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Characterization of long-range transported bioaerosols in the Central Mediterranean

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HIGHLIGHTS

• Distinctive air masses origins show different bacterial communities.
• North African air masses show a relatively low number of genera with high abundance.
• European long-range air masses show a highly diverse and even community.
• Bioaerosol community correlates moderately with chemical composition.
• Potential pathogens are more abundant in European and Regional samples.

GRAPHICAL ABSTRACT

ABSTRACT

Airborne bacteria were characterized over a 2-y period via high-throughput massive sequencing of 16S rRNA gene in aerosol samples collected at a background mountain European Monitoring and Evaluation Programme (EMEP) Network site (Monte Martano, Italy) located in the Central Mediterranean area. The air mass origin of nineteen samples was identified by air mass modelling and a detailed chemical analysis was performed. Four main origins (Saharan, North-western, North-eastern, and Regional) were identified, and distinct microbial communities were associated with these air masses. Samples featured a great bacterial diversity with Protobacteria being the most abundant phylum, and Sphingomonas followed by Acidovorax, Acinetobacter and Stenotrophomonas the most abundant genera of the dataset. Bacterial genera including potential human and animal pathogens were more abundant in European and in Regional samples compared to Saharan samples; this stressed the relevance of anthropic impact on bacterial populations transported by air masses that cross densely populated areas. The principal aerosol chemical characteristics and the airborne bacterial communities were correlated by cluster analysis, similarity tests and non-metric multidimensional scaling analysis, explaining most of
Saharan dust

1. Introduction

The presence and diffusion of bioaerosols (bacteria, viruses, fungi, and other dead or living organisms including biological debris) in the Earth atmosphere impact ecosystems, climate, and human health (Burrows et al., 2009a; Burrows et al., 2009b; Fröhlich-Nowoisky et al., 2016; Pöschl and Shiraiwa, 2015). The biosphere directly emits bioaerosols into the atmosphere, which subsequently enables their dispersion and transport even at long distances (Desprès et al., 2012; Womack et al., 2010). In the course of atmospheric transport, bioaerosols may undergo further chemical and physical transformation, stress, and biological aging upon interaction with UV radiation, photo-oxidants, and various air pollutants like acids, nitrogen oxides, ozone, and aromatic compounds. All these processes can limit or even suppress the vitality of the living fraction of bioaerosol and therefore affect their capacity to diffuse and to colonize new ecosystems (Womack et al., 2010). Due to the above challenges, the present knowledge on the ability of viruses and bacteria to spread in the air and diffuse infections and more in general diseases is still immature and demands a wide spectrum of investigation (Middleton, 2017; Morawaska and Cao, 2020; Polymenakou, 2012).

Most of the previous studies in the Mediterranean area have been limited to advections of air masses from the Sahara Desert only. The occurrence and impact of this type of air mass, very rich in desert dust, are frequent and well documented (Escudero et al., 2006; Formenti et al., 2011; Goudie and Middleton, 2001; Pey et al., 2013). Saharan dust particles can be transported over long distances towards Europe (Amato et al., 2016; Barnaba et al., 2017; Cusack et al., 2012) and America (Garrison et al., 2014; Prospero et al., 2005). However, although Saharan dust is recognized as one of the most relevant sources of atmospheric aerosol and bioaerosol on a global scale, the Central Mediterranean is a geographic area profoundly affected by the circulation of air masses of different origin and distinguished by nature, type, quality, and extent of contributions (Cusack et al., 2012; Kallos et al., 2014, 2007; Petroselli et al., 2018a, 2018b). Due to the very different characteristics of the source areas, these air masses are expected to carry different bacterial populations and specific chemical markers and pollutants. Moreover, only a few studies have used molecular-based approaches to investigate the relationships of different air masses with the bacterial communities in the Mediterranean area. In such studies, bioaerosol characterization was conducted by a low-throughput approach (cloning and sequencing of 16S rRNA gene), while High-Throughput Sequencing (HTS) approaches were used in an even smaller number of cases. Most of the previous studies on aerosol-associated microbial communities in the Mediterranean area have been focused on intense Saharan intrusions sampled in the proximity of the dust sources (Gat et al., 2017; Katra et al., 2015; Mazar et al., 2016; Polymenakou et al., 2008), or after a long-range transport over the Mediterranean basin (Federici et al., 2018; Rosselli et al., 2015; Sanchez De La Campa et al., 2013). Much less is known about the specific characteristic of the bacterial communities transported by air masses from continental Europe.

