



MOLECULAR BIOLOGICAL TOOL

Profile and Identify Dominant Members of a Microbial Community

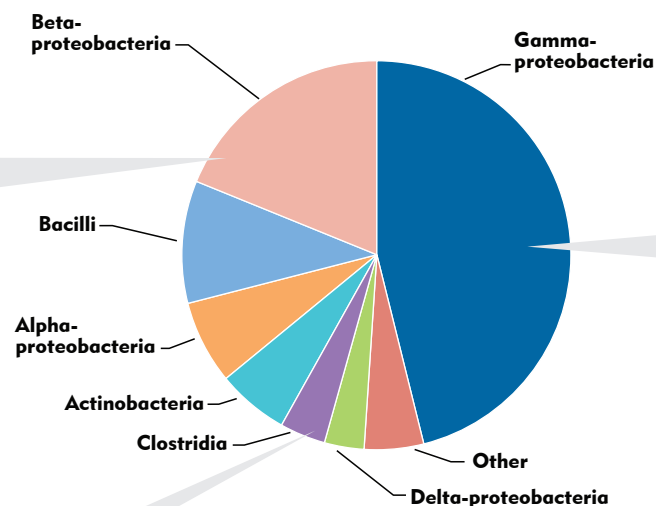
Environmental Bioremediation is a complex process mediated by the diverse metabolic activities of various indigenous microorganisms functioning in consortia and communities and impacted by site-specific geochemical factors. Bioremediation has been applied to metal/radionuclide reduction and degradation of petroleum hydrocarbons, chlorinated solvents, polychlorinated biphenyls, and nitro-aromatics just to name a few.

Next Generation Sequencing (NGS) is a high-throughput DNA-based technique that offers the advantages of scalability and speed in providing in-depth resolution of microbial community members in contaminated environments. 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 microbial classes between samples can provide insight into differences or changes in microbial communities by contaminated site, over time, or in response to process operations and remedial actions.

<p>Denitrification</p> <p><i>Azoarcus</i> is capable of mineralizing halobenzoates under denitrifying conditions.</p>
<p>Hydrocarbon Degradation</p> <p><i>Ralstonia</i>, <i>Burkholderia</i>, and other Betaproteobacteria completely mineralize various hydrocarbons (e.g., PAHs) under aerobic conditions.</p>
<p>Heavy Metal Reduction</p> <p><i>Achromobacter</i> sp. mediates anaerobic reduction of hexavalent chromium.</p>
<p>Radionuclide Immobilization</p> <p>Certain species of anaerobic clostridia have been shown to reduce uranium(VI) to uranium(IV).</p>



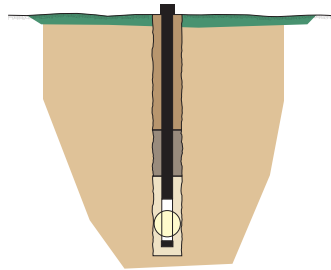
<p>Potential Hydrocarbon Degradation</p> <p><i>Ubiquitous Pseudomonas</i> spp., frequently found in contaminated soils, degrade polycyclic aromatic hydrocarbons.</p> <p><i>Acinetobacter</i> spp. utilize n-alkanes as carbon sources.</p>
<p>Polychlorinated Biphenyl Degradation</p> <p><i>Pseudomonas</i>, <i>Acinetobacter</i>, <i>Aeromonas</i>, and <i>Vibrio</i> degrade mono-, di-, tri-, and some tetrachlorinated PCBs.</p>
<p>Metal Reduction</p> <p>Gammaproteobacteria possess a variety of metal-reducing capabilities as a result of anaerobic respiration.</p>
<p>Pesticide and Dye Elimination</p> <p>Activities of some Gammaproteobacteria degrade pesticides and decolorize dyes.</p>

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



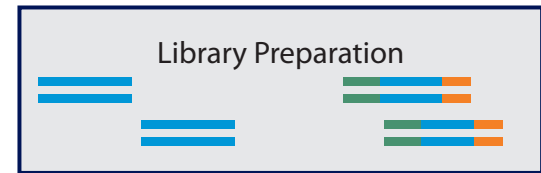
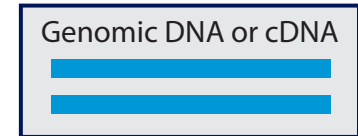
Samples (groundwater, soil, Bio-traps, etc.) are collected and shipped overnight on ice.

DNA Extraction



DNA is extracted from samples upon arrival

Template Preparation



Results



Results are emailed to project contact