NAPPFAST
NCSU APHIS Plant Pest Forecasting System

BRIEF WEATHER BASED PEST RISK MAPPING PROJECT

RISK ASSESSMENT:

Xylella fastidiosa subsp. *pauca*, Citrus Variegated Chlorosis

Cooperative agreement between NCSU and

USDA-APHIS-PPQ-CPHST-PERAL

I. Rationale

We developed this risk assessment to assess the climatic favorability of the United States for Citrus Variegated Chlorosis (CVC).

Image: (L) www.ars.usda.gov/Research//docs.htm?docid=8361; (R) http://www.padil.gov.au/viewPestDiagnosticImages.aspx?id=499

II. Life History and Biology

Citrus variegated chlorosis (CVC) of *Citrus* spp. is caused by *Xylella fastidiosa* subsp. *pauca*, a fastidious Gram-negative bacterium (Schaad et al., 2004; Wickert et al., 2007; Van Sluys et al., 2003). The pathogen can move via contaminated budwood, root grafting, seeds, and insect vectors (Li et al., 2003). This bacterium is transmitted specifically by the Hemiptera:

Cicadellidae and Hemiptera: Cercopidae species such as the glassy-winged sharpshooter (*Homalodisca coagulata* (Say)), which has become established in California (Redak et al., 2004), and the native *Homalodisca liturata* (Park et al., 2006). In the United States the most common vectors of Pierce's disease on grapes (caused by *Xylella fastidiosa* subsp. *fastidiosa*), which could also transmit CVC, are *Xyphon* (*Carneocephala*) *fulgida* (Nottingham), *Draeculacephala minerva* (Ball), *Graphocephala atropunctata* (Signoret), and *Oncometopia* spp. (Nielson, 1979; Purcell and Frazier, 1985; Turner and Purcell, 1959).

While *Xylella fastidiosa* subsp. *fastidiosa* cannot cause disease on *Citrus* spp., *X. f.* subsp. *pauca* can cause disease on *Vitis* spp. (Bi et al., 2007; Hopkins and Purcell, 2002). *Xylella f.* subsp. *fastidiosa* is limited by cold temperatures: 1) more than two days of temperatures below -12.2^{o}C or more than four days of temperatures below -9.4^{o}C (Sutton, 2005) and 2) multiple exposures of infected grape vines of 1.5 to 24 hours to temperatures ranging from –12 to 0°C (Purcell, 1977). Purcelll (1997) did not observe an upper limit of temperature for growth in *X. f.* subsp. *pauca*, indicating that summer growth in infected plant material is unhindered. Feil and Purcell (2001) observed an upper limit for growth in *X. f.* subsp. *fastidiosa* at 34°C.

Since *X. fastidiosa* are xylem-dwelling bacteria, seemingly uninfected plants may harbor the pathogen (Bi et al., 2007) (Table 1). The ability of *X. fastidiosa* to survive at replicating levels without causing disease can be a source for initial inoculum (Bi et al., 2007) and spatial analysis of epidemics in vineyards next to orchards has established a localized effect of the orchard on Pierce's disease (Park et al., 2006). This phenomenon of spread from orchards to vineyards may also be caused by overwintering of the insect vectors in the orchards. For example, citrus trees have been shown to be the preferred overwintering area for *Homalodisca coagulata* (Blua et al., 1999, Blua et al., 2001).

III. Prediction Model

The CVC prediction model was created using the NCSU-APHIS Plant Pest Forecast System (NAPPFAST). The NAPPFAST system uses a web-based graphical user interface to link climatic and geographic databases with templates for biological modeling. The NAPPFAST system includes two daily weather databases with over 30 years of records. The global database is based upon the National Centers for Environmental Prediction (NOAA/NCEP) Global Reanalysis II data set (Kalnay et al., 1996). This data set is a numerical grid created for use as input data for meteorological models. The spatial resolution of the grid is 28 km, which has been resampled from a 1.875 degree (210 km) resolution. Station data from the International Station Hourly (ISH) data (Lott et al., 2001) were used to supplement the NCEP backbone. The North American database includes over 2000 stations for North America (Magarey et al., 2007). The input weather data was interpolated to a 10 km^2 resolution using a 3-D multivariate interpolation (Splitt and Horrel, 1998). The database includes both native variables (e.g., air temperature) and derived variables (e.g., leaf wetness).

