

Creation of a Species-Level Cephalopod Phylogeny to Resolve Major and Minor Clades



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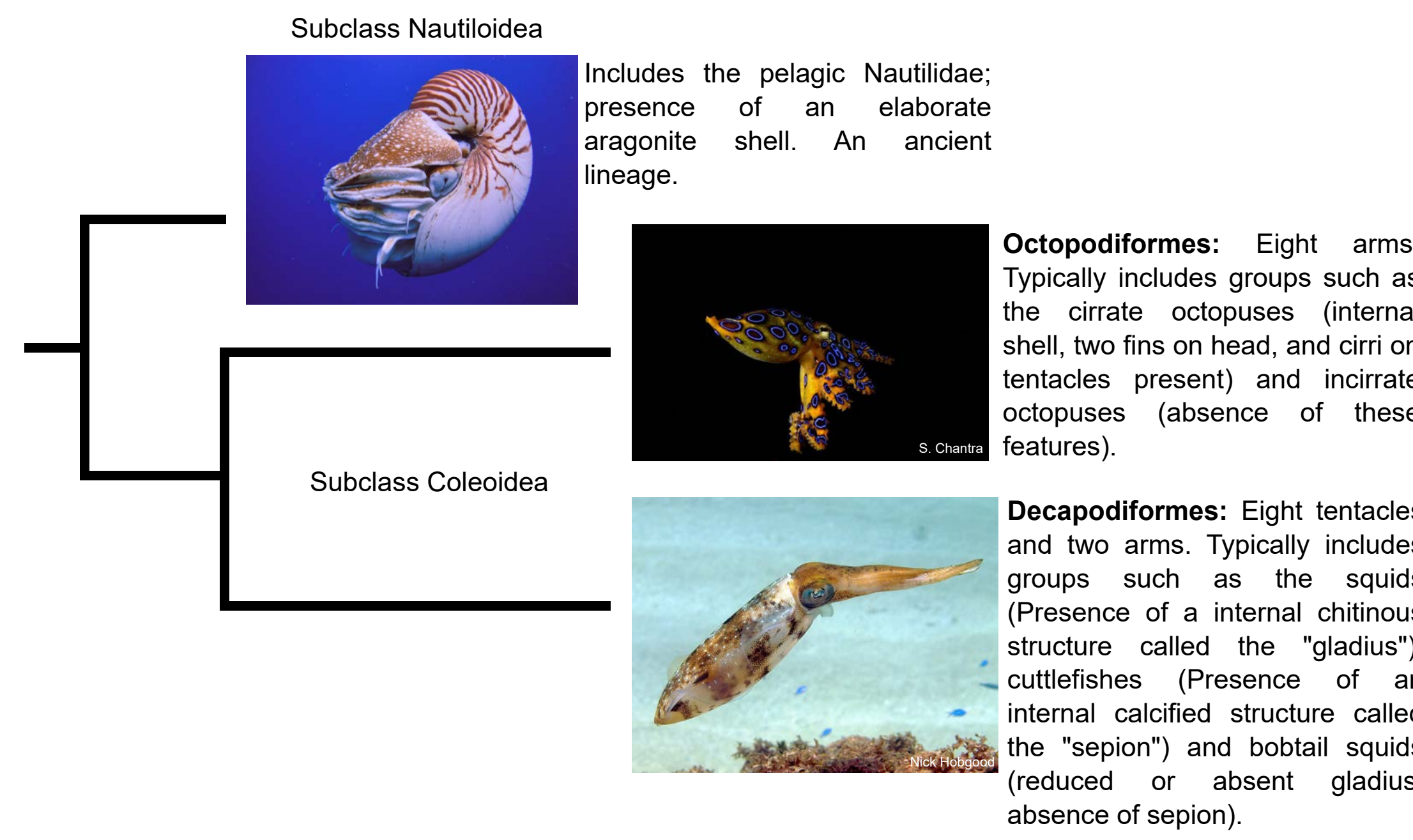


Introduction

Cephalopods (Mollusca : Cephalopoda) are a diverse Class of marine invertebrates consisting of over 800 described species.

The systematic relationships of and between many clades of cephalopods are still unclear, demonstrating the need for a robust phylogeny.

