Exploring Life at Deep-Sea Hydrothermal Vents
... and what does it have to do with Medicine?

Stefan M. Sievert
Woods Hole Oceanographic Institution
ssievert@whoi.edu
http://www.whoi.edu/people/ssievert
Who is there? Who is active? What process(es) are they mediating and at what rate(s)?

Salt marsh Deep-sea vents Shallow-water vents Oxygen minimum zones

CHEMOSYNTHESIS
Chemical Energy + Carbon Dioxide
↓
Living cells

Who is there? Who is active?

What process(es) are they mediating and at what rate(s)?

Abundance, Diversity Functions (Meta ‘Omics’)
Rates Geochemistry Interactions (biotic, abiotic)

http://www.whoi.edu/groups/sievertlab
Outline

• Introduction to Deep-Sea Vents
  – Geological and Physical Setting
  – Chemosynthesis

• Microbial Processes and Symbiosis – Link to Medicine

• Fieldwork at 9°N East Pacific Rise
  – Study site and approach
  – Productivity of subseafloor biosphere

• Synthesis
Discovery of Deep-Sea Hydrothermal Vents only ~40 years ago in 1977

Submarine Thermal Springs on the Galápagos Rift


16 March 1979, Volume 203, Number 4385

John (Jack) Corliss (OSU)

Bob Ballard (WHOI)
Discovery of Deep-Sea Hydrothermal Vents only ~40 years ago in 1977

John (Jack) Corliss (OSU)

Bob Ballard (WHOI)
Global Distribution of Hydrothermal Vent Fields
Global Distribution of Hydrothermal Vent Fields

[Map showing the global distribution of hydrothermal vent fields with various labels and symbols indicating active and unconfirmed vents along different tectonic features.]

Legend:
- Mid-ocean ridge
- Arc volcano
- Back-arc spreading center
- Intra-plate volcano & Other
- Ridge & Transform
- Trench
- Exclusive Economic Zones

- Active
- Unconfirmed

Physical Setting

Sievert et al., 2008
Physical Setting

Sievert et al., 2008
Physical Setting

Subsurface of diffuse-flow or warm-water vent:

- Mixing of hydrothermal fluids with seawater below the seafloor
- Creates conditions conducive for microbial growth
“Food chain” at deep-sea vents: Conceptual framework

- **A**: Hydrothermal Fluid
- **B**: Microbial Oxidations ($H_2S$, $H_2$, $CH_4$, etc.)
  - **B1**: Free-living Bacteria
  - **B2**: Procaryotic Symbionts
- **C**: Planktonic Plume Biota, Benthic Grazers, Symbiotic Invertebrates and Their Scavengers

*Figure modified from Jannasch, 1995*
“FOOD CHAIN” AT DEEP-SEA VENTS:
CONCEPTUAL FRAMEWORK

Chemical Energy -> Chemosynthesis

Hydrothermal Fluid

Microbial Oxidations (H₂S, H₂, CH₄, etc.)

Free-living Bacteria

Procaryotic Symbionts

Planktonic Plume Biota, Benthic Grazers, Symbiotic Invertebrates and Their Scavengers

Figure modified from Jannasch, 1995
“FOOD CHAIN” AT DEEP-SEA VENTS: CONCEPTUAL FRAMEWORK

Microbes are at the Base of Ecosystem by Mediating the Transfer of Energy from Geothermal Source to Higher Trophic Levels
Chemosynthesis

Hydrogen sulfide (H₂S)

Carbon dioxide (CO₂)

RedOx reaction

Energy

more microbes

Photosynthesis – Foundation for life on land and surface ocean

Chemosynthesis – Foundation for life at hydrothermal vents

Autotrophy

Oxygen (O₂) or nitrate (NO₃⁻)
Meanwhile, at the bottom of the ocean...

Do you think life exists at the surface of the ocean?

Nah. There are no hydrothermal vents up there. What would they use for energy?

Mmm, true.
What's in common?

