

ENVIRONMENTAL REMEDIATION



The Industry Leader in Innovative Molecular Biological Tools for Environmental Remediation, Providing the Actionable Data and Insight You Need to Make the Best Site Management Decisions



SUPERIOR CUSTOMER SERVICE

Over 200 clients report 100% customer satisfaction in working with Microbial Insights. Our goal is to not only provide you the most accurate data and expert interpretation, but to make it easy! From our MBTs, to our sample collection tools, and the access to our Database, at Microbial Insights we pride ourselves on being a trusted partner to our clients.



UNPARALLELED ACCURACY

Our MBTs provide accurate quantification of specific contaminant degrading microorganisms and functional genes, characterization of microbial communities, and conclusive evidence of contaminant degradation. The accuracy and precision of our analyses have been repeatedly proven in inter-lab comparisons with competitors, academia and national laboratories.

EXPERT ANALYSIS

For nearly three decades, Microbial Insights has been a leader in the industry. Our highly skilled scientists, who are accomplished and recognized in the fields of molecular biology and environmental remediation, provide expert interpretation and analysis of your data, making your path to site resolution and closure easier and more seamless.



COST EFFECTIVE

The data our MBTs provide, combined with our expert analysis, helps you make more informed management decisions, eliminate unnecessary site activities, and optimize a remediation strategy to cost-effectively reach site goals. Moreover, we only recommend the MBTs best suited to answer your specific site management question.



UNBIASED REPORTING

We do not sell bioaugmentation cultures or treatment products. We provide superior analysis, robust data and expert interpretation, so you can make the best possible remediation decisions that fit your specific needs, budget and timeline.



INNOVATIVE

We are continuously advancing the field of molecular microbiological tools and bringing those advancements to the Environmental Remediation industry through our active engagement in R&D and the Microbial Insights Databases.

Since 1992, Microbial Insights has been a trusted partner with environmental consultants, site owners, regulators, and government agencies for their Environmental Remediation testing, analysis, and services. Microbial Insights has extensive expertise and leverages our highly accurate, cost-effective, and informative molecular biological tools (MBTs) to provide the actionable data needed to help our clients select and implement effective remediation strategies.

ISSUE: Leaks, spills and historical manufacturing and disposal practices have led to the release of pollutants (chlorinated solvents, petroleum products, etc.) into the environment. Environmental Remediation is performed to destroy, degrade or remove these contaminants from soil, groundwater, and sediments.

IMPACT: Contamination of soil and groundwater + Toxicity + Loss of natural resources including drinking water.

THREATS: Health + Safety + Environmental Consequences.

PATH TO RESOLUTION: Our superior molecular biological tools and data interpretation provide you with the detailed insight you need to make informed site management decisions. Our MBTs provide quantification of specific contaminant degrading microorganisms and functional genes, comprehensive characterization and identification of microbial communities, and conclusive evidence of contaminant degradation. Our expert interpretation is 100% unbiased. Microbial Insights does not sell bioaugmentation cultures or treatment products. We provide the MBTs and reporting that help you make the most informed decisions for your sites, based on the best possible data and analysis.

OUR SUPERIOR TOOLS:







CENSUS®qPCR (quantitative polymerase chain reaction) is a DNA based method to accurately quantify specific microorganisms (e.g. *Dehalococcoides, Dehalobacter*) and functional genes (e.g., vinyl chloride reductase, anaerobic benzene carboxylase) responsible for biodegradation of contaminants.

QuantArray®, an advanced qPCR method, quantifies a broad spectrum of contaminant degrading microorganisms and functional genes in a single analysis for more comprehensive and cost-effective evaluation of biodegradation potential. Microbial Insights offers two versions of QuantArray for the Environmental Remediation industry: QuantArray-Chlor and QuantArray-Petro

Next Generation Sequencing (NGS) is a term for a group of advanced technologies that determine the exact order of nucleotides in DNA molecules. Based on the sequence of certain genes, NGS can identify microorganisms present in the sample down to the genus and even species level to answer the question: Who is there?

See microbe.com to learn more about these additional ER Tools

Dehalococcoides ER Compound Specific Isotope Analysis ER Stable Isotope Probing ER Phospholipid Fatty Acid Analysis ER

In Situ Microcosms ER Metagenomics ER Proteomics ER

Abiotic Panel ER
Magnetic Susceptibility ER
Oil Retention and pH

Buffering ER Bio-Trap Sampling ER Min-Trap Sampling ER



CENSUS® qPCR ADVANTAGES:



ACCURATE

Direct analysis of sample DNA removes the need to grow the bacteria, thus eliminating biases associated with traditional approaches. Microbial Insights is ISO/IEC accredited for qPCR and has proven the accuracy of our CENSUS qPCR and QuantArray assays.



