1. Introduction

The Sahel of West Africa, which is generally identified as a zone that runs from Senegal eastward to Ethiopia with a latitude range of 10°–18°N, is well known for the multidecadal precipitation anomalies that have been observed throughout the late twentieth century (Nicholson, 1993). The Sahel’s precipitation regimes are divided into a dry season that spans from October through May and a wet season between June and September. Saharan dust outbreaks are generated throughout the year (wet and dry seasons in West Africa), with the Sahara acting as the largest source of dust in the world, producing some 400–700 × 10⁶ t of dust per year (Goudie & Middleton, 2001). This dust is transported downstream to Europe, the Caribbean, and the United States. However, large quantities of Saharan dust are transported into West Africa, especially during the dry season.

During the dry season, PM₁₀ surface dust concentrations can reach hazardous levels with Marticornea et al. (2010) and Diokhane et al. (2016), showing frequent daily surface PM₁₀ concentrations exceeding 500 μg m⁻³, which is 10 times the World Health Organization (2006) recommended daily levels of 50 μg m⁻³. During the summer season, Toure et al. (2019) show that PM₁₀ monthly concentrations at Dakar, Senegal fall below the U.S. Environmental Protection Agency criteria of unhealthy levels (250 μg m⁻³), and monthly values are approximately 50 μg m⁻³ during August and September. The reduction in summer PM₁₀ and PM₂.₅...
concentrations are associated with the onset of the monsoon layer in June as Saharan dust is carried above the monsoon in the Saharan Air Layer and transported downstream to the Caribbean (Carlson & Prospero, 1972; Leone et al., 2009). During the peak of the monsoon period in August and September, PM$_{10}$ and PM$_{2.5}$ are further reduced through precipitation scavenging.

The impact of high dust concentrations on nontransmissible respiratory disease (e.g., asthma, bronchitis) on the population of West Africa and Senegal is poorly quantified, but studies conducted outside of Africa (Europe, Asia, Caribbean, and United States) show that high dust concentrations are linked directly or indirectly to respiratory and cardiovascular disease (de Longueville et al., 2013; Zhang et al. 2016). Numerous studies have identified high PM$_{2.5}$ concentrations as a risk factor (Dockery et al., 1993; Neuberger et al., 2007), with PM$_{2.5}$ contributing to infant mortality in West Africa (Heft-Neal et al., 2018). Bauer et al. (2019) suggest that there are 780,000 premature deaths annually with dust aerosols being responsible for a significant fraction of the premature deaths. PM$_{2.5}$ can penetrate deep into the lungs exacerbating existing respiratory diseases such as asthma, bronchitis, acute respiratory infection, and chronic obstructive pulmonary disease (Esmaeil et al., 2014; Zhang et al., 2016). In Senegal, Toure et al. (2019) have found a high prevalence of asthma across all ages, especially in the capital city of Dakar, during 2015 and 2016. In addition, Toure et al. (2019) have found a high prevalence of bronchitis and a very high prevalence of acute respiratory infection for children under 5 years of age. A number of studies have examined the linkages between Saharan dust and Meningitis during the dry season (Agier et al., 2013; Deroubaix et al., 2013; Martigny & Chiapello, 2013). In Senegal, Diokhane et al. (2016) showed that a larger number of meningitis cases occurred when higher dust concentrations that were measured and simulated occurred during 2012 as compared to 2013.

Bioaerosols are part of the background environment and may have local sources, but can also exist on the surfaces of dust particles. Brągoszewska and Pastuszka (2018) identified significant variations in urban areas between winter and spring. Viruses, bacteria, and fungi can serve as bioaerosols with a large range in size from 0.02 μm to several hundred microns. Similar to other aerosols, bioaerosols can have negative health impacts such as allergies or cause respiratory infections (Brągoszewska & Pastuszka, 2018; Mouli et al., 2005). While bioaerosols associated with Saharan dust may have a local source in the desert, they are transported into downstream (sometimes thousands of kilometers) regions and may differ from locally produced bioaerosols.

Dust-borne microorganisms, including bacteria and fungi, have been identified (Griffin, 2007; Kellogg et al., 2004; Prospero et al., 2005; Shinn et al., 2003). Some of the microorganisms are identified as pathogens (Bacillus, Pseudomonas, and Burkholderia) that could potentially affect respiratory health (Kellogg et al., 2004; Shinn et al., 2003). Allen et al. (2015) analyzed arid to semiarid soils in Mali, Morocco, Sudan, Niger, and Nigeria using molecular analysis and found Bacillus, a dominant bacteria. The microorganisms can pose a health risk, especially in highly populated centers. Thus, analytical protocols able to probe these microorganisms that are of interest to public health and national defense (Bottos et al., 2014). Different species of pathogenic and nonpathogenic bacteria are constituents of desert dust. However, the presence of potentially pathogenic microorganisms on dust particles could contribute to various health effects, particularly in the respiratory system.

