Prokaryotic Community Structure and Functional Insights of Cephalopod Gut Microbiomes from the Rio Grande do Sul Shelf-Break

Maria Eduarda Castro do Nascimento, André Oliveira de Souza Lima, Juliano Lauser Coletto, Noemi Petrucci

Área: Pesquisa

Next Generation Sequencing (NGS) has revolutionized the study of microbial communities by enabling direct analysis of environmental DNA, bypassing the need for culturing techniques. This approach is essential for investigating complex ecosystems such as the gut of marine organisms, where a multitude of microbes with diverse ecological functions coexist. Cephalopods, especially squids, are critical components of marine ecosystems, functioning as links between different trophic levels due to their voracious prey consumption and high production rates. Recent studies have shown that cephalopod microbiomes are significantly influenced by the host's phylogeny, habitat, and diet, with unique microbial consortia hosted by each species. Despite their ecological importance, the understanding of cephalopod ecology remains fairly limited. Our study, conducted in collaboration with the Laboratory of Molecular Genetic (LGM) at Univali and the Federal University of Rio Grande (FURG), focuses on the Argentine shortfin squid (Illex argentinus) and the recently reclassified neon flying squid (Ommastrephes cylindraceus). These species were chosen due to their distinct ecological roles and commercial significance. Illex argentinus is a key species in commercial fisheries, contributing significantly to the economy and food supply, while Ommastrephes cylindraceus plays a crucial role in marine ecosystems and sustainable fisheries management. Sampling was conducted along the continental shelf-break off the coast of Rio Grande do Sul, Brazil, a region known for its complex interplay of different water masses including Tropical Water (TW), Coastal Water (CW), Subtropical Water (SW) and Subantarctic Water (SAW). This environment is strongly influenced by upwelling cycles, proximity to the Subtropical Convergence, and freshwater discharge from La Plata River and Patos Lagoon, creating nutrient-rich conditions. These factors significantly impact phytoplanktonic production, prokaryotic microbial communities and ecological dynamics. Samples of digestive content were collected during a deck fishing campaign (part of the INCT-TRIATLAS-II project) between November 21 and November 25, 2023, from three distinct collection stations, representing a range of marine depths and environmental conditions. From the squids gut samples, DNA was extracted and sequencing was performed through the MinIon Oxford Nanopore platform of the 16S rRNA prokaryotic gene, aiming to characterize the composition and diversity of microbial communities, as well as investigate how the microbiome function varies with depth, performing functional prediction analyses to identify possibly occurring metabolic pathways. Our preliminary results demonstrate higher species richness in I. argentinus and shallower depths, as well as a predominance of the order Cellvibrionales, associated with high seasonal abundances in coastal environments. Meanwhile, in O. bartramii there was a lower species richness, with Mycoplasmatales predominating among

samples in higher depths. Functional prediction resulted in metabolism of cofactors and vitamins, biosynthesis of secondary metabolites and lipid metabolism peaking at medium depths (1899 m), more specifically higher carotenoid biosynthesis, carbohydrate metabolism, phenylpropanoid biosynthesis and atrazine degradation were found on medium depths, while bisphenol degradation, limonene and pinene degradation, bacterial toxins and benzoate degradation were higher at shallower depths (1693 m). These results indicate the presence of pollutants across different water masses, as well as a possible influence of deeper water masses influencing medium depths with a nutrient

Palavras-chave: Cephalopods; Gut Microbiome; Continental Shelf-Break

Instituição vínculo: Universidade do Vale do Itajaí (UNIVALI); Laboratório de Genética Molecular (LGM - UNIVALI)
Grupo de Pesquisa: Ciência e Tecnologia Ambiental
Parceiros / colaborações: University of Perugia (UNIPG); Universidade Federal do Rio Grande (FURG)