Industrial Genomics in Oil & Gas
Science, Solutions, Results

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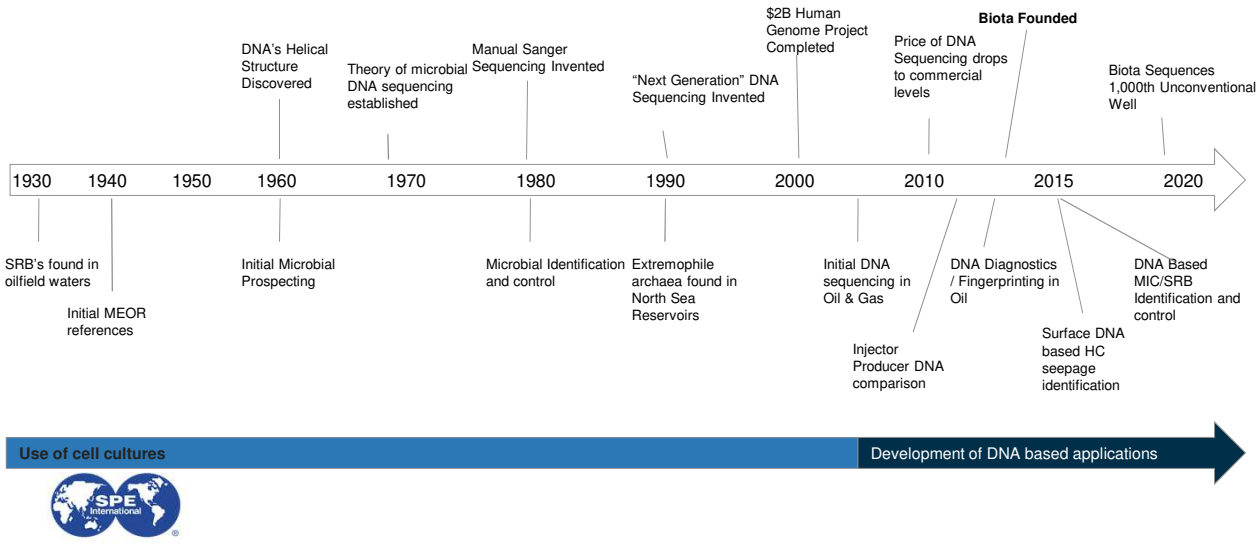
Content

- Foundation for Industrial Genomics in Oil & Gas
- Workflow
- Solutions
  - Conventional, Unconventional
- Case studies
- Outlook

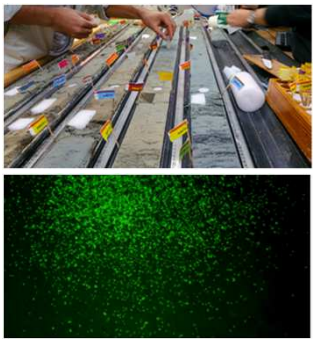
Industrial Genomics - A New Diagnostic with Historic Roots



Microbiome and Bioinformatics

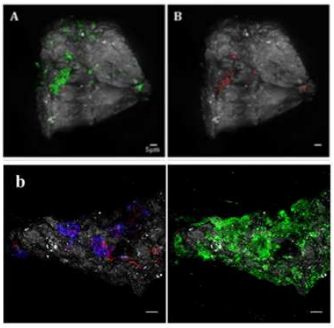
The Subsurface Microbiome – Preserved, but also changing

Ocean Bed Core (2020



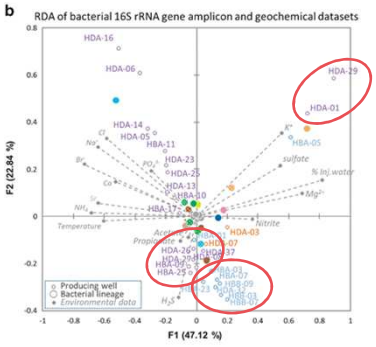
"Living" bacteria isolated from 100 million year old clay Sciencemag 2020/07

Pyrite Mine in Spain (2018)



Diverse, connected communities in um pore space
Nature January 2018

Halfdan Oilfield (2016)



Microbiome through production lifecycle (DOE, Shell)
Nature / ISMEJ May 2017

Characterizing the microbiome – Speed vs Resolution

qPCR / ddPCR *How many?*

Marker Gene Sequencing *Which ones?*

Metagenomics *What can they do?*

Metatranscriptomics *What are they doing?*

DNA Extraction

Target Amplification

Next Generation Sequencing

Data Science / Bioinformatics

OTU / ASV / DNA
Marker
Taxonomy
Phylogeny
α & β diversity
Functional Inference

Gene Calling
Functional Annotation
Taxonomy

Speed / Diagnostic

Detail / Discovery

Single target vs whole genome sequencing

- Amplicon Sequencing – High throughput
- Conserved Primer to amplify variable region
  - Sequence difference resolves different organisms
  - Sample diverse group of organisms
  - 16srRNA gene is a typical target
  - Primer design impact results
- Not all species can be resolved through amplicon sequencing
- Not an exact measure based on variance of 16s rRNA genes in different species
- Synthetic Spike in to evaluate data quality and determine absolute abundance evolving

- Metagenomics – High detail
- Resolve Taxa to species and even to strains
- Not efficient – requires millions of sequences per samples
- Contains information about metabolic pathways
- Requires deep sequencing as most abundant microbes dominate the signal

Sequencing target and quality considerations

Why 16S rRNA?

