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RESEARCH

The juvenile Antarctic whelk *Neobuccinum eatoni* maintains a specialized microbiome in its proboscis even in adulthood

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Abstract

Microbiomes are crucial for the health, physiology, and environmental adaptation of marine multicellular organisms. In Antarctica, marine invertebrates have developed unique physiological functions and adaptive strategies to withstand extremely cold and unstable conditions. However, diversity and role of the microbiome of Antarctic mollusks remains largely unexplored. In the present study, we investigated the diversity, and the putative functional role of the microbiome of the proboscis of the whelk *Neobuccinum eatoni*, one of the endemic species that dominate the Antarctic benthic ecosystems. We compared the microbiomes of both juveniles and adults and female and male specimens to understand potential changes across different life stages and the sex of the host. In addition, we investigated the microbiome of *N. eatoni*'s habitat to explore possible transmission pathways between host and environment. Results showed the presence of a microbiome core shared among all the individuals of *N. eatoni,* which remained stable across different life stages and sexes, accounting, on average, for up to 91% of the total microbiome. The core was mostly represented by bacterial members belonging to the genera *Sulfurospirillum*, *Mycoplasma*, and *Polaribacter*. These bacteria are characterized by putative metabolic functions specialized in chemoheterotrophy and the reduction of sulfur compounds, thus supporting *N. eatoni* in the degradation/digestion processes of even the most refractory food sources. In addition, the absence of these bacteria in the sediments of the surrounding environment suggests a vertical transmission of the microbiome through the whelk generations. These findings expand knowledge of the diversity and key role of the microbiome in Antarctic invertebrates providing insights into the microbiome contribution to holobiont survival to polar environments.

Keywords Microbiome · Life stages · *Neobuccinum eatoni* · Antarctica

Introduction

Over the past two decades, the widespread application of -omics and microbiological approaches has advanced our knowledge of the close relationships between marine organisms and their microbiome, highlighting its key role in host life (McFall-Ngai et al. 2013; Apprill 2017). A growing body of research underscores, indeed, the microbiome's role as a dynamic component of marine organism physiology (e.g., life stages, sex, health state, feeding activity; Jackson et al. 2018; Chiarello et al. 2018; Carrier et al. 2018, 2021; McQueen et al. 2023; Velasquez et al. 2023), ecological interactions, and survival in a rapidly changing ocean (Pantos et al. 2015).

Microbiota associated with marine organisms can vary, not only with the physiology of the host and environmental conditions but also in different body organs and tissues (e.g., gut, skin, gills), suggesting specialized functions (Verhoeven

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et al. 2017; Jackson et al. 2018). For example, gut-associated microbes may primarily be involved in nutrient processing, while skin or gill-associated microbiota may play a more significant role in host defense against pathogens and interaction with the external marine environment (Aronson et al. 2017; Legrand et al. 2018; Bennice et al. 2024). This body region-specificity of microbiomes can also provide insight into their origin or source, as microbiota may be acquired from the environment, shaped by the host's diet and digestive processes (Carrier et al. 2021; Velasquez et al. 2023), or transmitted vertically from parents to offspring (Bright and Bulgheresi 2010; de Oliveira et al. 2020).

Host-microbiome associations may also be crucial in coping with the extreme conditions of Antarctic ecosystems (González-Aravena et al. 2016; Herrera et al. 2017; Papale et al. 2020; Buschi et al. 2023) where subzero temperatures, extensive sea ice coverage, and prolonged periods of darkness during the polar winter can affect food webs (Chown et al. 2015; Wing et al. 2018; Rossi et al. 2019; Griffiths et al. 2024). Recent investigations have even revealed the key role of microbiome in the resistance to freezing in Antarctic polychaetes (Buschi et al. 2024).

