

GENOME SEQUENCING

The Complete Genome Sequences of 11 Species of Kingbirds (Tyrannus, Tyrannidae, Passeriformes)

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Biodiversity Genomes

We present the complete genome sequences of 11 species of kingbirds. Illumina sequencing was performed on genetic material from wild-caught and museum specimens. The reads were assembled using a *de novo* method followed by a finishing step. The raw and assembled data are publicly available via Genbank.

Introduction

The genus *Tyrannus* currently consists of 13 suboscine species distributed throughout the western hemisphere (Winkler, Billerman, and Lovette 2020). Commonly known as “kingbirds”, this genus is within the tyrant flycatcher family Tyrannidae, the most speciose family of birds on Earth. Although kingbirds only average 20 cm in length, they are known for their aggressive territorial behavior.. They are typically found in semi-open or open areas, where they employ a sit-and-wait foraging strategy from exposed perches, catching insects in midair. Like other members of Tyrannidae, kingbirds primarily consume insects but also incorporate fruit and, in some cases, small vertebrates such as lizards into their diet (Winkler, Billerman, and Lovette 2020). Despite their shared ecological traits, members of *Tyrannus* exhibit considerable variation in morphology and plumage. Most are black, gray, or olive above and white or yellow below, with long, pointed wings and broad bills suited for aerial insectivory. A distinctive feature of all *Tyrannus* species is an often concealed crest of red, orange, or yellow feathers that can be erected (but rarely are). Some species also possess long, deeply forked tails, such as *T. forficatus* and *T. savana*, that may enhance aerial maneuverability or serve as visual signals in display behaviors (Roeder et al. 2019).

Methods

Single wild-collected individuals and museum specimens were sampled for this study. Blood samples were collected from adult *T. forficatus*, *T. tyrannus*, and *T. verticalis* in Arkansas, USA during the 2022-2023 breeding season. Tissue and toe pad samples for the remaining species were obtained from the following museum collections: the Academy of Natural Sciences of Drexel University (*T. niveigularis*; #184813), Burke Museum (*T. melancholicus*; #82569), Delaware Museum of Natural History (*T. vociferans*; #25263), the Field Museum of Natural History (*T. crassirostris*; #394000), the National Museum of Natural History (*T. caudifasciatus*; #395620 and *T. cubensis*;

#395604) the University of Kansas Biodiversity Institute Ornithology Collection (*T. couchii*; #89449), and Yale Peabody Museum (*T. albogularis*; #137544)

DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard protocol. 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 Hi-Seq platform in paired-end, 2 × 150 bp format. The resulting fastq files were trimmed of adapter/primer sequence and low-quality regions with Trimmomatic v0.33 (Bolger, Lohse, and Usadel 2014). The trimmed sequence was assembled by SPAdes v2.5 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

All data, including raw reads and assembled genome sequence, is available via Genbank.

taxname	raw_reads	assembled_genome
<i>Tyrannus albogularis</i>	SRR31107683	JBQPN000000000
<i>Tyrannus caudifasciatus</i>	SRR23994958	JAUCNE000000000
<i>Tyrannus couchii</i>	SRR31107786	JBQPO000000000
<i>Tyrannus crassirostris</i>	SRR31107743	JAUESG000000000
<i>Tyrannus cubensis</i>	SRR23995626	JAUBOB000000000
<i>Tyrannus forficatus</i>	SRR17839038	JAQXXM000000000
<i>Tyrannus melancholicus</i>	SRR31103376	JAUCNP000000000
<i>Tyrannus niveigularis</i>	SRR31107681	JBQPM000000000
<i>Tyrannus tyrannus</i>	SRR17839680	JAQYSJ000000000
<i>Tyrannus verticalis</i>	SRR23995013	JAUCNF000000000
<i>Tyrannus vociferans</i>	SRR31107656	JAUELM000000000

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