

# Potato Yellow Vein Virus: A model for emerging potato diseases and climate change

H. Gamarra<sup>1</sup>, H. Juarez<sup>1</sup>, D. Giraldo<sup>1</sup>, I. Barker<sup>1</sup>, S. Fuentes<sup>1</sup>, G. Muller<sup>1</sup>, F. Morales<sup>2</sup>

<sup>1</sup>International Potato Center, Av. La Molina 1895, La Molina, Lima, Peru; <sup>2</sup>International Center for Tropical Agriculture, Apartado Aéreo 6713, Cali, Colombia.  
Corresponding author: Ian Barker (i.barker@cgiar.org)

## Abstract

The emergence and management of plant viruses transmitted by insect vectors is an important problem, particularly in developing countries, where phytosanitary capacity may not be adequate. Key factors responsible for the emergence of new plant diseases include: the intensification of agricultural trade (globalization); changes in cropping systems and climate change. Potato yellow vein virus (PYVV, genus *Crinivirus*) is a threat to potato cultivation in the Andean region because of its potential for wide and rapid dissemination through infected planting material and a ubiquitous insect vector: the whitefly species *Trialeurodes vaporariorum*. PYVV, has spread in the last 7-10 years throughout the Andean region of northern Peru. CIP is developing a risk prediction model of *T. vaporariorum* spread and indirectly PYVV (a model system for emerging diseases) using Geographic Information System (GIS) technology. The model predicts that PYVV could spread further south with apparent risk to southern Peru, Bolivia and Chile, based on the potential distribution of its vector. There is also some evidence of spread by seed since there are places where the disease is present but not the vector. We conclude that the model may be used to forecast potential occurrence of the vector and hence also PYVV under a given temperature and rainfall regime and be used to plan potential control measures. Species distribution modeling offers the possibility of predicting the potential distribution of the vector under different climate change scenarios and could estimate the potential risk of dispersion of the disease.

**Keywords:** Whitefly transmission, modeling distribution with GIS, ecological niche, maximum entropy, niche-based model, species distribution model.

## Introduction

The potato (*Solanum tuberosum* L.) is one of the most important crops around the world. This crop is affected by disease and pest like nematodes, insects, fungi, bacteria and viruses. An important potato disease is caused by Potato Yellow Vein Virus (PYVV, a tentative member in genus *Crinivirus*, family *Closteroviridae*) (Salazar *et al*, 2000). Its origin has been traced to Northern Ecuador and Southern Colombia (Alba, 1952; Tamayo and Navarro, 1984) and was later reported in Venezuela in 1977 and in Peru in 1996 (Salazar *et al*, 1998). Currently, this disease is present in Colombia, Ecuador, Venezuela and Peru (Alba, 1952; Tamayo and Navarro, 1984; Salazar, 1996) and causes around 50% yield reduction (Salazar, 1996).

Since then the virus spread via infected seed tubers throughout the Central Andes, particularly to the most important potato-producing areas of Northern Peru (SENASA, 2008) and Venezuela. The virus does not affect the size and morphology of plants; the typical yellowing of the veins appears between 30 and 40 days after infection, when stems and leaves are already formed (Saldarriaga *et al*. 1988).

A most widely used practice in the control of PYVV infection is the manual elimination or rouging of infected plants and the spraying of pesticides over the whole parcel at different times during the vegetative cycle, for the control of its vector. However, the use of pesticides increases costs and pesticide residue levels in agricultural products and soils contributes to ground water contamination (Bravo *et al*. 2004).

Furthermore, indiscriminate use of pesticides could eliminate natural biological control agents, thus increasing pest-insect populations, such as *Trialeurodes vaporariorum* (Westwood) (Hemiptera: Aleyrodidae), which is the PYVV.

The whitefly transmits the virus in a semi-persistent manner (Salazar et al, 2000; Diaz et al, 1990; Tamayo and Navarro 1984), other types of transmission are through tuber-seed, and underground stem-grafts (Alba, 1952, Salazar, 1998).

During the “El Niño” phenomenon (1997-1998), this vector and other important insects increase their populations consequently; the transmission of important viral disease is increased. Nowadays, the current climate changes could affect the *T. vaporariorum* population because temperature affects its development rate and consequently its damage on crops and diseases dissemination.

