

**ECOLOGICAL SOCIETY OF AMERICA 93RD ANNUAL MEETING
THE MIDWEST AIRLINES CENTER, MILWAUKEE, WI
AUGUST 3 – 8, 2008**

Incorporating effects of landscape heterogeneity on pathogen dispersal into spatially-explicit disease models

Alicia M. Ellis, UNC-Charlotte and Ross K. Meentemeyer, University of North Carolina, Charlotte.

Background/Question/Methods

Many spatially-explicit disease models have determined the probability of an area becoming infected or the force of infection in a particular area by calculating the straight line distances to known sources of infection, and incorporating a Euclidean-based dispersal kernel into a predictive disease model. However, these Euclidean-based dispersal kernels may only be appropriate for describing patterns of dispersal in homogeneous environments. The dispersal of most pathogens is influenced by a variety of landscape features such as the distribution of hosts, which may render Euclidean distances a less meaningful measure of the probability of reaching a given site. In these situations, the least-cost distance between sites based on the distribution of hosts and host habitat may be more appropriate.

In this study, we used a geographic information system (GIS) to examine the degree to which considering spatial heterogeneity of host habitat increases predictive power of dispersal kernel models for the emerging infectious disease Sudden Oak Death. Because the Sudden Oak Death pathogen (*Phytophthora ramorum*) is moderately dispersal limited, we hypothesize that conventional Euclidean-based dispersal kernels should not perform as well as models that incorporate heterogeneity into the dispersal estimation process. We first used a map of host (i.e., woodland) and non-host (e.g., grassland, agricultural land, residential developments) vegetation (derived from ADAR multispectral aircraft imagery) to calculate Euclidean and least-cost distances between 86 previously established plots in Sonoma County, CA. We then used field data to model the number of infected leaves in each plot (a measure of disease severity) as a function of the local density of primary foliar hosts, abiotic variables (i.e., precipitation, temperature, canopy cover, solar radiation, and topographic moisture index), and the force of infection from surrounding plots. The force of infection was modeled as a negative

exponential dispersal kernel using either straight line or least-cost distances between plots.

Results/Conclusions

Our results demonstrate that although kernels based on Euclidean distances perform reasonably well in predicting disease severity, models that incorporate spatial heterogeneity of host habitat through least-cost path modeling perform better and are more epidemiologically relevant.