



Metagenomic Analysis of Genes Encoding Nucleoside Catabolism Pathways in the Microbiota of Deep-Sea and Shallow-Water Sponges

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Abstract

Deep-sea sponges harbor a diverse and abundant microbiota, which may play a crucial role in the sponge's biology. However, the functional roles of the microbiota in sponges remain largely unknown. In this study, we performed a metagenomic analysis of the microbiota of two deep-sea sponges, *Theonella swinhoei* and *Neamphius huxleyi*, and compared the results with those of a shallow-water sponge, *Chlorella*. The results showed that the microbiota of deep-sea sponges is more diverse and abundant than that of shallow-water sponges. The functional analysis revealed that the microbiota of deep-sea sponges is enriched in genes encoding nucleoside catabolism pathways, which may play a crucial role in the sponge's biology. This study provides the first metagenomic analysis of the microbiota of deep-sea sponges and highlights the importance of nucleoside catabolism pathways in the sponge's biology.

Electronic supplementary material

Supplementary data associated with this article are available in the following format:



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Keywords

Deep-sea sponges, microbiota, metagenomics, nucleoside catabolism

Introduction

Deep-sea sponges harbor a diverse and abundant microbiota, which may play a crucial role in the sponge's biology. However, the functional roles of the microbiota in sponges remain largely unknown. In this study, we performed a metagenomic analysis of the microbiota of two deep-sea sponges, *Theonella swinhoei* and *Neamphius huxleyi*, and compared the results with those of a shallow-water sponge, *Chlorella*. The results showed that the microbiota of deep-sea sponges is more diverse and abundant than that of shallow-water sponges. The functional analysis revealed that the microbiota of deep-sea sponges is enriched in genes encoding nucleoside catabolism pathways, which may play a crucial role in the sponge's biology. This study provides the first metagenomic analysis of the microbiota of deep-sea sponges and highlights the importance of nucleoside catabolism pathways in the sponge's biology.

the 16S rDNA region. The 16S rDNA region was amplified using the primer pair 16S-1 and 16S-2 (Table 1). The PCR products were purified using the High Pure PCR Purification kit (Roche Diagnostics, Mannheim, Germany) and sequenced using the primer pair 16S-1 and 16S-2. The sequencing was performed using the BigDye 3.1 sequencing kit (Applied Biosystems, Foster City, CA, USA) on an ABI3130XL DNA sequencer (Applied Biosystems, Foster City, CA, USA). The sequencing results were analyzed using the Geneious 5.6.2 software (Biomatters, Auckland, New Zealand). The sequences were compared with the GenBank database using the BLAST program (Altschul et al. 1990). The sequences were aligned using the ClustalW algorithm (ClustalX 1.8.1) and the phylogenetic tree was constructed using the Maximum Likelihood method (PhyML 3.0). The bootstrap values were calculated using 1,000 replicates.

Cymbastela concentrica

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Rhizobium

The 16S rDNA region was amplified using the primer pair 16S-1 and 16S-2 (Table 1). The PCR products were purified using the High Pure PCR Purification kit (Roche Diagnostics, Mannheim, Germany) and sequenced using the primer pair 16S-1 and 16S-2. The sequencing was performed using the BigDye 3.1 sequencing kit (Applied Biosystems, Foster City, CA, USA) on an ABI3130XL DNA sequencer (Applied Biosystems, Foster City, CA, USA). The sequencing results were analyzed using the Geneious 5.6.2 software (Biomatters, Auckland, New Zealand). The sequences were compared with the GenBank database using the BLAST program (Altschul et al. 1990). The sequences were aligned using the ClustalW algorithm (ClustalX 1.8.1) and the phylogenetic tree was constructed using the Maximum Likelihood method (PhyML 3.0). The bootstrap values were calculated using 1,000 replicates.

