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MITOGENOME ANNOUNCEMENT



## The mitochondrial genome of the bone-eating worm *Osedaxrubiplus*(Annelida, Siboglinidae)

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### ABSTRACT

*Osedaxrubiplus*(Annelida, Siboglinidae)uses heterotrophic bacteria to feed onvertebrate carcasses and is currently found in the Pacific, Antarctic and Indian Ocean.Here, we report its nearly complete mitochondrial genomes assembled for 2 individuals, one from the East Pacific and the other from the Southwest Indian Ocean. Recoveredmitogenomes were 15591 and 15972bp in length, with both consisting of 37 typical metazoan mitochondrial genes. All genes were transcribed from the same strand, and arranged in the same order as the other siboglinids, revealing conserved gene arrangement withinSiboglinidae. Phylogeneticanalysis of 13 protein coding genes confirms the placement of *Osedax*sister to the Vestimentifera+*Sclerolinum* clade.

### ARTICLE HISTORY

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### KEYWORDS

*Osedax*; mitogenome;  
Southwest Indian Ridge;  
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The bone-eating worms, *Osedax* spp., are specialists thriving in chemosynthetic ecosystems formed by whale falls and other vertebrate carcasses through out the world's oceans (Amon et al. 2014; Rouse et al. 2018; Zhou et al. 2020). They are siboglinid annelids and recent analyses (Li et al. 2015, 2017) placed them as sister to the Vestimentifera + *Sclerolinum* clade. Although the phylogenetic position is well understood, the mitogenome has not been well explored in *Osedax* (Li et al. 2015) and its gene arrangement is still unknown. Interestingly, all sequenced siboglinid mtDNA shared the same gene arrangement (Li et al. 2015). Thus, a wider taxon sampling is needed to better explore the mitogenome in *Osedax*.

Specimens of *O. rubiplus* were collected from East Pacific margin (43°54.52'N; 125°10.29'W, 1560 m) and Southwest Indian Ridge (49°38.685'E, 37°47.013'S, 2908 m), which have been deposited in Auburn University (vouch number: AUMNH 46876) and the Repository of the Second Institute of Oceanography, MNR (vouch number: RSIO49bone\_ind) respectively. One individual from each sampling site was used for genomic DNA extraction, sequencing, assembling and gene annotation following the methods described in Li et al. (2015) and Zhou et al. (2019) respectively. A maximum likelihood (ML) analysis based on concatenated alignments of the amino acid sequences of the 13 PCGs was conducted in IQtree 1.6.10 (Trifinopoulos et al. 2016) with substitution



model for each individual gene or partition determined by the program automatically.

Two mitogenomes of *Osedaxrubiplus* (GenBank accession numbers: MT108936 and MT108937, 15591 and 15972 bp in length respectively) contains 13 PCGs, 2rRNA genes and 22 tRNA genes. Consistent with other siboglinid mitogenomes, the 13 PCGs use ATG as the start codon, and a combination of TAA, TAG and T as stop codon. All genes are transcribed from the same strand, and arranged in the same order as other siboglinids, suggesting conserved gene arrangement in the family (Li et al. 2015).

Previous study revealed four major lineages in Siboglinidae: Vestimentifera, Frenulata, *Sclerolinum*, and *Osedax* (Rouse et al., 2004; Halanych 2005). Using the 13 PCGs of *Osedaxmucofloris* mitochondrion, Li et al. (2015) Li et al. (2017) suggested that *Osedax* is genetically closer to the Vestimentifera + *Sclerolinum* clade rather than to Frenulata. The maximum likelihood analysis in the present study robustly supports the sister relationship between the *Osedax* and Vestimentifera + *Sclerolinum* clade (Figure 1).

