

# Microbiological Genomics and Metabolize energy

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## Abstract

Marine sponges host a wide diversity of microorganisms, which have versatile modes of carbon and energy metabolism. In this study we describe the major lithoheterotrophic and autotrophic processes in 21 microbial sponge-associated phyla using novel and existing genomic and transcriptomic datasets. We show that the main microbial carbon fixation pathways in sponges are the Calvin Benson Bassham cycle (energized by light in Cyanobacteria, by sulfur compounds in two orders of Gammaproteobacteria, and by a wide range of compounds in filamentous Tectomicrobia), the reductive tricarboxylic acid cycle (used by Nitrospirota), and the 3-hydroxypropionate/4-hydroxybutyrate cycle (active in Thaumarchaeota). Further, we observed that some sponge symbionts, in particular Acidobacteria, are capable of assimilating carbon through anaplerotic processes. The lithoheterotrophic lifestyle was widespread and CO oxidation is the main energy source for sponge lithoheterotrophs. We also suggest that the molybdenum-binding subunit of dehydrogenase (encoded by *coxL*) likely evolved to benefit also organ heterotrophs that utilize various organic substrates.

Information on the biochemical pathways of carbon and energy metabolism in representatives of the deep lineage bacterial phylum Deferribacteres are scarce. Here, we report the results of the sequencing and analysis of the high-quality draft genome of the thermophiles chemolithoautotrophic anaerobe Deferribacter autotrophicus. Genomic data suggest that CO<sub>2</sub> assimilation is carried out by recently proposed reversible tricarboxylic acid cycle ("roTCA cycle"). The predicted genomic ability of D. autotrophicus to grow due to the oxidation of carbon monoxide was experimentally proven. CO oxidation was coupled with the reduction of nitrate to ammonium. Utilization of CO most likely involves anaerobic [Ni, Fe]-containing CO dehydrogenase. This is the first evidence of CO oxidation in the phylum Deferribacteres. The genome of D. autotrophicus encodes a Nap-type complex of nitrate reduction. However, the conversion of produced nitrite to ammonium proceeds via a non-canonical pathway with the participation of hydroxylamine oxidoreductase (Hao) and hydroxylamine reductase. The genome contains 17 genes of putative multiheme c-type cytochromes and "e-pilin" genes, some of which are probably involved in Fe(III) reduction. Genomic analysis indicates that the roTCA cycle of CO<sub>2</sub> fixation and putative Hao-enabled ammonification may occur in several members of the phylum Deferribacteres.

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## Introduction

Numerous diverse microorganisms reside in the cold desert soils of continental Antarctica, though we lack a holistic understanding of the metabolic processes that sustain them. Here, we profile

the composition, capabilities, and activities of the microbial communities in 16 physicochemical diverse mountainous and glacial soils. We assembled 451 met genome-assembled genomes from 18 microbial phyla and inferred through Bayesian divergence analysis that the dominant lineages present are likely native to

Antarctica [1]. In support of earlier findings, met genomic analysis revealed that the most abundant and prevalent microorganisms are metabolically versatile aerobes that use atmospheric hydrogen to support aerobic respiration and sometimes carbon fixation. Surprisingly, however, hydrogen oxidation in this region was catalysed primarily by a phylogenetically and structurally distinct enzyme, the group 1-hydrogenase, encoded by nine bacterial phyla. Through gas chromatography, we provide evidence that both Antarctic soil communities and an axenic Bacteroidota isolate (*Hymenobacter roseosalivarius*) oxidize atmospheric hydrogen using this enzyme [2].

The aerobic thermoalkaliphile *Caldalkalibacillus thermarum* strain TA2. A1 is a member of a separate order of alkaliphilic bacteria closely related to the Bacillales order. Efforts to relate the genomic information of this evolutionary ancient organism to environmental adaptation have been thwarted by the inability to construct a complete genome. The existing draft genome is highly fragmented due to repetitive regions and gaps between and over repetitive regions was unbridgeable.

