

Unraveling Coleoid phylogenetics through molecular diversity of mitochondrial genomes

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INTRODUCTION

Coleoids are a diverse clade of cephalopods characterized by their internal shell, ink sac, and arm hooks. They diverged from Nautilus approximately 415 million years ago (MYA) and subsequently split into Octopodiformes and Decapodiformes roughly 245 MYA¹. Establishing accurate phylogenetic relationships within this clade remains essential for understanding cephalopod evolution and facilitating comparative research across species. Molecular phylogenetics has become the primary approach for resolving cephalopod evolutionary relationships first documented in 1994 using partial mitochondrial 16S rRNA and since evolved to multiple mitochondrial genes, nuclear genes, complete mitochondrial genomes, and transcriptomes². However, previous phylogenetic studies have been constrained by limited genetic sequence availability and inadequate genomic diversity, which has hindered the accuracy of evolutionary reconstructions and left significant gaps in our understanding of coleoid relationships. Complete mitochondrial genomes provide multiple markers for phylogenetic analysis and can reveal evolutionary signatures. In this study, we examine how mitochondrial molecular diversity, including gene order variation, nucleotide composition, and variant hotspots influences evolutionary relationships across coleoid cephalopods. By integrating both complete and partial mitochondrial sequences, we evaluate how comprehensive taxonomic sampling refines our understanding of coleoid phylogeny.

