

Uncontrolled emergence: populations of root-knot nematodes are overcoming resistance in tomato

Root-knot nematodes cause more than € 500 million economic losses to the annual tomato production in Europe. Massive deployment of a single resistance gene in tomato has led to the emergence of nematode populations that overcame the resistance.

Early detection of resistance-breaking nematode populations is essential to prevent their uncontrolled spread. Molecular diagnostic tools for the detection of resistance-breaking populations are currently missing. This could lead to the unnoticed range expansion of these virulent populations.

In NEM-EMERGE, we are studying the four most damaging root-knot nematode species regarding tomato: *Meloidogyne incognita*, *M. javanica*, *M. arenaria* and *M. luci*. We are collecting virulent (= resistance-breaking) as well as avirulent (= controlled by resistance) populations for each species. By sequencing and comparing the genomes of these virulent and avirulent populations, we aim to identify genomic signatures associated with virulence.

These genomic signatures will enable stakeholders to develop accurate diagnostic tools. Farmers and tomato growers will be invited to use these diagnostic tools as early and widely as possible and to report the presence of virulent populations allowing the timely application of appropriate control measures.



Figure 1: Root systems of a resistant tomato rootstock cultivated in soil infested with a virulent (left) or an avirulent (right) *Meloidogyne incognita* population.

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Funded by
the European Union

Funded by the European Union under G.A. NO 101083727. Views and opinions expressed are however those of the author(s) only and do not necessarily reflect those of the European Union or European Commission. Neither the European Union nor the European Commission can be held responsible for them.