In Antarctica, mollusks, especially bivalves and gastropods, represent one of the most abundant biological components of benthic habitat (Griffiths and Waller 2016). In particular, Antarctic gastropod mollusks include the endemic *Neobuccinum eatoni* (Smith 1875), which inhabits both hard and soft substrates at depths ranging from 4 to 2350 m in the entire continent (Schiaparelli et al. 2006; Norkko et al. 2007). During the juvenile stage, whelks belonging to *Buccinidae* family, not yet being specialized predators, feed exclusively on carrion, including prey recently killed by their conspecific adult snails (Averbuj et al. 2012). As it matures, the adult whelk shifts its feeding strategies to dual behavior, acting both as a scavenger, feeding through its proboscis on seabed carcasses, and as a predator, primarily preying on filter-feeding bivalves like *Adamussium colbecki*, *Laternula elliptica*, and *Limatula hodgsoni* (Norkko et al. 2007; Aldea et al. 2008). This trophic flexibility allows it to adapt to the variability of food resources in the cold benthic ecosystems of Antarctica (Norkko et al.2007; Aldea et al. 2008).

Despite the important role that *N. eatoni* plays in Antarctic ecosystems, no study to date has investigated its microbiota across different life stages and according to different feeding strategies.

Mollusks rely on mutualistic relationships with microbes to survive and perform their ecological functions (McFall-Ngai 2014; Dar et al. 2017) such as nutrition and digestion (Aronson et al. 2017) and energy generation through chemosynthesis (Goffredi et al. 2004; Duperron et al. 2013). Such associations have been also documented in extreme environments like deep-sea vents and cold seeps, which are inhospitable to many other animals due to anoxic conditions and high hydrogen sulfide concentrations (Distel 1998; Ritt et al. 2012).

Microbiomes may enable some mollusks to digest unusual food sources, allowing hosts to adapt to metabolically challenging environments. For instance, the snail *Rubyspira osteovora* is one of the few organisms which are thought to rely exclusively on organically enriched bones using its specific microbiome to digest those (Aronson et al. 2017).

Exploring the microbiome of Antarctic invertebrates not only enhances our understanding of microbial diversity but also provides information on how it contributes to survival of their hosts in Antarctic ecosystems.

The present study aims to explore, for the first time, the microbiome (through metabarcoding of 16S rRNA genes) of the proboscis of the whelk *N. eatoni* in the coastal habitats of Tethys Bay (Ross Sea, Antarctica) to assess its diversity and putative functions across different whelk life stages (juveniles and adults) and sexes (males and females). Since it has been documented that microbiome of marine invertebrates can be transmitted and selected from the environment/preys through the oral/buccal apparatus (Tiede et al. 2017; Carrier et al. 2018, 2021; Benvenuti et al. 2024), this study also investigated potential horizontal transmission pathways from surrounding habitats, through the concurrent analysis of the microbiome of the *N. aetoni* habitat.

Material and methods

Study area and sample collection

Sampling activity was carried out during the XXXIV Italian Expedition in Antarctica at Terra Nova Bay (Ross Sea) in the framework of the Italian National Program of Antarctic Research (PNRA) in January 2018. A total of 10 specimens of the Antarctic whelk *Neobuccinum eatoni* were collected by scuba diving at around 25 m water depth in Tethys Bay (74°42.068' S; 164°02.514' E), a 3 km-long bay, next to the Mario Zucchelli Station, in the Ross Sea area (Fig. 1). Surficial sediment (the first 3 cm; n = 3) was also collected concurrently with *N. aetoni* specimens.

Since the Ross Sea is a marine protected area (CCAMLR 2016; Worm et al. 2017), we collected the lowest number of whelks necessary to produce a reliable dataset. Tethys Bay is a partially rocky and muddy area with scarce benthic vegetation, characterized by marked seasonality in sea ice dynamics, with coverage generally persisting until mid-December, leaving the area ice-free during the austral summer. This creates marked spatio-temporal variations in food availability for benthic communities, leading to shifts in resource use and transfer across food webs, and influencing their feeding strategies (Pusceddu et al. 1999; Calizza et al. 2018). Specimens were preserved in RNA later and stored at

