

Evaluating modern breeding tools for assessing root lesion nematode (*Pratylenchus penetrans*) resistance in red raspberry

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Figure 3: Panoramic photo of plants in field August 2022 at Mt. Vernon, WA. Photo by

Objectives

- ❖ Characterize RLN resistance and tolerance phenotypes in a diverse population of 270 red raspberry breeding lines and cultivars and 10 mapping populations
- ❖ Determine the effectiveness of ground-based and aerial spectral imaging data for assessing RLN damage
- ❖ Conduct a genome-wide association study for RLN resistance using phenotypic and genotypic information
- ❖ Develop and evaluate genomic prediction models for RLN resistance

Introduction



Figure 1: *Pratylenchus* spp. under microscope from inoculated raspberry plant. Photo by Savannah Phipps

Management of root lesion nematode, *Pratylenchus penetrans*, (RLN; Figure 1) is important for red raspberry production (Figure 2) in the Pacific Northwest due to the unique regional climate that fosters this productive, and highly profitable, specialty crop industry (Rudolph & DeVetter, 2015; Walters et al., 2017). As a result, economical and sustainable control methods are a priority. Resistant cultivars are an effective control method; however, there is currently limited understanding of the genetics involved in host resistance. Furthermore, phenotypic evaluation of nematode resistance is an intensive and destructive process, which has hindered research into the genetics of RLN resistance. This project is currently evaluating newer technologies such as genomic prediction and high-throughput imaging, which may accelerate screening and improve a breeder's ability to select for resistance. This project leverages the combined diversity of raspberry germplasm from breeding programs at Washington State University (WSU), British Columbia Berry Cultivar Development Inc. (BCBCDI), the United States Department of Agriculture (USDA)/Oregon State University (OSU), and germplasm at the National Clonal Germplasm Repository (NCGR) for assessment of RLN resistance.



Figure 2: Red raspberry 'Willamette' in field with A) nonfumigated and B) fumigated plants for *Pratylenchus penetrans* infestation. Photos by Inga Zasada

Methods

Plant Materials

- ❖ 270 red raspberry genotypes from the WSU Small Fruits breeding program, BCBCDI, USDA/OSU breeding program, and NCGR
- ❖ 296 individual seedlings from 10 mapping populations derived from a susceptible by resistant cross made by the BCBCDI

Field Experimental Design

- ❖ Paired non-inoculated and RLN inoculated plants randomized across 3 replications for diversity panel (Figure 3, 4)
- ❖ Non-replicated seedlings from 10 mapping population planted alongside diversity panel (Figure 3)



Figure 4: Examples of morphological diversity seen in field. A) 'Dorman Red' B) 'Jokgal' C) WSU 1478 D) 'Meeker'. Photos by Savannah Phipps.

