Comparative Genomic and Mitochondrial Phylogenetic Relationships of Ovulidae (Mollusca: Gastropoda) Along the Chinese Coast

Qiong Wu[1], Peng Xiang[1], ShiHao Fan[2], GuangCheng Chen[1], and BingPeng Xing[1]

[1]Third Institute of Oceanography Ministry of Natural Resources
[2]Independent Researcher

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Abstract

The Ovulidae family, closely related to Cypraeidae (cowries), comprises approximately 260–280 species predominantly inhabiting tropical and subtropical shallow marine environments. Traditional morphological classification within Ovulidae has been challenging due to significant variability influenced by their host organisms. In this study, we collected 15 Ovulidae species from China's offshore waters, including the first regional record of *Habuprionovolva aenigma* (M. Azuma & C. N. Cate, 1971). We sequenced the mitochondrial genomes of 14 species and found that, except for *H. aenigma*, they exhibit typical metazoan mitochondrial structures. Phylogenetic analyses based on mitochondrial genome data were conducted to elucidate relationships among Ovulidae genera. Notably, we discovered that the subfamily Prionovolvinae exhibits a unique mitochondrial tRNA gene order. Our results suggest that mitochondrial gene rearrangements occurred after the divergence of the Prionovolvinae and Ovulinae subfamilies. Additionally, we found that Ovulidae species display significantly higher Ka/Ks ratios compared to Cypraeidae, indicating different selective pressures possibly linked to their unique feeding habits. Based on these findings, we propose reclassifying certain genera from the Simniinae subfamily to the Prionovolvinae subfamily. This research enhances the understanding of Ovulidae phylogeny and provides genomic resources for future studies.

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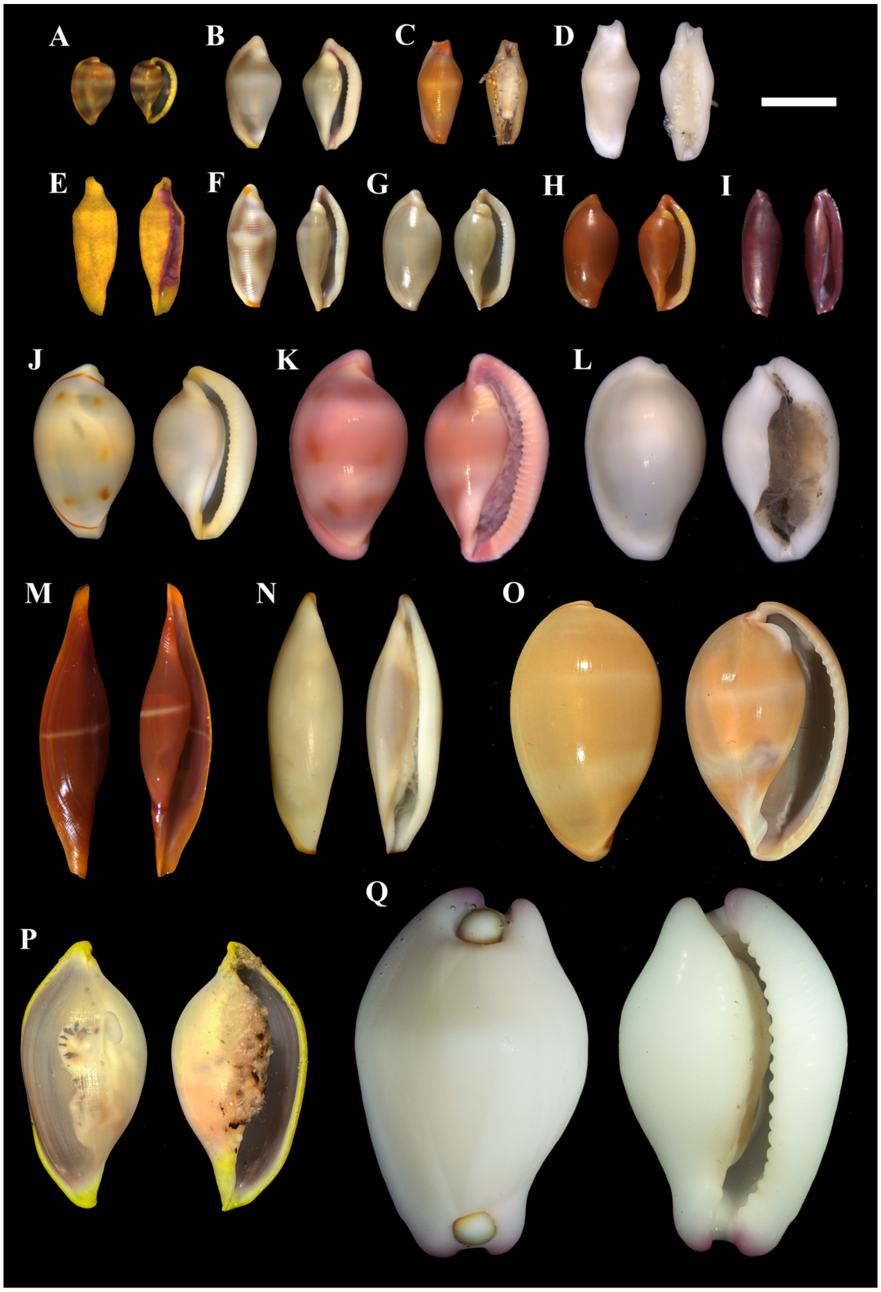
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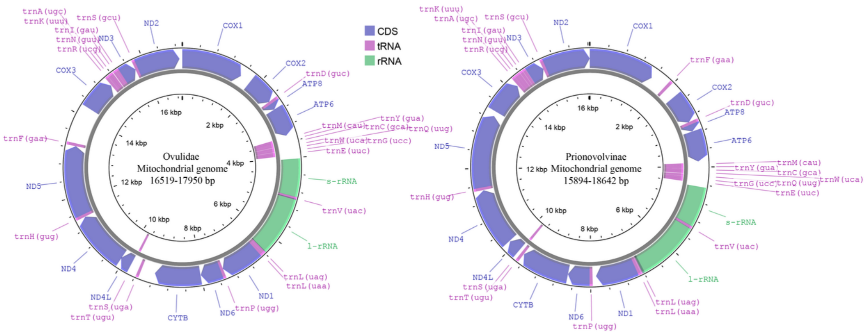

