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GENOME SEQUENCING

The Complete Genome Sequences of 13 Species of Brachycnemina (Cnidaria, Hexacorallia, Anthozoa, Zoantharia)

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Biodiversity Genomes

We present the complete genome sequences of 13 species of the zoantharian suborder Brachycnemina (Haddon, and Shackleton, 1891; Poliseno et al., 2020). Genome sequencing was performed on genetic material from single wild-collected individuals. For each species the sequence reads were assembled using a de novo method followed by a finishing step. The raw and assembled data are publicly available via GenBank.

Introduction

We present the assembled draft genome sequences from 13 extant species of the zoantharian suborder Brachycnemina. Detailed information about the specimen used for each species can be found in the Biosample linked to each genome assembly in GenBank.

Methods

DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard process. A paired-end sequencing library was constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The libraries were sequenced on an Illumina HiSeq platform in paired-end (2 × 150 bp) 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 sequences were assembled by SPAdes v2.5 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

All data, including raw reads and assembled genome sequence, are available via GenBank.

Isaurus tuberculatus	JAOEHV000000000
Palythoa caribaeorum	JAOCNB000000000
Palythoa grandiflora	JAOCPT000000000
Palythoa grandis	JAOEJH000000000
Palythoa heliodiscus	JAOBYJ000000000
Palythoa mutuki	JAODFW000000000
Sphenopus marsupialis	JAOBRF000000000
Zoanthus gigantus	JAOBBB000000000
Zoanthus pulchellus	JAOBRB000000000
Zoanthus sanctaehelenae	JAOTRI000000000
Zoanthus sansibaricus	JAPEIX000000000
Zoanthus sociatus	JAOBAY000000000
Zoanthus solanderi	JANCMA000000000

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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.

Haddon, A.C., and A.M. Shackleton. 1891. "Actiniae: I. Zoantheae." In *Reports on the Zoological Collections Made in the Torres Straits by Professor A.C. Haddon, 1888–1889*, 4:673–658. Scientific Transations of the Royal Dublin Society.

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.

Poliseno, Angelo, Maria Eduarda Alves Santos, Hiroki Kise, Brooks Macdonald, Andrea M. Quattrini, Catherine S. McFadden, and James Davis Reimer. 2020. "Evolutionary Implications of Analyses of Complete Mitochondrial Genomes across Order Zoantharia (Cnidaria: Hexacorallia)." *Journal of Zoological Systematics and Evolutionary Research* 58 (4): 858–68. https://doi.org/10.1111/jzs.12380.