

The complete mitochondrial genome of squat lobster, *Munida gregaria* (Anomura, Galatheaidea, Munididae)

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ABSTRACT

We determined the mitogenome sequence of *Munida gregaria* (Fabricius 1793) (Anomura, Galatheaidea, Munididae), which is the first complete mitogenome sequence in the family Munididae Ah Yong et al., 2010. The mitogenome of *M. gregaria* is 16326 bp in length and contains 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), two ribosomal RNAs (rRNAs) and two control regions (CRs). Mitogenome analysis of *M. gregaria* showed an extra copy of the CR and rearrangements of two PCGs (*nad2* and *nad3*) compared to the arthropod ground pattern. Additionally, it contains a tRNA (*trnY*) inversion and rearrangements of two PCGs (*nad1* and *nad3*) when compared with that of *Neopetrolisthes maculatus* and *Shinkaia crosnieri*, respectively. The phylogenetic tree confirmed that *M. gregaria* belongs to the superfamily Galatheaidea within Anomura. Our results will be useful for the detailed study of mitogenome evolution and the phylogenetic relationships among the superfamily in the infraorder Anomura.

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Munida gregaria (Fabricius 1793) is a benthic squat lobster species of the continental shelf and upper slope off southern South America, New Zealand, and southern Australia (Baba et al. 2008; Schnabel et al. 2011). Of 274 species in the genus *Munida*, this cold temperate species is suggested to be the only transpacific species in its family on both sides of the East Pacific Barrier, whose dispersal might have occurred by rafting on buoyant macroalgae via the Antarctic Circumpolar Current (Nikula et al. 2010; Perez-Barros et al. 2014; Macpherson 2015). Therefore, *M. gregaria* and its genetic information have great potential for studies on species expansion, gene exchange, circumpolar dispersal and phylogeography.

Individuals of *M. gregaria* were collected using hand net from a harbour in Punta Arenas, Chile (53°10'03S, 70°54'30W). Among them, one specimen was deposited in the Korea Polar Research Institute (KOPRI, Incheon, South Korea). Genomic DNA extraction, sequencing and gene annotation were performed according to the methods described by Song et al. (2015). Phylogenetic tree was constructed using MEGA 6.0 (MEGA Inc., Englewood, NJ) (Tamura et al. 2013).

The complete mitogenome of *M. gregaria* was 16326 bp in length (GenBank accession number: KU521508; Specimen deposit number: KPIV000001) and contained 13 protein-coding genes (PCGs), 22 transfer RNAs (tRNAs), two ribosomal RNAs (rRNAs) and two control regions (CRs).

The superfamily Galatheaidea comprises four families: Galatheididae Samouelle, 1819; Munididae Ah Yong et al., 2010; Munidopsidae Ortmann, 1898; Porcellanidae Haworth, 1825.

The complete mitogenomes have sequenced from only two families: *Shinkaia crosnieri* (Family Munidopsidae) and *Neopetrolisthes maculatus* and *Petrolisthes haswelli* (Family Porcellanidae) (Yang & Yang 2008; Shen et al. 2013; Tan et al. 2014). Here, we report the first mitogenome sequence of *M. gregaria* of the family Munididae. The mitogenome of *M. gregaria* has rearrangements of two PCGs (*nad2* and *nad3*), which is likely a common characteristic feature shared among anomurans, whereas most brachyurans follow the typical arthropod ground pattern. Additionally, the *M. gregaria* mitogenome contains a tRNA (*trnY*) inversion and rearrangements of two other PCGs (*nad1* and *nad3*) when compared with that in *N. maculatus* and *S. crosnieri*, respectively. Further, it has two CRs (CR1 and CR2) because of the presence of an extra CR (682 bp) between *trnS2* and *trnP*, whereas other anomurans species have only one CR (CR1 or CR2).

To infer the phylogenetic relationship of the *M. gregaria* mitogenome, we performed the maximum likelihood analysis by using the concatenated sequences of 13 PCGs from 15 selected species of the order Decapoda. *Munida gregaria* was grouped with *S. crosnieri* and formed a solid monophyletic group of the superfamily Galatheaidea within Anomura (Figure 1).

