microbialinsights

QuantArray®-Petro

MNA Assessment at a Crude Oil Impacted Site

PROJECT SUMMARY

- Site managers were considering MNA based on groundwater monitoring.
- QuantArray®-Petro revealed that concentrations of functional genes in pathways for aerobic and anaerobic biodegradation of BTEX and naphthalene were substantially greater in impacted wells than in the background well suggesting growth of these contaminant degraders within the dissolved plume.
- Based on converging lines of evidence, MNA was the selected remedy.

PROJECT CHALLENGE

Groundwater at a petroleum storage tank farm was impacted by the release of crude oil and condensate. Benzene, toluene, ethylbenzene, and xylenes (BTEX) were the primary concern, but polycyclic aromatic hydrocarbons (PAHs) also exceeded risk-based limits. Geochemical monitoring indicated variable redox conditions but confirmed utilization of DO and other electron acceptors. Site managers were considering monitored natural attenuation (MNA) but needed an additional line of evidence to support a decision.

SAMPLING AND MBT ANALYSIS

Along with chemical and geochemical monitoring, QuantArray-Petro was performed to quantify a broad spectrum of functional genes responsible for aerobic and anaerobic biodegradation of BTEX and naphthalene and to answer the following questions:

- What are the concentrations of aerobic and anaerobic BTEX and naphthalene degraders under existing conditions?
- Are concentrations of BTEX and PAH degraders in the dissolved plume greater than background?

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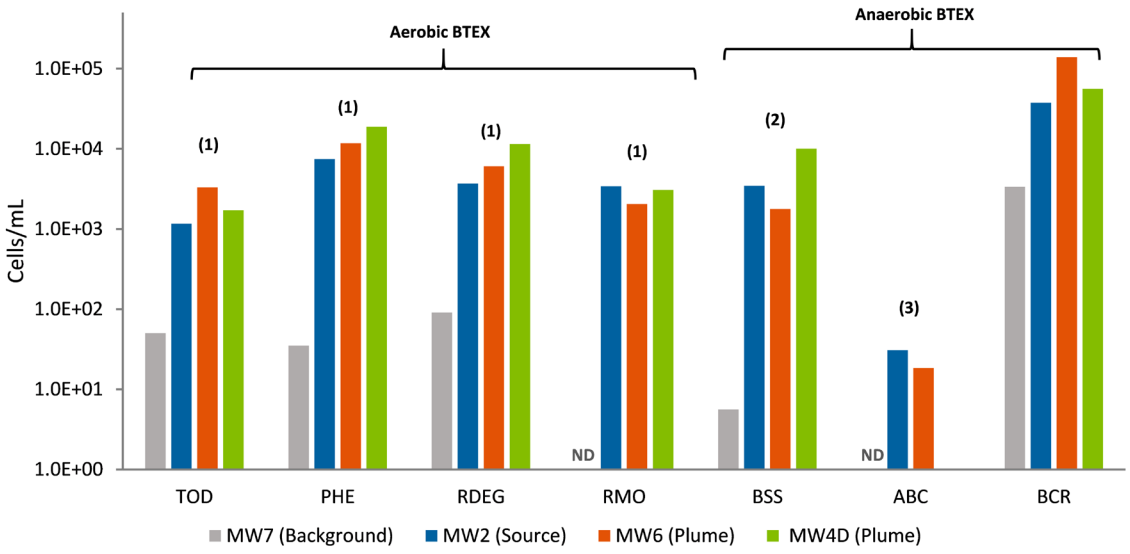
MNA EVALUATION

BTEX Biodegradation: As shown below, concentrations of functional genes involved in BTEX biodegradation were substantially greater at impacted monitoring wells MW2 (blue bars), MW6 (orange bars), and MW4D (green bars) than at the upgradient, background well MW7 (gray bars).



(1) More specifically, concentrations of toluene/benzene dioxygenase (TOD), phenol hydroxylase (PHE) and toluene/benzene monooxygenases (RMO and RDEG) genes were one to two orders of magnitude greater in impacted wells than in the background well MW7 (10^1 cells/mL).

(2) The results for functional genes responsible for anaerobic BTEX biodegradation were similar. Concentrations of benzylsuccinate synthase (BSS) genes were two to three orders of magnitude greater in impacted wells.

(3) Anaerobic benzene carboxylase genes (ABC), which were below detection limits in the background well MW7, were detected in impacted wells MW2 and MW6 indicating growth of bacteria capable of anaerobic benzene biodegradation within the dissolved plume. Finally, BCR genes, which encode an enzyme involved in anaerobic metabolism of a common aromatic metabolite and are often detected at relatively high concentrations in background samples, were still greater in the impacted wells.