We created a cold temperature exclusion model using thresholds developed for *X. f.* subsp. *fastidiosa* in *Vitis* spp. (grape) where the behavior of the pathogen is well understood. *Xylella f.* subsp. *pauca* and *X. f.* subsp. *fastidiosa* have 98% genetic similarity (Van Sluys et al., 2003). The CVC cold exclusion model had the following parameters: T_{min} = -12 and -9.4°C for 2 and 4 days, respectively. The frequency of years where the number of days exceeded each threshold was separately mapped for North America based on 10 years of climate data. We averaged the frequency maps for each threshold to create the annual cold exclusion map in ArcMap using the raster calculator. The cold exclusion risk map was then combined with the host acres of citrus and grape in the United States to create a final risk map.

IV. Results

We mapped the current distribution of this pathogen using data from Purcell (1997) and Schaad et al. (2004) (Fig. 1) and provided a map of the *Citrus* spp. and *Vitis* spp. cultivation in the United States (Fig. 2). The cold exclusion map (based on the average of the two cold exclusion thresholds probability maps, <-12°C for ≥2 days and <-9.4°C for ≥4 days) was used to create a NAPPFAST map to indicate where the bacteria would flourish (Fig. 3). The final risk map, a summation of the host acres and exclusion temperatures, shows that the entire production zone for *Citrus* spp. could be affected (Fig. 4). In California, the *Vitis* spp. production area would also become infected with *X. f.* subsp. *pauca* and have an opportunity to overwinter.

V. Discussion

Our analysis suggests that large areas of *Vitis* spp. production and all of the *Citrus* spp. production could become infected based on the conservative estimates of overwintering potential of *X. f.* subsp. *pauca* in host plants in the United States (Fig. 4). Furthermore, spread of this bacterium would be nearly exponential in these areas where native Hemiptera: Cicadellidae and Hemiptera: Cercopidae species exist because these vectors can quickly acquire the bacterium and spread it over their lifetime (Redak et al., 2004). Control of this disease is through eradication of infected crop plants, weedy host control, lowering of the vector numbers, and cold treatment of infected crop material. These control measures are expensive and also cause lost revenue due to exportation quarantines from the areas that would be affected.

VI. Authors

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VII. References Cited

Bi, J. L., C. K. Dumenyo, R. Hernandez-Martinez, D. A. Cooksey, and N. C. Toscano. 2007. Effect of host plant xylem fluid on growth, aggregation, and attachment of *Xylella fastidiosa*. Journal of Chemical Ecology 33:492-500.

Blua, M. J., P. A. Phillips, and R. A. Redak. 1999. A new sharpshooter threatens both crops and ornamentals. California Agriculture 53:22-25.

Blua, M. J., R. A. Redak, D. J. W. Morgan, and H. S. Costa. 2001. Seasonal flight activity of two Homalodisca species (Hemiptera:Cicadellidae) that spread *Xylella fastidiosa* in southern California. Journal of Economic Entomology 94:1506-1510.

CABI. 2007. *Xanthomonas oryzae* pv. *oryzae* (rice leaf blight). Commonwealth Agricultural Bureau International (CABI), Wallingford, UK.

Feil, H. and A. H. Purcell. 2001. Temperature-dependent growth and survival of *Xylella fastidiosa* in vitro and in potted grapvines. Plant Disease 85:1230-1234.

Hopkins, D. L. and A. H. Purcell. 2002. *Xylella fastidiosa*: Cause of Pierce's disease of grapevine and other emergent diseases. Plant Disease 86(10):10561066.

