

Molecular Deep Dive into Oilfield Microbiologically Influenced Corrosion: A Detailed Case Study of MIC Failure Analysis in an Unconventional Asset

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ABSTRACT

This work details a microbiologically influenced corrosion (MIC) failure analysis case study for a produced water pipeline. A pipeline in a shale and tight asset experienced heavy corrosion and ultimate failure within a 7-month period, with estimated corrosion rate at 161 mils per year (MPY), or 4.1 mm per year (MMPY). Upon removal by the inspection team, heavy white deposit buildup (a suspected microbial biofilm) was observed directly associated with the corrosion failure on top of a black scale underlayer. Detailed assessments were performed using ATP photometry, qPCR speciation, and 16S rRNA gene sequencing to profile the microbial population present, which was dominated by high-risk anaerobic microbial strains such as sulfate-reducing bacteria and methanogens. Scale analysis confirmed iron carbonate and iron sulfides associated with microbial iron metabolism and corrosion, and scanning electron microscopy explored surface morphology. This study will lay out detailed root cause analysis and include best practices for MIC diagnosis and recommendations for future prediction and prevention in oilfield assets.

Key words: biocorrosion, sulfide scale, carbon steel failure, sulfate-reducing bacteria, methanogens

INTRODUCTION

Microbiologically influenced corrosion (MIC) is a key oilfield problem associated with microbial activity, and can be described as the accelerated corrosion of surfaces (usually concrete or iron/steel) by the biological action of naturally present or externally introduced microorganisms. MIC incidents can occur anywhere that a system is exposed to the environment, where microorganisms can enter often via fluid flow and colonize various surfaces for their own growth. MIC is a persistent concern in practically any upstream, midstream, or downstream system where water could be present for microorganism colonization, including topside, subsurface, aerobic (with oxygen), anaerobic (without oxygen), and at extreme temperatures and salinities.¹⁻² This includes subsurface reservoir and well tubing, oilfield separators, fluid pipelines, water dump lines, relief valves, treatment facilities, etc. MIC failures result in process upsets, loss of containment, lost production opportunities, and increased operating expenses.

MIC is a complex issue throughout the oil and gas industry. A diverse population of microbial species are typically involved (including both bacteria and archaea), enhancing pipe/equipment corrosion by a variety of mechanisms including but not limited to: H_2S production (souring), biogenic acid production and pH acidification, and various electrochemical reactions.³ MIC is often divided into two categories. 1) Direct MIC involves electrochemical degradation of equipment integrity, often by direct uptake of electrons from metal surfaces by microorganisms (such as iron oxidation/reduction). 2) Indirect MIC can involve multiple mechanisms such as the production of harmful metabolites by microorganisms (e.g. acids, hydrogen sulfide) that have subsequent negative effects on equipment integrity, the formation of biofilms with deposition of cells/biomatter onto metal surfaces, and other metabolic processes that indirectly lead to corrosion or failures. Especially under anaerobic conditions, sulfate-reducing prokaryotes (SRP), including sulfate-reducing bacteria (SRB) and sulfate-reducing archaea (SRA) are particularly bad actors well known to the industry due to their production of H_2S and contribution to reservoir souring, H_2S -mediated indirect MIC, and iron sulfide scale formation.⁴ Other classes of microorganisms also play large roles in MIC, including sulfur-oxidizing bacteria (SOB) and various classes of acid-producing bacteria (APB) that can generate acetic acid, citric acid, or other organic acids associated with MIC. It is well documented that methanogens can cause significant corrosion of iron from the methanogenic process and reactions at iron pipe surfaces.⁵⁻⁶ Very recently the *micH* gene pathway has been identified as a potential key diagnostic indicator of methanogenic corrosion, allowing identification of methanogen strains capable of secreting extracellular [NiFe] hydrogenase enzymes that accelerate corrosion.⁷ Such a list of 'bad actors' is inherently incomplete due to the complexity of MIC, and the topic remains an area of significant investigation. Overall, MIC involves a variety of organisms consuming different energy sources and contributing to multiple microbial corrosion mechanisms.⁸ This creates a complex community (usually in the form of a solid sludge or scale-associated biofilm) that enhances local corrosion of critical production equipment.

In this report, a detailed MIC case study from an unconventional production asset is described. In April 2021, a production facility experienced a corrosion failure incident in a produced water pipe section after the primary well-head separator (**Figure 1**).

