FREQUENTLY ASKED QUESTIONS
Subsurface DNA Diagnostics™ service offerings include:

**DNA WellSpace®**
Estimate drainage height to optimize well placement

**DNA Target®**
Identify sweet spots for targeted stimulation

**DNA Surveillance®**
Monitor well connectivity to improve field development

**DNA Profile®**
Measure production over time for engineered completions
How can Biota’s Subsurface DNA Diagnostics™ add value?

The application of DNA sequencing to the oil industry provides operators with a novel data source for reservoir characterization to maximize production and NPV while minimizing environmental impact.

Subsurface DNA can be used to guide well spacing, determine oil potential, evaluate well connectivity, and understand production profiling.

Subsurface DNA is a non-invasive, high-resolution data source that enables integrated analysis across production life cycles and does not require downhole tool deployment or added environmental risk.

Subsurface DNA Diagnostics was recently deployed in the Wolfcamp Shale to estimate vertical drainage heights and landing zones for multiple laterals wells.¹

The results provide unprecedented reservoir insight, and have the potential to increase the EUR and NPV per section by several millions through optimized well spacing and production monitoring.

Additionally, Subsurface DNA has been used to monitor well-to-well communication over time, confirming subsurface fracture propagation and frac hits. These findings have the potential to save millions of dollars through targeted completion designs, ultimately increasing efficiency and asset value.

HOW IT WORKS

How does DNA analysis work?

Subsurface DNA is obtained from reservoir fluids (oil, water, emulsions), well cuttings, and/or cores. Samples are collected in the field and returned to the lab where DNA is extracted using techniques optimized specifically for oil field samples. Samples are then sequenced using next-generation DNA sequencing technology to return thousands of reads per sample.

After sequencing, the data are thoroughly checked to remove any sequences that may have been introduced by human and environmental contamination to ensure the highest Subsurface DNA signal fidelity.

¹ The results provide unprecedented reservoir insight, and have the potential to increase the EUR and NPV per section by several millions through optimized well spacing and production monitoring.
Biota provides the required materials and training to ensure sample integrity during collection and shipping. In addition to field samples, controls such as drilling muds, fracturing fluids, and other inputs to the system are collected for quality control. After collection, samples are kept cold during handling and shipping to minimize changes to the DNA.

**How is DNA sequencing different from tracers and geochemical analysis?**

Analyzing well performance and production profiling by Subsurface DNA is an independent method that can be deployed without any operational modifications or production interruptions.

Unlike tracers, which need to be added to stages and require supplemental oversight, Subsurface DNA requires no additional work since it relies on naturally occurring microbes.

Generally, tracers and geochemical measurements result in a few data points per sample, while Subsurface DNA returns a minimum of 5,000 sequences per sample, orders of magnitude more than other techniques.

In science wells and pilot projects where additional independent reservoir data sets exist, Subsurface DNA can be fully integrated with tracer, geochemical, and other data to provide independent validation and fully characterize the reservoir.

**How does DNA describe the subsurface?**

Geological controls, including depositional environment, lithology, diagenetic processes, and vertical/lateral heterogeneity ultimately drive modern microbial colonization and thus Subsurface DNA. Where reservoir and subsurface conditions change, these variations can be observed through alterations in microbial communities (Figure 1).

Figure 1. Subsurface DNA originates from microbes that live in the fracture networks and pore space of rocks. This DNA captures stratigraphy and lateral heterogeneity at a higher resolution than current methods applied to the subsurface.
How do you utilize Subsurface DNA variation across and within stratigraphy?

Initially, a stratigraphic profile will be made to correlate Subsurface DNA to well cuttings or core from the vertical section of a well. Well cuttings from the lateral wellbore will be used to extract Subsurface DNA and allows characterization of lateral subsurface heterogeneities. Produced fluids (oil, water) will be used in comparison to the vertical and lateral Subsurface DNA baselines to estimate vertical drainage height and production profile (Figure 2).

