Tafazzin Mutants Exhibit Differential Gene Expression in *Arabidopsis thaliana*

Cole Hayden,[1,3] Ruth Welti,[1,3] Zolian Zoong Lwe[2,3]

[1]Kansas State University, Division of Biology, [2]Kansas State University, Department of Biochemistry and Molecular Biophysics, [3]Kansas State University, Kansas Lipidomics Research Center

Tafazzin is a mitochondrial protein

- Tafazzin is an inner membrane mitochondrial protein that remodels the fatty acids of cardiolipin.
- Tafazzin is necessary for optimal electron transport chain function.
- Tafazzin is best characterized in mammals and yeast, but a homolog of taffazin was discovered in the model plant organism *Arabidopsis thaliana*.
- A tafazzin knockout mutant exhibits premature senescence (leaf-yellowing) (see images below).

Wild Type (WT)

Wild type plant at appr. 60 days after planting

Knockdown (KD)

Plant with knockdown mutation at appr. 60 days after planting

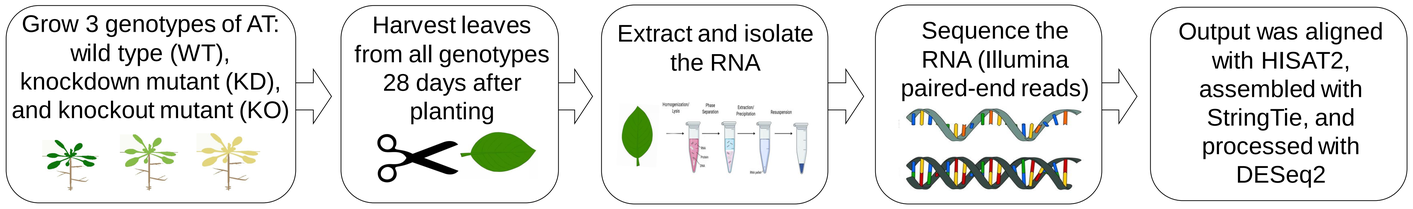
Knockout (KO)

Plant with knockout mutation at appr. 60 days after planting

Research Questions

1. How are genes differentially expressed when a cell has tafazzin deficiency?
2. What biochemical networks and pathways are associated with senescence when the cell has a tafazzin deficiency?

