Investigating Incidence and Type of Wood Decay Fungi in Almond

Bob Johnson[1], Franz Niederholzer[2] , Florent P. Trouillas[1], Dave Doll[3], Matteo Garbelotto[4], Luke Milliron[2] and Dave Rizzo[1]

[1]Department of Plant Pathology, University of California, Davis; [2]University of California Cooperative Extension, Yuba/Sutter/Colusa Counties, CA, [3]University of California Cooperative Extension, Merced County, CA, and [4]Department of Environmental Science, Policy and Management, University of California, Berkeley

Background

Wood decay fungi reduce the structural integrity of trees, leading to wind-driven collapses or “windfalls”, causing almond tree loss and lost production in many parts of California. Wood decay is caused by a wide array of fungi that colonize and digest the heartwood, and sometimes sapwood, in living trees. The last survey of wood decay diseases in California nut and fruit crops was conducted in 1988 by Adaskaveg and Ogawa. While this survey provided information on the identity of the major fungal species associated with heart-rot, it has had limited impact on disease control. Since this survey was completed the acreage of almond has more than doubled and new production techniques are allowing an expansion of land suitable for almond cultivation. For many decay fungi, there is not a clear understanding of the early stages of infection. This includes the source of inoculum, timing of infection, possible latent period, and specific virulence. The etiology and biology of wood decay diseases in orchard trees is overall poorly understood.

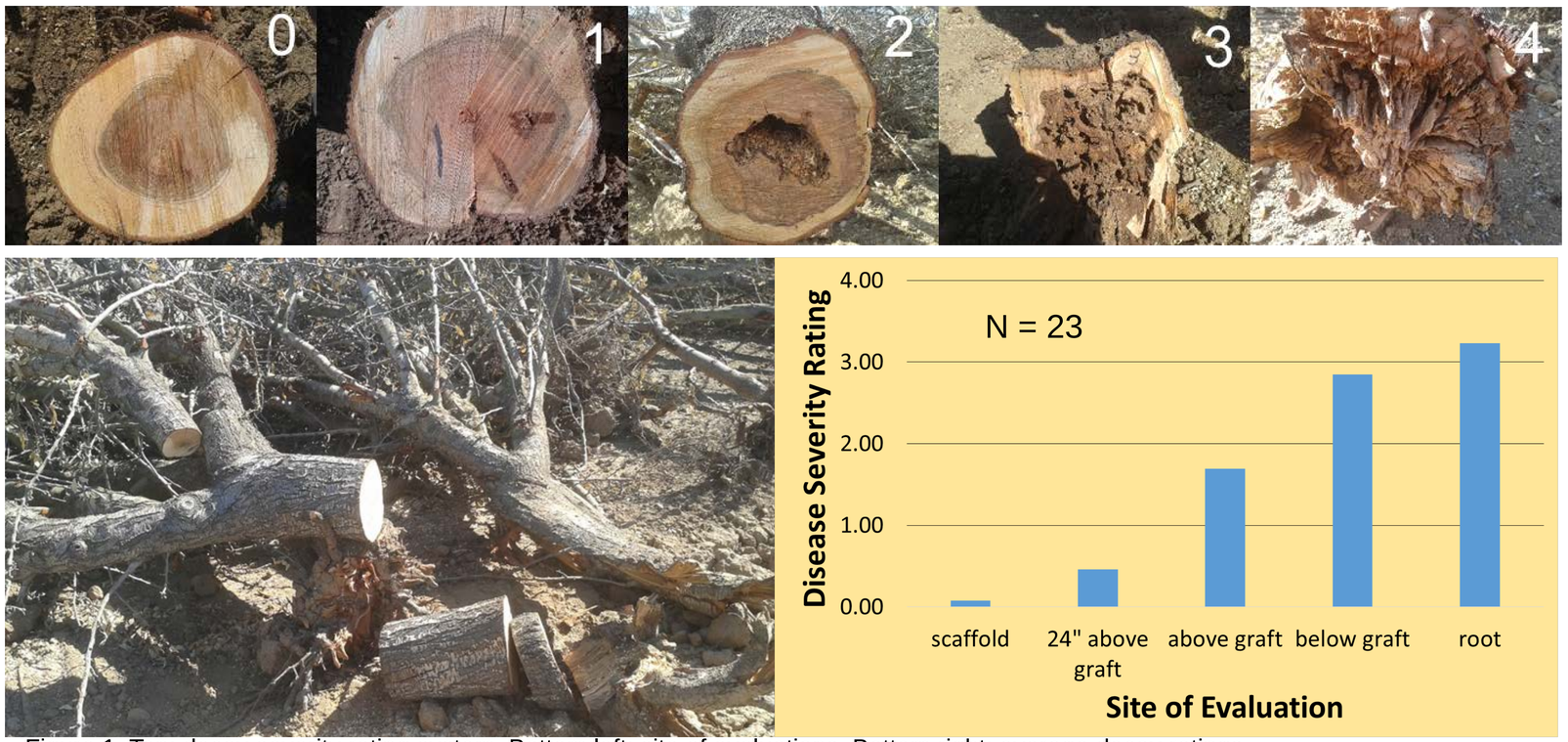

Figure 1. Top; decay severity rating system. Bottom left; site of evaluations. Bottom right; average decay ratings.

Figure 2. From top left moving clockwise: *Puctularia sp*., *Psathyrella sp*., *‘Hyphodontia’* sp., and *Trametes versicolor*.

Objectives

This project is investigating the main fungal associates with these diseases as well as their dissemination pathways and infection patterns within the individual tree and the orchard. It also aims to investigate infection processes as well as factors favoring tree susceptibility to disease including tree age, environmental conditions, and cultural practices.

Objectives for current year:

- **Identify the main fungi associated with heart-rot diseases of almond in California**
- **Determine the infection process in orchards**

Figure 3. Example of decay samples collected from down trees.

Results and Discussion

Cooperating growers were identified in Butte, Colusa, Yuba, and Yolo counties, and preliminary disease surveys began in the Fall of 2015. Individual fallen trees are being sampled as they become known. Using a chain saw approximately 1.5 inch wafers are cut from various points up the trunk of the tree (Figure 3). Additional cookies are collected from one or several scaffold limbs.

A recently removed orchard was also sampled shortly when trees were still windrowed, giving us access to exposed root systems.

We evaluated every tenth tree in every fifth row by assigning a disease severity rating from 0 (no evidence) to 4 (severe rot) to the root mass and each of four cuts: directly below the graft union, directly about the graft union, 24 inches above the graft, in a scaffold branch (Figure 1). Decay tended to be more severe in the roots and butt of the tree and very limited in the trunk and scaffold branches.

We collected representative samples of decay and plated decayed wood on to water agar amended with antibiotics. We extracted DNA from pure cultures and used PCR to amplify the internal transcribed spacer (ITS) regions. ITS positive samples were sequenced and BLAST was used for identification.

Preliminary analysis found several Basidiomycetes of interest in association with the decayed wood (Figure 2), however due to the nature of this disease it cannot be positively stated that they are primary cause of the decay at this time.

In early 2016 young almond trees will be inoculated with fungi identified in preliminary surveys. Trees will be observed for outward signs of the disease over the course of 2016 and will be destructively sampled after one year, to determine virulence and rate of spread with in the tree. The survey will allow us to reassess the fungal diversity associated with heart-rot diseases and will provide the baseline for completion of further objectives.