

# Novel gene rearrangement in the mitochondrial genome of *Pisidia serratifrons* (Anomura: Galatheoidea: Porcellanidae) and phylogenetic associations in Anomura

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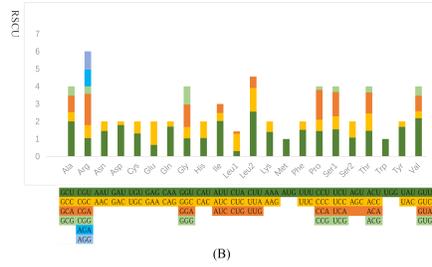
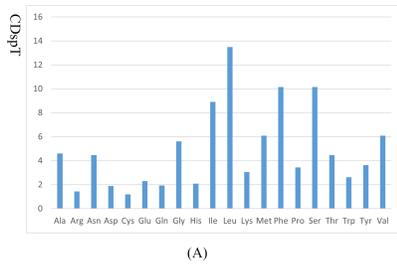
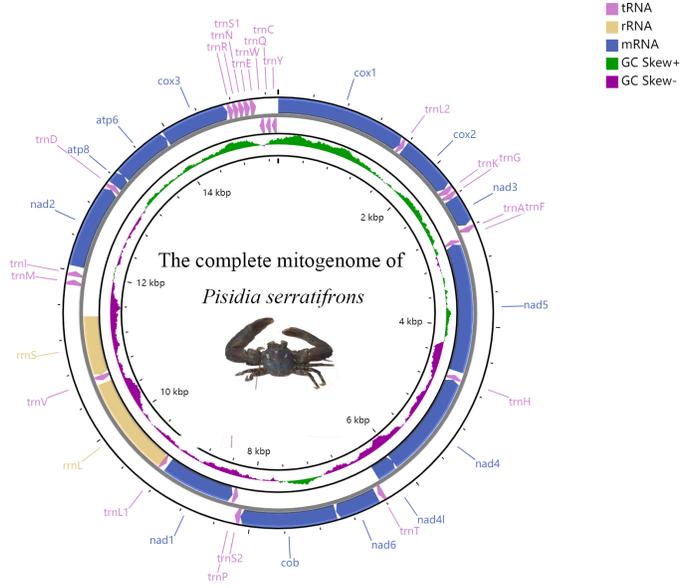
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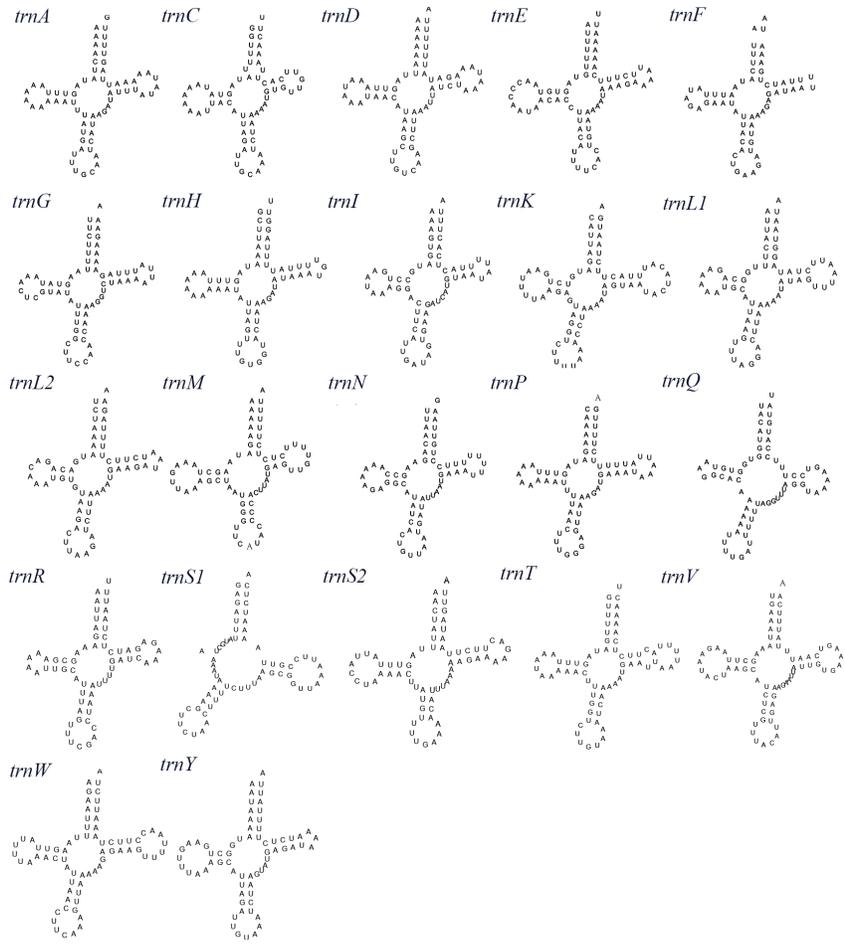
## Abstract

