

Trichinosis parasite gets DNA decoded (w/ Video)

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Trichinosis is caused by eating raw or undercooked pork or carnivorous wild game animals, such as bear and walrus, infected with the parasitic worm, *Trichinella spiralis*. While the disease is rarely deadly, some patients live for months or years with chronic muscle pain and fatigue until the worms eventually die. Photo by Jonathan Eisenback, Mactode Publications

Scientists have decoded the DNA of the parasitic worm that causes trichinosis, a disease linked to eating raw or undercooked pork or carnivorous wild game animals, such as bear and walrus.

After analyzing the genome, investigators at Washington University School of Medicine in St. Louis and their collaborators report they have identified unique features of the parasite, *Trichinella spiralis*, which provide potential targets for new drugs to fight the illness. The research

is published online Feb. 20 in [Nature Genetics](#).

While trichinosis is no longer a problem in the United States – fewer than a dozen cases are reported annually – an estimated 11 million people worldwide are infected. Current treatments are effective only if the disease is diagnosed early.

"It takes less than two weeks for the larvae to travel from the intestine to muscle, where they live," says lead author Makedonka Mitreva, PhD, research assistant professor of genetics at Washington University's Genome Center. "Once the worms invade the muscle, drugs are less effective. While the disease is rarely deadly, patients often live for months or years with chronic muscle pain and fatigue until the worms eventually die."

Today, trichinosis occurs most often in areas of Asia and Eastern Europe where pigs are sometimes fed raw meat, and meat inspections are lax.

The new research also has implications far beyond a single parasitic disease, the researchers say. *T. spiralis* is just one of many thousands of parasitic roundworms called nematodes that, according to the World Health Organization, infect 2 billion people worldwide, severely sickening 300 million. Other species of parasitic nematodes cause diseases in pets and livestock and billions of dollars of crop losses annually.

Among nematodes, *T. spiralis* diverged early, some 600-700 million years before the crown species, *C. elegans*, a model organism used in research laboratories. To date, the genomes of 10 nematodes, including five parasitic worms, have been decoded. The latest addition of the *T. spiralis* genome now allows scientists to compare species that span the phylum.

"*T. spiralis* occupies a strategic position in the evolutionary tree of nematodes, which helps fill in important knowledge gaps," explains senior author Richard K. Wilson, PhD, director of Washington University's Genome Center and professor of genetics. "By comparing [nematode](#) genomes, we have identified key molecular features that distinguish parasitic nematodes, raising the prospect that a single targeted drug may be effective against multiple species."

Over all, the genome of *T. spiralis* is smaller than that of *C. elegans*. It has 15,808 genes, compared to *C. elegans*' 20,000.

Moreover, about 45 percent of *T. spiralis* genes appear to be novel. These genes have not been found in other organisms and are not listed in public gene databases. The researchers say the worm's early evolutionary split or its distinctive lifestyle – it can't survive outside the body – may account for this extensive collection of enigmatic genes.

The researchers also found 274 families of proteins that are conserved among all nematodes and that do not exist in other organisms, including humans. Furthermore, they identified 64 protein families that are exclusive to parasitic nematodes.

"This provides opportunities for scientists to dig deeper into the distinctive features of parasitic nematodes that can be targeted with new drugs," Mitreva says. "If those drugs target molecular features unique to parasitic worms, it is more likely the side effects of those drugs will be minimal in humans."

More information: Mitreva M, Jasmer DP, Zarlenga DS, Wang Z, Abubucker S, Martin J, Taylor CM, Yin Y, Fulton L, Minx P, Yang S-P, Warren WC, Fulton RS, Bhonagiri V, Zhang X, Hallsworth-Pepin K, Clifton SW, McCarter JP, Appleton J, Mardis ER, Wilson RK. The draft genome of the parasitic nematode *Trichinella spiralis*. *Nature Genetics*.

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