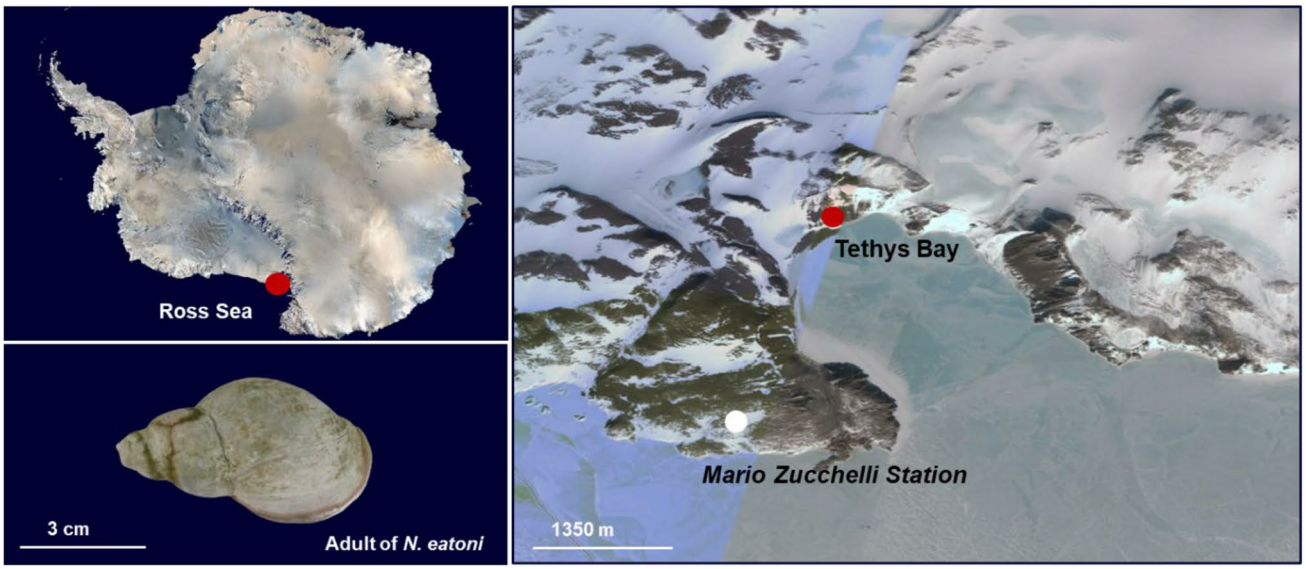


Fig. 1 Maps showing the location of Tethys Bay, within the Ross Sea, where the individuals of *Neobuccinum eatoni* investigated in this study were collected

− 20 °C both for taxonomic identification and microbiome characterization. Samples of surrounding sediments were collected using plexiglass cores and stored at − 20 °C (Buschi et al. 2023).

Morphological identification of *Neobuccinum eatoni* individuals

Individuals of *N. eatoni* were morphologically identified using dichotomous keys described according to Smith (1875) and the distinction between adults and juveniles was carried out measuring their size. In particular, shell length was measured from the apex of the shell to the hollow of the siphon, while shell width was measured at the level of the largest coil of the shell, following the horizontal axis perpendicular to the length. Four specimens were considered juveniles while six were adults. In the four juveniles, the shell length was 2–3 times shorter than that of adults and no reproductive organs were identified. In the adults, the presence/absence of a penis was used to determine the sex. All individuals of *N. eatoni* considered in this study are described in Table S1.

Molecular analysis of the microbiome associated with *Neobuccinum eatoni*

The external part of the proboscis (around 5 mm) from each individual of *N. eatoni* was used to extract DNA, through the Qiagen DNeasy Blood and Tissue Kit with a slight modification of manufacturer's instructions (i.e., extended incubation with proteinase K at 56 °C overnight to better lyse the outer sea star tissues). PCR amplifications were performed using the bacterial primer set 341 F: (5′-CCT ACGGGNGGCWGCAG- 3′) and 785R (5′-GACTAC HVGGGTATCTAAKCC-3′) identified by Klindworth et al. (2013) on an approximately ~400 bp fragment of the hypervariableV3 and V4 region of the 16S rRNA gene. The reaction mixture consisted of 37.5 µL of filtered and autoclaved Milli-Q water, 10 µL of 5× My Taq Reaction Buffer (Bioline), 0.25 µL of each primer (100 µM), 1 µL of My Taq HS DNA Polymerase (5 U/µL concentration), 1 µL of DNA extracted. The thermal cycling consisted of 2 min at 95 °C, followed by 35 cycles of 30 s at 95 °C, 30 s at 53 °C, and 45 s at 72 °C, with a final extension of 5 min at 72 °C. Successful DNA amplification was verified by 1% agarose gel electrophoresis using 10.000 × GelRed Nucleic Acid Stain (Biotium), 0.4 gr of agarose, 40 mL of TE Buffer for the gel preparation, and 2 µL of 5× GelPilot DNA Loading Dye (Qiagen), 2 µL of GeneRuler 1 kb DNA Ladder (Thermo Fisher Scientific) for the electrophoresis. The amplified DNA was sequenced on an Illumina MiSeq sequencer using V3 technology (2 × 300 bp) with the same primers used for the PCR amplification at LGC Genomics. Sequencing of a *N. eatoni* juvenile was unsuccessful.

