Raubold, Lina M., Rebecca N. Lopez-Anido, Stacy Pirro, Ángel Valdés, and Jessica A. Goodheart. 2024. "The Complete Genome Sequences of 7 Species of Nudibranchs (Nudibranchia, Gastropoda)." *Biodiversity Genomes*, May. https://doi.org/10.56179/001c.118546.

GENOME SEQUENCING

The Complete Genome Sequences of 7 Species of Nudibranchs (Nudibranchia, Gastropoda)

Lina M. Raubold[1], Rebecca N. Lopez-Anido[1], Stacy Pirro[2], Ángel Valdés[3], Jessica A. Goodheart[1]

[1] Division of Invertebrate Zoology, American Museum of Natural History, [2] Iridian Genomes, [3] Department of Biological Sciences, California State Polytechnic University

https://doi.org/10.56179/001c.118546

Biodiversity Genomes

We present genome sequences of 7 species of sea slugs from 4 genera. Illumina sequencing was performed on tissue from wild-collected museum specimens. The reads were assembled using a de novo method followed by a finishing step. The raw and assembled data are publicly available via Genbank.

Methods

Tissues from single, wild-collected individuals were used for this study. Three specimens were obtained from the Western Australian Museum (WAM) Marine Mollusca collection (Western Australian Museum 2023), and four were collected live for this study (CPIC, AMNH, MNHN). Live specimens were collected by hand while SCUBA diving and preserved in 95-100% EtOH for DNA sequencing.

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, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a final assembly finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

Species	Locality	Date Collected	Accession	Specimen_voucher
Bornella anguilla	Beagle Bay, Kimberley, WA, Australia	12 March 2008	JBDGEK000000000	WAMS:44513
Lomanotus vermiformis	Bocas del Toro, Panama	6 Aug 2004	JBBPDF000000000	CPIC:00556
Melibe bucephala	Seringapatam Reef, WA, Australia	27 Sept 2007	JBCJKE000000000	WAMS:31224
Melibe viridis	South Mole, Fremantle, WA, Australia	15 April 2019	JBCIKM000000000	WAMS:72630
Plocamopherus ceylonicus	Kwinana Grain Terminal Jetty,	21 June 2023	JBCJKF000000000	AMNH:IZC-00385163

Species	Locality	Date Collected	Accession	Specimen_voucher
	Rockingham, WA, Australia			
Plocamopherus imperialis	Koumac, New Caledonia	7 Nov 2018	JBCHJU000000000	MHNH-IM-2019-26525
Plocamopherus tilesii	Koumac New Caledonia	21 Nov 2019	JBBPCV000000000	MNHN-IM-2019-26526

Funding

Funding was provided by Iridian Genomes grant# IRGEN_RG_2021-1345: Genomic Studies of Eukaryotic Taxa. Field work in Australia was funded by the American Museum of Natural History, and work in New Caledonia was funded by the Gouvernement de la Nouvelle-Calédonie, Province Nord, Agence Française de la Biodiversité (AFB), the Lounsbery Foundation, and Office des Postes et Télécommunications (OPT).

Acknowledgments

We are grateful for specimens and support from Lisa Kirkendale and Corey Whisson at the Western Australian Museum, and collecting assistance from Henry Carrick for *Plocamopherus ceylonicus*. We also thank Rachel Colin for supporting field work in Bocas del Toro, Panama and facilitating export and collecting permits and Philippe Bouchet for the invitation to participate in the specimens "Our Planet Reviewed"—New Caledonia expeditions (2018–2019), a joint project of MNHN and Conservatoire d'Espaces Naturels (CEN) de Nouvelle-Calédonie.

Submitted: May 23, 2024 EDT, Accepted: May 28, 2024 EDT

REFERENCES

Bankevich, Anton, Sergey Nurk, Dmitry Antipov, Alexey A. Gurevich, Mikhail Dvorkin, Alexander S. Kulikov, Valery M. Lesin, et al. 2012. "SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing." *Journal of Computational Biology* 19 (5): 455–77. 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.

Western Australian Museum. 2023. "Western Australian Museum Provider for OZCAM." https://doi.org/10.15468/5qt0dm.