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THE GENOME OF THE YELLOW POTATO CYST NEMATODE, *GLOBODERA ROSTOCHIENSIS*, REVEALS INSIGHTS INTO THE BASES OF PARASITISM AND VIRULENCE. **Eves-van den Akker, S.¹, D.R. Laetsch², P. Thorpe³, C.J. Lilley⁴, E.G.J. Danchin⁵, M. DaRocha⁵, C. Rancurel⁵, N.E. Holroyd⁶, J.A. Cotton⁶, A. Szitenberg⁷, E. Grenier⁸, J. Montarry⁸, B. Mimee⁹, M. Duceppe⁹, I. Boyes¹⁰, J.M.C. Marvin⁴, L.M. Jones⁴, H.B. Yusup⁴, J. Lafond-Lapalme⁹, M. Esquibet⁸, M. Sabeh⁹, M. Rott¹⁰, H. Overmars¹¹, A. Finkers-Tomczak¹¹, G. Smant¹¹, G. Koutsovoulos², V. Blok³, S. Mantelin³, P.J.A. Cock¹², W. Phillips¹³, B. Henrissat^{14,15}, P.E. Urwin⁴, M. Blaxter², and J.T. Jones^{3,16}.** ¹Division of Plant Sciences, College of Life Sciences, University of Dundee, Dundee, DD1 5EH, UK, ²Institute of Evolutionary Biology, University of Edinburgh, EH9 3FL, UK, ³Cell and Molecular Sciences Group, Dundee Effector Consortium, James Hutton Institute, Dundee, DD2 5DA, UK, ⁴Centre for Plant Sciences, University of Leeds, Leeds, LS2 9JT, UK, ⁵INRA, Univ. Nice Sophia Antipolis, CNRS, UMR 1355-7254 Institut Sophia Agrobiotech, 06900 Sophia Antipolis, France, ⁶Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Cambridge, CB10 1SA, UK, ⁷School of Biological, Biomedical and Environmental Sciences, University of Hull, Hull, HU6 7RX, UK, ⁸INRA, UMR1349 IGEPP (Institute for Genetics, Environment and Plant Protection), F-35653 Le Rheu, France, ⁹Agriculture and Agri-food Canada, Horticulture Research and Development Centre, 430 Boul. Gouin, St-Jean-sur-Richelieu, Quebec, J3B 3E6, Canada, ¹⁰Sidney Laboratory, Canadian Food Inspection Agency (CFIA), 8801 East Saanich Rd, Sidney, BC V8L 1H3, Canada, ¹¹Laboratory of Nematology, Department of Plant Sciences, Wageningen University, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands, ¹²Information and Computational Sciences Group, James Hutton Institute, Dundee, UK, ¹³USDA-ARS Horticultural Crops Research Laboratory, Corvallis, Oregon, USA, ¹⁴CNRS UMR 7257, INRA, USC 1408, Aix-Marseille University, AFMB, 13288 Marseille, France, ¹⁵Department of Biological Sciences, King Abdulaziz University, Jeddah, Saudi Arabia, ¹⁶School of Biology, University of St Andrews, North Haugh, St Andrews, KY16 9TZ, UK.

The yellow potato cyst nematode *Globodera rostochiensis* is a devastating plant pathogen of global economic importance, classified into pathotypes of different plant resistance-breaking phenotypes. *G. rostochiensis* secretes effectors, some of which were acquired by horizontal gene transfer (HGT), from pharyngeal glands into the host to manipulate host processes and promote parasitism. We generated a high-quality genome assembly for *G. rostochiensis* pathotype Ro1 and identified putative effectors and HGT events, mapped gene expression through the life cycle focusing on key parasitic transitions, and sequenced the genomes of eight populations including three additional pathotypes. HGT contributed 3.5% of the predicted genes, ~8.5% of which are deployed as effectors. Over one third of all effectors were clustered in 21 “effector islands”. We identified a motif (DOG box) present upstream of representatives of 26 of 28 dorsal-gland effector families, and predicted a superset of putative effectors associated with this motif. We validated gland cell expression for two novel genes by *in situ* hybridisation, and catalogued DOG effectors from available cyst nematode genomes. Comparison of effector diversity between pathotypes highlights those which correlate with plant resistance-breaking. These resources rapidly establish *G. rostochiensis* as a model to study pathogenicity and virulence in plant-parasitic nematodes.

THE TRANSCRIPTOME OF *NACOBBUS ABERRANS* REVEALS INSIGHTS INTO THE EVOLUTION OF SEDENTARY ENDOPARASITISM IN PLANT-PARASITIC NEMATODES. **Eves-van den Akker, S.¹, C.J. Lilley², E.G.J. Danchin³, C. Rancurel³, P.J.A. Cock⁴, P.E. Urwin² and J.T. Jones^{5,6}.** ¹Division of Plant Sciences, College of Life Sciences, University of Dundee, Dundee, DD1 5EH, UK, ²Centre for Plant Sciences, University of Leeds, Leeds, LS2 9JT, UK, ³INRA, Univ. Nice Sophia Antipolis, CNRS, UMR 1355-7254 Institut Sophia Agrobiotech, 06900 Sophia Antipolis, France, ⁴Information and Computational Sciences Group, James Hutton Institute, Dundee, UK, ⁵Cell and Molecular Sciences Group, Dundee Effector Consortium, James Hutton Institute, Dundee, DD2 5DA, UK, ⁶School of Biology, University of St Andrews.

Within the phylum Nematoda, sedentary plant-parasitism is hypothesised to have arisen independently on at least four occasions. The most economically damaging plant-parasitic nematode species, and consequently the most widely studied, are those that feed as they migrate destructively through host roots causing necrotic lesions (migratory endoparasites) and those that modify host root tissue to create a nutrient sink from which they feed (sedentary endoparasites). The false root-knot nematode *Nacobbus aberrans* is rare in that it has both migratory endoparasitic and sedentary endoparasitic stages within its life cycle. It is widely accepted that the cyst and root-knot nematodes evolved sedentary endo-parasitism independently, as evidenced by essentially no overlap in effector repertoires, and distinctly different complements of cell wall degrading enzymes acquired via horizontal gene transfer. While the sedentary stage of *Nacobbus* appears to phenotypically have characteristics of both the root-knot and the cyst nematodes, genetic data we present supports this “intermediate” position. We present the first large scale genetic resource of any false-root knot nematode species. We used RNAseq to describe relative abundance changes in all expressed genes across the life cycle to provide interesting insights into the biology of this nematode as it transitions between modes of parasitism. A multi-gene phylogenetic analysis of *N. aberrans* with respect to plant-parasitic nematodes of all groups confirms its proximity to both cyst and root-knot nematodes. We present a transcriptome-wide analysis of both lateral gene transfer events and the effector complement. Comparing parasitism genes of typical root-knot and cyst nematodes to those of *N. aberrans* has revealed interesting similarities: genes that were believed to be either cyst nematode- or root-knot nematode-specific have both been identified in *N. aberrans*. Our results may provide insights into the characteristics of a common ancestor and the evolution of sedentary endoparasitism of plants by nematodes.