Because microbes are sensitive to environmental conditions, their DNA signatures will reflect changing reservoir conditions, such as fracturing, early flow back, and production. The magnitude of these changes range in size and Biota’s technology can closely monitor and detect changes in the reservoir at unprecedented resolution.

What is the impact of frac and workover fluid on the subsurface microbial communities?

The exact role that frac and workover fluid plays on impacting microbial communities remains under evaluation, but likely varies from location to location and by the amount and type of fluid used. Biota analyzes over 5,000 DNA sequences per sample, allowing for quantification and monitoring of microbial communities over time, even during operational changes.

SUBSURFACE SCIENCE

Where do the microbes live?

Most Subsurface DNA is obtained from microbes living in fractures, faults, and large interparticle pores (Figure 1).

Figure 2. Subsurface DNA varies significantly across stratigraphy and lateral heterogeneity. Biota measures these changes by extraction of Subsurface DNA from cuttings and produced fluids during production to estimate vertical drainage height and closely monitor how reservoirs change during production.
Microbes are very small, averaging 1 μm in diameter – small enough to live in some mineral matrix pores, including interparticle pores, and organic-matter pores, depending on reservoir lithology, diagenesis, and history.

The majority of microbial communities, however, are thought to be living in fracture pores. Pore space formed through faults, fractures, and joints provides sufficient space for microbial communities to survive, and provides conduits for preferential fluid flow delivering energy sources for these microbes. Estimates of fracture density in the Bakken, Permian, and Eagle Ford all provide sufficient fracture-associated porosity to account for the range of DNA features observed by Biota.

These microbes can live off a wide range of energy sources, with the specific energetic pathways being driven by geology and reservoir properties. Biota utilizes this connection to provide subsurface analysis with unprecedented resolution.

What are the thresholds for microbial survival in the subsurface?

Microbes exist in abundance within typical onshore reservoirs, such as the Bakken, Permian, Eagle Ford, and Montney Shale.

With respect to extremes, studies have shown that microbes are capable of reproducing at temperatures over 250 °F, pH ranges from 0 to 13, hypersaline solutions, and high-pressure environments over 15,000 PSI.²

Estimates indicate that between 75 and 94% of the Earth’s microbes reside in the deep subsurface.³ Previous work has conclusively demonstrated active microbial communities in deep terrestrial subsurface environments, including in oil and gas wells.⁴,⁵

Figure 3. Microbial communities were present during primary deposition of sedimentary rocks (left). However, they are not thought to have survived during burial and oil generation (center). Late stage fluid flow during uplift is thought to have deposited most of the microbes responsible for Subsurface DNA found today (right).
How did the microbes get to the deep subsurface?

Late stage fluid flow during original sediment deposition millions of years ago is thought to have deposited most of the microbes found today (Figure 3).

Post-diagenetic fluid mobilization and migration is thought to be the main driver of microbial input and colonization in the system. Although some microbes could have been deposited during primary deposition or early diagenetic pathways, it is estimated that the majority of sequenced DNA comes from microbes introduced in the later stages of geological uplift and fluid flow when reservoir conditions and fracture networks were more favorable for microbial colonization.6

What do microbes require for survival, given the harsh conditions of the subsurface?

Microbes are sensitive to their surrounding environment and have an extraordinary ability to adapt accordingly. This is accomplished by the use a wide range of chemical compounds for energy sources, depending on geology and reservoir conditions.

Energy sources for microbial growth can be acquired from pathways such as hydrocarbon oxidation, sulfate reduction, iron oxidation and reduction, methanogenesis, and nitrate reduction. Carbon for growth is either sourced from hydrocarbons, organic matter, or the carbon dioxide found in fluids and minerals.

Specific biochemical pathways depend on reservoir characteristics, such as primary depositional environment, paleo-redox conditions, and elemental concentrations. The diversity of possible metabolic pathways rooted to geologic history makes subsurface DNA a unique and powerful tool for understanding the subsurface.

REFERENCES


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