Enigmatic dual symbiosis in the excretory organ of *Nautilus macromphalus* (Cephalopoda: Nautiloidea)

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Symbiosis is an important driving force in metazoan evolution and the study of ancient lineages can provide an insight into the influence of symbiotic associations on morphological and physiological adaptations. In the ‘living fossil’ *Nautilus*, bacterial associations are found in the highly specialized pericardial appendage. This organ is responsible for most of the excretory processes (ultrafiltration, reabsorption and secretion) and secretes an acidic ammonia-rich excretory fluid. In this study, we show that *Nautilus macromphalus* pericardial appendages harbour a high density of a β-proteobacterium and a cocccoid spirochaete using transmission electron microscopy, comparative 16S rRNA sequence analysis and fluorescence in situ hybridization (FISH). These two bacterial phylotypes are phylogenetically distant from any known bacteria, with ammonia-oxidizing bacteria as the closest relatives of the spirochaete (above or equal to 87.5% sequence similarity) and marine *Spirochaeta* species as the closest relatives of the spirochaete (above or equal to 89.8% sequence similarity), and appear to be specific to *Nautilus*. FISH analyses showed that the symbionts occur in the baso-medial region of the pericardial villi where ultrafiltration and reabsorption processes take place, suggesting a symbiotic contribution to the excretory metabolism.

**Keywords:** symbiosis; cephalopods; *Nautilus*; excretion; bacteria; 16S rRNA

1. INTRODUCTION

The acquisition and maintenance of one or more organisms by another often leads to novel structures and metabolic pathways. Hence, the study of symbiotic systems has resulted in exciting discoveries, such as the role of symbiotic luminescent bacteria in the morphogenesis of the light organ in squid (*Euprymna scolopes*/*Vibrio fischeri* association; McFall-Ngai & Ruby 2000) or in the assimilation of inorganic molecules from hydrothermal vents by giant tube worms (*Riftia pachyptila* with its sulphide-oxidizing symbionts; Cavanaugh et al. 1985; Felbeck et al. 1981).

The evolutionary history of both the partners is also a major component of the symbiotic relationship, symbiosis being an important driving force of metazoan evolution (McFall-Ngai 2002). Therefore, the study of symbiotic associations in ancient lineages might provide an insight into the origin of major physiological adaptations. Thus, the symbiotic associations in the excretory organs of *Nautilus* (Schipp et al. 1985) are of particular interest, as these invertebrates are considered as ‘living fossils’ from the Cambrian (542–500 Myr ago). They are also the only extant cephalopods with an external chambered shell (filled with over 90% nitrogen gas) resembling that of extinct ammonoids (figure 1a; Norman 2000). A better comprehension of their life history, behaviour, ecology, physiology and metabolism is a means of understanding the success and eventual demise of the ammonoids (Boutilier et al. 1996; Staples et al. 2000).

In contrast to other extant cephalopods in which several organs are involved in excretion, in *Nautilus*, only the pericardial appendages are responsible for most of the three excretory processes (ultrafiltration, reabsorption and secretion; Martin 1983). The main end product of excretion is ammonia (Boucher-Rodoni 1989) and the contractile villi of the four pericardial appendages collect the blood from capacious sinuses (figure 1b) and secrete the acidic ammonia-rich fluid (up to 200 p.p.m., Schipp & Martin 1987) into the pericardial coelom from which it is finally excreted into the mantle cavity (figure 1a; Mangold et al. 1989).

Each pericardial appendage consists of numerous finger-like villi that are divided into an apical region covered with microvilli and a basal-medial region with crypt-like invaginations. The basal-medial villus segment is filled with a branched lacunar system (Schipp et al. 1985). An ultrastructural study of *Nautilus* pericardial appendages revealed symbiotic bacteria forming a dense fringe on the outer epithelium of the villi and its baso-medial invaginations (Schipp et al. 1985). Only a single bacterial morphotype was observed with a thin rod shape (0.25–0.35×1.5–2.2 μm) and a typical gram-negative cell wall (Schipp et al. 1990). The presence of bacteria in pericardial appendages, an ecological niche in

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ammonia, has led to several hypotheses about their potential role in the nitrogen metabolism of Nautilus, such as (i) detoxification by the symbionts via ammonia oxidation (Schipp et al. 1990) or (ii) the use of nitrogenous waste by the bacteria to produce the nitrogen gas filling the Nautilus shell and responsible for its neutral buoyancy (Boucher-Rodoni & Mangold 1994).

