

A transmission model for the Potato yellow vein virus-*Trialeurodes vaporariorum*- potato pathosystem

Heidy Gamarra¹ • Pablo Carhuapoma¹ • Jürgen Kroschel¹ • Jan Kreuze¹ •

¹ International Potato Center (CIP). DCE Crop Systems Identification and Climate Change Division • Av. La Molina 1895. La Molina. Lima 12. Perú

Background

- Potato yellow vein virus (PYVV, genus *Crinivirus*) is transmitted by the greenhouse whitefly *Trialeurodes vaporariorum* endemic to Colombia and Venezuela.
- As a consequence of climate change there is a risk of geographical range expansion of this virus, which has during the last 30 years spread South as far as Northern Peru.
- A temperature based phenology model implemented in the ILCYM software [1] was previously developed for the insect vector *T. vaporariorum* to predict changes in multiplication rate, survival and activity of the vector [2]. However the model does not take into account the effect of temperature on virus transmission efficiency.
- In this study, we developed a temperature dependent virus transmission sub-model to be integrated into the ILCYM software to enable predictions of risk and potential for virus spread on global, regional, or national scales (Figure 1).



Figure 1. Potato fields (left) and plants (center) showing symptoms of PYVV infection, which can reduce yields by 50% (right)

Methods & Results

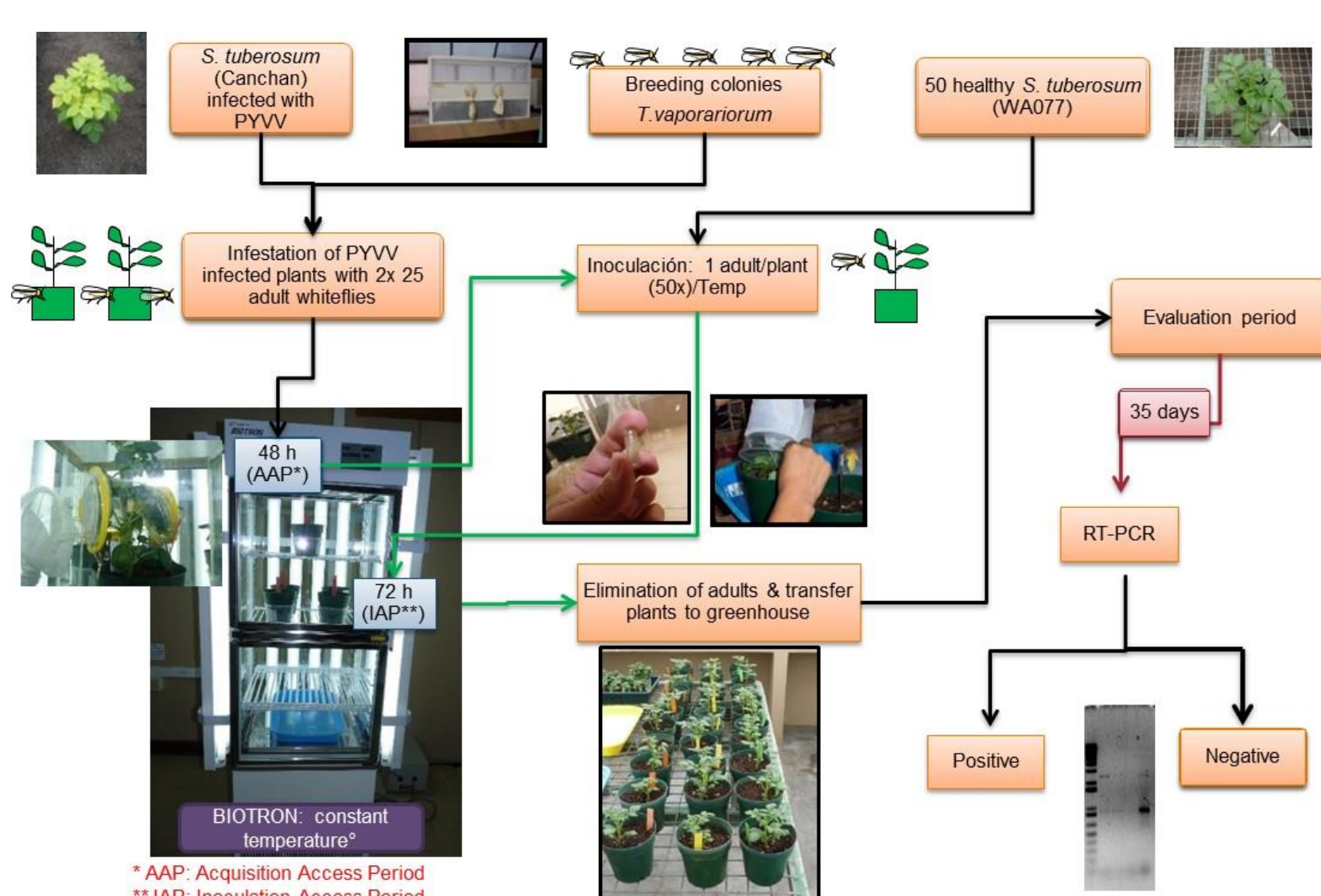


Figure 2. PYVV transmission by *T. vaporariorum* was determined at 8 constant temperatures between 10°C - 28°C by 50 single insect transmissions in 2 or 3 replications. The model was validated by transmissions at natural fluctuating temperatures during three distinct seasons at Lima, Peru, confirming the expected transmission rates.

