

Although quantification of *Dehalococcoides* has become an indispensable component of assessment, remedy selection, and performance monitoring at sites impacted by chlorinated solvents, additional bacterial groups such as *Dehalobacter* spp. and *Dehalogenimonas* spp. can play key roles in reductive dechlorination of chlorinated compounds. Moreover, reductive dechlorination is not the only potential biodegradation pathway—some chlorinated compounds are susceptible to aerobic (co)metabolic biodegradation mechanisms.

The diagram illustrates the biodegradation pathways of chlorinated ethylenes and ethane. The main pathway shows PCE being reductively dechlorinated to TCE, then to cis-DCE, VC, and finally Ethene. TCE can also be epoxidized to TCE Epoxide. VC can be epoxidized to VC Epoxide. Various side pathways involve aerobic oxidation to CO<sub>2</sub> or other intermediates like 1,1,2-TCA, 1,2-DCA, and Dichloroelimination products (DHB, DHG, DSB, DSB\*). Enzymes like SMMO, TOD, and ETN are indicated for specific steps.

## Anaerobic Reductive Dechlorination

- Quantification of important halo-respiring bacteria and key functional genes
- Assess reductive dechlorination of chloro-ethenes, -ethanes, -propanes, -benzenes, -phenols, and chloroform
- *Dehalococcoides*, TCE and vinyl chloride reductases, *Dehalobacter*, *Dehalogenimonas*, *Desulfotobacterium*, *Desulfuromonas*, *Dehalobium*

## Aerobic Cometabolism

- Several different types of bacteria can co-oxidize TCE, DCE, and vinyl chloride
- Gene targets include soluble and particulate methane monooxygenase (SMMO & PMMO), toluene dioxygenase (TOD), and toluene monooxygenases (RMO, RDEG, & PHE)
- Also includes genes encoding enzymes for aerobic metabolism of chlorinated benzenes (TOD & TCBO)

## Aerobic (Co)metabolism of Vinyl chloride

- Ethene oxidizing bacteria are capable of cometabolism of vinyl chloride
- In some cases, ethenotrophs can also utilize vinyl chloride as a growth supporting substrate
- The QuantArray targets key functional genes (etnC and etnE) involved in ethene utilization and vinyl chloride (co)metabolism

**Quantification of a multitude of key microorganisms and functional genes responsible for anaerobic biodegradation, aerobic co-metabolic processes, and even competing electron accepting processes.**

#### Reductive Dechlorination

- *Dehalococcoides* (DHC)
- tceA Reductase (TCE)
- BAV1 Vinyl Chloride Reductase (BVC)
- Vinyl Chloride Reductase (VCR)
- *Dehalobacter* spp. (DHB)
- Dichloromethane dehalogenase (DCMA)
- *Dehalogenimonas* spp. (DHG)
- *Desulfitobacterium* spp. (DSB)
- *Dehalobium chlorocoercia* (DECO)
- *Desulfuromonas* spp. (DSM)
- Chloroform Reductase (CFR)
- 1,1 DCA Reductase (DCA)
- 1,2 DCA Reductase (DCAR)

#### Aerobic Co-Metabolic

- Soluble Methane Monooxygenase (SMMO)
- Particulate Methane Monooxygenase (PMMO)
- Toluene Dioxygenase (TOD)
- Phenol Hydroxylase (PHE)
- Trichlorobenzene Dioxygenase (TCBO)
- Toluene Monooxygenase 2 (RDEG)
- Toluene Monooxygenase (RMO)

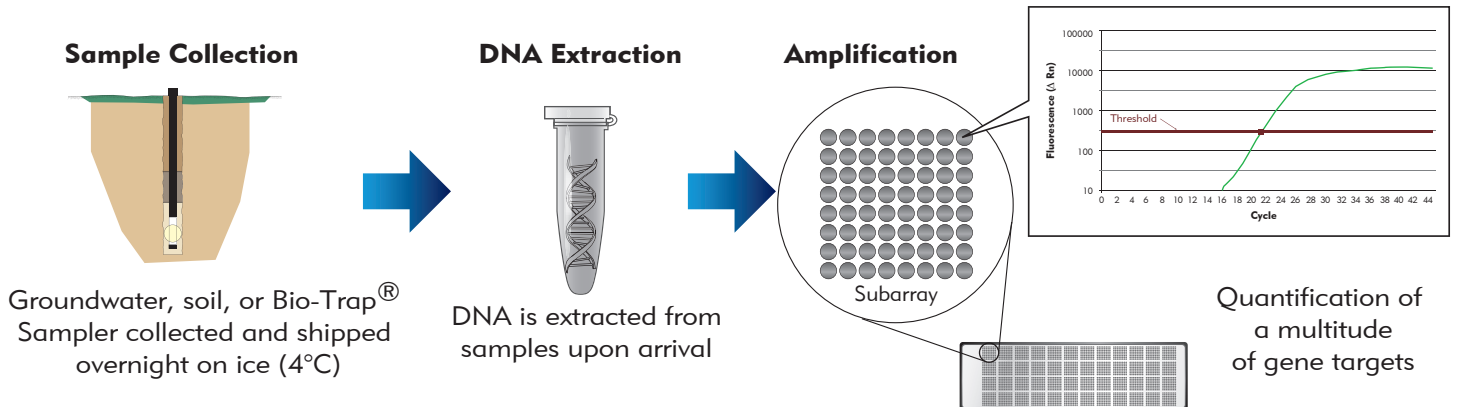
#### Aerobic (Co)Metabolism of vinyl chloride

- Ethene Monooxygenase (EtnC)
  - Epoxyalkane transferase (EtnE)
- Other Groups including Competitors
- Total Eubacteria (EBAC)
  - Sulfate Reducing Bacteria (APS)
  - Methanogens (MGN)

## How does it work?

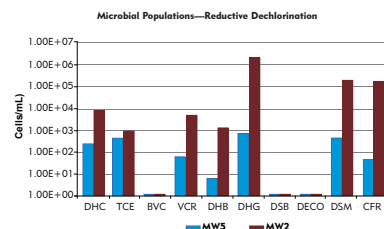
The QuantArray is a hybrid technology combining the highly parallel detection of DNA microarrays with the accurate and precise quantification of qPCR into a single platform. The key to the approach is nanoliter fluidics for low volume, solution phase qPCR allowing simultaneous quantification of different gene targets and therefore more comprehensive site assessment.

In many other respects, the QuantArray is the same as conventional qPCR with TaqMan® probes so you can expect the same level of accuracy and precision. qPCR is a process whereby many copies of a specific gene are generated. The gene copied during the process (target gene) is determined by short segments of DNA called "primers"



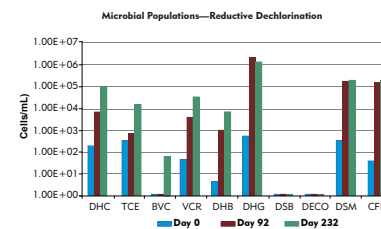
## Results

Sample Information	MW5	MW2
<b>Reductive Dechlorination (cells/mL)</b>		
<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 chlorothetica</i> (DECO)	<5.00E-01	<5.00E-01
<i>Desulfuromonas</i> spp. (DSM)	2.63E+02	1.02E+05
CFR	3.15E+01	1.03E+05



Quantification of a broad spectrum of different microorganisms and key functional genes responsible for various biodegradation pathways critical for site remediation.

## Assessment



QuantArray results are integrated with other site parameters to optimize site management