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BASED IN KNOXVILLE, TENNESSEE

Do You Dehalococcoides? WE DO!

Leading the Industry in Microbial Diagnostic Solutions

We *Dehalococcoides* and SO MUCH MORE!

Dehalococcoides spp. were the first isolated bacterial group capable of complete reductive dechlorination of tetrachloroethylene (PCE) to ethene.[1] The quantity of these bacteria possessing reductive dechlorination genes (functional genes) at sites impacted by chlorinated solvents informs methods for site remediation and monitoring. Quantify this important organism using CENSUS quantitative PCR.

Sites that have *Dehalococcoides* concentrations >10^4 cells/mL are expected to have "generally useful" reductive dechlorination rates.[2] Consistent with this, among sites around the world, *Dehalococcoides* concentrations correlate with complete reductive dechlorination of PCE to ethene, and ~80% of sites having > 10^4 *Dehalococcoides* cells/mL produce ethene —based on an analysis of Microbial Insight's Environmental Microbiology Database > 50,000 field sites, the largest collection of field concentrations of key microorganisms and functional genes. Check out Microbial Insights Database for more information.

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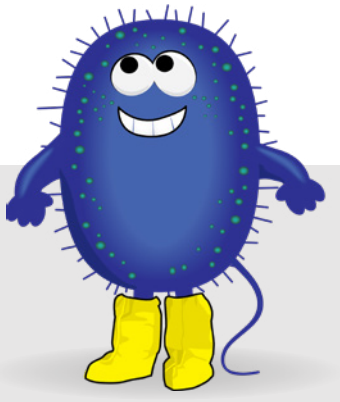
However, quantifying *Dehalococcoides* cell concentrations alone does not provide sufficient information for determining the potential for complete reductive dechlorination to ethene vs. the accumulation of daughter products (such as vinyl chloride, considered more carcinogenic than its parent compounds). By additionally quantifying the reductive dechlorination genes the overall potential for complete and efficient bioremediation of chlorinated ethenes is much easier to predict.

Although *Dehalococcoides* spp. are best known for their ability to degrade chlorinated ethenes, the same reductive dechlorination genes — tceA reductase (TCE), BAV1 vinyl chloride reductase (BVC), and vinyl chloride reductase (VCR) — can play an important role in the degradation of a broad range of chlorinated compounds, including some chlorinated ethanes (DCA), chlorinated benzenes (HCB, PeCB, TeCB, TCB), and chlorinated phenols (PCP, TeCP, TCP, DCP). Given their impressive capabilities for the biodegradation of such a large number of compounds it is important to quantify *Dehalococcoides* and their functional genes at contaminated sites impacted by any chlorinated compounds.

The innovative molecular-biological tool QuantArray®-Chlor is used to quantify *Dehalococcoides* and other key microorganisms and functional genes in order to assess the potential for reductive dechlorination and aerobic cometabolism of chlorinated compounds. By using QuantArray®-Chlor, site managers are able to make well-informed early decisions on the feasibility of monitored natural attenuation, the potential efficacy of biostimulation (e.g., adding an electron donor), or the need for enhanced bioaugmentation (adding *Dehalococcoides* with or without amendments such as buffer, electron donor, etc.). The inexpensive analysis can be performed on almost any type of sample (water, soils, sediments, Bio-Traps®, and others) and the actionable data generated by the tool ultimately translates to cost savings for site cleanup.

1. Maymo-Gatell, X., T. Anguish, and S.H. Zinder, *Reductive dechlorination of chlorinated ethenes and 1, 2-dichloroethane by "Dehalococcoides ethenogenes" 195*. Appl Environ Microbiol, 1999. **65**(7): p. 3108-13.
2. Lu, X., J.T. Wilson, and D.H. Kampbell, *Relationship between Dehalococcoides DNA in ground water and rates of reductive dechlorination at field scale.* Water Res, 2006. **40**(16): p. 3131-3140.



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