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Review article

A review on airborne microorganisms in particulate matters: Composition, characteristics and influence factors

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ABSTRACT

Airborne microorganisms (AM), vital components of particulate matters (PM), are widespread in the atmosphere. Since some AM have pathogenicity, they can lead to a wide range of diseases in human and other organisms, meanwhile, some AM act as cloud condensation nuclei and ice nuclei which let them can affect the climate. The inherent characteristics of AM play critical roles in many aspects which, in turn, can decide microbial traits. The uncertain factors bring various influences on AM, which make it difficult to elaborate effect trends as whole. Because of the potential roles of AM in environment and potent effects of factors on AM, detailed knowledge of them is of primary significance. This review highlights the issues of composition and characteristics of AM with size-distribution, species diversity, variation and so on, and summarizes the main factors which affect airborne microbial features. This general information is a knowledge base for further thorough researches of AM and relevant aspects. Besides, current knowledge gaps and new perspectives are offered to roundly understand the impacts and application of AM in nature and human health.

1. Introduction

AM are ubiquitous in the air, which mostly exist in the shape of attaching on the PM while few of individual, and they gradually become hot research objects with increasing studies on atmospheric PM (Munir, 2010). As important parts of PM, AM were the vital role in affecting human health, atmospheric chemistry, nucleation processes, and ecosystem interactions, they have biogeochemical connection with oceanic, atmospheric, and terrestrial environments (Bauer et al., 2003; Delort et al., 2010; Fröhlichnowoisky, 2016; Walser et al., 2015), so comprehending the microbial contents in the air has important scientific, health, and economic significances. Nevertheless, many traits of microbes, such as the actual identity, diversity, and abundance of different types as well as microbial temporal and spatial variability, are not well studied, therefore relevant researches about airborne microbial characteristics should be taken seriously from now. In most present researches about airborne microbial compositions and characters, the starting point is microbial integral distribution, and the emphasis is microbial constitutions and features in whole environment, but microenvironment and small environment also have high research value which less be studied. Size-segregated environments own study meaning because the most harmful effects of PM are related to the size of the particles (Kim et al., 2015). From culture-based methods to molecular biological techniques (Adhikari et al., 2004; Hospodsky et al., 2010; Katra et al., 2014; Kim et al., 2008; Lee et al., 2006), researchers generally have studied airborne microbial main compositions like bacteria, fungi, viruses and archaea with their concentration, size distribution and diversity in order to know their peculiarities. Besides, AM have variability caused by themselves and other factors. Common influence factors contain meteorological parameters, particles, source, time, location, and human and animal activities (Dallavalle, 1958; Haas et al., 2013; Peccia et al., 2001; Yadav et al., 2015), and they have different effects on AM. Over the last decade, the studies in field about influence factors exploration have increased gradually, but the concrete effect mechanisms are not clear that still need to be researched. The objective of this paper is to review knowledge about airborne microbial various characteristics and their influence factors. These aspects account for the manifold importance of the microorganisms in the atmosphere, provide preconditions of subsequent researches about impacts and solutions of AM on other sides like health risk assessment and allow insight in possible applications of these organisms.

2. Composition of AM

Microorganisms are omnipresent in the atmospheric environment, which mainly include bacteria, fungi, actinomycetes, viruses, pollen,

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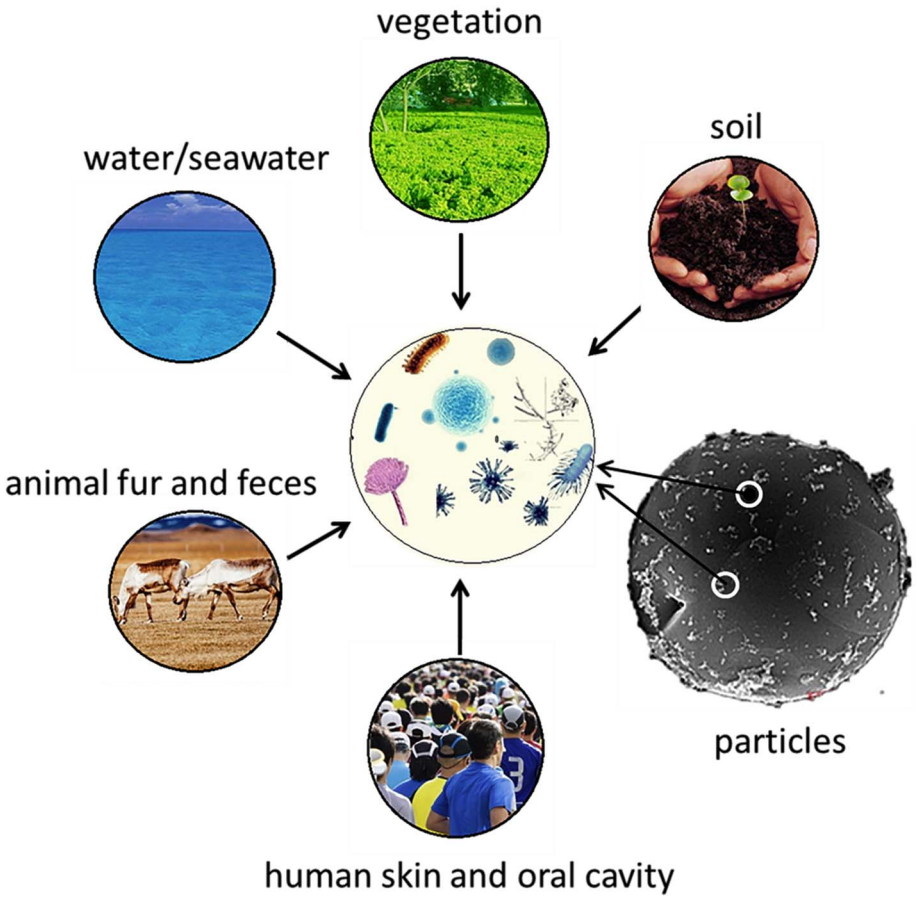

Fig. 1. Main sources of airborne microbes over particles.