In this frame, the present study aims at defining the patterns of the bacterial communities of atmospheric aerosol from distinct geographic regions reaching the Mediterranean. The samples were collected during different long-range transport events towards a background monitoring site located on the top of a mountain range (1100 m asl), in Central Italy. The low background aerosol concentrations make the site well suited to characterize long-range air mass transports. Samples were selected based on their provenance, unambiguously individuated by a modelling of the air masses. An HTS approach, combined with a thorough chemical analysis, allowed us to build a significant dataset including bacterial diversity and chemical composition. The hypotheses to be tested in this work are two-fold: (i) bacterial community structure associated with long-range transported aerosol in the Central Mediterranean area is significantly different based on the air mass provenance; (ii) there is a correlation between the main aerosol chemical characteristics and the airborne bacterial communities. To test these hypotheses, we investigated the chemical and microbial datasets by cluster analysis, similarity tests, and non-metric multidimensional scaling analysis.
allowed also to check the vertical distribution of dust over the MM site (see Fig. SM2).

Nineteen of these HVS samples (9 Saharian, 4 Regional, 4 Northwestern, 2 Northeastern), whose provenances were clearly identified, are considered in the present work.

2.2. Chemical analyses

The sampled filters underwent a thorough chemical characterization that included the investigation of both the inorganic and organic fractions of particulate matter.

Major ion composition was determined by ion chromatography (DIONEX 2100) after 30 min ultra-sonication in ultrapure water (18 MΩ). The quantified analytes were: Li⁺, Na⁺, NH₄⁺, K⁺, Mg²⁺, Ca²⁺, F⁻, HCOO⁻, MSA, Cl⁻, NO₂⁻, SO₄²⁻, oxalate, Br⁻, NO₃⁻, PO₄³⁻.

Concerning the elemental composition, the samples underwent a microwave-assisted acid-digestion process (CEM MARS-5) being treated with nitric acid (HNO₃ 65%, Millipore Suprapur) and hydrogen peroxide (H₂O₂ 30–32%, Carlo Erba Reagents) in 4:1 proportion. The samples were then analyzed by ICP-AES (Horiba ULTIMA 2000) equipped with an ultrasonic nebulizer (CETAC 5000). The determined elements were: Zn, Cr, Ni, Cu, V, Mn, Co, Ca, Ti, Fe.

Thermal-Optical-Transmittance (TOT, Sunset Laboratory Inc.TM) was used to determine elemental and organic carbon concentrations (EC/OC), following the NIOSH protocol. Finally, gas chromatographic-mass spectrometric analysis (GC Chrompack 3800 coupled with ITD-MS® Saturn 2000-Varian) was performed for the characterization of PAH and n-alkane fractions (Cartechini et al., 2015; Federici et al., 2018).

3. Results and discussion

3.1. General characteristics of air masses and PM samples

Nine Saharan dust advections and ten long-range transports from other geographical origin have been considered in this work. The air mass origins were identified on the basis of back-trajectory (BT) analysis. The BTs for the identified provenance groups are summarized in Fig. 1, for the 500 m endpoint. The other endpoints (50 and 1000 m above the ground) provided similar results and have been included in supplementary material (Fig. SM3). Saharan dust advection samples have been marked with the code SH. As for the other provenances, three main macro-areas have been identified, namely regional (RG), North-western (NW) and North-eastern (NE). RG air masses have been defined as those remaining over the terrestrial and marine sectors of central Italy for at least 48 h before sampling. Table 1 summarizes all the PM samples collected during 2014 and 2015.

