NEM-EMERGE
AN INTEGRATED SET OF NOVEL APPROACHES TO COUNTER THE EMERGENCE AND PROLIFERATION OF INVASIVE AND VIRULENT SOIL-BORNE NEMATODES

Genetic selection: managing potato cyst nematodes that have overcome current host plant resistances

The best solution to control *Globodera pallida* populations is to grow resistant potato cultivars, but the majority of the resistant cultivars contain the same resistance factor originating from *Solanum vernei*. This resistance gene has been effective for many years, but now we discovered that some ('virulent') potato cyst nematode (PCN) populations can no longer be stopped.

This 'breaking of resistance' can only be solved if we understand what was happened. For this, we need to know more about the nematode itself, about their spreading and about the host plant.

First, we will identify genomic regions linked to virulence of the nematode and develop a diagnostic molecular tool to map the spreading of virulent PCN populations. For this, we will sequence *G. pallida* populations that can overcome the resistance and perform genome scan analyses. Within Nem-Emerge, we have been identifying candidate genomic regions using virulent populations obtained in the laboratory. We have also collected natural populations with various levels of virulence, and are currently analysing them.

In a second step we will develop a proliferation model that will provide information on how virulent nematodes are likely to build up under different management regimes. We have published in 2024 a demo-genetic model considering the population genetic features of *G. pallida*, and the current work is to integrate it into existing decision support systems for farmers.

Last but not least we aim to identify new sources of resistance to control emerging virulent populations. We have decided to deeply study the resistance from *Solanum sparsipilum* which is conferred by a combination of two small genomic regions. After an enrichment step, which allows sequencing to be focused on resistance genes, potato genotypes from the initial cross between susceptible and resistant parents will be sequenced to identify markers linked to each of these regions.

Figure 1: Resistance test performed in the JKI greenhouses

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