Nautilus pericardial appendage bacteria were physiologically characterized as Pseudomonodales after their isolation in artificial culture media (Schipp et al. 1990). However, it is now widely acknowledged that culture methods reveal only a small fraction of the total bacterial diversity (Amann et al. 1990; Pace 1997). The aim of the present study was therefore to characterize the symbiotic bacteria in Nautilus macromphalus (Cephalopoda: Nautiloidea) excretory organs using culture-independent molecular approaches. The phylogenetic position of bacteria associated with the pericardial appendages was investigated by comparative sequence analysis of the 16S rRNA gene. Their localization within the organ was determined by catalysed reporter deposition (CARD) fluorescence in situ hybridization (FISH) and transmission electron microscopy (TEM). We also examined the potential function of the bacteria by investigating genes characteristic for nitrogen metabolism, namely amoA, nirS, nirK and nosZ, as respective indicators for aerobic ammonia oxidation, nitrite reduction and nitrous oxide reduction (Braker et al. 1998; Scala & Kerkhof 1998; Kowalchuck & Stephen 2001). The specificity of this bacterial–invertebrate association and its possible implications in Nautilus metabolism are discussed.

2. MATERIAL AND METHODS

(a) Specimen collection
Four N. macromphalus specimens by the method described by Zhou et al. (1996) using protease K for cell digestion and a standard chloroform–isooamyl alcohol extraction procedure. DNA was precipitated in isopropanol, washed with 70% ethanol, resuspended in 1 x TE buffer and stored in aliquots at −20°C.

(b) Transmission electron microscopy
Pericardial appendages from the four individuals were fixed at 4°C for 12 h in a fixative solution containing 3.2% glutaraldehyde in sterile seawater (pH 7.4) and washed in 0.05% of NaN₃ in sterile seawater (pH 7.4). After a brief rinse in 0.1 M pH 7.2 cacodylate buffer, adjusted to 900 mOsm with NaCl and CaCl₂ to improve membrane preservation, samples were fixed for 45 min in 1% osmium tetroxide at room temperature, then rinsed in distilled water, and post-fixed with 2% aqueous uranyl acetate for 1 h before embedding in epon–araldite. Semi-thin sections (0.5 µm thick) and ultra-thin sections (60 nm thick) were obtained using an Ultracut E microtome (LEICA). Transmission electron microscopy analyses were performed on a Philips 201 microscope operated at 75 kV accelerating voltage.

(c) DNA extraction
DNA was extracted from the pericardial appendages of four N. macromphalus specimens using the method described by Zhou et al. (1996) using protease K for cell digestion and a standard chloroform–isoamyl alcohol extraction procedure. DNA was precipitated in isopropanol, washed with 70% ethanol, resuspended in 1 x TE buffer and stored in aliquots at −20°C.