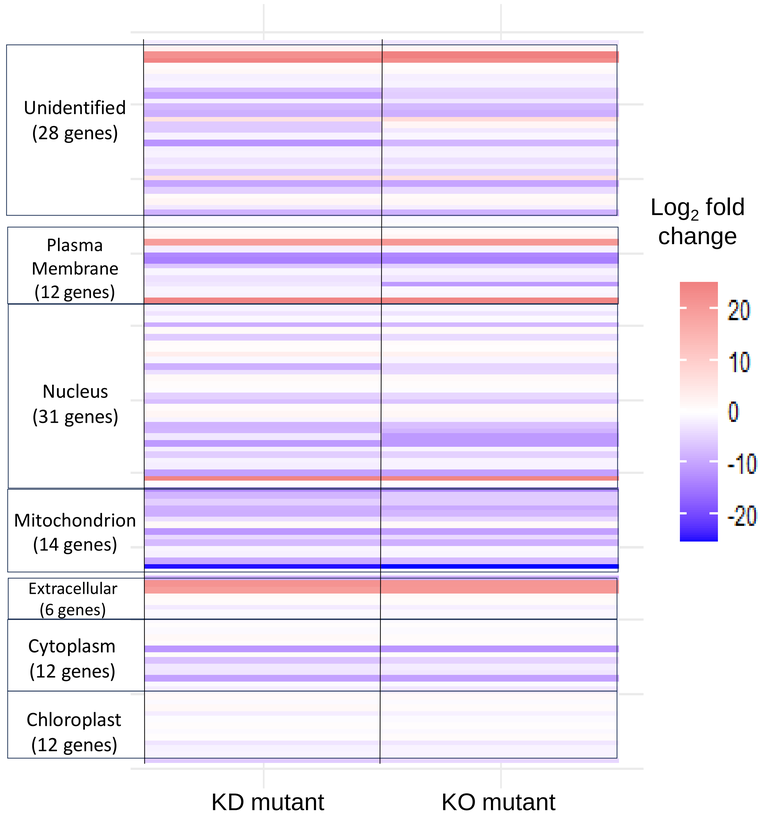
Methods



Results

Fig. 1: KO and KD mutants v. WT

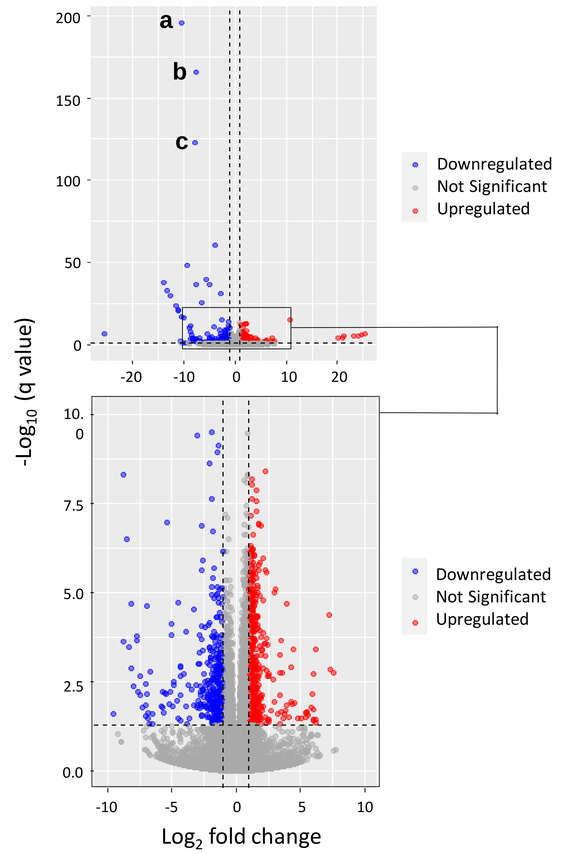
Log_2 fold change of all significantly differentially expressed genes in both mutants compared to WT, grouped by gene ontology term.



All (n = 123) genes whose q scores met the requirements of statistical significance (α = 0.05). Only cellular component gene ontological terms with 6 or more corresponding genes are labeled.

Fig. 2: KO mutant v. WT

Log_2 fold change vs $-log_{10}$ q value of gene expression in the KO mutant compared to WT.



Significance is defined as α = 0.05 and $|log_2$ fold change$| > 1$. A total of 25,838 genes are depicted above. 978 genes meet this definition of significance, although 3,205 genes meet the standard of statistical significance set by the alpha level when fold change is not considered.

Summary of Findings

Tafazzin mutants show **significant differential gene expression** in genes corresponding to gene products localized to **several cellular locations**.

KO and KD mutants

1. Most genes that show significant differential expression from WT are downregulated, and several of them are transcription factors.
2. There are many genes that appear to be expressed differently between the KD and KO mutants, although the significance of this difference varies.

KO mutant

1. Whereas only a little over one hundred genes showed significant differential expression in the KD mutant, several thousand genes show significant expression in the KO mutant.
2. The three most significant differentially expressed genes in the KO mutant (a, b, c) are related to the mitochondria or response to environmental stress.

Future Directions

- Explore the roles of differentially expressed genes in the various observed tafazzin mutant phenotypes, including senescence, cardiolipin production, and electron transport chain function.
- A long-term goal is to metabolically engineer plants to regulate senescence by regulating expression of senescence-promoting genes.

Acknowledgements

This research was funded by the United States Department of Agriculture-National Institute of Food and Agriculture (USDA-NIFA) under the AFRI Education and Workforce Development grant no. 2019-67032-29071 and USDA-NIFA (Hatch/Multi-State project 1013013). In the initial stage of the project, CH was the recipient of Johnson Cancer Research Center Undergraduate Research Award. The University of Kansas Genome Sequencing Core performed the sequencing of the RNA libraries.