Differences in the environmental characteristics of areas occupied by the insect can be examined by modeling species distributions, a technique that integrates locality data, GIS data, and modeling algorithms (Anderson et al., 2002; Anderson and Martinez-Meyer, 2004; Elith et al., 2006; Phillips et al., 2006). The resulting distribution model describes the common environmental and climatic characteristics of the known range of a given species or group of populations (Peterson, 2003; Soberón and Peterson, 2004). This approach has been used to predict species distributions (Illoldi-Rangel et al., 2004); to predict the potential geographic range of invading species (Peterson, 2003; Mau-Crimmins et al., 2006) and to predict changes in the distributions of fauna and flora associated with projected models of climate change (Peterson et al., 2002; Siqueira and Peterson, 2003; Oberhauser and Peterson, 2003; Thomas et al., 2004).

In crop species, GIS-based analyses have been used to predict yields of different cultivars in various geographic areas (Jeutong et al., 2000; Caldiz et al., 2002), to explore the distributions of wild relatives of crop species (Greene et al., 1999a, b; Hijmans and Spooner, 2001; Jarvis et al., 2004), and to model future distributions of crop pests and diseases (Bernardi, 2001).

CIP is interested in predicting and managing risk posed by emerging and re-emerging viruses and the effect of climate change. The models are important analytical tools for predicting, evaluating and understanding the dynamics of pest populations in ecosystems under a variety of environmental conditions and management practices. The aim of this work was: i) to generate data for vector and virus distribution in Peru, Ecuador and Colombia; ii) to estimate potential adaptability of the vector *T. vaporariorum* in the Andean region (using new modeling); and iii) to generate evidence of the potential distribution of the vector under climate change.

## **Materials and Methods**

### ***Insect distribution***

Two hundred and ninety nine distinct potato fields were sampled in the Andean region of Ecuador, Peru and Colombia during 2007 year, to obtain a spatially referenced data set for vector and virus occurrence. Visual inspection of presence/absence of *T. vaporariorum* was assessed in each potato field. Potato leaf samples were collected in the field and tested by nucleic acid spot hybridization (NASH) to confirm the presence of PVV. Position data for *T. vaporariorum* populations was recorded using a Garmin GPS 76s (Garmin International Inc., Olathe, Kansas, USA).

### ***Climate scenarios***

55 GIS data layers were used for either current [representing the year 2000] or future scenarios [representing the year 2050] from the WorldClim Global Climate GIS database (2.5 minute resolution) (Hijmans et al., 2005). These data included 36 monthly layers (maximum temperature, minimum temperature and rainfall) and 19 bioclimatic variables (annual mean temperature, mean diurnal temperature range, isothermality, temperature seasonality, maximum temperature of warmest month, minimum temperature of coldest month, temperature annual range, mean temperature of wettest quarter, mean temperature of driest quarter, mean temperature of warmest quarter, mean temperature of coldest quarter, annual precipitation, precipitation of wettest period, precipitation of driest period, precipitation seasonality, precipitation of wettest quarter, precipitation of driest quarter, precipitation of warmest quarter, and precipitation of coldest quarter).

### ***Insect distribution modeling***

Environmental conditions were related to the insect occurrence data using MAXENT 3.3.1 (Phillips et al., 2006). MAXENT is a recent implementation of a statistical approach called maximum entropy that characterizes probability distributions from incomplete information (Phillips et al., 2006).

Insect distributions were predicted using the locality data in Table 1. The Maxent algorithm was run using the default parameters including a maximum of 500 iterations with a convergence threshold of 0.00001. During model development, 50% of the localities were used for model training, while 50% of the localities were held back to test model accuracy.

Cumulative probability distributions ranging from 0 to 100 were generated for *T. vaporariorum* populations that represent a relative measure of the probability of occurrence for the modeled insect.

### ***Insect distribution modeling for future scenarios***

The model trained on the set of environmental layers was projected by applying it to a set of environmental layers under changing climate conditions. The CCM3-2050 model of NCAR (National Center for Atmospheric Research, Boulder, Colorado) from the WorldClim Global Climate GIS database (Hijmans et al., 2005) was used.