(d) 16S rRNA gene PCR amplification
Bacterial 16S rRNA gene PCR amplification was performed using GM3 (5’-AGAGTTTGATCMTGGCTC-3’) and GM4 (5’-TACCTTGTTACGACTT-3’) bacterial primers (Escherichia coli positions 8–23 and 1492–1477, respectively, Muyzer et al. 1995). The reaction mixture contained 50 pmol of each primer, 6 µg of bovine serum albumin, 200 µM of each dNTP, 10 mM Tris–HCl, 50 mM KCl, 1.5 mM MgCl₂, 0.1% Triton X-100, 0.01% gelatin and 1 U of Taq polymerase in a final volume of 50 µl. The amplification programme consisted of an initial denaturation at 94°C for 5 min, followed by 40 cycles of 94°C for 30 s, 55°C for 30 s and 72°C for 1 min, and a final extension at 72°C for 7 min. The amplified products were analyzed by electrophoresis on a 1% agarose gel and visualized by ethidium bromide staining. The DNA samples were then cleaned using the QIAquick PCR Purification Kit (Qiagen).
albumin, 2.5 μmol of each of deoxynucleoside triphosphate, 1X SuperTaq buffer and 0.2 U of Eppendorf Master Taq (Eppendorf, Hamburg, Germany) and the volume was adjusted with sterile water to 20 μl. PCR reactions were conducted in a thermocycler (Eppendorf, Hamburg, Germany), with an initial denaturing step (96°C for 5 min) followed by 25 cycles at 94°C for 1 min, 45°C for 1 min and 72°C for 3 min and a final elongation step at 72°C for 5 min. PCR bias was minimized by using only 25 amplification cycles and pooling four replicate PCR reactions. Amplified DNA was checked by 1.5% agarose gel electrophoresis and purified with a QiAquick PCR purification kit (Qiagen, Hilden, Germany).

**Cloning and sequencing**

A 16S rRNA clone library was constructed for each of the four Nautilus specimens. Purified PCR products were cloned by an insertion into a plasmid vector PCR4 TOPO TA Cloning (Invitrogen, Carlsbad, CA), following the manufacturer’s instructions. Positive clones were grown overnight in Luria–Bertani medium and E. coli plasmid inserts amplified in a 35 cycle PCR using M13F and M13R primers. The reaction mixture contained 50 pmol of each primer, 6 μg of bovine serum albumin, 2.5 μmol of each deoxynucleoside triphosphate, 1X SuperTaq buffer, 1X Enhancer and 0.2 U of Eppendorf Master Taq (Eppendorf, Hamburg, Germany) and the volume was adjusted with sterile water to 20 μl. The size of PCR products was checked by 1.5% agarose gel electrophoresis.

For each of the four individuals, 87–105 clones were sequenced partially in a variable region of the 16S rRNA gene (E. coli positions from 518 to approx. 1000), and a total of 81 representative clones were fully sequenced in both directions. After sequence assembly and alignment with SEQUENCER v. 4.5 (Gene Codes Corporation, Michigan), putative chimeric sequences were eliminated after analysis with BELLEROPHON (Huber et al. 2004). Sequencing reactions were performed using the BigDye Terminator v. 3.1 Cycle Sequencing Kit from Applied Biosystems on the ABI Prism 3130xl Genetic Analyser (Applied Biosystems, Foster City, Ca).

**amoA, nirK, nirS and nosZ amplification and sequencing**

Functional gene amplification was performed by PCR using specific primers and cycling conditions described by Holmes et al. (1995), Rothhauwe et al. (1997) and Purkhold et al. (2000) for the amoA gene (with A189–A682, AmoA1F–AmoA2R and AmoA3F–AmoA4R as specific primers and Nitrosonomas europa as a positive control), Braker et al. (1998) for the nirK gene (with NirK1F–NirK5R as specific primers and Ochrobactrum anthropi as a positive control) and the nirS gene (with NirS1F–NirS6R as specific primers and Paracoccus denitrificans as a positive control) and Scala & Kerkhof (1998) for the nosZ gene (with Nos661F, Nos2230R and Nos1773R as specific primers and Paracoccus denitrificans as a positive control). Thirty-five PCR cycles were used and PCR products were cloned and sequenced as described previously for the 16S rRNA gene.

