

Informal Comparative Review of *Phytophthora ramorum* Models

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DRAFT FOR REVIEW BY PARTICIPANTS OR CONFERENCE DELEGATES

Summary

Eight national-scale *P. ramorum* risk models were compared in a conference call and meetings. The models were sub-divided into two groups: those that used *P. ramorum* observations and those that do not. In general, models that use *P. ramorum* observations appear to predict a more restricted distribution than those that do not. A comparison of the models reveals a consistent national pattern of high risk in the coastal North-West and the central Appalachian Mountains, and low risk through the Great Plains. The models differ in predicting the extent of risk in the North East, coastal California, parts of the South East and the Northern Mid West. The greatest uncertainty appears to be: i) the extent of the Northern boundary of risk east of the Rockies; and ii) the degree of risk in the South East. Most likely comparing the output from multiple models gives decision makers more information than a single model alone.

Participants

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Objective

There have been numerous efforts to create predictive models for *Phytophthora ramorum*, causal agent of Sudden Oak Death. The purpose of this report is to review prediction models for *P. ramorum* which have been developed within the United States and Canada. With respect to this task, we have decided to limit the scope of this document to national scale risk models, although several other studies at the regional or state scale exist. The predictive models reviewed have been created by a variety of methods including rule-based relationships, infection models, training algorithms based on presence and absence data and a combination of methods. Since different modeling approaches may create different recommendations for survey, detection and eradication, APHIS Pest Detection and Management Programs requested a comparative review of models, particularly with respect to northern climates. To facilitate this task, an APHIS-CPHST sponsored a conference call with participants from the United States and Canada in September of 2005. This call was

followed with a meeting held in early November in Asheville, NC and sponsored by the US Forest Service.

Model Descriptions

The most important sub-division of the predictive models is their need for *P. ramorum* observations (distribution). Models that do not use *P. ramorum* observations use rules or models to predict pathogen distribution based on climate or other variables. (Smith, 2002; Smith et al., 2002; Kelly et al., 2005; Mentemeyer et al., 2004; Magarey et al., 2005a). Other models use rules or algorithms to predict *P. ramorum* distribution based on relationships between the observed pathogen distribution and climate or other variables (McKenney et al., 2003, Kelly et al., 2005). Models that do not use observed pathogen data may over simplify relationships with climate variables. For example, the NAPPFAST system (Borchert and Magarey, 2004) uses an infection model (Magarey et al., 2005b) combined with host distribution data; consequently, it may not reflect establishment. Including lethal cold temperature improves the prediction of establishment but there is some uncertainty about the lethal cold threshold since the data set (DEFRA, 2005) used to determine the lethal cold temperatures is quite limited. This leads to uncertainty in the northern boundary of risk in the NAPPFAST model. Models that use *P. ramorum* observations may underestimate disease risk due to the current restricted distribution. *P. ramorum* establishment in North America is currently confined to mild coastal climates; therefore, extrapolation based on presence/absence data may be problematic. Using a combination of models, such as the Kelly combination model, may improve this estimate (Kelly et al., 2005). Nursery observations are more widely distributed but may be questionable, since these observations do not represent establishments in ambient environment.

For each model, we compared the spatial resolution, the climate input variables, host data, requirement for *P. ramorum* observations, variables selection and outputs (Table 1). The spatial resolution varies from 1 to 10 km². Most models use annual or monthly climate variables (usually averages or sums); the NAPPFAST model uses daily climate data. Important variable selection is either “*A priori*,” using variables chosen by the modeler at the beginning of the analysis rather than “Through training,” using variables chosen by the model that best fit the observed pathogen distribution.

Model Performance

The final model output for the United States is presented for each group (Table 2). A comparison of the models reveals a consistent national pattern of high risk in the coastal North West and the central Appalachian Mountains, and low risk through the Great Plains. The models differ in predicting the extent of risk in the North East, coastal California, parts of the South East and the Northern Mid West. In our opinion, the greatest uncertainty is: i) the extent of the Northern boundary of risk east of the Rockies; and ii) the degree of risk in the South East. In general, models that use *P. ramorum* observations appear to predict a more restricted distribution than those that do not. Most likely comparing the output from multiple models gives decision makers more information than a single model alone.

Table 1—Characteristics of selected *P. ramorum* models.

