GENOME SEQUENCING

The Complete Genome Sequences of 23 Finch Species (Fringillidae, Passeriformes)

Louise Bodt^{1,2}, Taylor Hains^{1,3}, Daryl Coldren⁴, Stacy Pirro⁵, John Bates^{1,2}, Shannon Hackett^{1,2}

¹ Negaunee Integrative Research Center, Field Museum of Natural History, ² Committee on Evolutionary Biology, University of Chicago, ³ University of Chicago, Committee on Evolutionary Biology, ⁴ The Gantz Family Collections Center, Field Museum of Natural History, ⁵ Iridian Genomes https://doi.org/10.56179/001c.117726

Biodiversity Genomes

We present complete genome sequences of 23 species of finches from 6 genera.

Introduction

Birds in the Fringillidae family are true finches. There are three subfamilies, Fringillinae, Euphoniinae and Carduelinae (Zuccon et al. 2012). They are small to medium-sized, widespread, largely granivorous birds and are native to every continent except Antarctica and Australia. They also have colonized and differentiated on oceanic islands. They often have stout, conical-shaped bills (except Hawaiian honeycreepers) (Winkler, Billerman, and Lovette 2015). Some of European origin have been introduced to Australia and New Zealand. There are also introduced populations across the world, including in the United States and Argentina, where they share geography with native finches (North and South American siskins, redpolls, rosefinches etc.). Several species are common caged birds and historically have been kept as pets (e.g. European Goldfinches) or for human services (e.g. Canaries to detect carbon monoxide in coal mines).

Methods

Tissues 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, 2×150 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 v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras, O'Neill, and Pirro 2021).

Results and Data Availability

All raw read data and assembled genomes are available on Genbank:

Species	Genome	Specimen_voucher
Acanthis flamea	JAYJLY00000000	FMNH 95021
Carduelis citrinella	JAYRBP00000000	FMNH 343157
Carduelis corsicana	JAUYWN000000000	FMNH 343161
Linurgus olivaceus	JAYRCA00000000	FMNH 298894
Loxia leucoptera	0000000000MWWAL	FMNH 328157
Loxia pytyopsittacus	JAUYWL00000000	FMNH 126802
Serinus cacnicollis	JAUUDU00000000	FMNH 441104
Serinus flavivertex	JAYDBR00000000	FMNH 83958
Serinus nigriceps	JAUZTC00000000	FMNH 83996
Serinus pusillus	JAYRBO00000000	FMNH 66471
Serinus serinus	JAVCKY00000000	FMNH 185003
Serinus syriacus	JAWWM00000000	FMNH 343155
Spinus atriceps	JAVRMD00000000	FMNH 189863
Spinus crassirostris	JAYRBZ00000000	FMNH 391990
Spinus lawrencei	JAUZTD00000000	FMNH 177750
Spinus olivaceus	JAYRCE00000000	FMNH 481061
Spinus pinus	JAUUDX00000000	FMNH 437097
Spinus psaltria	JAYJLW00000000	FMNH 121653
Spinus spinescens	00000000000UYUAL	FMNH 220593
Spinus spinus	JAUUDX00000000	FMNH 185006
Spinus tristis	JAYRBQ00000000	FMNH 495559
Spinus yarrellii	JAYDZH00000000	FMNH 53368

Funding

Funding was provided by Iridian Genomes grant# IRGEN_RG_2021-1345 "Genomic Studies of Eukaryotic Taxa.

......

Submitted: May 18, 2024 EDT, Accepted: May 21, 2024 EDT

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. <u>https://doi.org/10.1089/cmb.2012.0021</u>.
- Bolger, Anthony M., Marc Lohse, and Bjoern Usadel. 2014. "Trimmomatic: A Flexible Trimmer for Illumina Sequence Data." *Bioinformatics* 30 (15): 2114–20. <u>https://doi.org/10.1093/</u> <u>bioinformatics/btu170</u>.
- Kieras, M, K O'Neill, and S Pirro. 2021. "Zanfona, a Genome Assembly Finishing Tool for Paired-End Illumina Reads." 2021. <u>https://github.com/zanfona734/zanfona</u>.
- Winkler, D. W., S. M. Billerman, and I. J. Lovette. 2015. *Bird Families of the World: An Invitation to the Spectacular Diversity of Birds*. Lynx Edicions.
- Zuccon, D., R. Prŷs-Jones, P. C. Rasmussen, and P. G. P. Ericson. 2012. "The Phylogenetic Relationships and Generic Limits of Finches (Fringillidae)." *Molecular Phylogenetics and Evolution* 62 (2): 581–96. <u>https://doi.org/10.1016/j.ympev.2011.10.002</u>.