OUANTITATIVE

Absolute quantification of the concentrations of specific microorganisms and functional genes encoding enzymes responsible for contaminant biodegradation gives site managers a direct line of evidence to evaluate remediation options and monitor remedy performance. Results reported as cells/mL, cells/g, etc.



INFORMATIVE

Is that a low, medium, or high concentration of contaminant degraders? With the MI Database, clients can retrieve percentile rankings of their CENSUS qPCR results to answer that question based on the tens of thousands of samples MI has received from sites around the world.



SENSITIVE

Practical Detection Limits (PDL) are as low as 100 cells per sample with a dynamic range over seven orders of magnitude. Low detection limits are particularly important when evaluating whether bioaugmentation is needed or an unnecessary expense.



SPECIFIC

Target specific bacterial groups (e.g., *Dehalococcoides*, *Dehalobacter*, *Dehalogenimonas*) and functional genes (e.g. vinyl chloride reductases, anaerobic benzene carboxylase) responsible for contaminant biodegradation.



COST EFFECTIVE

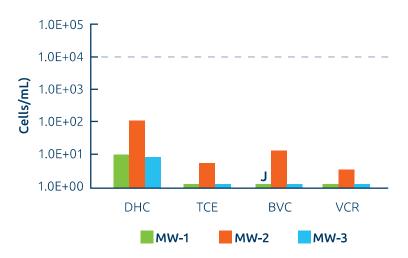
CENSUS qPCR is inexpensive and ultimately saves money by providing the actionable data needed to make the right site management decisions. Fast turnaround time (7-10 days), with rush service available, so you can make decisions and take action quickly.

CENSUS qPCR® (quantitative polymerase chain reaction) is a DNA based method to accurately quantify specific microorganisms (e.g. *Dehalococcoides*, *Dehalobacter*) and functional genes (e.g. vinyl chloride reductase, anaerobic benzene carboxylase) responsible for biodegradation of contaminants.

Along with contaminant concentrations and geochemical parameters, the concentrations of specific microorganisms and functional genes responsible for contaminant biodegradation is a key component of remedy selection and performance monitoring at sites impacted by chlorinated solvents, petroleum hydrocarbons, and emerging contaminants.

Use CENSUS qPCR to help answer...

- How feasible is MNA? Is enhanced bioremediation needed? Is bioaugmentation needed?
 - What are the concentrations of contaminant degraders under existing conditions?
 - Are degrader concentrations greater in impacted wells than background wells?
 - Based on the MI Database, are concentrations of contaminant degraders low, medium, or high in the plume?



- Is enhanced bioremediation effective?
 - Did concentrations of contaminant degraders and functional genes increase in response to treatment?
 - Are additional types of degraders and functional genes now detected that were previously below detection limits?

In the figure, CENSUS qPCR for *Dehalococcoides* (DHC) and functional genes demonstrated that bioaugmentation was not necessary and that bioatimulation should be the remediation strategy.



QuantArray® ADVANTAGES:



ACCURATE

Direct analysis of sample DNA removes the need to grow the bacteria, thus eliminating biases associated with traditional approaches. Microbial Insights is ISO/IEC accredited for qPCR and has proven the accuracy of our CENSUS qPCR and QuantArray assays.



OUANTITATIVE

Absolute quantification of the concentrations of specific microorganisms and functional genes encoding enzymes responsible for contaminant biodegradation gives site managers a direct line of evidence to evaluate remediation options and monitor remedy performance.



COST EFFECTIVE

QuantArray saves money because site managers can make highly informed decisions based on comprehensive assessment of anaerobic and aerobic biodegradation of a variety of contaminants by a multitude of microorganisms and pathways in a single analysis.



INFORMATIVE

Is that a low, medium or high concentration of contaminant degraders? With the MI Database, clients can retrieve percentile rankings of their QuantArray results to answer that question based on the tens of thousands of samples MI has received from sites around the world.



SENSITIVE

Practical Detection Limits (PDL) are as low as 100 cells per sample with a dynamic range over seven orders of magnitude. Low detection limits are particularly important when evaluating whether bioaugmentation is needed or an unnecessary expense.



SPECIFIC

Target specific bacterial groups and functional genes responsible for contaminant biodegradation.

QuantArray®, an advanced qPCR method, quantifies a broad spectrum of contaminant degrading microorganisms and functional genes in a single analysis for more comprehensive and cost-effective evaluation of biodegradation potential. Microbial Insights offers two versions of QuantArray for the Environmental Remediation industry:

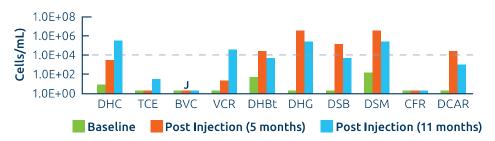
QuantArray®-Chlor quantifies key microorganisms (e.g., *Dehalococcoides, Dehalobacter*, etc.) and functional genes (e.g., vinyl chloride reductase, methane monooxygenase, etc.) to assess potential for reductive dechlorination and aerobic cometabolism of chlorinated solvents such as TCE.

