Geophysical Research Abstracts Vol. 20, EGU2018-17289, 2018 EGU General Assembly 2018 © Author(s) 2018. CC Attribution 4.0 license.



## Microbial diversity and metabolic potential of desert soil and the resulting dust aerosols

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Deserts are well known to be major sources of dust, which is transported as aerosols across local, regional and even transcontinental scales. Aerosols affect the scattering of light and absorb thermal infrared energy, having a significant impact on Earth's radiative balance. Dust has been shown to have negative effects on human well-being, as it has been associated with inducing respiratory, allergic, and cardiovascular diseases. Earlier studies proofed dust particles to serve as a carrier for microorganisms, such as fungal spores, viruses, bacteria, archaea, and protozoa. By this mechanism, microorganisms may spread and colonize new regions and habitats, but also pathogenic organisms may use this mode of transportation and dispersal. Numerous surveys have described the long-range transport and the transatlantic respectively transcontinental deposition of desert dust particles mobilized and emitted from the Sahel and Arabian Peninsula. However, only limited investigations focused on the examination of microbial community composition and the metabolic potential of the airborne desert dust microbiome.

This study's aim is to examine dust filter samples in comparison with soil samples from the source region of dust. Doing this, we want to i) quantify the microbial load, ii) determine the microbial composition, iii) analyze the metabolic potential, and iv) investigate the pathogenicity of microorganisms occurring in dust as compared to soil samples. For our study we collected total suspended particle (TSP) samples of dust on Barbados, the easternmost island in the Caribbean, on Cyprus, an island in the Eastern Mediterranean, and during the Air Quality and Climate Change in the Arabian Basin (AQABA) ship expedition leading through the Mediterranean Sea and around the Arabian Peninsula. Desert soil samples have been collected in the Sahara, which may serve as a source region for the long-range-transport of dust collected during all three campaigns and also in the vicinity of the dust collection sites, i.e. on Barbados, Cyprus, and on the Arabian Peninsula. The genetic material of the environmental samples will be quantified by means of qPCR and will be identified, metabolically and functionally characterized by means of shotgun metagenomic DNA sequencing. The pathogenicity will be determined by applying a chromogenic assay followed by a cell culture approach.

We expect our study to provide new insights into the microbial presence, its taxonomic diversity, metabolic potential, and pathogenicity of dust associated microorganisms in comparison to soil samples originating from the potential source regions. These results may allow drawing conclusions on the mechanisms during dust formation as well as its alteration during transport.