





Screening for new sources of resistance against plant-parasitic nematodes in wild tomato

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Abstract

Plant-parasitic nematodes are a devastating threat to many vegetables. For crops such as tomato, nematodes lead to yield losses of up to 20%. Important nematode parasites include the root-knot nematodes (RKNs), which attack over 4,000 plant species and generate billions of dollars in crop losses annually worldwide. In addition, farmers are now finding RKNs in their supposedly resistant tomato crops in increasing numbers. The *Mi-1* gene, discovered in wild tomatoes, has been the only source of resistance against the RKNs *Meloidogyne incognita*, *M. javanica*, and *M. arenaria*. However, this has put RKNs under high selection pressure to overcome *Mi-1*-mediated resistance. To search for new sources of resistance, we examined forty accessions of wild and weedy tomato plants. These plants naturally evolved in areas with varying levels of RKN activity, so we expect some will have developed effective defenses against RKNs. The tomato accessions were grown under greenhouse conditions and exposed to juveniles of the second stage of *M. incognita*. We obtained data on plant growth as well as fitness and galling numbers of *M. incognita* during three weeks of infection. We find four highly susceptible accessions, seven tolerant accessions, and nine accessions with low gall numbers, suggesting a great potential as sources of resistance against *M. incognita* infection. In susceptible accessions, we observed typical yellowing, stunting, and wilting symptoms. Crop damage results from a complex interaction in which RKNs start injecting effector proteins with their saliva into host cells to dampen the plant's defense response. To understand this process better, we performed genome-wide gene expression profiling on a subset of accessions to link root gene expression to tomato resistance to *M. incognita*. Preliminary analyses showed that expression of two genes was negatively correlated with nematode galling. One is *DHRS4*, which encodes dehydrogenase/reductase SDR family member 4 and is implicated in biosynthesis of calystegines, which are alkaloid secondary metabolites. The other is *MYB60*, which encodes a MYB transcription factor that is known to regulate root growth. Expression of its ortholog in *Arabidopsis thaliana* shows induction of expression early during cyst nematode infections. Our observations and experiments show the tremendous potential of some of the tolerant and resistant accessions and the possibility of finding novel genes that can contribute to RKN resistance.