The Genetic Basis for Bacterial Mercury Methylation

Contact: Liyuan Liang (liangl@ornl.gov, 865-241-3933)
DOE/Office of Science/Biological & Environmental Research

Objective

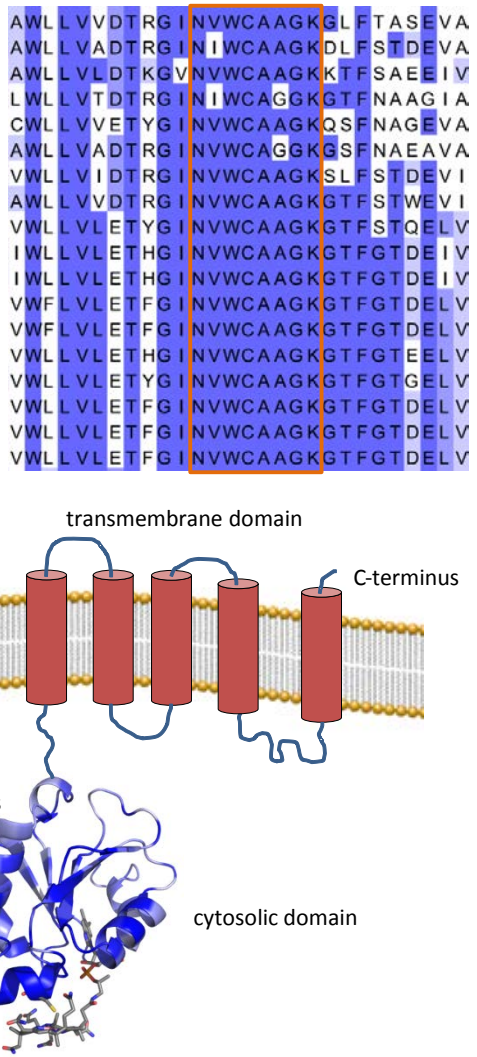
- Identify genes and enzymes responsible for microbial mercury (Hg) methylation, which have eluded scientists for decades.

New Science

- By combining chemical reasoning and genomics, we discovered two genes – *hgcA* and *hgcB* – that are required for Hg methylation. The encoded proteins are predicted to be a B_{12}-dependent methyl carrier and its auxiliary ferredoxin.
- Deleting each of these genes in *Desulfovibrio desulfuricans* ND132 and *Geobacter sulfurreducens* PCA abolished Hg methylation; activity was restored only with reintroduction of both genes.
- This two-gene cluster is present in all known Hg-methylating bacteria and archaea, and homologs have been found in the genome sequences of more than 50 diverse microorganisms.

Significance

- This discovery will enable detection of Hg methylating organisms and assessment of the extent of methylmercury production in the environment.



Homology model of *hgcA*

Parks, J.M., A. Johs, M. Podar, R. Bridou, R.A. Hurt, S.D. Smith, S.J. Tomanicek, Y. Qian, S.D. Brown, C.C. Brandt, A.V. Palumbo, J.C. Smith, J.D. Wall, D.A. Elias, and L. Liang. 2013. The genetic basis for bacterial mercury methylation. Science 339:1332-1335 (doi:10.1126/science.1230667).

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Methylmercury is a potent neurotoxin produced in natural environments from inorganic mercury by anaerobic bacteria. However, until now the genes and proteins involved have remained unidentified. Here, we report a two-gene cluster, *hgcA* and *hgcB*, required for mercury methylation by *Desulfovibrio desulfuricans* ND132 and *Geobacter sulfurreducens* PCA. In either bacterium, deletion of *hgcA*, *hgcB* or both genes abolishes mercury methylation. The genes encode a putative corrinoid protein, HgcA, and a 2[4Fe-4S] ferredoxin, HgcB, consistent with roles as a methyl carrier and an electron donor required for corrinoid cofactor reduction, respectively. Among bacteria and archaea with sequenced genomes, gene orthologs are present in confirmed methylators but absent in non-methylators, suggesting a common mercury methylation pathway in all methylating bacteria and archaea sequenced to date.

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