|  |  |
| --- | --- |
| 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: | March 20, 2023 |
| Progress Summary (in non-proprietary lay language suitable to be shared publicly): | |
| We collected fractions and extracts from sicklepod seeds and leaves that contain a compound that helps to repel herbivores. To figure out which compound it is, we'll be using a couple of different methods, including GC/MS and HPLC. HPLC will help us identify the exact compound that has the anti-herbivore property. This is great news for the environment, as it means we can reduce our reliance on harmful pesticides and other synthetic chemicals in agriculture. | |
| **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.   1. Conduct chromatography and mass spectrometry analysis to identify target anti-herbivore compounds in weeds: The fractions and extracts containing the anti-herbivore compound(s) were successfully prepared from the seed and leaf tissues of sicklepod. The next step will be to identify the target compound(s) using GC/MS and HPLC. The phenolic compounds will undergo loading onto a C18 column and elution with a gradient of solvent B (82% (v/v) acetonitrile, 0.04% (v/v) phosphoric acid) ranging from 0-15%. The detected peaks will be identified at 280 nm by comparing them with the retention times of standards. 2. Conduct quantitative trait loci analysis to identify molecular markers associated with anti-herbivory compounds in weeds: We have not started this objective yet. | |