At each geographic data point, ILCYM uses the functions f , g & q (Fig. 3) of *T. vaporariorum* to calculate the annual transmission potential (PAT), and generates risk maps (Figs. 4 & 5), with the following expressions:

$$PAT_{(Longitude, Latitude)} = \frac{\sum_{k=1}^{365} ((p_k)(s_k))(o_k)}{365}$$

The accuracy of the model was estimated using georeferenced data on presence or absence of the virus from field surveys performed in Colombia, Ecuador and Peru during 2007-2010, determining the PAT value with best prediction capability (Table 1):

	Presence	Absence
Estim_Presence	83	360
Estim_Absence	32	1034
Total	1509	

Table 1. Accuracy of prediction using PAT : $((83 + 1034)/(1509)) * 100 = 74\%$.

Regions where the PAT is >3 indicates temperature conditions where a certain proportion of *T. vaporariorum* population can transmit the virus throughout the year representing the regions where the risk is highest. In zones, where the PAT is less than 3, the risk of transmission of PYVV is reduced, however a risk of virus presence is maintained (PAT > 0.2).

Bibliography.

1. Sporleder M et al. 2013. Insect life cycle modelling (ILCYM) software – A new tool for regional and global Insect Pest Risk Assessments under current and future climate change scenarios. CAB International 2013. Potential Invasive Pest of Agricultural Crop (ed. J. Peña) 23: 412 – 427
2. Gamarra H. et al. 2016. Greenhouse whitefly, *Trialeurodes vaporariorum*. In: Pest Distribution and Risk Atlas for Africa- Potential global and regional distribution and abundance of agricultural and horticultural pests and associated biocontrol agents under current and future climates. Kroschel J et al. (eds.). CIP, Lima, Peru.