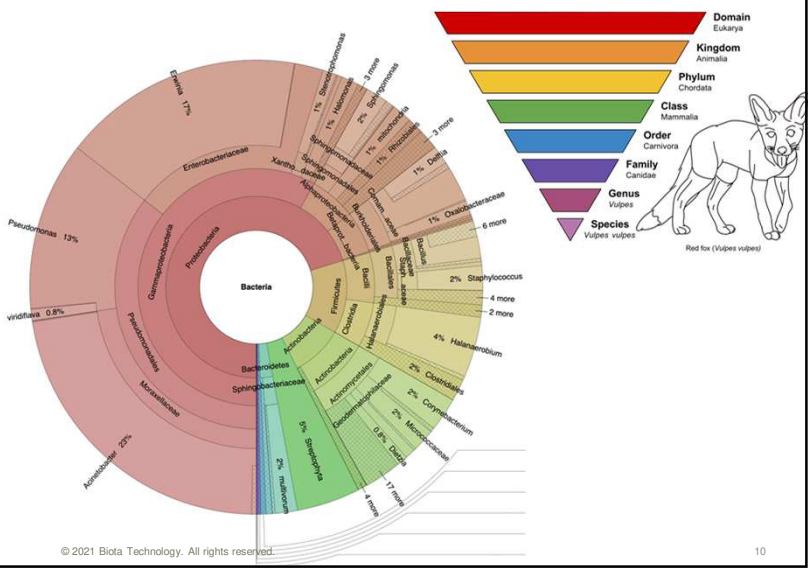
- Function of 16S rRNA is essential for protein synthesis. All bacteria and archaea contain the gene that codes for it.
- Similarity allows for easy targeting. Small variations in DNA are sufficient to differentiate distinct organisms.
- All DNA is extracted, the 16s gene is targeted and copied in the PCR amplification and sequenced.
- Unique DNA markers are identified representing different bacteria.

Quality control considerations

- Biomass – Subsurface samples are typically low in biomass (comparable low concentration of microbes). PCR typically required for sequencing.
- DNA marker assignment – 100% match between samples and multiple times observed in one sample.
- Negative controls – Measure the background signal from e.g. reagents to disassociate from the signal.

Krona Plot – A view of the microbial community

- Krona plots present the microbial community in their taxonomic hierarchy (e.g. species, genus)
- Some classifications are ambiguous because the microbes we observe in the oil and gas industry are novel to those previously observed
- The microbes we see here are consistent with those we've seen in the subsurface



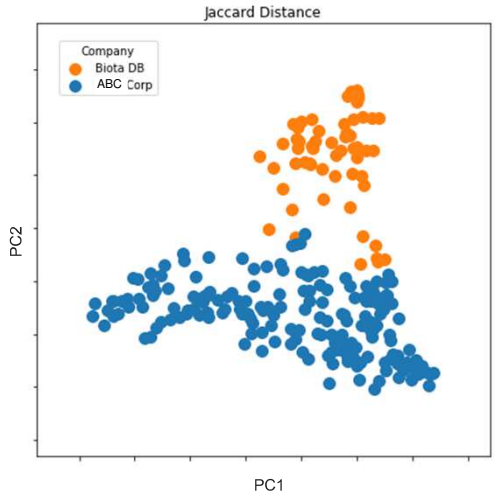
DNA Similarity Plot Across the Bakken

Plot Background

- The similarity between sets of DNA markers from ABC Corp produced fluids from 19 wells were compared at all observed time points
- Determined by counting the number of shared DNA marker counts in each sample.
- Shorter distances between two points indicate greater similarity in terms of presence and abundance of DNA marker counts
- ABC Corp wells were compared to a subset of other Bakken fluids in Biota's database

Interpretation

- Produced fluids from ABC Corp and other operators form distinct clusters
- Fluid differentiation may be drive by changes in geology, fluid composition, or operations (chemical treatment plan, etc)

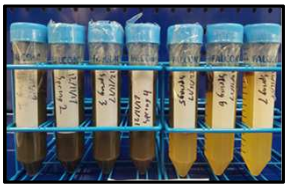


Diagnostic Workflow

DNA Diagnostics for high resolution fluid tracking

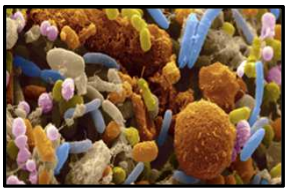
Webinars

Subsurface Samples



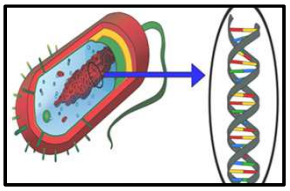
Fresh cuttings and produced fluids contain diverse microbial communities present in the subsurface

Subsurface Microbial Community



Microbes exploit physical and chemical changes within the subsurface

DNA Extraction & Sequencing



Microbes contain unique DNA sequences associated with different spatial regions

DNA Diagnostics

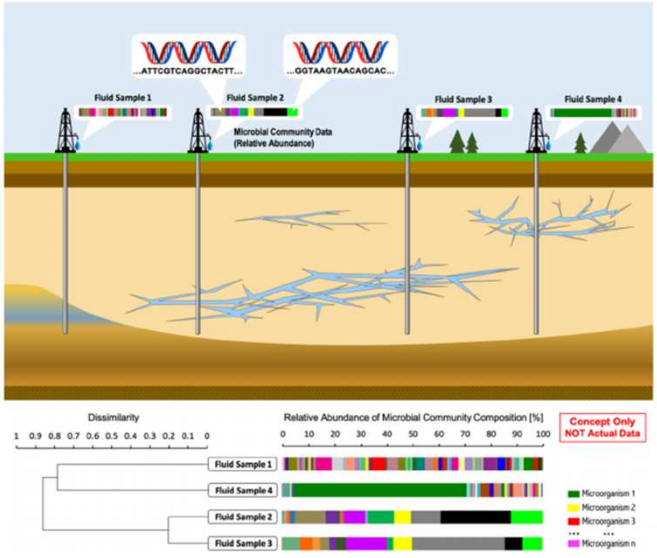
Bioinformatics and machine learnings enables the tracking of fluid origin, movement and well to well similarities

Images: www.themocracy.com.