**Phylogenetic reconstruction**

Sequences were compared with those in the database by using BLAST (Altschul et al. 1994), FASTA (Pearson & Lipman 1988) and RDP (Cole et al. 2005), and highly similar sequences were included in the analysis. The 16S rRNA sequence data were analysed using the ARB software package (Ludwig et al. 2004; www.arb-home.de) and assigned to a database of approximately 40 000 16S rRNA sequences. Only sequences above 1300-nt were used for alignment and tree construction. Sequence alignment was performed according to the 16S rRNA secondary structure with the Integrated Editor and then corrected manually. Preliminary analysis of 35 full-length sequences of Nautilus symbionts was performed using the quick-add parsimony methods of ARB to select an appropriate dataset. Phylogenetic trees were then reconstructed using distance and parsimony methods with different filter sets (none, termini, ebacteria and β-proteobacteria) on ARB (Ludwig et al. 2004; www.arb-home.de). The 28 sequences were finally analysed by maximum-parsimony (dnapars) and maximum-likelihood (dnaml) methods in the PHYLIP software package (Felsenstein 2002) with bootstrap analyses (1000 replicates) to test the robustness of each topology.

**CARD–FISH**

Pericardial appendage tissues from the four Nautilus specimens were fixed for CARD–FISH in 2% paraformaldehyde in sterile seawater at 4°C for 4 h. After two washes in 1X phosphate buffered saline (PBS: 10 mM phosphate and 130 mM NaCl), samples were stored at −20°C in a 1:1 mixture of 0.5X phosphate buffered saline and 50% ethanol. Fixed tissues were dehydrated in an increasing series of ethanol and xylene and embedded in paraffin. Histological sections (4 μm) were collected on gelatin-coated slides. Paraffin was removed from the sections with xylene (three 10 min treatments), and the sections were rehydrated in a decreasing ethanol series. Hybridization was performed in preheated chambers containing tissue wetted with hybridization buffer (0.9 M NaCl, 0.02 M Tris–HCl, 0.01% SDS, 1% blocking reagent, 10% dextran sulphate and 35% formamide). The sections were covered with a mixture containing 50 ng of horseradish peroxidase-labelled probe in 150 μl of hybridization buffer and then hybridized as described by Pernthaler et al. (2002). The slides were washed with 1X PBS for 10 min, MilliQ water for 1 min, 96% ethanol for 1 min, air dried and covered with an antibleaching agent (e.g. Citifluor AF1, Citifluor Ltd, London) amended with DAPI (final concentration 1 μg ml⁻¹) and a cover-slip. A total of about 120 pericardial appendage sections obtained from the four Nautilus specimens were visually examined for symbiont distribution and relative abundance using a DMLB epifluorescence microscope (Leica Microsystems SAS, France).