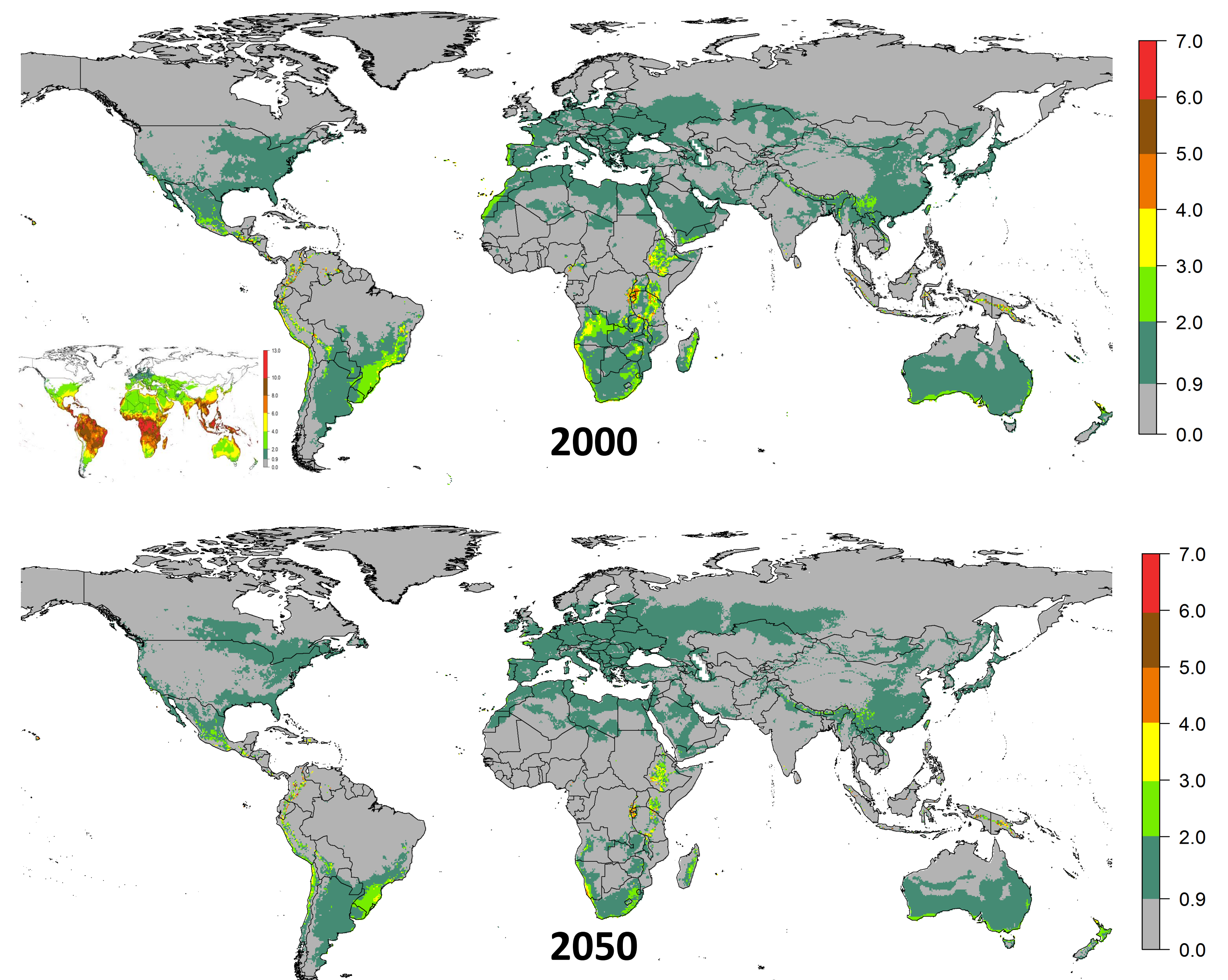


Figure 4. Annual transmission potential produces more precise risk maps for the risk of PYVV spread then using only the activity index (potential population growth) of *T. vaporariorum* (compare upper map to the inset on the lower left); using this approach, predictions are that transmission potential will reduce in tropical regions of the world, but increase in temperate regions under 2050 climate scenarios.