Use of DNA diagnostics in research environment

Webinars

- Stanford Research at Sanford Underground Research Facility, SD (2019)
- Uses technology co-developed by Biota's technology team
- Team analyzed formation water samples from Geothermal test wells
- Used microbial fluid signatures to ID well connectivity from natural fractures
- Hypothesis supported by analysis of coring run intersecting wells



Bringing Genomics Technology to Commercial Scale

Webinars

Challenge

- Low Biomass (Cuttings / Rock)
- High Background Signal (Mud, Surface equipment / handling)
- Downstream analysis requires quality subsurface signal
- Speed and scalability

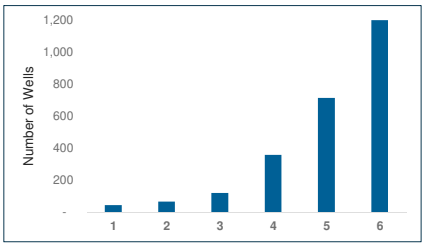
Solution

- Proprietary Extraction method
- Signal Amplification to captures major and minor markers
- Database to distinguish subsurface vs. surface signal
- High throuput lab and genomics pipeline

Broad range of operating conditions

- WBM + OBM
- Successful in High Temp environment (+250 °F already seen, 300F in literature)
- High API gravity oil – no limitations

Proven commercial scale



Step 1: Cuttings DNA Stratigraphy Baseline

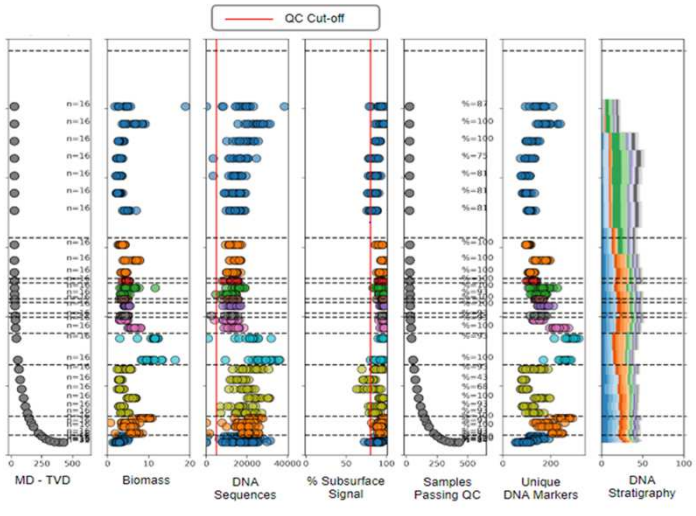
Webinars

Cuttings Baseline

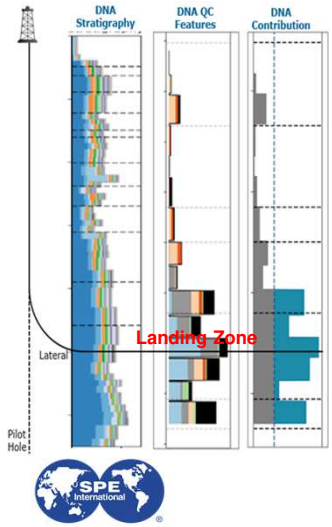
- Drill cuttings are acquired
- The plots on the right show the number of DNA extractions per depth, as well as QC measures and DNA Stratigraphy (relative abundance of top 20 DNA markers across all depths)
- Cuttings form the baseline to estimate drainage height and formation contributions when compared to fluid DNA markers
- Curves:
  - Biomass: an indication of concentration of microbes
  - Sequences: number of DNA sequences
  - Signal: QC metric with 80% cutoff
  - Standard QC: Depths and number of samples passing QC
  - Unique Markers: Number of unique DNA markers per depth
  - Stratigraphy: Relative abundance of top 20 DNA markers across depths

QC Criteria for Cuttings

- Subsurface signal above 80% and a minimum of 5000 DNA sequences are required for a sample to pass QC
- At least 5 QC-passed replicates from each unit (TVD or sub-formation) are required for that unit to be included in the downstream analysis



Step 2: Total Fluid Log



Fluid Samples

- Acquired at first accessible point on surface (wellhead or separator)
- DNA extracted and sequenced
- Data science comparison of DNA markers in fluids and cuttings

Data Science Interpretation

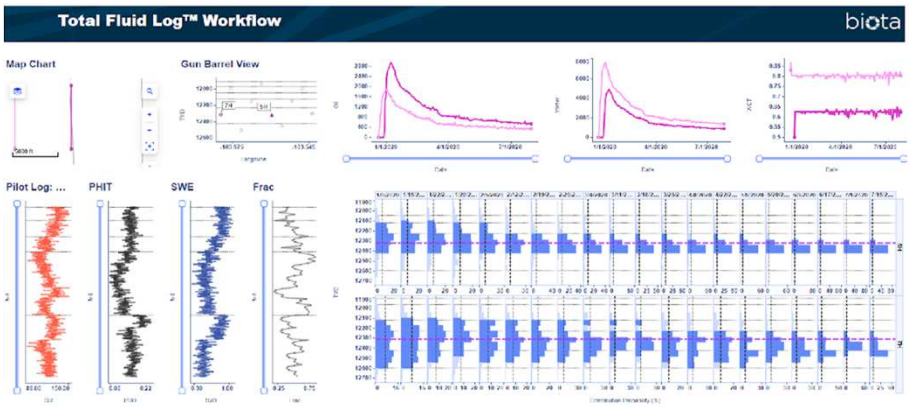
- Larger bar = increased probability relative to other depths
- Represents water + oil contributions
- Drainage height determined from depths with consistent above-average probabilities

Reservoir Engineering Considerations

- Bars are probabilities, and not volumetric contributions
- Bars should be scaled / considered in relation to oil in place and water in place
- DNA contributions likely include flow from areas that are propped open + natural fracture contributions
- DH will likely represent combined vertical drainage if 2 wells are communicating with one another
- DH's can be calculated with DNA markers weighted or not weighted by distance from landing zone -> Weighted approach likely better represents subsurface physical conditions