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Theonella swinhoei

Neamphius huxleyi

Materials and Methods

Sponge Sampling

The 16S rDNA region was amplified using the primer pair 16S-1 and 16S-2 (Table 1). The PCR products were purified using the High Pure PCR Purification kit (Roche Diagnostics, Mannheim, Germany) and sequenced using the primer pair 16S-1 and 16S-2. The sequencing was performed using the BigDye 3.1 sequencing kit (Applied Biosystems, Foster City, CA, USA) on an ABI3130XL DNA sequencer (Applied Biosystems, Foster City, CA, USA). The sequencing results were analyzed using the Geneious 5.6.2 software (Biomatters, Auckland, New Zealand). The sequences were compared with the GenBank database using the BLAST program (Altschul et al. 1990). The sequences were aligned using the ClustalW algorithm (ClustalX 1.8.1) and the phylogenetic tree was constructed using the Maximum Likelihood method (PhyML 3.0). The bootstrap values were calculated using 1,000 replicates.

DNA Extraction and Deep Sequencing

The 16S rDNA region was amplified using the primer pair 16S-1 and 16S-2 (Table 1). The PCR products were purified using the High Pure PCR Purification kit (Roche Diagnostics, Mannheim, Germany) and sequenced using the primer pair 16S-1 and 16S-2. The sequencing was performed using the BigDye 3.1 sequencing kit (Applied Biosystems, Foster City, CA, USA) on an ABI3130XL DNA sequencer (Applied Biosystems, Foster City, CA, USA). The sequencing results were analyzed using the Geneious 5.6.2 software (Biomatters, Auckland, New Zealand). The sequences were compared with the GenBank database using the BLAST program (Altschul et al. 1990). The sequences were aligned using the ClustalW algorithm (ClustalX 1.8.1) and the phylogenetic tree was constructed using the Maximum Likelihood method (PhyML 3.0). The bootstrap values were calculated using 1,000 replicates.



Figure 1. Genomic map of the shallow-water sponge *T. swinhoei* and deep-sea sponge *N. huxleyi*. The map shows the relative positions of the genes involved in nitrogen fixation and nitrification. The genes are labeled with names such as napA, hao, narX, nirK, nirS, nosZ, nrfA, and nxr. The map is divided into two main sections, x and y, with a central region labeled T.S. and N.H.