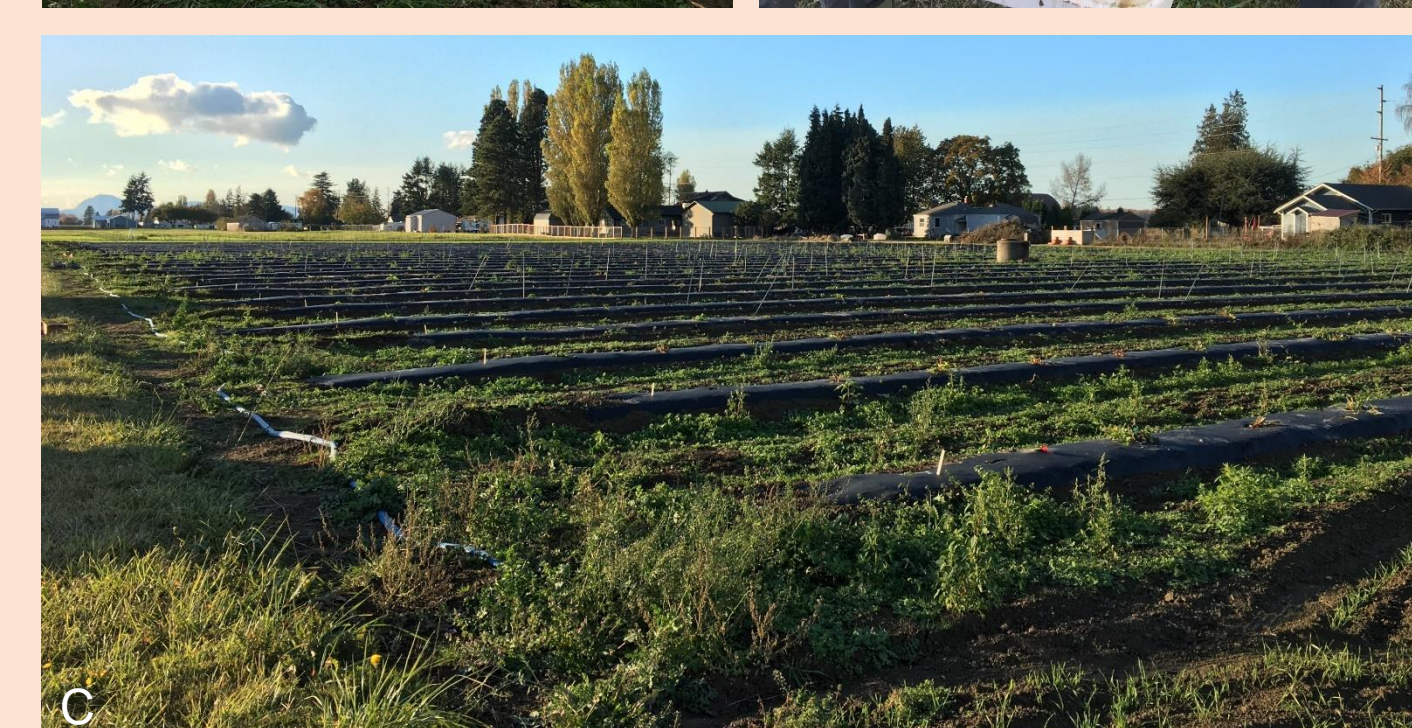


Figure 5: A) Harvesting of aboveground biomass B) Weighing and recording of aboveground biomass C) Completely pruned field in year 1. Photos by Savannah Phipps.

Genotypic Data Collection

- ❖ Genotyping-by-Sequencing following the protocol outlined in Bushakra et al. (2015)

GWAS Analysis

- ❖ FarmCPU in R with GAPIT (Lipka et al., 2012)

Genomic Prediction

- ❖ Develop single and multi-year data models

Phenotypic Data Collection

- ❖ Collected yearly
- ❖ Root sampling for nematode quantification
- ❖ Fresh weight aboveground biomass sampling (Figure 5) for plant nematode stress response
- ❖ Spectral data collection via drone fly-overs and smart devices for plant nematode stress response (Figure 6)

