

MITOGENOME ANNOUNCEMENT

The complete mitochondrial genome of the Japanese ghost shrimp *Nihonotrypaea japonica* (Crustacea, Decapoda, Axiidea)

SANGHEE KIM¹, DONG-HA AHN², JOONG-KI PARK³, SE-JOO KIM⁴, HAN-GU CHOI¹, & GI-SIK MIN²

¹Division of Life Sciences, Korea Polar Research Institute (KIOST), 12 Gaetbeol-ro, Yeosu-gu, Incheon 406-840, South Korea, ²Department of Biological Sciences, Inha University, Incheon 402-751, South Korea, ³Department of Parasitology, College of Medicine, Chungbuk National University, Cheongju 361-763, South Korea, and ⁴Deep-sea and Seabed Resources Research Division, Korea Institute of Ocean Science & Technology, Gyeonggi-do 426-744, South Korea

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Abstract

We determined the complete mitochondrial (mt) genome sequence of the Japanese ghost shrimp *Nihonotrypaea japonica* (Ortmann 1891) (Crustacea, Decapoda, Axiidea). The *N. japonica* mt genome is first represented in infraorder Axiidea, which, together with infraorder Gebiidea, belonged to infraorder Thalassinidea until recently. The genome sequence of *N. japonica* is 15,274 bp in size, and the gene arrangement and transcriptional polarity are partially different from that of the Japanese mud shrimp, *Upogebia major*, which belongs to the infraorder Gebiidea. We present the mt genome of *N. japonica*, which could provide useful molecular information to construct a stable classification for infraorder Thalassinidea and to better understand the phylogenetic relationship of Thalassinidea with other decapod groups.

Keywords: Complete mitochondrial genome, Decapoda, Japanese ghost shrimp, *Nihonotrypaea japonica*

The Japanese ghost shrimp *Nihonotrypaea japonica* (Ortmann 1891) (Crustacea, Decapoda, Axiidea) belongs to the group of burrowing thalassinideans in the order Decapoda. These crustaceans play an important role as bioturbators in benthic communities (Mukai and Koike 1984; Posey et al. 1991; Dworschak 2000; Felder 2001). Infraorder Thalassinidea was recently divided into two separate infraorders, Axiidea and Gebiidea, on the basis of morphological characteristics and molecular data (Robles et al. 2009). However, additional morphological characterization and molecular data are needed to ascertain whether Thalassinidea is monophyletic.

Recently, a complete mitochondrial (mt) genome of Gebiidea was determined from the Japanese mud

shrimp *Upogebia major* (Kim et al. 2011b). Additional data from representative species in Axiidea are required to better understand the phylogenetic relationships among the members of Thalassinidea. Here, for the first time, we present the mt genome of *N. japonica*, a representative of infraorder Axiidea (GenBank Accession No. KC236422). The mt genome was 15,274 bp in length, and, as in most metazoans, contained the typical 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), and 2 ribosomal RNAs (Figure 1 and Supplementary Table 1). The *N. japonica* mt genome was compared with that of *U. major* and *Homarus americanus* (as a representative of arthropod ground pattern) (Figure 1). The *U. major* mt genome showed that the

Correspondences: H.-G. Choi, Division of Life Sciences, Korea Polar Research Institute (KIOST), 12 Gaetbeol-ro, Yeosu-gu, Incheon 406-840, South Korea. Tel: + 82 32 260 6162. Fax: + 82 32 260 6301. E-mail: hchoi82@kopri.re.kr; G.-S. Min, Department of Biological Sciences, Inha University, 253 Yonghyun-dong, Nam-gu, Incheon 402-751, South Korea. Tel: + 82 32 860 7692. Fax: + 82 32 874 6737. E-mail: mingisik@inha.ac.kr

