Complete mitochondrial DNA sequence of the yeast *Zygosaccharomyces siamensis* (Saccharomycetes: Saccharomycetales) from fermented honey of the *Apis cerana japonica* in Japan

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**ABSTRACT**

Japanese *Apis cerana* honey is believed to ferment due to the presence of some yeast. We analyzed the complete mitochondrial genome of *Zygosaccharomyces siamensis*, a yeast involved in fermenting honey. *Zygosaccharomyces siamensis* was obtained from the honey collected from *A. cerana* hives under traditional beekeeping in the forest of the Minabe-Tanabe Ume system in Wakayama Prefecture, Japan. Its mitochondrial genome was identified as a 23,184 bp circular molecule containing 8 protein-coding genes (PCGs), 24 tRNA genes, and 2 RNA genes. The PCGs contained a common set of genes encoding ATPase subunits (ATP6, ATP8, and ATP9), three subunits of cytochrome *C* oxidase (COX1, COX2, and COX3), apocytochrome b (CYTB), and ribosome-associated protein (RPS3). In addition, two open-reading frames coding for LAGLIDADG endonucleases were predicted to be about 1100 bps. The average GC content was found to be 48.6%. The heavy strand was predicted to have 7 PCGs, 22 tRNA genes, and 2 rRNA genes, while the light strand was predicted to contain one PCG and two tRNA genes. Molecular phylogenetic analyses of the mitochondrial DNA genes strongly supported the result obtained from the phylogenetic analysis of partial ITS region sequences, grouping the monophyletic species within the genus *Zygosaccharomyces*. The complete mitochondrial DNA genome of this honey-fermenting yeast will provide useful information for understanding the basis of the honey fermentation process.
ribosome-associated protein (RPS3). Two open-reading frames encoding LAGLIDAG endonucleases were predicted to be 1122 and 1143 bp, respectively. Among the eight PCGs, the initiation codon ATG was found in five, ATA in two, and TTA in one gene. Seven PCGs used TAA as the stop codon, whereas one PCG used CAT as the stop codon. Phylogenetic analysis was conducted using seven mitochondrial PCG sequences from 32 closely related taxa (Figure 1). Zygosaccharomyces siamensis was found to be most closely related to Z. mellis. We expect that the complete sequence data of yeast mitochondrial DNA will provide useful information for understanding the genetic and molecular basis of honey fermentation by yeasts.

Disclosure statement
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**Data availability statement**

The data that support the findings of this study are openly available in DDBJ/GenBank at [https://www.ddbj.nig.ac.jp/index.html](https://www.ddbj.nig.ac.jp/index.html), accession number DRA009857.

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