

**Biomarker-based evaluation of white mold (WHM) resistance in peanuts**  
**FY25-26 Project Update - New Project**

Date: January 23, 2026

**Principal Investigators**

Joonhyuk Suh (Assistant Professor, Department of Food Science and Technology, University of Georgia)  
Nino Brown (Assistant Professor, Department of Crop and Soil Sciences, University of Georgia)

**Layman's Summary**

White mold (WHM) is currently the leading cause of peanut crop loss in the Southeastern region of the United States, resulting in an estimated economic loss of \$73.7 million in 2021 alone. While fungicides are effective, they are a major expense for growers. The most cost-effective long-term solution is developing peanut varieties with natural genetic resistance. However, current breeding methods rely on multiple years of field screening (visual selection), which is labor intensive and time-consuming. Our project aims to solve this bottleneck by developing a rapid, high-throughput biomarkers-assisted screening method. Much like a blood test can detect health issues in humans before symptoms appear, we are using metabolomics—the study of small chemical molecules—to identify chemical signatures (biomarkers) in peanut plants that predict resistance to WHM. This tool will enable breeders to identify resistant lines at the seedling stage, significantly speeding up the release of WHM-resistant cultivars.

**Objectives of The Project**

- 1) Identify biomarkers for WHM resistance in peanuts using a metabolomics approach
- 2) Uncover the relevant biological pathways through functional enrichment analyses

**Project Progress & Findings (Year 1):** Since the project start date, our team has successfully completed the critical first season of field trials and sampling.

- Field trials and sampling (Completed October 31, 2025): Three peanut breeding lines exhibiting differential resistance to WHM were selected under the guidance of Dr. Brown. These included 'Georgia-12Y' (highly resistant), 'Georgia007W' (moderate resistant), and 'Georgia-09B' (highly susceptible). All lines were cultivated at the University of Georgia's research plots in Tifton, Georgia, under standard experimental field conditions with consistent irrigation and fertilization. Root and stem samples were collected at approximately 140 days after planting (DAP). For each line, five biological replicates (n = 5) were obtained from four independent field plots. Four distinct groups were selected to compare chemical profiles: (i) healthy-resistant, (ii) healthy-susceptible, (iii) infected-resistant, and (iv) infected-susceptible.
- Sample preparation (Completed November 2025): The collected root and stem tissues were quenched in liquid nitrogen to arrest post-harvest metabolic activities and stored at -80°C. Samples were lyophilized using a freeze-dryer and ground into fine powders.
- Metabolomic analysis (Ongoing since December 2025): We are currently optimizing analytical methods for metabolomics using liquid chromatography-mass spectrometry (LC-MS). We are employing both reversed-phase (RP) and hydrophilic interaction (HILIC) modes to ensure we capture a broad range of metabolites.

**Future Plans**

- Metabolomic analysis (Year 1 samples): We will complete the chemical analysis of Year 1 samples to identify potential biomarker candidates.
- Replicate field trials and sampling (Year 2; estimated October 2026): We plan to repeat the field trials and sampling in Year 2. This is a **critical step** to rule out weather or soil variations and to identify reliable biomarkers truly associated with WHM resistance. Peer-review publication in scientific journals in horticulture also requires at least 2-3 years of field data.

**Budget Summary**

Category	Amount	Expended (to date)	Remaining
Salary & Wages (Grad Student)	\$9,858	\$1,877.03	\$7,980.97
Supplies (Lab & Field)	\$4,342	\$1,900.00	\$2,442.00
Travel	\$800	\$0	\$800
Total	\$15,000	\$3,777.03	\$11,222.97