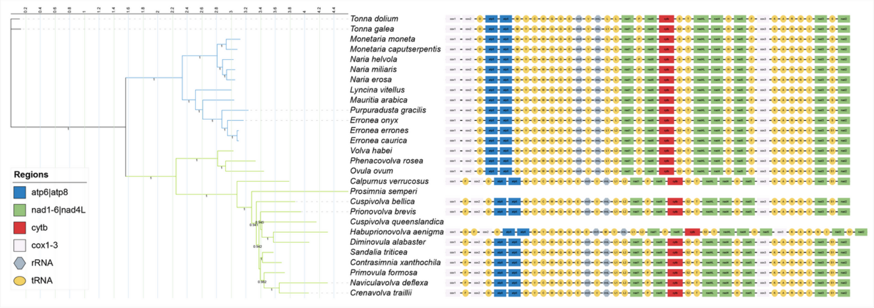

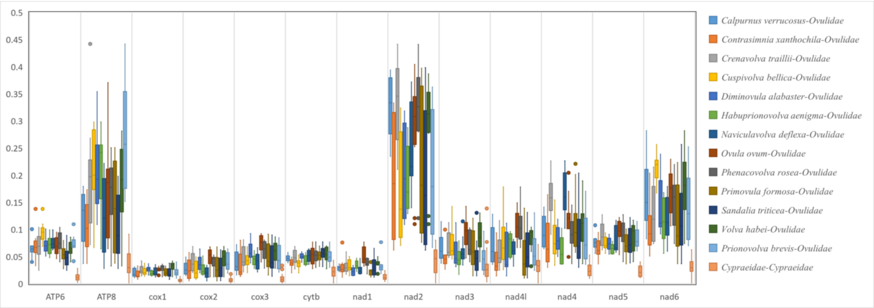

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