

NEXT-GENERATION SEQUENCING FOR MICROBIAL CHARACTERIZATION OF BIOVERMICULATIONS FROM A SULFURIC ACID CAVE IN APULIA (ITALY)

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Sulfuric acid cave systems host abundant microbial communities that can colonize several environments displaying a variety of morphologies *i.e.* white filamentous mats floating on the water surface, white creamy moonmilk deposits on the walls, and biovermiculations. Up to date, only few reports have described the microbiological aspects behind biovermiculation geomicrobiology of Italian sulfuric acid caves despite their overall abundance in the territory.

Here, we present the first characterization of biovermiculation microbial populations from Santa Cesarea Terme (Apulia, Italy) using a next-generation sequencing approach. In this area, four sulfuric acid caves located along the coastline of the Adriatic sea have been explored. The mixing of sea and upwelling acidic water characterizes these environments, where very peculiar microbiological communities are visible both floating on the water but also growing on cave walls. In particular, we focused our analysis on biovermiculations from Fetida cave. This cave opens at the sea level, and moving from the entrance to the deeper part, it is possible to observe a decrease of marine influence and a corresponding increase of the acidic effect of the upwelling waters. Biovermiculations copiously cover ceiling and walls mainly in the deeper and middle environments of the cave, while they are absent close to the entrance. From a morphological point of view, biovermiculations have a widespread range of colors going from grey to dark brown with an overall slimy appearance; dendritic morphologies alternate to very dense wall-covering sheets. Vermiculation samples from different locations within the cave (mid-section and the end) have been collected. Total DNA was extracted from each sample and 16S rDNA sequences were analysed through Illumina MiSeq platform. The main lineages found in all the samples included *Gammaproteobacteria*, *Betaproteobacteria*, *Alphaproteobacteria*, *Bacteroidetes*, *Planctomycetes* *Actinobacteria* and *Acidobacteria*. In particular, the samples from the deeper part of the cave had the highest abundance of *Acidobacteria* and showed the presence of *Epsilonproteobacteria* that can be related to bacterial sulfur-oxidizing activity typically occurring in sulfidic environments.