



Endolithic diversity of microorganisms on sandstone and implications for biogenic weathering

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Molecular methods allow a comprehensive view on uncultured microbial communities in dimension stone. In the presented study, we focus on depth profiles of microbial colonization in sandstones with different porosity and overall durability. All sandstones were taken from quarries where they were exposed to the environment for several years. Approximately 0.1 g of material from the stone surface, from 5 mm and from 30 mm depths was taken under sterile conditions and subjected to analysis of microbial DNA and culturing experiments. In particular, DNA was extracted from the material, the phylogenetic marker gene of eukaryotic organisms (18S rDNA) was amplified and used for generation of clone libraries, which were then analysed by sequencing. "Roter Wesersandstein" was just colonized at the material surface, predominantly with algal and fungal microorganisms. No environmental DNA could be isolated from depth profiles. From "Nebraer Sandstein" with high pore size (shown by thin sections), environmental DNA from depths down to 3 cm could be retrieved. Though the uppermost layer is dominated by microalgae (as concluded from the retrieved clones), the percentage of algal clones from 5 mm and 30 mm depths drop to 10 % of all clones. There, apart from filamentous fungi, moss clones clearly dominate the microbial community. At a depth of 30 mm, 70-80 % of the retrieved clones match to various mosses (Bryophyta). Though mosses do not form layers on the stone surfaces, moss rhizoids or protonemata must be abundant as endoliths inside the stone material. It is reasonable to assume that the rhizoids may contribute to an increase in pore size by active penetration of the clastic material, even though colonization of the surface by mosses is not obvious. This feature may imply stronger impact of stone decay induced by endolithic growth of bryophytes than hitherto observed.