The complete mitochondrial genome of the hydrozoan jellyfish *Turritopsis lata* Lendenfeld, 1885 (Cnidaria; Hydrozoa; Anthoathecata) with molecular phylogenetic analysis

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**ABSTRACT**

In this study, we sequenced and analyzed the complete mitochondrial genome (mtgenome) of the hydrozoan jellyfish *Turritopsis lata*. The mtgenome was a complete linear form (15,047 bp in length, 30.9% A, 42.1% T, 12.5% C, and 14.5% G), including 13 protein coding genes (PCGs) (cox1, cox2, cox3, atp6, atp8, nad1, nad2, nad3, nad4, nad4L, nad5, nad6, and cytB), 2 tRNAs (tRNA\(^{\text{Met}}\) and tRNA\(^{\text{Trp}}\)), and 2 rRNAs (12S and 16S rRNA). The genome structure of the *T. lata* was completely identical to those of other species within the subclass Hydroidolina. In addition, our molecular phylogenetic analysis using 13 PCGs within hydrozoans showed that *T. lata* was the closest to *Turritopsis dohrnii*.

The hydrozoan jellyfish *Turritopsis* are well-known to revert their life cycle to the juvenile polyp stage from adult medusae by rejuvaniation, and, thus, they are called ‘immortal jellyfish’ (Hasegawa et al. 2016). The jellyfishes are recorded worldwide from tropical to temperate waters (Miglietta et al. 2007), and their distribution patterns are region-specific depending on species (Miglietta et al. 2019). Although they are classified by morphology, their identification is difficult due to similar morphology among relatives (Kubota 2015). Alternatively, molecular analysis has been considered as a powerful tool to determine their taxonomic identities (Li et al. 2018), and mitochondrial genes and genomes are commonly used as molecular markers of taxonomy (Yuan et al. 2020). Geneious 9.1.3 (Geneious, Auckland, New Zealand), and MITOS (Bernt et al. 2013), respectively. A maximum-likelihood (ML) tree (JTT matrix-based model; 1000 bootstrap replications) was generated based on concatenated amino acid sequences of 13 PCGs in MEGA X (Kumar et al. 2018). The complete mtgenome of *T. lata* (GenBank accession no. MW399220) was linear in shape and 15,047 bp in length with 73% AT content. The genome contained 13 PCGs (cox1, cox2, cox3, atp6, atp8, nad1, nad2, nad3, nad4, nad4L, nad5, nad6, and cytB), two rRNAs (12S and 16S rRNA), and two tRNAs (tRNA\(^{\text{Met}}\) and tRNA\(^{\text{Trp}}\)). The arrangement of 17 mitochondrial genes of *T. lata* was completely identical to another order Anthoathecata species, including *T. dohrnii* (KT020766), *Clava multicorins* (JN700935) and *Hydra oligactis* (EU237491) (Seo et al. 2020). Mitochondrial PCGs of *T. lata* have two start codons (ATG/GTG) and three stop codons (TAA/TAG/ incomplete T). Especially, the incomplete T stop codon was found only in cox1.

The phylogenetic relationship within hydrozoans was inferred using amino acid sequences of 13 PCGs (Figure 1). The ML tree showed that the *T. lata* formed a sister relationship with *T. dohrnii*. In the present study, we provide additional complete mtgenome sequence data of *T. lata* to...
understand the abstruse phylogenetic relationship of hydrozoans.

**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](https://www.ncbi.nlm.nih.gov) under the Accession no. MW399220.

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