Major Cephalopod Lineages



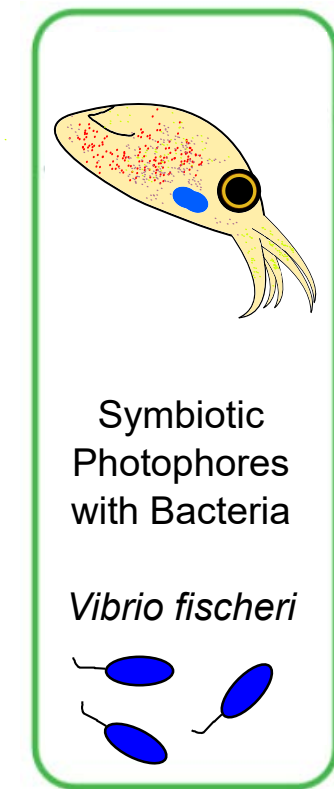
Previous studies' phylogenies are often poorly resolved, meaning that the relationships shown in the phylogeny are not highly probabilistic. In addition, poor taxon sampling and inadequate sampling strategies, such as picking one species to represent a genus, lead to inaccurate groupings.

Resolving the evolutionary relationships within a group forms the basis for studying ecological strategies that influence its diversification, complex trait evolution, and predicting how species will respond to anthropogenic stressors.

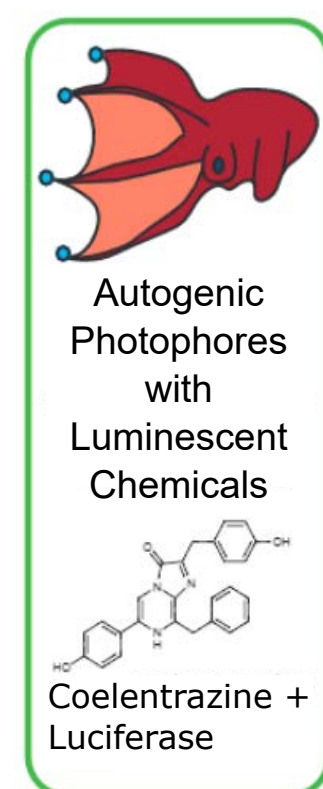
Bioluminescence: A Complex Trait

Complex traits functionally integrate many genes while simple traits use a few genes. Bioluminescence, the biological production and emission of light, involves complex morphological and physiological specialization. Photophores are specialized organs containing bioluminescence-producing structures, molecules, or symbionts. Many cephalopods are bioluminescent, which they use for defense, courtship, prey-capture, and more.

Symbiotic bioluminescence: Light is produced by symbiotic bacteria living within the photophore.



Autogenic bioluminescence: Light is produced by the organism itself, through a chemical reaction.



