Tiny ocean organism has big role in climate regulation

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A rosette going into the water in Bermuda to sample SAR11. Credit: Ben Temperton

Scientists have discovered that a tiny, yet plentiful, ocean organism is playing an important role in the regulation of the Earth's climate.

Research, published in the journal *Nature Microbiology*, has found that the bacterial group *Pelagibacterales*, thought to be among the most abundant organisms on Earth, comprising up to half a million microbial cells found in every teaspoon of seawater, plays an important function in the stabilisation of the Earth's atmosphere.

Dr Ben Temperton, lecturer in the department of Biosciences at the University of Exeter, was a member of the international team of researchers that has for the first time identified *Pelagibacterales* as a likely source for the production of dimethylsulfide (DMS), which is known to stimulate cloud formation, and is integral to a negative feedback loop known as the CLAW hypothesis.

Under this hypothesis, the temperature of the Earth's atmosphere is stabilised through a negative feedback loop where sunlight increases the abundance of certain phytoplankton, which in turn produce more dimethylsulfoniopropionate (DMSP). This is broken down into DMS by other members of the microbial community. Through a series of chemical processes, DMS increases cloud droplets, which in turn reduces the amount of sunlight hitting the ocean surface.

These latest findings reveal the significance of *Pelagibacterales* in this process and open up a path for further research.

Dr Temperton said: "This work shows that the *Pelagibacterales* are likely an important component in climate stability. If we are going to improve models of how DMS impacts climate, we need to consider this organism as a major contributor."

The research also revealed new information about the way in which the *Pelagibacterales* produces DMS.

Dr Temperton added: "What's fascinating is the elegance and simplicity of DMS production in the *Pelagibacterales*. These organisms don't have the genetic regulatory mechanisms found in most bacteria. Having evolved in nutrient-limited oceans, they have some of the smallest genomes of all free-living organisms, because small genomes take fewer resources to replicate.

"The production of DMS in *Pelagibacterales* is like a pressure release valve. When there is too much DMSP for *Pelagibacterales* to handle, it flows down a metabolic pathway that generates DMS as a waste product. This valve is always on, but only comes into play when DMSP concentrations exceed a threshold. Kinetic regulation like this is not uncommon in bacteria, but this is the first time we've seen it in play for such an important biogeochemical process."

Dr Jonathan Todd from UEA's School of Biological Sciences said: "These types of ocean bacteria are among the most abundant organisms on Earth - comprising up to half a million microbial cells found in every teaspoon of seawater.

"We studied it at a molecular genetic level to discover exactly how it generates a gas called dimethylsulfide (DMS), which is known for stimulating cloud formation.

"Our research shows how a compound called dimethylsulfoniopropionate that is made in large amounts by marine plankton is then broken down into DMS by these tiny ocean organisms called *Pelagibacterales*.

"The resultant DMS gas may then have a role in regulating the climate by increasing cloud droplets that in turn reduce the amount of sunlight hitting the ocean's surface."

Dr Emily Fowler from UEA's School of Biological Sciences worked on the characterisation of the *Pelagibacterales* DMS generating enzymes as part of her successful PhD at UEA. She said: "Excitingly, the way *Pelagibacterales* generates DMS is via a previously unknown enzyme, and we have found that the same enzyme is present in other hugely abundant marine bacterial species. This likely means we have been vastly underestimating the microbial contribution to the production of this important gas."

More information: The abundant marine bacterium Pelagibacter simultaneously catabolizes dimethylsulfoniopropionate to the gases dimethyl sulfide and methanethiol, *Nature Microbiology*, DOI: 10.1038/nmicrobiol.2016.65

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