



# How microbiomes are influenced by and influence migrating hydrocarbons

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## Summary

Resident microbial communities associated with prolific hydrocarbon seeps in the Gulf of Mexico were characterized by culture-independent DNA profiling of 16S ribosomal RNA (rRNA) genes. Multiple next generation sequencing technologies were deployed to obtain comprehensive microbial inventories from these environments. This approach enabled detection of more than 5 million ribosomal sequence tags and revealed that approximately one-third of the sequencing tags showed a similar distribution pattern among the piston core samples when compared to the major hydrocarbon constituents present in the seeps. Numerous correlated distributions, or associations, were found between particular microbial DNA sequences and specific hydrocarbons, suggesting a biochemical role in the transformation of these compounds. Quantitative polymerase chain reaction (qPCR) primers were designed to target these 16S rRNA gene sequences and were found to accurately detect and serve as sensitive bioindicators for these hydrocarbons in blind tests. These results highlight the role that microorganisms play in the dynamics of migrating hydrocarbons in marine sediments.