



HAL
open science

Genome scans on experimentally evolved *globodera pallida* populations to identify molecular basis of adaptation to GPAV(VRN) potato resistance

Delphine Eoche-Bosy, Magali Esquibet, Sylvain Fournet, Mathieu Gautier, Fabrice Legeai, Anthony Bretaudeau, Eric Grenier, Josselin Montarry

► To cite this version:

Delphine Eoche-Bosy, Magali Esquibet, Sylvain Fournet, Mathieu Gautier, Fabrice Legeai, et al.. Genome scans on experimentally evolved *globodera pallida* populations to identify molecular basis of adaptation to GPAV(VRN) potato resistance. Joint Meeting of the Society of Nematologists and the Organization of Nematologists of Tropical America (ONTA), 2016, Jul 2016, Montreal, Canada. 387 p. hal-01602955

HAL Id: hal-01602955

<https://hal.science/hal-01602955v1>

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

agua. La unidad de estudio fue una parcela conformada por 7 camellones con dos hileras de plantas cada uno. El cultivo de frutilla se encontraba alternado a intervalos irregulares con plantas de tomate, berenjena, cebolla de verdeo y malezas, irrigado por sistema de riego y manejo agroecológico del mismo. Se utilizaron dos camellones como puntos de aplicación y dos como control. El monitoreo de la plaga se realizó cada 15 días, a partir de la estimación del daño en el fruto, cuyos porcentajes variaron entre 0-10%. Una vez abandonada la cosecha, se realizaron nuevos monitoreos en los cuales se registró un daño promedio en los controles del 46%, mientras que en los camellones aplicados fue del 23%. A partir de estos datos preliminares podemos inferir que las diferencias entre los tratamientos son significativas, por tanto el uso del nematodo como agente de control de *L. insularis* podría representar una estrategia de control alternativa al manejo cultural, garantizando la producción de frutos con las características demandadas por el mercado.

GENOME SCANS ON EXPERIMENTALLY EVOLVED *GLOBODERA PALLIDA* POPULATIONS TO IDENTIFY MOLECULAR BASIS OF ADAPTATION TO *GPAV_{VRN}* POTATO RESISTANCE. **Eoche-Bosy, D.¹, M. Esquibet¹, S. Fournet¹, M. Gautier^{2,3}, F. Legeai^{1,4}, A. Bretaudeau^{1,4}, E. Grenier¹, and J. Montarry¹.** ¹UMR IGEPP, INRA, 35653 Le Rheu, France, ²UMR CBGP, INRA, IRD, Cirad, Montpellier SupAgro, 34988 Montpellier-sur-Lez, France, ³Institut de Biologie Computationnelle, 34095 Montpellier, France, ⁴IRISA, INRIA, 35042 Rennes, France.

In the current agronomical context of reduced use of pesticides, deciphering the genetic bases of pathogen adaptation to plant resistances is of major importance as it could help us to improve durability of these resistances. *Globodera pallida* is a major pest of potato and for which the promising resistance factor, QTL *GpaV_{vrn}*, has been identified in *Solanum vernei* and introduced into several new resistant cultivars in Europe. However, a previous study having employed an experimental evolution protocol, in which *G. pallida* lineages evolved on resistant or sensible potato genotypes, showed that *G. pallida* was able to overcome the resistance from *S. vernei*. The aim of the present study was to investigate the genomic regions involved in the resistance breakdown using a genome scan approach on the lineages resulting from the experimental evolution. A first low throughput genome scan was performed using 202 microsatellite markers distributed along the genome, using three different tests of neutrality based on genetic differentiation and heterozygosity. We identified eight outlier loci, several of which were found by multiple outlier detection methods and/or in two independent adapted lineages, indicative of genomic regions putatively involved in the resistance breakdown where several effectors of interest were identified. We also showed that the same adaptive genetic pathways seem to be involved in overcoming potato genotypes that harbored the same resistant QTL but differed in their genetic background. These results have validated the feasibility of a genome scan approach on biological material coming from a short term experimental evolution and led us to target more precisely the genomic regions involved in the adaptation. Thus a second high-throughput genome scan was performed using NGS data obtained through a whole genome resequencing of pools of individuals (Pool-Seq) that belonged to some of the lineages coming from the experimental evolution. 1.6 million SNPs are currently being used for a genome scan performed with the BAYPASS program. Identified outlier loci will allow us to target more precisely the best candidate genes involved in the adaptation and will also provide a molecular tool to follow virulence allele frequencies within wild *G. pallida* populations, which would be useful in order to conceive efficient strategies for maximizing the durability of potato resistance.

THE EMERGENCE OF *MELOIDOGYNE HAPLANARIA* IN FLORIDA, AND THE EFFECT OF INITIAL DENSITIES POPULATIONS ON TOMATO. **Espinoza-Lozano, L.^{1,3}, S. Joseph¹, W. Crow¹, L. Duncan², J. Noling², and T. Mekete¹.** ¹Department of Entomology and Nematology, University of Florida, Gainesville, FL, 32608, ²Department of Entomology and Nematology, University of Florida, Lake Alfred, FL 33850, ³Centro de Investigaciones Biotecnológicas del Ecuador, Escuela Superior Politécnica del Litoral, Guayaquil, Ecuador.

Root-knot nematodes are globally considered one of the most devastating plant-parasitic nematodes and are responsible for significant economic losses on a multitude of crops including tomato. The use of resistant varieties is a key tactic in the arsenal of management tools to control root-knot nematodes. In tomato, a single dominant gene referred to as the *Mi* gene has been widely used in plant breeding efforts and varietal development, which confers resistance to a number of the most economically important species of root-knot nematode found in Florida, including *Meloidogyne incognita*, *arenaria*, and *javonica*. *Mi*-virulent, resistance breaking isolates of these species, capable of reproduction and causing plant damage, have been detected in many areas of the world following the repeated use of these cultivars in field production. All too frequently, the discovery is also made that field populations of many different species of root-knot nematode are present in production fields, and those species that overcome the *Mi* resistance gene can proliferate and cause damage. *M. haplanaria* is an example of a root-knot nematode species recently reported in Florida affecting tomato crops that carry the *Mi* gene; this species was originally reported affecting peanut crops in Texas and Arkansas. Little is known about this nematode and its potential effect on tomato cultivars, including those conferred with the *Mi* gene. The main goal of the studies reported herein was to quantitatively describe the relationship between eight initial population densities of *M. haplanaria* on the resistant tomato cultivar “Sanibel” and the non-resistant cultivar “Rutgers”. Results from greenhouse and growth chamber studies will also be discussed.