METHODS

Data Sources³



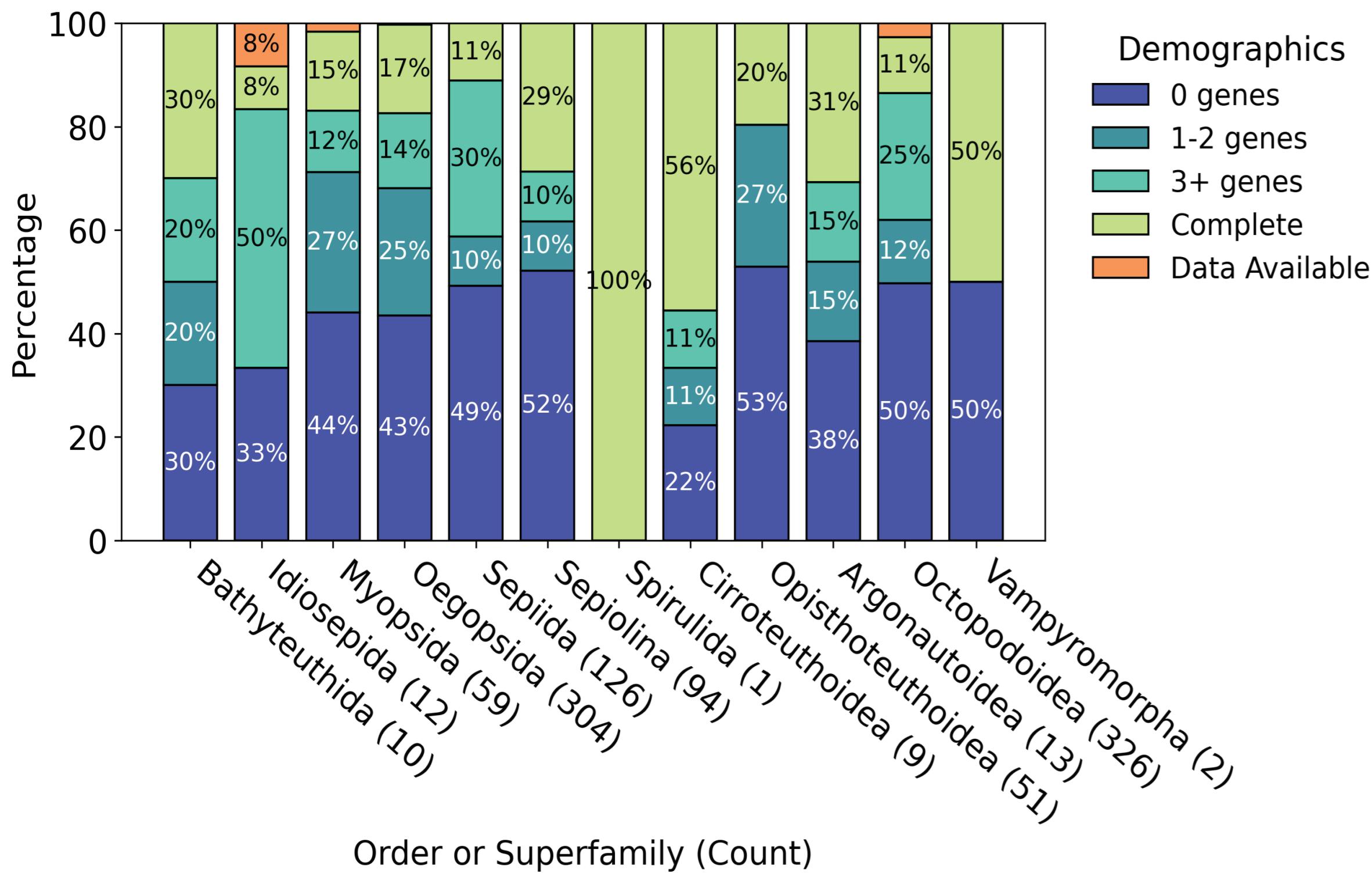
Mitochondrial Genome Construction

- Process sequencing/assembly data through GetOrganelle⁴
- Annotate assembly utilizing MITOS2
- Verify gene boundaries with closely related species