A specific probe was designed for each of the two 16S rRNA phylotypes found in N. macromphalus by using the PROBE, DESIGN function of ARB and the 16S rRNA accessibility information provided by Behrens et al. (2003). The specificity was checked by using BLAST (Altschul et al. 1994). The probe specific for the β-proteobacterial symbiont, NauBet66 (5′-AACGTTTCCTCGTTCCG-3′), was labelled with Alexa546 (Invitrogen, Carlsbad, Ca) and the probe specific for the spirochaete symbionts, NauSpiro255 (5′-TGGTACGCCTTACCCTA-3′), was labelled with Alexa647 (Invitrogen, Carlsbad, Ca). Stringency was evaluated at different formamide concentrations (10–50%) and 35% formamide chosen for all hybridizations, as this concentration led to optimal images (high specific signal and low background fluorescence). The general bacteria probe EUB338 (Amann et al. 1990) was used as a positive control and the NON338 probe (Wallner et al. 1993) as a negative control.
Figure 2. Transmission electron micrographs of *Nautilus macromphalus* pericardial appendages with symbiotic bacteria. (a) Transverse section of epithelial invaginations of a pericardial villus. The basal pole of each epithelial cell (EC) constituting the outer excretory epithelium is in contact with a blood lacuna, which is also in contact with ovoid cells (OC) characterized by numerous spherical electron-dense bodies. The apical pole of ECs is covered by bacteria, which are located in the pericardial lumen (lu). (b) Higher magnification of the excretory epithelium. Epithelial cells are characterized by numerous mitochondria (m) and the presence of basal infoldings (mp) in contact with the blood lacuna (BL). Bacteria (arrows) are observed either in contact with the microvilli (mv) of the apical pole or in the pericardial lumen (lu). N, nucleus; OC, ovoid cells. (c) Details of active transporters next to the blood lacunae. The basal pole of the epithelial cells possesses numerous podocyte-like structures (p) in contact with a strong basal lamina surrounded by mitochondria (m). These structures could represent an active ultrafiltration barrier consuming a large amount of energy provided by the mitochondria. BL, blood lacuna; bl, basal lamina. (d) Details of the inset in photo (a): distribution of symbiotic bacteria in the pericardial lumen. Two morphotypes of bacteria can be observed in TEM sections (identified by CARD–FISH as β-proteobacteria and spirochaetes; figure 4). The larger bacterial morphotype (white arrows) is located in the lumen or between the microvilli differentiated by the epithelial cells (EC), whereas the smaller bacteria are observed as small transverse sections in the lumen or as elongated bacteria with a parallel orientation to the microvilli (mv, black arrows). (e) Details of the spirochaete symbionts. The spirochaetes (s) possess the typical double membrane of gram-negative bacteria and are located between the microvilli (mv) of the epithelial cells (EC). m, mitochondria. (f) The β-proteobacteria symbionts are attached to the apical part of the microvilli (mv). These bacteria have a parallel orientation to the microvilli of the epithelial cells. They are characterized by bipolar appendages (black arrows). Inset: details of the polar appendage with a dense central filament. This appendage seems to be in contact with the microvilli through glycocalix fibres.
Table 1. Number of partial (from nucleotide 518 to approx. 1000 based on E. coli numbering) and nearly full 16S rRNA gene sequences (approx. 1450 nucleotides) obtained from cloned PCR products amplified from pericardial appendage DNA of four Nautilus macromphalus specimens.

<table>
<thead>
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<th>specimen source</th>
<th>number of partial sequences</th>
<th>number of full sequences</th>
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<tr>
<td></td>
<td>β-proteobacteria</td>
<td>Spirochaeta</td>
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<td>54</td>
</tr>
<tr>
<td>N2</td>
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<td>total</td>
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(i) *Nucleotide sequence accession numbers*  
The EMBL accession numbers for the two sequences described in this paper are AM399076 (β-proteobacteria) and AM399077 (spirochaetes).

### 3. RESULTS

(a) **Transmission electron microscopy**

Ultrastructural observations of pericardial villi in the baso-medial region showed an epithelial layer of excretory cells and a branched lacunar system (figure 2a,b). This epithelium was characterized by a polar organization consisting in (i) ‘labyrinth structures’ characteristic of active transporters next to the blood lacunae in the basal part (figure 2c), (ii) a high density of mitochondria in the medial part, and (iii) an apical border of high microvilli (figure 2d). Higher magnification confirmed a high density of extracellular bacteria associated with the microvilli, with two bacterial morphotypes regularly observed (figure 2d). In almost all the tissue sections examined, the cocccoid-shaped bacterium (1.53 ± 0.20 × 0.8 ± 0.07 µm) was located basally within the microvilli (figure 2e), while the rod-shaped bacterium (0.23 ± 0.06 × 2.2 ± 0.39 µm) appeared more apically attached by fine filamentous material to the microvilli (figure 2f).

(b) **Bacterial diversity and phylogeny**

Comparative bacterial 16S rRNA gene sequence analysis of a total of 385 partially sequenced and 81 fully sequenced clones from four *Nautilus macromphalus* pericardial appendages revealed two distinct bacterial phylotypes (table 1) with low sequence variation within each phylotype (below 0.4%). Phylogenetic analyses placed the two phylotypes within two phylogenetically distinct bacterial groups, the β-proteobacteria and the *Spirochaeta* (figure 3). Neither phylotype is closely related to symbionts from other hosts species or to free-living bacteria (below 90% sequence similarity) and they appear to be specific to their host.

