# QuantArray®

MOLECULAR BIOLOGICAL TOOL

*Simultaneously quantify microbes involved in Microbial Induced Corrosion and Oilfield Souring in a single analysis.*

Microbial induced corrosion (MIC) impacts nearly all industries and can exact a severe toll in terms of loss of production, O&M costs, deterioration of equipment and potentially the health, safety, and environmental consequences of corrosion related failure. MIC and souring are complex processes that depend on the actions and interactions of diverse bacterial communities of not only sulfate reducing bacteria but also acid producing bacteria, methanogens, iron oxidizers, slime formers, denitrifiers, and sulfur oxidizing bacteria. The QuantArray provides simultaneous quantification of key organisms and functional genes involved in MIC as well as oilfield souring providing a more comprehensive assessment.

| Target | Relevance |
|---|---|
| Total Bacteria | Monitoring total bacteria provides a general measure for evaluating bacterial growth in the system. |
| Total Archaea | Archaea are another domain of single celled microorganisms which can initiate and contribute to MIC. |
| Sulfate Reducing Bacteria | Sulfate reducing bacteria consume hydrogen, produce $H_2S$ and are probably the most commonly implicated group of microorganisms in the pitting corrosion of metals. |
| *Desulfovibrio* spp. | A specific genus of sulfate reducing bacteria implicated in MIC. |
| Sulfate Reducing Archaea | Sulfate reducing archaea consume hydrogen, produce $H_2S$ and have been implicated in MIC related piping failures. |
| *Archeoglobus* spp. | A specific genus of hyperthermophilic, sulfate reducing archaea implicated in MIC at elevated temperatures. |
| Methanogens | Methanogens utilize hydrogen for growth, can contribute to cathodic depolarization, and can cause corrosion rates comparable to sulfate reducing bacteria. |
| Fermenters | Anaerobic bacteria produce organic acids and hydrogen. Acid production can lead to localized drop in pH facilitating corrosion while hydrogen production can support growth of other MIC associated organisms including SRB. |
| Acetogens | Acetogenic bacteria are strict anaerobes that produce acetate from the conversion of $H_2$–$CO_2$, CO or formate. The presence of acetic acid is known to exacerbate carbon dioxide corrosion of carbon steel. |
| Nitrate Reducing Bacteria | Increasingly, nitrate addition is being used to stimulate growth of nitrate reducing bacteria as a bioexclusion strategy to combat SRB-mediated reservoir souring and MIC. |
| Iron Oxidizing Bacteria | Group of microorganisms commonly implicated in metal deposition and tubercle formation. |
| Manganese Oxidizing Bacteria | Like iron oxidizing bacteria, manganese oxidizing bacteria are capable of making deposits of metal oxides. |
| Sulfur Oxidizing Bacteria | Often aerobic bacteria oxidize sulfide or elemental sulfur producing sulfuric acid. Commonly implicated in corrosion of concrete. |
| Iron Reducing Bacteria | IRB reduce insoluble ferric iron to soluble ferrous iron potentially facilitating the removal of protective corrosion products formed on exposed iron alloy surfaces. However, other studies have suggested that the actions of IRB can inhibit corrosion through a variety of mechanisms. |
| *Geobacter* spp. | Generally considered a genus of iron reducing bacteria although some species are also capable of sulfate reduction. Some species been shown to significantly enhance the local corrosion of steel. |
| *Shewanella putrefaciens* | Anaerobic bacteria which utilize cathodic hydrogen as an energy source, reduce ferric iron and sulfite to ferrous iron and sulfide indicating that it can play a role in MIC. |
| Ammonia Oxidizing Bacteria | Ammonia oxidation or nitrification produces nitric acid causing corrosion of concrete and natural stone. Depending on alkalinity levels, nitrification in water systems can increase lead contamination and may increase copper solubility. |
| Nitrogen Fixing Bacteria | Nitrogen fixation converts nitrogen gas into ammonia which can be assimilated by organisms. Nitrogen fixation may become increasingly important in mature biofilms. |
| Exopolysaccaride Production | Gene involved in production of exopolysaccharide (EPS) and biofilm formation by some *Burkholderia* spp. |
| *Deinococcus* spp. | Genus of bacteria considered to be very efficient primary biofilm formers and therefore have been implicated in slime formation and biofouling. |
| *Meiothermus* spp. | Like *Deinococcus* spp., *Meiothermus* spp. are efficient primary biofilm formers and frequently implicated in slime formation and biofouling. |

