

Molecular Phylogenetics of Five *Corbicula* Species Determined by Partial 28S Ribosomal RNA Gene Sequences

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The bivalve superfamily Corbiculoidea (Order Veneroidea) has two families of special interest, Corbiculidae and Pisidiidae (Pisidiidae is also named Sphaeriidae). The genus *Corbicula* is present in freshwater, brackish-water, and estuaries in southeastern Asia, Africa, the Indian subcontinent, the Pacific Island, and South America where it is an important component of benthic communities in both lentic and lotic environments.

The present study is based on analysis of sequences from 5' end 28S ribosomal RNA (rRNA) gene of five common *Corbicula* species *C. fluminea*, *C. papyracea*, *C. leana*, *C. Japonica* *C. japonica* from Japan *C. largillierti* from China). Fifteen specimens of *Corbicula* were analyzed. In order to root the phylogenetic trees inferred from the data set, 28S rRNA gene sequence data of *Polymesoda maritime*, *P. caroliniana* and *S. corneum* were obtained from Genbank for the out groups, another member of the families Corbiculidae and Sphaeriidae .

Neighbor-joining analysis on the alignment of 412 base pairs of *C. fluminea*, *C. largillierti*, *C. papyracea*, *C. leana* and *C. japonica* (with *P. maritima*, *P. caroliniana* and *Sphaerium corneum* chosen as an outgroup) provides a robust molecular phylogeny for the genus. The results of the present study provide potential use of 28S rRNA gene sequence for phylogenies in the family Corbiculidae.