

Researchers profile symbiotic relationship between bacteria and filarial nematodes

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A microfilaria of *Brugia malayi*. Credit: Centers for Disease Control and Prevention, Wikimedia Commons

Filarial nematodes—microscopic, thread-like roundworms—currently infect up to 54 million people worldwide and are the leading cause of disability in the developing world. Now, researchers reporting in *PLOS Neglected Tropical Diseases* have described the relationship between one species of the worm, *Brugia malayi*, and a bacteria, *Wolbachia*, that lives in the worm's body. The symbiotic relationship, they found, could represent an Achilles' heel for the nematodes.

While medications currently exist to treat lymphatic filariasis and onchocerciasis, the two main diseases caused by filarial nematodes, the drugs are insufficient to eliminate the diseases by 2020 and researchers project that resistance will arise to some of the drugs. Most filarial nematodes are hosts to *Wolbachia* bacteria, and require the bacteria for their own development, reproduction, and survival. Until now, the molecular details of the relationship between the filarial nematodes and their [symbiotic bacteria](#) have been poorly understood.

A collaborative study by Elodie Ghedin, of the New York University, Sara Lustigman of New York Blood Center, and Thomas Unnasch of The University of South Florida measured levels of RNA molecules in both *B. malayi* and *Wolbachia* throughout the lifecycles of male and female [worms](#). Levels of RNA allow the researchers to get insight into which genes are being expressed in the two organisms at any given timepoint of development, and which pathways in the bacteria may be critical to the worm's development, reproduction and survival.

Genes encoding ribosomal proteins, DNA replication and repair machinery, oxidative stress, and purine biosynthesis were differentially expressed in *Wolbachia* during the development of *B. malayi* female worms, suggesting a role of the bacteria in worm reproduction. In addition, the bacteria in all stages of the worms studied expressed genes involved in the synthesis of heme—an iron cofactor—and the movement of molecules and nutrients. Moreover, the [bacteria](#) seemed to produce nucleotides not only for their own use, but for the worms when requirements for nucleotides were high—such as during oogenesis and embryogenesis.

"Our study provides novel insight into the complexity of the interactions between *B. malayi* and its [endosymbiotic bacteria](#), *Wolbachia*. We find that it is unlikely that this obligate [symbiotic relationship](#) relies on a single process or pathway, but rather on more complex interactions that

likely vary over the life cycle of the parasite," the researchers conclude. "Elucidation of essential pathways involved in the endosymbiosis... will allow for the identification of novel drug targets."

More information: Grote A, Voronin D, Ding T, Twaddle A, Unnasch TR, Lustigman S, et al. (2017) Defining *Brugia malayi* and *Wolbachia* symbiosis by stage-specific dual RNA-seq. *PLoS Negl Trop Dis* 11(3): e0005357. [DOI: 10.1371/journal.pntd.0005357](https://doi.org/10.1371/journal.pntd.0005357)

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