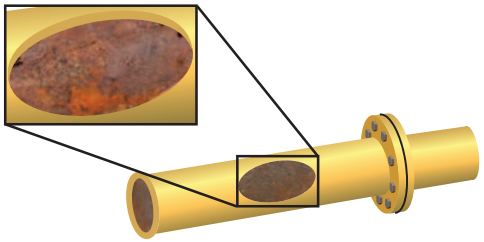
## How does it work?

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" and a TaqMan® "probe". As each gene copy is made, a fluorescent marker is released from the TaqMan® 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 qPCR, multiple primer sets are added to a reaction mixture to quantify multiple gene targets. Unlike multiplex qPCR, the QuantArray employs discrete through-holes for individual qPCR reactions ensuring that reaction kinetics are not compromised.

### Sample Collection

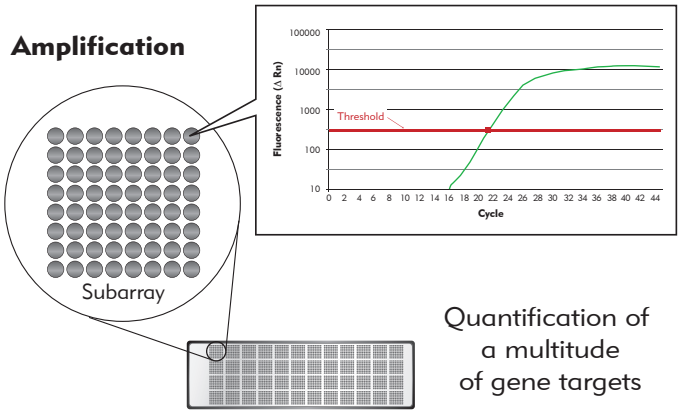


Samples (corrosion coupons, water, soil, Bio-Trap, etc.) are collected and shipped overnight on ice (4°C).

### DNA Extraction

DNA is extracted from samples upon arrival

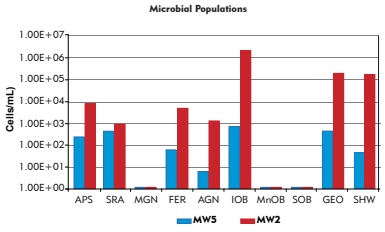
### Amplification




Quantification of a multitude of gene targets

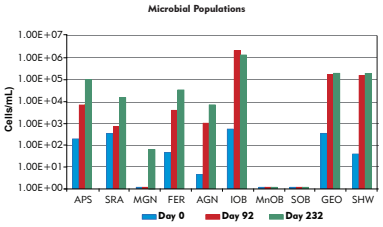
### Results

| Sample Information | Pipe 1 | Coupon 2 |
|---|---|---|
| *Microbiologically Influenced Corrosion (cells/mL)* | | |
| *Sulfate Reducing Bacteria (APS)* | 1.50E+02 | 4.58E+03 |
| *Sulfate Reducing Archaea (SRA)* | 2.80E+02 | 5.24E+02 |
| *Methanogens (MGN)* | <5.00E-01 | <5.00E-01 |
| *Fermenters (FER)* | 3.56E+01 | 2.76E+03 |
| *Acetogens (AGN)* | 3.80E+00 | 7.10E+02 |
| *Iron Oxidizing Bacteria (IOB)* | 4.20E+02 | 1.20E+06 |
| *Manganese Oxidizing Bacteria (MnOB)* | <1.00E+00 | <1.00E+00 |
| *Sulfur Oxidizing Bacteria (SOB)* | <5.00E-01 | <5.00E-01 |
| *Geobacter spp. (GEO)* | 2.63E+02 | 1.02E+05 |
| *Shewanella (SHW)* | 3.15E+01 | 1.03E+05 |




Quantification of a broad spectrum of different microorganisms and key functional genes responsible for MIC.

### Assessment




QuantArray results are evaluated along with operating parameters and conditions to optimize facility management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