Duststorms and bacterial diversity in the Mediterranean

Nikolaki S.[1], Zotou K.[1,2], Iakovidis M.[2], Stephanou E.[2], Bourtzis K.[1,3], Tsiamis G.[1]

[1]*Department of Environmental and Natural Resources Management, University of Patras, Agrinio, 30100, Greece*
[2]*Environmental Chemical Processes Laboratory, Department of Chemistry, University of Crete, Heraklion, Greece*
[3] *Present Address: Insect Pest Control Laboratory, Joint FAO/IAEA Programme of Nuclear Techniques in Food and Agriculture, Vienna, Austria*

Introduction

The Sahara region of Africa is the Earth's largest source of aerolized soil dust. African dust is transported to the Mediterranean region under particular meteorological conditions occurring during spring and summer. These dust events, inject a huge amount of microorganisms like fungal spores, bacteria, archaea and viruses, affecting visibility, climate, human health and the quality of life. Considering the importance of airborne microorganisms for human health, agricultural productivity and ecosystem stability, we assessed the bacterial composition during several sandstorm events in the South of Greece.

Materials and Methods

Air sampling was carried out from January 2013 until April 2014, in the coastal city Heraklion on the eastern Mediterranean Sea, during strong Saharan dust events. In total 22 samples (6 control samples and 16 event samples) have been characterized by Illumina amplicon sequencing using fusion primers U341F and 805R in order to amplify the V3-V4 region of the 16S rDNA gene. In total 519,707 sequences were analyzed using Qiime[1], Permutational multivariate analysis of Variance (Permanova)[2] and canonical analysis of principal coordinates (CAP)[3] implemented in primer 6+ software package.

Bacterial Distribution

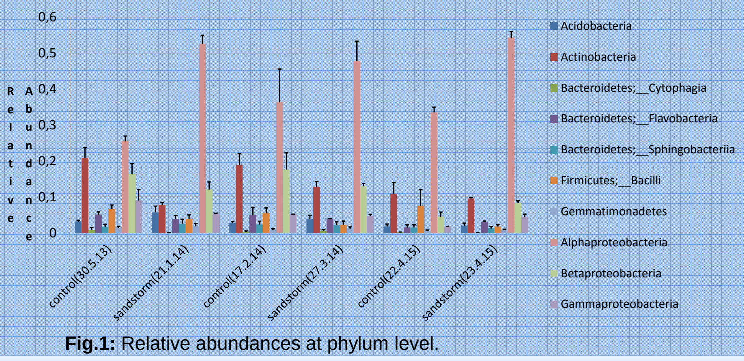

Fig.1: Relative abundances at phylum level.

Statistical analysis at order level

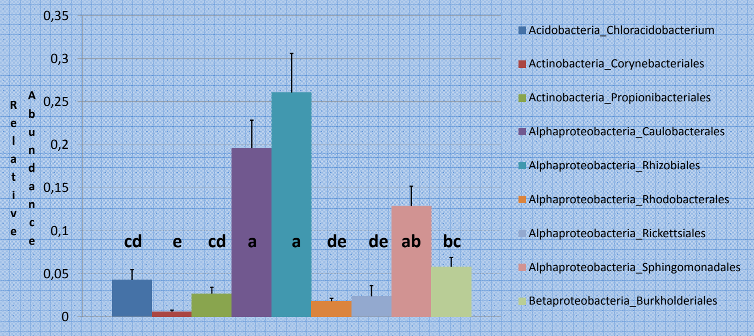

Fig.2: One way analysis of variance per OTU.

Results

- ➢The relative abundance of Alphaproteobacteria is higher followed by Actinobacteria and Acidobacteria (Fig.1).
- ➢Relative abundance of Alphaproteobacteria and specially members of family *Rhizobiaceae* is increasing during the sandstorm events (data not shown).
- ➢The level of Actinobacteria is reduced together with Betaproteobacteria (Fig.1).
- ➢Rarefaction curves determine that sampling depth was sufficient to accurately characterize the bacterial community being studied (data not shown).
- ➢*Caulobacterales* and *Rhizobiales* differ significantly from *Rhodobacterales* and *Rickettsiales (*Fig.2).
- ➢There is significant difference between control and events (Fig.3).
- ➢Species richness estimators and community diversity indices for sandstorms are increased compared to controls (data not shown).
- ➢Bray-Curtis similarity indicates distinct clusters in the ordination space between control and sandstorm communities that was quantitatively supported by high CAP reclassification rates (Fig. 3).

Future Plans

- ➢Characterize the bacterial communities that may be harmful for the human health.

Multivariable analysis of community structure

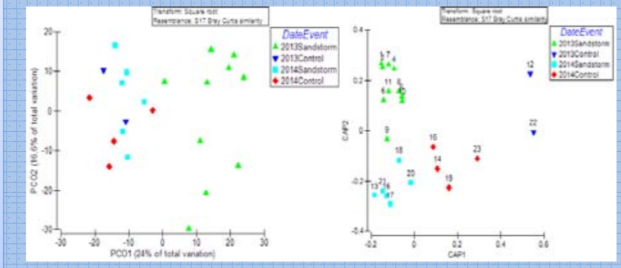

Fig.3: PCoA ordinations of Bray-Curtis similarities and CAP ordinations of bacterial communities.

References

[1] Caporaso et al., (2010). QIIME allows analysis of high-throughput community sequencing data, Nat. Methods.
[2] Anderson MJ (2001). A new method for non-parametric multivariate analysis of variance. *Aust J Ecol*.
[3] Anderson MJ, Willis TJ (2003). Canonical analysis of principal coordinates: A useful method of constrained ordination for ecology. *Ecology*.

Acknowledgments

"The project "CHEMISAND" is implemented under the "ARISTEIA" Action of the "OPERATIONAL PROGRAM EDUCATION AND LIFELONG LEARNING" and is co-funded by the European Social Fund (ESF) and National Resources.