Climate-driven global-risk maps for the establishment of Pierce's Disease of grapevines

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Abstract

The clonal lineage of the bacterium *Xylella fastidiosa* (Xf) responsible for Pierce's disease (PD) poses a threat to viticulture worldwide. Although this vector-transmitted disease has remained mainly restricted to the United States, recent introductions on the islands of Majorca (Spain) and Taiwan have raised concerns about the risk of spreading worldwide. To assess this risk, here we build a climate-driven epidemiological model that simulates PD progression. The model considers the temperature-dependent infection process based on a 3-year inoculation assay and assume local disease propagation when climatic conditions are favourable. The model was successfully validated with spatiotemporal data of the PD distribution in the United States yielding a remarkable ~90% accuracy. Thereafter the model was applied to the main winegrowing regions worldwide, specially focusing in Europe as a case study based on the distribution of the main vector, *Philaenus spumarius*. Our model simulation reveals that most wine-quality producing areas in China, Europe, Argentina, Chile, South Africa, and Australia currently thrive in non-risk or transient-risk zones. To a lesser extent, epidemic-risk zones with low to moderate risk indices appear in coastal zones such as Mallorca and Apulia, where Xf outbreaks have been already detected. The European case shows how models assuming a vector heterogeneous distribution yield lesser extended epidemic-risk zones than previous risk maps. Overall, a global expansion of PD epidemic-risk zones is projected for 2050, although with low increase in risk indices. Our study highlights the importance of considering climate variability and an invasive criterion to obtain precise risk maps for plant health decision-making.

Model construction

Standard SIR compartmental model for PD transmission

$$I(t) = I(0)\exp(\gamma(R_0 - 1)t)$$

Temperature-dependent infection process modeled with a climatic layer based on the temperature-dependent growht rate of Xf together with a 3-years inoculation assay (MGDD) and the winter curing effect (CDD)

$$\Pi(t) = \mathcal{F}(MGFF(t)) \cdot \mathcal{G}(CDD(t))$$

A spatially-homogeneous vector distribution is assumed except for Europe, where information on the spatial distribution of *P. spumarius* is available. The equation representing the evolution of the infected population is written as