Bioinformatics analysis

Raw sequences were analyzed through the QIIME2 pipeline (version 2019.4; https://qiime2.org/). Paired-end sequence files were loaded, and sequence pairs were analyzed using the DADA2 plugin (Callahan et al. 2016), which infers community composition in each sample by partitioning

sequences according to the respective error models, thus filtering for erroneous reads and chimaeras and resolving minimal variations between prokaryotic taxa; trimming parameters were set at 250 bp for forward-facing reads and 190 bp for reverse-facing reads. Paired sequences were then merged by the pipeline before producing an ASV table. Each sample was subsampled to 8040 sequences, the lowest number of sequences obtained among the samples, thereby obtaining a rarefied ASV table. The rarefied ASV table was used to generate the rarefaction curves and as input for the subsequent α diversity analyses. To infer the taxonomic affiliation of ASVs, a taxonomic classifier was first trained on the SSU region amplified by the primers utilized in the present study on the SILVA reference database v138 and then used on the ASVs identified (Quast et al. 2012). To compare the microbiomes associated with individuals of *N. eatoni* and those living in the surrounding sediments, sequences of microbiomes living in Tethys Bay, collected in the same expedition, and published by Buschi et al. (2023) were considered. To predict the relevant potential functions of microbiomes associated with *N. eatoni* and those living in the sediments a functional annotation using FAPROTAX database (Louca et al. 2018) was performed. This database maps prokaryotic taxa to putative functions using information based on functional annotations of cultivated representatives.

Statistical analyses

Significant differences (p-values < 0.05) were highlighted through a permutational analysis of variance (PERMANOVA) included in the PRIMER-E 6 software (Anderson et al. 2008), considering the factors *Life stage* (juvenile *vs* adult), *Sex* (male *vs* female) and *Source* (whelk *vs* sediment) in the diversity indices, the taxonomic composition (at the ASV and genus level) and putative functions of microbiomes of individuals of *N. eatoni* and surrounding sediments. A Bray Curtis similarity matrix, based on Square Root-transformed data of microbiome taxonomic composition at ASV level, was used to (1) identify the main ASVs responsible for differences between adults and juveniles through Simper analysis and (2) visualize the microbiome assemblage structure of *N. eatoni* individuals using a PCO analysis, where the ASVs identified by the Simper analysis were highlighted as vectors. Comparisons in taxonomic composition at the genus level and in putative functions of microbiomes between *N. eatoni* individuals and surrounding sediments were performed using the statistical packages provided by the STAMP program (Parks et al. 2014). In particular, heatmaps used to visualize the results were obtained using ANOVA as a statistical test and Welch's as a post-hoc test. Finally, a Venn diagram showing the shared and exclusive ASVs among the different groups of *N.eatoni* (juveniles, males and females) and sediments was built with the program InteractiveVenn.net (Heberle et al.2015).

Results

The microbiome of the *N. eatoni* proboscis in juveniles, and male and female individuals

