The complete mitochondrial genome sequences of *Trinorchestia longiramus* (Crustacea: Amphipoda: Talitridae)

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Abstract

The talitrid amphipods are common in sand beaches, estuarine marshes, shores of lakes and rivers around the world. They are detritivores and preys for birds and other animals, and play an important role in the food chain of ecosystem. Despite of their significance and vast diversity, no complete mitochondrial genome data have been available so far. Mitochondrial genomes contain the most informative sequences and gene arrangement for deeper phylogenetic analyses and they reflect evolutionary relationships and biogeography in the metazonas. In the present study, we describe the mitochondrial genome (mitogenome) sequences of talitrid *Trinorchestia longiramus*. *T. longiramus* was collected from the east coastal area in Korea. To analyze the mitogenome of the talitrid, we obtained the sequences of CO1, 12S, 16S, CO3 and Cytb in each talitrid using universal primers published or newly designed in our group and then, amplified the complete mitogenome of using long-PCR and genome walking techniques. As it has been reported that some species in extreme environment show unusual mt genome composition and structure, we attempted to compare mitochondrial genome feature of the species inhabiting in Korea. Also, we attempted to solve the ordinal relationships of Amphipoda in Class Malacostraca of Subphylum Crustacea by phylogenetic analysis using sequence data from mitochondrial protein-coding genes. Our result would provide a useful information for studying phylogenetic relationships of talitrid and be helpful in the further crustacean phylogenetic study.

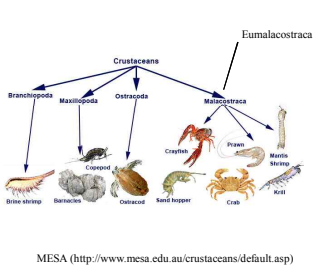
Sampling Site

Yong-hwa, Samcheok

Methods

- Sampling, DNA extraction, PCR amplification, and sequencing
  - DNeasy blood & tissue kit (QIAGEN, USA)
  - Partial sequences (CO1, CO3, 12S, 16S, Cytb, ND3)
  - Long PCR primers used in this work (Table 1)
  - Primer-walking technique (Biomedic, Korea)
- Gene identification and genome analysis
  - BioEdit v7.0.1 for alignment
  - DOGMA (http://dogma.ccbb.utexas.edu/) for annotation and location of genes

Materials



MESA (http://www.mesa.edu.au/crustaceans/default.asp)

Trinorchestia longiramus

Results and Discussion

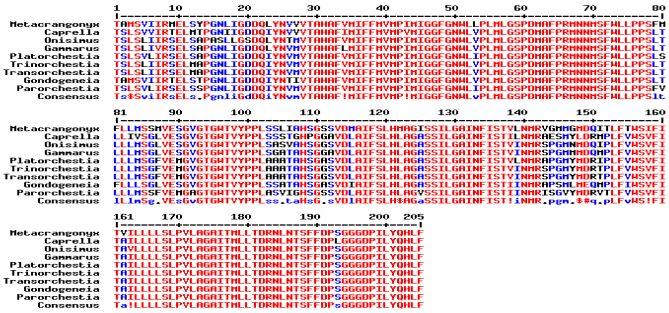


Fig 1. Alignment of protein and Phylogenetic tree based on COI genes.

Table1. Primers used to amplify parts of the mitogenome of *T. longiramus*.

Fragment	Primers	Sequence (5'-3')	Primer reference
Tali#83	taliCO1F	CACCAGCCAAGTGAAGTGAA	Cox1-12S
	tali12SR	ACGGGCGATCTGAACACTTA	
Tali#85	taliCO3F	AACCCTGACCGTTACACTCG	Cox3-Cytb
	talicytR	CGTCACCCAAAATTAAAGGA	
Tali#88	taliCO3R	AAATGTCCTTGGGTGAGACG	Cox3-Cox1
	taliCO1R	AGCCTTTCCTCGCATAAACA	
Tali#89	talicytF	AGGTTCTGGTAACCCTCTTGG	Cytb-16S
	tali16SF	AATATTTTGGCTGGGGCAGT	
Tali#90	tali16SR	AAAAGTTGAACAAACTCCCAAAA	in progress
	tali12SF	CGATAAACCGCGATTAGTTTG	

