



Biomolecular investigations for the identification of rock biodeteriogens in archaeological areas

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Rock-colonizing microorganisms form complex communities, such as subaerial biofilms, in which prokaryotic and eukaryotic autotrophs and heterotrophs are embedded within diverse extracellular substances, that enhance their survival. Rock substrates also harbour endolithic microorganisms, that are often overlooked because of their cryptic habitus. Such colonizers interact with mineral substrates by means of mechanical and metabolic mechanisms, thus modifying rock physical and chemical features. While these processes drive pedogenesis in natural environments, they give rise to biodeterioration of cultural heritage. Identification of the microorganisms colonizing lithic materials is a necessary prerequisite to understand their physical/chemical interactions with the substrates and eventually devise appropriate conservation strategies. Biodiversity of epi- and endolithic colonizers is certainly underestimated since studies have so far heavily relied on culture-dependent methods, thus neglecting uncultured microorganisms. In this research, funded by Fondazione CRT (Alfieri project), we have successfully extracted DNA directly from environmental rock samples collected from archaeological areas in the Alpine environment (the prehistoric paintings of Mompantero in the Susa Valley near Torino and the Roman Theatre of Aosta). Ribosomal DNA was PCR-amplified with fungal and cyanobacteria-specific primer pairs. NCBI BLAST searches with the sequences obtained have indicated that the examined rock substrates, alongside well-described fungal and cyanobacterial species, harbour uncommon biota, such as a pleosporalean ascomycete with unmatched ITS

sequences.