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1. methanotrophic bacterial endosymbiont of Bathymodiolus sp. genome assembly, contig: METH00, whole genome shotgun sequence
   14,012 bp linear DNA
   Accession: FNVW02000001.1 GI: 1183551330
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2. methanotrophic bacterial endosymbiont of Bathymodiolus sp. genome assembly, contig: METH01, whole genome shotgun sequence
   13,120 bp linear DNA
   Accession: FNVW02000002.1 GI: 1183551318
   BioProject BioSample Protein Taxonomy
   GenBank FASTA Graphics

3. methanotrophic bacterial endosymbiont of Bathymodiolus sp. genome assembly, contig: METH02, whole genome shotgun sequence
   12,430 bp linear DNA
   Accession: FNVW02000003.1 GI: 1183551307
   BioProject BioSample Protein Taxonomy
   GenBank FASTA Graphics

4. methanotrophic bacterial endosymbiont of Bathymodiolus sp. genome assembly, contig: METH03, whole genome shotgun sequence
   11,322 bp linear DNA
   Accession: FNVW02000004.1 GI: 1183551295
   BioProject BioSample Protein Taxonomy
   GenBank FASTA Graphics

5. methanotrophic bacterial endosymbiont of Bathymodiolus sp. genome assembly, contig: METH04, whole genome shotgun sequence
   10,919 bp linear DNA
   Accession: FNVW02000005.1 GI: 1183551283
   BioProject BioSample Protein Taxonomy
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6. methanotrophic bacterial endosymbiont of Bathymodiolus sp. genome assembly, contig: METH05, whole genome shotgun sequence

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Metabolic and physiological interdependencies in the *Bathymodiolus azoricus* symbiosis

Ruby Ponnudurai, Manuel Kleiner, Lizbeth Sayavedra, Jillian M Petersen, Martin Moche, Andreas Otto, Dörte Becher, Takeshi Takeuchi, Noriyuki Satoh, Nicole Dubilier, Thomas Schweder & Stephanie Markert

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Abstract

The hydrothermal vent mussel *Bathymodiolus azoricus* lives in an intimate symbiosis with two types of chemosynthetic Gammaproteobacteria in its gills: a sulfur oxidizer and a methane oxidizer. Despite numerous investigations over the last decades, the degree of interdependence between the three symbiotic partners, their individual metabolic contributions, as well as the mechanism of carbon transfer from the symbionts to the host are poorly understood. We used a combination of proteomics and genomics to investigate the physiology and metabolism of the individual symbiotic partners. Our study revealed that key metabolic functions are most likely accomplished jointly by *B. azoricus* and its symbionts: (1) CO_2 is pre-concentrated by the host for carbon fixation by the sulfur-oxidizing symbiont, and (2) the host replenishes essential biosynthetic TCA cycle intermediates for the sulfur-oxidizing symbiont. In return (3), the sulfur oxidizer may compensate for the host's putative deficiency in amino acid and cofactor biosynthesis. We also identified numerous 'symbiosis-specific' host proteins by comparing symbiont-containing and symbiont-free host tissues and symbiont fractions. These proteins included a large complement of host digestive enzymes in the gill that are likely involved in symbiont digestion and carbon transfer from the symbionts to the host.