As a general trend, the Saharan dust samples are characterized by higher aerosol mass concentrations with respect to the non-Saharan advections (see Table 2), i.e. an average +68.4% for PM₁₀ and +85.3% for PM₂·₅, defined as PM₁₀·PM₂·₅, and lower PM₂·₅/PM₁₀ ratio, reading 0.52 ± 0.18 for SH and 0.76 ± 0.12 for non-SH samples. The increase in the concentration of the coarse fraction is typical of natural crustal aerosol sources such as desert dust (Formenti et al., 2011). Moreover, Ca and Fe, typical crustal markers resulted higher in Saharan dust on average (Table 2). The insoluble fraction of Ca, defined as Cₐₙₐ₁-Ca²⁺, was close to 60% for Saharan dust, slightly lower for RG air masses and much lower for the NW. This is consistent with both the source area mineralogy and the different atmospheric processes during the long-range
transport (Avila et al., 2007). Biomass burning markers such as ammonium and organic carbon (OC) were higher in non-Saharan samples, and particularly enriched in NE samples, possibly due to the frequent wildfires recorded in Eastern Europe regions. The latter have been found to exert a distinct impact on the Monte Martano site, as previously reported in Petroselli et al. (2018a, 2018b). The average OC and EC values are in agreement with those reported in (Sandrini et al., 2014) at MM for the year 2009. Total PAHs were on average the highest for RG followed by SH and NE and NW air masses. Benzo(a)Pyrene, the reference PAH for health effects, has the same order in abundance.

3.2. Characterization of bacterial communities

Sequencing of 16S rRNA gene fragments led to the recovery of 1286659 high-quality sequences, which clustered, across all samples, into a total of 10,513 operational taxonomic units (OTUs) calculated at 97% of sequence similarity. The average number of OTUs per sample was 2239. Although a considerable fraction of the total biodiversity (18.6% on average) could not be classified at genus level, a total of 879 different genera were identified across all samples. Among them, a total number of 116 genera were found whose relative abundance transport (Avila et al., 2007). Biomass burning markers such as ammonium and organic carbon (OC) were higher in non-Saharan samples, and particularly enriched in NE samples, possibly due to the frequent wildfires recorded in Eastern Europe regions. The latter have been found to exert a distinct impact on the Monte Martano site, as previously reported in Petroselli et al. (2018a, 2018b). The average OC and EC values are in agreement with those reported in (Sandrini et al., 2014) at MM for the year 2009. Total PAHs were on average the highest for RG followed by SH and NE and NW air masses. Benzo(a)Pyrene, the reference PAH for health effects, has the same order in abundance.

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was higher than 0.5% in at least one sample. These genera were considered abundant (abundant genera hereafter) and further analyzed. 32 bacterial genera manifested a relative abundance higher than 0.5% on average in all samples; they are shown in Fig. 2. Overall, the most abundant genera were *Sphingomonas* (8.47%), followed by *Acidovorax* (3.89%), *Acinetobacter* (3.33%), *Stenotrophomonas* (3%), *Hymenobacter* (2.68%), *Methylobacterium* (2.57%), *Propionibacterium* (2.1%) and *Massilia* (1.85%). Most of these genera have already been described as members of airborne bacterial assemblages, both from urban and suburban environments and from dust storm intrusions (Chuvochina et al., 2011); however, it was also consistently retrieved in urban and suburban Chinese areas, together with *Sphingomonas* (Gao et al., 2017; Wei et al., 2015). *Methylobacterium* is known to be resistant to desiccation and to γ radiation together with *Arthrobacter*, also abundant in our samples (Favet et al., 2013). *Microvirga* was already found in desert-coming air-masses and some species of this genus can reduce nitrogen gas to ammonia (Favet et al., 2013; González-Toril et al., 2020). It should also be noted that some of the 32 most abundant genera are human- and animal-associated bacteria and include known pathogens, such as *Haemophilus*, *Staphylococcus*, *Streptococcus* and *Propionibacterium* (Brock et al., 2012). Moreover, we retrieved some bacterial genera that, despite being ubiquitous in the environment, also contain many opportunistic pathogens and a few pathogens, such as the *Pseudomonadales* *Acinetobacter* and *Pseudomonas*, or *Clostridium sensu stricto*. (Table 2)

