

Life in the dark: The role of microorganisms in the cave biogeochemical cycles

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Microorganisms play a crucial role in Earth's biogeochemical cycles on both short- and long-term scales. Understanding the extent of these interactions in specific environments is essential for assessing the impact of microbial communities on ecosystem dynamics. Cave systems are subterranean environments that vary in their genesis, host-rock types, and mineral inventories. For those caves isolated from the surface, the absence of light-driven photosynthetic processes makes them highly oligotrophic environments. Despite this, caves harbor an unexpected microbial diversity, often relying on chemotrophy and mutualistic interactions to sustain the development of complex communities. The resident microorganisms play key roles in speleothem formation and rock substrate alteration, atmospheric gas sequestration and oxidation (e.g., methane and hydrogen), and in the establishment of basal trophic networks. Although the microbial role in the subterranean ecosystem functions is fundamental, their contributions to biogeochemical cycling within caves have never been assessed using a large-scale systematic approach. To address this, we performed whole-genome metagenomic sequencing using both short-read (Illumina) and long-read (Oxford Nanopore) strategies, coupled with publicly available metagenomic data. In total, we compiled and analyzed a dataset of 154 metagenomes representing cave systems worldwide, encompassing diverse cave types (i.e., quartzite, limestone, sulfidic, and basaltic caves) and sample matrices (e.g., biofilms, soil, and water). We investigated microbial distribution across different cave systems and their roles in the biogeochemical cycling of major elements, such as sulfur, nitrogen, carbon, and iron. Our findings provide key insights into the diversity and ecological roles of cave microorganisms, shedding light on the evolution and adaptation of life in the absence of sunlight.