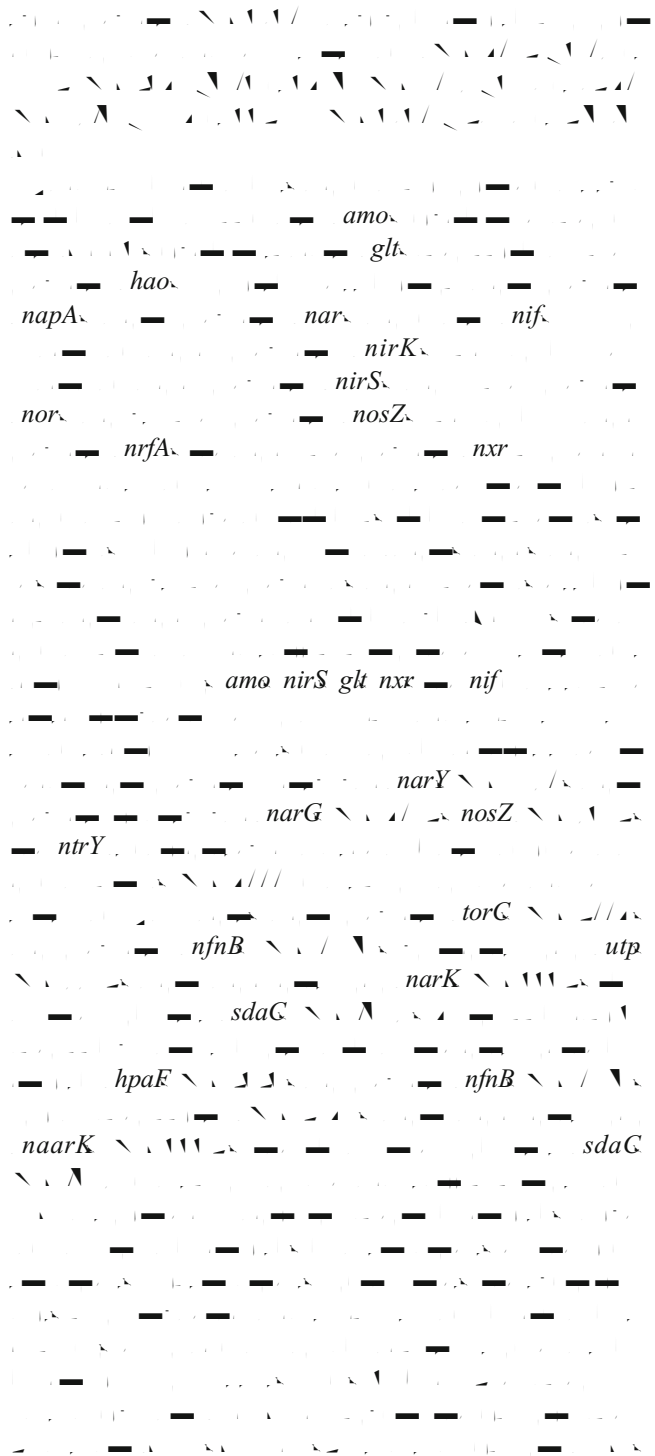
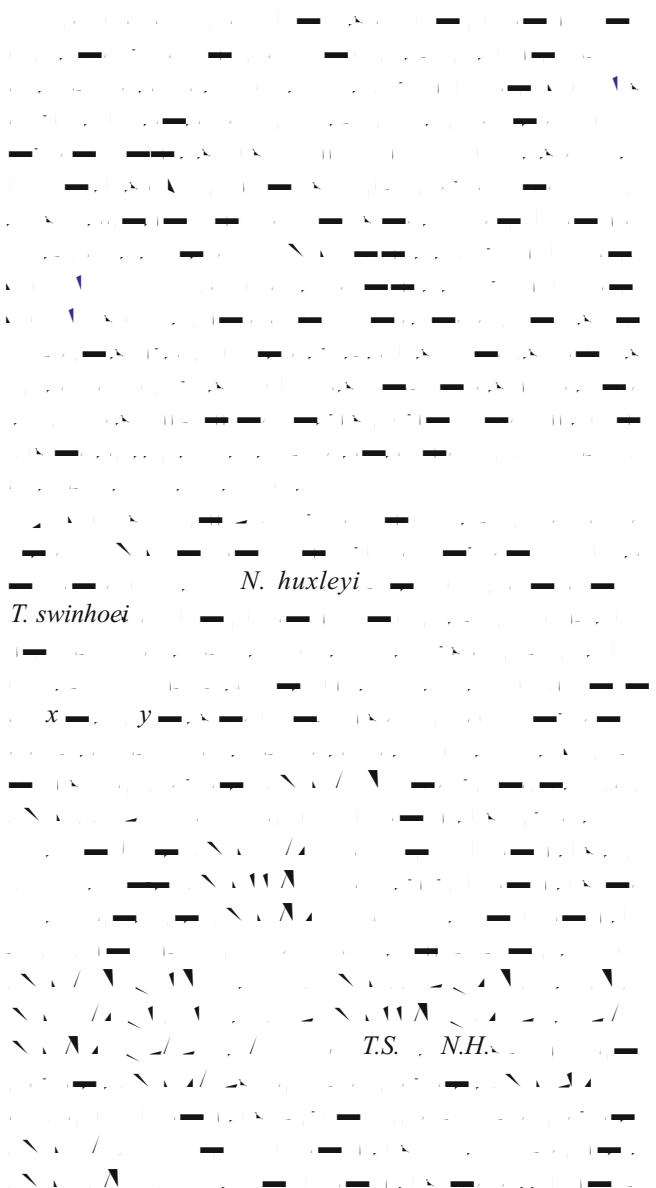


Figure 1. The effect of the number of trials on the number of correct responses. The number of correct responses was plotted against the number of trials for each participant. The number of correct responses was plotted against the number of trials for each participant. The number of correct responses was plotted against the number of trials for each participant.