**Table 2**

Aerosol mass concentration and chemical variables average values. Comparison between the investigated Saharan dust advections and non-Saharan (NE, NW, RG and total non-SH average) samples. Errors are given as standard deviations. Mean values for the 2014/2015 are also reported. All data in μg m⁻³ except when indicated.

| Sample | PM₁₀ (μg m⁻³) | PM₂.₅ (μg m⁻³) | PM_coarse (μg m⁻³) | PM₁₀/PM₂.₅ | Ca²⁺ (μg m⁻³) | Fe (μg m⁻³) | Ti (μg m⁻³) | NH₄⁺/NO₃⁻ | NO₃⁻/SO₄²⁻ | K⁺ (μg m⁻³) | SO₄²⁻ (μg m⁻³) | OC (μg m⁻³) | EC (μg m⁻³) | ΣPAH (pg m⁻³) | BaP (pg m⁻³) |
|--------|--------------|----------------|-------------------|-------------|-------------|------------|-----------|--------------|---------------|-------------|----------------|-------------|-----------|----------------|-------------|
| SH     | 35.1 ± 29.4  | 15.4 ± 9.6     | 19.7 ± 20.0       | 0.52 ± 0.2  | 3.0 ± 3.0   | 1.2 ± 2.1  | 0.06 ± 0.7 | 0.10 ± 0.9   | 1.8 ± 0.6     | 0.15 ± 0.2   | 1.4 ± 1.4     | 3.3 ± 1.5   | 0.3 ± 0.2  | 280 ± 150     | 11 ± 8       |
| NE     | 14.5 ± 4.2   | 10.1 ± 0.9     | 4.5 ± 3.3         | 0.71 ± 0.2  | 0.14 ± 0.2  | 0.3 ± 0.2  | 0.02 ± 0.2 | 0.46 ± 0.2   | 0.64 ± 0.3    | 0.19 ± 0.05  | 4.2 ± 0.5     | 3.9 ± 1.7   | 0.3 ± 0.1  | 200 ± 130     | 7.9 ± 5      |
| NW     | 7.3 ± 1.9    | 5.0 ± 0.5      | 2.3 ± 1.6         | 0.70 ± 0.1  | 0.38 ± 0.3  | 0.3 ± 0.2  | 0.02 ± 0.0 | 0.39 ± 0.2   | 2.9 ± 0.2     | 0.05 ± 0.07  | 1.2 ± 1.5     | 1.9 ± 0.5   | 0.3 ± 0.1  | 53 ± 14        | 1.3 ± 1.3    |
| RG     | 12.1 ± 5.9   | 9.4 ± 4.0      | 2.7 ± 2.2         | 0.81 ± 0.1  | 0.66 ± 1.0  | 0.3 ± 0.2  | 0.1 ± 0.0  | 0.46 ± 0.8   | 0.68 ± 0.8    | 0.07 ± 0.1   | 2.3 ± 0.9     | 3.2 ± 1.7   | 0.2 ± 0.1  | 440 ± 700     | 16 ± 28      |
| 2014/2015 | 10.6         | 7.7            | 3.9              | 0.73        | 1.0         | 0.7        | 0.05       | 0.29 ± 0.2   | 0.9 ± 0.5     | 0.26 ± 0.1   | 1.7 ± 1.4     | 2.8 ± 0.9   | 0.20 ± 0.1 | 230 ± 220     | 16 ± 28      |

**Fig. 2.** Cluster dendrogram and associated barplot of the relative abundance of the most abundant genera in each air-mass sample. Cluster analysis was performed on the 116 genera whose abundance was higher than 0.5% in at least one sample (abundant genera). Barplots represent only the 32 bacterial genera that showed a relative abundance higher than 0.5%. Chloroplasts were also included in the analysis.
sensu stricto and Clostridium XI (Brown, 2014). However, analyses based on 16S rRNA sequences do not allow to distinguish pathogenic from non-pathogenic species or strains.