## **Results and discussion**

A preliminary full model based on 66 observations with presence of *T. vaporariorum* points yielded a very widespread and diffuse damage probability surface (Fig. 1), probably because of the many different climate types that comply with the basic parameters represented in the points analyzed.

Based on known occurrences of cultivated *T. vaporariorum* populations, distribution maps predicting the possible areas where this insect might occur were generated (Fig. 1). Predictions were highly significant based on a binomial probability distribution test calculated from the held back test localities (Area Under curve (AUC): training data 0.994 and  $p$  values  $< 0.001$ ).

The minimum temperature for January, isothermality (the mean diurnal range divided by the Annual Temperature Range) and total rainfall for October and July estimate an overall relative contribution of 85.75% of the environmental variables to the Maxent model. The observation that *T. vaporariorum* adapts well to elevations above 1000 masl poses an important question. This species is widely adapted in a region extending from more than 11°N in Colombia to 17°S Peru. Therefore, the altitude limit does not seem to be related to temperature, since temperature varies widely over this latitude range. However, the annual temperature range increases with increasing distance from the equator.

Three particular regions highlighted in the map (Fig. 1, left), the northern highland of Colombia- Venezuela and the northern highland Peru-Ecuador, are areas where *T. vaporariorum* has caused only direct feeding damage to different crops (Anderson and Morales, 2005). The three areas (the central highlands of Bolivia, northern valley of Chile and the west part of Brazil) are shown on the map (Fig. 1 left) as a potential target for *T. vaporariorum*. These observations are interesting because the highland climate is quite similar to the climate found on the presence of *T. vaporariorum*. Even though, future conditions varied strongly between models. This preliminary map (Fig. 1, right) has resulted in major outbreaks in the highlands of Ecuador and Peru.

The results obtained in this study also suggest that countries, such as Bolivia, Chile and Brazil, should be particularly alert to the possible introduction of *T. vaporariorum* in vegetative material, considering the existence of environmental conditions suitable for the adaptation of this whitefly species.

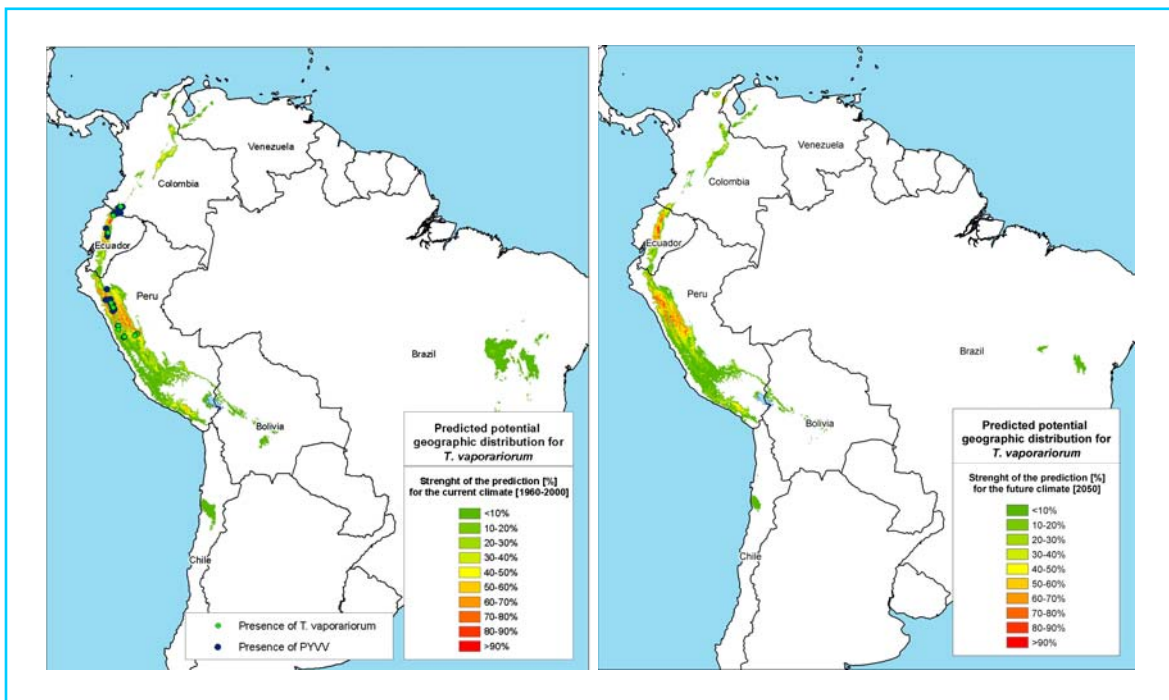
On the other hand, PYVV has been detected in northern of highland areas of Peru, Ecuador and Colombia affecting annual field crops of potato (Salazar et al, 1996).

