

MITOGENOME ANNOUNCEMENT

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## Complete mitochondrial genome of Kishi velvet shrimp, *Metapenaeopsis dalei* (Rathbun, 1902) (Crustacea: Decapoda: Penaeidae) in the East China Sea

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### ABSTRACT

We determined the complete mitochondrial genome of *Metapenaeopsis dalei* (Rathbun, 1902), which is collected from East China Sea (124°E and 33.5°N). Total mitochondrial genome length of *M. dalei* was 15 939 bp, in which 13 proteins, two ribosomal RNAs, 22 transfer RNAs and a putative control region were encoded. The gene arrangement of *M. dalei* was well conserved with nine known Penaeidae mitochondrial genomes from *COX1* to *tRNA<sup>Tyr</sup>*. The protein-coding genes started with ATN except for *COX1* in which ACG is used. Four genes (*COX2*, *COX3*, *ND3* and *ND5*) exhibited an incomplete stop codon. Nucleotide sequence identity of *M. dalei* mitochondrial genome to those of nine Penaeidae species ranged from 78% to 80%. Based on the COI region, *M. dalei* is most closely related to *Penaeus notialis*.

### ARTICLE HISTORY

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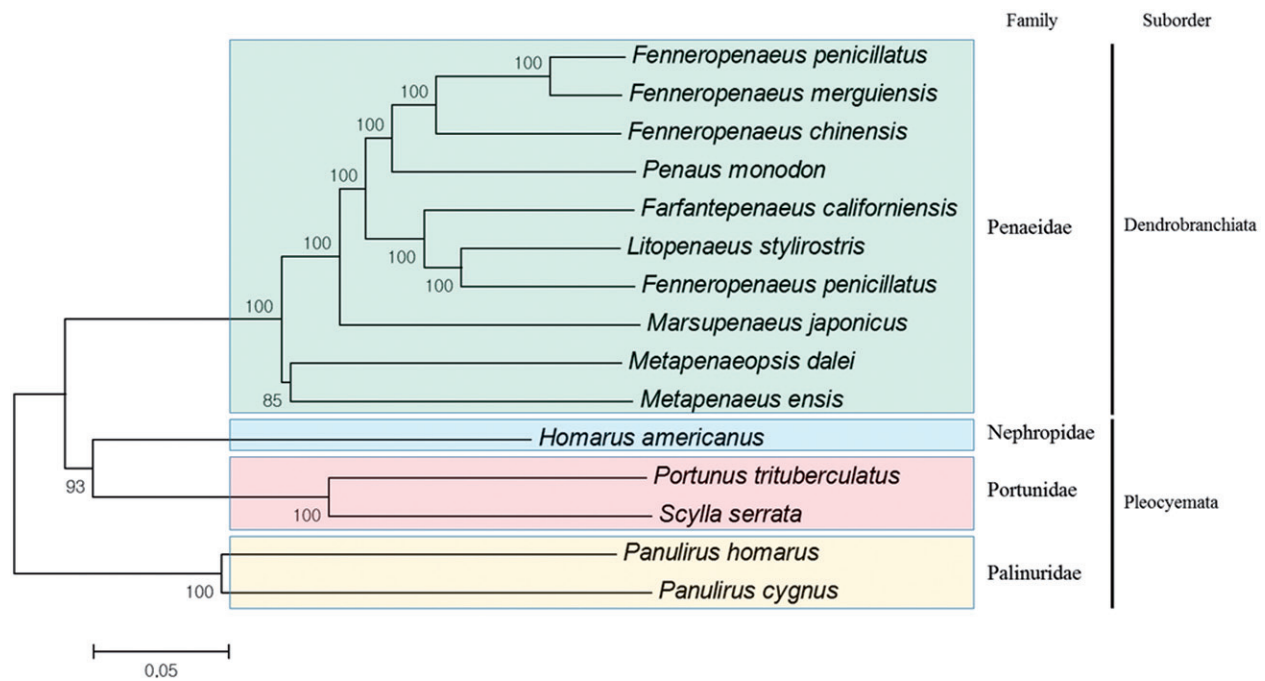
### KEYWORDS

