

MITOGENOME ANNOUNCEMENT

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The complete mitochondrial genome sequence and gene organization of *Trematomus bernacchii* (Perciformes: Nototheniidae) with phylogenetic consideration

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ABSTRACT

In this study, the complete mitochondrial DNA sequence was obtained from *Trematomus bernacchii*. The full length of mitogenome was 16 018 bp, including 20 transfer RNA genes, a 16S ribosomal RNA genes and an incomplete 12S rRNA, 12 protein-coding genes and an incomplete ND6 protein-coding gene, and 2 non-coding regions: control region (D-loop) and origin of light-strand (L-strand) replication (OL). Most genes were located on the heavy-strand (H-strand), while ND6 and seven tRNA genes were located on the L-strand. *T. bernacchii*'s mitogenome was comprised of 24.52% for A, 25.44% for C, 20.38% for G and 29.66% for T, with a higher A + T content (54.18%). From the NJ phylogenetic tree, it revealed that *T. bernacchii*'s was genetically closest to species *Dissostichus eleginoides* among seven species within sub-order Notothenioidei. This study could lay the foundation for the future studies in species identification, taxonomic status, molecular systematics, stock evaluation and conservation genetics for *T. bernacchii*'s.

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
KEYWORDS

Complete mitogenome;
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Trematomus bernacchii belongs to genus *Trematomus*, family Nototheniidae, suborder Notothenioidei, order Perciformes, whose body is mostly covered by darker spots. *T. bernacchii* is native to the Southern Ocean, which lives on the seafloor at depths from very shallow waters to 700 m and is adapted to living in waters of extremely low temperature. It feeds on various invertebrates and small fishes, and also is known to eat some algae. According to its abundance, circumpolar distribution and relatively easy collection, *T. bernacchii* has become a mainly species for physiological and biochemical studies to investigate the plasticity of this highly stenothermic family of fishes and the mechanism of adaptation to such a cold stable environment (Davison et al. 1994). These stenothermal species strictly dependent upon low temperature, due to their display in some cases upper lethal thermal limits of 6–8 °C (Somero & Devries 1967). In recent years, the studies about the location of gene sequence of Antarctic fishes have been widely done and the results are not always consistent (Zhuang & Cheng 2010). The research on the complete mitochondrial genome is thought to be a powerful tool for species identification, phylogeny and evolution research of *T. bernacchii* (Zhang & Georges 2014). Therefore, the examination on the mitogenome of *T. bernacchii* is very essential.

Adult fish of *T. bernacchii* was collected near Zhongshan Station (68°S, 70°W). After freezing at –80°C, it was

transported to East China Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences for storage and DNA extraction. In this study, the complete mitochondrial genome of *T. bernacchii* (GenBank number: KU166863) was firstly reported. This genome was 16 018 bp in length, including 20 transfer RNA genes, a 16S ribosomal RNA genes, an incomplete 12S rRNA, 12 protein-coding genes an incomplete ND6 protein-coding gene, and a putative control region. The location of genes in mitochondrial genome is not similar to other species in Nototheniidae, which lacked tRNA^{Glu} and tRNA^{Pro}, and its 12S rRNA and ND6 were not complete. This might because high frequency of gene duplications and rearrangement of mitochondrial genomes in *T. bernacchii* (Liu et al. 2012). The location of other genes is similar to the one of other species, as that most genes were located on the H-strand, while incomplete ND6 and seven tRNA genes (tRNA^{Gln}, tRNA^{Ala}, tRNA^{Asn}, tRNA^{Cys}, tRNA^{Tyr}, tRNA^{Ser} and tRNA^{Pro}) were located on the L-strand but different with the crustacean species. The mitogenome of *T. bernacchii* was comprised of 24.52% for A, 25.44% for C, 20.38% for G and 29.66% for T, with a higher A + T content (54.18%), which was similar to other teleost fish that an obvious anti-guanine bias commonly observed. The putative origin of light strand replication was found between tRNA^{lys} and ATPase8, with a length of 22 bp. Eleven protein-coding genes started by ATG, while COI gene was initiated by GTG. In

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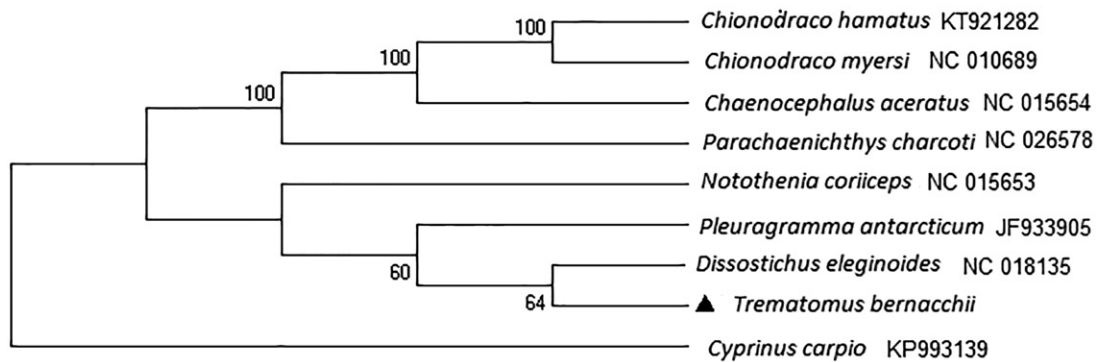


Figure 1. Phylogenetic relationship of *Trematomus bernacchii* within suborder Notothenioidei. *Trematomus bernacchii* was highlighted with a black triangle.

total, four types of stop codons (TAG, TAA, TA – and T –) were detected in these protein-coding genes.

The phylogenetic relationship of *T. bernacchii* within suborder Notothenioidei was analyzed using 13 concatenated protein-coding genes. A neighbour-joining (NJ) tree was constructed by software MEGA 5.1 (Figure 1). The tree topologies showed that *T. bernacchii* first grouped with *Dissostichus eleginoides*, then grouped with *Pleuragramma antarcticum* and *Dissostichus eleginoides*, and had obvious differentiation with the species of *Cyprinus*, *Chionodraco*, *Chaenocephalus*, and *Parachaenichthys*.

Declaration of interest

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