

VERSION 3

## OPEN BACCESS

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**Protocol status:** Working We use this protocol and it's working

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# © Collecting needle and branch samples for terpenoid and expression analysis V.3

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PlantCompGenomics



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**ABSTRACT** 

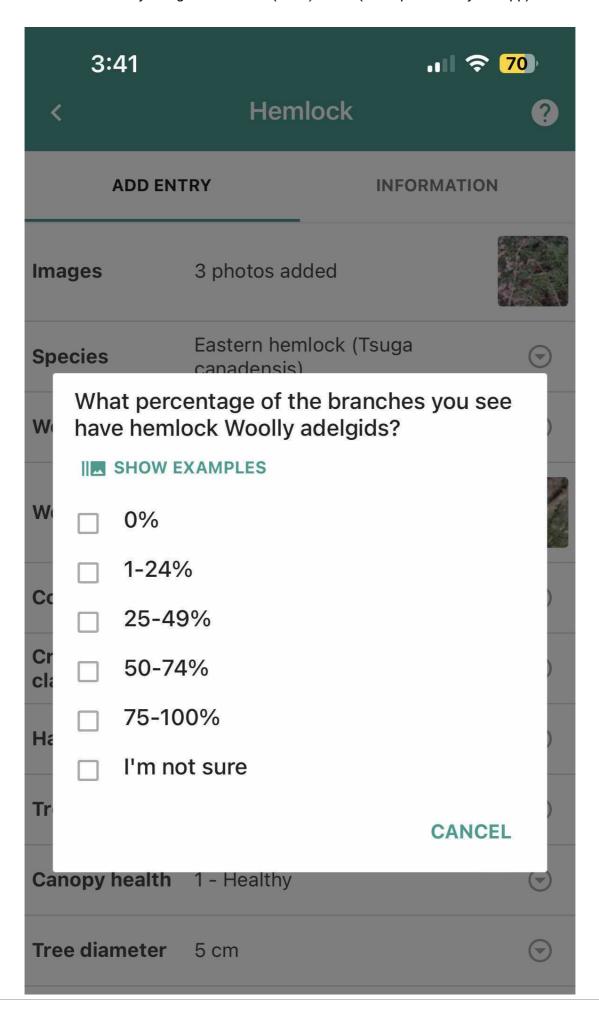
This protocol is used by the PCG group for sampling needle and branch tissue from hemlock conifers for terpenoid analysis, as well as RNA expression analysis.

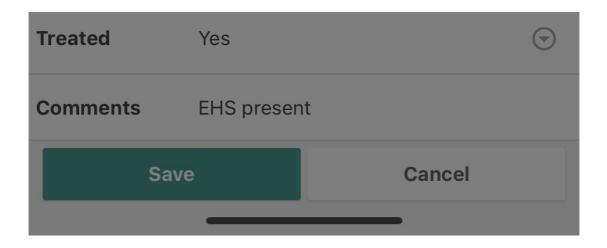
**IMAGE ATTRIBUTION** 

The image was taken by Dr. Karl Fetter

## **TreeSnap Observation**

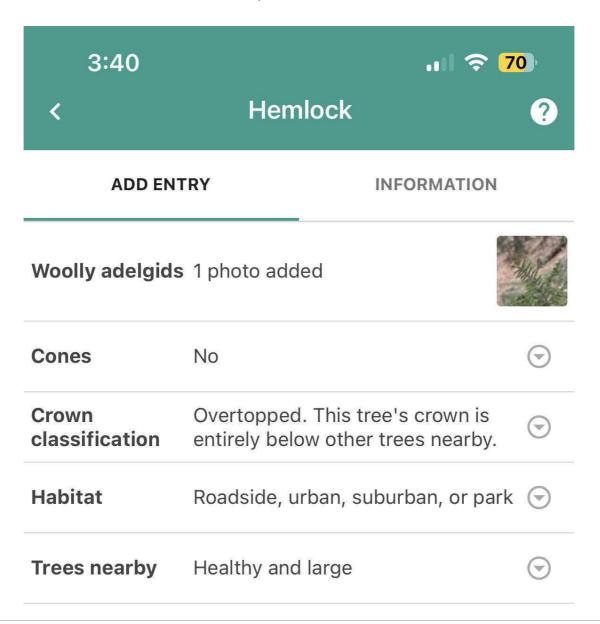
for hemlock woolly adelgid infestation (HWA) levels (scale provided by the app).