3.3. Dependence of bacterial diversity on air mass origin

The results of the cluster analysis on the database containing only the abundant genera, summarized by the dendrogram in the right panel of Fig. 2, were used for a data-driven visualization of the samples that are reported in the barplot following the dendrogram order. The average 1-D distances reported in the dendrogram revealed a high β-diversity among the bacterial communities of the SH samples, which however generally clustered together. At genus level, the structure of bacterial communities clearly showed differences due to the sample provenance rather than to other factors such as seasonality. Interestingly, among the PM samples, the non-Saharan samples collected during regional movements of air masses (RG) and, to a lesser extent, during long-range intrusions (NE and NW), showed a high richness of genera with low abundance, indicating a highly diverse and even community. Conversely, PM during Saharan intrusions showed a lower richness of genera, indicating that these microbial communities were dominated by fewer typical phylotypes. This is in contrast with previous studies, which generally reported higher diversity during dust intrusion events compared to non-dust events (González-Toril et al., 2020; Griffin, 2007; Mazar et al., 2016; Polymenakou et al., 2008; Sanchez De La Campa et al., 2013). It may be hypothesized that, in the case of central Italy, both regional air masses and long-range intrusions from NE and NW mainly cross more heterogenous areas than Saharan intrusions, thus collecting a wider variety of microorganisms. Particularly, when BTs indicated that regional air masses were prevalent, it is also possible that local sources played a major role in shaping bacterial communities. In fact, a wide variety of potential local sources, such as soil surface, leaf surface, water bodies and even animal faeces, have been reported to influence airborne bacterial and fungal community structure (Bowers et al., 2011; Mu et al., 2020; Qi et al., 2020; Sadyš et al., 2014).

To gain further insights about similarities and differences among all the aerosol samples and hypothesize possible effects of the air masses with different origins, a non-metric multidimensional scaling (NMDS) analysis was performed using the computation of Bray-Curtis distances between bacterial communities. This statistical method has been applied to the database containing only the abundant genera, and results are shown in Fig. 3. The results of NMDS analysis showed a good clustering (stress value <0.15) of the samples according to their provenance group. In particular, the NMDS1 dimension (x-axis, Fig. 3) seems to separate well the different clusters, and particularly the Saharan dust samples from the others, while NMDS2 describes the variability within each group.

NMDS is a helpful exploratory analysis but does not allow explaining the similarities or dissimilarities among samples, and additional information from other analysis is needed. For example, samples associated with RG and NW air masses show a partial overlap in the NMDS analysis, which is understandable based on the phenomenology of back trajectories (see Fig. 1). In fact, RG air masses at MM tend to the terrestrial and marine western sectors of peninsular Italy while samples of NE origins, although limited in number in present study, form a distinct cluster in NMDS and show a different pattern in the back-trajectory plot. On the other hand the similarity between NW_20141022, SH_20150506, and RG_20150607 samples as for the NMDS1 can be explained considering the source characteristics. In order to support the NMDS results we run a principal component analysis (PCA, results in Fig. SM4, Supplementary Material) based on chemical variables. The result indicates that similarity of the three samples is also driven by common chemical characteristics. In particular, the Na concentration, combined with the Benzo(a)Pyrene to Benzo(e)Pyrene ratio, suggests a similar residence time in the atmosphere and collective

![Fig. 3. Representation of NMDS analysis of air-mass samples, based on the 116 abundant genera (see text). Chloroplasts were also included in the analysis.](image-url)
marine influence (Simo et al., 1991), configuring the SH_20150506 sample as an atypical Saharan dust intrusion.