Barcode; decapod crustacean; mitochondrial genome; Palaemon

The Kishi velvet shrimp, *Metapenaeopsis dalei* (Decapoda: Penaeidae) is distributed along the coastal and brackish waters in North China, Korea and Japan (Holthuis 1980; Cha et al. 2001). As *M. dalei* is one of the commercially important shrimp species in southern and western coastal waters in Korea, its basic biology and life history have been documented (Choi & Hong 2001a,b; Choi et al. 2003, 2005). *Metapenaeopsis dalei* belongs to the genus *Metapenaeopsis*, which includes the most diverse species among Penaeidae prawn. Although its morphological characteristics has been reported such as the asymmetrical petasma in males (Dall et al. 1990), relatively little information on the molecular phylogeny has been published (Tong et al. 2000; Cheng et al. 2015). To our best knowledge, no mitochondrial genome sequences belonging to genus *Metapenaeopsis* is currently listed in GenBank database. Here we provide the first report about full mitochondrial genome sequence of genus *Metapenaeopsis*. The *M. dalei* examined in this study was collected in the East China Sea (124°E and 33.5°N) during the regular survey by National Fisheries Research and Development Institute (NFRDI) in Korea.

Total mitochondrial genome of *M. dalei* was here determined by the contig assembly obtained by next generation sequencing (NGS) using MiSeq platform (Illumina, San Diego, IL) and ambiguous sequences were reconfirmed by the typical Sanger sequencing strategy of the cloned

PCR products. A 15 939 bp of full length mitochondrial genome (GenBank accession no. KU050082) encoded 13 proteins, two ribosomal RNAs and 22 transfer RNAs, as well as a putative control region. The gene arrangement of all known mitochondrial genomes of Penaeidae including *M. dalei* was well conserved from *COX1* to *tRNA<sup>Tyr</sup>*. The protein-coding genes start with ATN except for *COX1* in which ACG is used. Four genes (*COX2*, *COX3*, *ND3* and *ND5*) exhibit an incomplete stop codon (T–). The length of LrRNA and SrRNA gene was 1355 bp and 850 bp, respectively. The tRNA genes were spread over the entire genome and were located on both strands. Twenty of them were identified using tRNAscan-SE 1.21 (Lowe & Eddy 1997) and the other variable two tRNA genes (*tRNA<sup>Asn</sup>* and *tRNA<sup>Ser(4672~4738)</sup>*) were confirmed by the comparison of mitochondrial genomes of previously known nine Penaeidae prawns (Figure 1). The mitochondrial genome encoded 22 tRNA genes ranging in size from 65 to 72 nucleotides. The putative control region (996 bp) is the major non-coding region with a high A+T content in *M. dalei* (80.8%), which is the most variable region within the total mitochondrial genome. Nucleotide sequence of *M. dalei* mitochondrial genome shared 78–80% identity to those of nine Penaeidae species, showing the highest identity to *Metapenaeus ensis*. When only COI region was compared, *M. dalei* is most closely related to *Penaeus notialis*



**Figure 1.** Phylogenetic tree of mitochondrial genomes from six species belonging to Palinuridae with other decapod crustaceans. Phylogenetic tree was constructed using molecular evolutionary genetics analysis ver. 6.0 (MEGA6, MEGA Inc., Englewood, NJ) program with the minimum evolution algorithm. The evolutionary distances were computed using the Kimura 2-parameter method. Total mitochondrial genome sequences used for the analysis include 10 from Penaeidae (*Fenneropenaeus penicillatus*; NC\_026885, *Fenneropenaeus merguensis*; NC\_026884, *Metapenaeus ensis*; NC\_026834, *Marsupenaeus japonicus*; NC\_007010, *Litopenaeus stylirostris*; NC\_012060, *Litopenaeus vannamei*; NC\_009626, *Fenneropenaeus chinensis*; NC\_009679, *Farfantopenaeus californiensis*; NC\_012738, *Penaus monodon*; NC\_02184 and *Metapenaeopsis dalei*; KU050082), two from Portunidae (*Portunus trituberculatus*; NC\_005037, *Scylla serrata*; HM590866), two from Palinuridae (*Panulirus homarus*; NC\_016015, *Panulirus Cygnus*; NC\_028024) and one from Nephropidae (*Homarus americanus*; NC\_015607).

(Pérez-Farfante, 1967), which is caught in eastern Atlantic and west African coast.

## Disclosure statement

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