

Complete mitochondrial genome sequence of Japanese cockle *Fulvia mutica* (Cardiidae)

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The complete mitochondrial genome (mt-genome) sequence of *Fulvia mutica* (Veneroida; Cardiidae) was determined. The genome is 19,110 bp in size and contains 42 genes, including the ATP synthase subunit 8 gene (*atp8*). All genes are on the same strand, as in other marine bivalves. It is extremely different in gene arrangement and size from that of *Acanthocardia tuberculata*, the only species belonging to Cardiidae with complete genome sequence data. The presence of putative *atp8* genes in two additional reported bivalve species, *A. tuberculata* and *Sinonovacula constricta* was also inferred by revising their deposited sequence data. It was suggested that *atp8* genes of heterodont bivalves could be translated to 37–39 amino acid sequences highly conserved within families, excluding *Hiatella arctica* with 53 amino acids. The mt-genome of *F. mutica* also contains two large duplicated regions related to different sequence motifs. One of the regions consists of five nearly identical copies of the 154 bp motif that includes a transfer RNA gene for cysteine. This region exhibited polymorphism in the number of repeats among individuals, suggesting the existence of a variable number of tandem repeats, which was expected to provide valuable information for developing useful genetic markers for phylogenetic study and population genetics.

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