Step 3: Data integration and visualization

- Petrophysical Data
- Production Data
- Time based
- Data Exploration



Solution Space

Conventional Plays – One baseline, Answers throughout asset life

Samples During Drilling Phase

Sidewall Cores

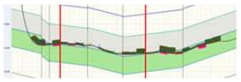
Well Cutting

Bottom Hole Fluids (MDT

Samples During Production Phase

Wellhead / Surface Fluids

Life of asset

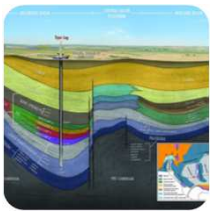


Customer / Public Data

Subsurface Mapping	Production Allocation	Enhanced Oil Recovery	Corrosion and Flow Assurance	Advanced Surveillance

▪ Structural Map
▪ Formation Identification
▪ Fault Identification
▪ Compartmentalization
▪ Corrosion & H2S potential
	▪ Commingled well contributions
	▪ Zonal contributions
	  ▪ Stacked pay
	  ▪ Complex reservoirs
	▪ Well to well communication
	▪ Zonal isolation
		▪ Vertical / Areal sweep efficiency
		▪ Identify channels / blockages
		▪ Early breakthrough indication
		▪ Injected vs formation water
			▪ SRB / MIC presence
			▪ Corrosion and H2S and prediction
			▪ Treatment effectiveness
			▪ Upstream and Midstream
				▪ Water source identification
				▪ Zonal isolation
				▪ Wellbore Integrity

Unconventional Plays: Capital Efficiency, Base Production Management

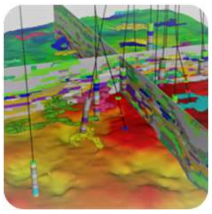


GEOLOGY

- Bench testing
- Natural fractures & fault validation
- Well placement

COMPLETIONS

- Completion optimization
- Frac barrier effectiveness



RESERVOIR

- Well spacing
- Well interference
- Water sourcing
- Modeling Restrains

PRODUCTION

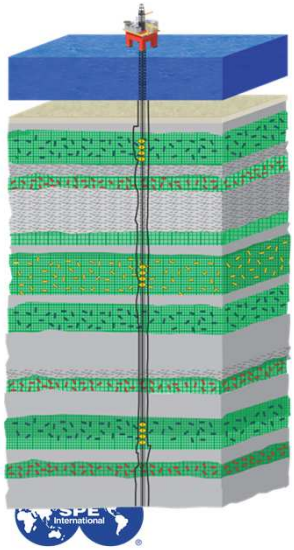
- Choke management
- Operational impacts

'One Diagnostic. Multiple Answers'

Case Studies

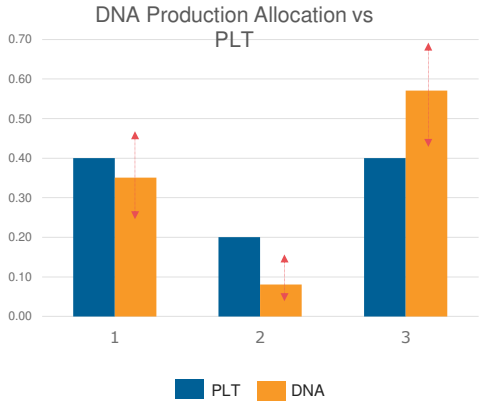
Conventional

Production Allocation / Zonal Contributions
Monitoring multi-zone completions in the deep-water Gulf of Mexico



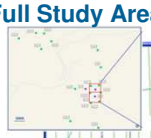
GOM Case Study (Super Major)

- Monitor relative contribution from three pay zones within a single commingled wellbore
- Apply subsurface DNA diagnostics to produced fluids
- Stored cuttings, MDT and commingled fluid samples
- DNA analysis provided qualitative reservoir monitoring and EOR optimization



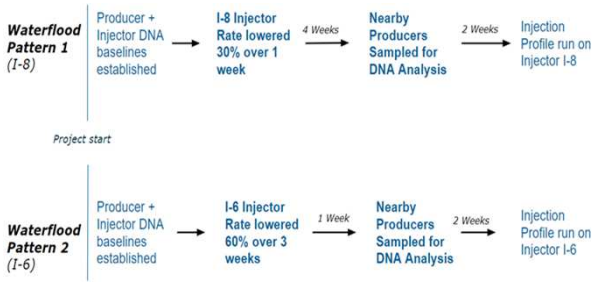
EOR / Waterflooding
Study Design and Objectives

Full Study Area



Focused Study Area

Sampling Timeline along Focused Study Area



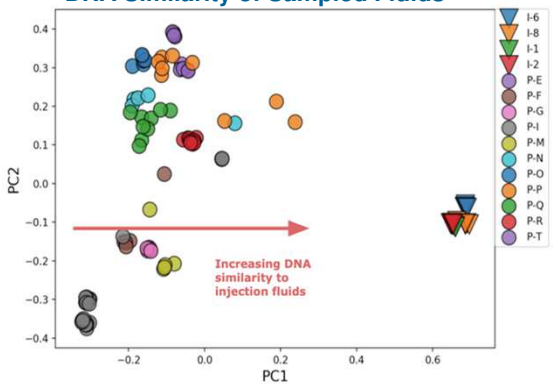
Study Objectives

- Differentiate Injection fluids from Produced fluids using DNA markers
- Assess Areal and Vertical Conformance using DNA markers

