Complete mitochondrial genome of *Gloydius saxatilis* (Viperidae: Crotalinae) from Korea

Yun Sun Lee, Min Seock Do, Hye Sook Jeon, Sang-Cheol Lee, Ji-Hwa Jung, Jae-Hwa Suh and Junghwa An

*Gloydius saxatilis* (Emelianov, 1937) is a venomous pit viper species endemic to Asia (Russia, China, and the Korean Peninsula) and belongs to the family Viperidae. Despite being assessed as Least Concern in IUCN Red List because of its large distribution in forest areas and mountainous zones, *G. saxatilis* in Korea has been decreasing due to poaching. The genetic information and biological data about this species are lacking. Also, many researchers in Korea used *G. intermedius* and *G. shedaoensis* as an alternative name of *G. saxatilis* (David and Vogel 2015). In this study, we determined the complete mitogenome of *G. saxatilis*.

*Gloydius saxatilis* tissue samples (NIBR00000625204) were collected from Samcheok-si, Gangwon-do, South Korea (37.109 N, 129.180 E) and stored in the National Institute of Biological Resources (NIBR: https://www.nibr.go.kr) in Incheon, South Korea. Genomic DNA was extracted using the DNeasy Blood and Tissue Kit (Qiagen, Germantown, MD). Average library insert size of 550 bp was construction and next-generation-sequencing was performed on the IlluminaNovaSeq6000 platform at DNA Link Inc. (Seoul, South Korea). Genomic DNA was extracted using the DNeasy Blood and Tissue Kit (Qiagen, Germantown, MD). The raw data were generated with 150 bp paired-end lengths. De-novo assembly was performed using GetOrganelle version 1.6.4 (Jin et al. 2020). Gene structures of the mitochondrial genome were annotated with GeSeq (Tillich et al. 2017), while tRNA detection was predicted by ARAGORN version 1.2.38 (Laslett and Canback 2004) and tRNAscan-SE version 2.0.5 (Lowe and Chan 2016). Mitogenome sequence of *G. saxatilis* was submitted in GenBank (accession no. MW143075).

The complete *G. saxatilis* mitogenome sequence was 17,223 bp in length and contained two non-coding control regions (CRs), 13 protein-coding genes (PCGs), two ribosomal RNA genes (rRNAs), 22 transfer RNA genes (tRNAs), and origin of light (OL)-strand replication. The genome structure and order of the genes were similar to other Crotalinae species. Phylogenetic analysis based on the 13 concatenated PCGs indicated that *G. saxatilis* closely related to *G. intermedius* and *G. shedaoensis.*

**ABSTRACT**

In this study, we sequenced the complete mitochondrial genome of *Gloydius saxatilis* using Illumina next-generation sequencing. The total length of the mitogenome was 17,223 bp, and contained 13 protein-coding genes (PCGs), two ribosomal RNA genes (rRNAs), 22 transfer RNA genes (tRNAs), two non-coding control regions (CRs), and the origin of light (OL)-strand replication. The genome structure and order of the genes were similar to other Crotalinae species. Phylogenetic analysis based on the 13 concatenated PCGs indicated that *G. saxatilis* closely related to *G. intermedius* and *G. shedaoensis.*
was based on the 13 concatenated PCGs and mitogenome data corresponding to 35 individuals of 27 Crotalinae species obtained from GenBank. This phylogenetic analysis indicated that \textit{G. saxatilis} closely related to \textit{G. intermedius} and, \textit{G. she daoensis} (Figure 1). In conclusion, this study provides a new additional high-quality mitogenome database for further evolutionary and molecular research on Crotalinae.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**ORCID**

Ji-Hwa Jung [http://orcid.org/0000-0002-7135-7088](http://orcid.org/0000-0002-7135-7088)

**Data availability statement**

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov](https://www.ncbi.nlm.nih.gov) under the accession no. MW143075.

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