## MITOGENOME ANNOUNCEMENT

# Complete mitochondrial genome of the northern mauxia shrimp Acetes chinensis (Decapoda, Dendrobranchiata, Sergestoidae)

# SANGHEE KIM<sup>1</sup>, JIYEON KIM<sup>2</sup>, HAN-GU CHOI<sup>1</sup>, JOONG-KI PARK<sup>2</sup>, & GI-SIK MIN<sup>3</sup>

<sup>1</sup>Korea Polar Research Institute (KORDI), 7-50 Songdo-dong, Yeonsu-gu, Incheon 406-840, Republic of Korea, <sup>2</sup>Department of Parasitology, College of Medicine, Chungbuk National University, Cheongju 361-763, Republic of Korea, and <sup>3</sup>Department of Biological Sciences, Inha University, Incheon 402-751, Republic of Korea

(Received 18 October 2011; accepted 26 October 2011)

#### Abstract

Here, we report the first complete mitochondrial genome sequence of northern mauxia shrimp *Acetes chinensis* (Decapoda, Dendrobranchiata, Sergestoidae). The genome sequence was 15,740 bp in size, and the gene content, gene order and transcriptional polarity were almost identical to the pancrustacean ground pattern, with the one exception that an extra  $trnS_I^{AGC}$  was adjacent to the original  $trnS_I^{AGA}$ . The two tandemly duplicated  $trnS_I$  showed a high sequence similarity (82.3%), with almost identical secondary structure lacking a DHU arm. Comparison of codon usage suggests that both of the  $trnS_I$  genes were functional.

**Keywords:** Mitochondrial genome, gene duplication,  $trnS_1$ , northern mauxia shrimp, Acetes chinensis

The northern mauxia shrimp (Acetes chinensis, Hansen 1919) (Decapoda, Dendrobranchiata, Sergestoidae) is one of the most economically important fished shrimps in East Asia because they are widely used as marine resources in fermented foods, dry products and industrial food ingredients (Oh and Jeong 2003; He et al. 2006). This planktonic shrimp is distributed across the Northwest Pacific Ocean, including China, Japan and Korea, and has an important function in the food webs in coastal waters, acting as predators of small organisms, or prey for large animals such as marine fishes (Oh and Jeong 2003). In this study, we present the complete sequence of the mitochondrial (mt) genome of A. chinensis (the GenBank accession number: JN689221). Specimens of A. chinensis were collected from Daekwang Beach in Imja Island (35°06'N, 126°04'E), Jeollanam-do province, Republic of Korea. The complete mt genome of A. chinensis

is 15,740 bp in size, and contains 38 genes (13 protein-coding genes, 2 rRNA genes and 23 tRNA genes). The genome content, gene order and transcriptional polarity of A. chinensis mtDNA were almost identical to the pancrustacean ground pattern, with the one exception that an extra  $trnS_1^{AGC}$  was adjoined to the original copy of  $trnS_1^{AGA}$  (Kim et al. 2011). Changes of tRNAs at the A-R-N-S1-E-F cluster (located between *nad3* and *nad5*) frequently occur in the arthropods as a "hot spot", but available data present mostly gene rearrangements (Dowton et al. 2003; Sun et al. 2005; Kilpert and Podsiadlowski 2006). However, A. chinensis mtDNA showed a novel tRNA cluster, A-R-N- $S_1^{AGA}$ - $S_1^{AGC}$ -E-F, which was due to an insertion of an extra copy of  $trnS_1^{AGC}$  adjacent to the original  $trnS_1^{AGA}$ . Notably, there was no intergenic space or overlapped nucleotide (nt) between the two S<sub>1</sub> tRNAs, although duplication/loss events give rise

Correspondences: G.-S. Min, Department of Biological Sciences, Inha University, 253 Yonghyun-dong, Nam-gu, Incheon 402-751, Republic of Korea. Tel: + 82 32 860 7692. Fax: + 82 32 874 6737. E-mail: mingisik@inha.ac.kr; J.-K. Park, Department of Parasitology, College of Medicine, Chungbuk National University, Cheongju 361-763, Republic of Korea. Tel: + 82 43 261 2843. Fax: + 82 43 272 1603. E-mail: jkpyou@chungbuk.ac.kr

ISSN 1940-1736 print/ISSN 1940-1744 online © 2012 Informa UK, Ltd. DOI: 10.3109/19401736.2011.643878



Figure 1. (A) Circular map of the mitochondrial genome of *Acetes chinensis*; (B) sequence comparison between  $trnS_1^{AGA}$  and  $trnS_1^{AGC}$ . In the top line, (,) and a dot indicate the anticodon stem and the loop, respectively. Identical nucleotides are presented by the vertical line. The red letters indicate the anticodon.

to the multiple intergenic spacers (Yamauchi et al. 2003; Sun et al. 2005) (Figure 1 and Supplementary Table S1). Very recently, a pseudogene-like  $trnS_1^{AGC}$ located between trnN and trnF was reported in the snapping shrimp Alpheus distinguendus, in which the functional  $trnS_1^{AGA}$  was not present (Qian et al. 2011). There have been some reports on mt gene duplication, where one of the duplicates was shown to become a pseudogene or deleted, due to the strong selective pressure for genome minimization (Zevering et al. 1991; Sasuga et al. 1999; Yokobori et al. 2004). However, a comparison of codon usage corresponding to each of the two tRNA duplicates in A. chinensis showed that both of the  $trnS_1$  genes were functional, although there was a preference of  $trnS_1^{AGA}$  (1.96%) over  $trnS_1^{AGC}$  (0.27%) (Supplementary Table S2).