Sponges (phylum Porifera) are ancient cosmopolitan filter feeders. They play an important role in nutrient recycling by transforming dissolved organic matter (DOM) into detrital particulate organic matter, thereby making it available for other invertebrates in nutrient poor environments. Symbiotic microbial communities of 268 different sponge species include more than 60 bacterial and archaeal phyla in total, with all sponges hosting symbionts of at least 13 different phyla. Sponge symbionts are often specific to one or a few hosts with the exception of a few cosmopolitan symbiotic species that are found in diverse hosts around the globe. These sponge-associated symbionts can be categorized based on their nutritional strategies, for instance (photo- and chemo-) autotrophic, organ heterotrophic, and lithoheterotrophic. Photoautotrophic and chemoautotrophic organisms harvest energy from light or inorganic compounds for inorganic carbon fixation. Autotrophic ally fixed carbon may later be used as the main carbon source by other organ heterotrophic or lithoheterotrophic microorganisms that co-occur in the same sponge [3]. Despite relying on the external carbon supply for biomass, lithoheterotrophic organisms can gain energy from inorganic sources.

## Microbial Genetics

Microbial genetics is a subject area within microbiology and genetic engineering. Microbial genetics studies microorganisms for different purposes. The microorganisms that are observed are bacteria, and archaea. Some fungi and protozoa are also subjects used to study in this field. The studies of microorganisms involve studies of genotype and expression system. Genotypes are the inherited compositions of an organism. (Austin, "Genotype," n.d.) Genetic Engineering is a field of work and study within microbial genetics. The usage of recombinant DNA technology is a process of this work. The process involves creating recombinant DNA molecules through manipulating a DNA sequence. That DNA created is then in contact with a host organism. Cloning is also an example of genetic engineering [4].

Since the discovery of microorganisms by Robert Hooke and

Antoni van Leeuwenhoek during the period 1665-1885 they have been used to study many processes and have had applications in various areas of study in genetics. For example: Microorganisms' rapid growth rates and short generation times are used by scientists to study evolution. Robert Hooke and Antoni van Leeuwenhoek discoveries involved depictions, observations, and descriptions of microorganisms. *Mucor* is the microfungus that Hooke presented and gave a depiction of. His contribution being, *Mucor* as the first microorganism to be illustrated. Antoni van Leeuwenhoek's contribution to the microscopic protozoa and microscopic bacteria yielded to scientific observations and descriptions. These contributions were accomplished by a simple microscope, which led to the understanding of microbes today and continues to progress scientists understanding [5]. Microbial genetics also has applications in being able to study processes and pathways that are similar to those found in humans such as drug metabolism.

## Bacteria

Bacteria have been on this planet for approximately 3.5 billion years, and are classified by their shape [9]. Bacterial genetics studies the mechanisms of their heritable information, their chromosomes, plasmids, transposons, and phages. Gene transfer systems that have been extensively studied in bacteria include genetic transformation, conjugation and transduction. Natural transformation is a bacterial adaptation for DNA transfer between two cells through the intervening medium. The uptake of donor DNA and its recombination incorporation into the recipient chromosome depends on the expression of numerous bacterial genes whose products direct this process. In general, transformation is a complex, energy-requiring developmental process that appears to be an adaptation for repairing DNA damage [6]. Bacterial conjugation is the transfer of genetic material between bacterial cells by direct cell-to-cell contact or by a bridge-like connection between two cells. Bacterial conjugation has been extensively studied in *Escherichia coli*, but also occurs in other bacteria such as *Mycobacterium smegmatis*. Conjugation requires stable and extended contact between a donor and a recipient strain is DNase resistant, and the transferred DNA is incorporated into the recipient chromosome by homologous recombination. *E. coli* conjugation is mediated by expression of plasmid genes, whereas mycobacterial conjugation is mediated by genes on the bacterial chromosome. Transduction is the process by which foreign DNA is introduced into a cell by a virus or viral vector. Transduction is a common tool used by molecular biologists to stably introduce a foreign gene into a host cell's genome [7].