N. huxleyi
T. swinhoei

Discussion

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Fig. 2

T. swinhoi
 yellow N. huxleyi
 green
 circles

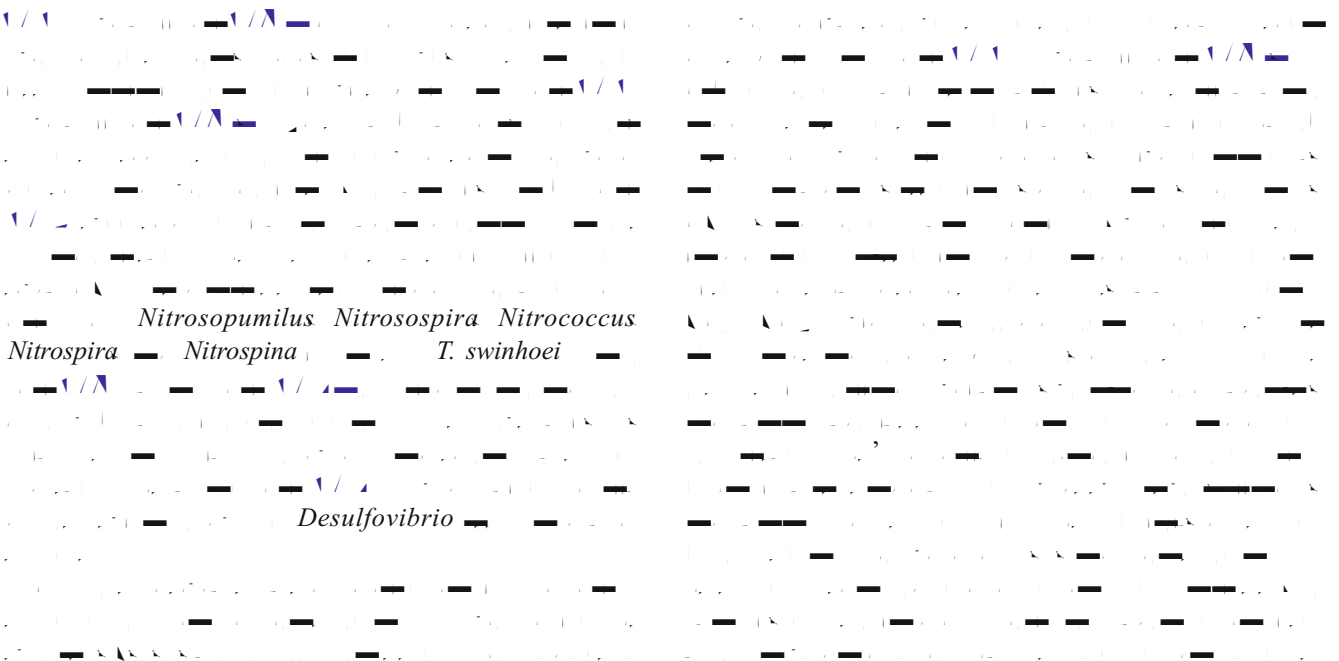
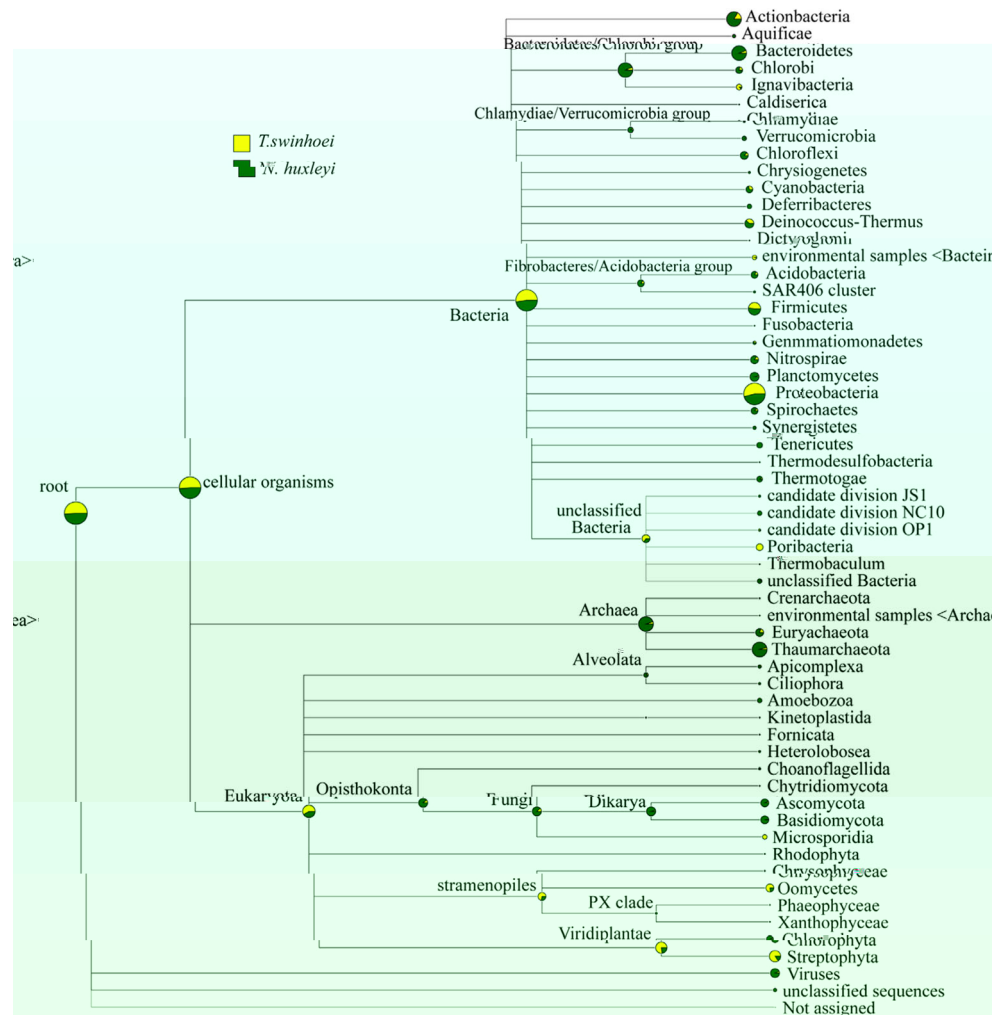


