



## **The Primary Results of Analyses on The Archaeal and Bacterial Diversity of Active Cave Environments Settled in Limestones at Southern Turkey**

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The microbial diversity of cave sediments which are obtained from three different caves named Insuyu, Balatini and Altınbeşik located at Southern Turkey has been investigated using molecular methods for biomineralization . The total number of 22 samples were taken in duplicates from the critical zones of the caves at where the water activity is observed all year round. Microbial communities were monitored by 16S rRNA gene based PCR-DGGE (Polymerase Chain Reaction - Denaturing Gradient Gel Electrophoresis) methodology. DNA were extracted from the samples by The PowerSoil<sup>®</sup> DNA Isolation Kit (MO BIO Laboratories inc., CA) with the modifications on the producer's protocol. The synthetic DNA molecule poly-dIdC was used to increase the yield of PCR amplification via blocking the reaction between CaCO<sub>3</sub> and DNA molecules. Thereafter samples were amplified by using both Archaeal and Bacterial universal primers (ref). Subsequently, archaeal and bacterial diversities in cave sediments, were investigated to be able to compare with respect to their similarities by using DGGE. DGGE patterns were analysed with BioNumerics software 5.1. Similarity matrix and dendograms of the DGGE profiles were generated based on the Dice correlation coefficient (band-based) and unweighted pair-group method with arithmetic mean (UPGMA). The structural diversity of the microbial community was examined by the Shannon index of general diversity (H). Simultaneously, geochemical analyses of the sediment samples were performed within the scope of this study. Total organic carbon (TOC), x-ray diffraction spectroscopy (XRD) and x-ray fluorescence spectroscopy (XRF) analysis of sediments were also implemented. The extensive results will be obtained at the next stages of the study currently carried on.