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Data Article

Mitogenome data of *Hylobates abbotti* Kloss, 1929 (Abbott's Gray Gibbon)

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ABSTRACT

Complete mitochondrial genomes provide valuable insights into species identification, accompanied by their respective geographic variation, molecular taxonomy, conservation strategies, and phylogenetic relationships among primates. This data article presents the complete mitochondrial genome sequence of *Hylobates abbotti* (Abbott's gray gibbon), a species endemic to southwest Borneo, previously classified as a subspecies of *Hylobates muelleri* (the Bornean gibbon). The mitogenome is 16,501 base pairs in length, comprising 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes, and a control region. A phylogenetic tree was constructed using the maximum likelihood (ML) method, offering insights into the evolutionary relationships within the genus *Hylobates*. The mitogenome has been deposited at GenBank under the accession number PQ867516.

Specifications Table

Subject	Genomics
Specific subject area	Molecular Systematics, Conservation Genetics
Type of data	Table, Figure Raw, Analyzed
Data collection	Buccal swab DNA sampling DNA extraction: Genomic DNA extracted using QIAamp® Blood & Tissue Kit (Qiagen, Germany) Library Preparation and Sequencing hardware: Qubit high sensitivity dsDNA assay (Thermo Fisher Scientific), Bioruptor (Diagenode), Fragment Analyzer (Agilent) and sequenced using the NovaSEQ6000 platform. Data analysis hardware: Adapter-trimmed using fastp v0.21, A de novo assembly based on Megahit v1.29 assembler, mitogenome assembly within mitoZ v3.5 pipeline. Phylogenetic analysis: IQ –TREE 2.2 was used to construct the Maximum Likelihood phylogenetic tree.
Data source location	The individual was rescued from Sibu, Sarawak, Malaysia, by the Sarawak Forestry Corporation (SFC) and is currently housed at Matang Wildlife Centre for rehabilitation.
Data accessibility	Repository name: GenBank Data identification number: WGG06 GenBank Accession number: PQ867516 Direct URL to data: https://www.ncbi.nlm.nih.gov/nuccore/PQ867516
Related research article	Not applicable

1. Value of the Data

- The complete mitochondrial genome sequence of *Hylobates abbotti*, an endemic primate from southwest Borneo, provides critical insights into species identification, molecular taxonomy and conservation strategies, while contributing to a deeper understanding of evolutionary relationships within the family Hylobatidae.
- This dataset highlights the critical role of high-quality mitogenome metadata, enabling researchers to strengthen their conclusions, improve population-level analyses, and enhance the validity of evolutionary, and conservation-related insights.
- The mitogenome sequence serves as vital reference for exploring the evolutionary history of *H. abbotti* and provides a comparative framework for studying primate evolution at both species-specific and broader taxonomic levels.

2. Background

Complete mitochondrial genomes serve as essential tools in species identification, revealing geographic variation, molecular taxonomy, conservation strategies, and phylogenetic relationships among primates. Gibbons (*Hylobates* spp.), small apes known for their distinctive calls and arboreal lifestyle, remain underrepresented in genetic studies, particularly in Borneo.

Initially, *H. abbotti* (Abbott's gray gibbon) was classified as a subspecies of *Hylobates muelleri* (the Bornean gibbon) [1,2]. However, subsequent research revealed distinct physical character-