The identification of respiratory pathogens is essential in many low income West African countries where there are significant numbers of residents living in poverty, which are also experiencing population growth, exposing more individuals to poor air quality. In many cases, vulnerable populations (poor, young, elderly, disabled, and sick) have limited capacity to pay for hospital visits and medicine and hence have the highest risk. Identifying potential respiratory pathogens on dust aerosols may improve treatment and improve health outcomes. The primary objective of this study is to identify bacteria associated with dust collected from Cheikh Anta Diop University, located in Dakar, Senegal, from 2013 to 2016 using two different collection techniques. We also identify bacteria and potential pathogens with the goal of follow-up studies using genomic techniques similar to Allen et al. (2015).

### 2. Materials and Methods

#### 2.1. Determining the Occurrence of Dust Events in Dakar Senegal for Sampling

We determine whether dust was present in Dakar, Senegal on the day of collection, through used satellite visible satellite images, visibility reports from the airport, aerosol optical depth satellite or ground-based...
measurements in Mbour, Senegal, and observed particulate matter (PM) concentrations (Table S1 in the supporting information) measured in Dakar, Senegal, by the Centre de Gestion de la Qualité de l’Air, from the Direction de l’Environnement et des Etablissements Classés (Ministry of Environment and Sustainable Development) (Diokhane et al., 2016).

We also used the Hybrid Single Particle Lagrangian Integrated Trajectory Model HYSPLIT model (Stein et al., 2015) to identify the potential origin of dust using 5-day back trajectories with the endpoint being Dakar, Senegal. Back Trajectories are based on Global Data Assimilation System (GDAS) with a resolution of 1° × 1°, and we assume isentropic vertical motions, which are appropriate for desert locations where precipitation is not likely. This assumption has been used by Drame et al. (2011) to follow Saharan dust that was found above Dakar, Senegal, in July 2010.

In Table S1 we show the environmental conditions associated with the dust collection during 2013–2016. We used two sampling techniques to collect dust, spatula sampling, and airborne sampling. The sampling occurred throughout the year with eight samples during the NH summer (21 June to 20 September), four samples during the spring (21 March to 20 June), two samples during autumn (21 September to 20 December), and three samples during the winter (21 December to 20 March). For the spatula method, a sufficient amount of dust (visible) had to accumulate on the glass surface before the sample was taken and hence, additional dust events may have occurred prior to the sampling. The sampling using the suspended aerosol sampler occurred on days when dust would have been present from visible satellite images although, during the summer season, dust is located above the monsoon layer with small particles gravitationally settling over Dakar, Senegal.

### 2.2. Deposited Dust Sampling

The aerosol samples were collected on the roof of the Laboratory of Atmospheric and Oceanic Physics Siméon FONGANG of the Ecole Superior Polytechnic of the Cheikh Anta Diop University of Dakar using a sterile spatula that allowed scraping for the samples. Dust samples were collected in 20 ml certified non-pyrogenic and noncytotoxic sterile Falcon Tubes with medical-grade packaging to ensure sterility. Eleven samples were obtained over the period between August 2013 and April 2015 (supporting information Table S1).

### 2.3. Airborne Dust Sampling

During 2016, direct airborne dust sampling was conducted using the QuickTake® 30 air sampling pump with a BioStage® viable aerosol single-stage impactor (SKC Inc., Eighty Four, PA, USA) during 2016 (supporting information Table S1). The BioStage® impactor has 400 2.5-μm pores and operates at a flow rate of 28.3 L/min. The dust particles passing through the pores are deposited on a Nutritive Agar previously prepared and incorporated into the apparatus for a predetermined time before being transported to the laboratory. Airborne dust samples take place for approximately 3–8 hr on the roof of LPSO-SF. The Nutrient Agar medium is then incubated at 30°C for 24 to 48 hr (Liang et al., 2013). Dust samples were taken in January and February of 2016, but there was insufficient bacteria for identification. Hence, four measurements during June of 2016 are used for identifying bacteria using airborne sampling.

### 2.4. Isolation and Identification of Bacteria

Standard microbiological protocols were used in storing, isolating, and evaluating the phenotypic characteristics of viable culturable bacteria (Allen et al., 2015).