Furthermore, we performed a SIMPER analysis to highlight the genera that typify each community. The results of pairwise comparison between the dust samples individuated by the above analysis is shown in Fig. 4. In the plot genera are reported along descending triangles based on their average contribution to the Bray-Curtis dissimilarity. SH samples are represented at the center of the plot, for convenience, and share common genera with all the other groups. The genera that mostly contributed to characterize Saharan intrusions were Sphingomonas, Acidovorax and Stenotrophomonas. Although Sphingomonas represents a quite ubiquitous genus, it is often found in desert-originated air samples (Griffine et al., 2006). Family Comamonadaceae, to which the genus Acidovorax belongs, has been reported both in Saharan dust layers deposited in Alpine snow (Meola et al., 2015) and in Asian long-range transport plumes (Smith et al., 2013). By contrast, Stenotrophomonas was more frequently described as a major member of bioaerosols from anthropic activities, such as wastewater treatment (Han et al., 2019) and livestock and poultry production (Chien et al., 2011). Moreover, SH samples were characterized by higher abundances of genera Bacillus, Adhaeribacter and Hymenobacter than NW and RG samples. Bacillus has been often described as one of the most abundant genera in Saharan dust samples (Griffin, 2007; Sanchez De La Campa et al., 2013). Adhaeribacter and Hymenobacter can be particularly abundant in arid soils and desert sands (Favet et al., 2013).

In contrast, chloroplasts were significantly more abundant in non-Saharan than Saharan samples. This is not surprising, since areas crossed by air masses from RG, NW and NE provenances are more vegetated than northern Africa. Interestingly, most of the other genera that were more abundant in the European or in Regional samples are human and/or animal associated bacteria, such as Lactobacillus, or they also include pathogens, such as Streptococcus, Propionibacterium and Haemophilus (Brock et al., 2012; Brown, 2014). An interesting case is represented by Acinetobacter: since it is ubiquitous in soil and water and easily transported by air, it has recently proposed as an indicator of airborne transport from the Sahara (Barberán et al., 2015). However, despite its presence in our Saharan samples, it was significantly more abundant in the NE group. Overall, we could therefore hypothesize that bacterial communities transported by non-Saharan air masses were significantly affected by the crossing of densely populated areas. Therefore, although it has been demonstrated that a number of diseases are linked to desert aerosols (Middleton, 2017), the concern about Saharan intrusions might be reduced from a public health point of view in this context, since air masses from European and regional origin were more enriched in human-associated bacteria than Saharan air masses. A more detailed boxplot representation of the distribution of...
the 116 more abundant genera for the four air mass origins is reported in Supplementary Material (Fig. SM5).

3.4. Correlations between microbiology and chemistry

Chemical and microbiological data were combined to check possible correlations between the variables and the sample provenances. In particular, some typical markers of Saharan dust, biomass burning, and industrial activities, the two latter being particularly enriched in non-Saharan samples, were identified among the chemical analytes. Moreover, the analysis of the β diversity showed that the microbial communities of long-range transported Saharan dust were significantly different from those sampled when other air masses were present, strongly supporting the hypothesis that desert dust can impact the bacterial composition of the aerosol at our latitudes (Gat et al., 2017; Mazar et al., 2016; Rosselli et al., 2015). On the contrary, non-Saharan samples...
showed similar communities among each other, which in fact clustered together (Figs. 2 and 3). Nevertheless, as observed for the chemical characteristics, even if similarities existed within the PM samples sharing the same origin, the differences were not negligible and suggested that each event was independent of the others. This has been already observed in previous works, at least for dust events. In fact, significant differences in bacterial community structure were reported during different dust events that impacted the same area, even when two events were very close in time (Federici et al., 2018; Yamaguchi et al., 2014).

In order to combine information about microbiology and chemistry, the NMD51 dimension from the statistical analysis on bacterial communities was correlated with the concentration of chemical variables, normalized against the PM values (w/w). Some of the statistically significant correlations ($p = ***$) are shown in Fig. 5.