Kalnay, E., M. Kanamitsu, R. Kistler, W. Collins, D. Deaven, L. Gandin, M. Iredell, S. Saha, G. White, J. Woollen, Y. Zhu, A. Leetmaa, R. Reynolds, M. Chelliah, W. Ebisuzaki, W. Higgins, J. Janowiak, K. C. Mo, C. Ropelewski, J. Wang, R. Jenne, and D. Joseph. 1996. The NCEP/NCAR 40-Year Reanalysis Project. Bulletin of American Society of Meteorology 77:437-471.

Li, W.-B., W. D. Pria Jr., P. M. Lacava, X. Qin, and J. S. Hartung. 2003. Presence of *Xylella fastidiosa* in sweet orange fruit and seeds and its transmission to seedlings. Phytopathology 93(8):953-958.

Magarey, R. D., G. A. Fowler, D. M. Borchert, T. B. Sutton, M. Colunga-Garcia, and J. A. Simpson. 2007. NAPPFAST an internet tool for the weather-based modeling of plant pathogens. Plant Disease 91:336-345.

Nielson, M. W. 1979. The leafhopper vectors of phytopathogenic viruses (Homoptera: Cicadellidae). U.S. Department of Agriculture Technical Bulletin (1382):1-386.

Park, Y.-L., T. M. Perring, R. K. Krell, C. A. Farrar, and C. Gispert. 2006. Saptial distribution of Pierce's disease in the Coachella Valley: Implications for sampling. American Journal of Enology and Viticulture 57(2):220-225.

Purcell, A. H. 1977. Cold therapy of Pierce's disease of grapevines. Plant Disease Reporter 61:514-518.

Purcell, A. H. 1997. *Xylella fastidiosa*, a regional problem or global threat? Journal of Plant Pathology 79(2):99-105.

Purcell, A. H. and N. W. Frazier. 1985. Habitats and dispersal of the leafhopper vectors of Pierce's disease in the San Joaquin Valley USA. Hilgardia 53(1):1-32.

Redak, R. A., A. H. Purcell, J. R. S. Lopes, M. J. Blua, R. F. Mizell III, and P. C. Anderson. 2004. The biology of xylem fluid-feeding insect vectors of *Xylella fastidiosa* and their relation to disease epidemiology. Annual Revue of Entomology 49:243-270.

Schaad, N. W., E. Postnikova, G. Lacy, M. Fatmi, and C.-J. Chang. 2004. *Xylella fastidiosa* subspecies: *X. fastidiosa* subsp *piercei*, subsp. nov., *X. fastidiosa* subsp. *multiplex* subsp. nov., and *X. fastidiosa* subsp. *pauca* subsp. nov. Systematic and Applied Microbiology 27:290-300.

Sutton, T. B. 2005. Progress Report: Pierce's Disease Risk Zones in the Southeast. Personal communication.

Turner, W. F. and H. N. Purcell. 1959. Life histories and behavior of five insect vectors of phony peach disease. U. S. Department of Agriculture Technical Bulletin 1188:1-32.

Van Sluys, M. A., M. C. de Oliveira, C. B. Monteiro-Vitorello, C. Y. Miyaki, L. R. Furlan, L. E. A. Camargo, A. C. R. da Silva, D. H. Moon, M. A. Takita, E. G. M. Lemos, et al. 2003. Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of *Xylella fastidiosa*. Journal of Bacteriology 185(3):1018-1026.

