

Methanotrophs: Could bacteria help protect our environment?

August 26 2015



Landfill burn off flare. Credit: Eddie Hagler/Public Domain

New insight into methanotrophs, bacteria that can oxidise methane, may help us develop an array of biotechnological applications that exploit methane and protect our environment from this potent greenhouse gas.

Publishing in *Nature*, scientists led by Newcastle University have

provided new understanding of how methanotrophs are able to use large quantities of [copper](#) for methane oxidation.

They have identified a new family of copper storage proteins called Csp that are present in a range of bacteria. These proteins store metal in a way that has not been seen previously and their widespread presence amongst diverse bacteria raises important questions about how bacteria use copper ions, which can also be toxic to cells.

The potential

Methane availability is rising as the extraction of natural gas booms, and more methane is escaping into the atmosphere. Methanotrophs are the primary biological mechanism for mitigating the release of methane by consuming it for carbon and energy. These organisms also have great potential in the biotechnological utilisation of methane, a readily renewable carbon source, for the production of bulk and fine chemicals and sustainable energy.

To oxidise methane, methanotrophs use an enzyme called methane monooxygenase whose essential cofactor is copper (some can also use iron). Understanding how methanotrophs handle copper is therefore of great importance for all potential applications of these organisms.

The scientists describe the discovery and characterisation of Csp1 from a methanotroph that can bind large quantities of copper and propose this is a protein that accumulates copper for methane oxidation.

Lead author Chris Dennison, Professor of Biological Chemistry at Newcastle University explained: "Methane is such a useful and plentiful commodity but we need more cost effective methods to unlock its potential. Using bacteria could be the best option so a better knowledge of how these bacteria operate is required.

"As copper is so important for the oxidation of [methane](#), all potential applications based on this reactivity requires knowing how methanotrophs acquire and store copper. The discovery of the Csps adds a new dimension to our understanding of this complex process."

Co-author Colin Murrell, Professor in Environmental Microbiology at the University of East Anglia, commented: "We have known that copper is a vital element for biological [methane oxidation](#) for over thirty years and this new information will really help us to formulate new strategies for exploiting these bacteria both in the laboratory and in the environment."

Method

Metalloproteomics was used to discover Csp1 in a highly complex mixture of proteins. The analysis of recombinant Csp1 using an array of biochemical and biophysical techniques has allowed copper binding by Csp1 to be understood at the molecular level. This includes determination of Csp1 crystal structures using the facilities at Diamond Light Source. A genetically modified methanotroph has been generated to demonstrate the physiological function of Csp1.

Dr Neil Paterson, a post-doctoral research associate at Diamond Light Source, said: "The ability of Diamond Light Source to provide tuneable X-ray energy allowed us to use the intrinsic copper ions within the protein to solve the crystal structure by X-ray diffraction and also define their oxidation state through X-ray fluorescence spectroscopy."

Structure

Csp1 possesses a four-helix bundle fold, a well-established structural motif for proteins. The striking feature of Csp1 is that multiple cysteine

residues, known to avidly bind copper, point into the core of the bundle that suggested a novel way of storing a metal. Copper-binding studies and the crystal structure of the protein with copper provide a detailed insight into how the four-helix bundle of Csp1 can be filled with [copper ions](#).

More information: A four-helix bundle stores copper for methane oxidation, Nicolas Vita, Semeli Platsaki, Arnaud Baslé, Stephen J. Allen, Neil G. Paterson, Andrew T. Crombie, J. Colin Murrell, Kevin J. Waldron, Christopher Dennison, *Nature*. [DOI: 10.1038/nature14854](https://doi.org/10.1038/nature14854)

Provided by Newcastle University

Citation: Methanotrophs: Could bacteria help protect our environment? (2015, August 26)
retrieved 10 April 2024 from
<https://phys.org/news/2015-08-methanotrophs-bacteria-environment.html>

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