Identification and Quantification of Proteins Produced by a Thermophilic Microbial Community Sampled at Three Temperatures.

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Abstract
The thermophilic microbial mat community found in Octopus Spring, Yellowstone National Park, has been studied by variety of methods. This study focuses on the proteins produced by the community. Three samples of the microbial mat in Octopus Spring were obtained at temperatures of 49˚C, 56˚C, and 67˚C. Proteins were extracted and amino acid analysis was performed on the separated green and red layers of the mat. Protein yields in the green layer were found to be 0.098% (49˚C), 2.82% (56˚C), and 0.13% (67˚C). In the red mat layer the protein yields found were 0.016% (49˚C), 1.07% (56˚C), and 1.25% (67˚C). There was a larger percentage of protein found in the 56˚C green mat sample compared to the amount found at the other temperatures. There was also overall more protein found in the green layer of the mat than in the red layer. The green layer samples were subjected to environmental proteomics using the iTRAQ method for quantification. 198 proteins were identified with $p<0.01$, and a false discovery rate of 3.37%. 108 proteins were quantified. The majority of proteins found were identified as chaperones, enzymes, and transporters from *Synechococcus sp. JA-3-A&B* and *Roseiflexus sp. RS-1*.