

# Science for Environment Policy

## Bacterial genes involved in making toxic methylmercury are identified

**Research into mercury** has identified two genes in bacteria that appear to be required for turning the metal into its most toxic form, methylmercury. The study adds to a growing body of research that helps us to understand the transformations that mercury undergoes in the environment and the microbes involved in these transformations.

**Mercury is harmful to animals and humans** and its more toxic form, methylmercury, can have devastating effects on the nervous system, leading to blindness, speech problems and developmental effects in the children of women exposed to mercury during pregnancy. Mercury is released into the environment by the burning of [fossil fuels](#) and other industrial processes. Some bacteria in coastal and freshwater environments are capable of transforming the metal into methylmercury, which can accumulate in high concentrations in food chains, for example, in fish.

However, until now, it was not known how the bacteria convert mercury into methylmercury. The new study claims to have solved this puzzle, and the researchers suggest that the understanding it brings to the methylmercury conversion process could potentially lead to new ways of limiting methylmercury production in the environment.

Bacteria that produce methylmercury ( $\text{CH}_3\text{Hg}^+$ ) do so by a process called 'methylation' – they add a methyl group ( $\text{CH}_3^-$ ) to a mercury ion ( $\text{Hg}^{2+}$ ) through a series of reactions that are not well understood by scientists. However, based on knowledge about the proteins involved in other bacterial methylation processes, the new study was able to identify the types of proteins that might be involved in mercury methylation.

The researchers also knew the genetic code that provides the blueprint for these proteins. Thus, by scanning for similar genetic sequences in methylating bacteria, they were able to identify genes encoding proteins with a potential role in transforming mercury into methylmercury.

The researchers named the first gene they identified *hgcA*, signifying mercury-carbon (Hg-C) bonding. The gene was found in *Desulfovibrio desulfuricans* ND132 – a mercury-methylating bacterium that had its genome sequenced in 2011. They suggest that *hgcA* encodes a protein in *D. desulfuricans*, which takes a methyl group from a folate compound and passes it to mercury. The *hgcA* gene was one of a pair; the other gene is called *hgcB*. Together, these may form key components of the mercury methylation pathway in bacteria.

When one or both of the genes were deleted by the researchers in two methylating species, the bacteria were still able to grow, but their ability to produce methylmercury was reduced. The researchers say other genes are probably involved in the methylation pathway. Similar genes were found in a number of other bacteria, but not in non-methylating species. One example of a species, among the more than 50 bacteria species identified in the current available genome database, that did have the genes was a human gut bacterium.

As the number of genome sequences grows, the researchers expect to detect a wide-spread species of methylating bacteria in a variety of environments. It is not yet clear whether all methylmercury-producing species require these genes to produce the toxic compound.



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