

## *Persistence of Impatiens Necrotic Spot Virus in Selected Floral Crop Systems*

### **PRINCIPAL INVESTIGATOR:**

James Moyer, Department of Plant Pathology, North Carolina State University, Raleigh, North Carolina.

### **RESEARCH TEAM:**

James Moyer, Elizabeth Parks, and Jan Speck, Department of Plant Pathology, North Carolina State University.

### **PROJECT OBJECTIVES:**

The objective of the project is to provide the ornamental industry with management tools to reduce their risk of *Tospovirus* epidemics. The goal of the current research is to obtain a better understanding of the molecular population genetics of impatiens necrotic spot virus (INSV) to identify the risk factors that lead to epidemics, the evolutionary forces that shape the virus, and the potential for the virus to spread into new areas.

### **ACCOMPLISHMENTS:**

Accomplishment of 2006 – 2008 objectives:

- We established collaborations in the floral industry to access virus samples that allowed us to create a database of 42 INSV isolates from 6 counties and 6 U.S. states.
- We not only characterized population diversity of INSV using OSA fragments, but we developed new tests for population subdivision, migration, targeting regions of the genome, natural selection, and recombination. These analyses are at the forefront of population genetics research, and represent a novel effort in the study of *Tospoviruses* and all negative-sense RNA viruses.
- We developed models for assigning attribution using *Tospovirus* populations and have since tested these on virus epidemics.

During FY 2009, we have sought to expand the statistical tools that we use to characterize INSV populations and to refine them into a usable system on a par with TSWV. The keystone of the research is to understand the population genetics of distinct populations. To this end, we previously applied the tests to INSV that we used to elucidate the geographic structure of tomato spotted wilt virus (TSWV). While these tests did find that INSV populations were geographically differentiated, the U.S. population had low statistical support for subdivision. We have extended this work to newly developed tests to examine how INSV differs from TSWV in this respect. New tests have shown that while INSV is geographically differentiated worldwide, the U.S. population is not strongly divided, implying that this population is nascent in its evolutionary history compared to TSWV. We incorporated this finding into our analysis, and proceeded to compare the U.S. population as a whole to other populations from which it was subdivided, such as New Zealand (NZ). This work shows that compared to the NZ population, the U.S. population has had more changes since divergence from their most recent common ancestor. Our findings will move forward the theoretical

understanding of not only Tospovirus evolution, but also that of other negative-sense RNA viruses. In addition, the manuscript that is currently in preparation will be the first publication on the analysis of the INSV genome since the initial INSV publications in the 1990's. The transformational advances include tools and a database for attribution (source identification) and epidemiological studies to assess disease and develop control strategies.

We have identified several commercial operations with chronic INSV problems and will be using these tools to reassess current controls and to explore potential avenues for survival of INSV in a floral cropping system.

**IMPACT:**

We recently had the opportunity to test our attribution system on an outbreak in the Western United States. Using our methods, we were able to identify the source of the outbreak and the naturally occurring isolates in the area.

**COLLABORATORS:**

We continue to work closely with AgDia. We will be working George Kennedy, an entomologist, and Kelly Ivors, an Extension Specialist.