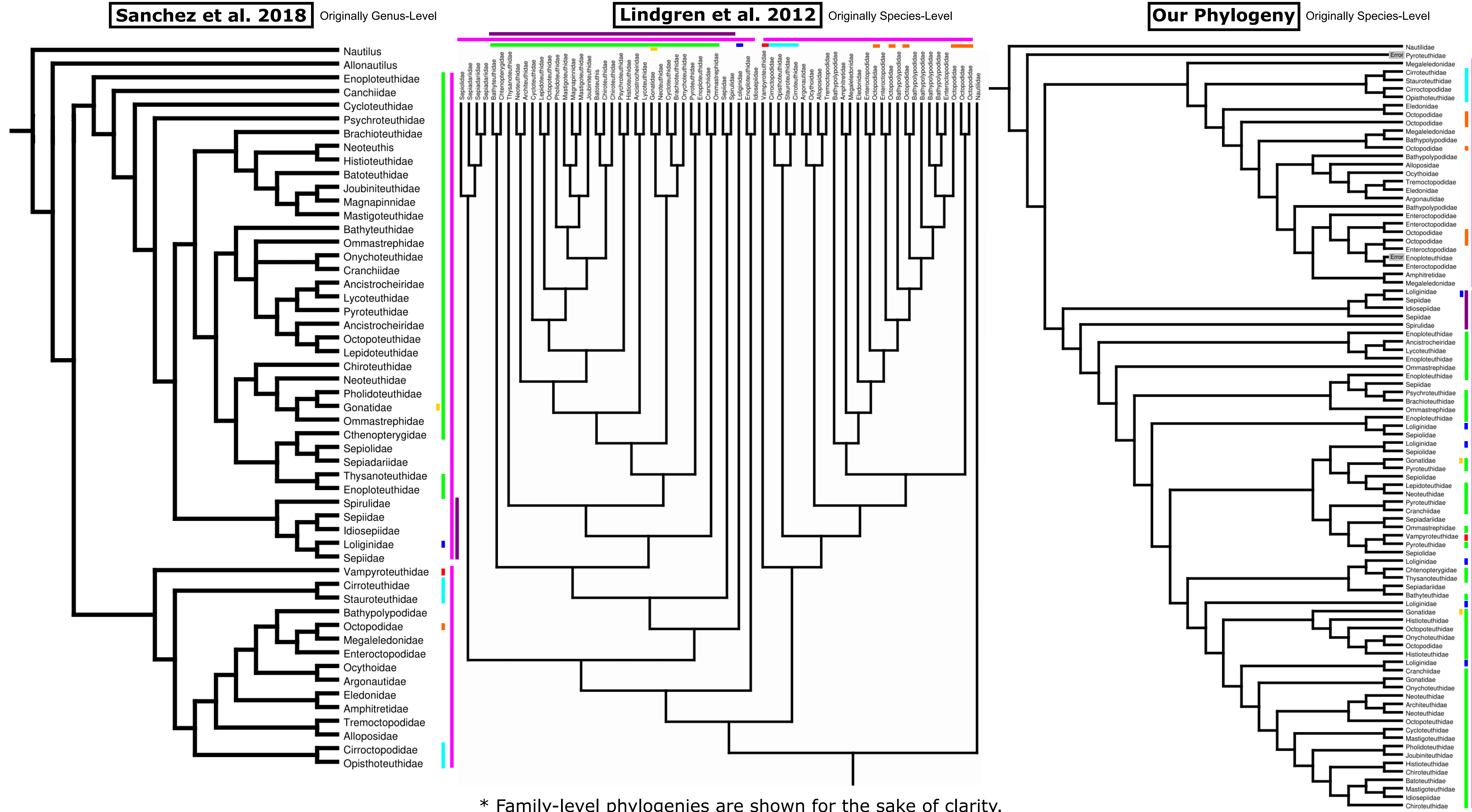
Objectives

- Resolve problematic relationships within Cephalopoda by creating a species-level phylogeny to assess major and minor clades.
- Compare the placement of major and minor clades in our phylogeny to other published phylogenies.
- Use this phylogeny as a tool to form and test phylogenetic hypotheses.

