

GENOME SEQUENCING

The Complete Genome Sequences of 29 Species of Ducks (Anatidae, Anseriformes)

Emily Griffith¹, Stacy Pirro²

¹ Drexel University, ² Iridian Genomes

<https://doi.org/10.56179/001c.122134>

Biodiversity Genomes

We present genome sequences of 29 species of ducks from 8 genera. Illumina sequencing was performed on tissue from wild-collected 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.

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

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

Species	Accession	Specimen_voucher
<i>Amazonetta brasiliensis</i>	JBBYHF000000000	UAM Bird:14628
<i>Anas acuta</i>	JAYRCF000000000	ANSP tissue:28083
<i>Anas aucklandica</i>	JBCATX000000000	ANSP skin:77177
<i>Anas bahamensis</i>	JBBYHN000000000	UAM Bird:36736
<i>Anas bernieri</i>	JAUEKP000000000	SHbern_V68VBK8SIL
<i>Anas capensis</i>	JAUELN000000000	REW671
<i>Anas carolinensis</i>	JBCAUC000000000	ANSP skin:189308
<i>Anas crecca</i>	JAYJLT000000000	ANSP tissue:27782
<i>Anas flavirostris</i>	JBCATY000000000	UAM Bird:24711
<i>Anas georgica</i>	JAUBNX000000000	KGM274
<i>Anas poecilorhyncha</i>	JBCJKG000000000	ANSP skin:128732
<i>Anas puna</i>	JBBYGV000000000	UAM Bird:38306
<i>Anas zonorhyncha</i>	JBCAUD000000000	ANSP skin:85306
<i>Lophonetta specularioides</i>	JAUJPM000000000	KGM821
<i>Mareca americana</i>	JAXIUU000000000	ANSP tissue:22592

Species	Accession	Specimen_voucher
Mareca falcata	JBBYGQ000000000	UAM Bird:21189
Mareca penelope	JAYRCD000000000	ANSP tissue:27964
Mareca sibilatrix	JAVKLD000000000	REW261
Sibirionetta formosa	JBCAUB000000000	UAM Bird:28790
Spatula clypeata	JBCATZ000000000	ANSP skin:190948
Spatula discors	JAUJJP000000000	REW001
Spatula querquedula	JAUJPN000000000	UWBM 36215
Spatula rhynchotis	JAVKLC000000000	UWBM 78156
Spatula smithii	JAWDEW000000000	REW674
Spatula versicolor	JBBYHG000000000	UAM Bird:17529
Specularias specularis	JAUJTY000000000	KGM271
Tachyeres brachypterus	JAULBN000000000	REW330
Tachyeres leucocephalus	JAVDPI000000000	KGM823
Tachyeres patachonicus	JBBYHP000000000	UAM Bird:20714

.....

Funding

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

Submitted: July 23, 2024 EDT, Accepted: July 24, 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. <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>.