The following protocol was used to identify microorganisms (bacteria and fungi) in dust samples, particularly bacteria: the introduction of 0.2 g of dust into 10 ml of buffered peptone water. Then, cascade dilutions ranging from $10^{-1}$ to $10^{-10}$ are carried out, and then 0.1 ml of each dilution is surface spread on the Plant
Count Agar medium, which is incubated for 72 hr to determine the mesophilic flora aerobic activity (Setlhare et al., 2014). On the third day, a macroscopic description of the colonies is made and isolated on Nutrient Agar medium for 24 hr.

A macroscopic reading of each isolated colony for the appropriate orientation of bacterial identification occurs after 24 hr of incubation for collected samples. Basic tests include Gram staining and a search for catalase and oxidase followed by purification on Nutritive to confirm the purity of the strain. Bacteria types are identified by carrying out the physiological and biochemical tests with conventional media. These tests include Voges-Proskauer, methyl red test, the use of carbohydrates, hydrolysis of casein, gelatin, and miniaturized galleries: API 20E®, API 20NE®, and API 50CH®.

A wide variety of bacteria types were visible on the agar media after incubation; however, not all of the bacteria can be identified. Strongly pigmented (colors from light to dark yellow, orange, and pink), bacterial colonies are thought to be a survival mechanism to protect against ultraviolet radiation in the air, or the effect of culturing (Bottos et al., 2014). It is known that only a small proportion (0.1–10%) of environmental bacteria can be cultivated under laboratory conditions; hence, the identified bacteria types are a subset of the total viable bacteria that can be detected (Theodorakopoulos, 2013). All bacteria types identified in this study can be found in Tables S2 and S3.

3. Results

3.1. Identified Microorganisms by Spatula Sampling

Fifty-one (51) culturable bacteria types were identified from 11 samples, of which 33 were Gram-positive (64.71%) and 18 Gram-negative (35.29%) (Figures 1a and 1b). The majority of the bacteria types identified are Gram-positive, and some are sporulated (Liang et al., 2013). The dominant groups in the 51 bacteria types are Micrococcus (33.33%), Bacillus (13.73%), Kyococcus (11.76%), Pseudomonas (9.80%), and Burkholderia (7.84%) successively. The genus Micrococcus is subdivided further by Micrococcus variants (11.76%), Micrococcus luteus (9%), Micrococcus roseus (5.88%), and Micrococcus agilis (3.96%).

Table S1 identifies dusty environmental conditions on 12 December 2013 and 3 March 2015 with PM10 values of 253 and 370 μg/m³, respectively. The identified bacterial species from 12 December 2013 include Staphylococcus aureus, Bacillus thuringiensis, Bacillus megaterium, and Rhizobium radiobacter. The identified bacterial species from 3 March 2015 includes Sphingomonas paucimobilis, Rhizobium radiobacter, Serratia plymuthica, and Micrococcus varians, which can cause respiratory diseases. The Micrococcus found in the collected samples is generally considered to be a saprophytic or commensal organism, but it can be an opportunistic pathogen, especially in hosts with a weakened immune system (Smith et al., 1999).

3.2. Identified Microorganisms From Airborne Sampling

Twenty-six (26) bacteria types (Figures 2a and 2b) were identified from the four samples, 23 of which were Gram-negative (88.46%) and 3 Gram-positive (11.54%). The majority of the bacteria identified by this technique are Gram-negative. The dominant groups in the 26 bacteria are Pseudomonas (38.61%), Burkholderia (26.92%), Micrococcus (11.54%), and Brucella spp (7.69%). In the dominant groups, the genus Pseudomonas had the highest percentage of the bacterial population and is represented by Pseudomonas luteola (29.72%), Pseudomonas pseudomallei (7.69%), and Pseudomonas aeruginosa (3.85%).

The samples from the four dates also show variations, with Pseudomonas being present on all 4 days (supporting information Table S4). The airborne samples from 20 and 24 June show different bacteria types, compared 6 and 10 June. Burkholderia and Micrococcus are in all samples except on 20 June and 12 June 2016, respectively. Enterobacter cloacae, Aeromonas hydrophila, Serratia rubidaea, and Micrococcus sedentarius are only present in the sample of 20 June 2016. However, Bacillus species are absent from airborne sampling suggesting that Bacillus were introduced into spatula samples from surrounding soils.
3.3. Possible Sahara Origin of Collected Dust Samples

For spatula sampling, Figure 3 shows 5-day back trajectories with the endpoint at Dakar, Senegal, for all November through March cases for 2013–2016 with all trajectories shown in Table S1. Back trajectories on 6 November 2013 (Figure 3a), 5 December 2013 (Figure 3b), 3 March 2015 (Figure 3d), and 25 January 2016 (Figure 3f) are shown.

