

GENOME SEQUENCING

The complete genome sequences of 4 species of Storks (Ciconiiformes : Aves)

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Biodiversity Genomes

We present complete genome sequences of 4 species of Ciconiiformes.

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

taxname	accession	specimen_voucher	country
Anastomus lamelligerus	JBFOX000000000	FMNH 192043	Somalia
Ephippiorhynchus senegalensis	JBPEW000000000	FMNH 85840	Swaziland
Leptoptilos crumeniferus	JBSEP000000000	FMNH 269478	Cameroon
Mycteria ibis	JBKOKA000000000	FMNH 192046	Somalia

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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*.
- 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>.