How Well Has the Spread of Sudden Oak Death Been Predicted by the Models in Northern California?[1]

Y. Valachovic[2], R. Cobb[3], and B. Twieg[2]

Abstract

Since *Phytophthora ramorum* established in the wildlands of California during the 1990s, the disease has spread rapidly throughout the state's coastal and adjacent counties, likely by a combination of human-aided events (e.g., nursery plant introductions) and natural dispersal. While human-aided events are almost impossible to predict, dedicated efforts have been made to model the natural spread of the disease throughout California. These models have been built upon aerial survey mortality data and/or extensive plot-level data gathered for infested and non-infested locations throughout the range of the disease in California and beyond, plus broader vegetation and weather data that dictate the pathogen's ability to infect hosts and further disperse. Some of these models have also sought to predict disease spread and intensity under various management scenarios.

While remaining cautious about model predictions, we find that the geographically explicit modeling efforts to date have been useful in predicting coarse scale patterns. This holds true even for the initial spread models developed in 2008 for the North Coast, where there is a rigorous dataset that supports actual disease spread. In retrospect, models that were run on a statewide scale (Meentemeyer and others 2004, 2008) predicted disease arrival and intensity well in some areas, but tended to overestimate disease spread and intensity further away from the infestation location(s) included when the model was first developed. In contrast, models with more limited geographic scope have, thus far, predicted spread rates surprisingly well. This is particularly true for an area (12 km X 85 km) of Humboldt County modeled by Filipe and others (2012) that accurately predicted the spread of the disease northward from the southern part of the county to within the proximity of the Van Duzen River by 2010. Another model that focused on the Mattole watershed slightly overestimated westward spread around Ettersburg, although the disease has been confirmed spreading north around a nearby infestation, where cryptic infection to the west may exist (Filipe and others 2013).

In reviewing the available *P. ramorum*-related modelling, we conclude that the modelling efforts to date have made significant advancements, but for land managers they should be viewed with the following limitations: 1) disease models can't predict new introductions or movement of ornamental plants; 2) while models exist for stand-level predictions (Cobb and others 2012), the lack of fine-scale data vegetation layers limits their application (see Twieg and others, this Proceedings for an example of stand-level model application); 3) available vegetation mapping

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[2] University of California Cooperative Extension, Humboldt and Del Norte Counties, Eureka, CA.

[3] University of California at Davis, Davis, CA 95616.

Corresponding author: yvala@ucanr.edu.

data layers that work well at the state scale (e.g. CalVeg) are not currently sufficient to provide site-level information and are not designed to give accurate host species-specific distributions for California bay laurel (*Umbellularia californica* Hook. & Arn.) or tanoak (*Notholithocarpus densiflorus* Hook. & Arn.); and 4) models are based on past weather trends and cannot predict future weather conditions and lack understanding of fine-scale climate variations. Of the models available, the recently developed SODDr statistical model is getting closer to being suitable for informing management decision making (Cobb and others 2012, Ross 2012), but is limited by data availability and requires a modicum of programming skills to parameterize and run. However, land managers should be aware that what is available to date can provide a prediction of probable pathogen establishment at broad spatial scales and shows very clearly the scope and scale of potential pathogen invasion and disease emergence. We look forward to future modeling products, such as the Tangible Landscapes approach (see Meentemeyer and others, this Proceedings) that can help forest managers tasked with difficult operational decisions.

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