CALIFORNIA STATE SCIENCE FAIR
2016 PROJECT SUMMARY

Name(s)
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Project Number
36659

Project Title
Sucrose Efflux Mediated by SWEET Proteins as a Crucial Aid for Whitefly Feeding

Abstract

Objectives/Goals
Bemisia tabaci is responsible for transmitting plant viruses causing the ongoing and devastating East African pandemics of cassava mosaic disease (CMD) and cassava brown streak disease (CBSD). Since the 1990s, there has been an unprecedented rise of cassava whitefly in the cassava-growing regions of East and Central Africa, which has in turn increased the spread of CMD and CBSD. However, areas of the world that cannot afford insecticides are subject to the devastating effects of B. tabaci feeding.
1. By investigating whether Bemisia tabaci reaches the phloem through the help of the sugar gradient secreted by SWEET sucrose transporter proteins, I hoped to gain some understanding of the feeding strategies of whiteflies.
2. I needed to determine which SWEET mutant, if any, had the least successful whitefly feeding.
3. If the whiteflies on a particular SWEET mutant showed increased difficulty in reaching the phloem, I needed to analyze the probing time of whiteflies (directly corresponding to less time feeding) and directionality of their stylets while probing.

Methods/Materials
Prior to infestation, I had 10 seeds per line for Col-0, the single mutants atsweet11 and atsweet12, along with the double mutant atsweet11, atsweet12. Each leaf was infested with either 1, 2, or 3 adults because the number of sheaths that was laid down is not definite. After feeding for 24 hours, the whiteflies were counted and removed, and whole leaves were stained with McBride's stain to track the stylet sheaths. I documented the number of stylets, bifurcations, and locations of said branches in the leaves, and compared the results from the mutants to Col-0.

Results
After analyzing the stylet destination, directionality, and the individual successes of whitefly feeding in the mutants and Col-0 using linear regression and chi-square goodness of fit tests, I determined that whiteflies on atsweet12 had the most difficulty and the least success in reaching the phloem for feeding.

Conclusions/Discussion
By inducing the gene expression of SWEET12 proteins, whiteflies had an extremely difficult time locating the phloem for feeding. This new knowledge of the feeding mechanisms of whiteflies is crucial to improving plant defenses against whiteflies. With this data, we can bioengineer plants through the manipulation of SWEET proteins to have natural defenses against these pathogens.

Summary Statement
I have determined that by directly inducing SWEET gene expression (particularly SWEET12) and therefore the sucrose gradient present in leaves, whiteflies feeding was greatly reduced.

Help Received
I give a tremendous amount of gratitude to Dr. Walling and Mr. Thomas for mentoring me through this project and allowing me to use UCR's whitefly colony and facilities. Mr. Thomas assisted me during the experiments and infestation, but the analysis and conclusions reached were conducted by myself.