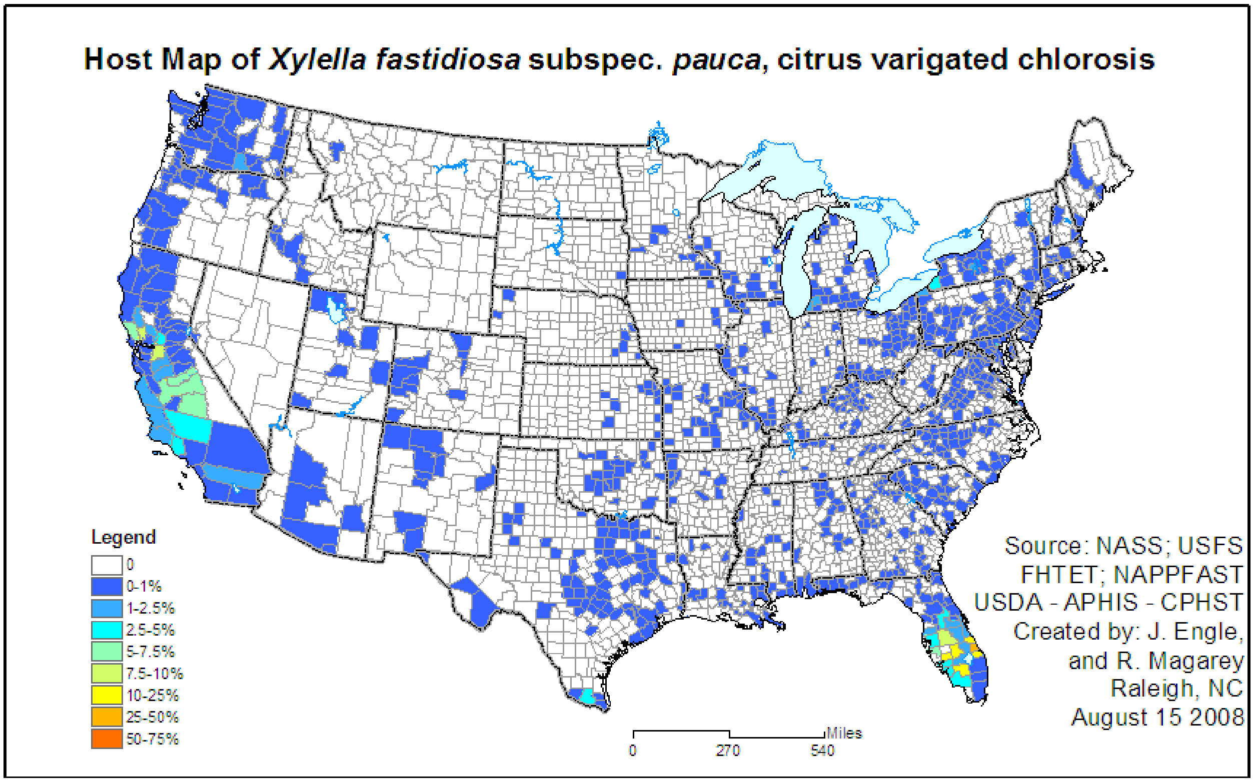
Wickert, E., M. A. Machado, and E. G. M. Lemos. 2007. Evaluation of genetic diversity of *Xylella fastidiosa* strains from citrus and coffee hosts by single-nucleotide polymorphism markers. Phytopathology 97(12):1543-1549.

VIII. Tables and Figures

Table 1. A host list for *Xylella fastidiosa* (CABI, 2007). Not all hosts can be infected with strains from other hosts, nor do all hosts that are infected become symptomatic.

Scientific name	**Common name**
Acer spp.	Maples
Brachiaria spp.	Singlegrass
Carya illinoinensis	Pecan
Citrus spp.	Citrus trees
Coffea spp.	Coffee
Conium maculatum	Poison hemlock
Cynodon spp.	Quickgrass
Cyperus spp.	Flatsedge
Digitaria spp.	crabgrass
Echinochloa frumentacea	Japanese millet
Fragaria vesca	Wild strawberry
Liquidambar styraciflua	Sweet gum
Lolium spp.	Ryegrass
Lolium multiflorum	Italian ryegrass
Medicago spp.	Medic
Medicago sativa	Alfalfa
Morus alba	Mora
Nerium oleander	Oleander
Poaceae spp.	Grasses
Prunus spp.	Almond, peach, plum
Pyrus spp.	Pear
Quercus rubra	Northern red oak
Rubus spp.	Blackberry, raspberry
Sambucus spp.	Elderberry
Taraxacum officinale complex	Dandelion
Trifolium spp.	Clovers
Ulmus spp.	Elm
Vitis spp.	Grapes

