

Mercury and Other Heavy Metals Influence Bacterial Community Structure in Contaminated Streams

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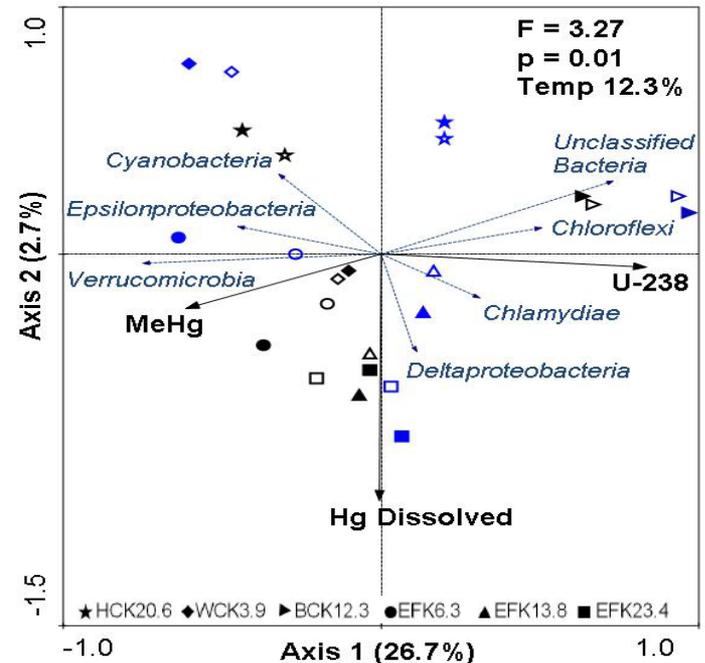
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➤ The influences of uranium (U), mercury (Hg) and methylmercury (MeHg) on the microbial community in contaminated streams were studied on the Oak Ridge Reservation.

➤ Redundancy analysis on bacterial community taxonomical data obtained through GS 454 FLX pyrosequencing of environmental 16S rDNA indicated:

- The bacterial community corresponded significantly to seasonal and geochemical factors.
- The *Verrucomicrobia* and ϵ -*proteobacteria* correlated positively with Hg and MeHg, but the sulfate-reducing δ -*proteobacteria* did not.
- There was little difference in the community structure between mid-channel and near bank samples.

This is the first study to indicate an influence by MeHg on the *in-situ* microbial community and suggests possible roles for these bacteria in the Hg/MeHg cycle.



Redundancy analysis of bacterial phyla from 24 stream sediments (six sites). Solid arrows represent geochemical parameters significantly associated ($p < 0.05$) with the variation in bacterial community structure and account for 29.4% of the variability. The remaining 70.6% of community variability between samples was not explained by measured parameters. Dashed arrows represent individual phyla ($|r| > 0.6$) significantly associated with Hg, MeHg, or U(VI). Arrow length correlates the relationship strength. Open symbols represent mid-channel, closed – near bank. Color coding: May – black; July – blue.

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High concentrations of uranium, inorganic mercury, Hg(II) and methylmercury (MeHg) have been detected in streams located in the Department of Energy reservation in Oak Ridge, TN. To determine the potential effects of the surface water contamination on the microbial community composition and the subsequent potential for MeHg generation, surface stream sediments were collected 7 times during the year from 5 contaminated locations and 1 control stream. Fifty nine samples were analyzed for bacterial community composition and geochemical parameters. Analysis of the community composition and geochemical data revealed that the *Verrucomicrobia* and the ϵ -*proteobacteria* were most closely correlated with MeHg while the δ -*proteobacteria* were more closely associated with Hg concentrations. The latter includes the sulfate-reducing bacteria and *Geobacter* spp., both of which are known to methylate Hg. However, no reports demonstrate that either the *Verrucomicrobia* or ϵ -*proteobacteria* can generate or degrade MeHg. These data suggest that an as of yet unknown function for either group in Hg biotransformations may exist and this is currently being investigated. This study is the first to indicate an influence by MeHg on the *in-situ* microbial community and suggests possible roles of the various bacteria in the overall Hg/MeHg cycle.

Vishnivetskaya T.A., J.J. Mosher, A.V. Palumbo, Z.K. Yang, M. Podar, S.D. Brown, S.C. Brooks, B. Gu, G.R. Southworth, M.M. Drake, C.C. Brandt, and D.A. Elias. 2011. Mercury and other heavy metals influence bacterial community structure in contaminated Tennessee streams. *Appl. Environ. Microbiol.* 77:302-311 (doi:10.1128/AEM.01715-10).