The *Nautilus macromphalus* β-proteobacterial symbiont is phylogenetically associated with a clade of free-living, ammonia-oxidizing bacteria from the family Nitrosomonadaceae with *Nitrosospira multiformis* and *Nitrosospira briensis* (Teske et al. 1994) as its closest relatives (87.5 and 87.4% sequence similarity, respectively). This phylogenetic affiliation is not strongly supported by bootstrap values (below 60%), but remained stable using different tree-building algorithms (parsimony and maximum likelihood) and filter sets (Hillis & Bull 1993).

The *Nautilus macromphalus* spirochaete symbiont belongs to a monophyletic group that includes free-living spirochaetes and symbionts of gutless marine oligochaetes. Within this group, the *Nautilus macromphalus* spirochaete symbiont forms a highly supported clade (bootstrap value above 99% in all treeing methods) with two free-living spirochaetes: *Spirochaeta bajacaliforniensis* (Fraisek & Stolz 1985) and *Spirochaeta smaragdinae* (Magot et al. 1997; 89.8 and 83.5% sequence similarity, respectively). Numerous attempts to amplify genes characteristic for aerobic ammonia oxidation (*amoA*), nitrite reduction (*nisSK*) and nitrous oxide reduction (*nosZ*) were unsuccessful, despite the use of a wide array of different conditions and successful amplification of these genes in positive controls.

(c) **In situ identification**

Examination of pericardial appendage longitudinal sections after hybridization with the universal EuB388 probe confirmed the presence of bacteria in the baso-medial region of *Nautilus macromphalus* pericardial villi, whereas the apical part of these villi was devoid of any bacteria (figure 4a). Hybridization with probes specific to the β-proteobacterial and spirochaetal sequences found in *Nautilus macromphalus* showed the coexistence of these two symbiotic bacterial phylotypes in all the examined specimens (figure 4b). The observed distribution of the spirochaetal and β-proteobacterial symbionts was similar in FISH and TEM sections. The β-proteobacterium-specific probe (NauBet66) hybridized to thin, rod-shaped bacteria was distributed principally in the invaginated epithelial areas (figure 4c,d). The spirochaete-specific probe (NauSpiro255) hybridized with cocccoid bacteria was generally found in the peripheral areas and closely associated with the pericardial epithelium (figure 4c,d). A non-quantitative, visual comparison of pericardial appendages from the four *Nautilus macromphalus* specimens showed a similar coexistence and distribution of the two symbiont phylotypes in most of the 120 sections examined. The hybridization patterns of the probes specific to the β-proteobacterial and spirochaetal symbionts of *Nautilus macromphalus* corresponded to those from the general eubacterial probe EuB388, suggesting that the two specific probes revealed all the bacteria present in the pericardial appendages.

### 4. DISCUSSION AND CONCLUSION

The present exhaustive molecular analysis (more than 100 clones per specimen) of *Nautilus macromphalus* pericardial appendages in combination with FISH clearly shows that these organs harbour only two symbionts, a β-proteobacterium and a spirochaete. This result supports
the hypothesis of a culture-related bias in the detection of \(\gamma\)-proteobacteria isolated in previous studies from cephalopod symbiotic organs (Schipp et al. 1990; Barbieri et al. 2001; Pichon et al. 2005; Pernice et al. 2007).

Symbioses for recycling nitrogenous waste products have evolved in a number of terrestrial invertebrates' lineages (Cochran 1985; Sasaki et al. 1996; van Borm et al. 2002; Schramm et al. 2003) and in gutless marine oligochaetes (Woyke et al. 2006). The \(N.\) \textit{macromphalus} bacterial symbiotic association occurs in a highly specialized organ, unique among cephalopods, and responsible for most of the excretory processes. The bacteria associated with the pericardial appendages are not closely related to any known bacteria. In addition, the \(\beta\)-proteobacteria symbionts are phylogenetically affiliated to \(\text{Nitrosomonadaeae,}\) an ammonia-oxidizing lineage that, to our knowledge, has not previously been found in symbiotic associations with animals.