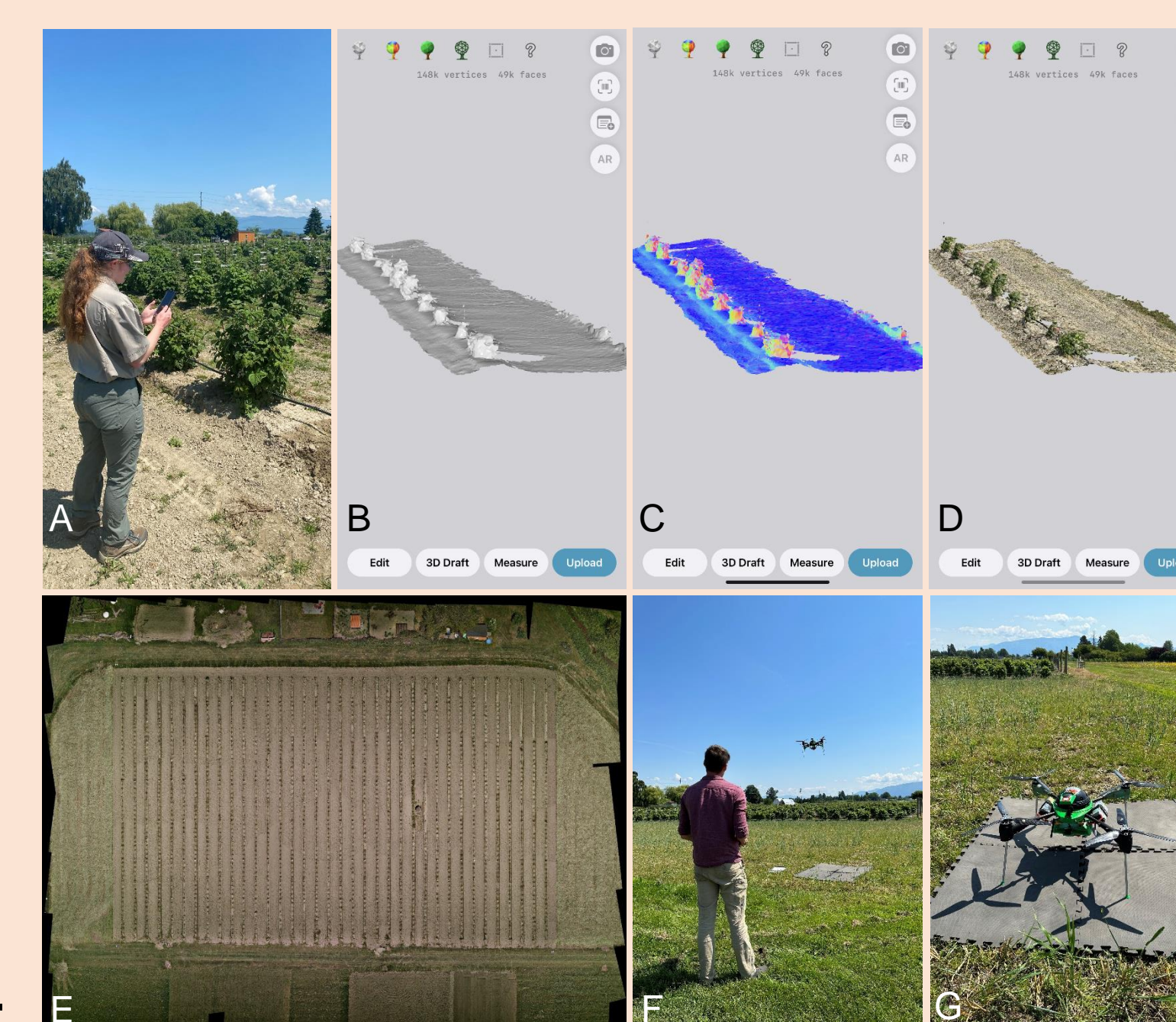


Figure 6: Examples of ground-based and aerial imaging in action. A) Savannah Phipps imaging in the AgerPoint Capture app with iPhone 14 Pro Max. Photo by Hannah Baker B-D) Example imaging results in the AgerPoint Capture app E) Stitched red-green-blue aerial orthomosaic of field trial from May 5, 2023. Photo by Alexander Gregory F) Alexander Gregory landing aerial drone after imaging. Photo by Savannah Phipps G) AgBOT mk 1 Quadcopter equipped with MicaSense RedEdge-MX multispectral sensor. Photo by Savannah Phipps

Future Work

Year 2

- ❖ Genetic marker screening Summer/Fall 2023
- ❖ Continued data collection May 2023 – October 2023
- ❖ Data exploration of first and second year spectral and biomass data (Figure 7)
- ❖ Begin developing genomic prediction models for nematode resistance

Year 3

- ❖ Final year of data collection
- ❖ Evaluate multi-year models for correlations between spectral data and biomass and nematode count data
- ❖ Conduct genome-wide association study with phenotypic and genomic data
- ❖ Evaluate genomic prediction models for multi-year data
- ❖ Publish results