Out of a total of 437,509 sequences, 372,982 sequences were obtained after the denoising and the chimaeras removal. The normalization to 8040 sequences for each sample exhaustively covered the diversity of the microbiome in all the individuals of *N. eatoni* investigated in this study (Supplementary Fig. 1). The number of observed ASVs in the juveniles, and in male and female adults, varied from 32 to 44 (mean value: 36.7 ± 3.2), from 19 to 42 (mean value: 33.7 ± 12.7), and from 29 to 44 (mean value: 37.0 ± 7.5), respectively, with the highest variability of values in the male adults. The values of the Shannon and Pielou's Evenness indices, in the three categories of individuals (juveniles, adult males and females), showed similar patterns to those of ASVs richness (Fig. 2A–C). No significant differences were found in the α-diversity indices considering the different life stages or the sex of the individuals investigated (Table S2). Conversely, significant differences were observed in the microbiome assemblage structure (at the ASV level) of *N. eatoni* between juveniles and adults (p-value < 0.05; Fig. 2D; Table S2). Moreover, on a total of 141 ASVs, 7 were shared in all individuals of *N. eatoni*, representing the core microbiome, whereas 39 and 59 were exclusively found in the juvenile and adult individuals, respectively (Figure S3).

The taxonomic annotation allowed us to identify a total of 38 different bacterial genera. The core microbiome (i.e., bacterial genera shared among all individuals of *N. eatoni*) was composed by 7 ASVs belonging to *Sulfurospirillum*, *Mycoplasma*, *Polaribacter*, *Marinifilum* genera and to *Flavobacteriaceae* family. Overall, they contributed, on average, for 73%, 83% and 79% to the total proboscis-associated microbiome of juveniles, males and females, respectively (Fig. 3B). A higher contribution of bacterial members belonging to *Mycoplasma* and *Marinifilum* was observed in adults than in juveniles (on average 24%, 37% and 32%, and 2%, 3% and 4%, in juveniles, males and females, respectively); conversely, higher abundances of *Sulfurospirillum* and *Flavobacteriaceae* were found in juveniles than in adults (on average 38%, 35% and 35%, and 4.6%, 1.9% and 0.5% in juveniles, males and females, respectively). Interestingly, higher contributions of *Polaribacter* members were observed in juveniles (29%) and females (27%) than in males (17%). The ASVs responsible for the significant differences between juveniles and adults, identified by the SIMPER