**Campylobacteria**
Formerly known as *Epsilonproteobacteria*
The 5300-year-old *Helicobacter pylori* genome of the Iceman

Frank Maixner,1† Ben Krause-Kyora,2† Dmitrij Turaev,3† Alexander Herbig,4,5† Michael R. Hoopmann,6 Janice L. Hallows,6 Ulrike Kusebauch,6 Eduard Egarter Vigl,7 Peter Malfertheiner,8 Francis Megraud,9 Niall O’Sullivan,1 Giovanna Cipollini,1 Valentina Coia,1 Marco Samadelli,1 Lars Engstrand,10 Bodo Linz,11 Robert L. Moritz,6 Rudolf Grimm,12 Johannes Krause,4,5,13 Almut Nebel,2† Yoshan Moodley,13,14† Thomas Rattei,3† Albert Zink18†

Eduard Egarter-Vigl (left) and Albert Zink (right) taking a sample from the Iceman in November 2010. Credit: © EURAC/Marion Lafogler

**Fig. 1.** *H. pylori*-specific reads detected in the metagenomic data sets of the Iceman’s intestine content samples. The color gradient displays the number of unambiguous *H. pylori* reads per million metagenomic reads. Control metagenomic data sets of the Iceman’s muscle tissue and of the extraction blank were included in the analysis. The different intestinal content sampling sites are marked in the radiographic image by the following symbols: asterisk, stomach content; circle, small intestine; square, upper large intestine; triangle, lower large intestine. The sampling site of the muscle control sample is highlighted in the Iceman overview picture (diamond).
Waite et al., 2017

<table>
<thead>
<tr>
<th>Legend</th>
<th>Temperature</th>
<th>Trophism</th>
<th>Lifestyle</th>
<th>Carbon</th>
<th>Nitrogen</th>
<th>Sulfur</th>
<th>Motility</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mesophilic</td>
<td>Heterotrophic</td>
<td>Campylobacter B</td>
<td>Anaerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td>Thermophilic</td>
<td>Mixotrophic</td>
<td>Campylobacter C</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Autotrophic</td>
<td>Campylobacter A</td>
<td>Anaerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Campylobacter</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Sulfurospirillum</td>
<td>Anaerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Helicobacter mustetalia</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Helicobacter B</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Helicobacter C</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Helicobacter himalayensis</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Helicobacter pametensis</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Helicobacter D</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Wolinella succinogenes</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>UBA6016 &amp;</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Sulfurimonas</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Sulfurcurvum</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Sulfurcurvum A sp. PC08-66</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Thiobulbus sp. ES</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Arcomicetor &amp;</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>UBA6211 &amp;</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Sulfurovum</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Nitrilactobacter salsuginis</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Hydrogenimonas thermophila</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Nitritotolerans sp. SB155-2</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Nautilia profundica</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Lebetimosa sp. JS138</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Cenminhibacter mediatianicus</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Hippea</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Desulfurella acetivorans</td>
<td>Aerobic, ADP-glucose, starch, Mn</td>
<td>NADH, NADPH, NAD, NADP</td>
<td>SR, P, X</td>
<td>Null</td>
</tr>
</tbody>
</table>

Waite et al., 2017
Deep-sea vent ε-proteobacterial genomes provide insights into emergence of pathogens!

Deep-sea vent chemoautotrophy has provided the core of virulence for important human/animal pathogens!
• Genome comparison of
  • 3 species of same genus
  • 3 species from different genera, but same habitat

• Most genes are lineage specific

• Select habitat specific genes

Zhang & Sievert, 2014
Campylobacteria inhabit a variety of niches at deep-sea hydrothermal vents.

Campbell et al., 2006
Oxidation of Sulfide Coupled to Reduction of $O_2$ and $NO_3^-$ in Chemoautotrophic *Campylobacteria*

- **Aerobic S-oxidizers** use periplasmic nitrate reductase (NAP).
- **Use** cbb3 cytochrome oxidase.
- **Adapted** to low concentrations of nitrate and oxygen:
  - Adapted to low concentrations of nitrate and oxygen
  - -> Vents/animal hosts
- **Citric acid cycle in pathogens utilizes enzymes of reductive citric acid cycle in chemoautotrophs**

*soxABCDXYZ*
Colonization of animate and inanimate surfaces at deep-sea vents

- Facilitation of larval settlement
- Trophic interactions
- Symbiotic associations

Sievert & Vetriani, 2012
From deep-sea volcanoes to human pathogens: a conserved quorum-sensing signal in Epsilonproteobacteria

Ileana Pérez-Rodríguez1,2,3, Marie Bolognini1,2, Jessica Ricci1,2,4, Elisabetta Bini1,2,5 and Costantino Vetricani1,2

1Department of Biochemistry and Microbiology, Rutgers University, New Brunswick, NJ, USA and 2Institute of Marine and Coastal Sciences, Rutgers University, New Brunswick, NJ, USA