**Figure 3.** HYSPLIT back trajectories for (a) 6 November 2013; (b) 5 December 2013; (c) 10 March 2014; (d) 3 March 2015; (e) 25 January 2016; and (f) 20 February 2016.
2016 (Figure 3e) show air arriving at Dakar, Senegal, had a desert origin. For 12 December 2013, there is some evidence of desert trajectories that pass across Mauritania (Figure 3b). Back trajectories for 3 March 2015 show potential sources of dust coming from Southern Algeria, which is a major source of dust in Senegal (Jenkins & Gueye, 2018). Unfortunately, there was not enough material for 25 January 2016 when the origins of dust arriving at Dakar is from Sahara desert locations (Figure 3e).

In contrast to late fall and winter seasons, airborne dust samples during June of 2016 show a different origin of air arriving at Dakar, Senegal (Figures 4a–4d). HYSPLIT back trajectories for 10, 12, 20, and 24 June show that air arriving at Dakar comes from the Northeast in the lower troposphere with sinking occurring on the southward journey. The back trajectories on 20 June (Figure 4c) suggest some influence of desert areas in Morocco or Mauritania prior to arriving in Dakar. This may help to explain the differences in observed bacteria types at Dakar, Senegal, among airborne samples in June 2016. However, it should be noted that all summer 5-day back trajectories have a common origin over the Tropical Eastern Atlantic in the lower troposphere. The surface origin remains unclear, but a Sahara influence with surface dust vertical transported into the Saharan Air Layer cannot be ruled out.

4. Discussion

Similar to earlier works (Griffin, 2007; Kellogg et al., 2004), the majority of bacteria isolated in this study could be responsible for respiratory pathologies and have a negative effect on human health. This includes Micrococcus, Bacillus, Kytococcus (11.76%), Pseudomonas, Burkholderia, and Brucella spp. Micrococcus luteus has been reported as the causative agent in cases of pneumonia, sepsis, endocarditis, and meningitis.
Transmission is possible by contact with contaminated objects and/or surfaces. Transmission by inhalation of contaminated droplets and/or aerosols is also possible (Dada & Aruwa, 2014).

Airborne bacteria have been measured in different environments (Liang et al., 2013), but the composition of microbial populations in air varies widely in space and time (Barberán et al., 2015). In this paper, we focus on those bacteria associated with dust transport from possible Saharan sources. We note that sampling with the QuickTake® 30 sample pump is more selective because it has a filter with pores of 2.5 μm, while the scraping with the spatula does not establish any size restrictions. Similarly, sampling with the spatula was carried out over a nonspecific time, while the sampling times with the pump are defined beforehand. In addition, scraping with the spatula could carry away bacteria from the soil and create a bias in the results compared to the objectives of the study. The 51 bacteria types found in our spatula samples could be bacteria usually found in the soil, the marine environment, and on human skin as described by Kellogg et al. (2004). For example, Bacillus species that are predominant in soil constitute 13.73% of the identified bacterial isolates (Kellogg et al., 2004). Bacillus species were also determined as a common bacteria species from soils at multiple locations at Allen et al. (2015).

There are potential respiratory diseases from many of the identified bacteria, especially for immune-compromised individuals. These include Pseudomonas, Burkholderia, Micrococcus, and Bacillus. Gram-negative bacteria were identified from airborne and spatula samples and can cause inflammatory reactions that can exacerbate allergies and asthma (Adhikari et al., 2014). Toure et al. (2019) show a high prevalence of asthma, bronchitis and acute respiratory infection spatially across Senegal during dusty period in the winter season.

5. Conclusion

Microbial populations transported by dust storms have the potential to affect ecosystems and public health in the Sahel and downstream in the Caribbean, Southeastern United States, Brazil, and Europe (Groß et al., 2015; Prospero, 1999; Prospero et al., 1981). In this study, we identified bacteria, which could be pathogens, present on Saharan dust aerosols that were observed with dust events in the Dakar region from 2013–2016 to identify possible linkages to respiratory health. From the samples, 77 bacteria were isolated, and the majority of bacteria could cause respiratory diseases. Conventional culture techniques confirm that microorganisms present in suspended dust are viable but only reveal the low percentage of microorganisms that grow on a given medium. Several bacteria found in the studies of Kellogg et al. (2004), including Bacillus, Micrococcus, and Staphylococcus are identified in our study. These bacteria are potentially responsible for respiratory infections, especially in immune-compromised patients.

However, many demanding fungi and bacteria, as well as all viruses, cannot be detected by this classical method of microbiology. Future work will focus on the use of direct DNA extraction techniques similar to Allen et al. (2015) but with a focus on airborne during dust events. Because of limited winter season samples, additional airborne sampling is required and traditional and genomic methods will be used for identifying bacteria species.

CONFLICT OF INTEREST

The authors declare no conflicts of interest relevant to this study.

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