



Keynote Speaker  
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## ORGANOHALIDE-RESPIRING BACTERIA IN THE MARINE ENVIRONMENT

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Abstract Organohalide compounds are widespread in the environment as a result of both anthropogenic activities and natural production. Organobromine compounds, including brominated flame retardants, have gained widespread use, and are now common anthropogenic contaminants of aquatic sediments. The marine environment is also a rich source of a great variety of natural organobromine compounds, such as those made by sponges. Reductive dehalogenation is thought to be an important process in the overall cycling of these compounds. Organohalide-respiring bacteria (OHRB), which utilize organohalides as electron acceptors for energy conservation, can readily be enriched and have been isolated from diverse marine environments, including organohalide-contaminated sediments, pristine sites, as well as marine sponges. Based on their metabolic versatility they can be classified into facultative vs. obligate OHRBs. The growth of obligate OHRBs is restricted to organohalide respiration, while facultative OHRBs are more versatile in their metabolism and can utilize diverse electron acceptors other than organohalides. Although an increasing number of OHRBs have been isolated, it is apparent that their diversity and distribution is even more extensive. For example, the capacity of organohalide respiration appears to be widely distributed in members of marine *Deltaproteobacteria*. A comprehensive survey of *Deltaproteobacteria* genomes revealed that approximately 10% contain reductive dehalogenase (RDase) genes, which are found within a common gene neighborhood, and their gene expression were experimentally verified. The tested *Deltaproteobacteria* strains were shown to reductively dehalogenate bromophenols and utilize them as terminal electron acceptors in organohalide respiration. Their debrominating activity was not inhibited by sulfate or elemental sulfur and these species are either sulfate or sulfur reducing bacteria. Organobromine-rich sponges provide a particular specialized niche for organohalide-respiring microbes. Using a combination of cultivation-based and molecular analyses, we have demonstrated that geographically and taxonomically disparate sponges harbor populations of dehalogenating bacteria that form stable populations within the sponge animal that function in the cycling of organohalide compounds. The dehalogenating strains enriched to date are closely related to *Desulfoluna spongiiphila*, suggesting a cosmopolitan association between *Desulfoluna* spp. and various marine sponges. The identification of reductive dehalogenase genes in diverse marine *Deltaproteobacteria*, and the confirmation of their dehalogenating activity through functional assays and transcript analysis extends our knowledge of the distribution and diversity of organohalide-respiring bacteria. *Deltaproteobacteria* may play an important role in natural organohalide cycling which may have a major impact on the fate of organohalide pollutants, such as brominated flame retardants, in the marine environment.



### Biography

Dr. Max Häggblom is Distinguished Professor and Chair of the Department of Biochemistry and Microbiology. He earned his Ph.D. in General Microbiology from the University of Helsinki and after a Post-Doctoral Appointment at New York University joined the faculty of Rutgers University. Since 2011 he has served as Editor-in-Chief of FEMS Microbiology Ecology. His research interests are in microbial ecology, environmental biotechnology and in the bioexploration, cultivation and characterization of novel microbes. A common theme is the “unusual appetites” of bacteria in the Anthropocene, including the metabolism and detoxification of xenobiotic chemicals or natural products, such organohalides. His group has worked extensively on characterizing anaerobic bacteria involved in dechlorination and debromination and assessing their *in situ* metabolic activities.