

Editorial

Bioaerosols: Composition, Meteorological Impact, and Transport

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The characterization and the main properties of biogenic airborne particles (or bioaerosols) comprising both living and dead microorganisms (such as bacteria, fungi, viruses, pollen, and microbial fragments) are currently of increasing interest in the scientific community. They are a ubiquitous component of the atmosphere that present a significant role in their transport and dispersal across the globe. Due to their small size, some of the bioaerosols have a relatively long atmospheric residence time and, therefore, they can be transported over long distances. Numerous studies have emphasized that biological airborne particles may be suspended as individual cells, but they can also be attached to other particles or found as agglomerates of many cells. Therefore, the abundance and speciation of bioaerosols are of increasing interest due to their possible effects on human health, agriculture, biogeochemical cycles, and atmospheric processes, even for their role as cloud condensation nuclei. The great importance of investigating the impact of meteorological parameters, atmospheric pollutants, seasonal variations, and PM chemical species on bioaerosol communities is also justified by the necessity to expand the risk assessment models related to their aerial dispersion. In addition, these kinds of analyses may also encourage biosurveillance technologies that could be useful in national policies for preventing the dispersion of pathogenic biological agents.

In the scientific community devoted to bioaerosol characterization, the study of pathogenic species identified in aerosol samples is a topic of increasing interest. Romano et al. [1] reported a preliminary database of human and plant pathogenic and non-pathogenic species identified in PM₁₀ samples collected at a Central Mediterranean coastal site, as well as their seasonal dependence and associations with meteorological variables and PM chemical composition. The PM samples were investigated using the 16S rRNA gene metabarcoding approach, while Spearman correlation and redundancy discriminant analysis were used to examine the main relations. They detected 76 and 27 potential human and plant pathogens, respectively. The bacterial structure of both pathogenic and non-pathogenic species presented a clear seasonal dependence, without showing a significant correlation with meteorological parameters. Conversely, several potential plant pathogens were strongly correlated with temperature and wind speed and direction, especially in spring.

Particular attention should also be devoted to mountainous environments, since they could host many plants, bacteria, and fungi containing ice nuclei (IN) characterized by the ability to regulate freezing events and offer survival benefits, in addition to being able to trigger ice nucleation in cloud droplets affecting the radiation budget and the hydrological cycle. In fact, the initial formation of precipitation in clouds is mainly due to inorganic and organic/biological ice nuclei. As reported by Georgakopoulos [2], different species of bacteria and fungi could act as efficient biological ice nuclei at low temperatures, since they were found and characterized in different precipitation samples such as snow, rain, and hail. Georgakopoulos [2] analyzed the presence of biological ice nuclei in snow samples from Greece by characterizing ice nucleation active bacteria. All samples were characterized by the presence of particles or other active materials such as ice nuclei at low temperatures,



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belonging to the genus *Pseudomonas* that is generally common in plants and soils. To estimate the atmospheric importance of alpine IN, Seifried et al. [3] collected aerosol samples in August 2019 from a mountainous site in the Austrian Alps, close to a forest of silver birches that generally release IN from their surface during and after rainfall. Samples were analyzed to determine their ice nucleation activity, while the corresponding bioaerosol communities' morphology and auto-fluorescence were studied using microscopic procedures. High concentrations of IN were identified below the canopy, showing a freezing compartment comparable to that of birch samples. The work by Seifried et al. [3] represented the first examination of aerosol emission sources in alpine environments focusing on birches. Another important topic related to birch pollen characterization is its interactions with air pollution, radiative balance, and atmospheric dynamics. In fact, some events characterized by high levels of both air pollutants and aeroallergens expose sensitive individuals to a dangerous mixture of airborne particles. To this end, Skjoth et al. [4] analyzed the effects of the interactions between meteorology and particles on the concentrations of birch pollens by means of the WRF-Chem atmospheric model. In more detail, they presented a case study of a birch pollen episode coinciding with a desert dust outbreak using the model results, pollen samplings, and meteorological measurements. They observed that the lowest parts of the atmospheric boundary layer presented a vertical profile able to favor the long-range transport, while the pollen samples were characterized by different types that flower at different times. Therefore, Skjoth et al. [4] were able to prove that the atmospheric conditions favored meteorological feedback processes that could alter the long-range transport of both air pollutants and airborne pollen particles. Considering the interactions between aeroallergens and meteorological variables, Hajkova et al. [5] studied the effects of winter oilseed rape (*Brassica napus*) in the Czech Republic since it represents one of the main pollen allergens. They analyzed several meteorological variables in the period of 1991–2012 using the PhenoClim phenological model to identify the best predictor among them of the beginning of flowering of *Brassica napus* at different monitoring sites in different climatic zones. Hajkova et al. [5] clearly proved that the beginning of flowering of the *Brassica napus* advanced progressively in timing in the selected period, while the most accurate predictor for the beginning of flowering was the mean air temperature.

