MICROORGANISMS ASSOCIATED WITH PITTING CORROSION IN A MODEL FLOW CELL SYSTEM

Jennifer Busch-Harris*
Robert H. Webb
Gary Jenneman
ConocoPhillips
222 GB Bartlesville Technology Center
Highway 60 & 123
Bartlesville, OK 74004
Voice: 918-661-5053
Fax: 918-661-1320
Jennifer.Harris@conocophillips.com

Kathleen Duncan
University of Oklahoma
Norman, OK

Kerry Sublette
University of Tulsa
Tulsa, OK

Microbiologically influenced corrosion (MIC) is a significant source of pitting corrosion affecting oil and gas pipelines, wells, and a variety of surface facilities. The cost of MIC includes the loss of product due to leaks, cleanup costs for damage to the environment caused by leaks, and the cost of preventive measures. Monitoring bacteria for control of MIC has typically focused on sulfate-reducing bacteria (SRB). However, since SRB are a diverse group which vary considerably in their propensity to influence corrosion, determining whether or not corrosive SRB species are present is desirable in order to target the application of biological control agents in an appropriate, cost-effective manner. This project uses molecular methods to identify the SRB and other potentially significant bacteria in biofilms contributing significantly to corrosion. We sampled biofilm bacterial communities from bench-scale flow cells designed to provide a model system for the examination of pitting corrosion in pipelines. The microbial feedstock for the experiment was obtained from a pipeline after enrichment for SRB. Six biofilm flow cells were constructed from PVC pipe, maintained at 40oC under anaerobic conditions and fed from a reservoir containing a synthetic brine medium and the enriched microbial feedstock. Two flow cells were controls that received no chemical treatment, two received corrosion inhibitor A and two received corrosion inhibitor B. The flow cells contained mild steel strip coupons and Biotraps to sample biofilm bacteria and monitor corrosion. After 30 days treatment, flow cells were dismantled and samples distributed for determination of viable biofilm bacteria (SRB and general heterotrophic acid-producing bacteria), microbial identification using DNA sequencing methods and PLFA, and rates of pitting corrosion. A preliminary analysis indicates chemical treatments not only affect the rate of pitting corrosion, but also alter the composition of the microbial community as determined by PLFA and DNA sequence analysis. The average pitting rate was determined from the deepest pit measured on corrosion coupons placed into the flow cells. The average pitting rate was 25 mpy for untreated coupons inoculated with microbial feedstock. Coupons treated with corrosion inhibitor had variable pitting rates; one corrosion inhibitor enhanced MIC pitting rates while another corrosion inhibitor decreased pitting rates (5.6 mpy ,$p<0.05$) vs. the control. Microbial communities from coupons treated with both corrosion inhibitors were more diverse than microbial community isolated from the untreated coupons. Microbial communities isolated from the reservoir feedstock were less diverse than those identified from coupons in the flow cells. The reservoir feedstock was heavily dominated by SRB similar to Desulfovibrio indonensis, a species known to be involved in biocorrosion. In contrast, SRB sequences similar to that of Desulfovibrio lkalitolerans, which has not been examined for biocorrosion, were more abundant on the coupons. The coupons also contained higher proportions of SRB sequences similar to Desulfomicrobium, Desulfacinum, and Geoalkalibacter. Coupons contained proportionately fewer SRBs but more clostridia, Betaproteobacteria, Gammaproteobacteria, Thermotogae and Synergistes. Communities from the treatment with the lowest fraction of SRB and highest proportion of clostridia contain a methanogen. Many, but not all, of the SRB and other sequences from the coupons were similar to those of organisms and sequences found in oil facilities and reservoirs.

###