

GENOME SEQUENCING

The complete genome sequences of 2 species of African honeyguides (Indicatoridae, Piciformes)

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Biodiversity Genomes

We present complete genome sequences of 2 species of African honeyguides.

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	accession
Indicator exilis	JBFNWZ000000000
Indicator maculatus	JBLLKV000000000

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