

# Update: Estimate of Oak and Tanoak Mortality Caused by *Phytophthora ramorum* in California Forests

Meentemeyer, R.<sup>1</sup>, Shoemaker, D. A.<sup>1</sup>, Cushman, H.<sup>2</sup>, Swiecki, T. J.<sup>3</sup>, Rizzo, D. M.<sup>4</sup>

<sup>1</sup> University of North Carolina-Charlotte, Center for Applied GIS [rmeente@email.uncc.edu](mailto:rmeente@email.uncc.edu); <sup>2</sup> Sonoma State University, Department of Biology, 1801 E. Cotati Avenue, Rohnert Park, CA 94928

<sup>3</sup> Phytosphere Research, 1027 Davis Street, Vacaville, CA 95687, USA; <sup>4</sup> University of California, Department of Plant Pathology, One Shields Avenue, Davis, CA 95616

## Principle Objective: Estimation of tree mortality attributed to Sudden Oak Death (SOD) on known hosts at a statewide scale.

### Introduction

This study examines mortality impacts of the emerging forest disease sudden oak death (SOD), caused by the invasive fungal-like pathogen *Phytophthora ramorum*. This disease has reached epidemic levels in many coastal forests of California and southwestern Oregon,

where it has led to the death of potentially millions of oak (primarily *Quercus agrifolia*, *Q. kelloggii* and *Q. parvula* var. *shrevei*) and tanoak (*Lithocarpus densiflorus*) trees and affected more than 25 other native plant species with non-fatal leaf and twig infections. In response to the threat of this disease, researchers have established numerous field plots in California forests to examine biological and environmental factors that contribute to the presence and impacts of *P. ramorum*. But, because plot locations of many projects have been concentrated in areas of high disease severity and/or are not evenly distributed across infested regions, it has not been possible to produce unbiased estimates of oak and tanoak mortality at the statewide scale.

### Phase 1: Compilation of Plot Data into Single Database

Currently the monitoring plot network is made up of 1109 plots across California established by three research groups (see map). The UC Davis group has established 507 plots (500 m<sup>2</sup> each) in multiple forest types in coastal areas from Monterey County to Del Norte County, the Sonoma State group has established 202 randomly located plots (225 m<sup>2</sup> each) in mixed evergreen forests across a 275 km<sup>2</sup> area in Sonoma County, and Phytosphere Research has established approximately 400 plots (200 m<sup>2</sup> each) in several forest types across Marin, Sonoma and Napa counties. Plot variables (Table 1.) will be integrated between various projects for consistency and entered into a new relational database. Presence of *P. ramorum* has been confirmed via culturing in most plots and stored along with other variables in a relational database within a Geographic Information System (GIS). Status: *In progress.*

Table 1. Basic variables anticipated for use in analysis.

Disease	Vegetative	Topographic	Climatic
Plot Level Mortality	CalVeg Vegetative Alliance	Topographic Moisture Index (TMI)	Seasonal Max, Min Temperature
Species: Canker and Foliar Host	Canker Hosts Spp.	Aspect	Minimum Mean Temp
Number Symptomatic Stems	Foliar Hosts Spp.	Elevation	Minimum Precipitation
Total Stems	dbh	Location (X, Y)	Maximum Mean Temp

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### Phase 2: Examine Plot Network for Bias, Target Data Gaps

To assess the sampling efficiency of the existing plot network we will statistically test the hypothesis that the proportion of forest types (Table 2) sampled is equal to the proportion of forest types within infested landscapes. These tests will be conducted in a GIS environment via

intersection of plot locations and established remote sensing derived vegetation maps. Further, the spatial arrangement of the network will be tested for evidence of non-random distribution, i. e. clustering. Specific remedies will be prescribed to correct biases identified by this analysis, including the addition of randomly located plots within undersampled vegetation types (Phase 3b). Status: *In progress.*

### Phase 3a: Preliminary Estimation of Mortality

Analysis of existing plot data will be made using geostatistical methods and multivariate regression. The resultant predictive model will be applied to the known extent of infestation using raster based modeling. Results will be spatially explicit and include:

- Total mortality attributed to *P. ramorum* (Individuals and biomass)
- Stand Effects
  - stem mortality/total # stems per plot
- Incidence
  - infected canker host stems/total # canker host stems per plot

### Phase 3b: Establish New Plots and Re-Apply Model

The addition of data from new plots within the monitoring network will test the initial predictive model. Parameters will once again be tested for significance and applied in a raster modeling environment. Anticipated completion Summer, 2006.

Table 2. Vegetative Alliances describing canker-host distribution.

SOD Host Alliances	Canker-Host Constituents		
Redwood	Tanoak	Madrone	Canyon Live Oak
Coast Live Oak	Coast Live Oak	Madrone	Interior Live Oak
Interior Hardwood Mix	Tanoak	Canyon Live Oak	Madrone
Douglas Fir	Tanoak	Black Oak	Canyon Live Oak