and a little archaea (Stetzenbach et al., 2004). The atmosphere is considered as one of habitats for AM originated from soil, water/seawater, vegetation and else places (Fig. 1). Though atmosphere owns some hard conditions such as high solar radiation, low moisture and nutrients and large dispersing capability, it gradually evolved into one of the habitats for microbes, there are still a large amount of microbes in the air now (Henderson and Salem, 2016). According to estimation, nature has about 40 thousand bacteria, 1.5 million fungi and 130 thousand virus, but actually the species, found and detected by current research methods, are little (Hawksworth, 2001). Under various settings, microbial compositions are distinguishing (Fig. 2), but the trends of scale in microbes are the similar that generally detected bacteria are the most about 80%, next are fungi, finally are others. These microbes can exist in the air mostly depend on PM which are primary carriers for AM, and the pattern AM existing on PM is adhesion, a way for AM to establish community and sustain life in a particular habitat. Meanwhile, PM can offer AM nutrients to prevent starving conditions and maintain AM's metabolism with likely high nutrients on surface of PM when air settings around PM haven't enough nutrients, and PM also can provide the occupants with a shield as decreasing harm by ultraviolet radiation (Kharangate-Lad, 2015; Maier and Gentry, 2015). Compared with AM on PM, the AM that exist as individuals may be more likely to die. AM attaching to particles gradually form many abundant and mutable communities as numerous microbial species and different shares of each microbial constituent, which generate microbial diversity over PM (Lighthart, 2000). The diversity and interaction among these microbes will have an effect on themselves and external environment. Airborne microbial composition can provide rich information about themselves, like their portions, properties and characters, and comprehensive knowledge can help researchers lay a foundation for subsequent studies about AM.

2.1. Bacteria

The study topics of AM are constantly increasing, which ranged from exploring their existence and metabolic activity in atmosphere to researching their potential pathogenicity and influence on climate and human health (D'Arcy et al., 2012; Polymenakou, 2012; Salonen et al., 2015; Šantl-Temkiv et al., 2015). Bacteria are common research objects with the concentration ranging between 10 and 10^7 cell per·m^3 in the air detected by methods like culture methods, bio-molecular technology and quick estimation model (Albrecht et al., 2007; Bertolini et al., 2013; Bowers et al., 2012; Lange et al., 1997; Lee et al., 2010; Li et al., 2010; Liu et al., 2017b). Bacteria can exert a certain extent influence on many aspects, like Gram-negative bacterial contamination relate to endotoxins that can bring adverse effects, and some bacteria have infection and toxicity may result in various microbial diseases of human and plants when higher concentration (Liang et al., 2013; Traversi et al., 2011), and some may impact cloud development and atmospheric chemistry (Andreae and Rosenfeld, 2008; Burrows et al., 2009). Hence, bacterial characteristics are vital for AM studies to broaden the knowledge and deepen the cognition.

2.1.1. Size distribution

Different bacteria have respective sizes ranging from 0.1–5 μm, and each bacterium has particular shape feature that plays an important role in the adhesion on PM (DeLeon-Rodriguez et al., 2013; Grinshpun et al., 1995). With smaller size, bacteria are easier to attach to fine particles like $PM_{2.5}$ even smaller particles. Generally, particle size is an essential factor that determines PM's inhalable degree which have a crucial effect on human health, so bacterial size distribution is a significant content of researching health risk assessment exposure to airborne bacteria for human (Kawanaka et al., 2009). Hot research topics are more put on small particles including 'inhalable coarse particles'

