

## Complete mitochondrial genome of *Turritella terebra bacillum*

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### ABSTRACT

The complete mitochondrial genome of the *Turritella terebra bacillum* was 15 868 bp in length and contained 13 protein-coding genes, 22 transfer RNA genes and two ribosomal RNA genes. The overall base composition of *T. terebra bacillum* was A 28.85%, T 35.88%, C 16.21% and G 19.06%. Phylogenetic tree construction indicated that *T. terebra bacillum* was most closely related to *Volutharpa perryi*. This molecular information will contribute to better understand its evolution and population genetics.

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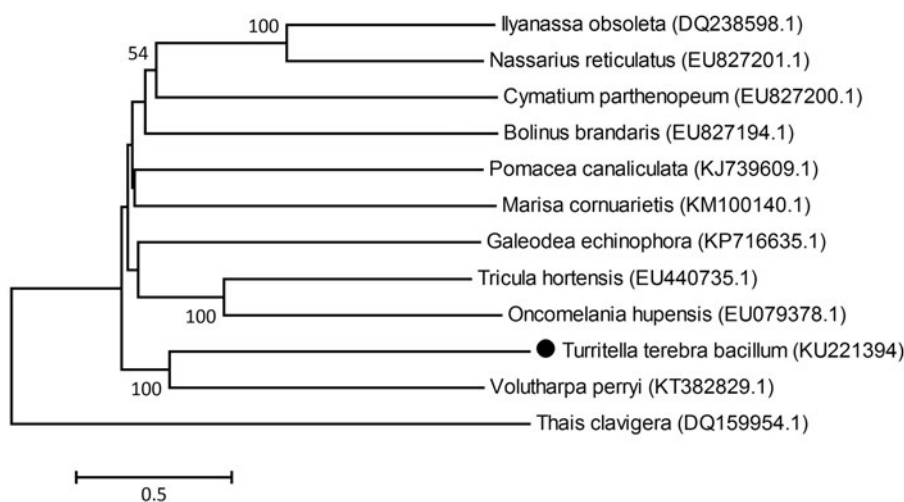
Mitochondrial genome;  
*Turritella terebra bacillum*;  
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*Turritella terebra bacillum* (Kiener 1844), which belongs to Prosobranchia, Mesogastropoda, Turritellidae, has certain value of nourishment and pharmaceutical. It is a fairly widespread species in southeast coastal region in China (Ma & Feng 1993; Xie et al. 1996). In order to obtain genetic information and understand the evolution of *T. terebra bacillum*, we sequenced its complete mitochondrial genome (GenBank accession no. KU221394).

*Turritella terebra bacillum* were obtained in Mazhan town, Wenzhou city, Zhejiang province (27°10'31.39"N, 120°32'22.61"E) and were stored in the fish herbarium of Zhejiang Ocean University. Initially, the spiral shell was

identified based on both the morphologic features and the *COX1* mitochondrial gene. Tissue samples for molecular analysis were reserved in absolute ethyl alcohol. The complete mitochondrial genome of *T. terebra bacillum* was extracted using the phenol–chloroform method. The PCR products were sequenced by Sanger's method.

The complete mitochondrial genome of *T. terebra bacillum* was 15 868 bp in length, containing 13 protein-coding genes, 22 transfer RNA genes (tRNA) and two ribosomal RNA genes (rRNA). The mitogenome base composition was A 28.85%, T 35.88%, C 16.21% and G 19.06%, A+T content (64.73%) was remarkably higher than the G+C content (36.53%),



**Figure 1.** Phylogenetic tree of *Turritella terebra bacillum* was constructed with the Neighbor-Joining method using the program MEGA 4.0. The numbers at each branch indicate the percentage bootstrap values.

which was similar to other mollusks (Boore 2006; Jiang et al. 2015). Thirteen protein-coding genes can be classified into two categories: *COX1*, *COX2*, *ND4L*, *ND4*, *ND5*, *ND2*, *ATP8*, *ATP6* and *ND3* were encoded by the light-strand, *COX3*, *CYTB*, *ND6* and *ND1* were encoded by the heavy strand. Eight protein-coding genes (*COX1*, *COX2*, *ND4L*, *ND5*, *ND2*, *ATP8*, *ATP6* and *ND3*) started with an ATG initiation codon, four protein-coding genes (*COX3*, *CYTB*, *ND6* and *ND1*) started with a CAT initiation codon, and only *ND4* used GTG as the initiation codon. Seven protein-coding genes (*COX1*, *COX2*, *ND4L*, *ND4*, *ND2*, *ATP6* and *ND3*) used TAA as the termination codon, *ND5* and *ATP8* used TAG as the termination codon, and four genes (*COX3*, *CYTB*, *ND6* and *ND1*) used TTA as the termination codon. The two ribosomal RNA genes, 16SrRNA (1357 bp) was located between *tRNA<sup>Leu</sup>* and *tRNA<sup>Val</sup>* genes and 12SrRNA (949 bp) was located between *tRNA<sup>Thr</sup>* and *tRNA<sup>Ser</sup>* genes.

In the mitochondrial phylogeny, *T. terebra bacillum* was most closely related to *Volutharpa perryi*. *Thais clavigera* was placed at the most basal position forming an individual clade, while other species formed another large cluster (Figure 1).

## Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

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