To improve the taxonomy and systematics of Porcellanidae within the evolution of Anomura, we describe the complete mitochondrial genomes (mitogenomes) sequence of *Pisidia serratifrons*, which is 15,344 bp in size, contains the entire set of 37 genes, and has an AT-rich region. The genome composition showed a high AT content of the mitogenomes was 74.29%, and exhibited a positive AT-skew (0.017) and a negative GC-skew (-0.246). Compared with the pan-crustacean ground pattern, at least five gene clusters (or genes) are significantly different with the typical genes, involving eleven tRNA genes and four PCGs, and the tandem duplication/random loss and recombination models were used to explain the observed large-scale gene rearrangements. The phylogenetic results showed that all Porcellanidae species clustered together as a group with well supported. Most Anomura superfamilies were found to be monophyletic, except Paguroidea. In general, the results obtained in this study will contribute to a better understanding of gene rearrangements in Porcellanidae mitogenomes and provide new insights into the phylogeny of Anomura.

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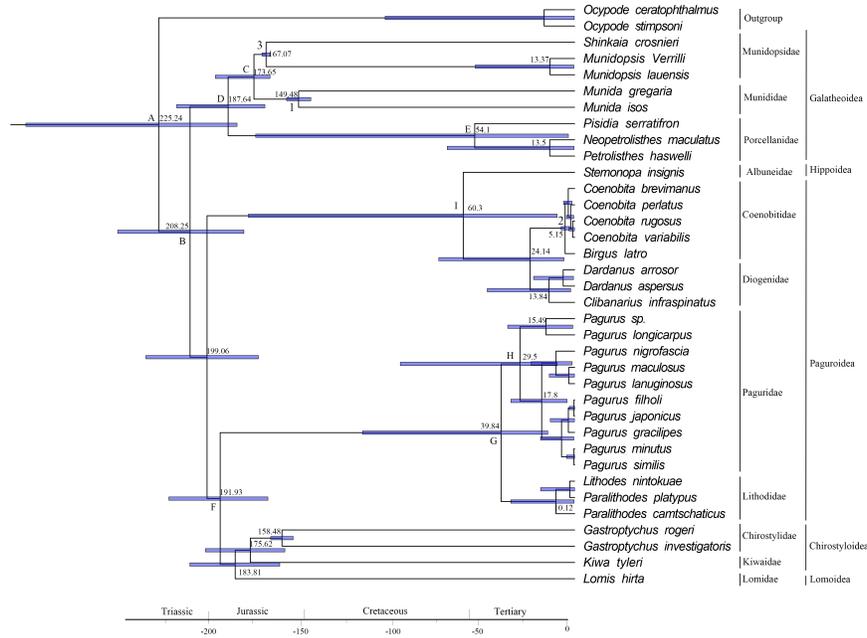
A Pancrustean ground pattern



B *P. serratifrons*







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Table1.doc available at <https://authorea.com/users/496832/articles/578077-novel-gene-rearrangement-in-the-mitochondrial-genome-of-pisidia-serratifrons-anomura-galatheoidea-porcellanidae-and-phylogenetic-associations-in-anomura>

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