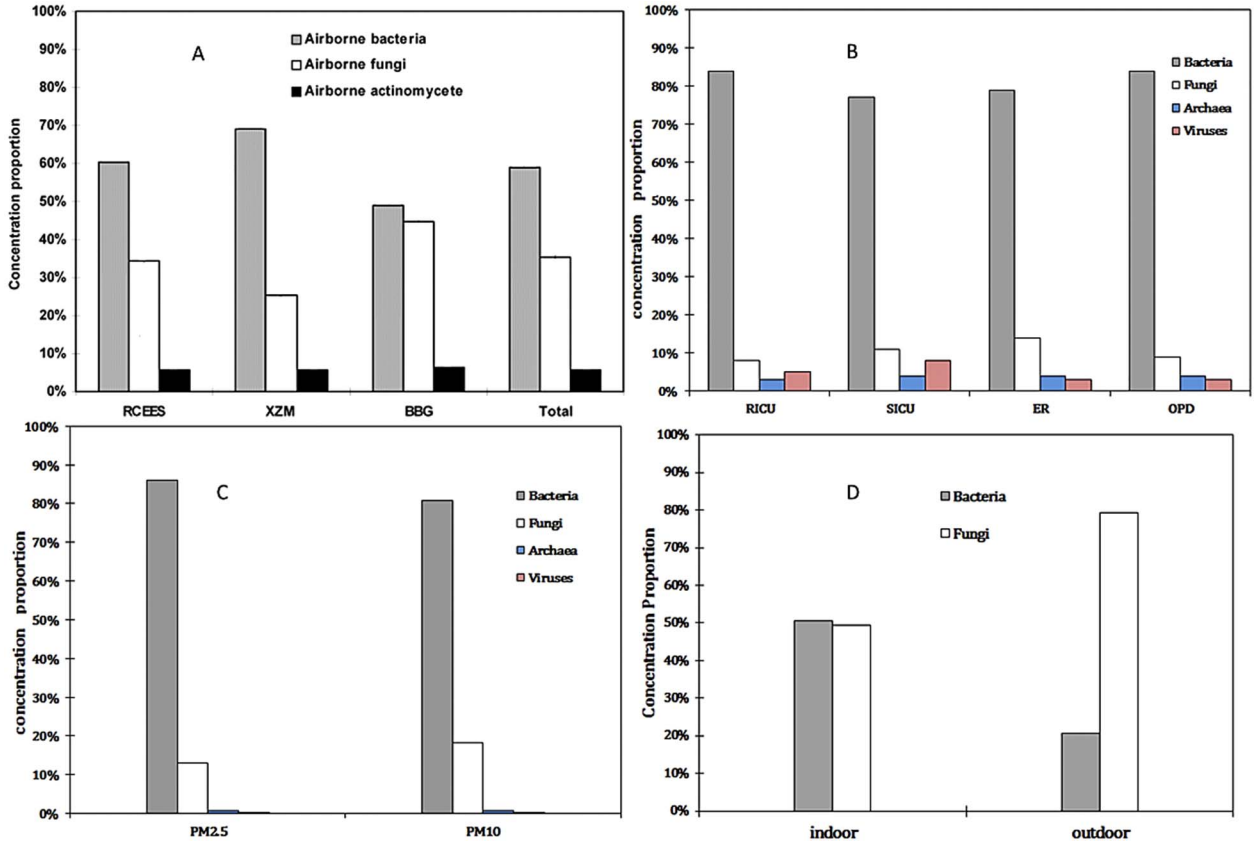

Fig. 2. Airborne microbial compositions under various settings, A) in three typical sites in Beijing, RCEES: Research Center for Eco-Environmental Sciences, XZM: Xizhimen, BBG: Beijing Botanical Garden (Fang et al., 2008); B) in a hospital environment, RICU: Respiratory Intensive Care Unit, SICU: Surgical Intensive Care Unit, ER: Emergency Room, OPD: Outpatient Department (Tong et al., 2017); C) in different particles (Cao et al., 2014); D): in food courts, indoor and outdoor (Rajasekar and Balasubramanian, 2011).

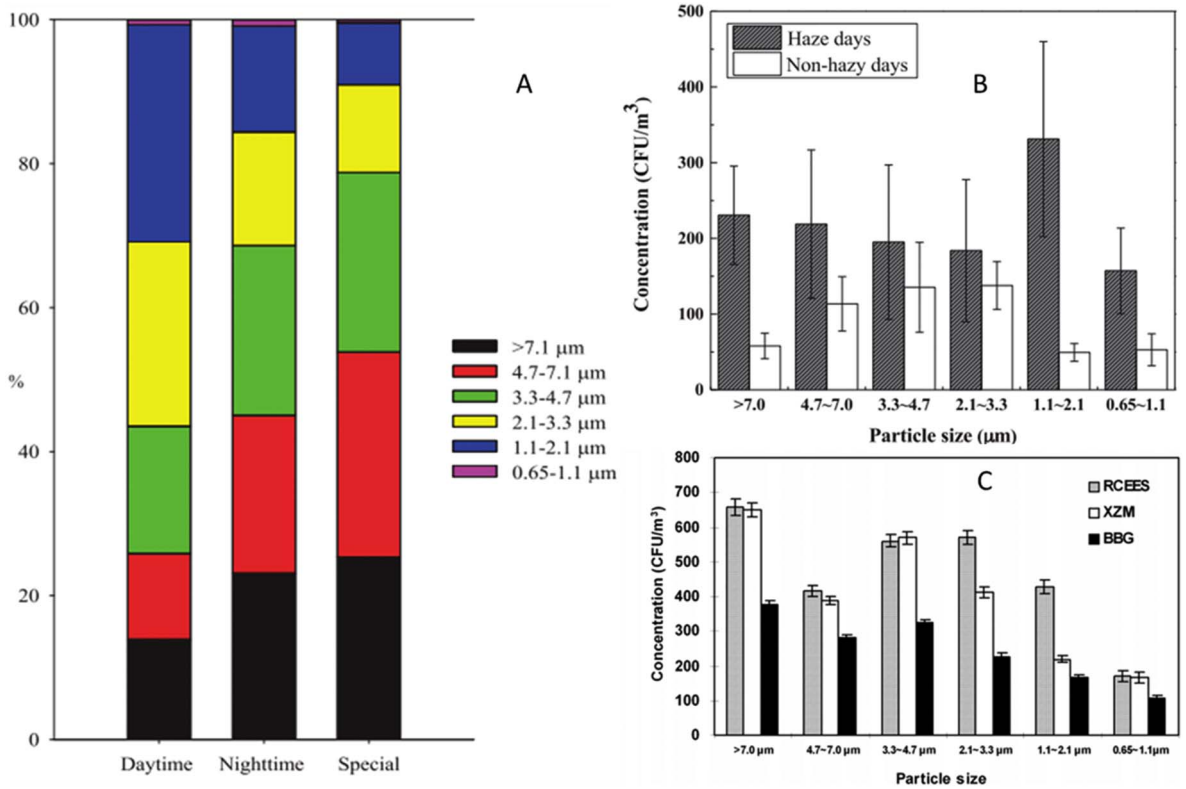

Fig. 3. The concentration and proportion of airborne bacteria in size-segregated particles, A) (Dybwad et al., 2014); B) (Li et al., 2015); C) RCEES: Research Center for Eco-Environmental Sciences, XZM: Xizhimen, BBG: Beijing Botanical Garden (Fang et al., 2008).

with a diameter of 2.5 to 10 μm and 'fine particles' which smaller than 2.5 μm in diameter. Because coarse particles, aerodynamic diameter larger than 10 μm, will be captured by vibrissa and can't enter body inner, they are less harmful to health than the former (Frąk et al., 2014; Kim et al., 2015). To research microbial size distribution, multi-stage sampler is used because it can more comprehensively, concretely and accurately embody this characteristic than single-stage. In researches which studied with Andersen six stage viable particle samplers, bacterial size distribution mainly concentrated on aerodynamic diameters from 1.1 to 2.1 μm and larger than 7.1 μm. The distinction of the two depended on temperature in sampling stage, diameters were 1.1 to 2.1 μm in warm, while another in cold (Raisi et al., 2012; Rajasekar and Balasubramanian, 2011). Actually under different environments, the size-distribution patterns have some distinctions (Fig. 3). Bacteria decreased with decreasing particulate size partly since the study environments were breeding settings in which bacteria had better conditions to grow and propagate (Zhao et al., 2011; Zheng et al., 2013). Studying with 8-stage Andersen samplers at poultry-feeding operations, authors indicated that size-related differences occurred in the aspect of airborne bacterial abundance, diversity, and concentration, and those bacterial features varied with particle sizes could facilitate an understanding of potential health risk of bacteria on human and poultry (Gao et al., 2017b). Meanwhile, different bacteria had respective variation tendency for particle sizes, although there were some differences on size distribution, bacteria mainly attached to particles with diameters larger than 2.1 μm (Blais Lecours et al., 2012). Actually, like mentioned above, single bacterial cell size is smaller than particles, there are a mass of nutrients and bacterial slime coat on the bacteria that make bacterial size bigger but still are smaller than particles, so there were bacteria presenting in smaller size range between 0.65 and 1.1 μm (Grinshpun et al., 1995; Lighthart, 1997; Raisi et al., 2012). In present relevant researches, there are some errors caused by sampling methods and microbial detection means, and the short of sufficient evidences is a hinder to observe bacterial size distribution on tiny particles, so further researches on airborne bacterial size distribution can use optimized sampling and detection approaches.