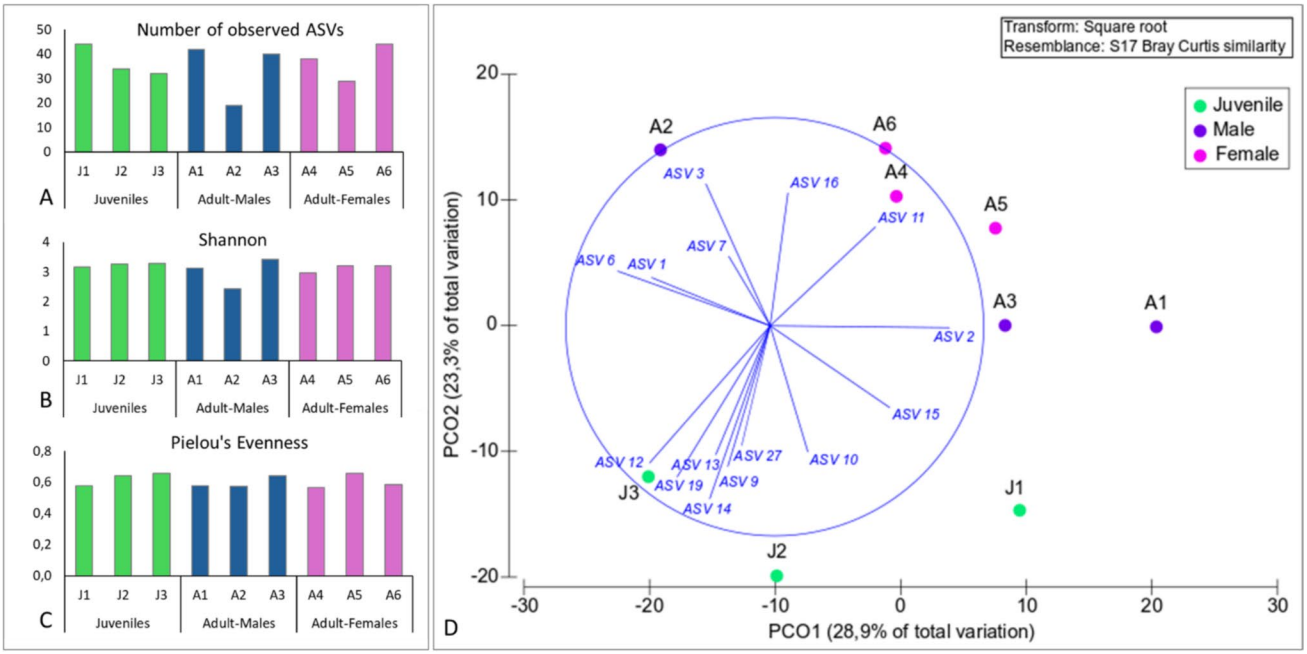


Fig. 2 ASV richness (**A**), Shannon (**B**), Pielou's evenness (**C**) indices of α-diversity and microbiome assemblage structure at ASV level (**D**) calculated on Bray Curtis dissimilarity of microbiomes associated with the proboscis of individuals of *Neobuccinum eatoni* collected in Tethys Bay. Vectors in blue highlighted the ASVs responsible for the main differences between juveniles and adults reported in Table S4

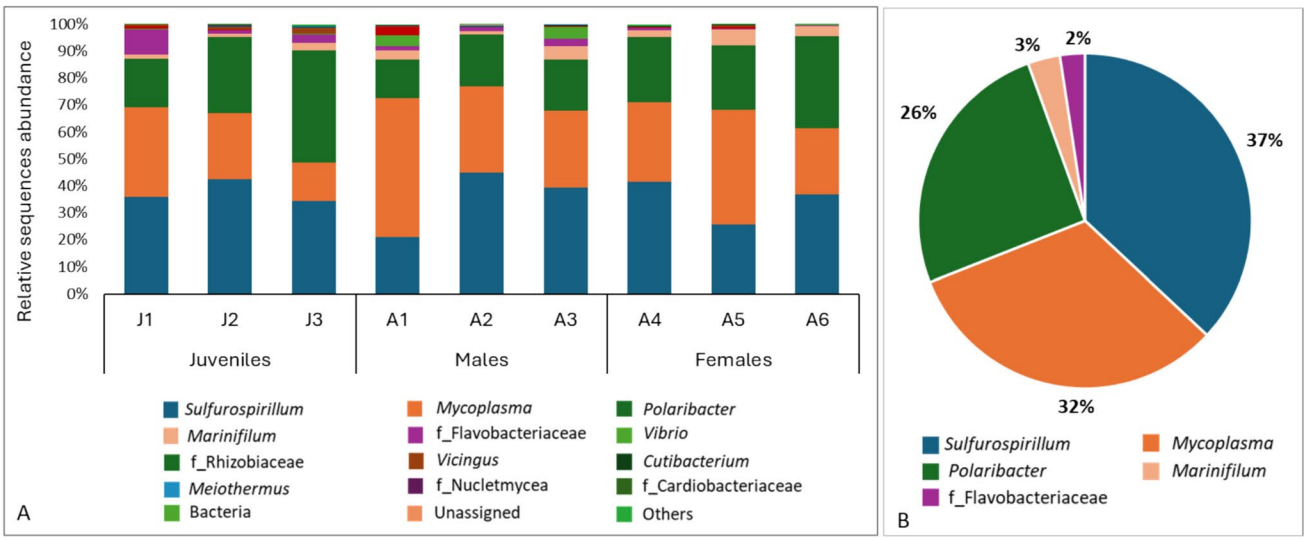


Fig. 3 Relative abundance of sequences of the microbial taxa associated with the different individuals of *Neobuccinum eatoni* (**A**). Others refer to all the bacterial taxa with a contribution of less than 0.2% in each sample. Taxonomic composition of the core microbiome, represented by 7 ASVs shared in all individuals of *N. eatoni* (**B**)

analysis (Fig. 2D), belong to the main bacterial genera that are part of the core (*Mycoplasma*, *Polaribacter* and *Sulfurospirillum;* Table S4). Moreover, the relative abundance of bacterial members of the *Vicingu*s genus accounted, on average, 1.3% in juvenile microbiomes and remained below 0.2% in adults. Bacterial members belonging to *Vibrio* genus in males contributed, on average, for 3% whereas in juveniles and females only for 0.2%.