Another aspect addressed in two works belonging to this Special Issue is the relation between bioaerosol particles and the global pandemic caused by severe acute respiratory syndrome coronavirus SARS-CoV-2. Analyzing new techniques and procedures for the disinfection of indoor air, many studies proved the efficiency of essential oils in the control of bioaerosol concentrations. To this end, Mirskaya and Agranovski [6] investigated the antimicrobial activity of the most common essential oils in Australia. They used a new device useful for bacterial, viral, and fungal inactivation on various surfaces and in aerosol form and proved that it was able to provide a sufficient aerosol concentration to efficiently inactivate microorganisms both on the surface and in airborne form. The results reported by Mirskaya and Agranovski [6] appeared to be encouraging for the advancement of bioaerosol-inactivating techniques and for air quality control purposes. Another important aspect strictly connected to the interaction between bioaerosols and the global pandemic is the appropriate use of masks, since this is necessary for effectively preventing the transmission of airborne bioaerosols. In particular, it is necessary to evaluate how long the living components of bioaerosols can be viable on masks. Lee et al. [7] evaluated the viability of airborne *Bacillus subtilis* accumulated on face masks. They proved that the bioaerosols survived on the masks immediately after the masks were used, and the bacteria amount significantly increased after one day of storage. Then, the viable cell amount in the filtered bioaerosols progressively decreased, and the viability of *B. subtilis* in bioaerosols on the masks presented a high variability strictly related to the mask material. Finally, Lee et al. [7] also proved that bioaerosols containing living components were still present in mask surfaces even after six days of storage.

Bioaerosols also represent an important component in our cities largely affecting urban, indoor, and industrial area air quality. Regarding urban air quality, Korneykova

