

Analysis of complete mitochondrial genome of fiddler crab *Uca (Tubuca) arcuata* (De Haan, 1835) (Arthropoda, Malacostraca, Decapoda)

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ABSTRACT

In this study complete nucleotide sequences of the mitochondrial genome of fiddler crab *Uca arcuata* (De Haan, 1835) were determined and characterized. The length of mitochondrial genome for *U. arcuata* is 15,955 bp. This is the third and the longest record of complete mitochondrial genome from the family Ocypodidae. Furthermore, phylogenetic relationships were evaluated due to mitochondrial protein-coding genes. Phylogenetic tree suggests that *U. arcuata* belongs to the monophyletic family Ocypodidae and has sister group relationship with the genus *Ocypode*.

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Ocypodidae is a semi-terrestrial crab family which consists of two subfamily and four genera. Among the four genera, the genus *Uca* can be easily distinguishable by extreme size difference between the claws in males (Reaney et al. 2008). There are 114 valid species in the genus (WoRMS Editorial Board, 2016). Among them only complete mitochondrial genome of *Ocypode cordimanus* (Sung et al. 2016) and *O. ceratophthalmus* (Tan et al. 2014) have been reported. In this study the complete mitochondrial genome of *Uca arcuata* has been determined and characterized. Furthermore, phylogenetic relationship of the species was reconstructed based on the amino acid sequences of mitochondrial genes.

The species were collected from Bang La mangrove forest, Vietnam (20°46'16,22"N–106°40'05,93"E) on 01 July 2016 (Marine Biodiversity Institute of Korea accession number MABIK Lot No 0002829). Mitochondrial genes were assembled and annotated using MITObim (Hahn et al. 2013) and MITOS (Bernt et al. 2013). The annotation of mitochondrial genome sequences was refined using Geneious software version 9.1.4 (Kearse et al. 2012). The phylogeny of *U. arcuata* was reconstructed with the maximum likelihood statistical method using MEGA 6 (Tamura et al. 2013). mtREV with Freqs (+F) model used for amino acid substitution and bootstrap method were replicated 1000 times for the test of phylogeny. For reconstruction, the complete mitochondrial genomes of the species were retrieved from the GenBank and amino acid sequences of all protein-coding genes except *ATP8* gene were used for the analysis.

The length of complete mitogenome for *U. arcuata* (GenBank accession number KX911977) is 15,955 bp and the nucleotide composition of the genome is 35.7% A, 18.8% C, 11.1% G, and 34.4% T. This is the first complete mitochondrial genome record for the genus and the third record for the family. The mitochondrial genome consists of 13 protein-coding, two ribosomal RNA and 22 tRNA genes. It has a putative control region (735 bp) which is located between 12S rRNA and tRNA-Ile. This control region is also observed in the other Ocypodidae records, but the control region of *U. arcuata* has the highest A–T (79%) content among them. The gene order and direction of the mitochondrial genome is similar to the other Ocypodidae mitochondrial genomes. *U. arcuata* has the shortest 16S rRNA gene (1082 bp). There are 9 overlapping regions between 1 and 7 bp in length and 19 intergenic sequences ranging from 1 to 249 bp lengths. The largest intergenic sequence is located in tRNA-Met and NAD2 genes. This intergenic sequence does not appear in the other Ocypodidae records. The phylogenetic relationship shows that *U. arcuata* is close to a lineage which consists of *O. ceratophthalmus* and *O. cordimanus* species (Figure 1). They belong to the monophyletic Ocypodidae family. Previous six nuclear and two mitochondrial gene-based molecular study (Tsang et al. 2014) showed that in the superfamily Ocypodoidea, Ocypodidae has sister group relationship with Mictyridae and Macrophthalmidae, and Dotillidae early branched. The present phylogenetic reconstruction shows similar relationship. This complete mitochondrial sequence

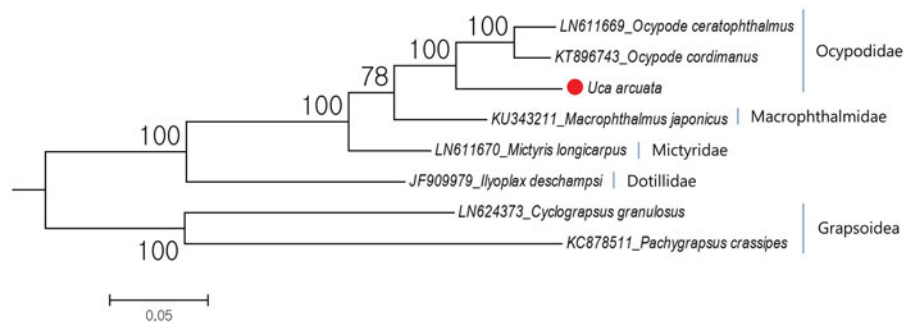


Figure 1. Phylogenetic tree of *Uca arcuata* in the superfamily Ocypodoidea based on protein-coding genes of mitochondrial genome. The species belongs to the superfamily Grapsoidea, chosen as a representative of outgroup and *U. arcuata* marked with a dot.

provides molecular systematic usage for the reconstruction of Ocypodidae phylogeny.

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Disclosure statement

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