- Use LuxS/AI-2 as quorum sensing mechanism
- Expressed in situ in vent biofilms
- Stability under harsh conditions?
ChePep Controls Helicobacter pylori Infection of the Gastric Glands and Chemotaxis in the Epsilonproteobacteria


Colonization of gastric glands
Microbial succession on basalt rock: Foundation for Ecosystem

Bacterial diversity and successional patterns during biofilm formation on freshly exposed basalt surfaces at diffuse-flow deep-sea vents

Gulmann et al, 2015
Cooperative Associations: *Alvinella pompejana* and *Campylobacteria* episymbionts

- Worms colonize outside of black-smoker chimneys
- Most eurythermal animal known, can tolerate 60°C
- Colonized by highly specific assemblage of *Campylobacteria*

Cary et al, 1997
Cooperative Associations:
*Alvinella pompejana* and *Campylobacteria* episymbionts

- Worms colonize outside of black-smoker chimneys
- Most eurythermal animal known, can tolerate 60°C
- Colonized by highly specific assemblage of *Campylobacteria*

Model of **predicted** metabolic processes in the episymbiont community based on annotation of the episymbiont metagenome

- Filamentous bacteria provide food and can provide protection from high levels of sulfide and toxic metals (arsenic, cadmium, copper).
- Highly specific association, requiring microbe-host recognition

**Riftia pachyptila: A unique symbiosis**

- **Plume:** Takes up sulfide, oxygen, and carbon dioxide to deliver to symbiotic chemosynthetic bacteria which produce sugars to feed the worm.

- **Throphosome:** Houses symbiotic bacteria.

- **Tube:** Provides protection.

---

*Image: Antarctic Riftia pachyptila.*
Horizontal endosymbiont transmission in hydrothermal vent tubeworms

Andrea D. Nussbaumer¹, Charles R. Fisher² & Monika Bright¹

- Symbiont is newly acquired from environment w/ each generation
- Symbiont acquisition reminiscent of infection
- Symbionts penetrate skin of settled tubeworms
- ‘Infected’ tissue develops into trophosom

Figure 2 | Symbiont acquisition and early development of recently settled vestimentiferans. Schematic sagittal drawings of animals reconstructed
Activity and Productivity of the Subseafloor Biosphere
“This flux of bacteria from the vents must be supported by the production of a large population of bacteria living within the rock mass, lining the walls of fissures (and fractures) through which the hydrogen sulfide-laden fluids ascend.”

“and that they may significantly influence the chemistry of the system.”

“The generation time for these populations of sulfur-oxidizing bacteria in situ is not known, but, unlike phytoplankton blooms, their productivity is, presumably, continuous.”

- Corliss et al, 1979, Science, 1979
One of first studies to measure primary production at deep-sea vents

In 1980, after follow up study

“In view of the complexity of the entire vent system and the limited amount of sampling possible, a useful quantification of deep-sea primary production is quite out of reach at this time.”

Today

“In view of the complexity of the entire vent system and the limited amount of sampling possible, a useful quantification of deep-sea primary production is quite out of reach at this time.


This goal is now within reach
‘CRAB SPA’ AT 9°50’N ON EAST PACIFIC RISE
A MODEL SYSTEM TO STUDY CHEMOAUTOTROPHIC PROCESSES AT DEEP-SEA VENTS

Crab Spa at Tica
Temp: ~24 (30°C in ‘07)
H₂S: 300 µM (1 mM in ‘07)
H₂: ~5 µM
pH: 5.8
O₂: <2 µM, NO₃⁻: <7µM
Sampled in Jan ‘07, Jan ‘08, Oct ‘08, May ‘10, May ‘12, Jan ‘14, Nov ‘14, May ‘17
NATIONAL DEEP SUBMERGENCE FACILITY AT WHOI: ALVIN, JASON & SENTRY
‘Crab Spa’
‘Snow Blower’
Seawater (SW) O₂, NO₃⁻, SO₄²⁻ (3°C)

Hydrothermal Fluid (HF) H₂S, H₂, CH₄ (>275°C)

Exiting fluids depleted in H₂, H₂S, NO₃⁻, O₂ relative to conservative mixing; enriched in cells

→ Chemosynthesis below seafloor!