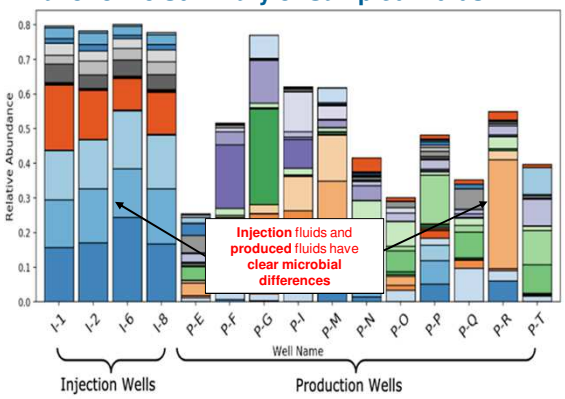
Sawadogo, Jordan , Ursell, Luke , Reeve, Nicolai , and Mathias Schlecht. "Mature Fields - Optimizing Waterflood Management Through DNA Based Diagnostics." Paper presented at the Abu Dhabi International Petroleum Exhibition & Conference, Abu Dhabi, UAE, November 2020. doi: https://doi.org/10.2118/202912-MS

EOR / Waterflooding
Differentiating DNA Markers among produced and injection fluids

DNA Similarity of Sampled Fluids



Taxonomic Summary of Sampled Fluids



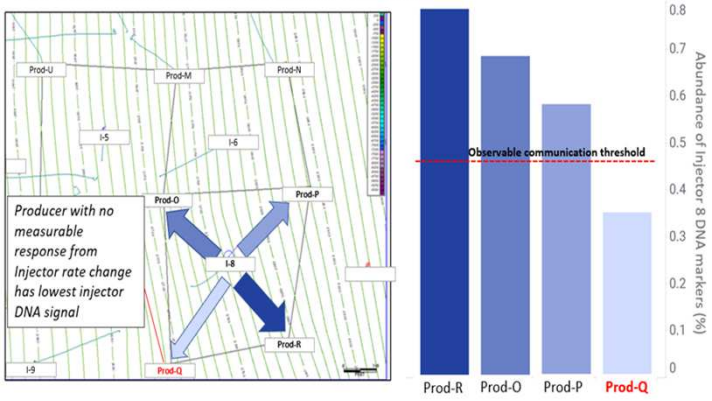
Sawadogo, et.al. ADIPEC 2020. doi: https://doi.org/10.2118/202912-MS

EOR / Waterflooding
Assessing Areal Conformance using DNA Markers

Methodology

- Injector I-8 rate decreased 30% over 1 week
- Pressure – Production responses observed in the field
- Producers sampled for DNA analysis
- Quantified injection DNA markers in Producers
- Compared DNA areal conformance to field data

I-8 Areal Conformance using DNA markers



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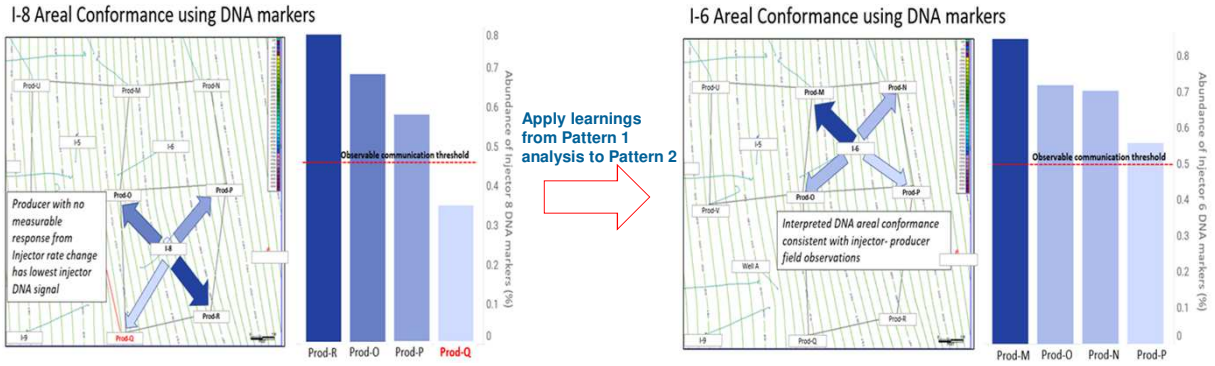
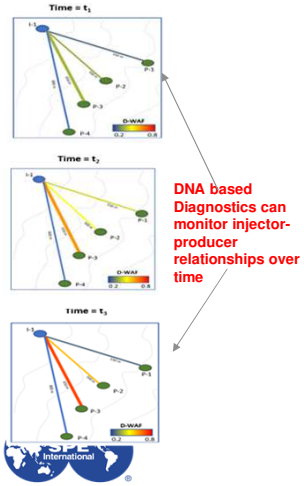
EOR / Waterflooding
Assessing Areal Conformance using DNA Markers



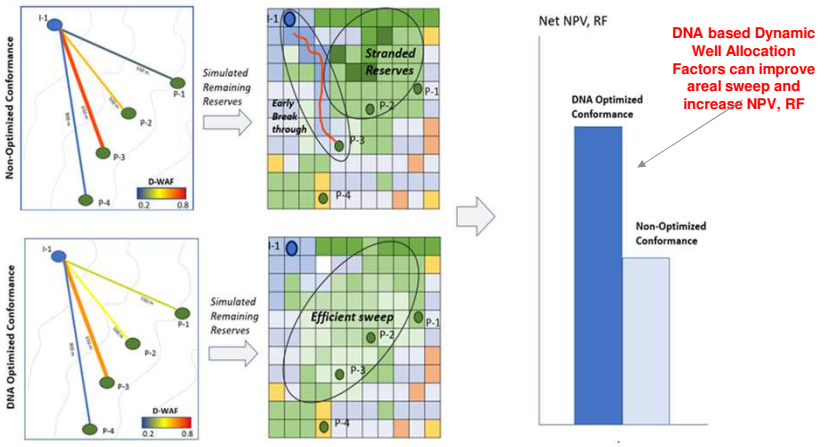
Sawadogo, et.al. ADIPEC 2020. doi: https://doi.org/10.2118/202912-MS

EOR / Waterflooding
Dynamic Well Allocation Factors (D-WAFs)