No significant differences were observed in the putative functions of microbiomes considering the different life stages or the different sexes. In fact, on average 37% and 61% of the microbiomes of the proboscis of all *N. eatoni*

individuals were characterized by putative functions related to sulfur respiration and chemoheterotrophy, respectively (Fig. 4B). A higher contribution of bacteria involved in fermentation and nitrate reduction was observed in the microbiome of males (3%) compared to the microbiome of juveniles and females (on average 0.3%).

The microbiome of the *N. eatoni's* habitat

The most abundant bacterial members found in the sediments surrounding *N. eatoni* individuals belonged to the Cyanobacteria phylum and the genera *Eudorea*, *Lutimonas*, *Blastopirellula*, which contributed, on average, for 9%, 8%, 7% and 5% to the total assemblage, respectively (Fig. 4A). An important contribution was also provided by bacterial members classified as "others" (i.e., relative contribution below 0.2%), which corresponded to the 8% of the total assemblage.

The main putative functions identified in the microbiome of sediments were related to chemoheterotrophy (50%), sulfate respiration (16%) and oxidation of dark hydrogen (15%; Fig. 4B; Fig. S2).

Significant differences were found between microbiomes of *N. eatoni* individuals (in terms of α-diversity, taxonomic composition at the ASV and genus levels and putative functions) and surrounding sediments (p-value < 0.05; Table S2). The microbiomes of the sediments showed 94% dissimilarity with those associated with *N. eatoni*, sharing



Fig. 4 Heatmaps showing the taxonomic composition at the genus level (**A**) and putative functions (**B**) of the microbiomes of *Neobuccinum eatoni* individuals (A1-A3: male adults; A4-A6: female adults; J1-J3: juveniles) and surrounding sediments (S1, S2). "Others" refer to all the bacterial taxa with relative contribution below 0.2%

only 8.5% of the total identified ASVs detected in *N. eatoni* (12 of 141 ASVs; Figure S3). Among those, 7 ASVs were shared exclusively between sediment and adult specimens and 4 ASVs shared exclusively between sediment and juvenile specimens (Figure S3). No ASVs belonging to the core microbiome in *N. eatoni* were detected in the sediments as well as to the dominant bacterial genera that have been detected in the proboscis microbiome (i.e., *Sulfurospirillum, Mycoplasma, Polaribacter, Marinifilum*).

Discussion

There is evidence that the microbiome of marine mollusks can have a key role in the well-being of these organisms (McFall-Ngai 2014; Dar et al. 2017), especially in increasing their metabolic capabilities (Goffredi et al. 2004; Duperron et al. 2013; Aronson et al. 2017) and adaptation to the environmental changes (Wegner et al. 2013). However, information on microbiomes of Antarctic mollusks as well as their transmission pathways are still largely unexplored.

In this study, we investigated the microbiome associated with the proboscis of one of the most abundant mollusks in the Ross Sea, *Neobuccinum eatoni*, to gain insight into diversity (across different life stages and sexes) and potential contribution of microbes in the whelk's predatory and scavenging feeding activities.

The proboscis microbiome was characterized by similar richness and evenness between life stages (juveniles and adults) and sexes (males and females). However, the high number of exclusive taxa in the microbiome of both juvenile and adult whelks suggests a change also in the host's needs and feeding behavior during the transition to adult life. The development of a diversified microbiome in *N. eatoni* proboscis could be associated with changes in predatory strategies during its development and consolidation of the buccal structures (e.g., proboscis, radula; Büchner-Miranda et al. 2021; Le Bourg et al. 2021).

Despite a relevant contribution of exclusive bacterial taxa in the proboscis microbiome of *N. eatoni* juveniles and adults (38 ASVs in juveniles and 58 ASVs in adults, including males and females; Fig. S3), the results of our study highlight the presence of a core microbiome. This core, characterized by bacterial taxa mainly belonging to the genera *Sulfurospirillum*, *Mycoplasma* and *Polaribacter*, represents a major part of the microbiome (on average 79%) of the proboscis of all individuals. This finding indicates that a large portion of the microbiome remains stable throughout the *N. aetoni* life stages.