Group	Model Name	Spatial Resolution	Climate Input Variables	Host Data	<i>P. ramorum</i> Presence/absence data required?	Important Variable Selection	Output
USFS Smith	Rule based	Unknown	Monthly max, min temperature, rainfall,	Unknown	No	<i>A priori</i>	Survey grids
CPHST NAPP-FAST	NAPPFAST	10 Km ²	Daily average temperature, daily total leaf wetness hours, annual extreme min temperature	Forest cover data USFS 1991	No	<i>A priori</i>	Probability
UCB Kelly	Rule-based		Total annual precipitation, total annual frost days, average minimum temperature, average maximum temperature and average maximum august temperature (Day Met)	Deciduous, conifer, mixed (National Land Cover Data 1992)	No	<i>A priori</i>	Ranked
UCB Kelly	Logistic Regression			Land Cover Data 1992)	Yes	Through training	Probability
UCB Kelly	Classification and Regression Tree	1 km ²		Hardwood diversity index (Digital tree range maps for North America)	Yes	Through training	P/A based on # runs
UCB Kelly	Genetic Algorithm			Percentage forest basal area in red and live oak group (USFS N. Eastern Research Station)	Yes	Through training	P/A based on # runs
UCB Kelly	Support Vector Machines				No (1-class) Yes (2-class)	Through training	P/A based on # runs
McKenney Natural Resources Canada	Bioclimatic Regression	10 Km ²	Annual Mean Temperature Mean Diurnal range Max, min, mean Temperature of warmest and coldest Periods Temperature Annual Range Precipitation of Warmest/coldest Quarter	Not used in this version of model	Yes Nursery data also used	Through training	?????

Table 2. Model results

Group	Map
USFS Smith	
CPHST NAPFFAST No lethal cold exclusion (Magarey et al., 2005; Borchert and Magarey, 2005)	
CPHST NAPFFAST Lethal cold exclusion (Magarey et al., 2005; Borchert and Magarey, 2005; DEFRA, 2005)	
UC Berkeley Kelly Rule-based (Kelly et al., 2005)	

Table 2. Model results


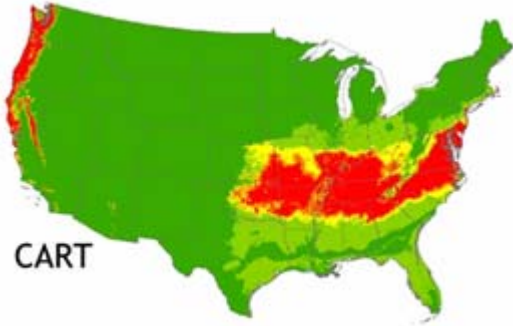


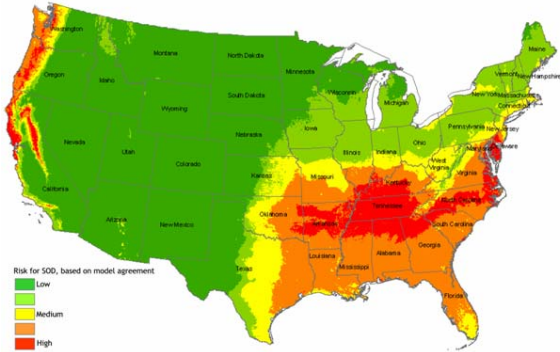
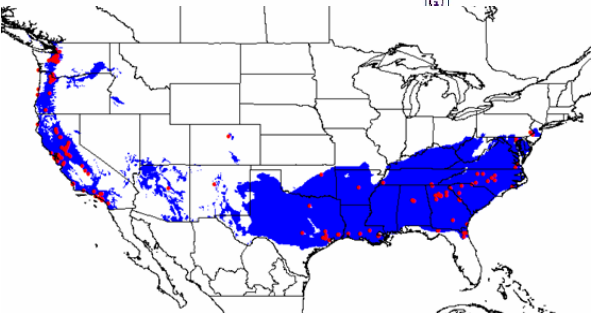
Group	Map
UC Berkeley Kelly Logistic Regression (Kelly et al., 2005)	 <p data-bbox="656 573 818 646">Logistic Regression</p>
UC Berkeley Kelly Classification and Regression Tree (Kelly et al., 2005)	 <p data-bbox="667 919 748 951">CART</p>
UC Berkeley Kelly Genetic Algorithm (Kelly et al., 2005?)	 <p data-bbox="656 1308 737 1339">GARP</p>
UC Berkeley Kelly Support Vector Machines (Guo et al., 2005)	 <p data-bbox="678 1675 743 1707">SVM</p>

Table 2. Model results

Group	Map
UC Berkeley Kelly Combination (Kelly et al., 2005)	 <p>Risk for SDD, based on model agreement</p> <ul style="list-style-type: none">LowMediumHigh
Natural Resources Canada <i>McKenney</i> (<i>Mc Kenney et al., 2003</i>)	

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