Concept



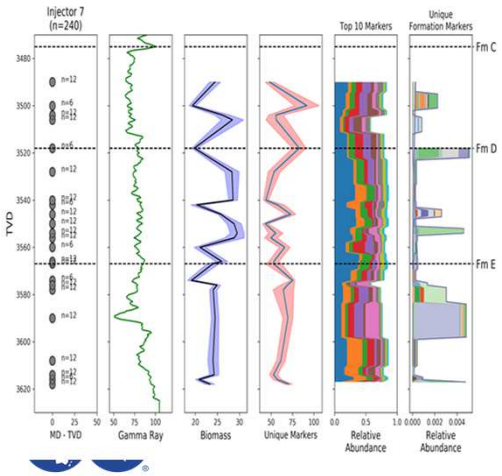
Proactive Optimization of Waterflood Management



Sawadogo, et.al. ADIPEC 2020. doi: https://doi.org/10.2118/202912-MS

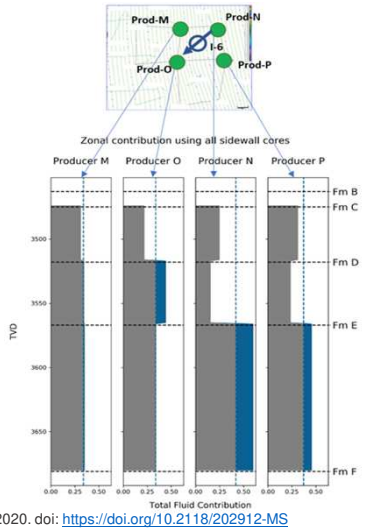
EOR / Waterflooding
Rock + Fluids DNA Based Diagnostics

Creating a DNA Baseline from Core Samples



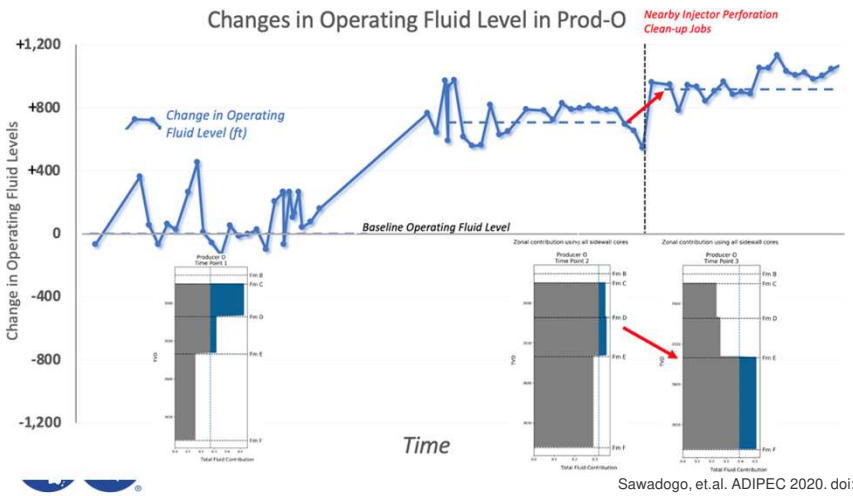
Total Fluid Logs

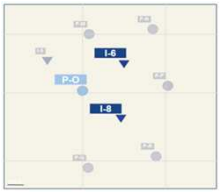
Allocate produced fluid DNA markers using overlapping markers in core baseline



Sawadogo, et.al. ADIPEC 2020. doi: https://doi.org/10.2118/202912-MS

EOR / Waterflooding
Total Fluid Logs can Identify Changes in Vertical Conformance





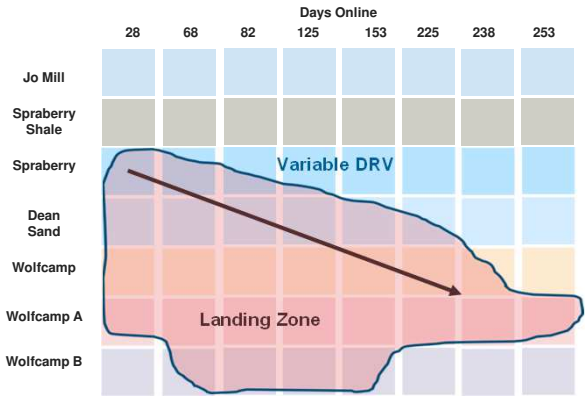
Sawadogo, et.al. ADIPEC 2020. doi: https://doi.org/10.2118/202912-MS

Case Studies

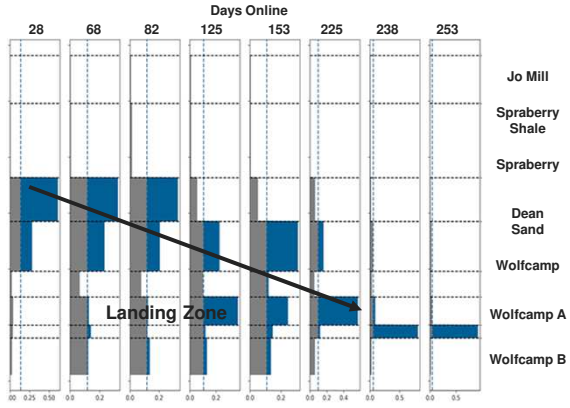
Unconventional

Modeling Restrains:
Reducing uncertainty by assessing drainage heights over time

Total Fluid Contribution demonstrated a reduction in drainage height over 253 days into production



Modeling Fluid Changes Over Time



Total Fluid Contribution

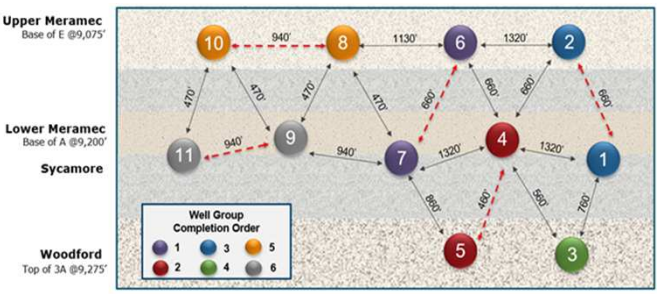
STACK Case Study
Study Background and Objectives

