Characterization of Microbial Community in Lascaux Cave by High Throughput Sequencing

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The Lascaux Cave in South-Est France is an archeological landmark renowned for its Paleolithic paintings dating back c.18.000 years. Extensive touristic frequenting and repeated chemical treatments have resulted in the development of microbial stains on cave walls, which is a major issue in terms of art conservation. Therefore, it is of prime importance to better understand the microbial ecology of Lascaux Cave. Like many other caves, Lascaux is quite heterogeneous in terms of the nature and surface properties of rock walls within cave rooms, as well as the succession of rooms/galleries from the entrance to deeper areas of the cave. Lascaux Cave displays an additional levels of heterogeneity related to the presence of discontinuous stains on certain types of cave walls. We compared the microbial community (i.e. both prokaryotic and eukaryotic microbial populations) colonizing cave walls of different rooms/galleries, in and outside stains and in different cave layers, in successive years. Quantitative PCR analysis of cave wall samples gave in the order of 10^2 copies of 18S rRNA genes and 10^5 copies of 16S rRNA genes per ng of DNA, indicating significant colonization of all cave walls by micro-eukaryotes and especially bacteria. Illumina metagenomic analyses of cave wall samples was carried out based on four ribosomal DNA markers targeting bacteria, archaea, fungi, and other micro-eukaryotes. The results showed that the four microbial communities were highly diverse in and outside stains, as several hundred genera of microorganisms were identified in each. Proteobacteria were more prominent within stains whereas Bacteroidetes and Sordariomycetes were more prominent outside stains. High-throughput sequencing also showed that the nature/surface properties of cave walls were the main factor determining the structure and composition of microbial communities, ahead of the other heterogeneity factors studied i.e. location within the cave, presence of stain and sampling season. This work provides a global view of the microbial community of Lascaux Cave, which could be useful to guide conservation efforts.