Title: What could be the genetic mechanisms behind mercury methylation and why has it eluded us for so long?

Dwayne A. Elias[1], Jerry M. Parks[1], Alexander Johs[1], Mircea Podar[1], Romain Bridou[2], Richard A. Hurt[1], Steven D. Smith[2], Stephen J. Tomanicek[1], Yun Qian[1], Steven D. Brown[1], Craig C. Brandt[1], Anthony V. Palumbo[1], Jeremy C. Smith[1], Judy D. Wall[2], and Liyuan Liang[1]

1. Oak Ridge National Laboratory; 2. University of Missouri

There have been numerous investigations regarding the biological generation of methylmercury (MeHg) ranging from macro-ecological studies to the molecular scale. However, at the heart of the issue lies a central question; what are the genes and proteins that convert divalent mercury (Hg(II)) to MeHg, which remain unknown.

While identification of these genes/proteins would be highly desirable and considered a substantial step forward in our understanding of Hg(II)/MeHg biochemistry, broader implications must also be considered such as answering the ongoing questions of; 1) a possibly broader phylogenetic diversity of Hg-methylating organisms that is currently known, 2) the degree of conservation between methylating genes, 3) possible advantages to the organism itself for expending energy to methylate Hg(II) and 4) whether such genes/proteins have a “native” biochemical function or are dedicated to methylating metals.

Recent bioinformatic and physiological studies in our laboratories suggest some plausible candidates that may be regarded as high value targets and may merit further investigation. These results also suggest differences at the level of genome-wide comparisons between Hg-methylators and non-methylators and will be presented in the broader physiological, metabolic and ecological context.