

Researchers Get to Root of Nematode Genome

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Root-knot nematodes, stained red, move through a plant root.

(PhysOrg.com) -- North Carolina State University scientists and colleagues have completed the genome sequence and genetic map of one of the world's most common and destructive plant parasites – *Meloidogyne hapla*, a microscopic, soil-dwelling worm known more commonly as the northern root-knot nematode.

The research could help lead to a new generation of eco-friendly tools to manage the ubiquitous parasitic worm, which, along with other species of root-knot nematode, causes an estimated \$50 billion in crop and plant damage yearly, says Dr. Charles Opperman, professor of plant pathology at NC State, co-director of the Center for the Biology of Nematode Parasitism and the corresponding author on a scientific paper describing the research. The resulting sequence data has been deposited in public databases, so other researchers interested in the root-knot nematode – how it develops, establishes a host-parasite interaction or evades host defenses, for example – are now able to use the map of the parasite's

genes as a tool to discover more specific information about the parasite.

The northern root-knot nematode is the smallest multicellular animal genome completely sequenced, says Dr. David McK. Bird, professor of plant pathology at NC State, co-director of the Center for the Biology of Nematode Parasitism and a co-author of the paper.

The study is published online this week in *Proceedings of the National Academy of Sciences*. Researchers from the University of California, Davis; the University of California, Berkeley; and the Joint Genome Institute also contributed to the research.

The northern root-knot nematode has been developed into a key model species in the study of plant-parasitic nematodes, and the completion of the genome sequence will further empower researchers to ask highly specific questions about the evolution and nature of parasitism. "A key facet to making *M. hapla* the premier model species for plant-parasitic nematodes is the development of a genetic map by our colleague, Dr. Valerie Williamson, at the University of California-Davis. The combination of a complete genome sequence with the genetic map makes this a unique and powerful system for the in-depth study of nematode-host interaction" Opperman says.

Besides being extremely important for the development of new and effective management strategies, the researchers say that the information gleaned from the genome sequence and genetic map will help scientists learn more about what they call the "themes of parasitism."

"All parasites have to do the same things to infect their hosts, whether the hosts are plants, animals or humans," Bird says. "Plants offer an advantage over those systems because they are easier to manipulate experimentally, and enable us to perform detailed experiments not easily done in animals, and not possible in humans."

The study shows that *M. hapla* has a somewhat smaller genome when compared with other microscopic worms like *Caenorhabditis elegans*, one of the models of scientific studies of animals. The northern root-knot nematode genome might be smaller, the researchers say, because the inside of the host plant's root provides an isolated environment compared to the soil.

"Having 99 percent of the genome sequenced allows you to not only know what's there, but to compare it to other nematodes to see what's missing from this genome," Bird says. "Finding potential Achilles' heels, what the nematode is getting from the plant and how is it really interacting with the plant are all more possible now."

The genome's reduced size made it easier to assemble the sequence, Opperman says. "In combination with an extensive database of plant parasitic nematode expressed genes from a previous project led by our Center for the Biology of Nematode Parasitism, this system provides a powerful platform for study of these important parasites," he added.

Although *M. hapla* was previously not known to be as widespread as other species of root-knot nematode, the cool-climate worm is now taking root in warmer climes, perhaps due to global climate change. The worm has been detected recently in Ugandan soils and other tropical and subtropical regions, for example. The expansion of range to new climates makes finding ways of controlling it even more critical, the researchers say.

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