



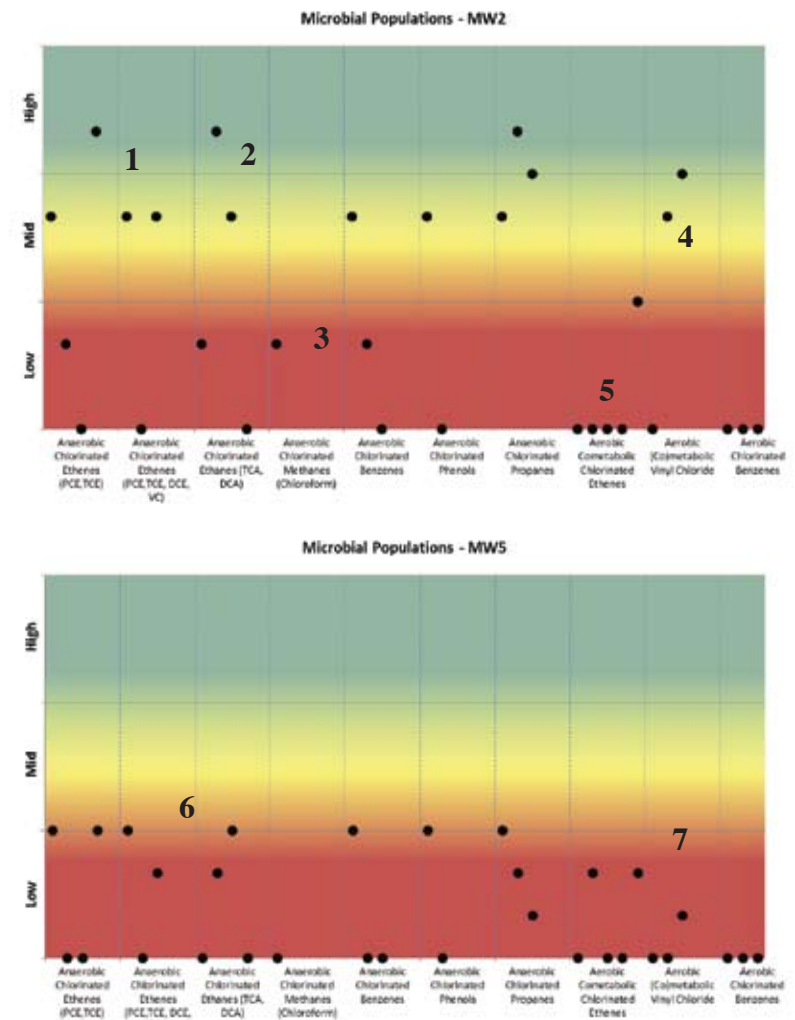
Simultaneously quantify microbes responsible for reductive dechlorination, aerobic cometabolism, and competing processes in a single analysis

QuantArray Case Study

A portion of an industrial site was impacted by trichloroethene (TCE), 1,1,2-trichloroethane (TCA), 1,2-dichloroethane (DCA), and to a lesser extent chloroform, cis-1,2-dichloroethene (DCE) and vinyl chloride. Groundwater samples were obtained from select monitoring wells and submitted for QuantArray analysis to aid in evaluating monitored natural attenuation (MNA), enhanced anaerobic bioremediation, and aerobic cometabolism as possible site management strategies.

The Microbial Population Summary figures present the concentrations of target populations (e.g. *Dehalococcoides*) and functional genes (e.g. vinyl chloride reductase and soluble methane monooxygenase) compared to typically observed values to give an overview of the potential for biodegradation of groups of compounds by anaerobic and aerobic pathways.

1. At MW2, bacterial populations capable of reductive dechlorination of TCE, DCE, and vinyl chloride were detected at moderate to high concentrations.
2. Likewise, at least two bacterial groups capable of anaerobic biodegradation of TCA and DCA were detected in the MW2 sample. Coincidentally, the vinyl chloride production observed at the site may be due to dichloroelimination of TCA rather than reductive dechlorination of DCE.
3. The potential for reductive dechlorination of chloroform appears limited based on a relatively low population of *Dehalobacter* spp.
4. Functional genes encoding enzymes responsible for aerobic (co)metabolism of vinyl chloride (etnC and etnE) were detected at moderate concentrations.
5. Overall however, microbial populations and concentrations of functional genes (e.g. soluble methane monooxygenase) capable of aerobic cometabolism of chlorinated ethenes were low.
6. At MW5, bacterial populations capable of reductive dechlorination of TCE, DCE, vinyl chloride, TCA, and DCA were detected but at relatively low concentrations.
7. The potential for aerobic cometabolism of chlorinated ethenes also appears limited under existing site conditions.



