

GENOME SEQUENCING

The complete genome sequences of 3 species of African barbets (Lybiidae, Piciformes)

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Biodiversity Genomes

We present complete genome sequences of 3 species of African barbets.

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

All raw data and assembled genomes are available via Genbank.

taxname	accessions
Buccanodon duchaillui	JBFNXXB0000000000
Pogoniulus atroflavus	JBFNGO0000000000
Pogoniulus bilineatus	JBFPDQ0000000000

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