

GENOME SEQUENCING

The Complete Genome Sequences of Five Species of Vipers (Viperidae, Squamata)

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Biodiversity Genomes

We present the complete genome sequences of five species of vipers: *Agkistrodon piscivorus*, *Crotalus aquilus*, *Crotalus enyo*, *Crotalus mitchellii*, and *Crotalus viridis*. Illumina sequencing was performed on DNA extracted from wild-caught specimens. The reads were assembled using a de novo method followed by a finishing step. The data is publicly available via Genbank.

Methods

Single wild-collected vipers individuals were sampled. DNA extraction was performed using the Qiagen DNAeasy genomic extraction kit using the standard protocol. 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 is available via Genbank.

taxname	NCBI:txid	genome_accession
<i>Agkistrodon piscivorus</i>	8715	JBKKFQ000000000
<i>Crotalus aquilus</i>	8743	JBLLKR000000000
<i>Crotalus enyo</i>	125865	JBLLKU000000000
<i>Crotalus mitchellii</i>	384065	JBKKFL000000000
<i>Crotalus viridis</i>	8739	JBKOIX000000000

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