

M.L. 2016 Project Abstract

For the Period Ending July 30, 2021

PROJECT TITLE: MITPPC Sub-project 3: Genetic Control of Invasive Insect Species: Phase I
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APPROPRIATION AMOUNT: \$296,655

AMOUNT SPENT: \$296,655

AMOUNT REMAINING: \$0

Sound bite of Project Outcomes and Results

We have demonstrated (in lab cages) a powerful new approach to combat invasive insect pests. Genetically engineered male insects would be released to mate with wild females, who would not have offspring. This can crash a wild population, and it is applicable to any sexually reproducing insect.

Overall Project Outcome and Results

With the overall goal of demonstrating our innovative genetic biocontrol approach in the pest insect Spotted Wing *Drosophila*, we had three specific objectives on this project: (i) demonstrate a proof-of-concept in the model laboratory insect and close cousin to SWD, *Drosophila melanogaster*, (ii) translate what we learned from *D. melanogaster* into the SWD species, and (iii) study the genome sequence of wild SWD so we can precisely design our engineered biocontrol agents to effectively suppress wild SWD populations in Minnesota.

Our outcomes and results for the first objective exceeded project expectations. We succeeded in making the proof-of-concept in *D. melanogaster*, and the engineered insects were 100% incompatible with wild-type flies. We made over a dozen versions. We also added additional genetic control elements to automatically sort the males from females, making the technology more economical to deploy for pest control.

We did not meet our objective two milestones (completing the engineering of SWD), however, we made good progress in that direction. Near the end of the award, we succeeded in making our first transgenic SWD flies, so we should be able to move quickly now in finishing the engineering process.

Our results from the third objective exceeded expectations. While we initially planned to sequence the genome of 20 wild-caught flies, we instead invented a new approach that allowed us to sequence the relevant genes from over 10,000 wild flies. We are using this data in our current engineering efforts with SWD.

This was a high-risk/high-reward project. We were able to overcome a tremendous amount of technical risk on the project so far, and the approach is looking very promising. We plan to continue to make progress towards Objective 2 in our second Phase of this project.

Project Results Use and Dissemination

We have disseminated our results through the normal channels available to academic labs (regional, national, and international conferences and workshops; peer-reviewed publications; patents; etc.). We are most proud of two high-impact publications from this work. The first was published in [Nature Communications](#) in 2020, and the

[second](#) is currently undergoing peer review at a top-ranked journal. We will have at least two additional papers submitted in the next year that stem from this project.