

# Oil reservoir bacteria

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Oil reservoirs are populated with complex microbial consortia adapted to an extreme environment. Microbiological and molecular biological methods may be applied to characterize and understand the microbial communities in reservoirs and the influence on oil quality and oil production.

## Oil microbiology

Our activities are concentrated on:

- Microbial Enhanced Oil Recovery
- Upgrading of heavy oils
- Reservoir characterization - metagenomics
- Metagenomic based monitoring
- Bioprospecting in extreme environments
- Biosurfactants and emulsifying agents

## Reservoir character characterization

- Cultivation and characterization of microorganisms and microbial consortia at reservoir conditions
- Quantification of microbes associated with souring (e.g. sulphate-reducing prokaryotes)
- Characterization of entire microbial communities by analytical tools (metagenomic and PCR-based methods)

## Competence

- Bioprospecting in natural environments (including oil reservoirs) for strains and biological compounds (biopolymers, biosurfactants) with high potential for use in microbial EOR strategies
- High throughput screening of strain collections and metagenome libraries



- Cultivation and characterization of microorganisms at reservoir conditions
- Ex situ production of microbial products (microbial strains, biopolymers, bio-surfactants) up to 300 L scale
- Systems scale characterization of producing strains for performance improvement (full scale 'omics analysis)
- Detailed understanding of microbial consortia structure in oil reservoirs to evaluate a potential impact of EOR methods
- Methods for stimulating growth and metabolic activity of indigenous microorganisms by injection of nutrients
- Injection of defined metabolic active exogenous microorganisms (render monitoring and controlling the treatment possible)
- Core flooding experiments

## Facilities

- Facilities for anaerobic work and work with (poly)-extremophilic microorganisms
- High pressure cultivation cells (~250 bar)
- Modern molecular biology lab's for 'omics and meta'omics, including next generation sequencer - Illumina MiSeq
- Automated high throughput screening facilities
- Advanced fermentation laboratories
- Attune Acoustic Focusing flow cytometer
- Ultra high resolution mass spectrometry - FT-ICR-MS (SINTEF's mass spectrometric instrument platform)
- Access to Core flooding rigs (SINTEF Petroleum)

## SINTEF's mass spectrometric instrument platform

### Unique possibilities for ion research

- GC-MS for identification of organic compounds
- LS-MS-QQQ tracer analysis (ppq sensitivity)
- FT-ICR-MS 12 T ultra-high resolution MS identification (only instrument in Scandinavia, ca 20 world-wide)
- ICP-MS analysis of elements
- FFF – field Flow fractionation – Enables characterization of nanoparticles, polymers, asphaltenes and aggregates

## OIL RESERVOIR – PROJECT ILLUSTRATION

### Study of the microbial communities in two physically separated sub-surface oil reservoir on the North Sea Continental Shelf

#### Reservoir characterization

The first to use direct metagenome sequencing on pressurized samples for largely unbiased representative picture of consortium structure.

- **Extremely high sequence similarity of species in the two studied wells (different to surface organisms)**
  - Very slow evolution after separation (> 20 million years ago)
- **Where do they originate from?** Deep surface continuum?
- Potential for new, sequenced based methods in exploration?

## Outlook:

- Re-sampling, or time-series from new pristine reservoirs
- New sample material from more distant reservoirs
- New sample material from reservoirs with different in situ conditions (NCS and abroad)
- **Open for collaboration with new partners!!**

Lewin et al. (2013) "The microbial communities in two apparently physically separated deep sub-surface oil reservoirs show extensive DNA sequence similarities", *Environ. Microbiol.*, doi: 10.1111/1462-2920.12181. [Epub ahead of print]

Wentzel et al. (2013) "Deep sub-surface oil reservoirs as poly-extreme habitats for microbial life" *Polyextremophiles*, *COLE* 27: 439-466.

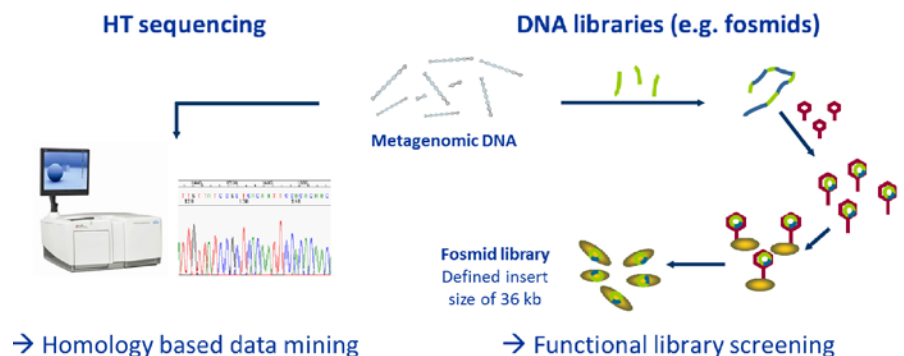
## Enzyme bioprospecting

Bioprospecting for enzymes by data mining and functional screening of an oil reservoir genome library.

- Extreme habitats harbor specialized microbes with metabolic functions of potential interest for industrial bioprocesses
- Metagenomes from extreme habitats represent attractive sources for the discovery of new enzymes for added value generation
- Oil reservoirs are poly-extreme (temperature, pressure, salt, toxic compounds)

Enzyme classes of special interest successfully approached by data mining and functional screening

- PAH and LCA converting enzymes (Upgrading of crude oil and oil fractions)
- Lipases, esterases (Chemical production, biofuels)
- Carbonic anhydrases (CO2 capturing and storage)
- Glycoside hydrolases, e.g. cellulases, xylanases (Degrading of biomass for biorefineries)
- Others (proteases, etc...)



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