Bacteria of the *Dehalococcoides* (Dhc) group play a key role in the detoxification of chlorinated ethenes. While a variety of bacteria dechlorinate tetrachloroethene (PCE) and trichloroethene (TCE) to cis-1,2-dichloroethene (cis-DCE), the reductive dechlorination of DCEs and vinyl chloride (VC) to the innocuous ethene has been firmly linked to the presence and activity of Dhc bacteria. Documented successes of biostimulation and bioaugmentation with Dhc-containing consortia at contaminated sites have given bioremediation credibility as a viable in situ technology for achieving plume control and reducing source zone contaminant flux. To support the decision-making process for selecting the most efficient remedial technology (e.g., monitored natural attenuation or biostimulation with/without bioaugmentation) and for monitoring the progress of bioremediation, molecular biological tools (MBTs) that specifically target Dhc nucleic acids have been designed. MBTs monitor Dhc biomarker gene abundance over temporal and spatial scales and provide useful information about the progress and performance of the reductive dechlorination process, especially when analyzed in conjunction with contaminant data and geochemical parameters.

Currently used Dhc biomarker gene targets for monitoring Dhc presence and abundance rely on the 16S rRNA gene and three dehalogenase genes (i.e., tceA, vcrA and bvcA) implicated in the reductive dechlorination of chlorinated ethenes. Nucleic acids are typically obtained from groundwater samples collected from suitable monitoring wells. To generate information about Dhc biomarker gene abundance, the method of choice is quantitative real-time PCR (qPCR). The qPCR data are used for site assessment and bioremediation monitoring, and to support the decisions on technology selection.

To increase confidence in the microbial MBT data, a systematic evaluation of the key steps leading from the environmental sample to quantitative information of Dhc abundance is being conducted under the auspices of SERDP- and ESTCP-funded projects. The key goals are to design a comprehensive suite of Dhc biomarker targets along with sampling and analysis procedures that generate information about the true abundance and activity of Dhc bacteria in contaminated aquifers. The challenges in interpreting Dhc DNA and RNA (i.e., transcript) biomarker data will be discussed and brought into context for making site management decisions.