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GENOME SEQUENCING

The Complete Genome Sequences of 7 Species of *Epizoanthus* (Epizoanthidae, Zoantharia, Hexacorallia, Cnidaria)

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Biodiversity Genomes

We present the complete genome sequences of 7 species of the zoantharian genus *Epizoanthus*. Illumina sequencing was performed on genetic material from single wild-collected individuals. The reads were assembled using a de novo method followed by a finishing step. The raw and assembled data are publicly available via GenBank.

Introduction

The Epizoanthidae are a family of zoantharians with a worldwide distribution (e.g. Ryland and Ward 2016; Kise et al. 2019). We present the assembled genome sequences from 7 extant species of this genus. 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 library was sequenced on an Illumina Hi-Seq platform in paired-end, 2 × 150 bp format. The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was 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 draft genome sequence, are available via GenBank.

Epizoanthus fatuus	JAOCZQ000000000
Epizoanthus illoricatus	JANVCK000000000
Epizoanthus planus	JANVCE000000000
Epizoanthus ramosus	JANVCJ000000000
Epizoanthus rinbou	JANVCH000000000
Epizoanthus scotinus	JANUFV000000000
Epizoanthus stellaris	JAOBYG000000000

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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.

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.

Kise, Hiroki, Javier Montenegro, Merrick Ekins, Takeya Moritaki, and James Davis Reimer. 2019. "A Molecular Phylogeny of Carcinoecium-Forming *Epizoanthus* (Hexacorallia: Zoantharia) from the Western Pacific Ocean with Descriptions of Three New Species." *Systematics and Biodiversity* 17 (8): 773–86. https://doi.org/10.1080/14772000.2019.1693439.

Ryland, John S., and Helen Ward. 2016. "Carcinoecium-Forming Epizoanthus [Hexacorallia: Zoantharia] and the Biology of E. Papillosus in the Eastern Atlantic, with Special Reference to the Cnidom." *Zootaxa* 4088 (4): 489–514. https://doi.org/10.11646/zootaxa.4088.4.2.