

# mi QuantArray®

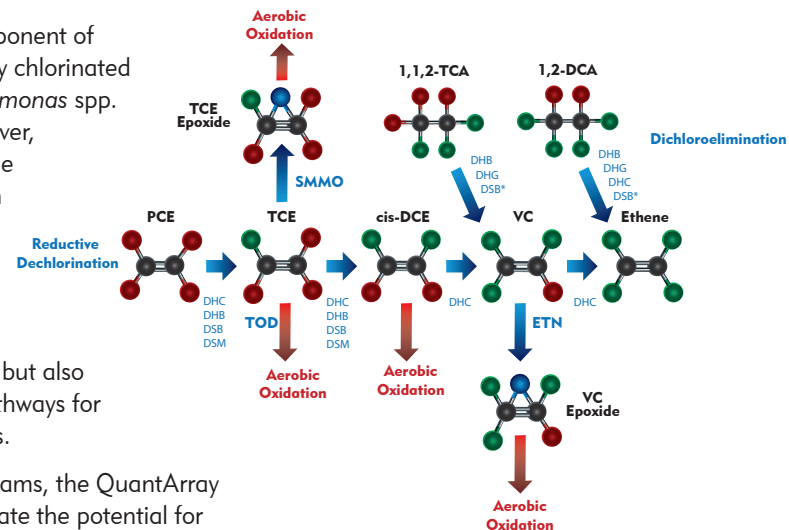
MOLECULAR BIOLOGICAL TOOL

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

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 Chlorinated QuantArray not only provides quantification of a variety of halo-respiring bacteria (*Dehalococcoides*, *Dehalobacter*, *Dehalogenimonas*, *Desulfitobacterium*, etc.) to assess the potential for reductive dechlorination of chloroethenes, chloroethanes, chlorobenzenes, chlorophenols, and chloroform but also includes quantification of functional genes involved in aerobic (co)metabolic pathways for biodegradation of chlorinated solvents and even competing biological processes.

When combined with chemical and geochemical groundwater monitoring programs, the QuantArray provides site managers with the ability to simultaneously yet economically evaluate the potential for biodegradation of a spectrum of common chlorinated contaminants through a multitude of anaerobic and aerobic (co)metabolic pathways to give a much more clear and comprehensive view of contaminant biodegradation.



## 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*, *Desulfitobacterium*, *Desulfuromonas*, *Dehalobium*, dichloropropane reductase

## Aerobic Cometabolism

- Several different types of bacteria can co-oxidize TCE, DCE, and vinyl chloride
- Gene targets include soluble methane monooxygenase (SMMO), 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)
- *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)
- Toluene Dioxygenase (TOD)
- Phenol Hydroxylase (PHE)
- Trichlorobenzene Dioxygenase (TCBO)
- Toluene Monooxygenase 2 (RDEG)
- Toluene Monooxygenase (RMO)
- Dichloromethane dehalogenase (DCMA)

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

- Ethene Monooxygenase (EtnC)
- Epoxyalkane transferase (EtnE)

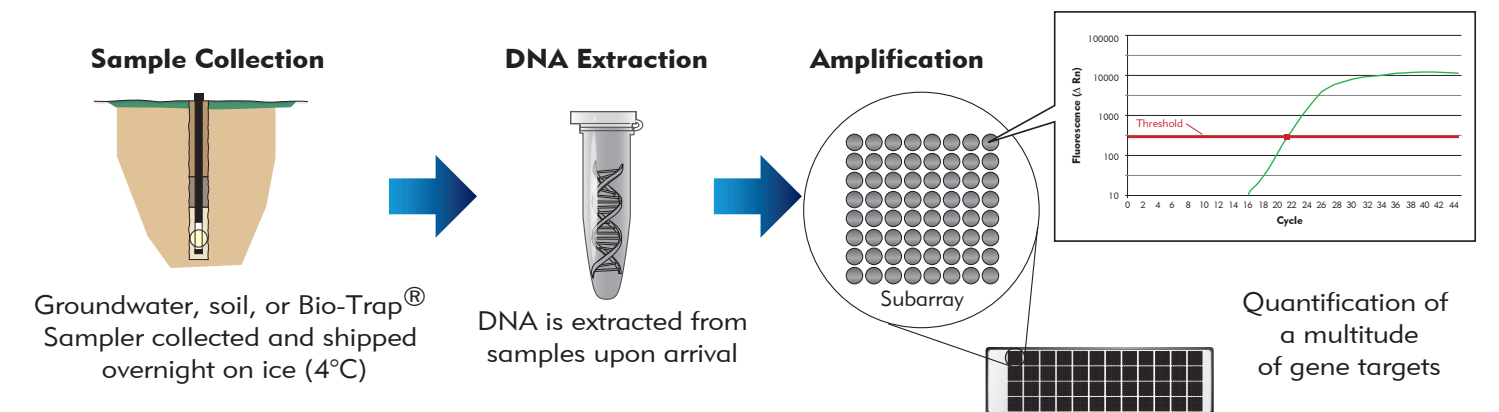
#### Other Groups including Competitors

- Total Eubacteria (EBAC)
- Sulfate Reducing Bacteria (APS)
- Methanogens (MGN)

## How does it work?

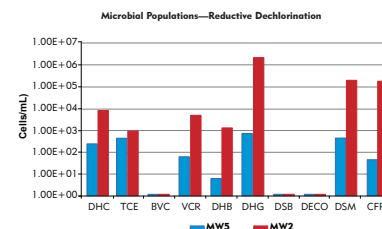
The QuantArray is a hybrid technology combining the highly parallel detection of DNA microarrays with the accurate and precise quantification of qPCR into a single platform. The key to the approach is nanoliter fluidics for low volume, solution phase qPCR allowing simultaneous quantification of different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



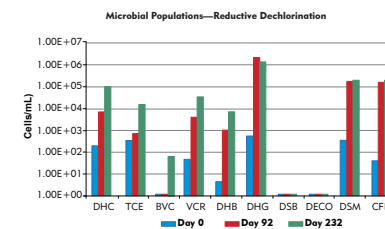
## Results

Sample Information	MW5	MW2
<i>Reductive Dechlorination (cells/mL)</i>		
<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 chloroethenica</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