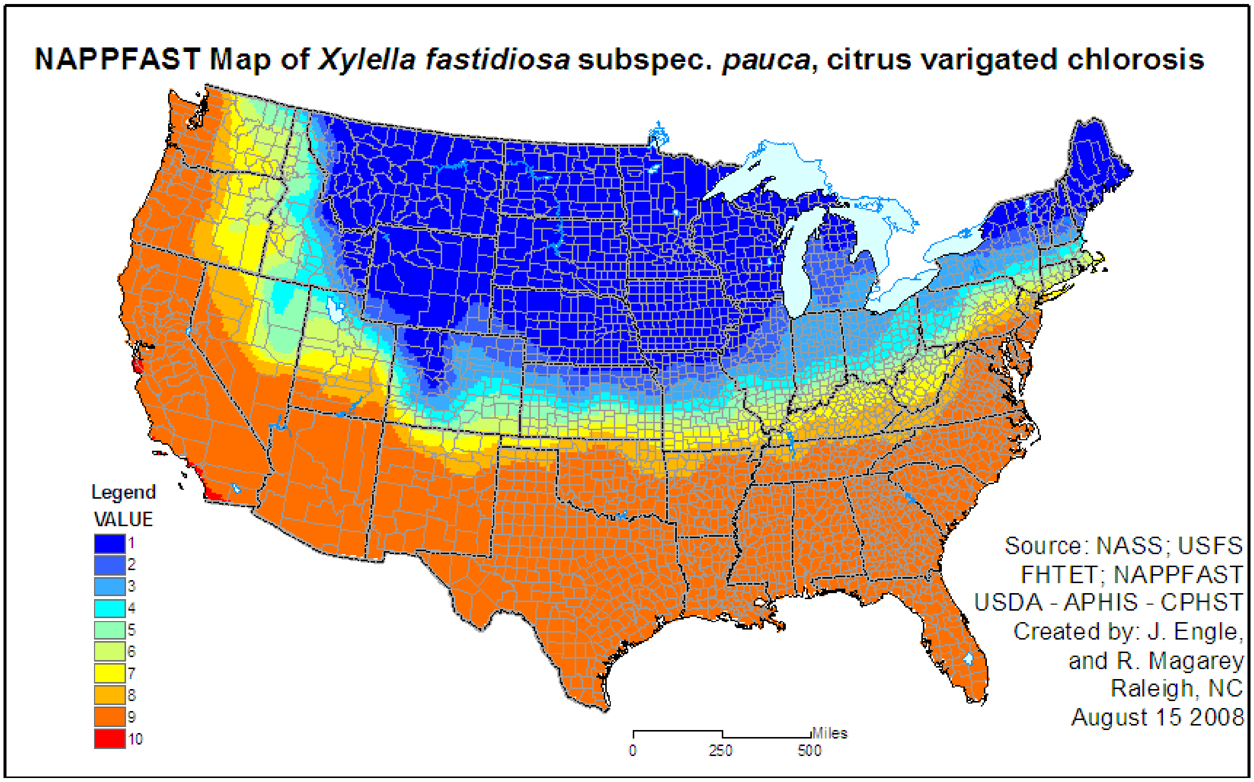
Figure 1. Areas of the world where *Xylella fastidiosa* subsp. *pauca* has been reported to occur (highlighted in green).



Host Map of *Xylella fastidiosa* subspec. *pauca*, citrus varigated chlorosis

Source: NASS; USFS FHTET; NAPPFAST
USDA - APHIS - CPHST
Created by: J. Engle, and R. Magarey
Raleigh, NC
August 15 2008