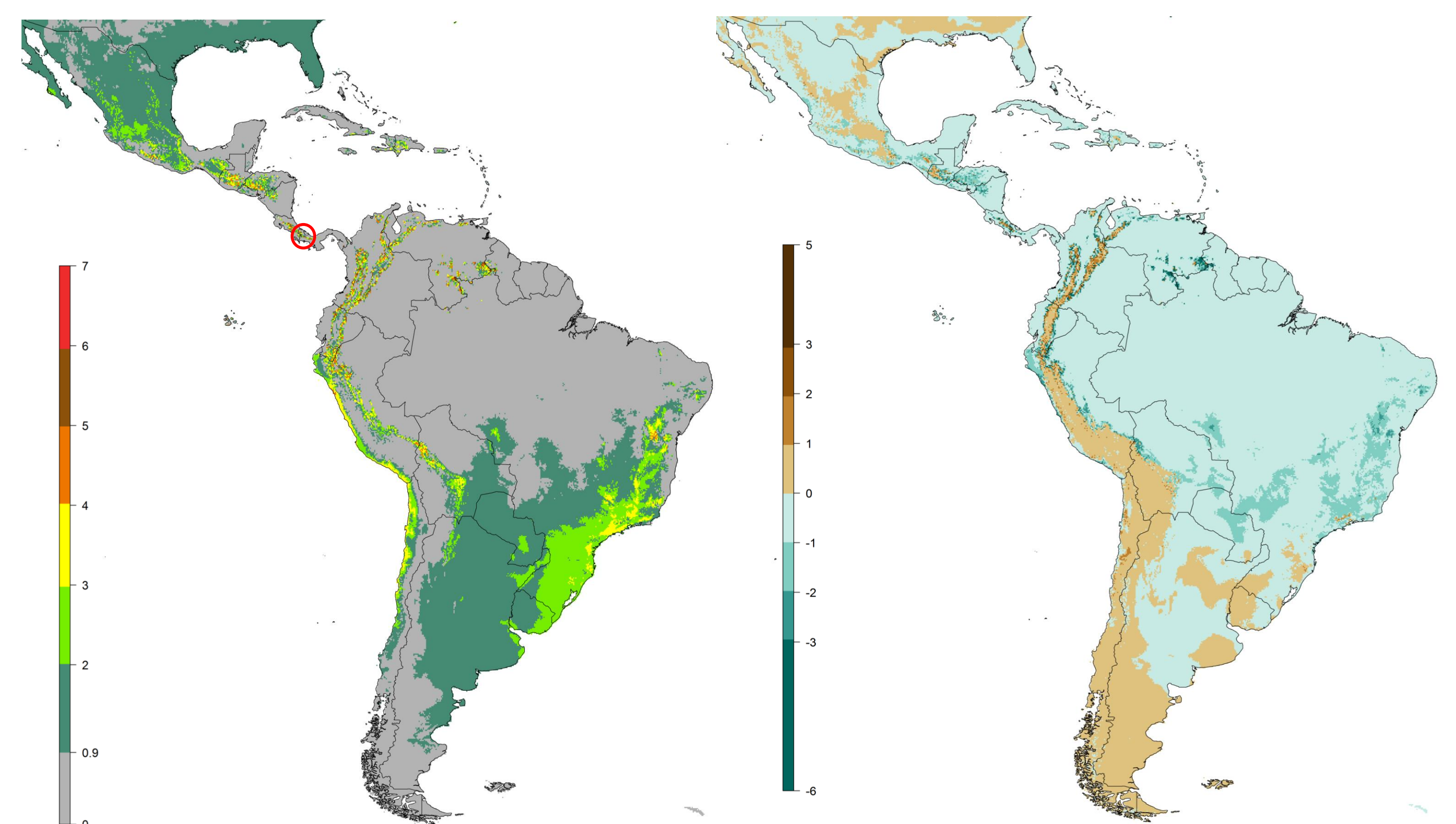


Figure 5. Predicted annual potential transmission risk for PYVV by *T. vaporariorum* in Latin America for the year 2000 (left), the red circle in Western Panama indicates a region predicted at high risk for virus transmission and was visited for surveillance confirming the presence of the virus; the map on the right, shows the change of this risk between 2000 and 2050 (right)

Using the maps a region in western Panama that was predicted to have high PAT risk (red circle in Fig 5) and PYVV had not yet been reported was identified and targeted for sample collection which confirmed abundant presence of the virus.

Conclusions & Recommendations

- The combination of *T. vaporariorum* phenology and PYVV transmission models identifies regions at risk of virus dissemination in support of surveillance.
- PYVV is predicted to have potential to spread to the southern regions of Peru, Bolivia, Chile and Argentina, and will increase in the future.
- Validation may be improved by removing surveyed regions of southern Peru, where PYVV is not yet present, and by including percentage of plants infected per surveyed field.
- The model could be modified for local epidemiological forecasting & decision support.