Webinars

Study Background:

- Development in STACK, Canadian County
- 1st Full Section Development
  - Development informed by offset pilots
  - 4 Targets across 11 Wells
  - Variable well spacing and completion design
  - Rich Data Acquisition Program

Full Section Gun Barrel View



Study Objectives:

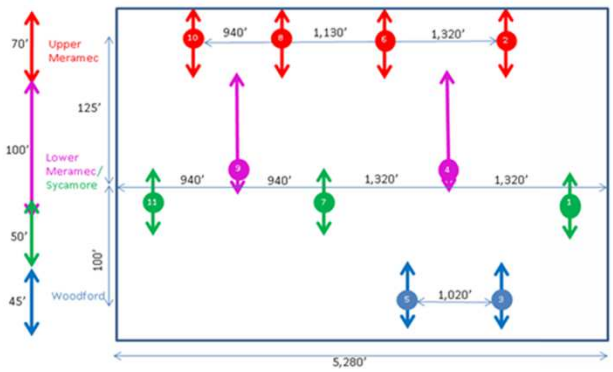
- Assess impact of completion order
- Assess impact of interwell communication

Sawadogo, Jordan , Haggerty, Matthew , Mallory, CharLee , Huchton, Jake , DeAngelis, Whitney , and Courtney Price. "Impact of Completion Design and Interwell Communication on Well Performance in Full Section Development: A STACK Case Study Using DNA Based Diagnostics." Paper presented at the SPE Annual Technical Conference and Exhibition, Virtual, October 2020. doi: https://doi.org/10.2118/201726-MS

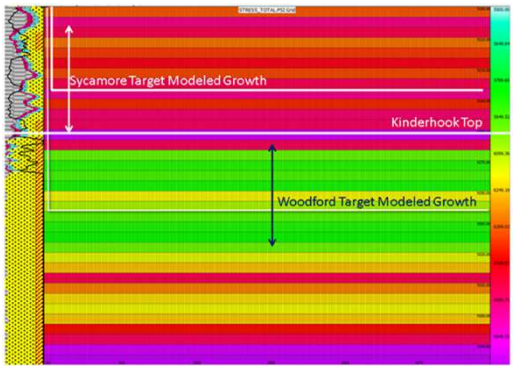
STACK Case Study
Completion Design and Anticipated Fracture Growth

Webinars

Modeled Fracture Growth across Full Section



Modeled Sycamore + Woodford Fracture Growth

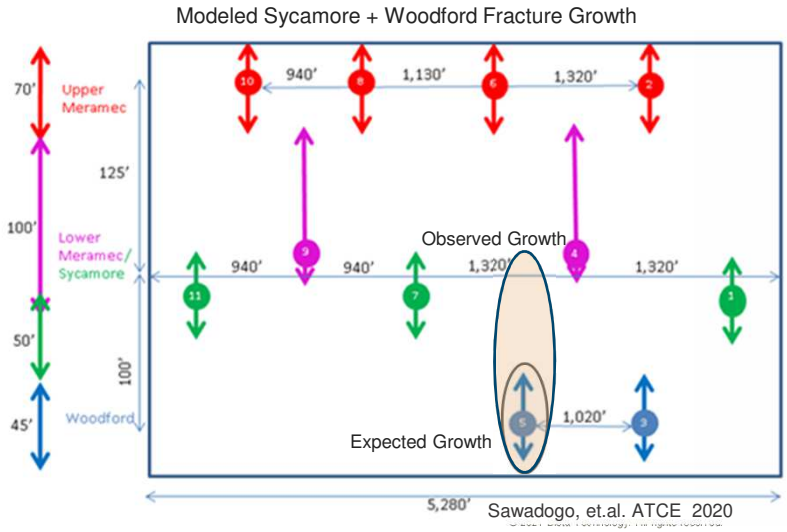


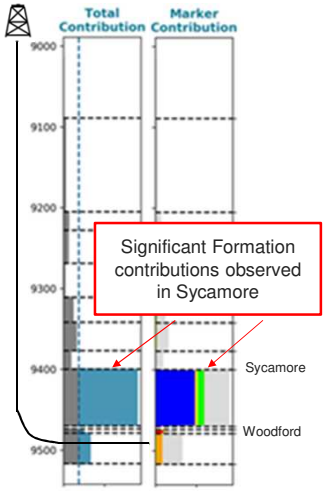
Constructed using offset logs, tracer data, pressure data

Sawadogo, et.al. ATCE 2020

Modeled growth shows fracture growth constrained to landing zone due to geological features

STACK Case Study
Results I: Upwards Communication Across Perceived Deterrents to Fracture Growth





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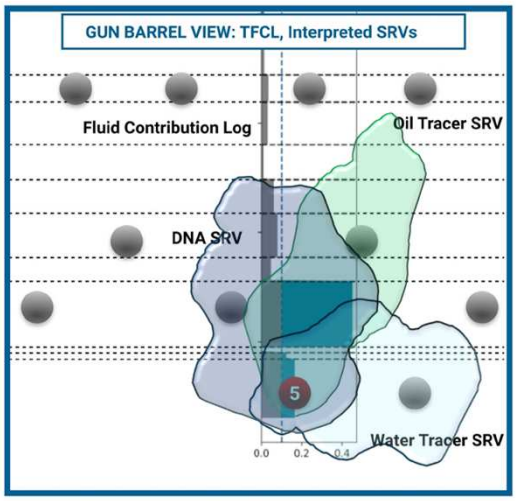
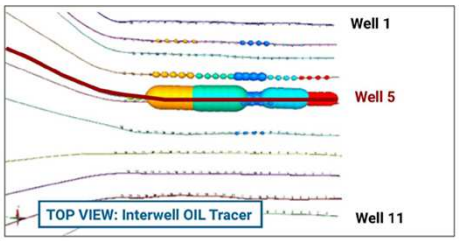
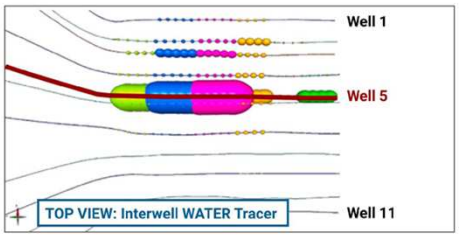
STACK Case Study
Identifying Intervening Formation Contributions from Tracer and DNA Data