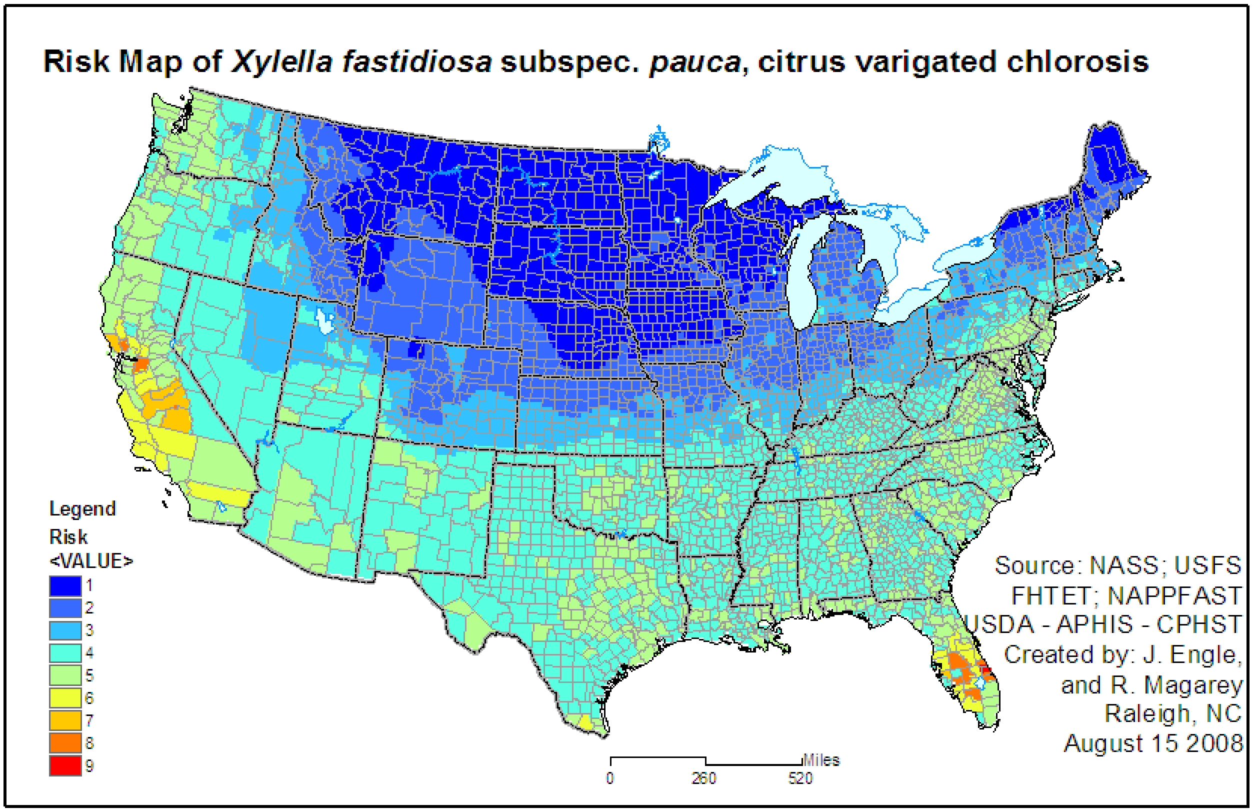
Figure 2. Percentage of county acres in the United States where *Citrus* spp. and *Vitis* spp. are commercially cultivated from data downloaded from the NASS website. Weedy or wild hosts have been excluded due to the inability to accurately estimate distribution and acreage.



NAPPFAST Map of *Xylella fastidiosa* subspec. *pauca*, citrus varigated chlorosis

Source: NASS; USFS FHTET; NAPPFAST USDA - APHIS - CPHST Created by: J. Engle, and R. Magarey Raleigh, NC August 15 2008

Figure 3. Areas of the United States where temperatures are expected to limit the overwintering ability of *Xylella fastidiosa* subsp. *pauca* are lower in value while areas where the bacteria would be able to flourish are closer to a value of ten. The NAPPFAST map was based on ten years of historical weather data.


Risk Map of *Xylella fastidiosa* subspec. *pauca*, citrus varigated chlorosis

Source: NASS; USFS FHTET; NAPPFAST USDA - APHIS - CPHST
Created by: J. Engle, and R. Magarey
Raleigh, NC
August 15 2008

Figure 4. The relative biological potential (risk) of the United States for establishment of *Xylella fastidiosa* subsp. *pauca* in *Citrus* spp. and *Vitis* spp. commercial cultivation as well as alternate weedy hosts not listed.