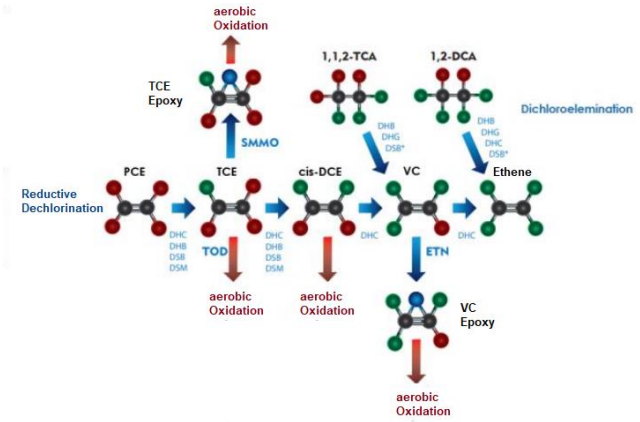
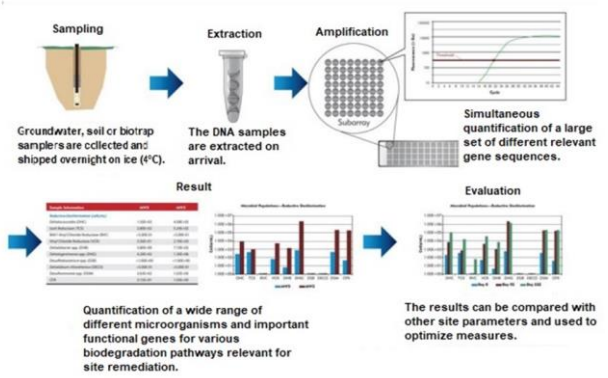
QuantArrayChlor®

QuantArrayChlor® is a molecular biology assay that simultaneously quantifies individual microbial species as well as functional genes for aerobic, cometabolic and anaerobic microbial degradation of chlorinated hydrocarbons in one single analysis.
QuantArrayChlor® allows the quantification of a variety of halorespiring bacteria (Dehalococcoides, Dehalobacter, Dehalogenimonas, Desulfitobacteriu, etc.) to evaluate the potential for reductive dechlorination of chloroethenes, chloroethanes, chlorobenzenes, chlorophenols, and chloroform and the quantification of functional genes involved in aerobic (co)metabolic pathways or competitive biological processes. Combined with chemical and geochemical groundwater data, the QuantArray provides the ability to simultaneously and economically assess the potential for biodegradation of the full spectrum of common chlorinated contaminants with a variety of anaerobic and aerobic (co)metabolic pathways to provide a clear and more comprehensive view of biodegradation.





he array includes analyses for:
•Quantification of key halorespiring bacteria and key functional genes.
- Reductive dechlorination of chlorinated ethenes, ethanes, propanes, benzenes, phenols and chloroform.
- Dehalococcoides spec. TCE and vinyl chloride reductases, Dehalobacter, Dehalimonas, Desulfitiobacterium, Desulfuromonas, Dehalobium.
•Various species of bacteria can cooxidize TCE, DCE and vinyl chloride:
- Analyses include soluble and particulate methane monooxygenase (s-MMO & p-MMO), toluene dioxygenase (TOD) and toluene monooxygenases (RMP, RDEG & PHE).
- Also included are genes encoding enzymes for aerobic metabolism of chlorinated benzenes (TOD & TCBO).
•Ethenotrophic microorganisms can cometabolize vinyl chloride. In some cases. Ethenothrope microorganisms use vinyl chloride as a growth substrate.
- Analyses include subunit genes of epoxyalkane coenzyme M transferase (EaCoMT),
- genes of the alkenes monooxygenase alpha-subunit.
As a result, it is possible to determine whether microorganisms are detectable at the site that are capable of degrading CHCs, to quantify them if necessary and to clarify the degradation mechanisms.

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