

GENOME SEQUENCING

The complete genome sequences of 3 species of African Woodpeckers (Picidae, Piciformes)

Frank Bapeamoni¹, Bertin Murhabale Cisirika², Charles Kahindo², Balekage Balezi Charles¹, Mushagalusa Satira Fidel², Stacy Pirro³, Ben D. Marks⁴

¹ Faculté des Sciences, Université de Kisangani, Kisangani, République Démocratique du Congo, ² Département de Biologie, Faculté des Sciences, Université Officielle de Bukavu, Bukavu, République Démocratique du Congo, ³ Iridian Genomes, ⁴ Field Museum, Gantz Family Collections Center, Bird Collection, Chicago, IL, USA

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Biodiversity Genomes

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

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.

taxame	accession
Sasia africana	JBIGID0000000000
Campethera nivosa	JBFTWP0000000000
Campethera caroli	JBGGHU0000000000

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