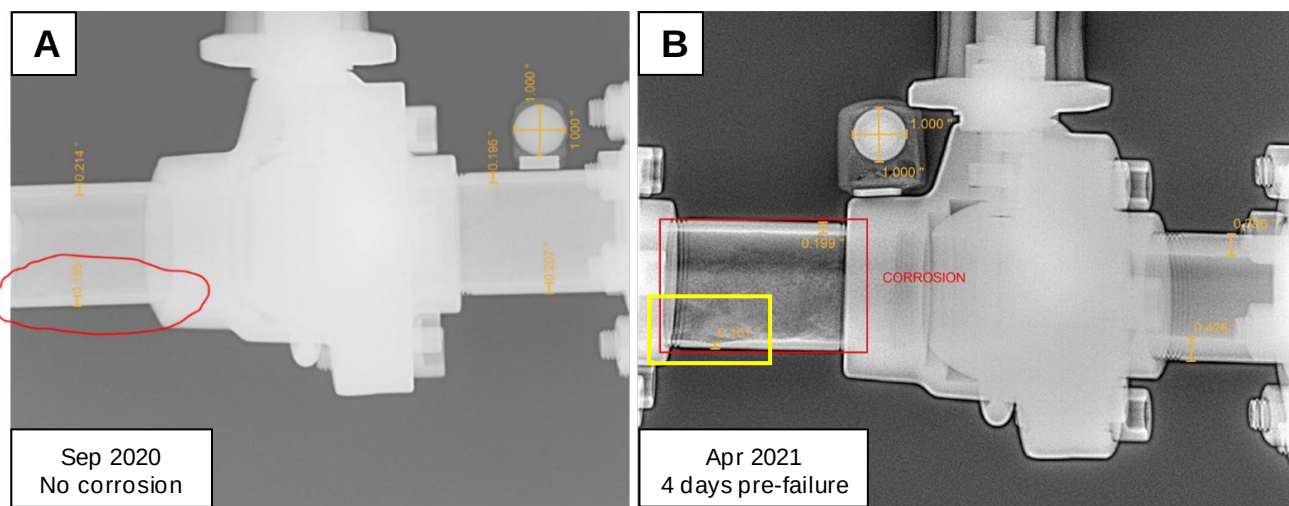


Figure 1: X-ray inspection images of pipeline in service. (A) shows pipe section of interest (red circle) in good condition during routine inspection in Sep 2020 with 0.195" (0.495 cm) wall thickness. (B) later inspection days before failure in 2021 showed same pipe section (red box) in poor condition with wall thickness of 0.101" (0.257 cm) near threads.

X-ray inspection of the produced water line showed no corrosion issues in September 2020 (see **Figure 1A**). However, upon inspection on April 13, 2021 (**Figure 1B**), there was significant corrosion and reduction in pipe thickness, with estimated corrosion rate at 161 mils per year (MPY), or 4.1 mm per year

(MPPY). Note that the yellow box in **Figure 1B** highlights the ‘left-most’ section near the threads, which upon failure analysis (see **Figure 2A**) showed the highest levels of deposit growth and corrosion. The pipe material is ASTM⁽¹⁾ A106 Gr. B carbon steel. The scale/microbial growth associated with the pipe corrosion and failure is presumed to have occurred over the 7-8 month period between X-ray inspections, as the pipe appeared in pristine condition during the September inspection. Monitored ATP testing of produced water for planktonic bacteria levels had remained below concerning levels (typically <100,000 ME/mL), leading to a false sense of security in terms of microbial control. The system was also known to have significant CO₂ levels (~3 mol% or 30,000 ppm in gas phase), with produced water typically at ≥20,000 ppm total dissolved solids (TDS), ~100 ppm sulfate, near neutral pH, and moderate temperatures (70-100°F, or 21-38°C). Temperature readings were subject to some uncertainty as cooling may have been allowed before data collection. After failure the corroded pipe section was removed and immediately shipped with all internal solid deposits intact for detailed root-cause lab analysis, described herein.

EXPERIMENTAL PROCEDURE

Upon reception approximately 4 days after the produced water line failed and was removed for shipment, the pipe failure sample was photographed (see **Figure 2**) and stored at -20°C before microbial and solids analyses. General analytical methods were as follows:

Sample collection

Deposit samples were removed by physical scraping with a 70% ethanol sterilized spatula from two major areas/layers visible in the pipe interior: 1) white surface deposits near areas of highest corrosion, and 2) black underlayer deposits away from highest corrosion areas.

