

GENOME SEQUENCING

The complete genome sequence of *Vulcanoctopus hydrothermalis* (Octopodidae, Octopoda)

T. Martin Schmeing¹, Taylor Hains^{2,3}, Stacy Pirro⁴, Janet R. Voight²

¹ Department of Biochemistry and Centre de Recherche en Biologie Structurale, McGill University Montréal QC H3G 0B1 Canada, ² Negaunee Integrative Research Center, Field Museum of Natural History, USA, ³ Committee on Evolutionary Biology, University of Chicago, USA, ⁴ Iridian Genomes

<https://doi.org/10.56179/001c.163650>

Biodiversity Genomes

We present complete genome sequence of *Vulcanoctopus hydrothermalis*, an octopod apparently endemic to the hydrothermal vents of the East Pacific Rise.

Introduction

Vulcanoctopus hydrothermalis, apparently restricted to the hydrothermal vents of the East Pacific Rise, has a morphology stunningly distinct from that of the morphologically conservative octopuses of *Muusoctopus*. Regardless, the two genera are members of the same clade (Strugnell et al. 2009). The different generic names were retained as they have been argued to be “sufficiently different” to merit it. *Vulcanoctopus hydrothermalis* prey on swarms of the amphipod *Halice hesmonectes* that live in warm (2-8°C) water wafting from diffuse vents (Voight 2005). The octopods are also found in ambient seafloor temperatures, as they venture at least 50 m from active vents.

Methods

A single, wild-collected individual was used for this study. The tissue sample was provided by the Field Museum, specimen voucher **FMNH 307183**. It was collected by the HOV ALVIN on dive 3936 at 10° 46.246'N 103° 39.412'W at 2763 m depth on Nov. 17, 2003.

DNA extraction was performed using the Qiagen DNEasy genomic extraction kit using the standard process. Paired-end sequencing libraries were constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The libraries were sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150bp format. The resulting fastq files were trimmed of adapter/primer sequences and low-quality regions with Trimmomatic v0.33 (Bolger et al. 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras et al. 2021).

Results and Data Availability

Taxname	raw_reads	genome
Vulcanoctopus hydrothermalis	SRR26078688	JAYRBU000000000

.....

Funding

Funding was provided by Iridian Genomes, grant# IRGEN_RG_2021-1345
Genomic Studies of Eukaryotic Taxa.

Submitted: June 18, 2026 EDT. Accepted: June 25, 2026 EDT. Published: June 25, 2026 EDT.

REFERENCES

- Bankevich, Anton, Sergey Nurk, Dmitry Antipov, et al. 2012. “SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing.” *Journal of Computational Biology*. <https://doi.org/10.1089/cmb.2012.0021>.
- Bolger, Anthony M., Marc Lohse, and Bjoern Usadel. 2014. “Trimmomatic: A Flexible Trimmer for Illumina Sequence Data.” *Bioinformatics* 30 (15): 2114–20. <https://doi.org/10.1093/bioinformatics/btu170>.
- Kieras, M., K. O’Neill, and S. Pirro. 2021. “Zanfona, a Genome Assembly Finishing Tool for Paired-End Illumina Reads.” <https://github.com/zanfona734/zanfona>.
- Strugnell, J., J. R. Voight, P. C. Collins, and A. L. Allcock. 2009. “Molecular Phylogenetic Analysis of a Known and a New Hydrothermal Vent Octopod: Their Relationships with the Genus *Benthooctopus* (Cephalopoda: Octopodidae).” *Zootaxa* 2096: 442–59. <https://doi.org/10.11646/zootaxa.2096.1.27>.
- Voight, J. R. 2005. “Hydrothermal Vent Octopuses of *Vulcanoctopus hydrothermalis*, Feed on Bathypelagic Amphipods of *Halice hesmonectes*.” *Journal of the Marine Biological Association, U.K.* 85: 985–88. <https://doi.org/10.1017/S0025315405011999>.