et al. [8] reported a mycological analysis of different outdoor urban environments in Russia considering the chemical composition of dust deposited on the leaves of dominant tree species to be an indicator of air quality, and evaluating the impact of different factors such as climate zone, type of substrate, and anthropogenic load. Dangerous fungi species were absent in the air of recreational zones, while, in contrast, they were present on leaves and in road dust. Korneykova et al. [8] also proved that the aerosol chemical composition significantly influenced the diversity in fungi species and that the substrate is fundamental in determining the sensitivity of outdoor mycobiome to air pollution levels. The sources, the diversity, and the variability in urban airborne bacterial communities were also investigated by Metaxatos et al. [9] in Athens, Pollegioni et al. [10] in Rome, and Song et al. [11] in Manchester. In detail, Metaxatos et al. [9] characterized the microbiome in aerosol samples by means of the analysis of 16S rRNA genes. They were able to prove the diversity in airborne bacteria and their variability over time in Athens during three seasons in 2019. The identified OTUs belonged to Phyla *Actinobacteria*, *Firmicutes*, *Proteobacteria*, *Bacteroidetes*, *Cyanobacteria*, and *Fusobacteria*. They were also able to detect several opportunistic or potential pathogens in their urban monitoring sites and to identify soils, plants, animals, and humans as being possible sources. Then, Pollegioni et al. [10] investigated the airborne microbiome associated with PM10 samples and their main local sources in Rome. They selected three different monitoring sites (located in a green area, in a residential area, and in a polluted area close to the traffic roads) characterized by different air pollution levels. They detected PM10 samples from air, paved road surfaces, and leaf surfaces and, then, they analyzed them by means of the bacterial 16S rRNA gene and the fungal internal transcribed spacer (ITS) region, in addition to chemical speciation. They proved that the resuspension of road dust from vehicular traffic could contribute to an increase in microbial exchanges and that the amount of extremotolerant microbes was strictly related to an increase in both air pollution levels and human pathogenicity in fungal communities. Song et al. [11] aimed to detect bioaerosol communities in Manchester using high-throughput sequencing approaches (based on the 16S rRNA gene of prokaryotes, ITS region of fungal DNA, and 18S rRNA gene of eukaryotes) and to find their potential sources. Essentially, they found that a potential application of bioaerosol profiling could be useful for identifying the source of atmospheric aerosols. In fact, the marine-environment-associated bacteria and archaea were relatively more abundant in relation to air masses of marine origin. In contrast, an OTU belonging to *Methylobacterium*, which includes many species resistant to heavy metals, was relatively more abundant in relation to samples with higher metal concentrations. Then, regarding the indoor air quality, Mostafa et al. [12] studied the PM and bioaerosol concentrations associated with different indoor aerosol sources such as candles, cooking, electronic cigarettes, tobacco cigarettes, mosquito coils, and incense, trying to quantify each effect in an examination room using a diffusion aerosol spectrometer. Mostafa et al. [12] proved the significant increase in PM concentrations during electronic cigarette usage and tobacco cigarette burning, and tried to test some strategies to guarantee an improvement in indoor air quality. Regarding the interaction between bioaerosol concentration and industrial area air quality, Affek et al. [13] presented the results obtained by applying biofilters to treat waste gases at different industrial sites in Poland. In detail, they used two different types of materials as beds in the biofilters that supported microbial growth, observing high numbers of culturable bacteria and fungi. No correlation between the number of microorganisms and the respiratory activity in the biofilter beds was determined, while biofilters were seen to reduce or increase bioaerosol emissions from industrial plants, depending on the microbial content in the waste gases. Affek et al. [13] also proved that both the type of biofilter bed and the number of microorganisms in the bed affected the final bioaerosol emission only for biofilters that treated waste gases with low microbial concentrations.

Finally, this Special Issue also included two promising studies related to the development of a novel bioaerosol chamber. The behavior of the microorganisms in this kind of chamber can be simulated with computer models to assess the possible risks associated

with the emission from animal houses via exhaust air. Therefore, Clauß et al. [14] developed a new bioaerosol chamber to quantify the survival rates of *Staphylococci* under outdoor air conditions as a function of different environmental variables. In particular, they were able to prove that the survival rates of *Staphylococci* presented a decrease with increasing temperature, global radiation, and ozone concentration and with decreasing relative humidity. Then, Santarpia et al. [15] used a different technique based on a captive aerosol growth and evolution (CAGE) chamber to examine the changes in the fluorescence spectra of bioaerosols when subjected to ambient outdoor conditions. Using the measurements taken via a TSI UV-APS and a single-particle fluorescence spectrometer, they detected changes in both the fluorescence spectral profile and intensity from *Bacillus thuringiensis* spores and MS2 bacteriophage particles. Therefore, they hypothesized that bioaerosol particles can be considerably modified using atmospheric aging processes and that these variations could alter measurements via ultra-violet light induced fluorescence.

In conclusion, this Special Issue aimed to review the existing state of knowledge on bioaerosol relationships with meteorological parameters, particulate matter chemical components, and sources identifying the potential factors responsible for the bioaerosol community structure and its seasonal variations. Both chamber and real-world studies characterizing bioaerosols were included within this Special Issue. In more detail, different topics on bioaerosol instrumentation for its detection and monitoring focusing on specific innovative methods were addressed, as well as ones related to pathogenic species.

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