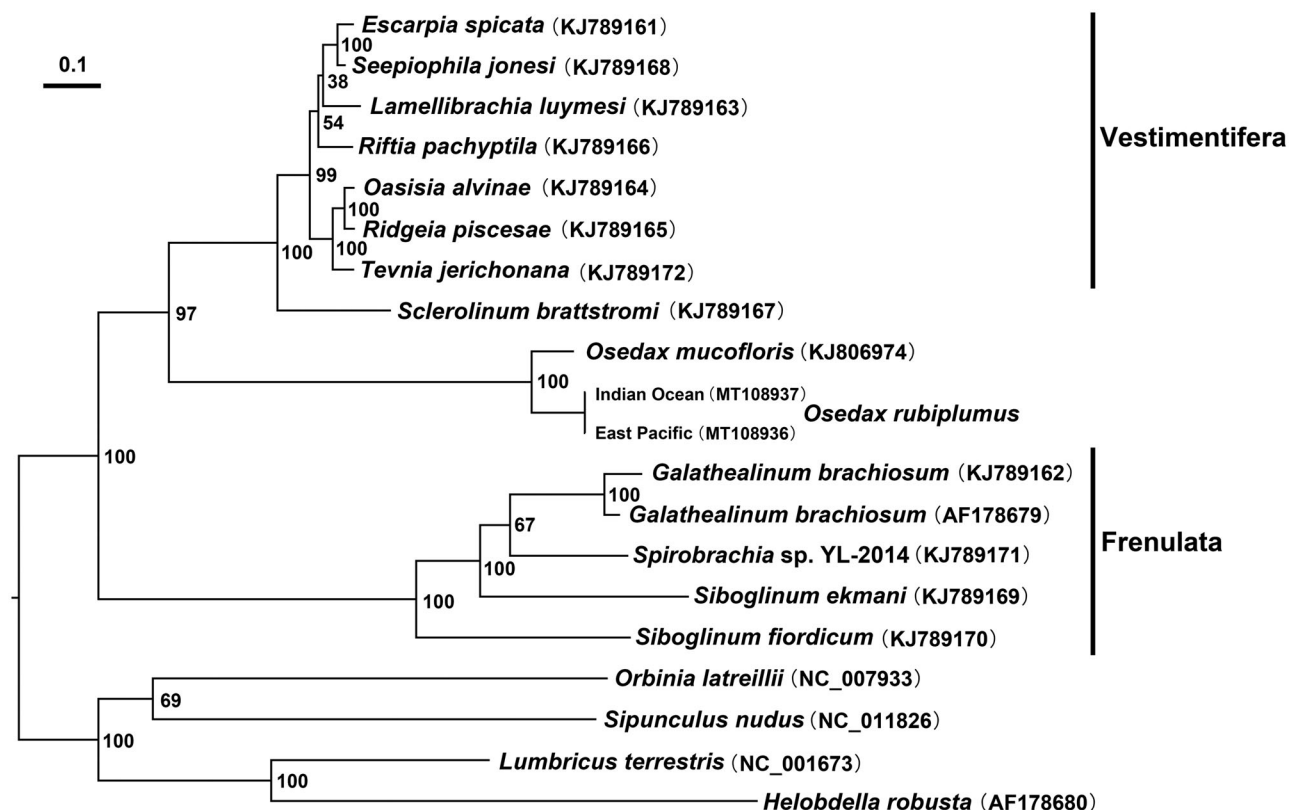
### Disclosure statement

The authors declare no conflict of interest. The authors alone are responsible for the content and writing of the paper.

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**Figure 1.** Maximum likelihood (ML) analysis based on the concatenated amino acid (AA) sequences of 13 PCGs. ML bootstrap values are indicated at each node. *Helobdellarobusta*, *Lumbricusterrestris*, *Orbinialatreillii* and *Sipunculusnudus* serve as the outgroup.

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## Data availability statement

All sequences generated or used in the present study are deposited in NCBI GenBank (<https://www.ncbi.nlm.nih.gov>) and the accession numbers are detailed in Figure 1.

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