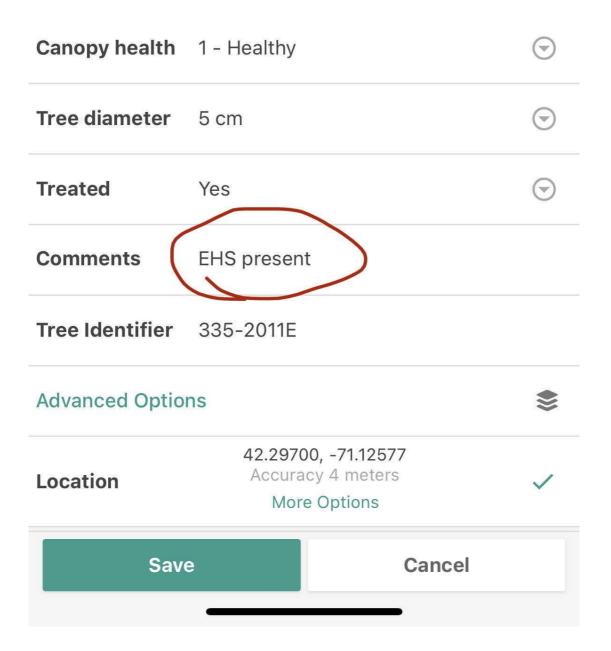




Pop-up box displaying the levels of infestation of HWA to record

1.1 Use the comment field to enter: *EHS present* OR *EHS absent* to record the hemlock scale.





highlighting where to place additional notes on individual sampled. EHS is important to log.

- 1.2 Take at least 3 photos with TreeSnap. This includes at least one of the trees itself, one photo of the tree tag if that is present, and one photo of the collection vial with the label as well.
- **1.3** Geolocation will be recorded automatically but TreeSnap can also connect with a more precise external GPS device.
- **1.4** Note DBH in appropriate column

1.5 Note any other observation you may have-including plant condition (Excellent/Good/Poor), and placement of individual (lower canopy, full sun, etc.)

## **Prepare sampling sheet**

2 The sample sheet would look like this:- Link to spreadsheet

#### Collection

3 You will collect two



You will collect two sets of samples from each tree. One for RNA extraction for transcriptomics and one for metabolomics. The first needs less material so we will use the 5ml tubes. The latter needs more material and will use the 10ml tubes. The first should include two branches that are approximately 5 cm in length. The second should include four branches, ideally taken from different locations around the tree

#### **Safety information**

For RNA collections- please use gloves, and spray RNase before collections (separate vial-5ml cryovial)

- 4 Metabolomics- You would use 2 10ml vials. You will be able to fit 4 branches (5cm) in each tubeso sample from one direction of the tree, then collect the three other branches from the other sides of the tree (you would ideally try to sample around the individual)
- 5 RNA- You would use one 5ml vial. For this, 2 branches would be more than sufficient to fit into the vial. Ideally, you would want to sample from 2 different locations of the individual.

#### **Safety information**

It is important to wear gloves while collecting samples for RNA analysis!

## **Placing in Liquid Nitrogen**

6

Close cryovials, and place the vial slowly into the LN dewar. Be wary of LN splashing out, and wear appropriate gear, and stay at a distance.



Safety information

Use appropriate wear while handling liquid nitrogen

## Cleaning before sampling from new individual

7 Clean trimmers between trees with ethanol (spray bottle).



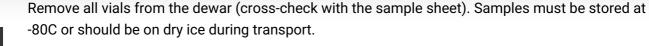
Note

For the collection of RNA- spray clippers and gloves with RNase and ethanol

- 8 Use a clipboard to manually record notes on a pre-printed spreadsheet with sample names.
- **9** After returning from the field, ensure that notes are consistent with TreeSnap entries. These entries can be amended after collection as needed.

### **Post-sampling and Pre-shipping**

10





Cross-check all samples at this stage with your sample sheet.

## **Shipping**

11 Shipping instructions will be provided via email. Shipments must be sent on dry ice. You will be

shipping separate parcels for the Metabolomics and RNA samples.

#### Note

Please separate the RNA and terpenoid vials before shipment

12 Log all data and samples in a Google sheet, or send over sample sheet so that we log your data