Fig. 3

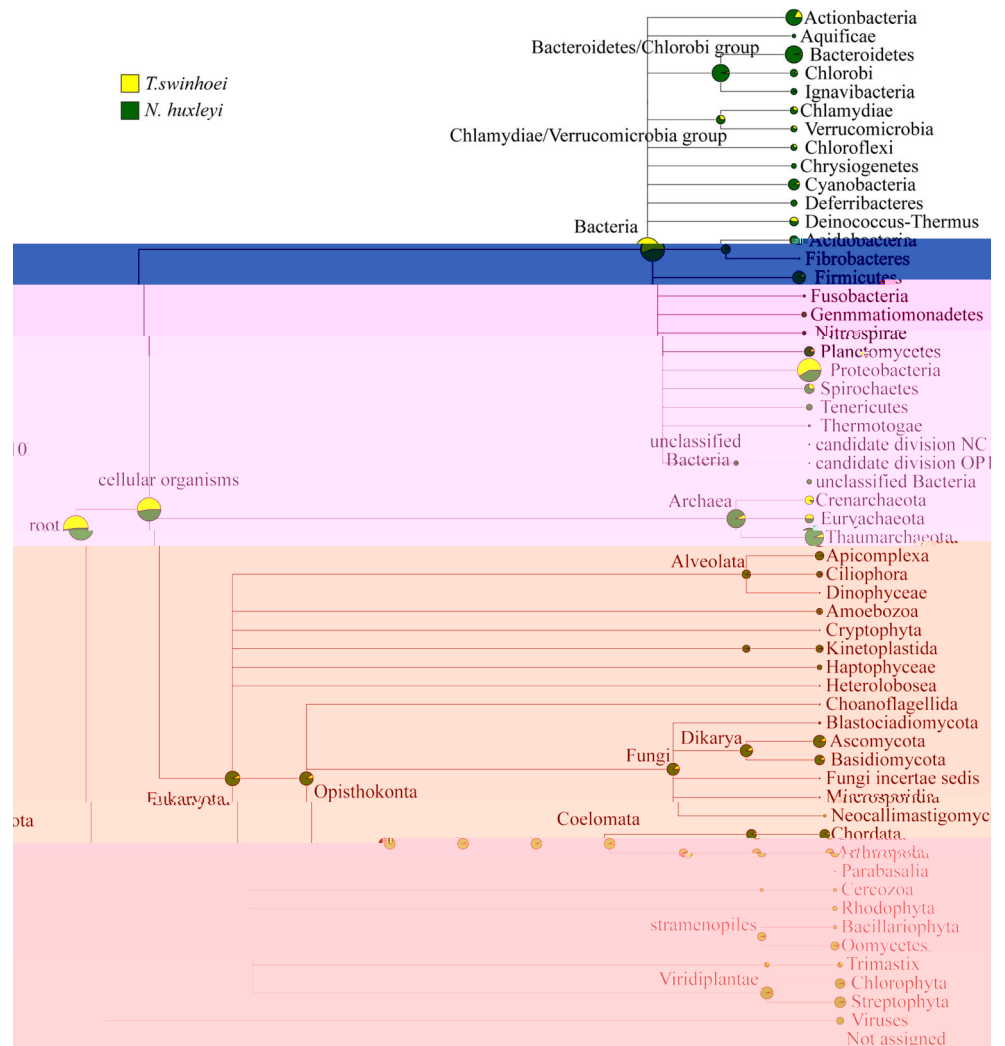
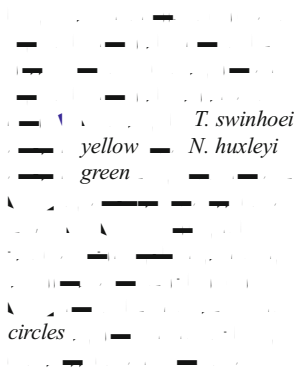
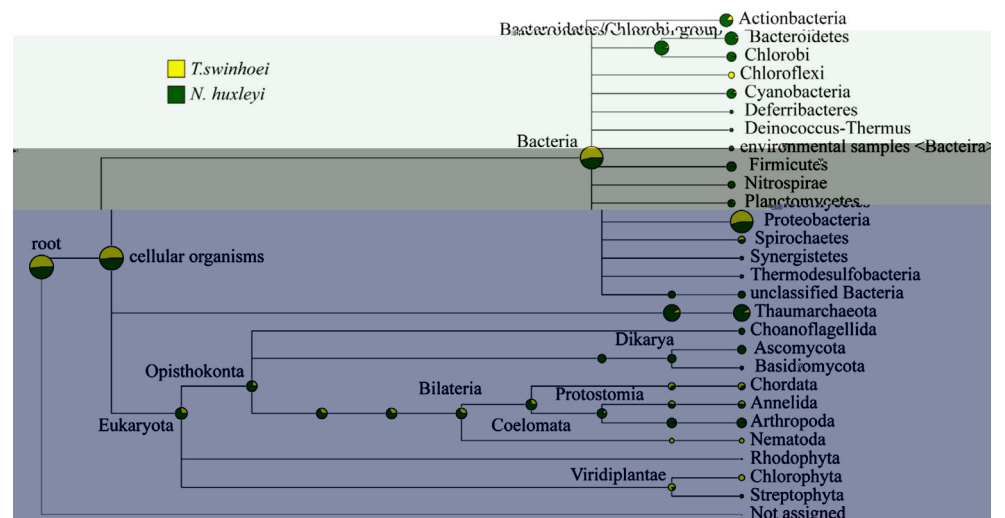
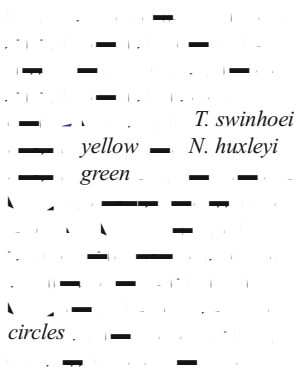


Fig. 4



N. huxleyi

N. huxleyi

T. swinhoei

T. swinhoei

N. huxleyi

Compliance with Ethical Standards

Conflict of Interest

Reference

- Aplysina aerophoba*
- *Prochloron*
- Xestospongia muta*
- Suberites zeteki*
- Mycale armata*
- Haliclona*
- Theonella swinhoei* — *Xestospongia testudinaria*

[illegible]

Arenosclera brasiliensis