There is also some evidence of spread by seed since there are places where the disease is present but not the vector.

The southern of Peru, located over 1000 masl, is a marginal area for *T. vaporariorum*. Nevertheless, a prolonged dry period in the July-December of 2008 resulted in major outbreaks of *T. vaporariorum* in potato and ornamental plants, causing considerable direct damage on the plants and an indirect risk in transmitting PYVV (Anderson and Morales, 2005). This observation suggests that once *T. vaporariorum* reaches high populations in a region due to the presence of suitable reproductive hosts, pesticide abuse (overuse causing elimination of natural enemies and development of pesticide-resistant *T. vaporariorum*) and favorable climatic conditions (dry and temperature weather), the probability of PYVV outbreaks increases.

**Table 1. Distribution of *Trialeurodes vaporariorum* using the locality data**

Country	Place	COD_CULT	ZONE_UTM	LON_DEG	LAT_DEG	ALTITUDE	PYVV	T_VAPORA	S_FENOLO
Peru	Yungay	3	18	-77.680	-9.173	3047		x	Flowering
Peru	Yungay	1	18	-77.669	-9.168	3034	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3031	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3027	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3025	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3024	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3024	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3022	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3022	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3023	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3025	x	x	Tuberization
Peru	Yungay	1	18	-77.669	-9.168	3023	x	x	Vegetative development
Peru	Yungay	1	18	-77.669	-9.168	3022	x	x	Vegetative development
Peru	Yungay	1	18	-77.669	-9.168	3022	x	x	Vegetative development
Peru	Shancayan	2	18	-77.672	-9.515	3045		x	Tuberization
Peru	Chiquian (Obraje)	1	18	-77.158	-10.137	3141	x	x	Vegetative development
Peru	Chiquian (Obraje)	1	18	-77.158	-10.137	3142	x	x	Vegetative development
Peru	Chiquian (Obraje)	1	18	-77.158	-10.137	3146	x	x	Vegetative development
Peru	Chiquian (Obraje)	1	18	-77.158	-10.137	3145	x	x	Vegetative development
Peru	Chiquian (Obraje)	1	18	-77.158	-10.137	3134	x	x	Vegetative development
Peru	Chiquian (Obraje)	1	18	-77.158	-10.137	3140	x	x	Vegetative development
Peru	Chiquian (fuera de Chiquian)	1	18	-77.161	-10.149	3480	x	x	Vegetative development
Peru	Chiquian (fuera de Chiquian)	1	18	-77.161	-10.149	3485	x	x	Vegetative development
Peru	Namora(Cau-cau)	1	17	-78.288	-7.207	2876	x	x	Vegetative development
Peru	Namora(Cau-cau)	1	17	-78.287	-7.206	2882	x	x	Tuberization
Peru	Namora(Cau-cau)	1	17	-78.287	-7.206	2883	x	x	Tuberization
Peru	Namora(Cau-cau)	1	17	-78.287	-7.206	2887	x	x	Tuberization
Peru	Namora(Cau-cau)	1	17	-78.287	-7.206	2882	x	x	Tuberization
Peru	Namora(Cau-cau)	1	17	-78.287	-7.206	2886	x	x	Tuberization
Peru	Namora(Cau-cau)	1	17	-78.287	-7.206	2885	x	x	Tuberization
Peru	Namora(Cau-cau)	1	17	-78.287	-7.206	2885	x	x	Tuberization
Peru	Malcas	2	17	-78.137	-7.511	2880	x	x	Vegetative development
Peru	Malcas	2	17	-78.143	-7.509	2052	x	x	Vegetative development
Peru	Malcas	2	17	-78.143	-7.509	2049	x	x	Vegetative development
Peru	Malcas	2	17	-78.143	-7.509	2050	x	x	Vegetative development
Peru	Malcas	2	17	-78.143	-7.509	2053	x	x	Vegetative development
Peru	Huarimba (entrada Cajabamba)	2	17	-78.104	-7.602	2296	x	x	Vegetative development