Among the main bacterial genera found associated with *N. eatoni*, *Sulfurospirillum* is represented by members, often microaerophilic, adaptable to different metabolic conditions, specialized in degrading fermentation products through anaerobic respiration of a wide variety of terminal electron acceptors, including sulfur and nitrogen compounds (Goris and Diekert 2016). They have been detected in several extreme environments such as oil-contaminated sites and hydrothermal vents (van der Stel and Wosten 2019), as well as associated with guts of marine invertebrates (Zhang et al. 2017; Lim et al. 2022). Their versatile energy metabolism may explain their presence in very specific but diverse ecological niches, such as the proboscis of *N. eatoni* investigated in this study.

A relevant contribution to the microbiome by bacterial taxa belonging to the *Mycoplasma* genus (as observed in our study, i.e., 32% on average) appears to be a regular pattern in the microbiome of marine mollusks from different coastal and deep-sea habitats worldwide (Davis et al. 2013; Duperron et al. 2013; Akter et al. 2023; Schoinas et al. 2023; González-Aravena et al. 2024).

Previous investigations have suggested an important role of this genus in host digestion, especially in acquiring energy from refractory food sources (Duperron et al. 2013; Aronson et al. 2017) and in biomass conversion for host growth (Bozzi et al. 2021; English et al. 2023). Specific energy acquisition pathways involving chitin and arginine deiminase have been identified in *Mycoplasma* from the molluscan gut, suggesting its contribution to the host metabolism (Pimentel et al. 2021).

Based on this documented information, we can infer that the relevant contribution of *Mycoplasma* in the microbiome of *N. eatoni*'s proboscis may be associated with host ability to act as a scavenger, feeding on carcasses in the seabed (Norkko et al. 2007).

The bacterial core of the *N. eatoni* proboscis was also represented by a relevant contribution of *Polaribacte*r, whose members are psychrophilic and typically present in polar seawater such as those of the Antarctic Ross Sea (Silvi et al. 2016; Kim et al. 2018; Gui et al. 2021; Cordone et al. 2022). They have also been found in mutualistic association with different marine mollusks (Fernandez-Piquer et al. 2012; Hyun et al. 2014) including gastropods (Kim et al. 2017; Jeong et al. 2022), where they potentially act as organic matter degraders (Lo Giudice et al. 2018; Wang et al. 2024).

The analysis of putative functions in the investigated microbiomes showed that nearly all bacterial taxa associated with the proboscis of *N. eatoni* were involved primarily in sulfur respiration (61%) and in chemoheterotrophy (37%). All these findings, taken together, suggest a specialized role of the *N. buccinum* microbiome in food degradation and digestion processes.

We also found that only 8.5% of the whelk microbiome was shared with the microbiome of the surrounding sediment and, at the same time, it was absent in the microbiome core. Therefore, we can hypothesize that bacterial members of

this microbiome fraction were horizontally transferred or selected from the environment, while core bacteria were vertically transmitted through host generations (Bright and Bulgheresi 2010; Kwan et al. 2017).

Conclusions

Our study provides new insights into diversity and potential role of the microbiome in Antarctic invertebrates. We found that the proboscis of *N. eatoni* is characterized by a specialized microbiome, which remains possibly stable during its different life stages and between male and female individuals, although a minor fraction of bacterial taxa changes during the transition phases from juvenile to adult life. In particular, the proboscis microbiome is dominated by a microbiome core represented by the genera *Sulfurospirillum*, *Mycoplasma*, and *Polaribacter*. These bacterial members are likely to be involved in food degradation/digestion, including the more refractory food utilized by the scavenger Antarctic whelk. Since these bacterial genera were not present in the surrounding sediments, we suggest that the microbiome core of *N. eatoni* proboscis could be primarily acquired through vertical transmission across host generations.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s00300-025-03388-4.

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Author contributions C.C. conceived the study. M.L.M., M.T. collected the samples. E.B. conducted the molecular and bioinformatic analysis. E.B. wrote the first draft of the manuscript, and all authors participated in the writing and revision of the manuscript. All authors have read and agreed to the published version of the manuscript.

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Data availability Sequence data that support the findings of this study have been deposited in Sequence Read Archive under the Bioproject name"PRJNA1175597: Microbiome of proboscis of Neobuccinum eatoni".

Declarations

Conflict of interest The authors declare no competing interests.

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