

The genome of a subterrestrial nematode reveals an evolutionary strategy for adaptation to heat

Deborah J. Weinstein¹, Sarah E. Allen^{1†}, Megan N. Guerin¹, Maggie C. Y. Lau², Mariana Erasmus³, Kathryn C. Asalone¹, Kathryn Walters-Conte¹, Gintaras Deikus⁴, Robert Sebra⁴, Gaetan Borgonie⁵, Esta van Heerden^{3§}, Tullis C. Onstott², John R. Bracht¹

AFFILIATIONS

1 Biology Department, American University, Washington DC 20016, USA; 2 Department of Geosciences, Princeton University, Princeton, NJ 08544, USA; 3 UFS/TIA Saense Platform, Department of Microbial, Biochemical, and Food Biotechnology, University of the Free State, Bloemfontein 9301, South Africa; 4 Department of Genetics and Genomic Sciences and Icahn Institute for Genomics and Multiscale Biology, Icahn School of Medicine at Mount Sinai, New York, New York 10029, USA; 5 Extreme Life Isyensya, Gentbrugge, 9050 Belgium; † Current: Biology Department, Cornell University, Ithaca, NY, 14853, USA; § Current: iWater Pty Ltd, 5 Walter Sisulu Road, Bloemfontein 9301, South Africa.

ABSTRACT

The nematode *Halicephalobus mephisto* was originally discovered inhabiting a deep terrestrial aquifer 1.3 km underground. *H. mephisto* can thrive under conditions of abiotic stress including heat and minimal oxygen, where it feeds on a community of both chemolithotrophic and heterotrophic prokaryotes in an unusual ecosystem isolated from the surface biosphere. Here we report the comprehensive genome and transcriptome of this organism, identifying a signature of adaptation: an expanded repertoire of 70 kilodalton heat-shock proteins (Hsp70) and *avrRpt2*-induced gene 1 (AIG1) proteins. We find that positive selection has driven the expansion of Hsp70 genes, which are also transcriptionally induced upon growth under heat stress. We further show that AIG1 may have been acquired by horizontal gene transfer (HGT) from a rhizobial fungus. Over one-third of the genes of *H. mephisto* are novel, highlighting the divergence of this nematode from other sequenced organisms. This work sheds light on the genomic strategies of adaptation to heat in the first complete subterrestrial eukaryotic genome.