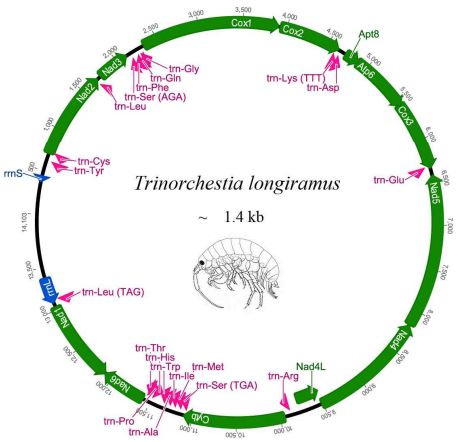


Fig 2. Mitochondrial genome maps of *Trinorchestia longiramus*. The transcriptional directions are indicated by arrowheads.

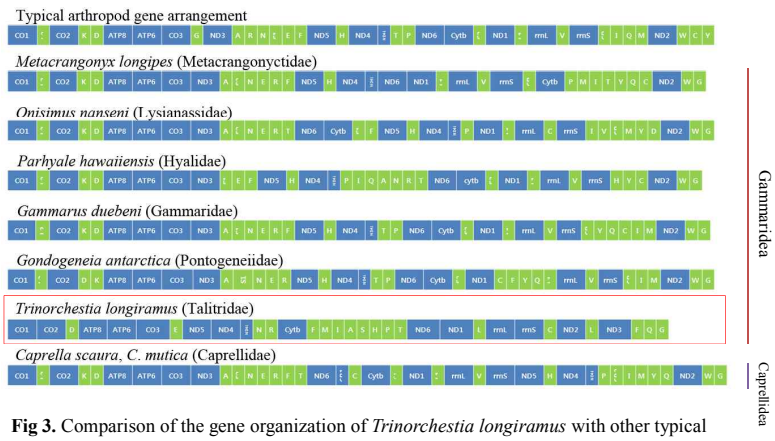


Fig 3. Comparison of the gene organization of *Trinorchestia longiramus* with other typical arthropod mitogenomes (e. g. *Drosophila yakuba*, *Daphnia pulex*) and closely-related species.

- The first Talitrida complete mitochondrial genome from *Trinorchestia longiramus* with a typical set of 37 genes (13 PCGs, 2 rRNAs and 22 tRNAs genes)
- *Trinorchestia longiramus* mt genome shows the distinctive features such as ND3 translocation.
- In further study, comparison between polar and non-polar talitrid mt genomes as well as between Arctic and Antarctic ones to explore an interaction between adaptation to a harsh environment and mt genome arrangement.

References

1. Maria M. et al., 2009. The compelete mitochondrial genome of the subterranean crustacean *Metacrangonyx longipes* (Amphipoda): A unique gene order and extremely short control region, Mitochondrial DNA, 20(4): 1-12.
2. Jang-Seu Ki et al., 2010. Complete mitochondrial genome sequence of the Arctic gammarid, *Onisimus nanseni* (Crustacea; Amphipod): Novel gene structures and unusual control region features, Comparative Biochemistry and Physiology Part D 5: 105-115.
3. Atsushi Ito et al., 2010. The complete mitochondrial genome of *Caprella scaura* (Crustacea, Amphipoda, Caprellidea), with emphasis on the unique gene order pattern and duplicated control region, Mitochondrial DNA, 21(5): 183-190.
4. Lukas Krebes and Ralf Bastrop, 2012. The mitogenome of *Gammarus duebeni* (Crustacea, Amphipoda): A new gene order and non-neutral sequence evolution of tandem repeats in the control region, Comparative Biochemistry and Physiology Part D 7: 201-211.

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