

GENOME SEQUENCING

Complete Genome Sequences of the Diamondback Terrapin, Eastern Mudsnaill, and their Shared Fluke Parasite (*Pleurogonius malaclemys*)

Garrett James Maggio¹, Stacy Pirro², John P. Wares³, April Monica Houghton Blakeslee¹

¹ East Carolina University, ² Iridian Genomes, ³ University of Georgia

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Biodiversity Genomes

We present the complete genome sequences of the diamondback terrapin (*Malaclemys terrapin*), the eastern mudsnaill (*Ilyanassa obsoleta*), and the terrapin fluke parasite (*Pleurogonius malaclemys*).

Methods

Tissue samples used in this study were obtained from a wild-collected specimen of *Ilyanassa obsoleta*, a salvaged road-mortality specimen of *Malaclemys terrapin*, and a specimen of *Pleurogonius malaclemys* (the “terrapin fluke”) recovered from a mudsnaill host. The intertwined ecology of these species is represented in the life cycle of the fluke, which infects mudsnails as intermediate hosts before being trophically transmitted to terrapins serving as a definitive (i.e., final) host. The terrapin road mortality was sampled during nesting season in 2022 from Jekyll Island, GA and consisted of skin and muscle tissues. The mudsnaill and fluke samples were obtained from Wellfleet, MA in 2025. The mudsnaill sample consisted of foot tissue and the fluke sample consisted of metacercarial cysts. 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 et al. 2014). The trimmed sequence was assembled by SPAdes v3.15.4 (Bankevich et al. 2012) followed by a finishing step using Zanfona (Kieras et al. 2021).

Data Availability

taxname	accession
Malaclemys terrapin	JBYAWA0000000000
Ilyanassa obsoleta	JBWIDO0000000000
Pleurogonius malaclemys	JBXGTI0000000000

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