

Microbiological Profiles and Risk Exposures in Topside Production Systems of FPSOs in West Africa

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ABSTRACT

Microbiological risk evaluation of topside systems of four floating production storage and offloading in West Africa was carried out over a period of four years. Field samples were taken, and DNA analyzed using next-generation sequencing technology to identify and classify the microbial population present on the facilities. Several classes of bacteria and archaea were sequenced and identified from the samples, including those that have been shown to play key roles in biofouling, microbiologically influenced corrosion and biogenic hydrogen sulphide generation in oil and gas production systems. The classic microbial population according to metabolic classes associated with oil and gas production systems were identified. The study found that of the 137 microbial genera identified, 45.3% were associated with biofouling, 29.9% with microbiologically influenced corrosion, 29.1% with a H₂S/MIC risk and a 2.9% population did not have a clear link to any of these risks. There was at least 98% relative abundance of bacteria population in the samples from all FPSOs, implying a significant exposure to the risks posed by microbial growth and proliferation.

Key words: biocorrosion, biofouling, MIC, SRB, FPSO

INTRODUCTION

The incidence and proliferation of microbial population in oil and gas production facilities can have undesirable consequences on upstream, midstream and downstream production systems. Microbes thrive in the anaerobic conditions encountered in these systems and are supported by nutrients and metabolites found in produced water. Although the majority of process and water injection systems are susceptible to microbial fouling, the development of microbial activity is exacerbated by specific

conditions such as stagnant fluids or the presence of deposits.¹ Threats of microbiologically influenced corrosion (MIC) and other challenges associated with microorganisms have become valid as more cases are reported. While MIC, biofouling (BF), and reservoir souring are three of the most common problems associated with microbes, many other production issues can be attributable to microbial activity including: employee infections, filter plugging, loss of injectivity, and metal sulfide deposits.²

Bacteria capable of reducing sulfate (sulfate reducing bacteria, SRBs) to produce hydrogen sulfide (H₂S) and other bacteria that generate organic acids as a byproduct of their metabolism (acid producing bacteria, APBs) have long been “blamed” as the sole mediators of MIC.^{3,4} However, in recent times, test methods long employed in academic and healthcare research have been extended to the oil and gas investigation tool-kit resulting in an expanded identification of types of microbes involved in MIC. DNA sequencing techniques such as denaturing gradient gel electrophoresis (DGGE) and Sanger sequencing are able to reliably identify bacteria and archaea to the genus level. More recently (within the last 2-3 years), highly sensitive and accurate next-generation DNA sequencing (NGS) technologies, which can identify microbes to the species and strain level, have been applied to the oil and gas space.⁵

Eight distinct metabolic classes of microbes are recognized in oilfield environments: acid producers, iron oxidizers, iron reducers, general heterotrophs, methanogens, nitrate reducers, sulfur oxidizers, and sulfur reducers.⁵ Each metabolic class is made up of dozens (if not hundreds) of different genera of Bacteria and Archaea. Importantly, microbes can possess multiple types of metabolic pathways that can be utilized in different environments, therefore necessitating their inclusion in multiple classes: NACE 31205 provides detailed descriptions of many of these eight classes of microbes.⁶

Briefly, acid producing bacteria and archaea (APB/APA) contribute to MIC through their ability to produce various organic acids that can reduce the local pH underneath biofilms. Iron oxidizing bacteria and archaea (IOB/IOA) by stripping iron (and often manganese) from the surface of pipelines and vessels, and iron reducing bacteria and archaea (IRB/IRA) by depositing iron onto pipelines and vessels, are able to generate pits and tubercles associated with MIC. While general heterotrophic archaea and bacteria (GHA/GHB) do not directly cause MIC or souring, many species play important roles in forming biofilms and contributing to biofouling. In the oilfield, methane production by methanogens (Met) is fueled by electrons from hydrogen ions stripped from the steel surface itself, thereby causing MIC. Nitrate reducing bacteria and archaea (NRB/NRA) are not generally thought of as contributors to MIC, although incomplete nitrate reduction to nitrite can be corrosive. Sulfate reducing bacteria and archaea (SRB/SRA) are the most notorious causes of MIC and souring.^{3,4}

This work is intended to assess the microbiological risks that the target floating production storage and offloading (FPSOs) are exposed, through a thorough analysis of the facilities’ microbiological data collected over a period of five years. The study provides an understanding of the prevalence and distribution of microbial population at different points on the FPSO production system, provides a clearer understanding of the risks posed by these microbes to the facility, and therefore provides the momentum for a well-targeted microbial control program that would ensure that the integrity of the producing assets are maintained, personnel safety is enhanced and production is less impacted.

EXPERIMENTAL PROCEDURE

DNA Extraction

Prokaryotic DNA was isolated from fluid samples that were sent to the microbiology laboratory for analysis. Fluids were captured on a 0.45µm filter in the field to decrease changes to the microbial

population during shipping and the entire filter was processed for extraction. The UltraClean Soil DNA Kit* (MoBio) was used to extract DNA from each of the samples following the manufacturer's instructions.

Next-generation DNA sequencing

Microbial speciation was performed using semiconductor-based NGS with the IonTorrent platform* (Life Technologies, Carlsbad, CA). Several pilot studies were conducted to verify that the NGS approach was able to identify all of the bacterial species identified via the DGGE pathway. Briefly, following DNA extraction a ~200bp portion of the 16S rRNA gene was amplified via PCR using oligonucleotides designed to target both bacteria and archaea. These amplified sequences (amplicons) were purified via E-Gel SizeSelect gels* (Life Technologies) and then quantified with the Qubit dsDNA HS assay* (Life Technologies). Once quantified, the individually barcoded amplicons were pooled in an equimolar ratio and subjected to emulsion PCR and enrichment using the Ion OneTouch system* (Life Technologies). The pooled samples were then loaded onto a prepared Ion 314 Chip* and run on an Ion Personal Genome Machine* (Life Technologies). Data assembly, metagenomic analysis, and taxonomic identification was performed using the SeqMan NGen software* (DNASTAR Inc., Madison, WI) and exported into Microsoft Excel 2010* (Microsoft, Redmond, WA) for final reporting.

Data analysis

Results of analyses of samples collected from the various FPSOs between 2017 and 2020 were collated into a database maintained and analyzed in the spreadsheet used above. Descriptive tables and figures from the data were generated using the same spreadsheet.

RESULTS AND DISCUSSION

A total of 25 samples were collected from several vessels from the operational facilities of four FPSOs in West Africa between 2017 and 2021. The sample locations were the sea water injection systems (SW) including – injection pumps, multimedia filters, deaerators and discharge pumps; crude separation (CS) equipment including – separators, oil treaters and wash tank; and produced water (PW) treatment vessels including – degassing drums, induced gas floatation units, hydrocyclones and slop tanks.

Identification of the microbial population to the genus level indicated there was 134 Bacteria genera, representing 97.8% of the identified organisms and 3 Archaeal genera, representing just 2.2% (Table 1). This bacterial: archaeal ratio was seen for each of the four FPSOs (Figure 1). Geissler *et al* found a 91% to 9% Bacterial to Archaeal ratio in prokaryotic speciation in samples collected between 2009 and 2013.⁷

Table 1
Microbial genera from all four FPSOs

Genera	No. of isolates	Percentage
Bacterial genera	134	97.8%
Archaeal genera	3	2.2%
Total microbial genera	137	

*Trade name