Phylogenetic, phylogeographic, and taxonomic insights into New Zealand's bathymodioline mussels (Bathymodiolinae)

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High regional endemism displayed in deep sea taxa suggest that understudied regions of the world may host a variety of previously unrecognized species. Nearly 95% of New Zealand's exclusive economic zone (EEZ) contains deep ocean, yet it is vastly unexplored and the true species richness of this region is unknown. Mussels of the subfamily Bathymodiolinae exploit deep sea chemosynthetic habitats including hydrothermal vents, cold seeps, and organic falls by harboring gill-borne symbionts that metabolize inorganic compounds such as hydrogen sulfide. Phylogenetic analyses suggest fall obligate bathymodioline mussels are ancestral to the subfamily, and organic falls were exploited as evolutionary "stepping stones" to reach derived deep sea habitat including vents and seeps. Organic falls and their obligates are therefore crucial to understand the evolutionary history of Bathymodiolinae yet are comparatively understudied and taxonomically messy. Using fall obligate bathymodioline mussels collected in the New Zealand EEZ, I will apply a multi-gene approach to construct a robust, molecular dated phylogeny that allows interrogation of phylogenetic and phylogeographic patterns. Preliminary sample processing and phylogenetic analyses suggest multiple novel linages of bathymodioline mussels may be present in New Zealand, supported by unique morphologies and deep lineage splits between taxa. However, further molecular sampling and phylogenetic analyses are still required prior to formal taxonomic descriptions.