

## 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

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**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  $trnS_1^{AGC}$  was adjacent to the original  $trnS_1^{AGA}$ . The two tandemly duplicated  $trnS_1$  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  $trnS_1$  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-S<sub>1</sub>-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<sub>1</sub><sup>AGA</sup>-S<sub>1</sub><sup>AGC</sup>-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  $S_1$  tRNAs, although duplication/loss events give rise

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- 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 sinensis* (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 triuberculatus* (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 bimoei*; Gekkonidae). *J Mol Evol* 33:431–441.

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