2.1.2. Dominant species

On PM, bacteria have different dominant species in various environments. Atmosphere habitat is considered as an extreme environment, but AM can live well in the air with nutrients supported by cloud, rainwater and particles (Womack et al., 2010). Although atmosphere provides survival conditions for AM, due to microbial different intrinsic properties, different microbes can adapt themselves to one certain environment better and develop into preponderant species in disparate atmospheric settings. Therefore, dominant species of bacteria is a worth research content which is effective in providing more insight into the dominant species with their features and exploring biodiversity of the atmosphere. According to researches about airborne bacteria under diverse environments, researchers can find that bacterial communities have respective characteristics. It is reported that bacteria exposure level mainly has correlation with various factors like human oral cavity, human skin indoors, and wind, temperature, relative humidity (RH) alfresco, so bacterial composition has a close correlation with one concrete environment. *Streptophyta*, *Bacillus*, *Corynebacteria*, *Pseudomonas*, *Acinetobacter* and so on often were detected in retail stores (Hoisington et al., 2016), and *Sphingomonas*, *Staphylococcus*, *Bacillus* were common bacteria in residences (Adams et al., 2014), in office buildings, *Micrococcus*, *Staphylococcus* became dominant (Bonetta et al., 2010), while in underground subway station, wastewater treatment plant (WWTP), suburban, hospital, coastal region, city and so on, the dominant bacterial species had fine distinctions (Table 1). In addition, pathogenic bacteria sometimes were also found on particles, such as *Enterococcus casseliflavus* in a hospital WWTP and *Proteus sp.*, *Proteus mirabilis*, *Escherichia coli*, *Enterobacter aerogenes*, *Providencia alcalifaciens* and *Morganella sp.* commonly were detected in researches (Han et al., 2013; Uhrbrand et al., 2017). For these pathogenic bacteria, researchers should devise effective ways to keep them within safe limits owing to their obvious harm to humans. These dominant species may belong to different attributes which are divided into Gram-positive and Gram-negative. Among cultivable bacteria, the Gram-positive bacteria, generally dominant bacteria isolated from bioaerosol, take up a great part of all detected genera in different studies (Amato et al., 2007; Fröhlichnowoisky et al., 2011; Raisi et al., 2012). And the proportion of Gram-positive bacteria is about 80% (Table 2). On the contrary, in Fahlgren et al.'s (2010) research about coastal airborne bacteria, Gram-negative bacteria were more than Gram-positive in all samples, which because the dominant sources were coastal airborne bacteria that containing more Gram-negative bacteria (Fahlgren et al., 2010). These proportions are not changeless, maybe changing with other parameters, but overall these trends are basically constant (Kowalski et al., 2017). These results indicated that the bacterial composition of Gram-positive and Gram-negative were different between various sampling locations, and were influenced by bacteria origin, if bacterial origin mostly belonged to marine place, Gram-negative would occupy a fairly large proportion. Bacterial species composition over PM is a vital part for researchers to discover the microorganism potential sources by principal component analysis and backward air mass trajectory analysis and other methods, and dominant species are the main research objects (Lee et al., 2007; Seifried et al., 2015). There are several important factors in a health risk assessment, one of which is the nature of the microbe including microbial concentration and pathogenicity, so the study of dominant species can provide preliminary preparation and basis.

2.1.3. Diversity

Over PM, bacterial composition is complex with multiple genera and species, so in this microenvironment, AM forming many microbial communities show their diversity. Diversity generally is analyzed by traditional separation culture methods and molecular biological technologies, the former is skillful but restrictive, and the latter is more precise like high-throughput sequencing (pyrosequencing analysis targeting 16S rRNA sequences and metagenome sequences). There are some indexes can illustrate microbial diversity features. α-Diversity index, calculated by the kinds of species and abundance, is a significant gist to evaluate microorganism community level. This index mainly includes community diversity (Shannon and Simpson), community richness (Chao and ACE), npShannon and Good's Coverage. Larger Shannon index values indicate the richer species in the environment and the more evenly distributed the species, larger Simpson index indicates that the higher the species diversity of the sample, the more evenly distributed among the various individuals and vice versa, and larger Chao values represent more species contained in the sample. β-Diversity describes the relationship between microorganisms and environmental factors. The both indexes are important microorganism parameters reflecting microbial community with their diversity. Gao et al. (2016a) reported six $PM_{2.5}$ clone libraries with average index values of Shannon, Simpson, Chao 1, ACE and Good's Coverage respectively. In this study, Simpson indexes value reflected the samples had high evenness, while other data showed low richness (Gao et al., 2016a). Genitsaris et al. (2017) had a study of atmospheric bacterial variability in an urban area, and reported that the values of the Simpson index ranged between 0.81 and 0.95 except one sample, and the Shannon index showed similar patterns with the Simpson index (Genitsaris et al., 2017). This result indicated that the majority of the samples manifested relative homogeneity in the field of the sequences number. Fahlgren et al. (2010) collected 8 samples, the Shannon index of them were from 1.2 to 3.9 in different sampling time, the data showed a high abundance and diversity in most samples (Fahlgren et al., 2010; Straat et al., 1977). The abundance of AM varied in a degree with many factors including sampling time and site et al., and these indexes effectively represented the situation of diversity for bacterial community on particles under different conditions. The diversity

Table 1
Different dominant bacterial genera in different study environments.

