

Predicting the Spread of Sudden Oak Death in California: Spatial-Temporal Modeling of Susceptible-Infectious Transitions¹

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Abstract

The number of emerging infectious diseases is thought to be increasing worldwide - many of which are caused by non-native, invasive plant pathogens in forest ecosystems. As new diseases continue to emerge, the ability to predict disease outbreaks is critical for effective management and prevention of epidemics, especially in complex spatially heterogeneous landscapes. Mathematical modeling of susceptible-infectious transitions in plant epidemics often incorporate spatial dynamics, but are rarely applied to real-world landscape data using geographic information systems (GIS). In spite of the challenges, application of epidemic models to GIS data provides several opportunities, including the ability to map high risk locations for management and early detection of disease outbreaks, assess ecological and economic impacts of disease in specific geographic regions, and visualize potential outcomes of management actions. Here, we present a spatial-temporal model of the spreading forest pathogen *Phytophthora ramorum*, causal agent of sudden oak death. Our goal was to develop a spatially-explicit epidemic model that predicts susceptible-infectious (SI) transitions at discrete time steps using a geographic cellular automata approach. To increase understanding and guide management, we examined 1) the ability of the modeling approach to predict the geographic distribution of disease spread, 2) the degree to which rates of disease spread vary through time and space, and 3) the influence of stochastic variability on epidemic outcomes. We first describe a generic mathematical model for a susceptible-infectious epidemic that simulates spatial and temporal patterns of disease spread on a weekly time step for application at large spatial scales. Next, we describe how data from field and lab studies were used to parameterize the driving system variables, including daily rainfall and temperature, host abundance and susceptibility, human population density, and pathogen dispersal characteristics. The parameterized model was implemented (1990 to 2005) in a GIS to simulate disease spread across California at a spatial resolution of 250 x 250 m. Model performance was also evaluated in the GIS by examining the spatial correspondence between predicted patterns of disease spread and 784 geo-located field observations of disease presence. The nature of prediction errors was examined by ecoregion, vegetation composition, and climate. The model predicts almost 80 percent of the spatial variability in current patterns of disease spread and identifies numerous forest ecosystems at high risk of infection. We believe the application of epidemiological models to realistic landscapes in a GIS can allow for a rigorous validation of model performance using geo-located field data of disease presence and can be used as an effective management tool to identify actual landscapes at high risk to disease spread.

Key words: *Phytophthora ramorum*, biological invasions, emerging infectious disease, spatial modeling, forest management, model validation, dispersal, GIS.

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