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The complete mitochondrial genome of the subarctic red king crab, *Paralithodes camtschaticus* (Decapoda, Anomura)

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Abstract
We determined the complete mitochondrial (mt) genome sequence of the red king crab, *Paralithodes camtschaticus* (Decapoda, Anomura). *P. camtschaticus* is one of the largest arthropods and the most expensive commercially available gourmet seafood. The genome sequence of *P. camtschaticus* is 16,720 bp in size and its gene content, gene order, and transcriptional polarity are almost identical to those of the hermit crab *Pagurus longicarpus*, which is thought to be derived from a common ancestor. However, *P. camtschaticus* mtDNA showed tRNA translocation in two blocks compared to that of *P. longicarpus.* Prior to this study, complete mt genomes of only two species of Anomura have been reported. Thus, our genomic data will provide additional information for constructing the decapod phylogeny.

Keywords: Paralithodes camtschaticus, *mitochondrial genome, Anomura, Decapoda, subarctic red king crab*

The red king crab *Paralithodes camtschaticus* (Tilesius, 1815) (Decapoda, Anomura, Lithodidae) is one of the most expensive commercial seafoods. *P. camtschaticus* inhabits the subarctic regions of the Pacific Ocean, such as the Bering Sea, Barents Sea, and Gulf of Alaska. It can be found between the intertidal zone and a depth of 300 m, where the temperature ranges from − 1.7 to 18°C (Rodin 1989; Pavlova et al. 2007). *P. camtschaticus* is an omnivorous feeder that eats a wide variety of species, including worms, mollusks, and fish (Feder and Jewett 1981). This crab is also a food source for seals, sea lions, octopuses, and sea otters (Powell and Nickerson 1965; Abrunhosa and Kittaka 1997; Falk-Petersen et al. 2011). Thus, *P. camtschaticus* plays an important role in maintaining a balanced marine ecosystem. Recently, more attention has been paid on several king crabs that are considered as invasive species in both the Arctic and the Antarctic. In the 1960s, *P. camtschaticus* was first introduced to the Barents Sea in the Arctic, and now, it has an increasing distribution range. In the Antarctic, a large population of a king crab species, *Neolithodes yaldwyni*, was first reported in Palmer Deep on the west Antarctic Peninsula shelf, probably due to global warming (Smith et al. 2012). The introduction of the alien species can reduce native benthic diversity and biomass through predation and competition. Therefore, the potential impact of king crabs on the ecosystem must be carefully investigated (Falk-Petersen et al. 2011).

In this study, we determined the complete sequence of the mitochondrial (mt) genome of *P. camtschaticus* (GenBank accession number: JX944381). The complete mt genome of *P. camtschaticus* is 16,720 bp in size, comprising 37 genes (13 protein-coding genes, 2 rRNA genes, and 22 tRNA genes), which is typical for most metazoans (Figure 1 and Supplementary Table 1). The gene content, gene order, and

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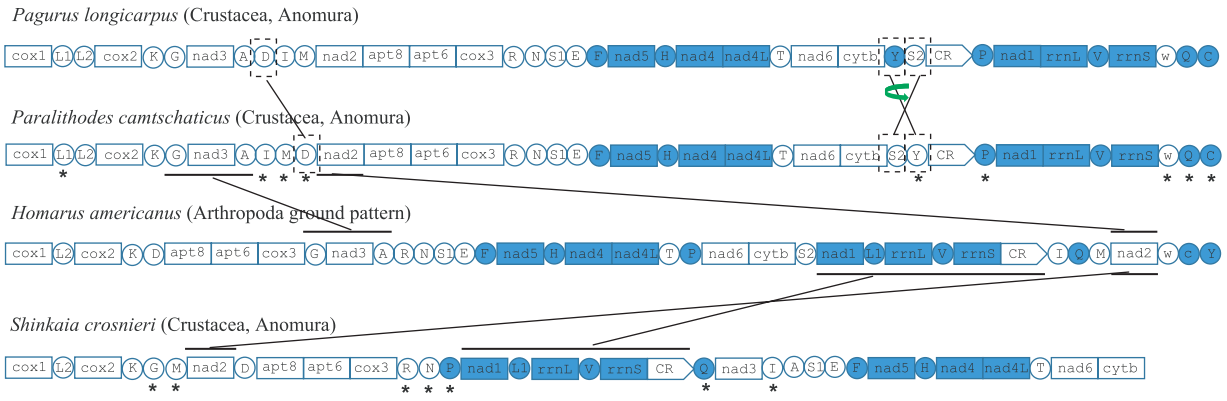

Figure 1. Gene structure comparison of the *P. camtschaticus* mt genome, ancestral pancrustacean pattern (*Homarus americanus*), and two anomuran decapod mitogenomes (*P. longicarpus* and *S. crosnieri*). Each tRNA gene (represented by a circle) is indicated by a letter, which corresponds to the appropriate amino acid. Gene translocation from the ancestral order is represented by the horizontal thick line linked to a diagonal line. Gene inversion is specified by the rotated arrow with lines. Asterisks under tRNA genes indicate rearrangement from the ancestral order. The gene rearrangement between *P. camtschaticus* and *P. longicarpus* is represented by the dotted box.

transcriptional polarity are almost identical to those of the hermit crab *Pagurus longicarpus*, with the exception of the rearrangements of three tRNAs—*trnD*, *trnY*, and *trnS*$_2$ (Hickerson and Cunningham 2000). The gene structure of *P. camtschaticus* is identical to that of *P. longicarpus*. However, its gene arrangement differs significantly from that of the anomuran *Shinkaia crosnieri* (Yang and Yang 2008) found in hydrothermal vents. When the location of tRNA was excluded from the comparison, for simplicity, the *P. camtschaticus* mitogenome showed two translocated genes, *nad2* and *nad3*, respectively, whereas *S. crosnieri* showed large block rearrangements (*nad1-rrnL-rrnS*) along with a *nad2* translocation. In addition, the *P. camtschaticus* and *P. longicarpus* mitogenomes contained well-conserved ancestral tRNA blocks, *R-N-S*$_1$*-E-F*, which are found in most arthropods as *A-R-N-S*$_1$*-E-F* clusters (Dowton et al. 2003; Kim et al. 2011). The similarities among the gene orders of the *P. camtschaticus* (superfamily Lithodidae) and *P. longicarpus* (Paguroidea) mitogenomes and their considerable differences when compared to that of *S. crosnieri* (Galatheoidea) are in agreement with the phylogeny of recent molecular studies (Ahyong et al. 2009; Tsang et al. 2011), which support the derivation of king crabs from asymmetrical hermit crabs, also known as the "hermit to king" hypothesis (Cunningham et al. 1992).

Anomurans comprise 7 superfamilies, 17 families, and approximately 1500 species (Ahyong et al. 2009), including hermit crabs, squat lobsters, porcelain crabs, mole crabs, and king crabs. Although numerous studies using both morphological and molecular data have been conducted (McLaughlin et al. 2004; Tsang et al. 2011), the phylogenetic relationships among anomuran internal groups remain to be fully elucidated. Thus, the genetic information of *P. camtschaticus* determined in this study will provide additional information for understanding the evolution of the anomuran mt genome and phylogeny.

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