Overall, the QuantArray-Petro results indicated growth of high concentrations of a diverse spectrum of aerobic and anaerobic BTEX degraders within the dissolved plume and thus provided a supporting line of evidence for BTEX biodegradation under existing site conditions.

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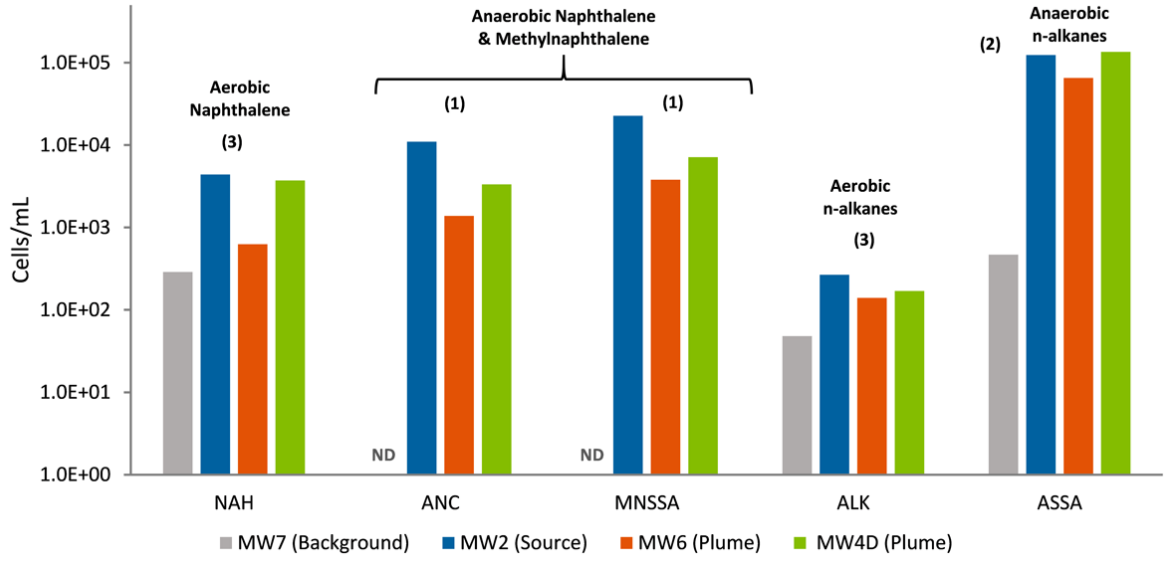
MNA EVALUATION (CONT.)

PAH Biodegradation: Concentrations of functional genes responsible for PAH and alkane biodegradation were substantially greater in impacted wells (MW2, MW6 and MW4D) than in the background well (MW7) demonstrating growth contaminant degraders within the dissolved plume.



(1) Anaerobic naphthalene carboxylase (ANC) and methylnaphthylsuccinate synthase (MNSSA) genes, which were below detection limits in the background well MW7, were detected at high concentrations (10^3 – 10^4 cells/mL) in PAH-impacted wells.

(2) Concentrations of alkylsuccinate synthase (ASSA) genes which initiate anaerobic biodegradation of alkanes were more than two orders of magnitude greater in the impacted wells.

(3) While somewhat less readily evident than for the anaerobic pathways, concentrations of naphthalene dioxygenase (NAH) and alkane monooxygenase (ALK) were also notably higher in petroleum-impacted samples.

As with BTEX degraders, the QuantArray-Petro results indicate growth of high concentrations of aerobic and particularly anaerobic naphthalene and alkane degraders providing a strong line of evidence for PAH and alkane biodegradation under existing site conditions.

Decision: MNA was selected as the site management strategy based on converging lines of chemical, geochemical, and microbiological evidence. Contaminant concentrations were stable or decreasing. Geochemistry provided indirect evidence of microbial activity and electron acceptor availability. QuantArray-Petro demonstrated growth of high concentrations of aerobic and anaerobic BTEX, PAH, and alkane degraders within the dissolved contaminant plume.

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KEY BENEFITS

QuantArray-Petro was a critical line of evidence that directly impacted site management decisions.

- **Actionable:** Along with contaminant trends and geochemistry, QuantArray-Petro results demonstrating high concentrations of functional genes for aerobic and anaerobic BTEX and naphthalene biodegradation was a key factor in selecting MNA.
- **Saved Money:** Enhanced remediation options were not necessary and MNA was accepted.
- **Comprehensive & Cost-Effective:** Petroleum products are complex mixtures of hydrocarbons. In a single analysis, QuantArray-Petro quantified a broad spectrum of functional genes responsible for aerobic and anaerobic biodegradation of BTEX, PAHs and other contaminants of concern.

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