Geophysical Research Abstracts Vol. 21, EGU2019-7904, 2019 EGU General Assembly 2019 © Author(s) 2019. CC Attribution 4.0 license.



## Unraveling the secrets of antique marble statues by metagenomics

Katja Sterflinger, Hakim Tafer, Caroline Poyntner, and Guadalupe Pinar University of Natural Resources and Applied Life Sciences, ACBR, Vienna, Austria (katja.sterflinger@boku.ac.at)

Every step in the history of an object leaves its own genetic fingerprint represented by DNA, a specific microbiome that allows us to get an idea of everything that it has been through during its history. The microbiome can be primarily used as an indicator for the state of conservation of the object, but it may additionally release relevant information about the geographical and climatic regions through which an object passed and the conditions under which it was stored or buried.

High-throughput molecular methods are undergoing a revolution allowing the analysis of smallest traces of DNA from ancient objects. Emerging technologies, together with the development of bioinformatics pipelines, enable to assign single DNA molecules to a certain animal, plant, microorganisms or even to humans. The biological information contained in cultural heritage objects is a bio-archive of the history of the objects, offering a kind of fingerprint for current and future comparisons.

This work presents data derived from a high-throughput metagenomics DNA analysis performed on three valuable and possibly smuggled marble statues of an unknown origin. The results enabled to infer the possible relation among the statues, as well as the conditions of their storage and their geographical shift. These data help to reconstruct the history of these objects, a kind of time travel.

These strategies offer an immense potential and reveal more information than we could have imagined shortly before. Nevertheless, it is important to note that these techniques pose a challenge concerning the interpretation of the immense amount of data generated.

Keywords: high-throughput molecular methods, biological information, bio-archive