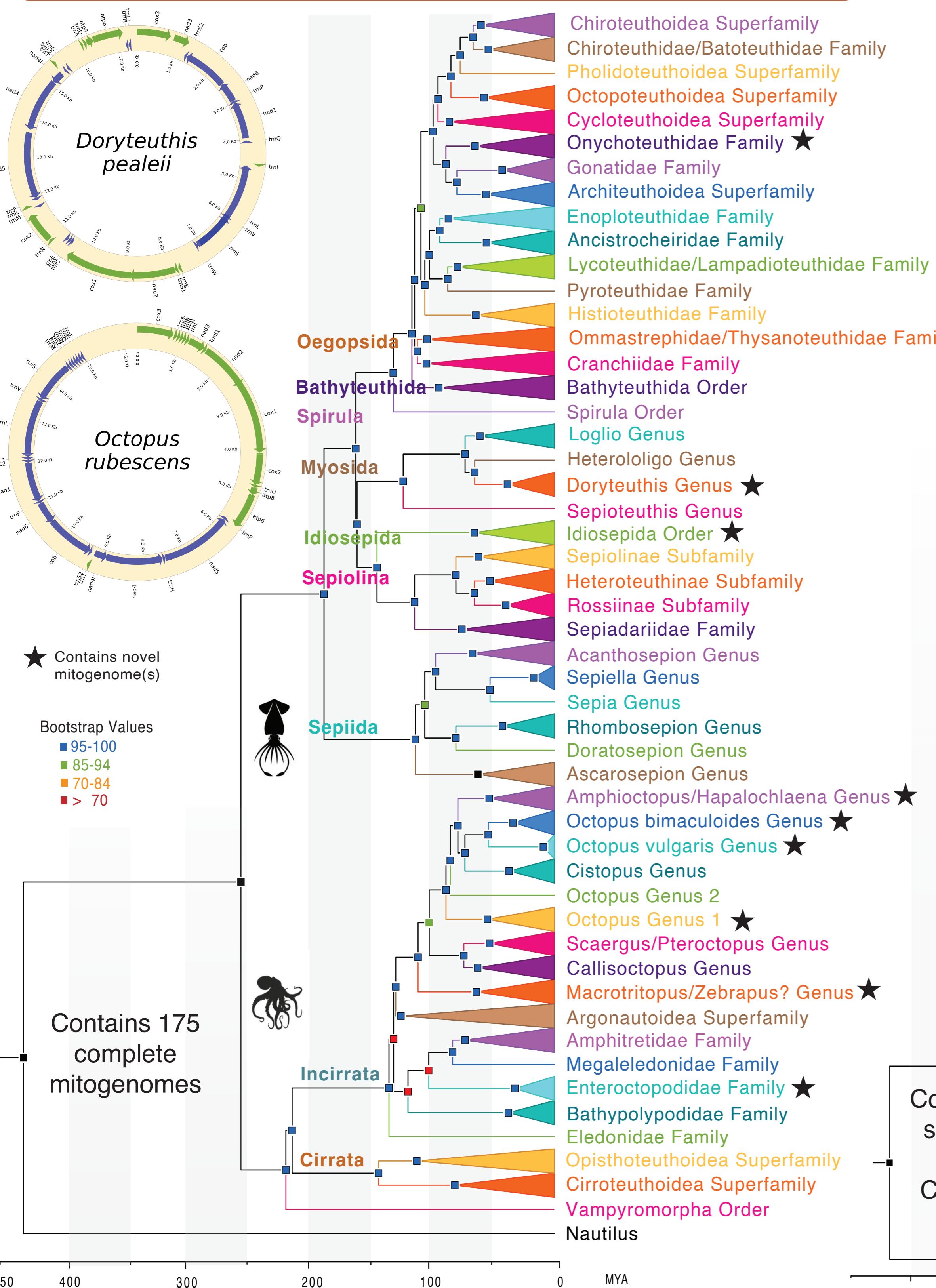


RESULTS

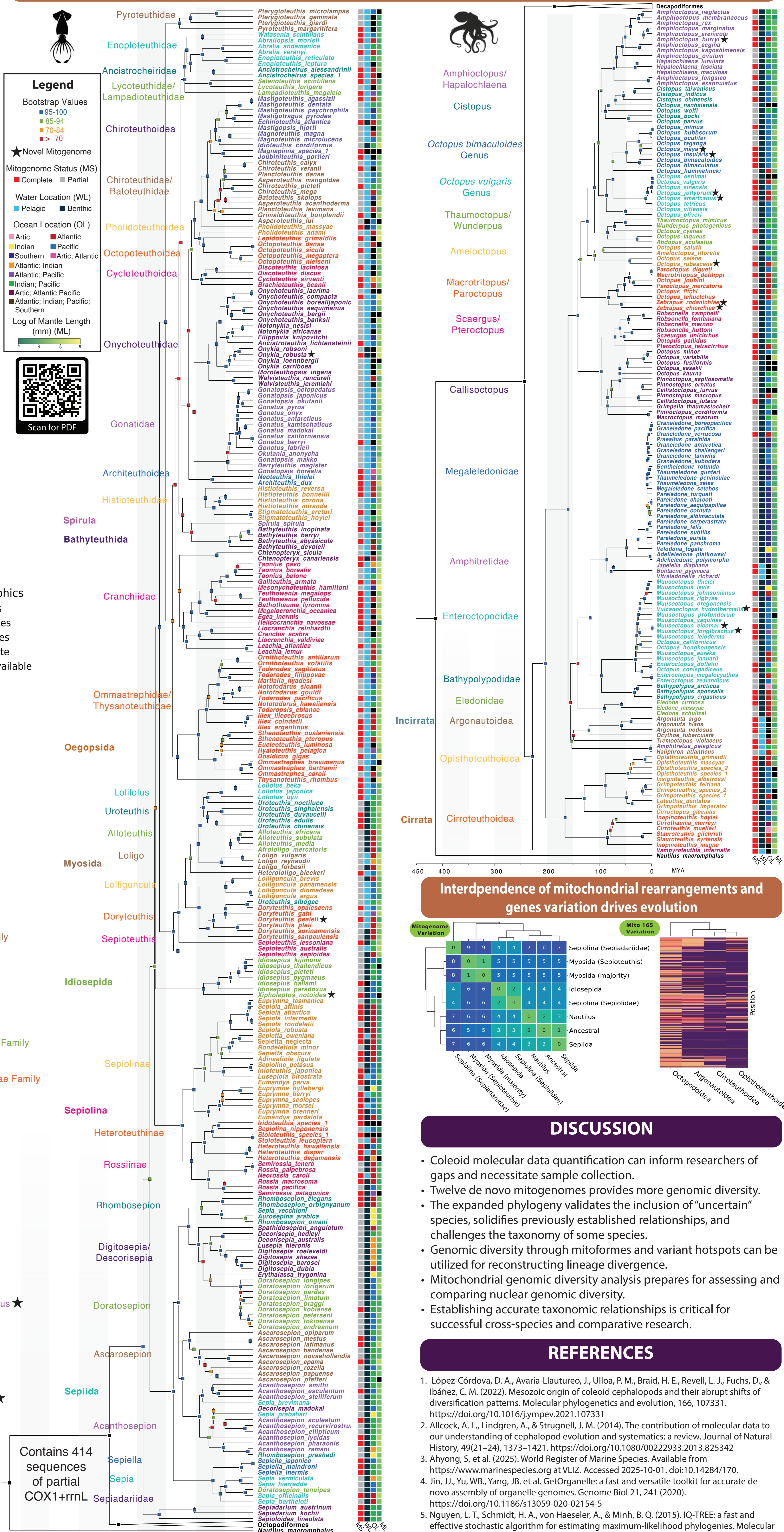
Mitochondrial genomic mining reveals approximately half of coleoids have available data



De novo mitogenome assemblies offer more diversity in complete mitogenome phylogeny



Established morphological and ecological diversity parallels mitochondrial molecular diversity



DISCUSSION

- Coleoid molecular data quantification can inform researchers of gaps and necessitate sample collection.
- Twelve de novo mitogenomes provides more genomic diversity.
- The expanded phylogeny validates the inclusion of "uncertain" species, solidifies previously established relationships, and challenges the taxonomy of some species.
- Genomic diversity through mitoforms and variant hotspots can be utilized for reconstructing lineage divergence.
- Mitochondrial genomic diversity analysis prepares for assessing and comparing nuclear genomic diversity.
- Establishing accurate taxonomic relationships is critical for successful cross-species and comparative research.

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