

Scientists sequence genomes of microscopic worms beneficial to agriculture

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Infective juvenile nematodes (*Steinernema glaseri*) emerging from infected insects (waxworms). Each nematode is about 1 millimeter in length. Credit: Adler Dillman, UC Riverside.

Many nematodes (worms) have specialized as pathogens, including those that serve as deadly insect-attacking parasites, making them effective biocontrol agents.

Now a research team led by a scientist at the University of California, Riverside has sequenced the genomes of five nematodes, specifically, microscopic round worms likely to be involved in parasitism and widely used in agriculture as an organic pesticide.

"In sequencing these particular nematodes we hoped to learn something about parasite biology and the evolution of nematodes in general," said Adler R. Dillman, the lead researcher and an assistant professor of parasitology in the Department of Nematology. "Although these nematodes are widely used in biological control against agricultural insect pests, their efficacy in the field is limited. Now with the genomic sequence we will be able to use this genetic information in efforts to improve the efficacy of these parasites to prevent insect damage of important crops."

Study results appear online in *Genome Biology*.

The five nematodes - *Steinernema carpocapsae*, *S. feltiae*, *S. glaseri*, *S. monticolum* and *S. scapterisci* - are used both commercially and in home gardens, and are marketed as beneficial nematodes. *Steinernema* are considered insect pathogenic because they can rapidly kill an insect host.

Dillman explained that his research team also learned more about [gene regulation](#) and the evolution of genomes in general as it compared the five sequences with other nematodes.

"For example, *Caenorhabditis elegans*, better known as *C. elegans*, is the best known [nematode](#) in the world and is a heavily studied model organism," Dillman said. "Scientists have learned a lot about

development, gene regulation, and cancer biology, among other things, by studying *C. elegans*. Now that we have sequenced these additional nematodes, we can compare the sequences to discover new regulatory sequences and motifs."

The research helps scientists' understanding of how the information encoded in a genome is regulated and used. Dillman expects that the five sequences will be used in subsequent studies by many researchers around the world. Further, these genome sequences will serve as the foundation of a research program he is building at UC Riverside.

"UCR is unique in having a Department of Nematology with experts studying a variety of nematodes and their importance in agriculture, ecology, and parasitism," Dillman said. "UCR is uniquely poised to make use of the immense data that results from this kind of genomic study."

One of the remaining biological mysteries is understanding how genes "know" when to turn off and on. Dillman explained that the elusive instructions that provide this information to genes is found in the non-coding regions of DNA - stretches of DNA that do not encode information for protein synthesis.

"The difficulty is in finding such pieces of informative DNA," he said. "Scientists have found that one way to identify these regions is to compare the genomic sequences of multiple related species and to search for regions of the genomes that contain the same or similar strings of letters - nucleotides - even though those parts of the genomes do not encode instructions for making proteins."

By sequencing the genomes of five insect-parasitic microscopic worms and comparing them to other well-studied species, his research team was successful in identifying some of these elusive genetic elements that

control when genes are turned on or off.

"In particular we found instructions in the genome for turning on and off genes that are involved in the development of neurons and muscle tissue," Dillman said. "We have also found a number of gene families that seem to be involved in the parasitism of insects by worms and we are excited to continue studying these in future experiments."

More information: *Genome Biology*,
www.genomebiology.com/2015/16/1/200

Provided by University of California - Riverside

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