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.