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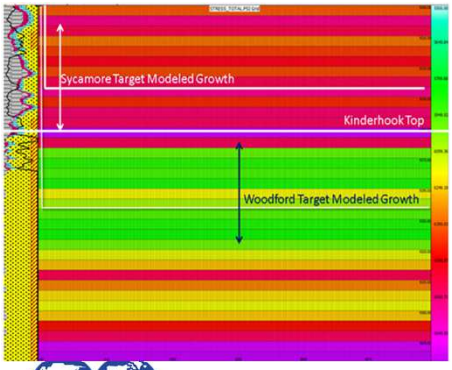
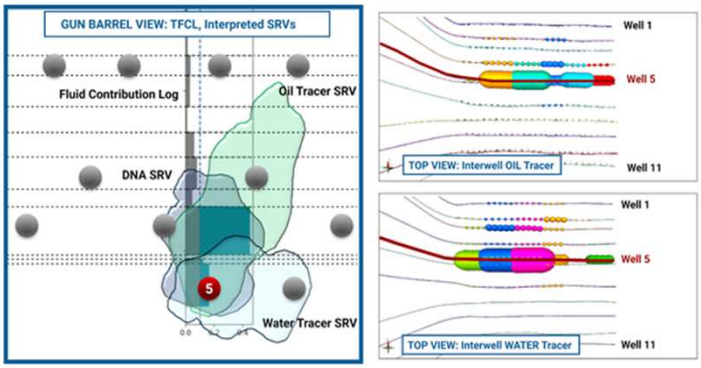
STACK Case Study
Results Summary: Comparing Anticipated vs Observed Woodford Fracture Growth

Modeled Woodford Fracture Growth



Observed Woodford Fracture Growth



Woodford targets eliminated from future development program based on integrated analysis

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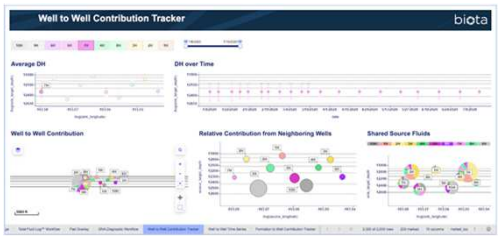
Evolving applications

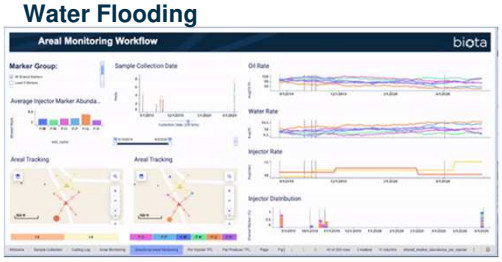
Fluid only answer products – insights without a cuttings baseline

Webinars

Well to Well Communication

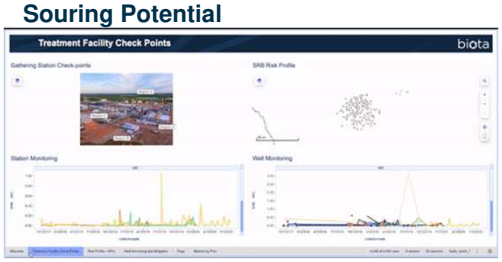


Water Flooding



Formation Contribution across Field

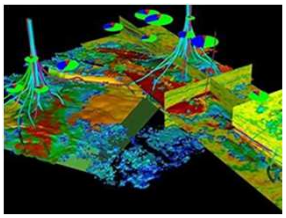
Souring Potential



Going beyond Oil & Gas

Webinars

OIL & GAS



ENERGY TRANSITION

ASSET INTEGRITY

ENVIRONMENTAL

Conclusion

DNA Diagnostics – A scalable, sustainable solution

- **Total fluid analysis:** Total fluid movement of combined oil and water
- **Low risk:** Non-disruptive to well operations; no shutdown time and lost production
- **Sustainability:** environmentally safe and friendly; low carbon footprint
- **4D:** Long-term monitoring with no sample storage
- **High Resolution:** Unique fluid profiling by measuring well cuttings and produced fluid
- **Scalable:** Field level analysis with 2 week turn around on fluid results
- **Integrated:** Analysis integrated with type curves, logs, completion designs and operational events
- **Affordability:** A fraction of the cost of other diagnostics and affordable long-term monitoring

Conclusion

- DNA diagnostics is a fast-evolving field
- Complimentary, digital data set
- Data integration unlocks the full potential
- Broad and increasing application space
- Decisions enabled impact financial and environmental sustainability

Thank You

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Recommended Reading

- Sawadogo, Jordan , Ursell, Luke , Reeve, Nicolai , and Mathias Schlecht. "Mature Fields - Optimizing Waterflood Management Through DNA Based Diagnostics." Paper presented at the Abu Dhabi International Petroleum Exhibition & Conference, Abu Dhabi, UAE, November 2020. doi: https://doi.org/10.2118/202912-MS
- Sawadogo, Jordan , Haggerty, Matthew , Mallory, CharLee , Huchton, Jake , DeAngelis, Whitney , and Courtney Price. "Impact of Completion Design and Interwell Communication on Well Performance in Full Section Development: A STACK Case Study Using DNA Based Diagnostics." Paper presented at the SPE Annual Technical Conference and Exhibition, Virtual, October 2020. doi: https://doi.org/10.2118/201726-MS