

GENOME SEQUENCING

Short read genome assemblies of 11 species of *Xenopus* (Pipidae, Anura)

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Biodiversity Genomes

We present complete genome sequences of 11 species of *Xenopus* frogs.

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 manufacturer's protocol. Paired-end sequencing libraries were constructed using the Illumina TruSeq kit according to the manufacturer's protocol. 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).

Results and Data Availability

Species	Ploidy	Accession	Specimen ID	Sex
<i>Xenopus borealis</i>	4n	SRR35968864	Evans_17C3	F
<i>Xenopus boumbaensis</i>	8N	SRR35972782	AMNH17285	M
<i>Xenopus fischbergi</i>	4n	SRR35973704	Evans_18DF	F
<i>Xenopus fraseri</i>	4n	SRR35964371	BJE4204	F
<i>Xenopus itombwensis</i>	8n	SRR38286237	BJE3376	M
<i>Xenopus lenduensis</i>	8n	SRR38285470	Evans_lendu_20	M
<i>Xenopus longipes</i>	12n	SRR38285167	Evans_male101	M
<i>Xenopus muelleri</i>	4n	SRR35972780	Evans_17B3	F
<i>Xenopus parafraseri</i>	4n	SRR35972781	BJE3065	F
<i>Xenopus pygmaeus</i>	4n	SRR35964928	Evans_15	F
<i>Xenopus wittei</i>	8n	SRR38285187	BJE4311	F

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