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Role of EPS in cryptoendolithic communities in an arid habitat

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Within the barren sandstone outcrops found in the Grand Staircase-Escalante National Monument in southern Utah, diverse microbes exist in the pore spaces of the rocks. Dominated by cyanobacteria, these communities harbor a diverse collection of bacteria, including potential iron-reducing bacteria. As a community, these cryptoendolithic microbes affect the larger landscape through their production of extracellular polysaccharide (EPS). Through the production of EPS and filamentous cells, these communities harden the stone surface, making it more resistant to the effects of wind and water. Cell mass and EPS also clog pores within the rock surface, reducing the rate of water infiltration. These physical effects resulting from EPS production are likely passive phenomena. EPS extracted from these communities can bind ferrous iron, potentially arising from the activity of iron-reducing bacteria. Biochemically, active preparations of the EPS were rich in uronic acids, making the polysaccharides acidic in nature. Fractions of the EPS obtained from lab grown consortia include a soluble fraction found in culture supernatants and an insoluble component that is tightly associated with the cell mat. We have found that cobalt ions will interfere with the iron binding activity of the EPS, suggesting that these EPSs bind multiple cations. Functionally, the EPS would serve to sequester and concentrate available cations from the ecosystem, making them available for uptake by cyanobacteria and other community members for metabolic purposes. When we include the movement of water through the communities via evaporation, we hypothesize that the system serves as a bio-filter to capture essential metal ions.

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Microbiome and virome of a *C. difficile* patient cured by fecal transfer 5 years ago

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Fecal transplantation (FT) is a promising therapeutic option for antibiotic-refractory *Clostridium difficile* infection. FT utilizes donor feces with complex bacterial and viral communities to limit *C. difficile* and inflammation. Ultimately, bacterial communities were donor similar, suggesting sustainable stool engraftment. A central rather unexplored role in FT is played by phages, the most abundant viruses, which largely influence bacterial communities in response to environmental changes. They are activated during obesity and inflammation and promote bacterial lysis and reduction of microbiota complexity as indicators of disease. In light of the fact that phages behave differently in the intestine than under laboratory conditions, more research is needed. Here, we describe the dynamic microbiota changes of a *C. difficile* patient cured by FT since five years, the longest follow-up period so far. We reported on the microbiome and recently also analyzed the virome by deep sequencing and observed that low abundance of phages correlated with recovery of the patient and absence of inflammation. Thus, healthy microbiota appears to be characterized by low phage abundance. This has been described to correlate with high microbiome complexity. In accordance, the cured patient's microbiota had similar complexity as the donor's. Although viruses were likely transferred, the patient established a virome distinct from the donor. Surprisingly, we detected *Chlorella* virus-related sequence, an algae-specific giant virus, for the first time in the human intestine. Similarities of the phage-bacterial interplay in the intestine and the better understood marine ecosystems as reported by the TARA Oceans-EMBO expedition participants in 2016 are striking. Based on these findings, we will discuss technical difficulties encountered with virome analyses possible implications of intestinal viruses on future microbiota and other phage therapies.

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