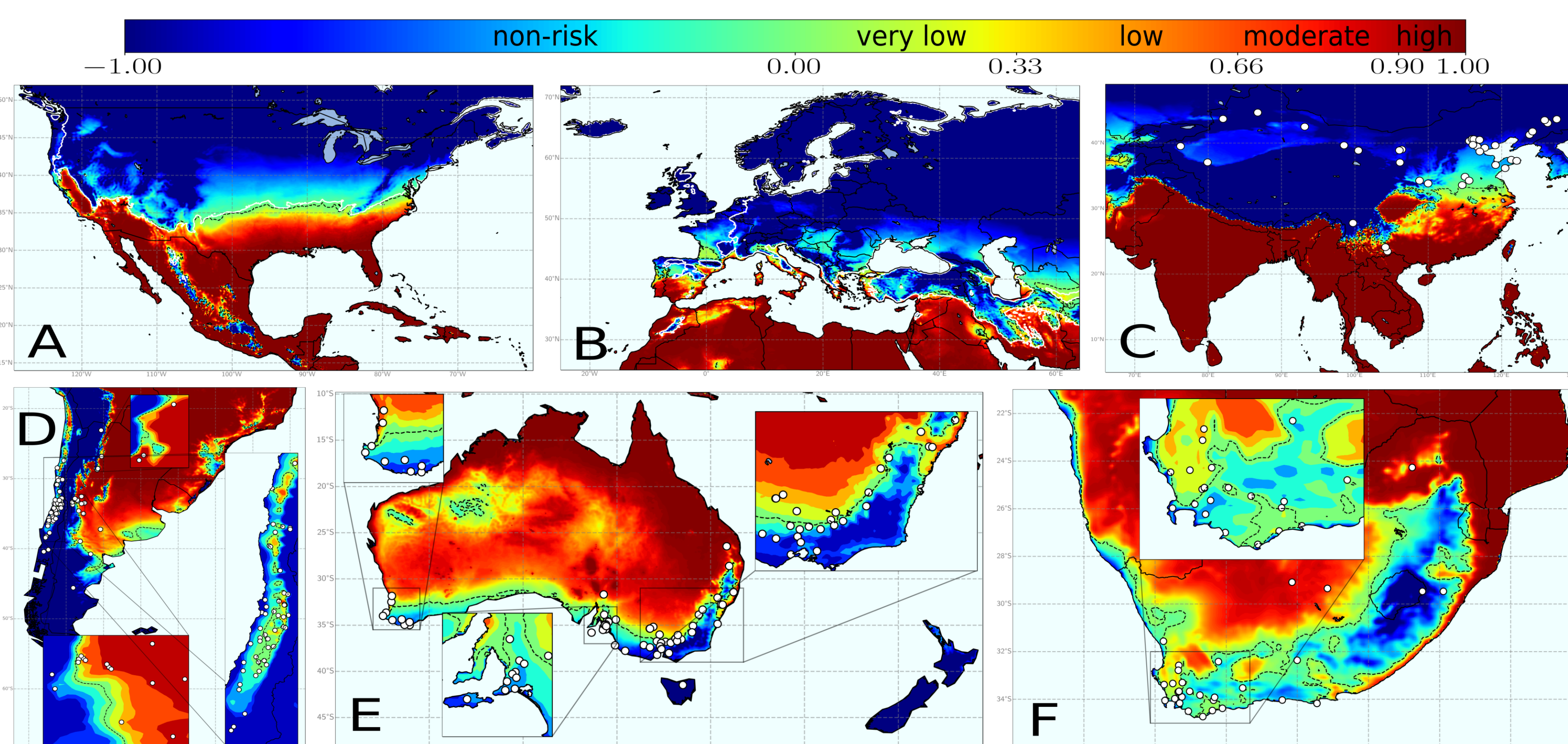$$I_j(t) = I_j(t-1)e^{\gamma(R_0-1)}\Pi_j(t)$$
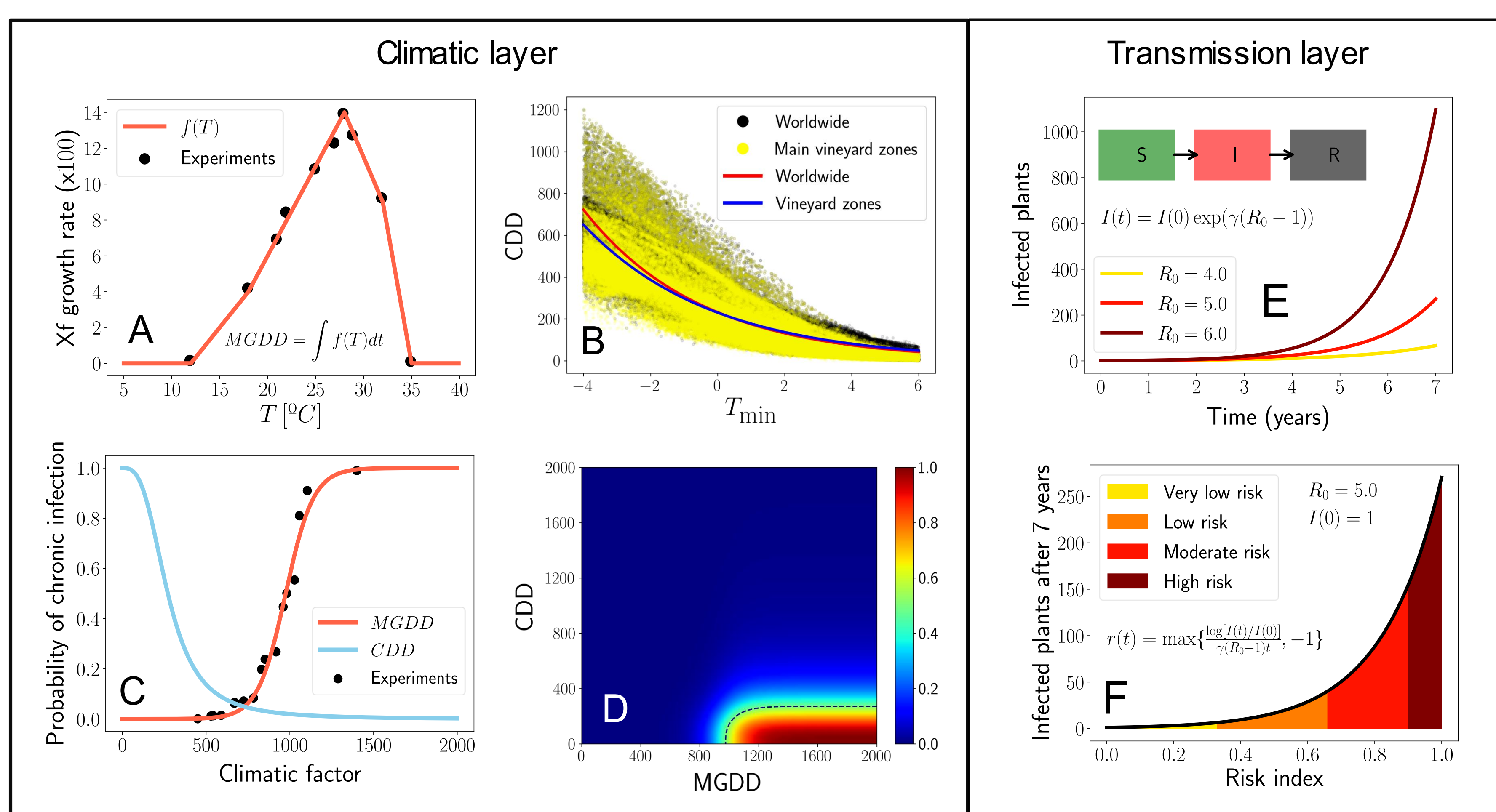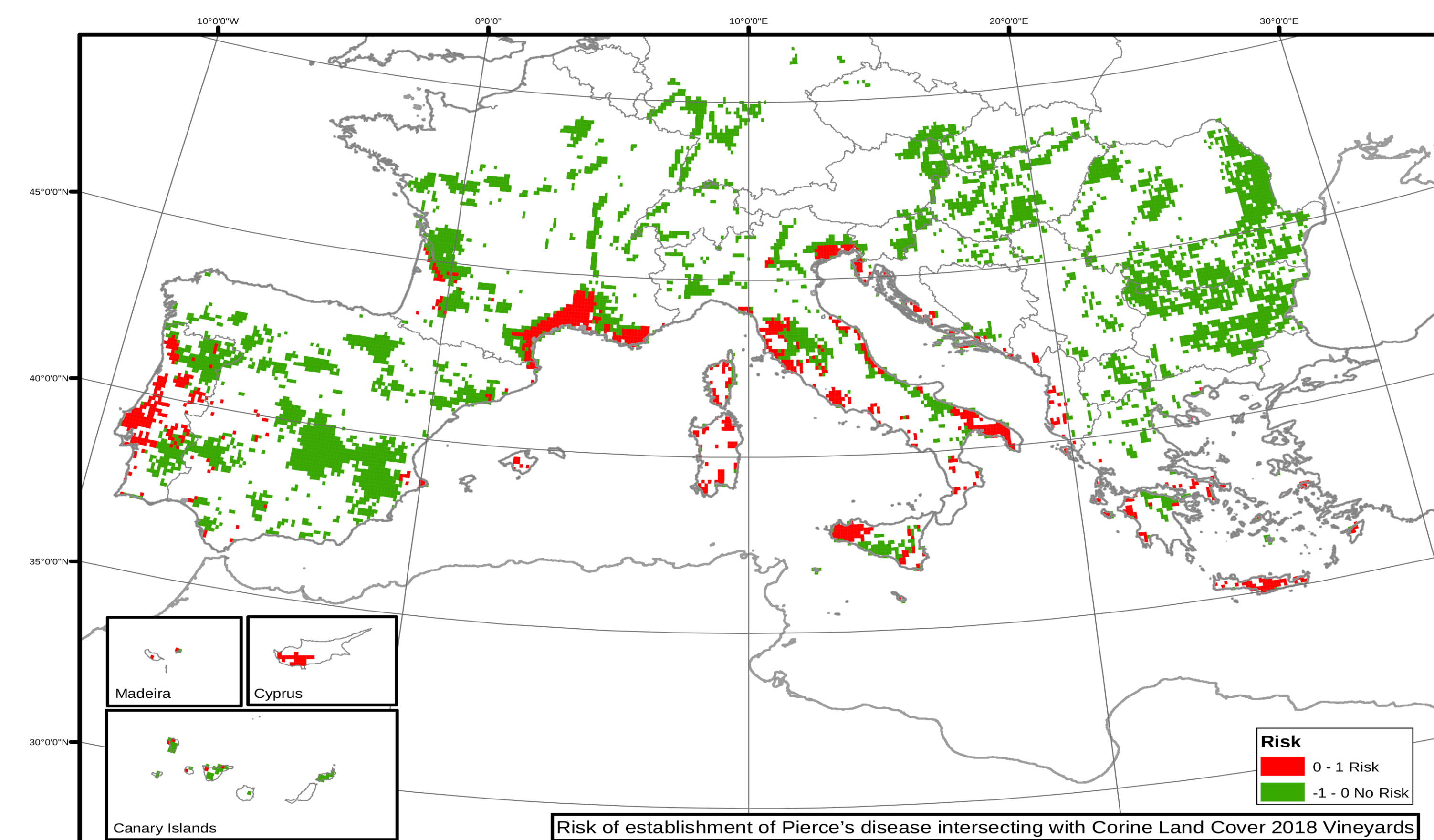

Model validation

TABLE II. **Validation of model predictions.** The items are locations where PD was present or absent. TP corresponds to true positives and TN to true negatives according to our model with $R_0 = 8$.

Year	Presence	Absence	TP	TN	Accuracy
2001	16	5	15	3	86%
2002	12	2	11	1	86%
2005	4	2	4	1	83%
2006	8	0	4	0	50%
2015	53	0	51	0	96%
TOTAL	93	9	85	5	88%

Homogeneous vector distribution

Heterogeneous vector distribution

Risk of establishment of Pierce's disease intersecting with Corine Land Cover 2018 Vineyards

Risk
0 - 1 Risk
-1 - 0 No Risk

Conclusions

■ The model was successfully validated with ~90% accuracy.

■ Most wine-quality producing areas in non-risk or transient-risk zones.

■ Epidemic-risk zones with low to moderate risk indices appear in coastal zones.

■ Heterogeneous vector distribution yield lesser extended epidemic-risk zones.

■ Expansion of PD epidemic-risk zones for 2050, but with low increase in risk indices.

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