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GENOMIC RESOURCES NOTE

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Abstract

This article documents the public availability of (i) genomic sequence data and 43 microsatellite loci for the bat species, *Lasiurus borealis* and *Lasiurus cinereus*, and (ii) complete mitochondrial and partial nuclear genomes for two jack species, *Caranx ignobilis*, *Caranx melampygus*.

Table 1 contains information on the focal species, data type and resource developed, as well as access details for the data. The authors responsible for each genomic resource are listed in the final column. Full descriptions of how each resource was developed and tested are uploaded as Appendices S1 and S2 (Supporting information); both Table 1 and Appendices S1 and S2 (Supporting information) are sorted by the generic name of the focal taxon.

Table 1 Information on the focal species, data type and resource developed, as well as access details for the data. The authors responsible for each genomic resource are listed in the final column.

Species (no. of individuals)	Data type	Resources	Authors
Caranx ignobilis, C. melampygus	Mt and nuclear genomic sequence assembly	*Sequence data:* Available from NCBI SRA under PRJNA220978; SRR1002875 (*C. ignobilis*) and PRJNA220978; SRR1002876 (*C. melampygus*) *Assembled contigs:* Available from Dryad for both *C. ignobilis* and *C. melampygus* as FASTA files under accession DOI:10.5061/dryad.6gr7t *Mitochondrial genomes (complete)*: Available from NCBI GenBank under accessions KF649842 (*C. ignobilis*) and KF649843 (*C. melampygus*) *Nuclear genome contig annotation*: Available from Dryad for both *C. ignobilis* and *C. melampygus* as FASTA files of all potential and BLAST-annotated ORFs, as well as gene lists relative to *Danio* and *Takifugu* under accession doi:10.5061/dryad.6gr7t	Santos, Scott R.

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Table 1 (Continued)

Species (no. of individuals)	Data type	Resources	Authors
		Alignments: Available from NCBI SRA under PRJNA220978; SRR1002927 (*C. ignobilis*) and PRJNA220978; SRR1002928 (*C. melampygus*) Putative SNPs and indels: Available from Dryad for both *C. ignobilis* and *C. melampygus* as unfiltered and filtered VCF files under accession doi:10.5061/dryad.6gr7t	
Lasiurus borealis (1 for sequencing; 23 for marker screening), *L. cinereus* (1 for sequencing; 23 for marker screening)	Genomic sequence assembly and microsatellite discovery	*Sequence files*: Raw sequence files with quality scores (.fastq) are available for each species from the NCBI Sequence Read Archive: PRJNA225945 *Alignments*: One aligned sequence file (.bam) for each individual is available from NCBI Sequence Read Archive: PRJNA225945 *Scripts*: Shell script outlining pipeline for sequence alignment and consensus sequence calling is available as File S1 from DRYAD entry doi:10.5061/dryad.70254 *Microsatellite loci*: Table 2 of Appendix S2	Keller, Stephen R.; Trott, Regina; Pylant, Cortney; Nelson, David M.

Supporting Information

Additional Supporting Information may be found in the online version of this article:

Appendix S1. Complete mitochondrial and partial nuclear genomes for the jack species *Caranx ignobilis* (Forsskål, 1775) and *C. melampygus* (Cuvier, 1833) (Perciformes:Carangidae) from the High Hawaiian Islands.

Appendix S2. Genome-wide microsatellite marker development from next-generation sequencing of two non-model bat species impacted by wind turbine mortality: *Lasiurus borealis* and *L. cinereus* (Vespertilionidae).