

Please use this form to clearly and concisely report on project progress. The information included should reflect quantifiable results that can be used to evaluate and measure project success. Comments should be limited to the designated boxes. Technical reports, no longer than 4 pages, may be attached to this summary report.

Project Number:	2022-47
Project Title:	Exploitation of weed species extracts as an effective and environmental friendly strategy to control insects and deer in soybean
Organization:	Mississippi State University
Project Lead Name:	Te Ming (Paul) Tseng
Report Period:	December 15, 2023

Progress Summary (in non-proprietary lay language suitable to be shared publicly):

In our research, the primary goal is to identify and develop a natural deer repellent that can be used in soybean crops. This repellent aims to protect soybean plants from damage caused by both deer and insects, ultimately safeguarding soybean yields and promoting more sustainable agriculture. We have extracted plant's DNA to find out which genes are responsible for making these helpful compounds. We started with 10 genetic markers, but we plan to look at more in the future. So far, we've taken DNA from the leaves of the plants and used a special method called polymerase chain reaction (PCR) to make copies of the genes we're interested in. We have also run all the PCR products in the gel. However, we haven't done the full analysis to see how these genes are linked to the compounds that keep herbivores away.

Detailed Progress Status:

The objectives proposed were (1) conduct chromatography and mass spectrometry analysis to identify target anti-herbivore compounds in weeds, and (2) conduct quantitative trait loci analysis to identify molecular markers associated with anti-herbivory compounds in weeds.

- 2. Conduct quantitative trait loci analysis to identify molecular markers associated with anti-herbivory compounds in weeds:** Presently, we have initiated the screening of a subset comprising 10 simple sequence repeat (SSR) markers, with intentions to broaden this screening effort in forthcoming months. DNA isolation from leaves followed, and polymerase chain reaction (PCR) was used to facilitate amplification of genetic regions corresponding to the target anti-herbivore compound(s) as identified within objective 3. We have almost completed running all the PCR products in the agarose gel and have captured images of each gel containing the DNA bands.

The statistical analysis of these markers and, consequently, the linkage analysis to anti-herbivory traits, have not been conducted at this stage. These highly promising markers will continue to serve as pivotal components in subsequent greenhouse-based breeding experiments, aimed at the meticulous selection of soybean lines characterized by the coveted anti-herbivory trait(s).