Comunità Batterica e Composizione Chimica in Campioni di PM10: Nuovi Approcci di Analisi Integrando Differenti Tecniche

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Introduction

BIOAEROSOL

number concentration $\sim 10^4 \text{ m}^{-3}$

mass concentration $\sim 1 \text{ μg m}^{-3}$


Bioaerosol represents about 10% of the total aerosol mass


Bacteria 80.8%

Archaea 0.8%

Viruses 0.1%

Eukaryota 18.3%

AEROSOL
Outline and Main Goals

- **The structure of the airborne bacterial community** was characterized in PM10 samples to investigate its relationships with the **chemical composition** in a Central Mediterranean site affected by aerosol particles of different type and origin.

- We analyzed both **winter** (January-March 2018) and **spring** (May-June 2018) PM10 samples to study the **seasonal variations** of the relationships between the bacterial community structure and the chemical elements.

- The **16S rRNA gene metabarcoding approach** was used for the DNA extraction and the PM10 sample bacterial structure characterization (both at the phylum and at the genus taxonomic level). PM10 samples were chemically characterized for more than 30 species, including **OC, EC, ions, and metals**.

- The **PCA (Principal Component Analysis)** and the **RDA (Redundancy Discriminant Analysis)** were applied to the bacterial phylum/genus relative abundances and the chemical species mass concentrations, allowing identifying the main relations among the investigated parameters.
Monitoring Site

Aerosol & Climate Laboratory
Mathematics and Physics Department
University of Salento (Lecce, Italy)

from Perrone et al. (2015)
Instrumentation and Methodology
(Airborne Bacterial Community Characterization)

10 winter PM10 samples (January-March 2018)

10 spring PM10 samples (May-June 2018)

Hydra Dual Sampler
FAI Instruments

PM Sampler
Gravimetric Method

PM10 Sample 1
Instrumentation and Methodology
(Chemical Species and Oxidative Potential)

ION Mass Concentration
ION Chromatography
Gilson 222-XL auto sampler
(University of Florence)

Metal Mass Concentration
Varian 720-ES Inductively Coupled Plasma Atomic Emission Spectrometer
(University of Florence)

OC and EC Mass Concentration
Sunset Carbon Analyzer Instrument
(University of Salento)

Oxidative Potential
DTT and AA depletion rate methods
(University of Ferrara)

PM10 Sample 2
Characterization of Airborne Bacterial Phyla in PM10 Samples

Geographical location and meteorological conditions of the monitoring site

Effects on the airborne bacteria dispersion

Variability of the bacterial community composition

**Cyanobacteria (18.80%)**

**Proteobacteria (45.56%)**

**Actinobacteria (11.43%)**


from Romano S. et al. (2019) “Comunità Batterica e Composizione Chimica in Campioni di PM10: Nuovi Approcci di Analisi Integrandoci Differenti Tecniche”
Characterization of Airborne Bacterial Genera in PM10 Samples

We found a different structure of the airborne bacterial community at the phylum and at the genus taxonomic level.

Role of the Meteorology and the Long-Range Transport

Meteorological Parameters, Bacterial Phyla Relative Abundances → PCA Input Parameters

Heavy Rain Samples
(S5, S9, S11, S13)

Continental Samples
(S1, S2, S10)

Desert Dust Samples
(S3, S6, S12)

Marine Samples
(S4, S7, S8)

Late Spring Samples
(S14, S15, S16, S17, S18, S19, S20)

from Romano S. et al. (2019) Sci. Total Environ. 697 (134020)
Redundancy Discriminant Analysis

Chemical species mass concentrations (red arrows) = predictive variables

Bacterial PHYLA relative abundances (green arrows) = response variables

Main pollution sources identified by Positive Matrix Factorization (PMF) (black arrows): mixed anthropogenic MAN, sulphate SUL, heavy oils – secondary marine OSM, soil dust SDU, reacted dust RDU, and sea salt SES

In spring, most of the bacterial phyla were associated with chemical species characterizing the OSM, RDU, and SES sources.

The chemical species arrows in the RDA triplot were on average spread in the canonical axis plane over a wider angle in spring than in winter, suggesting that the correlation coefficients among chemical species likely decreased in spring. The spring-summer air mass aging, which favored the mixing of particles of different type/source, likely contributed to this result.

From Romano S. et al. (2020) Sci. Total Environ. 730, 138899
We found that in winter OP_m was associated with Cyanobacteria (generally found in aquatic habitat), the “marine samples” S4 and S8 and the “heavy rain samples” S5 and S9.

In spring, OP_m values were strictly related to Firmicutes and the desert dust sample S12.
Main Results

- **Proteobacteria** (46%), **Cyanobacteria** (19%) and **Actinobacteria** (11%) were the most abundant airborne bacterial phyla identified in winter and spring PM10 samples collected in Lecce, a Central Mediterranean monitoring site.
- “Continental”, “marine”, “heavy rain”, “desert dust”, and “late spring” clusters were identified by PCA taking into account the long-range transport, the meteorological parameters, and the bacterial phyla relative abundances.
- The Redundancy Discriminant Analysis technique highlighted that most of the relationships among bacterial phyla/genera and chemical species are highly season-dependent.
- The oxidative potential values obtained by AA and DTT assays presented similar associations with the analyzed bacterial phyla and chemical species, as proved by RDA triplots.
- The analyses reported in this work have shown that the PM bacterial structure must be accounted to properly estimate the toxicity of PM10 samples and to assess the chemical species role.
Grazie per l’attenzione!!!

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