



HAL
open science

Transcriptomic particularities among species of globodera

M. Sabeh, Eric Grenier, M. St-Arnaud, B. Mimee

► **To cite this version:**

M. Sabeh, Eric Grenier, M. St-Arnaud, B. Mimee. Transcriptomic particularities among species of globodera. Joint Meeting of the Society of Nematologists and the Organization of Nematologists of Tropical America (ONTA), Jun 2016, Montreal, Canada. 387 p. hal-01602956

HAL Id: hal-01602956

<https://hal.science/hal-01602956>

Submitted on 3 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - ShareAlike 4.0 International License

root-galling (scale 0 – 8) and egg production 70 days after inoculation. Each isolate x carrot genotype combination was replicated four times and the test was conducted twice. The most resistant genotypes across isolates were derived from Brasilia 1252 and HxB, a cross between Homs and Brasilia. Ping Ding and Western Red also exhibited effective resistance across isolates. Of 29 *M. incognita* isolates, three were slightly more aggressive on Homs and Ping Ding, whereas the Brasilia sources were unaffected by those more aggressive isolates. The *M. incognita* isolates included ones known to be virulent on the tomato *Mi-1* gene or the cowpea *Rk* gene, but there was no correlation between virulence on the *Mi-1* and *Rk* genes and ability to parasitize resistant carrot genotypes. Two isolates of *M. arenaria* and seven isolates of *M. javanica* were avirulent on the carrot resistance sources, whereas variation in ability to parasitize resistant carrots was found among 11 *M. hapla* isolates.

IMPACT OF CONCURRENT INFECTION BY *PRATYLENCHUS PENETRANS* AND *FUSARIUM VERTICILLIOIDES* ON CORN SEEDLINGS. Rush, T.A. and A.E. MacGuidwin. Plant Pathology Dept., University of Wisconsin-Madison, Madison, WI 53706.

Pratylenchus penetrans (Pp) and *Fusarium verticillioides* (Fv) are soilborne pathogens of corn. Infection by either pathogen damages roots and can inhibit plant growth and development with the potential to reduce yield. The severity and time course of symptoms caused by a fungal potato pathogen are increased when potato is infected by population densities of Pp too low to cause disease and it has been reported this phenomenon extends to the Fusarium-corn pathosystem. Our objective was to determine the fate of corn seedlings infected by both pathogens soon after planting using a scenario of low disease pressure for Pp. Four treatments, 1) non infested control, 2) Pp only, 3) Fv only, and 4) Pp+Fv were replicated six times in a complete randomized block design for two hybrids, Pioneer 9910X and Pioneer 1105YHR. Seeds were surface sterilized and pre-germinated. Treatments receiving Fv were soaked in a suspension of conidia or sterile water for 24 hrs before planting in cones filled with 700cm³ of pasteurized loamy sand soil. The Fv isolated, transformed to express GFP, was obtained from Iowa State University. Inoculum of 1000 Pp in water or water only was added to the hole before placing the seed. Nematodes were recovered from monoxenic root explant cultures by incubating roots on Baermann funnels. Plants were grown in a growth chamber under a, 14- hr photoperiod at 28 C and watered daily starting at 7 days after planting. Plant height, measured from the soil line to the tip of the tallest leaf, was recorded every day and used to calculate an area under the growth curve (AUGC). Thirty days after planting, plants were harvested and data collected for fresh and dry weight of plant organs. Nematodes were recovered from soil and roots and infection by the fungus was verified using fluorescence microscopy of plant tissues and morphology of conidia isolated from roots, stems and first leaf. The experiment was repeated twice and the data analyzed using SAS PROC MIXED. The Pioneer 9910X hybrid exposed to Fv only had lower ($P < 0.05$) dry root weights and lower values for AUGC as compared to the other three treatments. There were no differences between the Pp+Fv and control plants, indicating that concurrent infection by Pp mitigated the effect of the fungus. Absolute population densities of Pp per cone (roots and soil) and Pp per gram of dry root were not different for the Pp and Pp+Fv treatments. The Fv fungus was only recovered from plants receiving the conidial inoculum. No effects of any treatment were detected for the Pioneer 1105YHR hybrid. Studies are in progress to determine if Pp and Fv interact during the infection and colonization processes.

TRANSCRIPTOMIC PARTICULARITIES AMONG SPECIES OF *GLOBODERA*. Sabeh, M.^{1,3}, É. Grenier², M. St-Arnaud³, and B. Mimee¹. ¹Saint-Jean-sur-Richelieu Research and Development Center, Agriculture and Agri-Food Canada, Saint-Jean-sur-Richelieu (Qc), Canada J3B3E6; ²Institut National de Recherche Agronomique, Biologie des Organismes et des Populations appliquée à la Protection des Plantes, Domaine de la Motte, BP 35327, 35653 Le Rheu cedex France; ³Institut de Recherche en Biologie Végétale, Université de Montréal and Jardin Botanique de Montréal, Montréal (Qc), Canada H1X2B2.

Globodera spp. are major plant parasitic nematodes affecting Solanaceous plants including potato, tomato, eggplant and tobacco. Each species secretes specialized proteins called *effectors* to outwit plant defenses, allowing them to have a unique host range. RNA sequencing of the J2 parasitic stage was used to identify sequence variations and expression differences in effector genes that could explain species specificity for their host. *G. rostochiensis*, *G. pallida*, *G. mexicana* and *G. tabacum* were chosen for their economic importance, distinctive host range and high genetic similarity. Two distinct populations of each species were used to avoid finding intra-species variations. *G. rostochiensis* was directly compared to *G. tabacum* because of the difference in their primary host (*S. tuberosum* and *N. tabacum*) and *G. pallida* to *G. mexicana* because of the broader host range of *G. pallida*. RNA sequencing was performed on an Illumina HiSeq2500 producing an average of 29M sequenced 125bp paired-reads per sample. Data analysis was achieved using CLC Genomics Workbench. Clustering of gene expression patterns highlighted several differentially expressed effector genes. SPRYSEC and RBP-1 genes were overexpressed in *G. rostochiensis* compared to *G. tabacum*. On the other hand, CLE-1 and SKP-1 were overexpressed in *G. tabacum*. For the other pair, pectase lyase genes and ENG-3 were overexpressed in *G. pallida* while Gpx and CM-1 were overexpressed in *G. mexicana*. For sequences variations, only large variation (≥ 3) in effector genes sequences were searched for, as they are more prone to affect the molecular interactions of the protein. Fairly large insertions (8 and 5 bp) were found in *G. rostochiensis* SPRYSEC-4 and -5 as compared with its orthologue in *G. tabacum*. Important variations were also found in *G. pallida*'s IC5, SPRYSEC-1 and -19 genes as well as in pectase lyase when compared with orthologues in *G. mexicana*.