

GENOME SEQUENCING

The Draft Genome Sequences of 63 Species of Catfish (Ariidae, Siluriformes)

Melissa M. Rincon Sandoval<sup>1</sup>, Stacy Pirro<sup>2</sup>, Ricardo Betancur<sup>1</sup>

<sup>1</sup> Department of Biology, The University of Oklahoma, <sup>2</sup> Iridian Genomes  
<https://doi.org/10.56179/001c.117717>

Biodiversity Genomes

We present genome sequences of 63 species of catfish from the Ariidae family. 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:

Amissidens hainesi	JANZXU000000000
Ariopsis seemanni	JAOANJ000000000
Arius gadora	JAODTS000000000
Arius madagascariensis	JANZXT000000000
Bagre pinnimaculatus	JAPEKL000000000
Batrachocephalus mino	JAOBAL000000000
Brustiarius nox	JAODHU000000000
Brustiarius proximus	JAOXJH000000000
Brustiarius solidus	JAODKP000000000
Cathorops aguadulce	JAPEIY000000000
Cathorops dasycephalus	JAPEKN000000000
Cathorops festae	JAODXR000000000
Cathorops hypophthalmus	JAPEKO000000000
Cathorops melanopus	JAODLJ000000000
Cathorops multiradiatus	JAPEKM000000000
Cephalocassis borneensis	JAOPUC000000000

---

Amissidens hainesi	JANZXU000000000
Cephalocassis melanochir	JAODOG000000000
Chinchaysuyo labiata	JAODLF000000000
Cinetodus carinatus	JAODOI000000000
Cinetodus crassilabris	JAODKQ000000000
Cinetodus froggatti	JAODOL000000000
Cochlefelis danielsi	JAODKR000000000
Cochlefelis spatula	JAODKX000000000
Galeichthys feliceps	JAODTV000000000
Genidens genidens	JAODOH000000000
Genidens machadoi	JAOTJA000000000
Genidens planifrons	JAOANL000000000
Hemiarus dioctes	JAODID000000000
Hemiarus stormii	JAODOD000000000
Nedystoma dayi	JAODIC000000000
Nedystoma novaeguineae	JAODLB000000000
Nemapteryx armiger	JAODOB000000000
Nemapteryx augusta	JAODHT000000000
Nemapteryx nenga	JAODOC000000000
Neorarius berneyi	JAODIF000000000
Neorarius graeffei	JALHSM000000000
Neorarius leptaspis	JAODTU000000000
Neorarius midgleyi	JAPEKJ000000000
Neorarius paucus	JAPUBO000000000
Neorarius pectoralis	JAPTHB000000000
Neorarius utarus	JAODOJ000000000
Netuma bilineata	JAODOK000000000
Notarius cookei	JAOEHH000000000
Notarius kessleri	JAOBAM000000000
Notarius lentiginosus	JAODVO000000000
Notarius quadriscutis	JANZLB000000000
Occidentarius platypogon	JAOBRE000000000
Osteogeneiosus militaris	JANZLE000000000
Plicofollis layardi	JAODHV000000000
Plicofollis nella	JAODOM000000000
Plicofollis tonggol	JAODOE000000000
Potamarius nelsoni	JAODKY000000000
Potamarius usumacintae	JAOEJH000000000
Potamosilurus coatesi	JAODKU000000000
Potamosilurus latirostris	JAODKZ000000000
Potamosilurus macrorhynchus	JAOBYD000000000
Potamosilurus velutinus	JAODLA000000000
Sciades assimilis	JAODJS000000000
Sciades dowii	JAODKS000000000
Sciades herzbergii	JAPFFA000000000
Sciades mastersi	JAODKO000000000
Sciades proops	JAODOF000000000
Sciades troschelii	JAODIB000000000

---

.....

## ***Funding***

Funding was provided by Iridian Genomes grant# IRGEN\_RG\_2021-1345: Genomic Studies of Eukaryotic Taxa.

Submitted: May 17, 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. <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.” 2021. <https://github.com/zanfona734/zanfona>.