AT1G10210's Role in Phenotypic Expression of *Arabidopsis thaliana*

John H. Walker and Michael J. Wolyniak

Department of Biology, Hampden-Sydney College, Hampden-Sydney, VA 23943

Introduction

A gene in *Arabidopsis thaliana*, AT1G10210, plays a role in auxin signaling pathways, intracellular signaling transduction, and regulation of gene expression. To better understand the importance of this gene, T-DNA has been inserted into this gene to disrupt the targeted gene's function on the cellular level. Therefore, the purpose of this research project is to determine the importance of the gene AT1G10210 in phenotypic growth. In this experiment, I hope to answer if this gene plays a role in leaf number and size, bolt height, number of seed pods, and plant vertical and horizontal height.

Arabidopsis thaliana is a small flowering plant that is widely used as a model organism in plant biology. It has a life cycle of 6 weeks (germination to mature seed), which makes it an ideal candidate for genetic research. It was the first plant to have its entire genome sequenced (Environment Makers, 2019). The targeted genes of the seeds encoded for a mitogen activated protein kinases (MAP Kinase). Kinases function in a signaling cascade. Therefore, with this process being disrupted due to T-DNA, this should have a profound effect on the phenotypic growth of the plant (Krysan, 1999). Arabidopsis introns are relatively small. Therefore, the insertion of 5-25 kilo-base pairs of T-DNA will thoroughly disrupt the function of the gene and will likely hinder phenotypic growth.

The most important aspect of the gene AT1G10210 is its role in the auxin signaling pathway. Auxin, a hormone, is one of the most influential plant growth regulators; it is a signaling molecule with great ability to induce growth responses throughout the plant life cycle (Schepetilnikov, 2017). The auxin signaling pathway modulates diverse aspects of plant growth and development, such as responses to light, organ patterning, general root and shoot architecture and vascular development. In short, the targeted gene plays a key role in the fitness of the plant. Although fitness is typically defined as an individual's ability to produce offspring or close kin that survive to reproductive age (Evolution Berkeley), I am more interested in the plant's ability to grow the fastest and produce the widest Rosetta.

Methods

Six single knockout lines and six double knockout lines of *Arabidopsis* seeds obtained from Arabidopsis Biological Resource Center. Within the six double knockout lines, two shared a targeted gene: AT1G10210. The control variable was the single knockout that had the same target gene as the double knock out line. Therefore, only one gene could account for alterations in phenotypic growth. Seed samples were distributed onto a damp filter paper, sealed in an air-tight container, and stored at 4 °C for 48 hours. Seeds were then distributed into moist potting soil and placed under a light, in which the light/dark cycle was 16/8 hours per day. Measurements were taken twice a week for 6 weeks. Data analysis was then performed on the dataset to determine if there is a statically significant difference in the variables.

Results

T-tests were performed on all the data sets. There is a statistically significant difference between the Rosetta width of CS69427 and SALK_022928, with a p-value of 0.039. Also, there is a significant difference in the Rosetta width of CS69430 and SALK_069399, with a p-value of 0.000506. Lastly, there is a significant difference in the number of seed pods in CS69430 and SALK_069399, with a p-value of 0.04423.

Conclusions

Based on the t-tests, there is a statically significant difference in the width of the rosetta in both sets of plants. Therefore, AT1G10210 plays

a role in the size of the rosetta of the Arabidopsis plant.

Although I have yet to find a specific correlation in the gene AT1G10210 and the gene responsible for leaf growth in White Oaks, I hope to eventually transition the findings from my research to genes vital for growth of *Quercus alba.* This is important because bigger and wider leaves absorb more carbon than pine needles, which in turn, could play a role in preserving the ozone layer of the Earth. Despite not finding a direct correlation, I will continue literature research in hopes to find a correlation between *Arabidopsis thaliana* and White Oak trees. The southeast is the largest timber producing region in the United States, accounting for 62% of the annual timber harvest (Forest Data). Hardwood forests are continually being harvested and replanted with *Pinus taeda*. My hopes are to find parallelisms between *Arabidopsis thaliana* and *Quercus alba,* or other commonly targeted hardwood trees, with the eventual goal of determining genes in White Oaks that are vital in plant height, leaf size and number, and root size, in order that human made alterations to forests be minimized.

REFERENCES

- Schepetilnikov, Mikhail, and Lyubov A. Ryabova. "Auxin Signaling in Regulation of Plant Translation Reinitiation." Frontiers, Frontiers, 26 May 2017, www.frontiersin.org/articles/10.3389/fpls.

- 2017.01014/full#:~:text=Auxin%20distribution%20is%20highly%20regulated%20in%20plants.&text=The%20classical%20nuclear%20auxin%20signaling,the%20cellular%20spatio%2Dtemporal%20context.
- Krysan, Patrick J., et al. "T-DNA as an Insertional Mutagen in Arabidopsis." Plant Cell, American Society of Plant Biologists, 1 Dec. 1999, www.plantcell.org/content/11/12/2283.
- "Growing Arabidopsis Thaliana: the Perfect Environment With a Growth Chamber – FDM – Environment Makers." FDM - Environment Makers, 9 Dec. 2019, www.dellamarca.it/en/how-to-grow-arabidopsis-thaliana/.
- TAIR - About Arabidopsis, www.arabidopsis.org/portals/education/aboutarabidopsis.jsp#:~:text=Arabidopsis%20thaliana%20is%20a%20small,such%20as%20cabbage%20and%20radish.
- "CURRENT U.S. FOREST DATA AND MAPS," - https://www.fia.fs.fed.us/slides/current-data.pdf

- ·   What about fitness? (n.d.). Retrieved March 02, 2021, from https://evolution.berkeley.edu/evolibrary/article/evo_27