Subseafloor Biosphere

Basalt

14:1 mix (SW:HF)

(25°C)

Open Questions:
- Subseafloor primary productivity?
- Identity & physiology of active organisms?
- Ecological niches?
Multifaceted Approach to Study Crab Spa Microbiome

- **Geochemistry**
  - **In situ**
  - Lab based

- **Samples w/ IGT fluid samplers**
  1. **Shipboard incubations**
  2. CARD-FISH
  3. Single-cell Amplified Genomes (SAG)

- **In situ filtration w/ LVP**
  1. 16S rRNA pyrotags
  2. Metagenome
  3. Metatranscriptome
  4. Metaproteome
  5. Lipids

---

Jesse McNichol, François Thomas

Florian Götz
Isobaric Gas Tight Sampler (IGT) to collect fluids for chemical analyses and investigating microbial activity at *in-situ* pressure and temperature.
**Shipboard Incubations with Hydrothermal Fluids under Simulated in situ Conditions**

- Added $^{13}$C-labeled bicarbonate to incubations conducted at *in situ* pressure, different temperatures and conditions.
- Analyses at single cell level with HISH-SIMS: Nanoscale-Secondary Ion Microprobe coupled with Halogen In Situ Hybridization.

McNichol et al. 2016 DSR-I, McNichol et al. 2018 PNAS
Nano-SIMS is mass spectrometry on individual cells

Wagner, 2009, Annual Review of Microbiology
SHIPBOARD GENERATED DATA

Jesse McNichol & François Thomas
Bacterial community composition during incubations

- Background (n=2)
- Control (n=3)
- H₂ only (n=3)
- NO₃⁻ only (n=3)
- O₂ (~80 μM) (n=2)
- O₂ (~110 μM) (n=2)
- NO₃⁻ + H₂ (n=3)
- NO₃⁻ + H₂, 50°C (n=2)

A) Percent probe-hybridized cells (% DAPI-stained)

- Campylobacteria
- Sulfurimonas
- Nautiliales

B) NMDS 1 vs NMDS 2

- Initial [O₂] in incubation (μM)
- Stress = 0.057

C) Sulfurimonas OTU abundance (%)

McNichol et al., 2018
Bacterial community composition during incubations

Sulfurimonas OTUs respond to differences in O₂ concentration -> niche partitioning?

McNichol et al., 2018
Estimations of Primary Productivity in Incubations of Hydrothermal Vent Fluids at *In Situ* Temperature and Pressure Determined by HISH-SIMS

- **A**
  - Bar chart showing biomass, identity, and activity data for different conditions.

- **B**
  - Percentage of carbon fixation attributed to *Nautiliales*.

- **Card-FISH**:
  - *Campylobacteria* 80-100%

- **Findings**:
  - *Campylobacteria* dominate carbon fixation!
  - Amendments increased carbon fixation
  - Active carbon fixation (and DNRA) also by *Nautiliales* (-> *Thioreductor*) at lower temperatures, w/o H₂, and under oxic conditions
  - Evidence for physiological versatility not currently reflected in cultures

**McNichol et al., 2018**
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Lower bound</th>
<th>Upper bound</th>
<th>Units</th>
</tr>
</thead>
<tbody>
<tr>
<td>Absolute carbon fixation rates(^1)</td>
<td>17.3</td>
<td>321.4</td>
<td>μg C ◦ L(^{-1}) ◦ day(^{-1})</td>
</tr>
<tr>
<td>Chemosynthetic growth efficiency(^1)</td>
<td>0.06</td>
<td>0.13</td>
<td>Fraction electron equivalents to Carbon fixation</td>
</tr>
<tr>
<td>Estimated in situ carbon fixation(^2)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(per L Crab Spa mixed fluid):</td>
<td>104</td>
<td>253</td>
<td>μg C ◦ L(^{-1})</td>
</tr>
<tr>
<td>(per L Crab Spa end-member fluid):</td>
<td>1.4×10(^3)</td>
<td>3.5×10(^3)</td>
<td></td>
</tr>
<tr>
<td>Estimated annual productivity(^3) of:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Crab Spa vent(^4)</td>
<td>6.1×10(^3)</td>
<td>1.5×10(^4)</td>
<td>g C ◦ y(^{-1})</td>
</tr>
<tr>
<td>Surrounding vent field(^5)</td>
<td>3.8×10(^6)</td>
<td>9.3×10(^6)</td>
<td></td>
</tr>
<tr>
<td>Global diffuse-flow vents(^6)</td>
<td>4.5×10(^{10})</td>
<td>1.4×10(^{12})</td>
<td></td>
</tr>
<tr>
<td>Standing stock(^7), Crab Spa</td>
<td>28.6</td>
<td>NA</td>
<td>g C</td>
</tr>
<tr>
<td>Biomass residence time(^8), Crab Spa</td>
<td>17</td>
<td>41</td>
<td>hours</td>
</tr>
<tr>
<td>Global standing stock(^6)</td>
<td>1.4×10(^9)</td>
<td>2.7×10(^9)</td>
<td>g C</td>
</tr>
</tbody>
</table>

