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The genome of Antarctic copepoda Tigriopus kingsejongensis and adaptation to life in the Antarctic Environment

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Antarctic marine invertebrates face extremely cold temperatures and many of decapod crustacean and fish groups became extinct because of extreme climate for over the last 30 million years. In that matter, species which have survived in Antarctic region may have evolutionary strategies and understanding their adaptation mechanisms in response to the extreme environment has received considerable attention. However, genome-wide studies about the molecular basis underlying these mechanisms is still limited to fishes and microbes. Here we present the first draft genome sequence and annotation for Antarctic copepoda Tigriopus kingsejongensis, the first Antarctic Crustacean to be sequenced. 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. The comparative genome analysis among 3,254 orthologs in 4 arthropod species (T. kingsejongensis, Tigriopus japonicus, Daphnia 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.