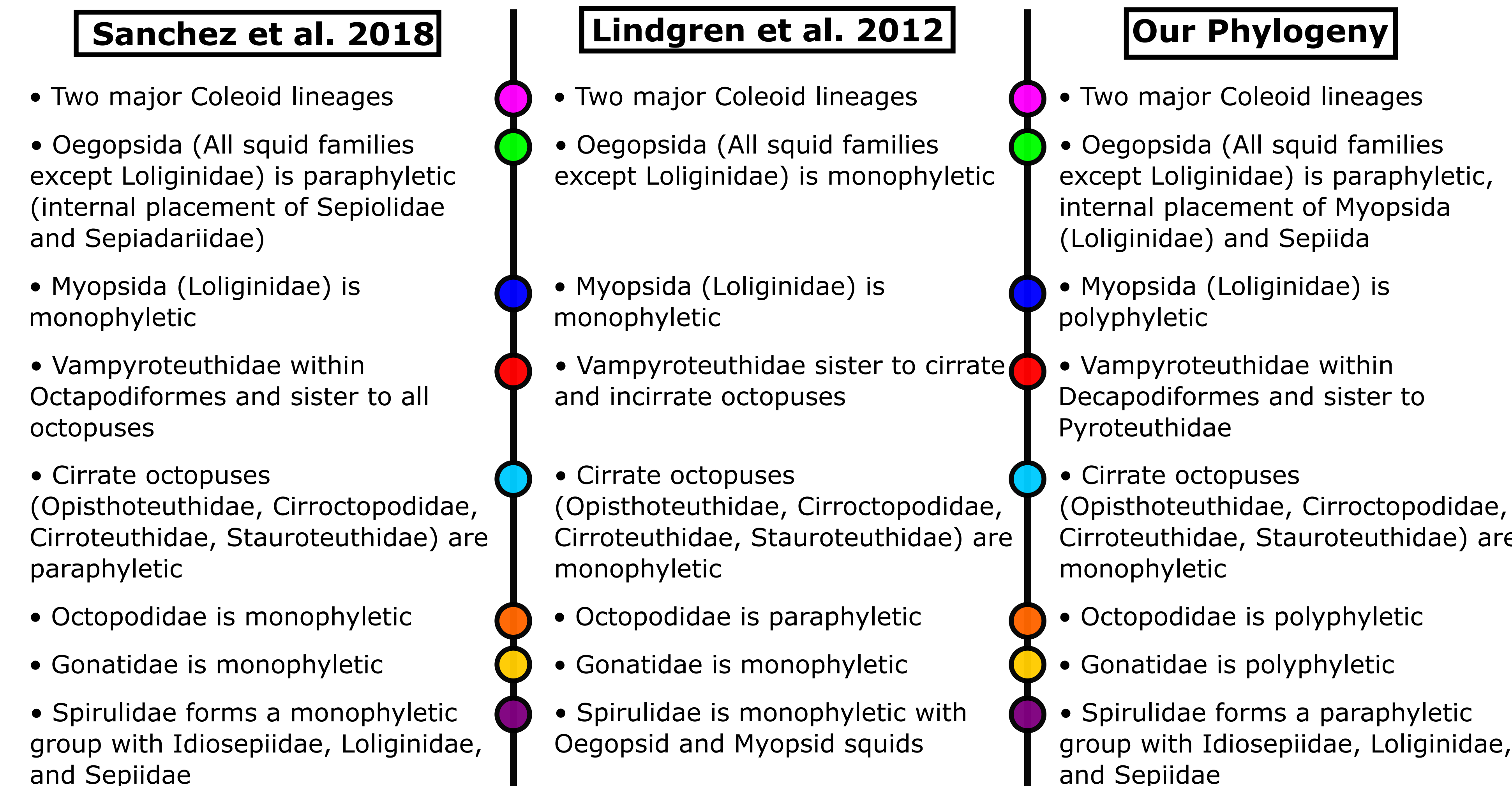
Methods for Phylogenetic Reconstruction

Publicly available short-read genetic data from NCBI was used, with the following molecular markers being used: *12S*, *16S*, *28S*, *actin*, *COI*, *COIII*, *Cyt-b*, *histone*, *myosin*, *ODH* (octopine dehydrogenase), *Pax-6*, *rhodopsin*, *18S* spacer region. The following programs were used: MAFFT, a multiple sequence alignment program, was used to create gene family alignments; IQ-TREE to create gene trees, and ASTRAL to concatenate the gene trees into one species tree.

Phylogenetic Analysis



Results



Discussion and Future Directions

- We found that while aspects of our phylogeny agree with some previous studies, the relationships within Cephalopoda become complicated when analyzed at the species level.
 - There is some agreement with previous studies, such as the recovery of two major Coleoid lineages and the monophyly of the cirrate octopuses.
 - Several major clades such as Oegopsida, Myopsida, and Octopodidae are not monophyletic and are in need of further taxonomic revision.
 - We show different placements of other minor clades such as Spirulidae, Vampyroteuthidae, and Gonatidae. The placement of the Vampyroteuthidae within the Decapodiformes disagrees with its placement in the two other studies analyzed.
 - We are using this phylogenetic framework to conduct ancestral state reconstruction of bioluminescence to determine the number of times this trait originated within Cephalopoda.
 - We can use this phylogeny to study the predictability and repeatability of evolution and the evolutionary dynamics of complex traits.
- Relevant literature:**
1. Lindgren, A. R., Pankey, M. S., Hochberg, F. G., & Oakley, T. H. (2012). A multi-gene phylogeny of Cephalopoda supports convergent morphological evolution in association with multiple habitat shifts in the marine environment. *BMC evolutionary biology*, 12(1), 129.
2. Sanchez, G., Sotomayor, D. H., Tuanapaya, S., Tongthorn, K., Winkelmann, I. E., Schmidbaur, H., ... & Gleadall, I. (2018). Genus-level phylogeny of cephalopods using molecular markers: current status and problematic areas. *PeerJ*, 6, e4331.
- Acknowledgements:** I would like to extend a sincere thank you to Bridget Vincent and Emily Lau for their mentorship, and to Dr. Todd Oakley for his wholehearted support. Use was made of computational facilities purchased with funds from the National Science Foundation (CNS-1725797) and administered by the Center for Scientific Computing (CSC). The CSC is supported by the California NanoSystems Institute and the Materials Research Science and Engineering Center (MRSEC; NSF DMR 1720256) at UC Santa Barbara.