Sequencing and analysis of the complete mitochondrial genome of *Hippopus porcellanus*

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ABSTRACT

In this study, the complete mitochondrial genome of *Hippopus porcellanus* was reported. The whole mitochondrial genome was 21,565bp in length with a typical mitochondrial genomic structure including 13 protein-coding genes, 23 transfer RNA genes, 2 ribosomal RNA genes and 1 control region (D-loop). Mitogenome base composition was biased toward A + T content, at 60.3%. A phylogenetic tree based on complete mitogenome sequences revealed that, *H. porcellanus* is closely related to *H. hippocus*, both of which belong to the genus *Hippopus*.

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located between tRNA-Met and COII, with an A+T content of 54.7%.

A neighbor-joining phylogenetic tree of *H. porcellanus* with five other closely related species was constructed with the complete mitochondrial genomes using MEGA6 (Tamura et al. 2013) (Figure 1). The result suggested that, *H. porcellanus* is closely related to *H. hippopus*, both of which belong to the genus *Hippopus*.

**Disclosure statement**

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

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**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/) under the accession no. MT755622. The associated BioProject, SRA, and Bio-Sample numbers are PRJNA704757, SRR13827840, and SAMN18054235, respectively.

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