

GENOME SEQUENCING

The Complete Genome Sequence of *Chlorophonia sclateri* (Fringillidae, Passeriformes), the Puerto Rican Euphonia

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Biodiversity Genomes

The Puerto Rican Euphonia (*Chlorophonia sclateri*) was recognized as an endemic species in 2023 based solely on morphological differences. A brightly plumaged finch that inhabits a variety of habitats, including lowland dry, scrub forests and shade-coffee plantations (Carlo et. al 2004). To provide molecular evidence for the genetic comparison of Antillean Euphonias, we present the whole genome sequence of *Chlorophonia sclateri*. Illumina paired-end reads were assembled by a *de novo* method followed by a finishing step. The raw and assembled data are publicly available via GenBank: Sequence Read Archive (SRR28963854) and assembled genome (JBFPDU000000000).

Methods

A single wild-collected museum specimen (FMNH 27046) was used for sequencing. DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard process. A paired-end sequencing library was constructed using the Illumina TruSeq kit according to the manufacturer's instructions. The library was sequenced on an Illumina NovoSeq platform in paired-end, 2 × 150 bp 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 v2.5 (Bankevich, Nurk, Antipov, et al. 2012) followed by a finishing step using Zanfona v1.0 (Kieras 2021) to make additional contig joins based on conserved regions in related species.

Data availability

Raw and assembled data are publicly available via GenBank.

Raw genome data: SRR28963854

Assembled genome: JBFPDU000000000

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