QuantArray®-Petro quantifies a suite of functional genes involved in aerobic and anaerobic biodegradation of BTEX, PAHs, and other petroleum hydrocarbons.

Along with contaminant concentrations and geochemical parameters, the concentrations of specific microorganisms and functional genes responsible for contaminant biodegradation is a key component of remedy selection and performance monitoring at sites impacted by chlorinated solvents or petroleum hydrocarbons.

Use QuantArray-Chlor or QuantArray-Petro to help answer...

- How feasible is MNA? Is enhanced bioremediation needed? Is bioaugmentation needed?
 - What are the concentrations of contaminant degraders under existing conditions?
 - Are degrader concentrations greater in impacted wells than background wells?
 - Based on the MI Database, are concentrations of contaminant degraders low, medium, or high in the plume?



- Is enhanced bioremediation effective?
 - Did concentrations of contaminant degraders and functional genes increase in response to treatment?
 - Are additional types of degraders and functional genes now detected that were previously below detection limits?

QuantArray-Chlor results showed site managers that bioaugmentation was not needed and that the subsequent electron donor injection not only promoted growth of *Dehalococcoides* (DHC) but also increases in a broad spectrum of other key halorespiring bacteria and functional genes.



NGS ADVANTAGES



IDENTIFICATION

Who is there? Next generation sequencing (NGS) provides comprehensive identification of microorganisms present in a sample down to the genus and even the species level.



RELATIVE ABUNDANCE

While not quantitative, NGS reports include the relative proportions of the microorganisms identified in the sample based on number of classified sequence reads.



REVEALING

NGS reveals the overall microbial community composition. Knowing which microorganisms are present and their relative abundances provides insight into the types of microbial processes might be occurring such as fermentation or metals reduction. In addition, NGS is commonly used at sites impacted by emerging contaminants where biodegradation pathways are unknown and therefore CENSUS qPCR and QuantArray assays are not available.



COMPATIBLE

Multiple lines of evidence can provide a more complete picture. At complex and challenging sites, NGS is often used for an overall profile of the microbial community composition while CENSUS qPCR or QuantArray is performed to quantify known contaminant degraders and functional genes.



DESCRIPTIVE

NGS reports include brief descriptions of the top genera identified in each sample. The descriptions highlight the metabolic capabilities commonly associated with the genus.



COMPARATIVE

Reports include statistical analysis that compares NGS results between samples to reveal important differences or shifts in the microbial community between monitoring wells, over time, or in response to treatment.

Next generation sequencing (NGS) is a term for a group of advanced technologies that determine the exact order of nucleotides in DNA molecules. Based on the sequence of certain genes, NGS can identify microorganisms present in the sample down to the genus and even species level to answer the question: Who is there?

Next generation sequencing (NGS) is a powerful molecular biological tool designed to answer the question: What microorganisms are present?

Use NGS to help answer...

- What microorganisms are present?
- How diverse is the microbial community?
- How did the microbial community change in response to site activities?
- Which microbes were relatively more or less abundant after treatment?
- What are the differences in the microbial communities along the dissolved plume?
- What biogeochemical processes are likely in each zone?
- Are different types of microbes present in downgradient areas?

Background MW-3				Source Area MW-1		
Genus	Reads	Percent	Genus	Reads	Percent	
Pseudomonas	337,932	44.9%	Rhodofe	erax 338,375	38.3%	
Methylotenera	121,349	16.1%	Geobaci	ter 155,421	17.6%	
Geobacter	115,818	15.4%	Sulfurita	alea 54,382	6.2%	
Dechloromonas	50,124	6.7%	V ► Dechlor	omonas 43,026	4.9%	
Sulfuritalea	39,649	5.3%	Azovibri	io 31,669	3.6%	
Rhodoferax	33,637	4.5%	/ Sulfuric	urvum 22,763	2.6%	
Azoarcus	29,117	3.9%	Plaromo	onas 18,810	2.1%	
Gallionella	24,697	3.3%	Syntrop	hus 14,797	1.7%	
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			Pseudoi	monas —	_	
			Methylo	otenera —	_	





microbe.com 865-573-8188

Microbial Insights, Inc. USA

Ship samples to:
ATTN: Sample Custodian
10515 Research Drive Knoxville, TN 37932 USA
865-573-8188







