

# Complete mitochondrial genome of *Sineleotris saccharae* (Perciformes, Odontobutiae) and phylogenetic analysis

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## Abstract

The freshwater sleeper, *Sineleotris saccharae*, endemic to southeastern of China belongs to the family of Odontobutiae. The composition of the Odontobutidae is controversial due to the lack of molecular data. Information about genetic characteristics of *S. saccharae* was still not reported. In the present study, we determined the complete mitochondrial genome of *S. saccharae* for the first time and analyzed its evolutionary relationship. The complete mitochondrial genome of *S. saccharae* was 16,487 bp in length, and consisted of 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), 2 ribosomal RNA (rRNAs) and a control region (CR). The gene arrangement and orientation of *S. saccharae* mitogenome was identical to those of other teleosts. Phylogenetic analysis by Maximum likelihood (ML) methods strongly supported the monophyly of Odontobutidae containing two clades. The genus *Odontobutis* was sister to the clade consisting of *Perccottus* and *Neodontobutis*. Meanwhile, *Microdous*, *Sineleotris* and *Micropercops* formed another clade. These data will be helpful for understanding the genetic information of *S. saccharae* and systematics of the odontobutids.

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