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Complete mitochondrial genome of the freshwater monogonont rotifer *Brachionus angularis* (Rotifera, Brachionidae)

Min-Sub Kim[a], Beom-Soon Choi[b], Erick Ochieng Ogello[c], Hee-Jin Kim[d], Atsushi Hagiwara[d,e], and Jae-Seong Lee[a,*]

[a] Department of Biological Sciences, College of Science, Sungkyunkwan University, Suwon 16419, South Korea
[b] Phyzen Genomics Institute, Seongnam 13558, South Korea
[c] Department of Fisheries & Natural Resources, Maseno University, Kisumu, Kenya
[d] Institute of Integrated Science and Technology, Nagasaki University, Nagasaki 852-8521, Japan
[e] Organization for Marine Science and Technology, Nagasaki University, Nagasaki 852-8521, Japan

ABSTRACT

The two complete mitochondrial genomes were sequenced from the freshwater monogonont rotifer *Brachionus angularis*. The mitochondrial genome sequences were 10,764 bp (mitochondrial DNA I) and 12,238 bp (mitochondrial DNA II) in size, respectively. Of 12 protein-coding genes (PCGs), one gene (*ND5*) had incomplete stop codon. Furthermore, the start codon for *CO1*, *ND4L*, *ND5*, and *CO2* was GTG, while the start codon for *ND3* was ATA, respectively, whereas the start codon for other PCGs was ATG. The base composition of 12 PCGs in *B. angularis* mitogenome showed 20.4% for A, 47.3% for T, 17.5% for C, and 14.8% for G, respectively. The mitochondrial genome A+T base composition (67.7%) of 12 PCGs was higher than G+C (32.3%), while the complete mitochondrial genome A+T base composition (66.3%) was higher than G+C (33.7%).

KEYWORDS: Monogonont rotifer, complete mitochondrial genome, *Brachionus angularis*, Kenyan strain

The freshwater rotifer *Brachionus angularis* consists of at least four subspecies (*Brachionus angularis angularis*, *Brachionus angularis bidens*, *Brachionus angularis caudatus*, *Brachionus angularis dolabratus*) (https://www.itis.gov/servlet/SingleRpt/SingleRpt?search_topic=TSN&search_value=58445#null). However, to date, there is no report on complete mitochondrial genome on *B. angularis*, while several complete mitochondrial genome of other *Brachionus* rotifers have been published; *Brachionus plicatilis* (Suga et al., 2008), *Brachionus koreanus* (Hwang et al., 2013; Hwang et al., 2014), *Brachionus rotundiformis* (Kim et al., 2017), *Brachionus calyciflorus* (Choi et al., 2019), *Brachionus paranguensis* (Choi et al., 2020a), and *Brachionus rubens* (Choi et al., 2020b). Thus, the species identification of *B. angularis* species complex would be helpful to better understand the phylogenetic relationship of *B. angularis* species complex clade. Also, *B. angularis* is considered as a model for aquaculture (Ogata et al., 2011; Ogello and Hagiwara, 2015), environmental biology (Ferrão-Filho Ada et al., 2002; Wang et al., 2016), and ecology (Yang et al., 2009; Yin et al., 2017; Zhang et al., 2010) in response to environmental factors. In this study, we identified two complete mitochondrial genomes of

[*] **CONTACT** Jae-Seong Lee, E-mail jslee2@skku.edu, Department of Biological Sciences, College of Science, Sungkyunkwan University, Suwon 16419, South Korea
http://orcid.org/0000-0003-0944-5172

the monogonont rotifer *B. angularis*.

The resting eggs of *B. angularis* were collected by netting from sediments of freshwater ponds (0°42'35.7"S and 34°49'11.3"E) in August 2014 (kindly provided by Dr. Erick O. Ogello, Kenya Marine and Fisheries Research Institute in Kenya) and maintained at the Laboratory of Professor Atsushi Hagiwara, Nagasaki University in Japan. The type of *B. angularis* (85.6 μm in length and 75.4 μm in width) was deposited in the Ichthyological collection of the Faculty of Fisheries, Nagasaki University (FFNU) under the accession no. FFNU-Rot-0003.

We sequenced *B. angularis* from whole body genomic DNA using the nanopore platform (Oxford Nanopore Technologies, Oxford, United Kingdom). *De novo* assembly was conducted by smartdenovo (https://github.com/ruanjue/smartdenovo). Of the assembled *B. angularis* 106 contigs (63,578,663 bp) with a polishing using Pilon V1.23 (https://github.com/broadinstitute/pilon/releases) and the 300 bp HiSeq2500 Illumina data, we obtained one complete mitochondrial DNA sequence with manual editing process. Also, to identify the second complete mitochondrial genome, we examined 134,733 contigs (80,281,057 bp) and compared with the complete mitogenome of the rotifer *B. rubens* after *de novo* assembly of 300 bp HiSeq2500 Illumina data with Newbler V2.9 (http://www.454.com).

