mi NGS
MOLECULAR BIOLOGICAL TOOL
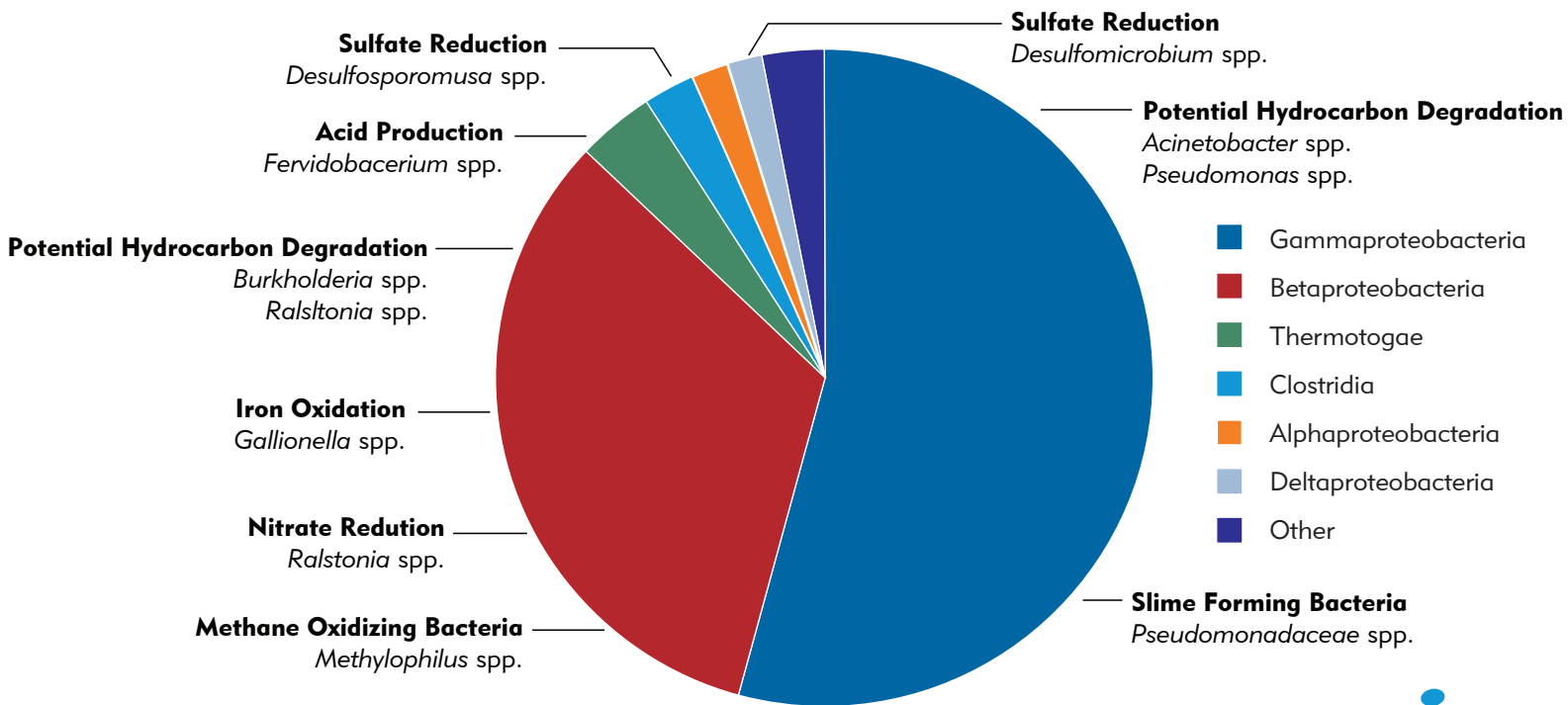
Characterize microbial communities associated with MIC

Microbial induced corrosion (MIC) is a complex phenomenon directly and indirectly attributed to diverse microbial communities of sulfate reducing bacteria, acid producing bacteria, acetogens, fermenters, slime formers, iron and manganese oxidizing bacteria, methanogens, and sulfur oxidizing bacteria among others.

Next-generation sequencing or high-throughput sequencing is a collection of advanced technologies for determining DNA sequences much more rapidly and less expensively than previous methods. No other technique yet developed provides more comprehensive characterization of the microbial community of an environmental sample or better answers the question: *Who is there?*

Identification: Next-generation or high-throughput DNA sequencing provides identification of microorganisms present in an environmental sample down to the genus level with no prior knowledge of the microbial community composition. Although function cannot always be predicted from phylogeny, comprehensive identification of the microorganisms present offers unprecedented insight into the potential microbial processes occurring in the environment.

Profile Comparisons: Comparisons of next-generation sequencing results between samples can reveal important differences or shifts in the microbial community by location, over time, or in response to changes in process operations and O&M activities.

Sulfate Reduction
Desulfosporomusa spp.

Acid Production
Fervidobacerium spp.

Potential Hydrocarbon Degradation
Burkholderia spp.
Ralsltonia spp.

Iron Oxidation
Gallionella spp.

Nitrate Redution
Ralstonia spp.

Methane Oxidizing Bacteria
Methylophilus spp.

Sulfate Reduction
Desulfomicrobium spp.

Potential Hydrocarbon Degradation
Acinetobacter spp.
Pseudomonas spp.

- Gammaproteobacteria
- Betaproteobacteria
- Thermotogae
- Clostridia
- Alphaproteobacteria
- Deltaproteobacteria
- Other

Slime Forming Bacteria
Pseudomonadaceae spp.

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How does it work?

While each platform is unique, the overall steps and the underlying concepts are similar. DNA is extracted from the sample and fragmented into a library of small segments that are amplified and subsequently sequenced in millions of parallel reactions. The sequencing step is similar to previous methods—the bases of each DNA fragment are sequentially identified from light signals emitted as the complement to each fragment strand is re-synthesized. The net result is a set of newly identified strings of nucleotides called "reads" that represent members of the microbial community present in the original sample.

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

Template Preparation

Genomic DNA or cDNA

Library Preparation

Library Amplification

Sequencing and Imaging

GCCAGCCGTGTTTACAGA…
GCCGGCTCTAGCTTCCGT…

Results

Results are emailed to project contact

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