## Extrusion Hypothesis

A highly complex but attractive theory to explain energy conservation in biologic systems is the chemiosmosis coupling of oxidative and photosynthetic phosphorylation's, commonly called the Mitchell hypothesis [8]. This theory attempts to explain the conservation of free energy in this process on the basis of an osmotic potential caused by a proton concentration differential (or proton gradient) across a proton-impermeable membrane. Energy is generated by a proton extrusion reaction during

membrane-bound electron transport, which in essence serves as a proton pump; energy conservation and coupling follow. This represents an obligatory “intact” membrane phenomenon. The energy thus conserved (again within the confines of the membrane and is coupled to ATP synthesis [9, 10]. This would occur in all biologic cells, even in the lactic acid bacteria that lack a cytochrome-dependent electron transport chain but still possesses a cytoplasmic membrane. In this hypothesis, the membrane allows for charge separation, thus forming a proton gradient that drives all bioenergization reactions.

## Conclusion

Based on the above discussion we conclude that microbial physiology even though it is a classical discipline still plays a very important role in both application-driven research (metabolic engineering) and in fundamental biological research (functional

genomics), as in many cases it is required to consider the effect of specific genetic modifications at the macroscopic level. In fact, both in metabolic engineering and functional genomics there is a move towards analysing the complete system, and here the approach of systems biology offers great promise. Returning to our introductory definition of microbial physiology it is, however, also clear that the aim of systems biology to describe at the quantitative level the interaction between all the components in the system is very similar to that of microbial physiology.

## Acknowledgement

None

## Conflict of Interest

None

## References

- 1 Jang HJ, Kim AS, Hwang JB (2012) Cytomegalovirus-associated esophageal ulcer in an immunocompetent infant: When should ganciclovir is administered. *Korean J Pediatr*. Dec 15 55: 491-3.
- 2 Yi F, Zhao J, Luckheeram RV, Wang C, Huang S, et al. (2013) The prevalence and risk factors of cytomegalovirus infection in inflammatory bowel disease in Wuhan, Central China. *Virology* 10: 43.
- 3 Li W, Fan H, Yiping L (2009) Postural Epigastric Pain as a Sign of Cytomegalovirus Gastritis in Renal Transplant Recipients: A Case-Based Review. *Transplant Proc* 41: 3956-8.
- 4 Sepkowitz KA (2001) AIDS-the first 20 years. *N Engl J Med* 344: 1764-72.
- 5 Nachega JB, Marconi VC, Gardner EM, Hong SY, Gross R, et al. (2011) HIV treatment adherence, drug resistance, virologic failure: evolving concepts. *Infect Disord Drug Targets* 11: 167-74.
- 6 Nachega JB, Mills EJ, Schechter M (2010) Antiretroviral therapy adherence and retention in care in middle-income and low-income countries: current status of knowledge and research priorities. *Current Opinion in HIV and AIDS* 5: 70-77.
- 7 Burgoyne RW, Tan DH (2008) Prolongation and quality of life for HIV-infected adults treated with highly active antiretroviral therapy (HAART): a balancing act. *J Antimicrob Chemother* 61: 469-73.
- 8 Huang L, Cattamanchi A, Davis JL, den Boon S, Kovacs J, et al. (2011) HIV-associated Pneumocystis pneumonia. *Proc Am Thorac Soc* 8: 294-300.
- 9 Beck CR, McKenzie BC, Hashim AB, Harris RC, Zanuzdana A, et al. (2013) Influenza vaccination for immunocompromised patients: summary of a systematic review and meta-analysis. *Influenza and Other Respiratory Viruses* 7 Suppl 2: 72-75.
- 10 D'Herelle F (2007) on an invisible microbe antagonistic toward dysenteric bacilli: brief note by Mr F D'Herelle, presented, Mr Roux. *Res Microbiol* 158: 553-54.