Dominant bacterial genera	Total amount of genera	Detected method	Study environment	Reference
Streptophyta, *Bacillus*, *Corynebacterium*, *Pseudomonas*, *Acinetobacter*	788	Pyrosequencing	Retail stores (United States)	(Hoisington et al., 2016)
Bacillus, *Kocuria*, *Staphylococcus*, *Sarina*, *Pseudomonas*	16	cb	Agricultural industry	(Awad et al., 2010)
Sphingomonas, *Pseudomonas*, *Chryseobacterium*, *Sejongia*	30	cb and ci	Vicinity of the Baltic Sea coast	(Fahlgren et al., 2010)
Vibrio, *Bacillus*, *Pseudoalteromonas*, *Psychrobacter*, *Salinibacterium*	31	16S	Coastal near-shore	(Dueker et al., 2012)
Staphylococcus, *Pseudomonas*, *Alcaligens*, *Corynebacterium*	9	cb	Food courts	(Rajasekar and Balasubramanian, 2011)
Micrococcus, *Staphylococcus*	nd	cb	Office building	(Bonetta et al., 2010)
Staphylococcus, *Bacillus*	11	cb	Wastewater treatment plant	(Kowalski et al., 2017)
Bacillus, *Micrococcus*, *Staphylococcus*	37	cb and partial 16S	Underground subway station	(Dybwad et al., 2012)
Pseudomonas, *Bacillus*	106	DGGE	Suburban (Toyama)	(Tanaka et al., 2014)
Streptomyces, *Bacillus*, *Kocuria*, *Corynebacterium*, *Paenibacillus.*	26	cb	Urban (Ahvaz)	(Goudarzi et al., 2014)
Micrococcus, *Staphylococcus*, *Kocuria*, *Pseudomonas*	55	16S	Urban (Hangzhou)	(Fang et al., 2016)
Afipia, *Oxalobacteraceae*, *Methylobacterium*	314	SSU	Upper troposphere	(DeLeon-Rodriguez et al., 2013)
Staphylococcus, *Micrococcus*, *Corynebacterium*, *Bacillus*	10	cb	Hospital	(Kiyoun et al., 2010)
Micrococcus, *Staphylococcus*, *Bacillus*, *Corynebacterium*, *Pseudomonas*	47	cb	Slaughtering plant	(Liang et al., 2013)
Sphingomonas	nd	16S	Ocean	(Seifried et al., 2015)
Staphylococcus, *Micrococcus*, *Pseudomonas*, *Proteus*	11	cb	Poultry farms	(Plewa and Lonc, 2011)
Bacillus	11	16S	Free troposphere	(Maki et al., 2013)

nd: no data.
cb: culture-based.
ci: culture-independent.
16S: 16S rRNA sequencing.
SSU: SSU rRNA gene sequencing.
DGGE: denaturing gradient gel electrophoresis.

Table 2
Proportion of Gram-positive and Gram-negative bacteria (%).

Gram-positive bacteria	Gram-negative bacteria	Reference
79	21	(Awad et al., 2010)
89	11	(Goudarzi et al., 2014)
80–85	15–20	(Liang et al., 2013)
82	18	(Gangamma, 2014)
68	32	(Orsini et al., 2002)

can reflect the state of the bacteria and their relationship to the environment, and microbial resources developments, ecosystem functioning, global change and human health are all closely related to microbial diversity, so microbial diversity are significant for relevant studies. To understand the diversity fully, more researches have to be conducted.

2.1.4. Variation

Bacterial concentration, diversity, size distribution and predominant species will change following temporal and spatial variation. Temporal change mainly include daily shift and seasonal shift, while spatial change generally refer to exploring microbial source and different characteristics of AM in distinguishing regions. In most cases, microbial abundance change diurnally, the maximum concentrations normally appear on 7:00–9:00 h and 17:00–18:00 h, and the minimum on 13:00–14:00 h in daylight, and bacterial level increase during the daytime compared with the nighttime. Tong (1999) detected both total and cultivable airborne bacteria reached the concentration peak at 18:00 h (Tong, 1999). Fang et al. (2007) reported that significantly higher bacterial concentrations were recorded at 09:00 h and 17:00 h than those at 13:00 h because of heavy human activities and traffic flow appearing in the two periods (Fang et al., 2007). In the livestock farm, due to closed environment and animals' influences, the diurnal variation of bacteria was complex, and the concentration peaks of bacteria on working days and weekends were different (Fig. 4). In conclusion, bacterial concentration diurnal variation in a great degree is shaped with multiplicate conditions such as sunrise, wind speed (WS), temperature, solar radiation and increasing of human activities. In addition to bacterial concentration, the size distributions also vary during a day and the temporal variation of bacteria would help to fully understand the possible harm at different times. Dybwad et al. (2014) researched temporal variability of airborne bacteria at a subway station, they observed a significantly larger fraction bacterium-containing particles between 1.1 and 3.3 μm during the daytime than night, while a significantly greater fraction of particles of > 3.3 μm was observed at night than during the day. These results indicated that bacterium-containing particles' diameter had an obvious diurnal variation (Dybwad et al., 2014). In addition, both on non-haze and haze days, aerodynamic diameter of AM fluctuated from 9:00 to 21:00 h, and changeless highest concentrations of airborne bacteria were observed at size ranges of 3.3–4.5 μm at 12:00 and 21:00 h (Gao et al., 2015). Meanwhile, bacterial diversity showed day-to-day variation, and dominant bacteria changed from daytime to nighttime. The author adopted two methods to analyze the diurnal variation of dominant bacteria, the results showed that the Andersen-derived and the SASS 3100-derived daytime diversity was dominated by *Micrococcus*, while the nighttime diversity was dominated by *Rhodococcus*, just the followed bacteria had few differences (Dybwad et al., 2014).

