The chemical communication between potato and cyst nematodes

Project lead: WR: Prof. Richard GF Visser; UvA Prof. Harro Bouwmeester,

Potato production is threatened by potato cyst nematodes (PCN).
Eggs of the nematodes can survive in the soil and will hatch in the presence of a hatching stimulant secreted by the roots of potato plants. In this project, we aim to develop a new strategy to improve yield stability of potato by using knowledge about the signaling relation between the host plant and the cyst nematodes.

Highlights:
In the second year, we have identified promising genotypes within the wild genotype collection of Plant Breeding. These have been propagated and multiplied and a set of around 40 genotypes were transferred to the lab of Nematology (WUR) for further in vitro studies.

A bioinformatic analysis of available Globodera genomes was conducted. Two globodera genomes (Globodera pallida v.0.8.d2b with 55% BUSCO score and Globodera rostochiensis) were previously structurally annotated and used for this analysis. We identified putative orthologs on all genes in the Dauer pathway in Globodera pallida and Globodera rostochiensis genomes. 68 nuclear hormone receptors were identified in G.pallida vs 284 in C.elegans.

An experiment to identify differentially expressed genes upon SolA treatment on Globodera pallida took place in 2020. Pooled nematodes were tested with three different treatments (water, SolA, PRD) on 7 timepoints and 5 technical replicates. Some bacterial contamination and background hatching was observed through the experiment. RNA was isolated from 96 samples, of which 95 were sequenced and analyzed. polyA-RNAseq libraries were made to limit the effect of bacterial RNA contaminations, and samples were sequenced in NovaSeq-6000. Sequencing output was 400Gb (4.5Gb per sample). Mapping rate to the G.pallida genome shows little contamination of libraries (80-89% mapping rate). PCA analysis of data shows clustering of water 0h, and no clustering of rest of samples, either by treatment or by time. Different corrections of data were tested (filtering of lowly expressed genes, scaling, and PERMANOVA) but did not result in improved clustering of samples. DGE analysis shows 73 differentially expressed genes in SolA vs 0h water, and 68 genes differentially expressed between PRD and 0h water and no biological process was found to be enriched. It is worth noting that the hatching rates in this experiment are lower in this experiment than expected (15% in water, 25% in SolA treatment and 50% in PRD) and hatching was observed during the time course. The biological noise may be related to the time of the year when the experiment was conducted and may have contributed to the limited differential gene expression seen in this experiment. We modified the experimental conditions in order to reduce biological noise for a new test in 2021.

Bottlenecks:
No significant bottlenecks have been encountered.

Planning:
We will perform crosses with plants producing a lot and no SolA to investigate the genetic nature of the production of the compound. Furthermore a new test RNAseq test (number of samples tbd) will be conducted in 2021.

Products:
No products have been developed at this time.