The exact mechanisms by which the symbionts are involved in \(N.\) \textit{macromphalus} excretion remain to be clarified. However, these bacteria are assumed to be involved in such a symbiotic function for several reasons: (i) the attachment and concentration of symbionts at the outer epithelium in the baso-medial region of the pericardial villi suggest that they could be active in ultrafiltration and/or reabsorption processes (figure 4a), (ii) the ultrastructure of this outer epithelium and its polar organization are characteristic of an energy-requiring, transport active tissue (Martin 1983; figure 2a–c), and (iii) the bacteria live in an ammonia-rich environment (Schipp & Martin 1987).

Cephalopods are ammonotelic, i.e. more than 70\% of their nitrogenous waste is excreted as ammonia (Boucher-Rodoni 1989). Excretion rates of ammonia are surprisingly low in \textit{Nautilus}, and it has been suggested that this waste compound is used for buoyancy through bacterial transformation of ammonia to dinitrogen gas (Denton 1974; Boucher-Rodoni & Mangold 1994). Direct transformation of ammonia to nitrogen is only known to occur under anaerobic conditions in the so-called ammox reaction driven by the recently discovered anaerobic planctomycete bacteria (Strous et al. 1999). In contrast, there are no known aerobic bacteria that can directly oxidize ammonia to nitrogen. Under oxic conditions in a process called nitrification, ammonia is first oxidized to nitrite by (among others) \(\beta\)-proteobacteria of the genera \(\text{Nitrosomonas}\) and \(\text{Nitrosospira}\) and then to nitrate by aerobic bacteria that can directly oxidize ammonia to nitrite (Strous et al. 1999).

Figure 3. The phylogenetic relationships of the spirochaetal and \(\beta\)-proteobacterial symbionts of \(N.\) \textit{macromphalus} (bold) inferred from \(16S\) rRNA gene analysis using maximum likelihood (ML; 1411 sites analysed). Numbers at each branch point are the bootstrap values for percentages of 1000 replicate trees calculated by MP (upper) and ML (lower) methods. Only values above 60\% are shown. Two cyanobacterial species (\textit{Trichodesmium thiebautii}: AF013027 and \textit{Merismopedia glauca}: AJ781044) were used as outgroups. AOB, ammonia-oxidizing bacteria.
Influence of symbiosis on adaptation  M. Pernice et al.

Figure 4. Schematic diagram (modified from Schipp et al. 1985, with kind permission of the author and Springer Science and Business Media) and distribution of *N. macromphalus* symbionts in a pericardial appendage villus. (a) Details of the inset in figure 1b: schematic diagram of a longitudinal section through a villus and general distribution of the symbiotic bacteria (CARD–FISH with universal eubacterial probe EUB388 in green). Direction of blood flow: secretion (white arrow), filtration (black arrow) and reabsorption processes (grey arrows). Scale bar, 500 μm. (b–d) Multicolour CARD–FISH images of *N. macromphalus* symbionts in transversal sections of a pericardial villus. The spirochaete symbionts (NauSpiro255 probe in red) are closely associated with the pericardial epithelium in peripheral areas. The β-proteobacterial symbionts (NauBet66 probe in green) are found in peripheral and invaginated areas and are less closely associated with the epithelium. In blue, *Nautilus* tissue is stained with DAPI. (b) Scale bar, 500 μm; (c, d) scale bar, 10 μm.
Nitrosococcus and nitrite is further oxidized to nitrate mainly by α-proteobacteria of the genus Nitrobit. Transformation of nitrate and nitrite to dinitrogen gas, i.e. denitrification, occurs under anoxic conditions and is driven by a wide range of very different bacteria.

No bacteria belonging to the Planctomycetales that are to date the only bacteria known to oxidize ammonia anaerobically to nitrogen were found in N. macromphalus. What we did find is β-proteobacteria most closely related to the nitrifying bacteria that oxidize ammonia to nitrite. However, none of the genes involved in these processes such as amoA, nirKS and nosZ were found in DNA extracted from N. macromphalus pericardial appendages so that other metabolic pathways of the symbionts must be considered.

