

GENOME SEQUENCING

The complete genome sequences of 8 species of African Bulbuls (Pycnonotidae, Passeriformes)

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Biodiversity Genomes

We present complete genome sequences of 8 species of African Bulbuls.

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, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

Andropadus latirostris	JBGBCZ000000000
Andropadus virens	JBGDLT000000000
Bleda syndactyla	JBFNHG000000000
Bleda ugandae	JBFCYF000000000
Criniger calurus	JBWZB000000000
Criniger chloronotus	JBFCYT000000000
Eurillas ansorgei	JBFNWW000000000
Phyllastrephus albigularis	JBFSWZ000000000

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REFERENCES

- Bankevich, Anton, Sergey Nurk, Dmitry Antipov, Alexey A. Gurevich, Mikhail Dvorkin, Alexander S. Kulikov, Valery M. Lesin, 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>.