Annual variation in diversity, type, ration and composition of airborne bacteria in the same area has a regular pattern. Selecting these bacterial features for longitudinal comparison in the same site, researchers find bacterial characteristics in the same season do not show significant change, and this is owing to bacterial seasonal stability, while in different sampling sites there are diverse distributions. Overall, bacterial characteristics, especially richness and the relative abundance, exhibit significant seasonality patterns. Concentration distributions in a year weren't uniform, considering temperature, region, terrain and bacterial autologous characters multi-factors, high concentrations were found in winter (Alghamdi et al., 2014; Fahlgren et al., 2010), in summer (Fang et al., 2007; Wang et al., 2010),in

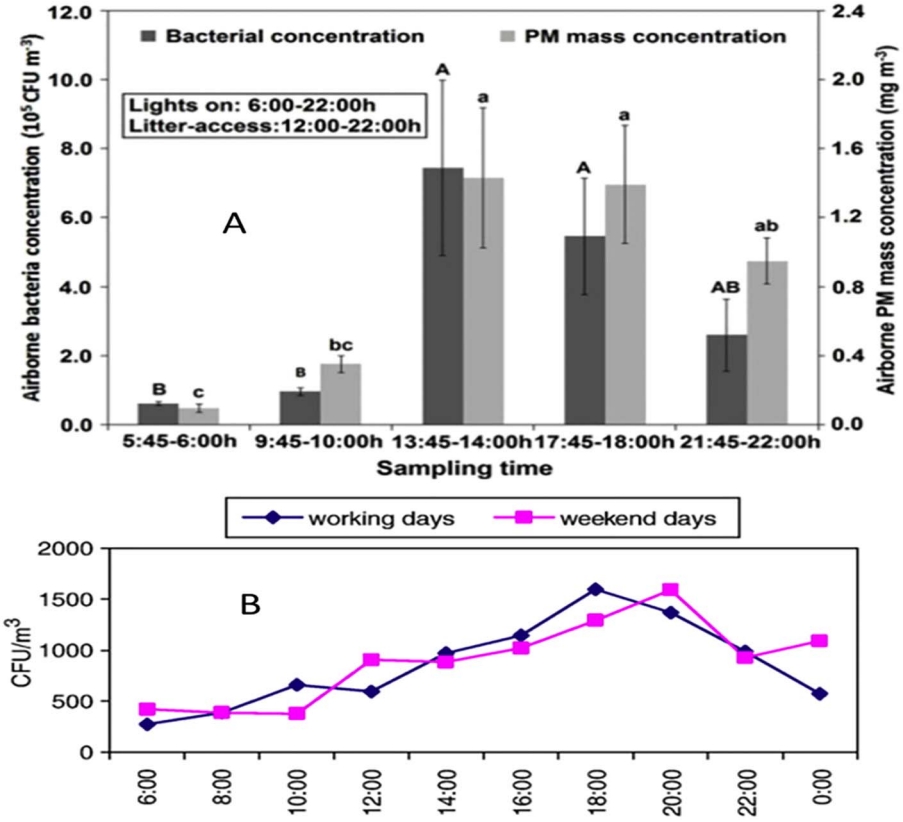

Fig. 4. Diurnal variations of airborne bacteria concentrations, A) (Zheng et al., 2013); B) (Abdel Hameed et al., 2009).

autumn (Fang et al., 2016; Kaarakainen et al., 2008). Tanaka et al. (2014) didn't find significant seasonal changes in the concentration of airborne bacteria (Tanaka et al., 2014), and that showed bacterial indeterminacy and variability under different researches. In addition to integral concentration variation, the dominant bacteria similarly owned temporal variation, like *Actinobacteridae* reached maximum abundance in the late summer while *Pseudomonadales* reached their highest levels during mid-spring (Bowers et al., 2013). As the report illustrated, in warm seasons, predominant microorganisms generally were retrieved in soil, while typically associated with plants in cold seasons (Gandolfi et al., 2015). The results also indicated that bacterial communities seemed mostly related to environmental conditions, in which season was the significant factor. Potential sources' relative contribution on bacterial community has a temporal variability, so bacterial communities variance correlates to temporal transition and potential sources, especially those located close to sampling sites (Bertolini et al., 2013; Gandolfi et al., 2015).

Bacterial sources' spatial distributions make bacterial communities own respective spatial variation characteristics. Under the same season, different sites have their own unique bacterial communities, and local sources and atmospheric dispersal are involved in the assembling of the communities. In present researches, a Geographic Information System is usually used to analyze the spatial distribution of bacteria, and backward trajectories are used to find the sources of bacteria (Agabou et al., 2013; Seifried et al., 2015), and these technologies supply more information about bacterial temporal and spatial variation. Temporal and spatial variability of bacterial communities are important contents for scholars to gain insight into atmospheric biodiversity and biogeography.

2.2. Fungi

Fungi are estimated to the most microbes contained in nature, and airborne fungal spore are primary biogenic aerosol particles (PBAP), but as many studies reported about microorganisms consisting in atmosphere, fungi generally just accounted for a fraction of all microbes. Compared with bacteria, fungal allergen is one of the predominant allergens, and fungi exposure has been more closely linked to allergic sensitization and symptoms of allergy and asthma (Medicine, 2000; Medicine, 2004; Swanson, 2001). Due to the pathogenicity of fungi and the airborne effects, researches about airborne fungi should get a comprehensive cognition of them, so that corresponding prevention and protection steps can be took.

2.2.1. Size distribution

Fungal concentration and size distribution vary with sampling sites as bacterial. The fungal concentration is 0–10^7 CFU·m^{-3} with different sizes (Sautour et al., 2009; Yu et al., 2013). Airborne fungi have inequable sizes. Some large hyphal fragments and multicellular spores are > 10 μm in size, unicellular spores' diameters are between 1 and 10 μm and parts < 1 μm, and that shows airborne fungi have a broad size distribution. Size is an important parameter that decides the taxonomic compositions of airborne fungi and influence inherent diversity of fungi, and in all aspects fungal size distribution manifests fungal significance (Yamamoto et al., 2012). Overall, size of fungal particle generally is bigger than bacterial particle, and fungi are found occurring on the fine particles (< 3.3 μm) in the conventionally with the maximum proportion and minimum proportion in the range of 2.1–3.3 μm and 0.65–1.1 μm, respectively, while in the most areas the size distribution represent a unimodal distribution pattern (Yu et al., 2013). Similar results showed by Fig. 5, with other articles discovered fungal particles being mainly distributed at 3.0–6.0 μm, 2.0–3.5 μm and 1.0–2.0 μm (Rajasekar and Balasubramanian, 2011), at 1.1–2.1 μm and 2.1–3.3 μm (Zuraimi et al., 2009), and at 2.1–3.3 μm and < 4.7 μm (Dueker et al., 2012; Xu et al., 2011). On different size-segregated PM, Lee and Liao (2014) researched the fungi size distribution in three size fractions: < 1 μm, 1–1.8 μm, and > 1.8 μm in agricultural farms and found that the median concentrations of cultivable fungi measured for