An alternative hypothesis is that the N. macromphalus β-proteobacterial symbionts are protein degraders, as suggested for the Acidovorax symbionts of earthworms (Schramm et al. 2003; Davidson & Stahl 2006) that are also β-proteobacteria, although only very distantly related to the N. macromphalus β-proteobacterial symbionts. The coelomic fluid proteins could thus be degraded to peptides and amino acids by the symbionts. This would facilitate their reabsorption and enable the host to conserve valuable nitrogen compounds otherwise lost through excretion.

Free-living spirochaetes are not only widespread in marine and limnic environments, but are also commonly found as commensals or parasites in animals and humans (Dubillier et al. 1999; Cabello et al. 2001; Prescott et al. 2003; Dröge et al. 2006). One of the closest relatives to the N. macromphalus spirochaete symbiont is S. maragdinae, a free-living, obligate anaerobe that ferments carbohydrates (Magot et al. 1997), suggesting fermentation as one possible metabolic pathway of the N. macromphalus spirochaetes. However, these symbionts could also have a completely different metabolism, just as spirochaete symbionts in termites, which are involved in the nitrogen nutrition of their host (Tayasu et al. 1994; Libburn et al. 2001).

Unexpectedly, the morphology of the N. macromphalus spirochaete symbionts observed with TEM (figure 2e) and FISH (figure 4d) was not the typical helical-shaped spirochaete but rather a coccoid morphology. However, the existence of coccoid spirochaetes was recently shown in anoxic freshwater sediments (Ritalahti & Loßler 2004) and in the digestive tract of termites (Dröge et al. 2006). The presence of such coccoid spirochaetes in N. macromphalus pericardial appendages supports the hypothesis that non-spiral spirochaetes are widespread in nature and not restricted to specialized ecosystems or to the termite hindgut (Dröge et al. 2006).

The high density of bacteria in N. macromphalus pericardial appendages, as estimated previously by flow cytometry (approx. 150 × 10^6 bacteria per gram of fresh tissue; Pernice et al. 2007), indicates that these symbionts may play an important role in the physiology of their host. Further investigations are needed to understand how exactly the β-proteobacteria and spirochaete symbionts are involved in N. macromphalus excretion. This could include the use of 15N tracer experiments coupled with multiple isotope imaging mass spectrometry to measure the assimilation of nitrogen compounds by symbionts in N. macromphalus pericardial appendages tissue at the cellular level (Luyten et al. 2006).

A further point of interest in the N. macromphalus symbiosis is the understanding of the factors that contribute to the distribution patterns of β-proteobacteria and spirochaete symbionts in the pericardial appendages. Indeed, the predominance of the β-proteobacteria symbionts in the cavities formed by baso-medial invaginations was clearly observed by CARD–FISH (figure 4b–d), while the spirochaete symbionts were evidenced mainly in the peripheral areas. Such spatial distribution may reflect an ecological equilibrium between the two symbiotic phyotypes. This allows the comparison of the N. macromphalus pericardial appendages with a micro-ecosystem harbouring two bacterial groups that have established their own ecological niche. Additional examination of N. macromphalus pericardial appendages by combining CARD–FISH with microsensor technology will help to relate the distribution of β-proteobacteria and spirochaete symbionts to microscale gradients of key factors, such as oxygen, ammonia, nitrite and nitrate (De Beer et al. 1997).

Finally, preliminary analyses of 16S rRNA sequences from N. pompilius specimens showed that N. macromphalus and N. pompilius share highly similar symbiont phylotypes (above 99.5% identity), suggesting that this symbiosis could be widespread among Nautilus species. With symbiosis being an important driving force of metazoan evolution (McFall-Ngai 2002), it would then be of interest to explore the N. macromphalus dual symbiosis from an evolutionary point of view to better understand where and when this symbiosis evolved.

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