

Distinguished Scientist Seminar Series

10:30-12:00 p.m.

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Building 66 Auditorium

Genome Biology of *Dehalococcoides*

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Abstract

Vinyl chloride (monochloroethene) is a human carcinogen and widespread priority pollutant associated with the commercial manufacture of some polymers as well as the microbial degradation of the industrial solvents perchloroethene and trichloroethene. Microorganisms of the genus *Dehalococcoides* have been shown to use chloroethenes and other organochlorine compounds as terminal electron acceptors in respiration (dehalorespiration), thereby contributing to bioremediation of contaminated sites. The first complete genome sequences of microorganisms able to couple growth with the reduction of vinyl chloride to ethene, *Dehalococcoides* sp. strains VS and BAV1, will be discussed. Comparative analyses of these genomes with two previously sequenced *Dehalococcoides* genomes revealed a stable 'core' genome comprised of more than 70% of all genes with high contextual conservation (synteny). This core genome is interrupted in two regions that have undergone multiple independent insertions, deletions, and rearrangements. These regions, termed 'high plasticity regions' (HPR), contain the majority of genomic islands (GEIs) in the four strains, a significantly elevated number of repeated elements including insertion sequences (IS), as well as 95% of the genes encoding the terminal reductases in dehalorespiration (*rdhA*). Notably, strains VS and BAV1 harbor their respective vinyl chloride reductase-encoding operons, *vcrABC* and *bvcAB*, in different genomic locations embedded in distinct GEIs with different predicted integration sites. Together with unusual codon usage bias, this suggests not only that vinyl chloride respiration is a horizontally acquired trait, but also that these operons were acquired independently and by different mechanisms. While the number of *rdhA* genes in the four genomes ranges from 11 in BAV1 to 36 in VS, only three *rdhA* orthologous groups were shared between the genomes, and of these three, only one type was found within a conserved gene context (synteny). Horizontal acquisition of novel *rdhA* genes is indicated for approximately one-third of the 96 total *rdhA* genes in the four genomes and is likely a fundamental ecological strategy for niche adaptation in *Dehalococcoides*.



Biographical Sketch

Alfred M. Spormann is a Professor at Stanford University in the Departments of Chemical Engineering, Civil & Environmental Engineering, and (by courtesy) Biological Sciences and Geological & Environmental Sciences. He is a microbial physiologist and biochemist who received his Ph.D. from the Philipps-University, (Marburg, Germany) and conducted postdoctoral research in the Departments of Biochemistry at the University of Minnesota (Minneapolis) and Stanford University. Among his honors and awards are the Otto Moensted Visiting Professorship (2003; Danish Technical University, Lyngby, DK), the Charles Lee Powell Foundation Research Award (2000-2002), an NSF CAREER award (1998), and a Terman Fellowship Award (1995; Stanford University). He is an editor of *Applied and Environmental Microbiology* and *Archives of Microbiology* and has served on several editorial boards and committees (including *Annual Review of Microbiology*). Currently, he is the director of the Hopkins Microbiology Course (Pacific Grove, CA), and was director of the Stanford Biofilm Research Center and co-director of the Microbial Diversity Course at the Marine Biological Laboratory in Woods Hole, MA.

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