

GENOME SEQUENCING

The complete genome sequences of 5 species of reptiles invasive in Puerto Rico

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Biodiversity Genomes

We present complete genome sequences of 5 species of reptiles invasive in Puerto Rico. Individuals were collected in the wild and represent species known to be established and reproducing (*Caiman crocodilus*, *Gymnophthalmus underwoodi*, *Malayopython reticulatus*) or first verified reports of species that could become established (*Chlamydosaurus kingii*, *Python bivittatus*).

Methods

Tissues from single, wild-collected individuals were used for this study. 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

taxid	species	specimen_voucher	bioproject
8499	Caiman crocodilus	UPRMGENRESCOL_4184_TJC1737	JBTXPI000000000
103699	Chlamydosaurus kingii	UPRMGENRESCOL_4185_TJC1738	JBTVYJ000000000
88867	Gymnophthalmus underwoodi	UPRMGENRESCOL_3211_TJC1727	JBTVYH000000000
1496311	Malayopython reticulatus	UPRMGENRESCOL_4148_TJC1732	JBTXPH000000000
176946	Python bivittatus	UPRMGENRESCOL_4186_TJC1733	JBTVYI000000000

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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* 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>.