



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 halorespiring bacteria (*Dehalococcoides*, *Dehalobacter*, *Dehalogenimonas*, *Desulfitobacterium*, etc.) to assess the potential for reductive dechlorination of chloroethenes, 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.

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Anaerobic Reductive Dechlorination

- Quantification of important halorespiring 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

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)
- Toleuene Monooxygenase 2 (RDEG)
- Toluene Monooyxgenase (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)

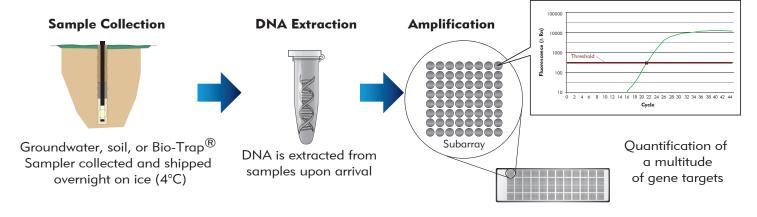
How does it work?

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. aPCR 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"

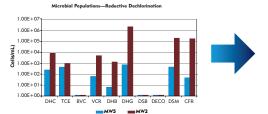
and a TagMan® "probe". As each gene copy is made, a fluorescent marker is released from the TagMan® probe, measured, and used to quantify the number of target genes present in the sample.

Other methods like multiplex qPCR have been described that achieve some level of parallel quantification. There is a fundamental difference between the QuantArray and multiplex qPCR however. For multiplex aPCR, multiple primer sets are added to a reaction mixture to quantify multiple gene targets. Unlike multiplex gPCR, the QuantArray employs discrete through-holes for individual qPCR reactions ensuring that reaction kinetics are not compromised.



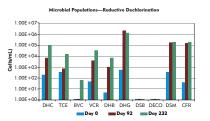
Results

Reductive Dechlorination (cells/mL) Dehalococcoides (DHC) 1 50F+02 4 58F+03 tceA Reductase (TCE) 2.80E+02 5.24E+02 BAV1 Vinvl Chloride Reductase (BVC) <5.00E-01 <5.00E-01 Vinyl Chloride Reductase (VCR) 3.56E+01 2.76E+03 Dehalobacter spp. (DHB 3.80E+00 7.10E+02 Dehalogenimonas spp. (DHG) 4.20E+02 1.20E+06 Desulfitobacterium spp. (DSB) <1.00E+00 <1.00E+00 Dehalobium chlorethenica (DECO <5.00E-01 <5.00E-01 Desulfuromonas spp. (DSM) 2.63E+02 1.02E+05 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



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