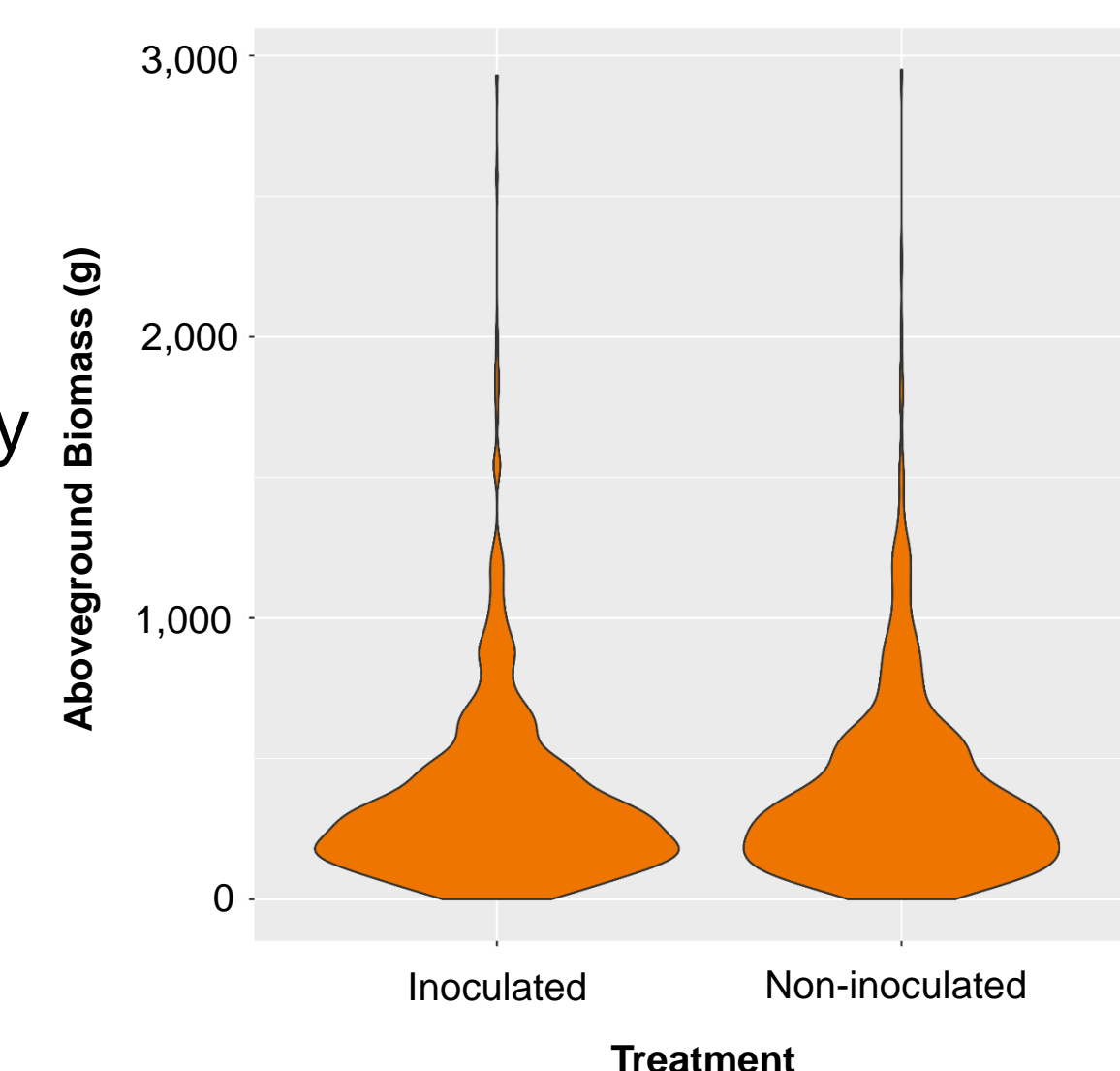


Figure 7: Violin plot distribution of first year aboveground biomass (grams) data between inoculated and non-inoculated plants.

Collaborations and Affiliations



Photo by Alexander Gregory

Funding



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