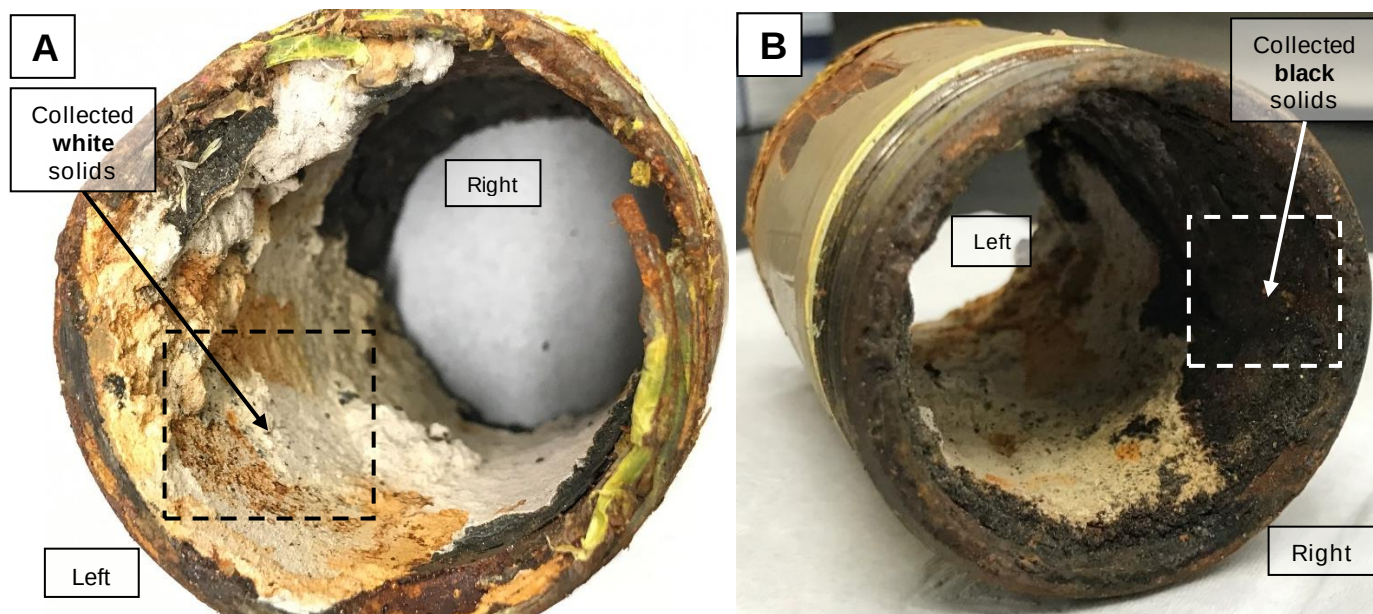


Figure 2: Images of failed pipe section as received. (A) Heavily corroded ‘left’ section of A106 Gr. B carbon steel pipe near failed threads is labeled, showing heavy white solid deposits on top of a black solids underlayer. Separate samples were taken from left-side white surface layer and right-side black solids layer (B). Removal of white solids surface revealed additional black underlayer, as well as corroded pipe walls and deep pitting.

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Adenosine triphosphate (ATP) photometry

Solid subsamples were massed and placed in 2 mL of a cell lysis and ATP extraction buffer for 10 min at room temperature, vortexing twice. Samples were then centrifuged and 1 mL of supernatant was removed for dilution and ATP quantification using a standard ATP photometer luciferase assay.

Quantitative polymerase chain reaction (qPCR)

DNA was extracted from solid samples (~100-200 mg solid used per sample) by microbead beating and chemical lysis using a soil DNA extraction kit. DNA was purified by the same kit, with inhibitor precipitation and silica spin columns. Eluted DNA was diluted 1:10 or 1:100 in Tris low-EDTA buffer and used directly for PCR or stored at -20°C. PCR reactions were run on a standard 96-well thermocycler with assay gene targets of universal 16S (for total prokaryotes), *mcrA* (for methanogens), *aprA* (for sulfate-reducing prokaryotes), *SoxB* (for sulfur-oxidizing bacteria), and *ITS* (for total fungi). All assays used SYBR-green chemistry, 40-cycle reaction programs, and standard curves generated with dilution series of positive control DNA.

16S rRNA gene sequencing

Solid samples were submitted for external analysis by an academic partner lab, performing 16S rRNA / ITS gene sequencing and microbiology database matching for taxonomic classification.

Scanning electron microscopy (SEM)

Samples were loaded onto aluminum stub sample holders with carbon tape. Samples were placed in a low vacuum chamber in a scanning electron microscope (SEM) in order to analyze in natural state with no sample preparation. Imaging of different phases was completed using backscattered electrons which separates heavier elements from lighter elements, imaged at 7.0 KV and 5000-20,000X magnification.

Quantitative X-ray diffraction (QXRD)

Due to sample size limitations and the minimum mass requirements of the QXRD instrument used, white and black layer samples were not able to be separately analyzed but submitted in bulk. For QXRD analysis, mixed white and black solids (~2g) were homogenized by mortar and pestle grinding and passed through a 40-mesh screen. The sample powder was solvent washed, further homogenized and mill ground, and dried before loading into a sample holder and analyzed by QXRD for at least 8 hours. Quantification of relative weight percentage composition was performed by proprietary software analysis.

RESULTS AND DISCUSSION

Microbial analysis

Upon lab reception of the pipe failure sample, significant corrosion and metal failure could be seen especially around the pipe threading. Also observed were large amounts of white solid deposits within the pipe, especially dense near the heavily corroded top section near the failed threads (**Figure 2A**). A thick black scale layer was observed underneath this surface white layer (and visible alone elsewhere in the pipe, **Figure 2B**). Separate white and black solid samples were taken for individual tests when analytical mass requirements allowed. ATP and qPCR microbial analysis yielded strikingly different results for the solid samples taken from the internal pipe deposits, which are shown in **Table 1** and **Figure 3** below.