

Mitochondrial genome of the acorn barnacle *Tetraclita rufotincta* Pilsbry, 1916: highly conserved gene order in Tetraclitidae

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ABSTRACT

The complete mitochondrial genome of the intertidal barnacle *Tetraclita rufotincta* Pilsbry, 1916 (Crustacea: Maxillopoda: Sessilia) is presented. The genome is a circular molecule of 15,236 bp, which encodes a set of 37 typical metazoan mitochondrial genes. All non-coding regions are 438 bp in length, with the longest one speculated as the control region (242 bp), which is located between *srRNA* and *trnK*. Comparison of the genome and those of three other species from Tetraclitidae shows that gene arrangement is identical, indicating that the mitochondrial gene order is highly conserved in the family. Moreover, in comparison with the pancrustacean ground pattern, the four species of Tetraclitidae share three large conserved gene blocks. Phylogenetic analysis based on 13 mitochondrial PCGs shows that *Chelonbia testudinaria* (Coronulidae) clusters with the four species of Tetraclitidae. Within Tetraclitidae, *T. serrata* clusters with *T. japonica*, and the two grouped with *T. rufotincta* with high support (BP = 100), with *T. divisa* as the most distantly related species (BP = 100).

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Barnacles of the genus *Tetraclita* are common intertidal inhabitants of tropical and sub-tropical waters (Newman and Ross 1976; Tsang et al. 2012). They are often the major space occupiers on the shore, playing important roles in the filter-feeding food chain and as foundation species affecting the structure and dynamics of intertidal communities (Barnes 2000). *Tetraclita rufotincta* Pilsbry 1916 is a common intertidal barnacle in the western Indian Ocean and east Africa (Achituv et al. 1997; Chan et al. 2009).





The work presents the complete mitochondrial genome of *T. rufotincta*. A specimen of *T. rufotincta* was obtained from the coastline in the Red Sea in Eilat, Israel, which is stored at the Biodiversity Research Museum, Academia Sinica, Taiwan. The mitochondrial genome encodes a set of 37 typical metazoan mitochondrial genes, including 13 protein-coding genes (PCGs), two ribosomal RNAs (rRNAs) genes, and 22 transfer RNAs (tRNAs) genes (GenBank accession number: KY865100). Four PCGs and two rRNAs are encoded on the light strand (*nd1*, *nd4*, *nd4L*, and *nd5*), while the other nine PCGs are located on the heavy strand.

In all 15 sessile barnacle mitochondrial genomes reported, the numbers of amino acids in four of the PCGs (*cox2*, *cox3*, *nd3*, *atp8*) are identical. Yet there are gene length variations in the remaining nine PCGs. The A + T composition of the first and second codon positions in the 13 PCGs of *T. rufotincta* is 49.3% and 66.3%, respectively, but that of the third codon positions elevates to 77.4%,

which is lower than values from the other sessile barnacles (Shen et al. 2015, 2016).

The gene arrangement of *T. rufotincta* is identical to the other three mitochondrial genomes available from Tetraclitidae (*T. divisa*, *T. serrata*, and *T. japonica*). Compared with the pancrustacean ground pattern, the four species from Tetraclitidae share three large conserved gene blocks (*trnM-nd2-trnW-cox1-trnL₂-cox2-trnD-atp8-atp6-cox3-trnG-nd3-trnR-trnN-trnA-trnE-trnS₁, trnT-nd6-cob-trnS₂*, and *nd1-trnL₁-lrRNA-trnV-srRNA*) (genes encoded on the light strand are underlined). There are large variations in gene rearrangement among the Sessilia barnacles (Tsang et al. 2017), but the four species from Tetraclitidae have the same gene order, indicating that it is highly conserved within the family.

To investigate the phylogenetic position of the Sessilia and the relationships within this order, phylogenetic trees are constructed based on nucleotide sequences of 13 PCGs from 19 complete mitochondrial genomes of Maxillopoda using phyML (<http://www.atgc-montpellier.fr/phyml/>). In the tree (Figure 1), *Chelonbia testudinaria* (Coronulidae) clusters with the four species from Tetraclitidae. Within Tetraclitidae, *T. serrata* clusters with *T. japonica*, and the two are grouped with *T. rufotincta* with high support (BP = 100), with *T. divisa* being the most distantly related taxon (BP = 100). Tsang et al. (2015) provide molecular evidence suggesting that the superfamily Tetraclitoidea is monophyletic, while Tetraclitidae is not monophyletic. Thus, taxon coverage of the mitochondrial genome

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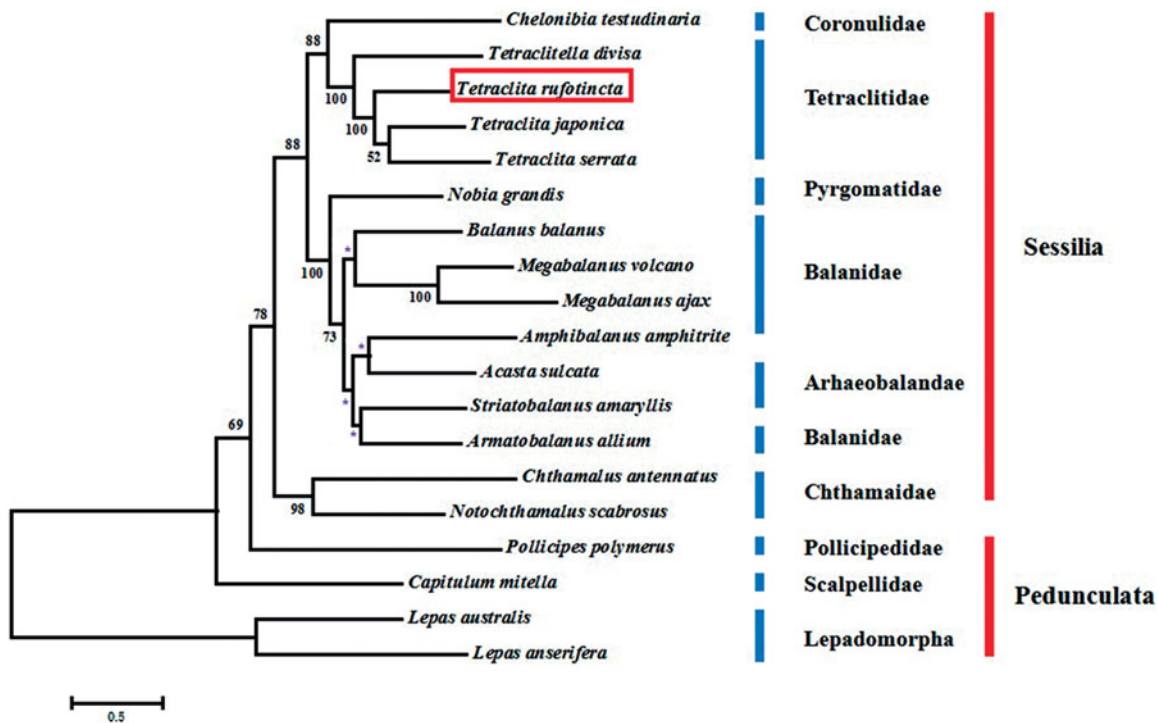


Figure 1. Maximum-likelihood phylogenetic tree based on 13 PCGs nucleotide acid sequences of *T. rufotincta* and 18 other Cirripedia species. Nodal supports are denoted on the corresponding branches for a bootstrap value $>50\%$ for ML, while * represents the value $\leq 50\%$.

data from the family Tetraclitidae should be increased in order to address the issues on the monophyly of Tetraclitidae and the phylogenetic relationships within the family.

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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