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

This project is generously funded through the Canadian AgriScience Cluster for Horticulture 4, in cooperation with Agriculture and Agri-Food Canada's AgriScience Program, a Sustainable Canadian Agricultural Partnership initiative, the Fruit and Vegetable Growers of Canada (FVGC), and industry contributors.

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

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 tenui*s.

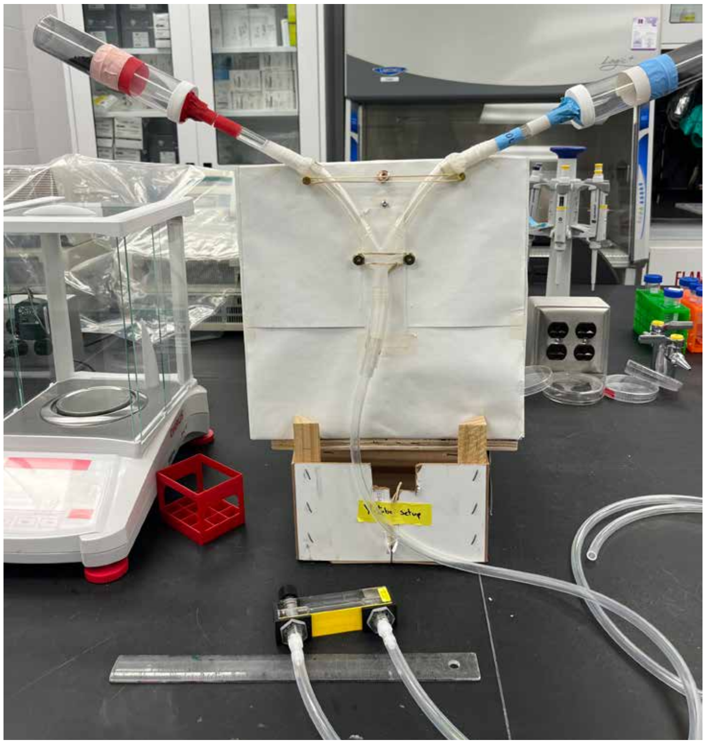
Researchers have been focused on breeding genetically improved strains of the native mirid species *Diciphus famelicus*, which appears to be one of the predominant species of the *Dicyphini* tribe in natural ecosystems across eastern Canada and has a broad genetic diversity. Two other native predator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

In 2025, the research team characterized the genetic variation of *D. famelicus* predators from three new sources collected in 2024. However, given these didn't represent new genetics, the researchers have proceeded with continued work to characterize existing isolines.

Over the past year, the researchers completed assessment of oviposition preference of predators on tomato, cucumber and sesame (*Dicyphus hesperus* and *N. tenuis*). The research team is assessing the potential of predation among native mirids and *N. tenuis* along with the effects of a multi-predator environment on plant distribution preferences.

Tests this winter examining intraguild interactions among four mirid species showed low overall levels of intraguild predation, with two significant cases: *Dicyphus famelicus* consumed 18 per cent of *D. hesperus* nymphs, and *D. hesperus* consumed 13 per cent of *Nesidiocoris tenuis* nymphs. These results suggest multiple mirid species can likely be released together without compromising biological control, but native species are unlikely to suppress the exotic *N. tenuis* through competition.

A greenhouse trial of mirid host preferences. Photo: Isabella Nardone



A mirid prey attraction assay. Photo: Isabella Nardone

Greenhouse trials in summer 2025 confirmed low intraguild predation between species and provided insight into plant and oviposition preferences. Both *D. hesperus* and *D. famelicus* adults strongly preferred mullein over tomato, while *N. tenuis* used both plants more evenly. Vertical positioning on tomato plants showed little pattern except for *D. famelicus*, which preferred the middle and lower sections when alone.

Oviposition patterns varied by species. *D. hesperus* consistently preferred mullein, *D. famelicus* showed no plant preference, and *N. tenuis* typically preferred tomato – except when paired with *D. famelicus*, then it shifted to mullein. Vertical oviposition on tomato was generally uniform, aside from *D. famelicus*, which favoured the middle of the plant. These details on mirid species distribution on different host plants can help researchers understand how likely species are to have either positive or negative interactions.

The research team is planning to acquire information on mirid species prey preferences through olfactory preference trials. These trials will provide essential information for each mirid species related to their ability to locate pests through volatile and olfactory cues.

KEY TAKEAWAYS:

- The research team characterized the genetic variation of *D. famelicus* predators from three new sources, but as they didn’t represent new genetics, the researchers have proceeded with continued work to characterize existing isolines.
- Researchers have found that multiple mirid species can likely be released together without compromising biological control, but native species are unlikely to suppress the exotic *N. tenuis* through competition.
- Vertical positioning on tomato plants showed little pattern except for *D. famelicus*, which preferred the middle and lower sections when alone.

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

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.

To understand ToBRFV genetic diversity, researchers have collected and analysed over 300 samples from greenhouse tomatoes in Ontario and Quebec since the research activity started. They've sequenced and assembled the full-length genome sequences of 40 Isolates. The research team combined these sequences with other Canadian ToBRFV genomes previously deposited in the public domain and conducted phylogenetic analysis.

Through computer-assisted comparison analyses, researchers have found that the genome sequences of Canadian isolates share high sequence identity when the movement protein (MP) is least conserved. At the genome level, most Canadian isolates are closely related to isolates from the United States and Mexico. However, several Canadian isolates appear distantly related, suggesting multiple introductions to Canadian production systems. This explains the difficulties and challenges in preventing ToBRFV spread and the unusual ability of ToBRFV to adapt to novel and existing resistance genes.

The research team has collected 25 samples from greenhouse tomatoes in British Columbia. They will do a molecular analysis of them over the next year.

Researchers have completed over 50 trials by screening about 20,000 tomato individual plants from the mutant population and have identified over 30 lines that showed resistance/tolerance to ToBRFV. The research team has started breeding work for next generation mapping to identify genes responsible for resistance in two identified resistant lines. In addition, they have successfully generated a new mutant population using the Roma tomato cultivar for screening for novel genetic resistance.

A tomato plant infected with Tomato Brown Rugose Fruit Virus (ToBRFV). Photo: Aiming Wang

Tomatoes at the market showing Tomato Brown Rugose Fruit Virus (ToBRFV) symptoms. Photo: Aiming Wang

KEY TAKEAWAYS:

- Researchers have found the genome sequences of Canadian isolates share high sequence identity with MP least conserved. This explains the difficulties and challenges in preventing ToBRFV spread and the unusual ability of ToBRFV to adapt to novel and existing resistance genes.
- The research team has successfully generated a new mutant population using the Roma tomato cultivar for screening for novel genetic resistance.