



Greenhouse Vegetable Research Activities

The greenhouse vegetable sector has two research activities with the Canadian AgriScience Cluster for Horticulture Cluster 4. These two activities are focused on protecting vegetables against pests and managing disease in tomatoes.

THE CLUSTER 4 GREENHOUSE VEGETABLE RESEARCH ACTIVITIES ARE:

ACTIVITY 9

Developing a systems approach to pest management on greenhouse vegetable crops: mirid predator selection

LEAD RESEARCHER – Roselyne Labbé, research scientist in greenhouse entomology with Agriculture and Agri-Food Canada at the Harrow Research and Development Centre

ACTIVITY 10

Novel approaches for the management of tomato brown rugose fruit virus (ToBRFV)

LEAD RESEARCHER – Aiming Wang, research scientist with Agriculture and Agri-Food Canada at the London Research and Development Centre

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Developing a Systems Approach to Pest Management on Greenhouse Vegetable Crops: Mirid Predator Selection



LEAD RESEARCHER

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To find new integrated pest-management strategies to protect greenhouse vegetable crops, a research team is studying two native North American mirid species: *Dicyphus discrepans* and *Dicyphus famelicus*, and one adventive species, *Nesidiocoris tenuis*.

Researchers are focused on breeding genetically improved strains of the native mirid species *Dicyphus famelicus*, which appears to be one of the predominant species of the *Dicyphini* tribe in natural ecosystems across eastern Canada and has a broad genetic diversity. Two other native predator species, *Dicyphus discrepans* and *Dicyphus hesperus*, are being assessed for their comparative biocontrol potential of common greenhouse pests, as well as if they are prone to causing fruit injuries.

Through surveys in Ontario and Quebec, researchers have established and maintained a total of 10 source populations of *Dicyphus famelicus* and one source population for each of *D. discrepans*, *D. hesperus* and *Nesidiocoris tenuis*. Genetic analysis for the 10 populations of *D. discrepans* found at least four distinct DNA sequences suggesting there is substantial genetic variation to support strain phenotypic selection.

From the 10 *D. famelicus* populations, researchers established 12 isofemale lines, which have been assessed through 723 tests for plant or prey feeding preferences. One line was found to be particularly predatory, with

predatory capacity being a heritable trait, which correlates with predator aggressivity.

The research team has started to explain biases in host plant selection for the four native and adventive mirid species, along with the impact of these host plants on population increase rates. They have found all *Dicyphus* species prefer to reproduce on mullein hosts, whereas the adventive *Nesidiocoris tenuis* has a preference for tomato.

Given the prevalence of *N. tenuis* in greenhouses around the world, researchers have focused on finding ways to control the species to reduce crop injury. This includes examining the efficacy of control products, assessing mass trapping approaches and reviewing exclusion screen dimensions. They are conducting trials to find the interactions between all four diverse mirid species and studying the impacts of LED lights and release rates in greenhouse environments.

Over the 2025–26 research season, the team is working to finalize the establishment of isofemale lines for *Dicyphus famelicus* and complete assessments of their feeding behaviour. This will allow researchers to pick the most promising strains to further assess their biological control potential on greenhouse crops.

KEY TAKEAWAYS:

- Genetic analysis for the 10 populations of *D. discrepans* found at least four distinct DNA sequences, suggesting there is genetic diversity for strain phenotypic selection.
- Researchers have found all *Dicyphus* species prefer to reproduce on mullein hosts, whereas the adventive *Nesidiocoris tenuis* has a preference for tomato.



