

# THE POTENTIAL IMPACTS OF AIRBORNE MICROBES IN DESERT DUST ON THE SE MEDITERRANEAN SURFACE SEAWATER

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## Abstract

Atmospheric dust events can create a transoceanic bridge, injecting a wide variety of airborne microorganisms. This study documents their potential impacts on the SE Mediterranean surface water (SEMS) production and ambient microbial population. Our results show a significant microbial variability in aerosol samples collected at the shoreline of the SEMS, and demonstrate that some heterotrophic airborne bacteria are active in sterile Mediterranean seawater and fix both C and N under some circumstances. Furthermore, we show that airborne microbes caused a specific decrease in ambient *Prochlorococcus* abundance, possibly triggered by some airborne viral infection or airborne bacterial predation on the *Prochlorococcus*' cells.

**Keywords:** *Aerosols, Levantine Basin, Atmospheric input, Bacteria, Primary production*

Aerosols and dust are periodically transported across the oceans and seas, supplying nutrients and trace metals to the surface water [1]. Additionally, aerosols may also contain a wide array of different airborne microorganisms (heterotrophic bacteria, viruses, cyanobacteria and fungi), which can easily be transported thousands of kilometers away from their origin within a few days [2]. The SEMS is an ideal marine system for studying the potential impact of aerosols and airborne microbes on surface microbial production, because it is an oligotrophic environment with low inorganic nutrients and low autotrophic and heterotrophic activity [3] that is subject to relatively high aerosol deposition throughout the year [4]. Thus, any external input of micro/macronutrients, along with airborne microbes, can have a relatively significant effect upon interaction with the ambient microbial populations, thereby having a potential impact on the system's production and ecological function [5]. The heterotrophic airborne microbial community exhibits high diversity (Fig. 1). A principle component analysis of the 16S rRNA gene, extracted from aerosol filters that represent different geographical origins (determined by air mass back trajectory), indicated similar biological signatures in filters of a similar source but different signatures in aerosols from dissimilar geographical origins (Fig. 1). Microcosm bioassay experiments in which aerosols were added to sterile (0.2- $\mu$ m filtered and autoclaved) SEMS were performed in order to assess the potential impact of airborne bacteria on bacterial abundance, production and N<sub>2</sub> fixation. A significant increase was observed in all parameters within a few hours (ANOVA,  $p < 0.05$ ), suggesting that airborne microbes can account for one-third of bacterial abundance and 50-100% of bacterial production and N<sub>2</sub>-fixation rates, following dust/aerosol amendments to surface SEMS (Fig. 1). Experiments in which dust collected during an intense dust storm (September 2015) was added to surface SEMS indicate that airborne microbes cause a rapid decrease in *Prochlorococcus* abundance and that the effect is dose-dependent (Fig. 2). While the addition of UV-killed (48h) aerosol resulted in a modest decrease in *Prochlorococcus*, possibly due to certain chemical toxicity effects, the addition of 'live' dust caused a much larger decline within 48 hours of the addition. We hypothesize that this effect can be attributed to some airborne viral infection or to bacterial predation on the *Prochlorococcus* cells. Our results suggest that dust/aerosol deposition can be a potential source of a wide array of microorganisms, all of which may affect microbial composition and food-web dynamics in oligotrophic marine systems such as the SEMS.

Fig. 1. Upper panel: (A) Representative air mass back trajectories analyses (3 days) derived from NOAA/ARL HYSPLIT-4 backward trajectories model showing the route and origin of the aerosols used in this study. Different colors represent different air mass trajectories; Middle East (gray, filters # 450,565,739), Sahara desert (red, filters # 576, 691 and dust collected in February 2015) and Eastern Europe (yellow, filters # 785, 738), (B) Taxonomic distributions of 16S rRNA genes analyses (family level) retrieved from the different aerosol samples, and (C) The genetic discrimination of bacterial phylotypes based on a/the principle component analysis (PCA) of the different dust sources. Lower panel: (E) Bacterial abundance, (F) bacterial production and (G) N<sub>2</sub> fixation rates following the addition of aerosol (collected during February 2015) to sterile SEMS surface water. The letters above the columns represent statistically significant differences (one-way ANOVA and a Fisher-LSD

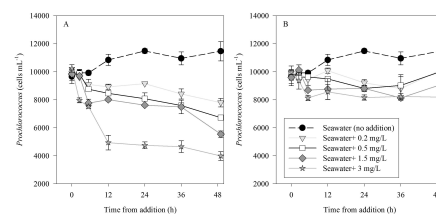


Fig. 2. Changes in the *Prochlorococcus* abundance in water collected from the SEMS following the addition of various amounts of (A) non-killed and (B) UV-killed aerosols collected during a dust storm in September 2015, Haifa, Israel.

## References

- 1 - Guieu C, Aumont O, Paytan A, et al. 2014. Global Biogeochemical Cycles deposition to Low Nutrient Low Chlorophyll regions. *Global Biogeochemical Cycles*: 11:79–98.
- 2 - Griffin DW. 2007. Atmospheric movement of microorganisms in clouds of desert dust and implications for human health. *Clinical Microbiology Reviews* 20: 459–77.
- 3 - Raveh O, David N, Rilov G, and Rahav E. 2015. The temporal dynamics of coastal phytoplankton and bacterioplankton in the Eastern Mediterranean Sea. *Plos One* 10: e0140690.
- 4 - Guerzoni S, Chester R, Dulac F, et al. 1999. The role of atmospheric deposition in the biogeochemistry of the Mediterranean Sea. *Prog Oceanogr* 44: 147–90.
- 5 - Rahav E, Ovadia G, Paytan A, and Herut B. 2016. Contribution of airborne microbes to bacterial production and N<sub>2</sub> fixation in seawater upon aerosol deposition. *Geophys Res Lett* 43: 1–9.