The nt sequences of duplicated genes are often very similar and/or nearly identical in some other metazoan species (Azevedo and Hyman 1993; Hyman and Azevedo 1996; Arndt and Smith 1998; Yokobori et al. 2004; Chen et al. 2008). In *A. chinensis*, the two tandemly duplicated  $trnS_1$  showed a high sequence similarity (82.3%), with almost identical secondary structure lacking a DHU arm (Supplementary Figure S1). A DHU arm was also lacking or incomplete in many other crustacean species (Kilpert and Podsiadlowski 2006; Ki et al. 2009).

The suborder Dendrobranchiata comprises two superfamilies: Penaeoidea and Sergestoidae. Until now, the six complete mtDNA sequences have been determined for species in Penaeoidea but none for Sergestoidae. The *A. chinensis* mtDNA is the first representative of the Sergestoidae. Along with gene duplication of  $trnS_1$ , this study will provide useful information to better understand the evolution of the mt genome in crustacean lineages.

#### Acknowledgements

This work was supported by the Polar Academic Program (PAP), KOPRI for G.-S. Min, and the Basic Research Program of the KOPRI (PE11030) for S. Kim and H.-G. Choi.

**Declaration of interest:** The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper.

## References

Arndt A, Smith MJ. 1998. Mitochondrial gene rearrangement in the sea cucumber genus *Cucumaria*. Mol Biol Evol 15:1009–1016.

- Azevedo JL, Hyman BC. 1993. Molecular characterization of lengthy mitochondrial DNA duplications from the parasitic nematode *Romanomermis culicivorax*. Genetics 133:933–942.
- Chen C, Dai CF, Plathong S, Chiou CY, Chen CA. 2008. The complete mitochondrial genomes of needle corals, *Seriatopora* spp. (Scleractinia: Pocilloporidae): An idiosyncratic *atp8*, duplicated *trnW* gene, and hypervariable regions used to determine species phylogenies and recently diverged populations. Mol Phylogenet Evol 46:19–33.
- Dowton M, Castro LR, Campbell SL, Bargon SD, Austin AD. 2003. Frequent mitochondrial gene rearrangements at the Hymenopteran *nad3-nad5* junction. J Mol Evol 56:517–526.
- He H, Chen X, Sun C, Zhang Y, Gao P. 2006. Preparation and functional evaluation of oligopeptide-enriched hydrolysate from shrimp (*Acetes chinensis*) treated with crude protease from *Bacillus* sp. SM98011. Bioresour Technol 97:385–390.
- Hyman BC, Azevedo JL. 1996. Similar evolutionary patterning among repeated and single copy nematode mitochondrial genes. Mol Biol Evol 13:221–232.
- Ki J-S, Park HG, Lee J-S. 2009. The complete mitochondrial genome of the cyclopoid copepod *Paracyclopina nana*: A highly divergent genome with novel gene order and atypical gene numbers. Gene 435:13–22.
- Kilpert F, Podsiadlowski L. 2006. The complete mitochondrial genome of the common sea slater, *Ligia oceanica* (Crustacea, Isopoda) bears a novel gene order and unusual control region features. BMC Genomics 7:241.
- Kim S, Lee SH, Park MH, Choi HG, Park JK. 2011. The complete mitochondrial genome of the American lobster *Homarus*

americanus (Crustacea, Decapoda). Mitochondrial DNA 22: 47-49.

- Oh C, Jeong I. 2003. Reproduction and population dynamics of *Acetes chinensis* (Decapoda: Sergestoidae) on the Western Coast of Korea, Yellow Sea. J Crustacean Biol 23:827–835.
- Qian G, Zhao Q, Wang A, Zhu L, Zhou K, Sun H. 2011. Two new decapods (Crustacea: Malacostraca) complete mitochondrial genomes: Bearings on the phylogenetic relationships within the Decapoda. Zool J Linn Soc 162:471–481.
- Sasuga JS, Yokobori S, Kaifu M, Ueda T. 1999. Gene contents and organization of a mitochondrial DNA segment of the squid *Loligo bleekeri*. J Mol Evol 48:692–702.
- Sun H, Zhou K, Song D. 2005. Mitochondrial genome of the Chinese mitten crab *Eriocheir japonica sinenesis* (Brachyura: Thoracotremata: Grapsoidea) reveals a novel gene order and two target regions of gene rearrangements. Gene 349: 207–217.
- Yamauchi MM, Miya MU, Nishida M. 2003. Complete mitochondrial DNA sequence of the swimming crab, *Portunus trituberculatus* (Crustacea: Decapoda: Brachyura). Gene 311: 129–135.
- Yokobori S, Fukuda N, Nakamura M, Aoyama T, Oshima T. 2004. Long-term conservation of six duplicated structural genes in Cephalopod mitochondrial genomes. Mol Biol Evol 21: 2034–2046.
- Zevering CE, Moritz C, Heideman A, Sturm RA. 1991. Parallel origins of duplications and the formation of pseudogenes in mitochondrial DNA from parthenogenetic lizards (*Heteronotia binoei*; Gekkonidae). J Mol Evol 33:431–441.

# Supplementary materials available online. Table S1, Table S2 and Figure S1