

Two *Corbicula* (Corbiculidae: Bivalvia) mitochondrial lineages are widely distributed in Asian freshwater environment

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We investigated the biogeography of Asian *Corbicula* using mitochondrial gene sequence variation for *Corbicula* members sampled from 24 localities of 8 Asian regions. A total of 210 individuals were genetically characterized by examining sequence variations of a 614 bp fragment of the mitochondrial cytochrome oxidase I (COI) gene. Phylogenetic analyses of the COI dataset revealed that *Corbicula* members are subdivided into two well-supported clades: estuarine and freshwater. A robust dichotomy between the Japanese/Korean (*C. japonica*) and Chinese (*C. fluminalis*) estuarine forms was evident, suggesting that these two regional populations represent a deep phylogeographic split. Our mitochondrial gene tree showed that among the freshwater members, two *Corbicula* mitochondrial lineages are the most common, having attained extensive geographic distribution in the Asian freshwater environment. While the present study provides significant biogeographic information on Asian *Corbicula*, a comprehensive phylogenetic study by cross-referencing the mitochondrial-based *Corbicula* phylogeny with nuclear gene data is required to fully understand the evolutionary origin(s) of triploidy/clonality in this genus.