Specifically, a significant correlation was found between NMD51 and PM$_{2.5}$ (i.e. PM$_{2.5}$/PM$_{10}$ ratio). PM ratio was lower for Saharan dust with the exception of the outlier SH$_{20141107}$ which corresponded to the weakest Saharan dust event, with a PM$_{10}$ concentration of 8.4 $\mu$g/m$^3$. The correlation was significant also between NMD51 and PM$_{coarse}$, which was higher for SH because Saharan intrusions are constituted by coarser particles. Organic carbon (OC) content correlated significantly with NMD51. OC in Saharan dust was lower than in non-Saharan samples because the latter can have a higher anthropogenic contribution. The highest OC/PM$_{10}$ values were found for SH$_{20140624}$ (which had also high sulphate concentration) and SH$_{20140522}$ of NW provenance. As stated above, also many bacterial genera that were significantly more abundant in non-SH than in SH samples (e.g. Lactobacillus, Streptococcus, Propionibacterium and Hue- mophillus) were generally related to anthropic and built environments. This confirms the relevance of the impact that densely populated areas may exert on bacterial populations transported by air masses.

Anthracene was the only PAH correlating significantly with NMD51, being higher for SH samples. The sum of low molecular weight PAHs (LW) was also higher for SH samples. Calcium concentrations showed no correlation with NMD51, which was interpreted as due to the high local contributions of this element. Iron, on the other side, was richer in SH samples and correlated negatively with NMD51. Ammonium and sulphate concentrations were generally higher for non-Saharan air masses. Innocente et al. (2017) also reported that high ammonium and sulphate concentrations were associated with long-range transport from north-west in Milan (North Italy), and those air masses presented a high percentage of Propionibacterium. This is in agreement with our SIMPER analysis, which indicated the genus Propionibacterium as significantly more abundant in NW than in SH samples (Fig. 4). However, Innocente and colleagues also reported that this correlation was weak, and ironic composition of air masses was much more clearly related to air mass provenance than to bacterial community structure.

Indeed, also in our case, since NMD51 was strongly correlated to air mass origin, it was not possible to fully understand whether variations in chemical variables were more correlated to variations in bacterial community structure or to dust provenance.

4. Conclusions

In this work, we have characterized the bacterial communities of 19 air masses of different origin, sampled as PM$_{10}$ at the remote site of Monte Martano, in Central Italy. This EMEP station is representative of the Central Mediterranean area. The main results of the present work can be summarized as follows:

- Four distinctive air masses were identified: previous similar work on this topic was substantially limited to Saharan (SH) dust air masses while in the present study we extended the characterization to regional (RG), North-Western (NW), and North-Eastern (NE) air masses.
- At genus level, the distribution of the bacterial populations in air masses clearly showed differences due to the sample provenance. In fact, PM$_{10}$ during Saharan intrusions showed a relatively low number of genera, while non-Saharan samples, particularly those collected during regional movements of air masses (RG), showed a high number of different genera with low abundance, indicating a highly diverse and even community.
- The abundance of bacterial genera including potential human and animal pathogens is higher in non-Saharan than in Saharan samples and stressed the relevance of anthropic impact on bacterial populations transported by air masses that crossed densely populated areas.
- A significant correlation was found between the NMD51 dimension from the statistical analysis on bacterial communities and specific chemical variables determined on the samples. Particularly, organic carbon and ammonium concentrations, which are markers of anthropogenic contribution, were found to increase along the sequence SH, NW, NE, and RG, and be also correlated to an increasing abundance of human and animal associated bacteria. However, the strong correlation between bacterial community structure and air mass origin hampered the possibility to disentangle the effects of variations in bacterial populations and of dust provenance on variations in chemical variables.

CRediT authorship contribution statement

CP, RS, BS, BM: chemical analysis, GLP; statistical analysis, SC: Atmospheric modelling: AF, IG, EF, EM, EC; CC: microbiological analysis.; DC: Conceptualization, Methodology, Data curation, Original draft preparation, CP, IG and DC. Writing and editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.scitotenv.2020.143010.

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