A female *D. discrepans*. Photo: Carly Demers



A female *D. famelicus*. Photo: Carly Demers





Novel Approaches for the Management of Tomato Brown Rugose Fruit Virus (ToBRFV)



LEAD RESEARCHER

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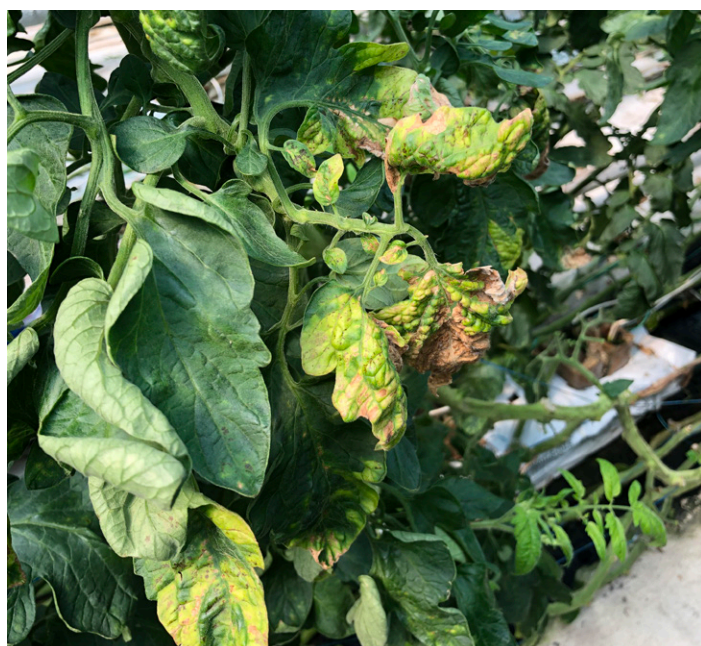
Researchers are working to stop Tomato Brown Rugose Fruit Virus (ToBRFV) from threatening Canadian greenhouse tomatoes and peppers. This research activity is studying the infection process and working to develop novel genetic resistance to ToBRFV. Researchers want to better understand how ToBRFV overcomes broad-spectrum resistance given by Tm-22 and bring back Tm-22-mediated resistance to ToBRFV.

Approximately 16,000 individual tomato plants have been screened, with 30 lines found to have resistance/tolerance to ToBRFV. Resistance in one line has been confirmed after four generations, while resistance in other lines is yet to be confirmed. The research team has cloned the resistance gene Tm22 and ToBRFV movement protein (MP). It was found neither are stable as they have a very short turn-over time. A tomato protein involved in ToBRFV MP degradation was identified.

By investigating the deficiency of two ToBRFV proteins, including coat protein (CP) and MP on virus replication and infection by generation of CP- and MP-deficient mutants followed by protoplast transfection and plant infection assays, it was found both CP and MP provide supplementary but not essential roles in virus replication at the early infection stage. Both MP and CP are necessary for ToBRFV infection.

Researchers have sequenced the full genome sequences of 28 isolates and partial genomic sequences of an additional 100 isolates. Most Canadian isolates were found to be closely related to isolates from the United States and Mexico. However, several Canadian isolates seem to be distantly related, pointing to multiple introductions to Canadian production systems. Two conserved residues in CP were found to be essential for ToBRFV infection.

Researchers are working to finish screening for ToBRFV resistance from the tomato mutant population, confirm resistance in future generations of identified lines, and initiate genetic work to identify the genes needed for resistance. The team will continue to



Tomato plants infected with typical tomato brown rugose fruit virus (ToBRFV) symptoms.

Photo: Aiming Wang

monitor ToBRFV diversity in Canada, and decode what causes ToBRFV break-down of Tm22 resistance. They are also assessing the incidence of ToBRFV and Pepino mosaic virus (PepMV) mixed infection.

KEY TAKEAWAYS:

- Approximately 16,000 individual tomato plants were screened with 30 lines found to have resistance/tolerance to ToBRFV. Resistance in one line has been confirmed after four generations, while resistance in other lines is to be confirmed.
- The research team has cloned the resistance gene Tm22 and ToBRFV movement protein (MP). It was found neither are stable, as they have a very short turn-over time. A tomato protein that is involved in ToBRFV MP degradation was identified.
- Most Canadian genome sequence isolates were found to be closely related to isolates from the United States and Mexico. However, several Canadian isolates seem to be distantly related pointing to multiple introductions to Canadian production systems.





Tomato plants infected with tomato brown rugose fruit virus (ToBRFV). Photos: Aiming Wang