTEIN 32 (MYB32)**

**WHIRLY 1 (WHY1)**

**WHIRLY 3 (WHY3)**

*Insertions sites were sequenced.

**Experimental Design**

Semi-quantitative RT-PCR was used to determined the level of transcript in homozygous mutants. Intensity of band correlates to the level of mRNA transcript accumulated. Lack of a band from *lrb2-2* suggests that it is likely a null allele.

**Future Directions**

- Create double and triple mutants between *lof1* and the homologous T-DNA mutants identified in this study
- Resulting phenotypes will give support for LOF1-interacting TFs’ involvement in LOF1 processes
- Gain a better understanding of how LOF1 functions
- May be able to apply this knowledge to crop species to improve crop yield

**Acknowledgements**

This work was supported by the National Science Foundation REU grant 1461297 to the UC-Riverside Center for Plant Cell Biology.


Contact Info:
Zoe Yeoh, yeohzo01@gettysburg.edu
300 North Washington Street, Gettysburg, PA 17325