The complete mitochondrial genome of the jellyfish Aurelia coerulea (Cnidaria and Scyphozoa) with phylogenetic analysis

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ABSTRACT

In this study, we sequenced the complete mitochondrial genome of the jellyfish Aurelia coerulea (A. coerulea). The mitochondrial genome was a linear form (16,748 bp long, 65.7% AT), consisting of 13 protein coding genes (PCGs) (cox1, cox2, atp8, atp6, cox3, nad2, nad5, nad6, nad3, nad4L, nad1, nad4, and cytB), 2 rRNAs (12S and 16S), and 2 tRNAs (trnM and trnW). Mitochondrial gene arrangement of the A. coerulea was identical when compared to already-known mitochondrial genomes of Aurelia species. The maximum-likelihood (ML) phylogenetic tree using of 13 mitochondrial proteins showed that A. coerulea collected from Korean waters was closely related to A. limbata.

Moon jellies of the genus Aurelia are widely distributed in the world’s oceans, and their outbreaks have been reported globally (Ki et al. 2008). All species in the genus are morphologically similar, making it difficult to distinguish between species. However, molecular studies indicate that there are at least 13 cryptic species in the genus (Dawson et al. 2005). Aurelia coerulea (A. coerulea or Aurelia sp.1) is a genetically and morphologically distinct form (Scorrano et al. 2017), and its occurrence has been reported from the Northwest Pacific oceans, the coasts of California, and the Mediterranean coasts, expanding geographic ranges (Dawson and Jacobs 2001; Ki et al. 2008; Scorrano et al. 2017). Thus, it is imperative to analyze the complete mitochondrial genome of the jellyfish to better understand the global distribution and the molecular phylogenetic relationship of the Aurelia. In the present study, we sequenced the complete mitochondrial genome of A. coerulea, and investigated their genomic structures and molecular phylogenetic relationships using mitochondrial proteins.

The specimens of A. coerulea were collected from Susanport (38°04′47.2″N, 128°40′27.9″E) in Yangyang, Korea, on 9 September 2015. Total genomic DNA was extracted from the jellyfish umbrella by using the cetyl-trimethylammonium bromide method (Ausubel et al. 1989) and the remaining part of the specimen was stored in the Department of Biotechnology, Sangmyung University, Korea (Accession No. R858). Next-generation sequencing (NGS) was subjected to part of the specimen was stored in the Department of Biotechnology, Sangmyung University, Seoul, South Korea. The complete mitochondrial genome was in accordance with previous molecular phylogenetic relationships and ecological adaptations of the organisms (Ramšak et al. 2012). By considering cryptic Aurelia species,
their mitochondrial genomes are still unknown, and further data should be recorded from the jellyfishes.

**Disclosure statement**

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