McNichol et al., 2018
**Ambient Deep-Sea Water:**
- 2°C
- 2.3 mM DIC
- 115 μM O₂
- 40 μM NO₃⁻
- 0 μM S²⁻, H₂
- 10⁴ cells/ml
- ~0% Campylobacteria

**Diffuse-Flow Fluid:**
- 25°C
- 8.2 mM DIC
- < 3.6 μM O₂
- < 6 μM NO₃⁻
- ~12 μM NH₄⁺
- ~ 200 μM S²⁻
- < 2 μM H₂
- 2-5 *10⁵ cells/ml
- ~80% Campylobacteria

**Hydrothermal Fluid:**
- >275°C
- 85 mM DIC
- 7.7 mM S²⁻
- 410 μM H₂
- 0 μM O₂
- 0 μM NO₃⁻
- 0 Cells

**Rates**
- 40 gC d⁻¹

**Flow rate:** 162 m³ d⁻¹

**Growth of Campylobacteria under e⁻-acceptor limitation**
- **Sulfide Oxidation w/ O₂ and NO₃⁻ to S⁰**
  - Mesophiles
  - Oxygen reduction: CBB3
  - Nitrate reduction: NAP, NIR, NOR, NOS
  - Sulfide oxidation: SQR, SOX (incomplete)
- **Hydrogen Oxidation w/ NO₃⁻ and S⁰**
  - moderate thermophiles, some mesophiles
  - DNRA and denitrification
  - Ni/Fe hydrogenase
Subseafloor productivity rivals above seafloor production by symbiotic associations!

- Diversity
- Pathways

\[ \begin{align*}
\text{NO}_3^- & \rightarrow \text{H}_2\text{O}, \text{N}_2, (\text{N}_2\text{O}), \text{NH}_4^+ \\
\text{CO}_2 & \rightarrow \text{Biomass} \\
\text{S}_2^- & \rightarrow \text{S}^0, (\text{SO}_4^{2-})
\end{align*} \]

\[ 40 \text{ gC d}^{-1} \]
Next Step: Incubations at the Seafloor

- Deployed and tested at Crab Spa, 9ºN EPR (2014, 2017)
- Directly correlate the measurement of these processes with community composition and gene expression
- Can perform repeated incubations
CONCLUSIONS

- *Campylobacteria* are dominant members of microbial communities at deep-sea hydrothermal vents
- Have conserved pathways and mechanisms that have allowed them to colonize a variety of environments, including humans
- Connection between environmental microbiology and medical microbiology, one can inform the other
- Deep-sea vents are potentially rich resource for bioactive compounds: high density, productivity, competition, etc.
- *Campylobacteria* dominate chemoautotrophy at Crab Spa
- Activity and rate measurements indicate very active community
- Processes thought to operate separately co-occur: aerobic/anaerobic, denitrification/DNRA, sulfide/hydrogen oxidation
- First direct estimates of subseafloor productivity, standing stock, and turnover!
- Subseafloor productivity rivals above seafloor production by symbiotic associations
Many thanks to...

SIEVERT lab
Florian Götz, Lara Gulmann, Jesse McNichol, François Thomas

WHOI
Jeff Seewald
Craig Taylor
Sean Sylva
Kerry McCulloch

University of Greifswald
Thomas Schweder
Stephanie Markert
Dörte Becher
Stephan Fuchs

UFZ Leipzig
Niculina Musat
Hryhoriy Stryhanyuk
Sabrina Lübke

Bigelow Lab
Ramurias Stepanauskas
Maria Pachiadaki
Jessica Labonte

Rutgers University
Costantino Vetriani
Ashley Grosche
Donato Giovanelli

UPMC Banyuls-sur-Mer
Nadine Le Bris
Erwan Peru

University of Maine
Jeremy Rich
Sean O’Neill

Carnegie Geophysical Lab
Dionysis Foustoukos
Ileana Perez-Rodriguez (now UPenn)

Georgia Tech
Leonid Germanovich

Joint Genome Institute
Tanja Woyke

Shipboard scientific parties (AT15-28, AT15-38, AT26-10, AT26-23, AT37-12)
Captain, crew, and pilots of R/V ATLANTIS and DSRV ALVIN and ROV Jason-II