

## **ADVANCES IN THE MANAGEMENT OF PTSL ASSOCIATED WITH *Mesocriconema xenoplax* IN PEACH TREES**

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Peach Tree Short Life (PTSL) is a complex disease syndrome that involves environmental (temperature, acid soils), cultural (site history, fall pruning) and biotic (ring nematodes) factors that significantly impact peach production especially on replant orchard sites. Peach tree death similar to PTSL has been observed since the 1930s in the southeastern U.S., though similar symptoms (tree decline and death) have been observed in Brazil, South Africa, Australia and Italy and with lesser injury (scaffold death) in California wherever ring nematodes (*Mesocriconema xenoplax* (Raski) Loof and de Grisse) are present in acid, coarse textured soils. Previous research has shown that PTSL is more a rootstock disease syndrome that is linked to ring nematode feeding injury and to a lesser extent to replant soil conditions and a variety of non-specific secondary pathogens. A 10-point cultural program implemented in the 1970s in South Carolina was reasonably effective up until the loss of the key pre-plant soil fumigant DBCP in 1979 and nematode control became less effective.

The significance of rootstock cultivar was recognized in the 1980s after the banning of DBCP when significant numbers of peach trees began dying from PTSL on peach (*Prunus persica*) seedling rootstocks other than Lovell, which exhibited some tolerance. In 1994, Clemson University and USDA-Byron, Georgia jointly released Guardian® 'BY520-9' rootstock, which provided excellent tree longevity on PTSL sites. However, this rootstock is not resistant to the *Armillaria sp.* soil fungus; therefore, new rootstocks are still needed that incorporate Guardian®'s PTSL tolerance into an *Armillaria* resistant rootstock. Fortunately, with current molecular biology tools and cost-effective genome sequencing, the genetic and molecular mechanisms of this tolerance are now being identified for future rootstock breeding. Once this genetic resistance is elucidated, it can be introduced into elite peach germplasm by introgression of the selected gene(s)/haplotype(s) using classical breeding strategies or by transgene techniques.

Field (phenotype) and molecular (genotype) research undertaken at Clemson University over the past 30 years has located unique sections of the peach genome that confer increased resistance to bacterial diseases including *Pseudomonas syringae* pv.

*syringae* as well as *Xanthomonas arboricola* pv. *pruni* (Xap). Results from earlier concurrent genetic field testing and genomic analysis of PTSL resistant and susceptible F<sub>2</sub> replicated progenies found 9 SSR loci correlated with a response to PTSL. These loci were distributed on four linkage groups (Linkage Group-1, LG-2, LG-4 and LG-6) with 4 of the 9 loci (EPDCU5100, Pacita 27, UDA008 and UDA029) accounting for most of the variance in PTSL tolerance or susceptibility. To detect QTLs in the peach genome related to the PTSL response, a genetic map with the SSR markers segregating in the F<sub>2</sub> populations was generated. The PTSL phenotypic data of the F<sub>2</sub> populations spanning 5 years were combined with the SSR molecular marker inheritance data. A QTL was identified to be associated with the response to PTSL. The upper terminus of LG2 where markers Pacita 27 and UDA029 are located appeared to be important for the genetic basis for PTSL tolerance or susceptibility because both analyses (SSR and QTL) identified this region.

More recently, genomic research has advanced our knowledge of the genetic mechanisms of how rootstock genotype influences the PTSL syndrome in peach. From the earlier SSR and QTL studies, 4 different F<sub>2</sub> families, derived from a cross between a PTSL susceptible rootstock Nemaguard and the tolerant rootstock Guardian<sup>®</sup>, and previously evaluated for PTSL tolerance in the field, were genotyped using Genotyping by Sequencing (GBS). Meta-analysis, which is used to refine QTL positions detected in family specific genetic linkage maps, revealed a total of six metaQTLs associated with PTSL, two each on linkage groups (LG) 1, 4 and 6, but not on LG2 though it was confirmed to have a QTL associated with response to nematodes. All metaQTLs except one showed significant effects on PTSL. Individuals heterozygous for one metaQTL with a haplotype originating from both Guardian<sup>®</sup> and Nemaguard, exhibited the best phenotypic performance. Both metaQTLs on LG4 exhibited the best PTSL field performance when the haplotype coming from Guardian<sup>®</sup> was in a homozygous state. Candidate gene analyses in the metaQTL genomic regions detected over 180 resistance genes, including genes associated with resistance to bacterial diseases. The Guardian<sup>®</sup> genome assembly revealed multiple duplications in resistance genes, most of them in two metaQTL regions, suggesting a disease resistance hot spot on chromosome 4 of the peach genome. MetaQTLs identified in this recent (unpublished) work suggested genomic regions associated with PTSL response in peach are also associated with response to

*Pseudomonas syringae* (bacterial canker), which is often the primary cause of death once ring nematodes infest, multiply, and damage peach roots, a process that predisposes trees to the PTSL syndrome.

We are currently incorporating this genetic information into the rootstock breeding program where similar research is being conducted with *Armillaria* resistant chromosome regions from select *Prunus sp.* genomes. In the near future, the integration of molecular genetics with traditional breeding will shorten the time interval to produce new rootstocks that better tolerate or resist parasitic nematodes and other root pathogens to prevent predisposition of stone fruit trees to bacterial canker and thus improve orchard productivity and profitability for fruit growers.