To our knowledge, this is the first report of the complete mitogenome in the family Munididae and will be useful for the detailed study of mitogenome evolution and phylogenetic relationships among the superfamilies in the infraorder Anomura.

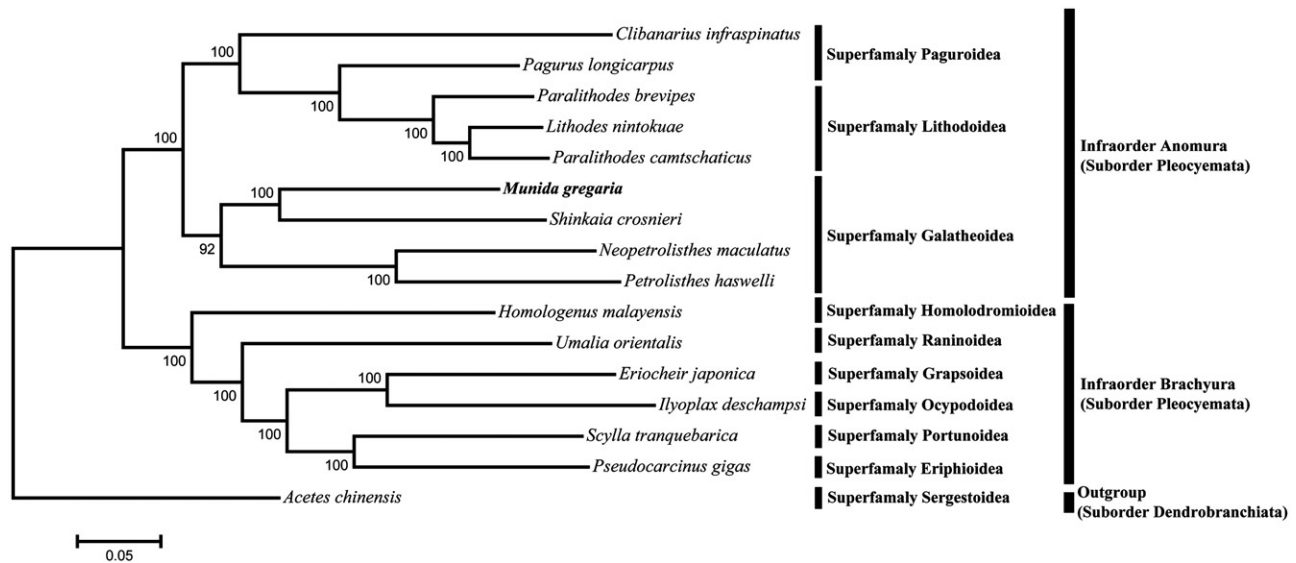


Figure 1. Maximum likelihood (ML) tree based on the mitogenome sequences of *Munida gregaria* (KU521508; this study) with 15 other selected species was constructed using MEGA 6.0 software. The bootstrap supports are shown on each node. The following mitogenomes were used in this analysis: *Clibanarius infraspinus* (NC_025776; Gan et al. 2015), *Pagurus longicarpus* (NC_003058; Hickerson & Cunningham 2000), *Paralithodes brevipes* (NC_021458; Yanagimoto & Kobayashi, unpublished), *Lithodes nintokuae* (NC_024202; Yanagimoto, unpublished), *Paralithodes camtschaticus* (NC_020029; Kim et al. 2013), *Shinkaia crosnieri* (NC_011013; Yang & Yang 2008), *Neopetrolisthes maculatus* (NC_020024; Shen et al. 2013), *Petrolisthes haswelli* (NC_025572; Tan et al. 2014), *Homologenus malayensis* (NC_026080; Hui et al. 2014), *Umalia orientalis* (NC_026688; Shi et al. 2015), *Eriocheir japonica* (NC_011597; Wang et al. 2014), *Ilyoplax deschampsii* (NC_020040; Ji et al. 2014), *Scylla tranquebarica* (NC_012567; Sangthong, unpublished), *Pseudocarcinus gigas* (NC_006891; Miller et al. 2005), and *Acetes chinensis* (NC_017600; Kim et al. 2012).

Disclosure statement

The authors declare no conflicts of interest. The authors alone are responsible for the content and writing of the manuscript.

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