

[예시-영문]

Genome sequencing of the Antarctic copepod *Tigriopus kingsejongensis*

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Introduction

Antarctic marine invertebrates have struggled to survive in extreme environmental conditions and have evolved to possess specialized life strategies. Thus, extant species in the Antarctic have received considerable attention for studying adaptation mechanisms and other fundamental biological knowledge of extremophiles. However polar organisms haven't been developed as the laboratory species because of the difficulties of the accessibility and cultivation of them. As most biological research has long relied on a small number of well-established model organisms, we are aware of limitations to expand our interest, basic biological knowledge and evolutionary mechanisms of the polar-adapted species. We paid attention on the Antarctic copepods to develop the laboratory cultivation methods and more, to examine the potential as model species. Copepods, the small crustaceans are highly diverged with long evolutionary history and can survive temperatures below 0°C in polar regions and 45°C in hot springs. These abilities to survive under a wide range of environments are also advantageous in genetic comparative analysis for physical, chemical and biological studies. We have cultured the Antarctic new species *Tigriopus kingsejongensis* along with *Tigriopus japonicus* which were collected in west coast in Korea for comparative analysis. Here we report the first draft genome sequence and gene annotation for Antarctic *Tigriopus kingsejongensis* [1] and the comparison of those of *T. japonicus*, temperate species in same genus. Based on these results, we want Antarctic *T. kingsejongensis* to become established as a model species, expand our research interest and therefore accumulate a valuable informations of polar organisms.

Results and Discussion

We sequenced genomic DNA and RNA of *T. kingsejongensis* using Illumina Miseq platform and the libraries were prepared with average coverage of 120.7x. The final assembly consists of 48,368 contigs with an N50 contig length of 17.5 kilobases (kb) and 27,823 scaffolds with N50 contig length of 138.2 kb and a total of 39,717 coding genes were inferred using the MAKER annotation pipeline approach. Gene content comparison showed that *T. kingsejongensis* shares 5,396 (60.1%) gene families with *Daphnia pulex*, 4,963 (55.3%) gene families with *Ixodes scapularis*, 3,688 (41.1%) gene families with *Mesobuthus martensii* and 2,909 (32.4%) gene families with *Tetranychus urticae* and total 2,367 gene

families were common to the five arthropods. The comparative genome analysis among 3,254 orthologs in four arthropod species (*T. kingsejongensis*, *Tigriopus japonicus*, *D. pulex* and *Drosophila melanogaster*) revealed the *T. kingsejongensis* specific signals of molecular adaptation in genes associated with mitochondrial electron transport, deacetylase activity, proteasomal ubiquitin-dependent protein catabolic process, endoplasmic reticulum, and tryptophan metabolism. This suggest that *T. kingsejongensis* have changed adaptation mechanisms such as energy production and metabolism, proteolytic complex, and sterol biosynthesis. The results have important implications for understanding of crustacean evolution and their adaptations to the Antarctic environment.

References

[1] Park, E.-O., S. Lee, M. Cho, S. H. Yoon, Y. Lee, and W. Lee, A new species of the genus *Tigriopus* (Copepoda: Harpacticoida: Harpacticidae) from Antarctica, *Proceedings of the Biological Society of Washington*, **2014**, 127, 138-154.

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