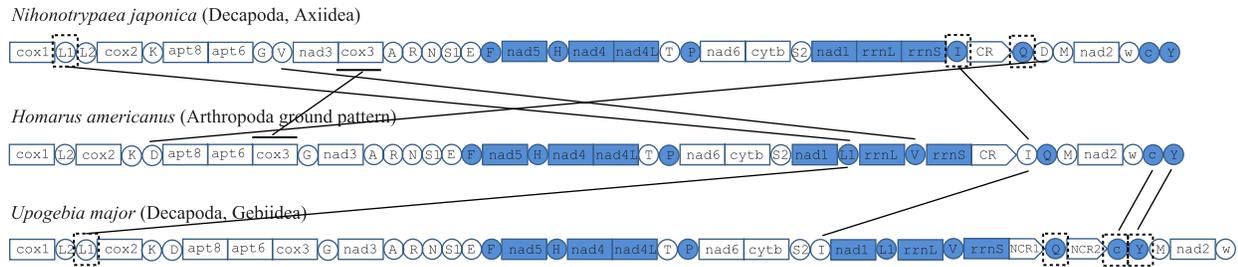


Figure 1. Comparison of the gene structure among the *N. japonica* mt genome, an ancestral pancrustacean pattern (*H. americanus*), and *U. major* mt genome. Each tRNA gene (represented by a circle) is indicated by a letter, which corresponds to the appropriate amino acid. Gene translocation from the ancestral order is represented by a thick horizontal line that is linked to a diagonal line. Gene inversion that differs from *H. americanus* is specified by a dotted box.

translocations were restricted only to tRNA genes, and that the order of the PCGs is identical to the arthropod ground pattern. The PCGs in the *N. japonica* mt genome showed the typical gene arrangement, except for *cox3* translocation. Interestingly, the *cox3* in *N. japonica* was separated from an ancestral gene cluster, *apt8-apt6-cox3*, which is highly conserved in most metazoans from Porifera to Chordata (King 2004). The *cox3* translocation has only been reported in the mt genomes of copepods in crustaceans and insects so far (Kim et al. 2012; Wei et al. 2010).

The *N. japonica* mt genome has a non-coding region (NCR) of 549 bp, whereas that of *U. major* showed two NCRs separated by *trnQ*. When compared with the arthropod ground pattern, the *N. japonica* mt genome showed rearrangements in the genes for four tRNAs (*trnD*, *trnI*, *trnL1*, and *trnV*), and the transcriptional polarity was reversed in *trnL1*, *trnI*, and *trnQ*. Note that the *N. japonica trnI* showed translocation as well as inversion of polarity, whereas the *trnI* in *U. major* showed translocation only in the same (original) direction as that of *H. americanus*. The position of *trnL1* is an interesting aspect of the *N. japonica* mt genome. In most arthropods, *trnL1* is located between *nad1* and *rrnL*. However, *trnL1s* of both *N. japonica* and *U. major* are located between *cox1* and *cox2*, but in the reverse order, i.e. *trnL1-trnL2* and *trnL2-trnL1*, respectively. Such positioning of *trnL1-trnL2* between *cox1* and *cox2* was also reported in the mt genome of *Pagurus longicarpus* (Anomura) (Hickerson and Cunningham 2000). This *trnL1* in *U. major* is considered as a duplication of the original *trnL1* located between *nad1* and *rrnL*, on the basis of the pancrustacean pattern (Kim et al. 2011a). In decapods, only two cases of extra genes have been reported from *U. major* and *Geothelphusa dehaani* (Brachyura), which also contains an extra *trnL1* (Segawa and Aotsuka 2005; Kim et al. 2011b). Unlike in the *U. major* mt genome, the original *trnL1* between *nad1* and *rrnL* was absent in *N. japonica* mt genome.

These unique differences in the locations of *trnL1* and *trnL1-trnL2* can be considered as criteria to explain the phylogenetic relationships between Axii-dea (*N. japonica*) and Gebiidea (*U. major*), as well as

among Thalassinidea, Anomura (*P. longicarpus*), and Brachyura (*G. dehaani*). Therefore, adding more mt genome data from the representative species from these groups will help to establish robust relationships among these decapods.

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