Peru	Huarimba (entrada Cajabamba)	2	17	-78.104	-7.602	2296	x	x	Vegetative development
Peru	Huarimba (entrada Cajabamba)	2	17	-78.104	-7.602	2299	x	x	Vegetative development
Peru	Huarimba (entrada Cajabamba)	2	17	-78.103	-7.602	2298	x	x	Vegetative development
Peru	Huarimba (entrada Cajabamba)	2	17	-78.103	-7.602	2297	x	x	Vegetative development
Peru	La Punta (Panao)	1	18	-76.045	-9.851	2322		x	Vegetative development
Peru	La Punta (Panao)	1	18	-76.046	-9.850	2327		x	Vegetative development
Peru	La Punta (Panao)	1	18	-76.047	-9.850	2327		x	Vegetative development
Peru	La Punta (Panao)	1	18	-76.047	-9.850	2327		x	Vegetative development
Peru	La Punta (Panao)	1	18	-76.047	-9.850	2328		x	Vegetative development
Peru	Huanin	1	18	-76.029	-9.903	2704		x	Vegetative development
Peru	Huanin	1	18	-76.029	-9.903	2714		x	Vegetative development
Peru	Huanin	1	18	-76.029	-9.903	2711		x	Vegetative development
Peru	Huanin	1	18	-76.029	-9.903	2704		x	Vegetative development
Peru	Huanin	1	18	-76.029	-9.903	2703		x	Vegetative development
Peru	Quicacan I	1	18	-76.236	-10.017	1992		x	Vegetative development
Peru	Quicacan I	1	18	-76.236	-10.017	1990		x	Vegetative development
Peru	Quicacan I	1	18	-76.236	-10.017	1990		x	Vegetative development
Peru	Quicacan I	1	18	-76.236	-10.017	1996		x	Vegetative development
Peru	Quicacan I	1	18	-76.236	-10.017	1997		x	Vegetative development
Peru	Quicacan I	1	18	-76.237	-10.018	2002		x	Vegetative development
Peru	Quicacan II	1	18	-76.223	-9.965	2014		x	Vegetative development
Peru	Quicacan II	1	18	-76.223	-10.056	2014		x	Vegetative development
Peru	Quicacan II	1	18	-76.223	-10.056	2011		x	Vegetative development
Colombia	Zaragosa	2		-77.4507	1.1553	1970		X	Vegetative development
Ecuador	Pillaro	1	17S	-78.536	-1.089	3016	x	x	Vegetative development
Ecuador	Pillaro	1	17S	-78.536	-1.088	3018	x	x	Vegetative development
Ecuador	Pillaro	1	17S	-78.536	-1.089	3019	x	x	Vegetative development
Ecuador	Imbarugua	2	17N	-78.107	0.392	2244		x	Maduration
Ecuador	Imbarugua	2	17N	-78.107	0.392	2244		x	Maduration



**Figure 1. Maps showing predicting potential geographic distribution of *Trialeurodes vaporariorum* using all occurrence records [66] under different climate scenarios: current climate is represented by the period 1960-2000 (left) and future climate is represented by year 2050 (right).**

## Conclusions

The climate probability model described here can be used to identify regions of Latin America prone to *T. vaporariorum*/PYVV crinivirus attack. Regions highlighted in the map (Colombia, Venezuela and the northern highland Peru-Ecuador) are areas where *T. vaporariorum* has caused only direct feeding damage to different crops (Anderson and Morales, 2005). The central highland of Bolivia, northern valley of Chile and the west part of Brazil are potential areas for *T. vaporariorum* adaptation. These observations are interesting because the highland climate is quite similar to that climate where *T. vaporariorum* was found to be present. Even though, future conditions varied strongly between models. This preliminary map has resulted in major outbreaks in the highlands of Ecuador and Peru.

The investigation conducted in Latin America will be repeated in other continents affected by *T. vaporariorum*, primarily in Africa and Europe in order to further validate the applicability of this model to other parts of the world.

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