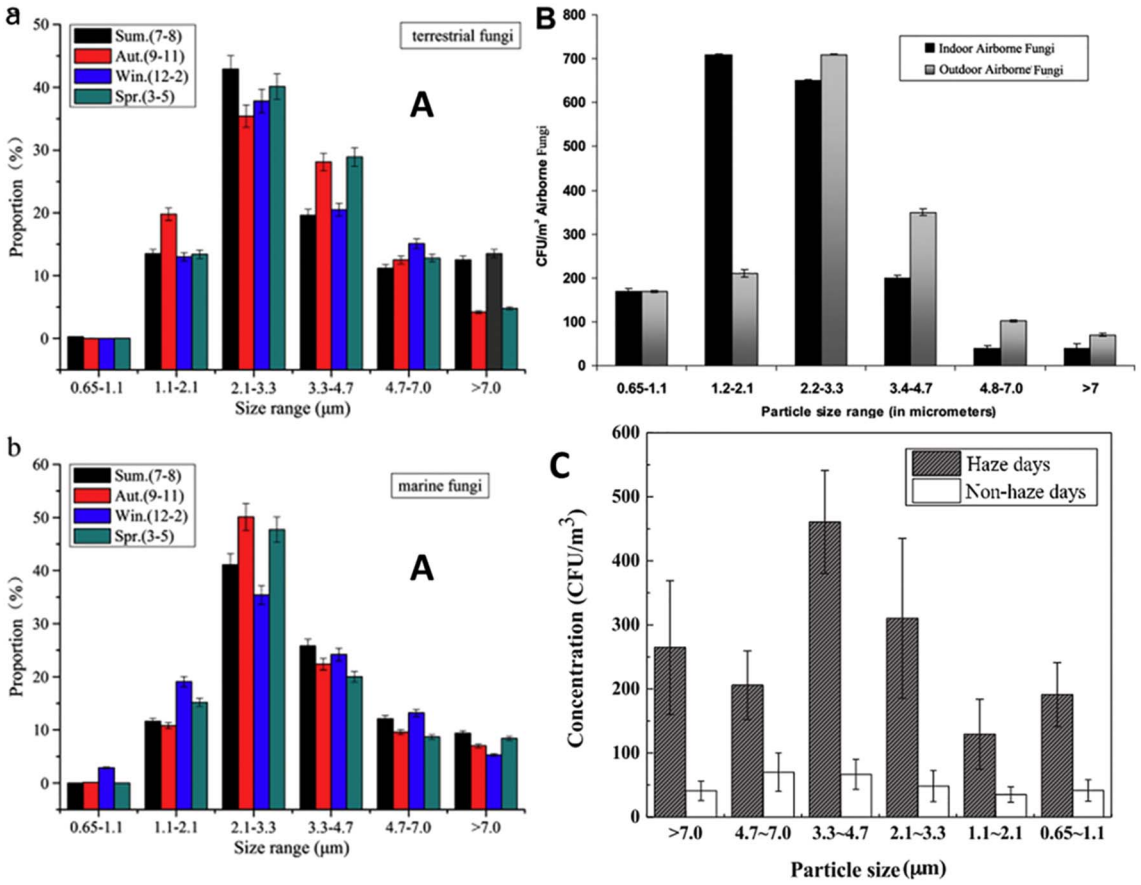

Fig. 5. Average size distribution of fungi, A) a. terrestrial fungi, b. marine fungi (Li et al., 2011); B) indoor and outdoor airborne fungi (Rajasekar and Balasubramanian, 2011); C) fungi in haze days and non-haze days (Li et al., 2015).

the size > 1.8 μm were higher than those for the sizes of 1–1.8 μm and < 1 μm (Lee and Liao, 2014). Sangkham and Sakunkoo (2014) got the results that the size distribution of airborne fungi were 1.1–2.1 (19.99%), > 7 (19.86%), 4.7–7.0 (15.75%), 3.3–4.7 (15.70%), 2.1–3.3 (15.65%), and 0.65–1.1 (13.00%) μm, respectively (Sangkham and Sakunkoo, 2014). These data indicated that fungi were usually found in small one which size were about > 1 μm. Of course, fungal size distribution weren't invariable, the size distribution pattern of the samples might be influenced by factors such as sources, seasons, weather situations, sampling sites and so on, like fine fraction and coarse fraction showed an increase on hazy and foggy days, respectively (Dong et al., 2016; Rajasekar and Balasubramanian, 2011). Fungal size distribution is closely correlative with fungal health threat because aerodynamic diameter is one of the master variables which determine microbial personal exposures, it can be said that the smaller size is, the greater danger is brought, so research fungal size distribution to evaluate the health risk degree. But in previous studies, size-segregated researches of fungi are insufficient, and detected methods also need to be improved to get more accurate and abundant data.

