

Genetic studies reveal how rat lungworm evolves

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Rat lungworm is a parasitic disease, spread through contaminated food, which affects the brain and spinal cord. Now, researchers report in *PLOS Neglected Tropical Diseases* that a detail analysis of the genetics of the rat lungworm parasite— *Angiostrongylus cantonensis*— reveal signatures of adaptive evolution that have let the parasite survive and may serve as future drug targets.

A. cantonensis is a roundworm with a complicated lifecycle that requires snails or slugs as an intermediary host. The parasite leads to central nervous system angiostrongyliasis in humans after ingestion of larvae in raw or undercooked snails or contaminated water or vegetables. The worm is the most common causes of eosinophilic meningitis in humans, an infection that can lead to death or permanent nervous system damage.

In the new work, Zhongdao Wu, of Sun Yat-sen University, China, and colleagues performed high-quality genetic sequencing of a well-defined laboratory strain of *A. cantonensis*. They isolated DNA and RNA from multiple stages of larvae and mature adult worms. They also compared the sequences to seven other nematode genomes that had been previously sequenced.

The researchers discovered that [transposable elements](#) make up 54.61% of the genome, more than in any other parasitic nematode. The expansion of retrotransposons and genes related to antioxidants, invasion, migration and digestion suggested adaptive evolution in these areas. There was also evidence of convergent evolution of extracellular

superoxide dismutase (EC-SOD) in *A. cantonensis* and flukes, which both require snails as hosts.

"These results provide an abundant data resource to study the biology and [evolution](#) of *A. cantonensis* and showed some potential targets against *A. cantonensis* and helminths with similar traits," the researchers say.

More information: Xu L, Xu M, Sun X, Xu J, Zeng X, et al. (2019) The genetic basis of adaptive evolution in parasitic environment from the *Angiostrongylus cantonensis* genome. *PLOS Neglected Tropical Diseases* 13(11): e0007846. doi.org/10.1371/journal.pntd.0007846

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