

# **Genomes of two millipede species shed light on their evolution, development and physiology**

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The rusty millipede *Trigoniulus corallinus* (Spirobolida)(left) and the orange rosary millipede *Helicorthomorpha holstii* (Polydesmida)(right). Credit: Wai Lok So, 2020

Millipedes, those many-legged denizens of the soil surface throughout the world, don't always get the recognition they deserve. But a new study by Jerome Hui of Chinese University of Hong Kong and colleagues puts them in the spotlight, sequencing and analyzing complete genomes from two very different millipede species. The study, publishing on September 29th in the open-access journal *PLOS Biology*, provides important insights into arthropod evolution, and highlights the genetic underpinnings of unique features of millipede physiology.

Millipedes and centipedes together comprise the Myriapoda—arthropods with multi-segmented trunks and many legs. Centipedes sport one pair of legs per segment, while millipedes bear two. Despite the apparent numeric implications of their names, different centipede [species](#) bear between 30 and 354 legs, and millipedes between 22 and 750. There are about 16,000 species of myriapods, including over 12,000 species of millipedes, but only two myriapod genomes have so far been characterized; a complete genome for the centipede *Strigamia maritima*, and a rough "draft" sequence of a [millipede](#) genome.

The authors of the new study fully sequenced the genomes of two millipede species, the orange rosary millipede *Helicorthomorpha holstii*, and the rusty millipede *Trigoniulus corallinus*, from two different orders, each distributed widely throughout the world. They also analyzed the gene transcripts (transcriptomes) at different stages of development, and the proteins (proteomes) of the toxin-producing "ozadene" glands.

The researchers found that two species have genomes of vastly different sizes—the orange rosary's genome is 182 million base pairs (Mb), while the rusty's is 449 Mb—which the authors showed was due mainly to the rusty millipede's genome containing larger non-coding regions (introns) within genes and [larger numbers](#) of repetitive "junk" DNA sequences.

Homeobox genes play central roles in body plan formation and segmentation during animal development, and the authors found lineage-specific duplications of common [homeobox genes](#) in their two species, which differed as well from those found in the previously published millipede genome. None of the three, however, displayed the massive duplications seen in the homeobox genes in the centipede [genome](#). They made further discoveries about the organization and regulation of the homeobox genes as well.

Many millipedes bear characteristic glands on each segment, called ozadene glands, which synthesize, store, and secrete a variety of toxic and noxious defensive chemicals. The authors identified multiple genes involved in production of these chemicals, including [genes](#) for synthesizing cyanide, as well as antibacterial, antifungal, and antiviral compounds, supporting the hypothesis that ozadene gland secretions protect against microbes as well as predators.

The results of this study provide new insights into evolution of the myriapods, and arthropods in general. "The genomic resources we have developed expand the known gene repertoire of myriapods and provide a genetic toolkit for further understanding of their unique adaptations and evolutionary pathways," Hui said.

**More information:** Qu Z, Nong W, So WL, Barton-Owen T, Li Y, Leung TCN, et al. (2020) Millipede genomes reveal unique adaptations during myriapod evolution. *PLoS Biol* 18(9): e3000636.

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