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DISCOVERING PAST GUT MICROBIOMES THROUGH NGS ANALYSIS: THE MUMMIES OF ROCCAPELAGO (MO)

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The gut microbiota plays a primary role in metabolism and immune response of host organisms. It is influenced by lifestyle, diet and environment but little is known about its ancestral state and evolution, especially in relation to past human dietary shifts, the impact of industrialization and the introduction of antibiotics. In the reconstruction of the ancestral state of gut microbiota, recent pioneering studies have focused on contemporary rural populations or ancient coprolites. This paper presents the first screening of microbiota by NGS technology from ancient human gut tissues. We collected samples from ten Roccapelago mummies (16th-18th c. AD) from different anatomical tissues (gut, skin, muscle). In addition, samples of soil and clothes were analyzed to detect environmental contamination. Paleodiet reconstruction by stable isotopes analysis (δ^{13}C and δ^{15}N) was performed on femurs and teeth. Moreover, information about diet, lifestyle and health were recovered from parish registers and historical documents.

DNA was extracted with a silica-based protocol and amplicons of 16S rRNA gene (V3 region) were sequenced on 454/Roche obtaining an average of 10.059 reads per sample. The bioinformatic analysis using the MICCA pipeline reveals a consistent diversification between tissues (gut vs muscle vs skin), with an enrichment of Actinobacteria in gut samples (18%) in respect to muscle and skin samples, despite Clostridiales are represented in all tissues analyzed. Interestingly, halophilic Gram-positive bacteria from Staphylococcaceae (6%) are found in gut samples. Investigation of a potential physiological basis of this association may lead to new insights into the reconstruction of past gut microbiomes.