

GENOME SEQUENCING

The Complete Genome Sequences of 38 Species of Elephantfishes (Mormyridae, Osteoglossiformes)

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Biodiversity Genomes

We present the complete genome sequences of 38 species of elephantfishes from 20 genera. Illumina sequencing was performed on genetic material from single wild-caught individuals. The reads were assembled using a *de novo* method followed by a finishing step. The raw and assembled data is publicly available via Genbank.

Introduction

The Mormyridae are a family of weakly electric freshwater fish found over most of Africa, with the exception of the Sahara, northernmost Mahgreb and southernmost Cape provinces. They are an important food source in Africa's inland regions where they are often the most abundant fish available (Sullivan and Lavoué 2022).

Elephantfishes possess organs that generate weak electric fields, and electroreceptors that can sense nearby objects and prey as distortions to their self-produced electric fields. They can detect the electric fields generated by prey in low visibility conditions (Carlson et al. 2019).

We present the complete genome sequences of 38 species of elephantfishes from 20 genera. Tissue samples were obtained from preserved museum specimens.

Methods

DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard process. 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 | specimen_voucher | raw_read_data | genome |
|-------------------------------|------------------|---------------|-----------------|
| Boulengeromyrus knoepffleri | CUMV 81643-2254 | SRR8717394 | JABJVO000000000 |
| Brevimyrus niger | CUMV 94596 | SRR8717240 | JAABNY000000000 |
| Brienomyrus brachyistius | CUMV 89979 | SRR8717393 | JAODOV000000000 |
| Brienomyrus longianalis | AMNH 257030 | SRR8717273 | JABJVP000000000 |
| Campylomormyrus numenius | CUMV 97364 | SRR8717166 | JAODOW000000000 |
| Campylomormyrus tamandua | CUMV 87879 | SRR8717220 | JABJVQ000000000 |
| Cryptomyrus ogoouensis | CUMV 98155 | SRR8717184 | JAOYFF000000000 |
| Cyphomyrus discorhynchus | CUMV 82809 | SRR8717165 | JABJVS000000000 |
| Cyphomyrus wilverthi | AMNH 253525 | SRR8717167 | JAODKV000000000 |
| Genyomyrus donnyi | CUMV 96735 | SRR8794244 | JAODJT000000000 |
| Gnathonemus echidnorhynchus | CUMV 96186 | SRR8794645 | JAODJU000000000 |
| Gnathonemus longibarbis | CUMV 90412 | SRR8794644 | JAODJV000000000 |
| Hippopotamyrus longilateralis | SAIAB 78793 | SRR9215643 | JAOXXE000000000 |
| Hippopotamyrus pictus | CUMV 94598 | SRR8793730 | JAODLC000000000 |
| Hyperopisus bebe | CUMV 91467 | SRR8794911 | JAODJW000000000 |
| Isichthys henryi | CUMV 84650-2051 | SRR8794571 | JAODJX000000000 |
| Ivindomyrus marcheii | CUMV 83105 | SRR8794910 | JAODJY000000000 |
| Ivindomyrus opdenboschi | CUMV 83107 | SRR8795503 | JAODJZ000000000 |
| Marcusenius schilthuisiae | CUMV 87790 | SRR8794570 | JAODKA000000000 |
| Marcusenius ussheri | CUMV 97730 | SRR8794646 | JAODKB000000000 |
| Mormyrops attenuatus | CUMV 88155 | SRR8844661 | JAODKC000000000 |
| Mormyrops boulengeri | CUMV 87730 | SRR8844538 | JAODLD000000000 |
| Mormyrops zanclostris | CUMV 96834 | SRR8844858 | JAODKD000000000 |
| Mormyrus hasselquistii | CUMV 94650 | SRR9055927 | JAODKE000000000 |
| Mormyrus iriodes | AMNH 263510 | SRR9056052 | JAAGVU000000000 |
| Mormyrus lacerda | SAIAB 87199 | SRR9215603 | JAABNX000000000 |
| Mormyrus proboscirostris | CUMV 96245 | SRR8844651 | JAODKF000000000 |
| Myomyrus macrops | AMNH 231025 | SRR6399006 | JAODKG000000000 |
| Myomyrus pharao | CUMV 96474 | SRR9214507 | JAODKH000000000 |
| Paramormyrops hopkinsi | CUMV 89281-5497 | SRR9214432 | JAODKI000000000 |
| Petrocephalus microphthalmus | CUMV 97508 | SRR6399355 | JAODKK000000000 |
| Petrocephalus schoutedeni | CUMV 97510 | SRR9214420 | JAODKL000000000 |
| Petrocephalus sullivanii | CUMV 79700 | SRR6410432 | JAODKM000000000 |
| Petrocephalus zakoni | CUMV 87787 | SRR9214598 | JAODKN000000000 |
| Pollimyrus isidori | CUMV 97714 | SRR9215378 | JABFDZ000000000 |
| Pollimyrus plagiostoma | CUMV 96188 | SRR9214508 | JABFEA000000000 |
| Stomatorhinus ivindoensis | CUMV 92286 | SRR9214431 | JABFEB000000000 |
| Stomatorhinus walkeri | CUMV 95160 | SRR9214424 | JAODUD000000000 |

Discussion

These published data have already been used in recent publications on mormyrid phylogenomics and taxonomy (Peterson et al. 2022; Sullivan et al. 2022) and will serve a resource for future studies of this group of fishes.

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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>.
- Carlson, Bruce A., Joseph A. Sisneros, Arthur N. Popper, and Richard R. Fay, eds. 2019. *Electroreception: Fundamental Insights from Comparative Approaches*. Cham, Switzerland: ASA Press & Springer International Publishing. <https://doi.org/10.1007/978-3-030-29105-1>.
- 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>.
- Peterson, Rose D., John P. Sullivan, Carl D. Hopkins, Aintzane Santaquiteria, Casey B. Dillman, Stacy Pirro, Ricardo Betancur-R, Dahiana Arcila, Lily C. Hughes, and Guillermo Ortí. 2022. “Phylogenomics of Bony-Tongue Fishes (Osteoglossomorpha) Shed Light on the Craniofacial Evolution and Biogeography of the Weakly Electric Clade (Mormyridae).” *Systematic Biology* 71 (5): 1032–44. <https://doi.org/10.1093/sysbio/syac001>.
- Sullivan, J.P., C.D. Hopkins, S. Pirro, R. Peterson, A. Chakona, T.I. Mutizwa, C. Mukweze Mulelenu, F.H. Alqahtani, E. Vreven, and C.B. Dillman. 2022. “Mitogenome Recovered from a 19th Century Holotype by Shotgun Sequencing Supplies a Generic Name for an Orphaned Clade of African Weakly Electric Fishes (Osteoglossomorpha, Mormyridae).” *ZooKeys*.
- Sullivan, J.P., and S. Lavoué. 2022. “Mormyridae - African Weakly Electric Fishes Scratchpad.” <http://mormyrids.myspecies.info>.