

## Complete mitochondrial genome of the Antarctic copepod *Tigriopus kingsejongensis* (Harpacticoida, Harpacticidae)

Dae-Sik Hwang<sup>a</sup>, Beom-Soon Choi<sup>b</sup>, Min-Chul Lee<sup>a</sup>, Jeonghoon Han<sup>c</sup>, Sanghee Kim<sup>d</sup> and Jae-Seong Lee<sup>c</sup>

<sup>a</sup>Research Institute of Environmental Health and Safety, Bucheon, South Korea; <sup>b</sup>Phyzen Genomics Institute, Seongnam, South Korea;

<sup>c</sup>Department of Biological Science, College of Science, Sungkyunkwan University, Suwon, South Korea; <sup>d</sup>Division of Life Sciences, Korea Polar Research Institute, Incheon, South Korea

### ABSTRACT

The complete mitochondrial genome was sequenced from the Antarctic harpacticoid copepod *Tigriopus kingsejongensis*. The sequenced genome size was 14,940 bp, possessing different gene order and contents to those of the congeneric species *T. japonicus* and *T. californicus* in the genus *Tigriopus*. The mitochondrial genome of *T. kingsejongensis* has 13 protein-coding genes (PCGs), 2 rRNAs, and 22 tRNAs. Of the 13 PCGs, *CO1*, *ND3*, *ATP6*, and *CO3* genes had incomplete stop codons T-, T-, TA-, and T-, respectively. Furthermore, the stop codons of the remaining 11 PCGs were TAA or TAG, while the start codon of 13 PCGs was ATG (*CO1*, *ND4*, *Cytb*, *ND2*, *ND1*, *CO2*, *ND6*, *ATP6*, *CO3* genes), ATT (*ND5*, *ATP8* genes), and ATA (*ND3*, *ND4L* genes), respectively. The nucleotide of 13 PCGs of *T. kingsejongensis* mitogenome showed 53.42, 52.17, and 49.10% similarities to the copepods *T. japonicus*, *T. californicus*, and *Amphiascoides atopus*, respectively, while the amino acid similarities were 64.38, 63.86, and 62.40%, respectively.

### ARTICLE HISTORY

Received 6 March 2019  
Accepted 23 March 2019

### KEYWORDS

*Tigriopus kingsejongensis*;  
Antarctic copepod;  
rearrangement

Until now, 13 species are retrieved from the genus *Tigriopus* (Huys 2001). Of them, five complete mitochondrial genomes of two *Tigriopus japonicus* (Machida et al. 2002; Jung et al. 2006) and three *Tigriopus californicus* (Burton et al. 2007) have been reported with a high similarity of the gene structure of the mitochondrial genome. However, despite the reported morphometry with *CO1* gene (Park et al. 2014), RNA-seq (Kim et al. 2016), and the whole genome (Kang et al. 2017), the taxonomical consideration of the copepod *Tigriopus kingsejongensis* based on complete mitogenome is still unavailable (Huys 2001; Park et al. 2014). Since *T. kingsejongensis* can be a good model for studying environmental adaptation (e.g. ultraviolet ray) in the genus *Tigriopus* (Han et al. 2016; Kang et al. 2017), we report the complete mitochondrial genome of the Antarctic copepod *T. kingsejongensis* to better understand the phylogenetic position of *T. kingsejongensis* within the genus *Tigriopus*.

The Antarctic copepod *T. kingsejongensis* was originally collected at 62°14'10.29"S, 58°46'38.67"W by Dr. Sanghee Kim (Korea Polar Research Institute, South Korea) and maintained in the Department of Biological Science, Sungkyunkwan University in South Korea (kindly provided by Dr. Sanghee Kim). We sequenced 800 bp mate-pair library of *T. kingsejongensis* from whole body genomic DNA using the Illumina HiSeq 2500 platform (GenomeAnalyzer, Illumina, San Diego, CA). *De novo* assembly was conducted by Minia (version 3.2.0) (<https://github.com/GATB/minia>) with K-mer 320.

