

**MICROBIAL COMMUNITY STRUCTURE
OF “CAVE SILVER” BIOFILMS FROM
THE SANFORD UNDERGROUND
RESEARCH FACILITY IN LEAD, SOUTH DAKOTA,
AS DETERMINED BY 16S rDNA SEQUENCING**

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ABSTRACT

“Cave Silver” biofilms, nicknamed for their silvery-iridescent appearance, are documented in cave and mining systems worldwide. Despite their name, “cave silver” biofilms are a complex microbial community. European studies identified high proportions of Actinobacteria, Proteobacteria, and unclassified phyla using Sanger sequencing methods. Samples collected from Sanford Underground Research Facility (Lead, South Dakota) were analyzed using Next Generation sequencing of 16S rDNA to compare their microbial community composition with those of European samples. Averages of all SURF samples show high proportions of Proteobacteria, Actinobacteria, Firmicutes, Chloroflexi, and unclassified phyla. Top class matches of Proteobacteria are Alphaproteobacteria, Gammaproteobacteria, and Deltaproteobacteria. The most abundant class of Actinobacteria is Actinomycetes. The high number of unclassified taxa indicate that “cave silver” contains many uncultured and unknown microorganisms. Comparison of SURF and European biofilms will reveal details of the similarities and differences among “cave silver” communities.