

First milestone reached towards ToBRFV High Resistance

A new virus affecting all varieties of tomato, known as the **Tomato Brown Rugose Fruit Virus (ToBRFV)**, was first discovered in Israel in 2014. Since then, it spread to countries in Europe, Asia, Africa and in parts of Mexico and the USA. Symptoms of ToBRFV include a rough leaf wrinkling (i.e. rugose) surface and bubbling with an accompanying mosaic pattern. The fruit has a browning calyx and is undersized. Fruit abortion may occur, and the remaining fruit will be blotchy, pale and may have brown, necrotic spots (Figure 1). Plants infected at an early stage of development will be stunted with poorly formed fruit while those infected later may not express symptoms until the fruit turns red.



Figure 1

In an effort to combat the virus, NRGene and PhiloSeed have partnered to create varieties resistant to ToBRFV. This collaboration for a DNA marker-based ToBRFV resistance trait integration has now reached a milestone with the first quantitative trait locus (QTL) discovered in a mapping population.

For more information please contact:

   www.nrgene.com • info@nrgene.com

Below is a brief summary of a QTL analysis of a bi-parental population segregated for resistance to ToBRFV. This analysis is the first part in a complete solution of QTLs and markers for high resistance (HR) to ToBRFV originating from a HR wild tomato variety source.



The first population of a wild tomato resistance source for ToBRFV was mapped using an ultra-dense genetic map. This process resulted in one highly significant QTL with the following characteristics:

- Genomic location (2Mbp QTL – patent pending) not previously described (LOD score of ~9, Figure 2).
- Mapping based on a heterozygous state, ensuring the disease resistance does not represent a recessive inheritance.
- QTL required but not sufficient to confer high resistance.
- Can be used in combination with other resistance loci for possible increased resistance.
- May confer resistance on its own in an homozygous state (currently under evaluation).

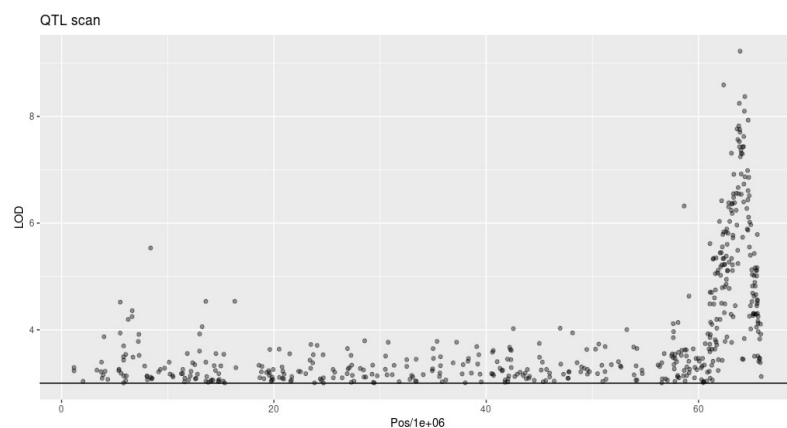


Figure 2 - Manhattan plot (LOD score) of the QTL region

Furthermore, under development is work with additional proprietary QTLs in a heterozygous state. The phenotype score used in this QTL analysis is based on the severity and timing of the ToBRFV symptoms starting from four weeks post-inoculation.

NRGene currently offers seeds containing the QTL and markers, with an additional QTL expected to be delivered in late 2022. Together, these QTLs are expected to confer HR (high resistance) in the same level as for the wild variety. Fast introgression of the QTL using Marker Assisted Back Cross (MABC) service is available

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