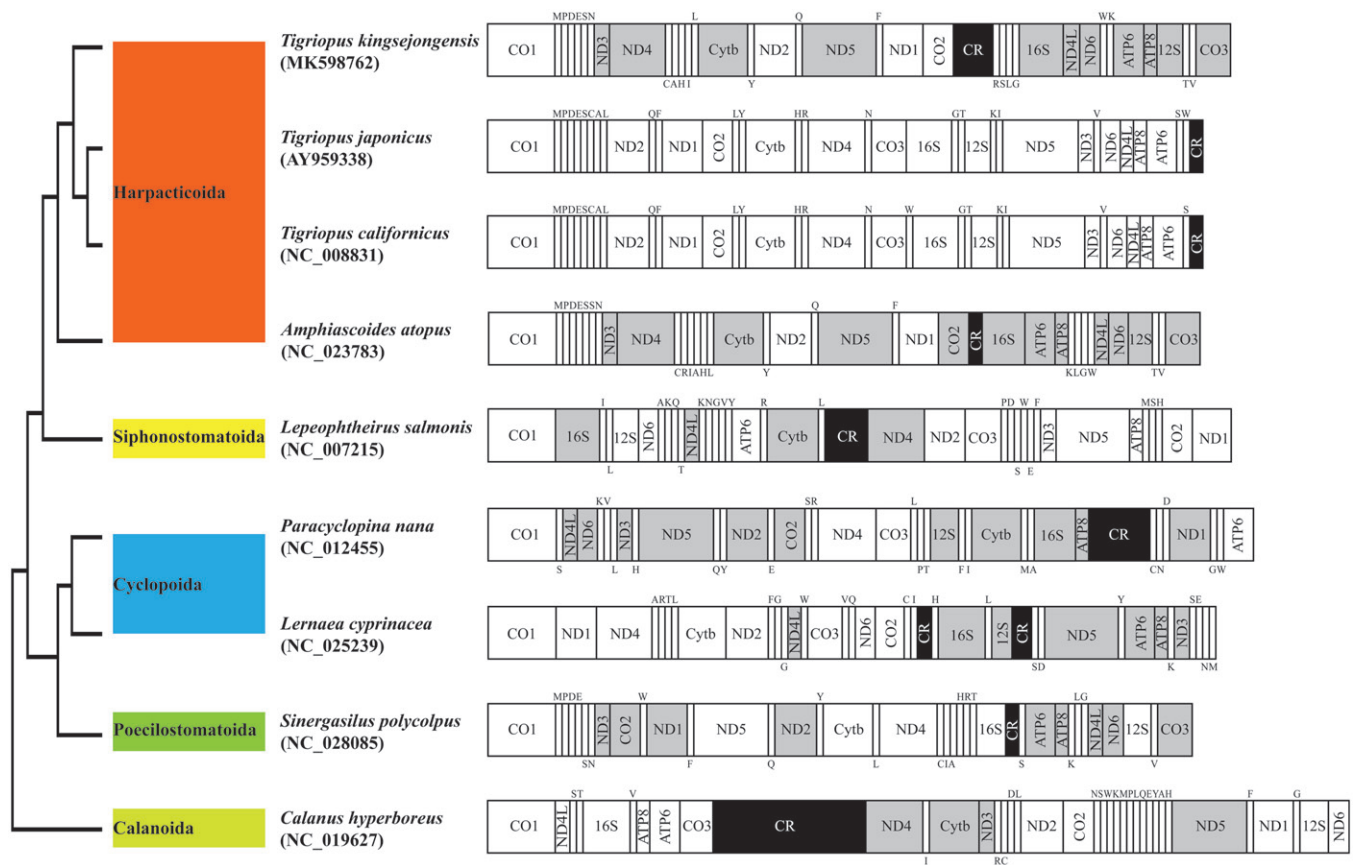
Of the assembled *T. kingsejongensis* 139,592 contigs with Newbler (version 2.9; identity 100) (<http://www.454.com>), nine supercontigs were obtained. After a manual curation of nine supercontigs with Consed (version 19.0) (<http://www.phrap.org/consed/consed.html>), a single contig was mapped to the mitochondrial DNA of *T. japonicus*.

The total length of the complete mitochondrial genome of *T. kingsejongensis* was 14,940 bp (GenBank accession no. MK598762). The mitochondrial genome of *T. kingsejongensis* contained 13 protein-coding genes (PCGs), 2 rRNAs, and 22 tRNAs. The direction of 13 PCGs of *T. kingsejongensis* was mostly different to those of a congeneric species *T. japonicus* (Machida et al. 2002; Jung et al. 2006) and *T. californicus* (Burton et al. 2007). Of the 13 PCGs in *T. kingsejongensis*, *CO1*, *ND3*, *ATP6*, and *CO3* genes had incomplete stop codons T-, T-, TA-, and T-, respectively. Furthermore, the stop codons of the remaining 11 PCGs were TAA or TAG, whereas the start codon of 13 PCGs was ATG (*CO1*, *ND4*, *Cytb*, *ND2*, *ND1*, *CO2*, *ND6*, *ATP6*, *CO3* genes), ATT (*ND5*, *ATP8* genes), and ATA (*ND3*, *ND4L* genes), respectively. Between the two sister species (*T. kingsejongensis* and *T. japonicus*), the similarities of amino acids and nucleotides of 13 PCGs were 64.38 and 53.42%, respectively, which demonstrated higher similarity compared to that of *T. californicus* (63.86% for amino acids and 52.17% for nucleotides) and *Amphiascoides atopus* (62.40% for amino acids and 49.10% for nucleotides).

