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Association of microbial community structure and iron oxidation rate in autotrophic mine biostalactites

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Biostalactites created by microorganisms using chemolithotrophic iron oxidation as a sole energy source frequently grow in acidic mine water (AMD) springs. Different primary producers may even dominate in individual stalactites showing similar physico-chemical characteristics. This phenomenon is known from a number of environments; however, the question whether community structure influences the efficiency of microbially catalysed geochemical processes remains unresolved despite numerous studies concerning microbial diversity and metabolic potential. The biostalactites represent a good model for analysing such kind of relationship since they are distinct objects in which iron oxidation rates can easily be determined, along with other relevant environmental features and microbial community structure.

We analyzed biostalactites from three abandoned underground mines in Bohemia and Slovakia. All stalactites grew at AMD seepages with pH between 2.5 and 3, iron content from 10 to ca. 250 mg/L and flow rates from 4 to over 300 mL/hour. Members of the genus *Ferrovum* represented the most abundant primary producers in most biostalactites. However, significant differences in the iron oxidation rate and the ability to lower Fe²⁺ concentration in the solution were observed even in adjacent stalactites. These differences corresponded neither to water chemistry nor to flow rate or other obvious parameters. Moreover, an absence of iron oxidation and strikingly different microbial community structure was recorded in some stalactites at all three study sites. This phenomenon occurred at a wide range of flow rates, Fe²⁺ concentrations and stalactite sizes.

Our findings support the view that results of microbially catalyzed processes are not simply determined by physic-ochemical conditions. However, contrary to the widely held notion, the (un)availability of suitable bacteria cannot explain our results, since all stalactites contained at least small abundances of identical iron oxidizers or thrived in proximity of viable iron oxidizing communities. More likely, biotic interactions within the microbial consortia caused the observed variability of the system's behaviour.