Microbial community composition of biofilms associated with sewer corrosion.

B.I. Cayford, G.W. Tyson, J. Keller, P.L. Bond

Advanced Water Management Centre, Level 4 Gehrmann Building (60), The University of Queensland, Brisbane, QLD 4072

Keywords: Microbial ecology; sewer corrosion

It is well established that the corrosion of concrete in sewer systems is the result of sulfur oxidising microbes converting hydrogen sulfide (H$_2$S) to sulfuric acid (H$_2$SO$_4$) (Parker, 1945). These microbes form biofilms that grow on exposed concrete surfaces in aerobic areas of the sewer, in particular the crown of gravity sewer pipes. The H$_2$S is produced in anaerobic environments such as pump stations, rising mains and the sediment at the bottom of gravity sewer pipes. In order to develop effective mitigation strategies, it is essential to characterize the microbial biofilm communities responsible and elucidate how their activities promote concrete corrosion. Previous studies have revealed that the sulfur cycle is central to this corrosion, therefore traditional management strategies have focused on controlling hydrogen sulfide levels through the use of chemicals to oxidise or precipitate hydrogen sulfide to prevent its availability for microbial oxidation. Historically, Acidithiobacillus thiooxidans (previously named Thiobacillus thiooxidans) has been considered the main sulfur oxidizing microorganism responsible for this process ((Parker (1945), Islander et al. (1991), Okabe et al. (2007)). We aim to perform the first comprehensive analysis of microbial communities associated with concrete corrosion.

In September 2009, a corrosion associated sewer biofilm was collected from a main gravity trunk site within the Sydney sewer network. DNA was extracted from this microbial community and the diversity of organisms was assessed by high-throughput 16S/18S rRNA gene amplicon sequencing (pyrotags) using universal primers. This cutting-edge technology provides the most comprehensive analysis of all microbes (bacteria, archaea and eukarya) within a sample. Pyrotag sequences were clustered based on sequence similarity (>97% identity) into groups of related sequences referred to as phylotypes (species).

Preliminary phylogenetic analysis revealed a total of 108 phylotypes, composing 72 bacterial and 36 eukaryotic representatives, no evidence of archaea was found. The majority of phylotypes represent low abundance organisms; only 10 phylotypes were present at greater than 1% of the community. More than 70% of the community was composed of three bacterial phylotypes from the Actinomycetales, Xanthomonadales, and Rhodospirillales (Figure 1). The dominance of these organisms suggests that they play a significant role in the corrosion process, either directly through the production of acids or indirectly through competition with acid producing bacteria. The Acidithiobacillales, which includes A. thiooxidans, had a relatively low abundance composing approximately 4% of the total community (exposed wedge of Figure 1). This study is the first to characterize the eukaryotic community found in sewer corrosion biofilms, although several fungi have been isolated from similar environments (Cho and Mori, 1995). The dominant eukaryotes were fungi and metazoa, which are known to graze on bacterial populations. A wide range of fungi are known to produce organic acids and as such may contribute to the corrosion process. Archaea have never been reported in previous studies and the use of universal primers and large number of sequences (3440) generated should have revealed if any were present in this study.
The results so far were unexpected considering previous research has suggested that *A. thiooxidans* is the major organism involved in concrete corrosion. This study suggests that the corrosion process is the result of the activity of a diverse microbial community. Analysis of biofilm samples and environmental monitoring data taken from Gold Coast (September 2009 and April 2010) is currently underway. Comparison of samples from different locations or time points will reveal the effects of the environmental and seasonal variation on the microbial community and any implications this may have on the corrosion process. Phylotypes that are consistently present are likely to play key roles in the corrosion process and identification of these organisms is crucial. Further research will reveal what role these new organisms play and allow for an improved understanding of the corrosion process.

**References**