**CONTACT** Jae-Seong Lee  [jslee2@skku.edu](mailto:jslee2@skku.edu)  Department of Biological Science, College of Science, Sungkyunkwan University, Suwon 16419, South Korea

© 2019 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.



**Figure 1.** Phylogenetic analysis. We conducted comparison of the mitochondrial genomes of nine copepods. Amino acids of 13 PCGs gene from nine copepods were aligned using MEGA software (ver. 10.0.1) with the ClustalW alignment algorithm. To establish the best-fit substitution model for phylogenetic analysis, the model with the lowest Bayesian Information Criterion (BIC) and Akaike Information Criterion (AIC) scores were estimated using a maximum likelihood (ML) analysis. According to the results of model test, maximum likelihood phylogenetic analyses were performed with the GTR + G+I model. Gray, the opposite direction of PCGs; Black, control regions; Upper and lower single letters indicate tRNA clockwise and anticlockwise, respectively.

The placement of *T. kingsejongensis* among four Harpacticoida species with known complete copepod mitogenomes with outgroup (Calanoida *Calanus hyperboreus*) was shown in Figure 1. Among the three *Tigriopus* spp., *T. kingsejongensis* showed strikingly different patterns of mitogenomic arrangement compared to two congeneric species (*T. japonicus* and *T. californicus*), yet was closely situated to *T. japonicus* compared to *T. californicus*. This phylogenetic tree of the copepods supports the finding of Wang et al. (2011). This information will be helpful for a better understanding of mitogenome evolution in the genus *Tigriopus*.

## Disclosure statement

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

## Funding

This work was supported by a grant from the Korea Polar Research Institute [PE19100] funded to Jae-Seong Lee.

## References

Burton RS, Byrne RJ, Rawson PD. 2007. Three divergent mitochondrial genomes from California populations of the copepod *Tigriopus californicus*. *Gene*. 403:53–59.

Han J, Puthumana J, Lee M-C, Kim S, Lee J-S. 2016. Different susceptibilities of the Antarctic and temperate copepods *Tigriopus kingsejongensis* and *T. japonicus* to ultraviolet (UV) radiation. *Mar Ecol Prog Ser*. 561:99–107.

Huys R. 2001. Copepoda - Harpacticoida. In: Costello, M.J. et al. (eds.) European register of marine species: a check-list of the marine species in Europe and a bibliography of guides to their identification. Collection Patrimoines Naturels 50:268–280.

Jung S-O, Lee Y-M, Park T-J, Park HG, Hagiwara A, Leung KMY, Dahms H-U, Lee W, Lee J-S. 2006. The complete mitochondrial genome of the intertidal copepod *Tigriopus* sp. (Copepoda, Harpacticidae) from Korea and phylogenetic considerations. *J Exp Mar Biol Ecol*. 333: 251–262.

Kang S, Ahn DH, Lee JH, Lee SG, Shin SC, Lee J, Min GS, Lee H, Kim HW, Kim S, et al. 2017. The genome of the Antarctic-endemic copepod, *Tigriopus kingsejongensis*. *GigaScience*. 6:1–9.

Kim H-S, Lee B-Y, Han J, Lee YH, Min GS, Kim S, Lee J-S. 2016. *De novo* assembly and annotation of the Antarctic copepod (*Tigriopus kingsejongensis*) transcriptome. *Mar Genomics*. 28:37–39.

Machida RJ, Miya MU, Nishida M, Nishida S. 2002. Complete mitochondrial DNA sequence of *Tigriopus japonicus* (Crustacea: Copepoda). *Mar Biotechnol*. 4:406–417.

Park E-O, Lee S, Cho M, Yoon SH, Lee Y, Lee W. 2014. A new species of the genus *Tigriopus* (Copepoda: Harpacticoida: Harpacticidae) from Antarctica. *Proc Biol Soc Wash*. 127:138–154.

Wang M, Sun S, Li C, Shen X. 2011. Distinctive mitochondrial genome of Calanoid copepod *Calanus sinicus* with multiple large non-coding regions and reshuffled gene order: useful molecular markers for phylogenetic and population studies. *BMC Genomics*. 12:73.