The complete mitochondrial genomes of *B. angularis* were 10,764 bp (mitochondrial DNA I; GenBank no. **MT875425**) and 12,238 bp (mitochondrial DNA II; GenBank no. **MT875426**) in size. Of 12 protein-coding genes (PCGs), one gene (*ND5*) had incomplete stop codon. Furthermore, GTG was identified as the start codon for *CO1*, *ND4L*, *ND5*, and *CO2* while ATA was the start codon for *ND3*, whereas the start codon for other PCGs was ATG. The base composition of 12 PCGs in *B. angularis* mitogenome showed 20.4% for A, 47.3% for T, 17.5% for C, and 14.8% for G, respectively. The mitochondrial genome A+T base composition (67.7%) of 12 PCGs was higher than G+C (32.3%), whereas the complete mitochondrial genome A+T base composition (66.3%) was higher than G+C (33.7%).

The placement of *B. angularis* in the genus *Brachionus* with 12 PGCs was shown in Figure 1. *B. angularis* was clustered with *B. rubens* and *B. calyciflorus* which are freshwater species, but was clearly separated from the marine species such as *B. rotundiformis*, *B. koreanus*, and *B. paranguensis*, possibly suggesting relationship between the differences in their natural habitat and mitogenome.

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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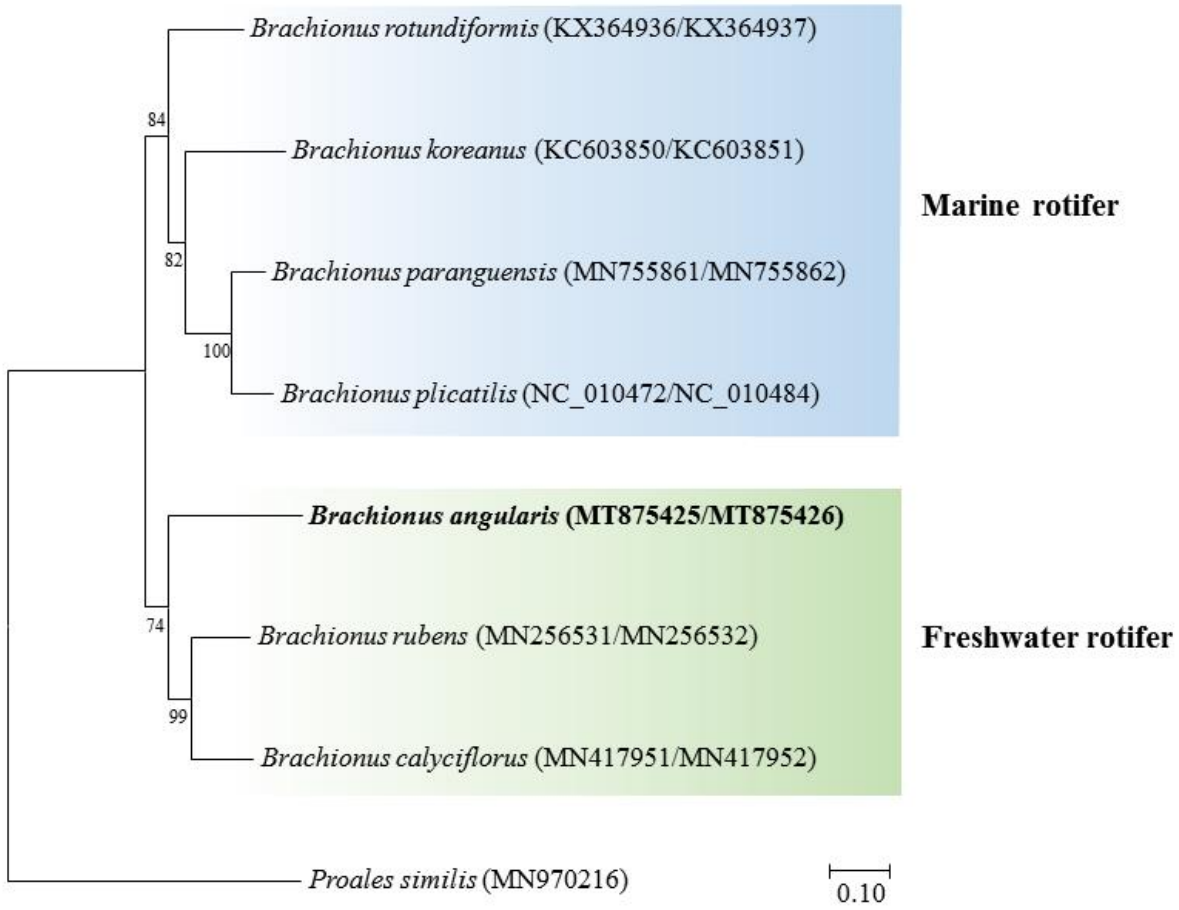

Figure 1. Phylogenetic analysis of mitochondrial DNA. We conducted a comparison of seven mitochondrial DNA genes of the genus *Brachionus*. The amino acid sequences of 12 mitochondrial DNA genes were aligned by ClustalW. Maximum likelihood analysis was performed by Mega software (ver. 10.0.1) with Gamma+LG+I model. The rapid bootstrap analysis was conducted with 1,000 replications with 48 threads running in parallel. The rotifer *Proales similis* (class Monogononta) served as outgroup. -Ln=28545.407996