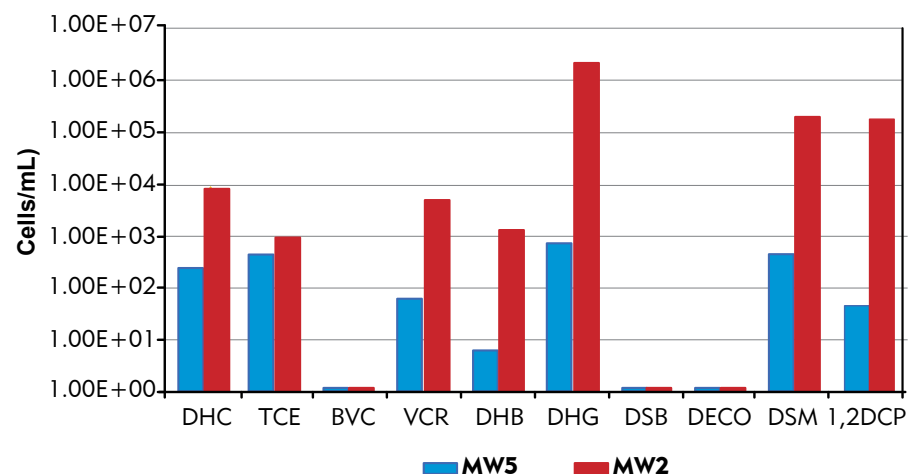
The low populations of bacteria capable of either reductive dechlorination (MW5) or aerobic cometabolism of chlorinated ethenes (MW2 and MW5) suggest that MNA may not achieve site remediation goals in an acceptable timeframe. With the moderate populations of dechlorinating bacteria at MW2 and at least the detection of dechlorinators at MW5, enhanced anaerobic bioremediation may be a feasible site remediation strategy.

Focusing on the QuantArray results for microbial populations responsible for reductive dechlorination...

Sample Information	MW5	MW2
Reductive Dechlorination (cells/mL)		
<i>Dehalococcoides</i> (DHC)	1.50E+02	4.58E+03
tceA Reductase (TCE)	2.80E+02	5.24E+02
BAV1 Vinyl Chloride Reductase (BVC)	<5.00E-01	<5.00E-01
Vinyl Chloride Reductase (VCR)	3.56E+01	2.76E+03
<i>Dehalobacter</i> spp. (DHB)	3.80E+00	7.10E+02
<i>Dehalogenimonas</i> spp. (DHG)	4.20E+02	1.20E+06
<i>Desulfitobacterium</i> spp. (DSB)	<1.00E+00	<1.00E+00
<i>Dehalobium chlorethenica</i> (DECO)	<5.00E-01	<5.00E-01
<i>Desulfuromonas</i> spp. (DSM)	2.63E+02	1.02E+05
1,2 DCP	3.15E+01	1.03E+05

1. *Dehalococcoides* and vinyl chloride reductase genes were detected at each well suggesting that bioaugmentation will not be required for complete reductive dechlorination of TCE to ethene. However, current *Dehalococcoides* concentrations are below the threshold proposed by Lu et al (2006) for generally useful rates of reductive dechlorination—electron donor addition may be necessary to stimulate growth of these key halo-respiring bacteria.
2. *Dehalobacter* spp. can utilize TCA and DCA as growth supporting electron acceptors. More recently, *Dehalobacter* strains have been implicated in the reductive dechlorination of chloroform and fermentation of dichloromethane.
3. *Dehalogenimonas* isolates couple growth to dichloroelimination of a variety of vicinally chlorinated alkanes including TCA, DCA, and DCP. Based in part on the high

Microbial Populations—Reductive Dechlorination



Dehalogenimonas population at MW2, the vinyl chloride production observed at the site may be due to dichloroelimination of TCA rather than reductive dechlorination of DCE.

4. Along with *Dehalococcoides*, *Dehalobacter*, and *Desulfitobacterium*, *Desulfuromonas* spp. are also capable of reductive dechlorination of PCE and TCE.

Based on QuantArray analysis in conjunction with traditional groundwater monitoring results, biostimulation through electron donor addition was selected as the remediation strategy.