2.2.2. Diversity

Fungal species diversity is a primary influence factor for health risk exposure, because fungal pathogen and allergen are ubiquitous in the air, clearly knowing that fungal composition can better make a health risk assessment. One of the important contents of fungal composition is dominant species. *Cladosporium*, *Aspergillus* and *Penicillium* have the highest frequencies in relevant reports (Bezerra et al., 2014; Kumari et al., 2016; Pyrri and Kapsanaki-Gotsi, 2011; Sepahvand et al., 2013; Sharma, 2011) (Table 3). These common genera own different degrees of pathogenicity and anaphylaxis, and fungal diversity have been shown to be associated with asthma development, so exploring fungal diversity can pave the way for subsequent researches about fungal influence on human health. Besides dominant species researches, analyzing fungal Shannon diversity index is also one of the study methods to research fungal diversity. In swine houses, Shannon index were about 4.5–6.0 and 5.5–6.0 in summer and winter, respectively, the results illustrated that the airborne had a high fungal diversity and winter was more conducive to the formation of high diversity than summer (Kumari et al., 2016). Yan et al. (2016) showed that fungi in TSP and PM_{10} samples had higher Chao1-values than $PM_{2.5}$ which were 169.8, 167.43 and 94.17, respectively, this result indicated higher richness in TSP and PM_{10} samples; Shannon index in TSP, PM_{10} and $PM_{2.5}$ samples were low with 1.905, 2.215 and 2.213 respectively, and a higher value of Shannon index in heavy-haze days indicated a higher diversity than non-haze and light-haze days though there was no significant difference ($p > 0.05$) (Yan et al., 2016). In tropical deciduous forest, the Shannon index was 3.1 and 3.6 that showed high diversity (Satish et al., 2007). The Shannon index, Shannon evenness, and Simpson's index values of airborne fungi were similar to the fungal samples which were obtained from soil and plants, and the result indicated fungi also owned a high diversity in the air (Fröhlichnowoisky et al., 2009). Because many fungi can't be cultured on media, using culture-dependent methods to explore fungal diversity ineluctably would underestimate the data and produce great errors. However, detected by sequencing, over 86% of genera were new-found compared with culture-based methods (Pashley et al., 2012). Tong et al. (2017) combined a culture-based method and DNA sequencing analysis with the Illumina MiSeq and HiSeq 2000 sequencing systems to find high diversity of fungi in hospital, and reported *Aspergillus* was the highest at species level (Tong et al., 2017). These showed that culture-independent methods were optimal ways with

Table 3
Different dominant fungal genera in different study environments.

Dominant fungal genera	Total amount of genera	Detected method	Study environment	Reference
Aspergillus, Candida, Penicillium, Rhizopus, Fusarium	28	cb	Campus and town	(Begum et al., 2011)
Nonsporulating fungi, Penicillium, Cladosporium, Yeast, Aspergillus	16	cb and PCA	Large office buildings	(Chao et al., 2002)
Cladosporium, Penicillium, Aspergillus, nonsporulating fungi	44	cb	Buildings and outdoor environments (United States)	(Shelton et al., 2002)
Penicillium, Aspergillus, Cladosporium	10	cb	Food courts	(Rajasekar and Balasubramanian, 2011)
Ascomycota, Basidiomycota, Schizophyllum, Cryptococcus, Epicoccum	588	qPCR plus 454 pyrosequencing	Urban setting (northeastern United States)	(Yamamoto et al., 2012)
Penicillium, Cladosporium, Aspergillus, Fusarium, Alternaria	20	cb	Hospital	(Sepahvand et al., 2013)
Aspergillus, Penicillium, Cladosporium	nd	cb	Agricultural farms	(Lee and Liao, 2014)
Acremonium, Aspergillus, Cladosporium, Penicillium	29	cb	Underground stations	(Bogomolova and Kirtsideli, 2009)
Penicillium, Aspergillus, Geotrichum, Cladosporium	25	cb	Child care centers	(Zuraimi et al., 2009)
Fusarium, Clavaria, Rhodotorula, Mortierella	30	qPCR and Illumina HiSeq sequencing	Swine houses	(Kumari et al., 2016)
Penicillium, Cladosporium, Alternaria, Mucor, Ulocladium	11	cb	Wastewater treatment plant	(Niazi et al., 2015)
Erysiphe graminis, Hansfordiella, Puccinia, Sporidesmium	18	Photomicrographs	Federal Capital Territory	(Ezikanyi, 2016)
Cladosporium, Alternaria, Fusarium, Penicillium, Sporisorium, Aspergilus	368	Illumina MiSeq Sequencing	campus	(Yan et al., 2016)
Cladosporium, Ustilago, Peniophora, Kavinia	72	Sequencing techniques	Campus	(Pashley et al., 2012)

nd: no data.
cb: culture-based.
PCA: principal component analysis.
qPCR: quantitative real-time PCR.

their high efficiency. Investigation of the diversity about airborne fungi can provide reliable results for microbial infection control and surveillance, whilst more accurate information can make it easier for researchers to develop a better solution proposal.

2.2.3. Variation

Existence of fungi in the air is affected by a mass of factors, therefore, fungi vary with these influences, which are reflected in temporal and spatial variation. Fröhlichnowoisky et al. (2011) illustrated biogeography in the air through analyzing fungal diversity over land and oceans, they compared each sampling method at several locations around the world, like Austria, Arizona, Brazil, China, Germany, Puerto Rico, United kingdom, Ocean, and found estimates of the total species richness of fungi ranging from about 135 to 1100 with the Chao1 estimator approach (Fröhlichnowoisky et al., 2011). In different regions, as the difference of sources, meteorological conditions, land-use types and anthropogenic activities, diversity of fungi are distinguishing, and this difference reflects the spatial variation of fungi (Núñez et al., 2016). One thing to emphasize is that land environment may be rich in fungi, which different from marine environment with rich bacteria. Besides, fungal concentration, size distribution and relative abundance change with time, and the fungal abundance peaked in early spring, summer, late autumn basing on different conditions (Bowers et al., 2013; Liao et al., 2004; Oliveira et al., 2005; Yamamoto et al., 2012). In addition, fungal concentration also varies in a day (Fig. 6). Different fungal species had diverse diurnal distributions, like *Aspergillus* showed double peak patterns at 10:00 h and 20:00 h, *Penicillium* and *Cladosporium*'s concentration peaks appeared at 20:00 h (Lin and Li, 2000), and the highest concentration of *Penicillium/Aspergillus* spores appeared at 10:00 h (Gillum and Levetin, 2007). Besides, fungal size distributions were different in different seasons and sites, like that fungal sizes were higher in winter than summer in outdoor, while it was adverse in indoor (Liao et al., 2004). During heavy haze days and non-haze days, the mean percentages of fine particles carrying cultivable airborne fungi were different in different seasons (Gao et al., 2015). High diversity and concentration of fungi and potentially high levels of fungal allergens occurred in springtime (Oh et al., 2014), in summer (Chao et al., 2002), in fall (Shelton et al., 2002) and in winter (Begum et al., 2011). Above all, time and space are significant factors influence on fungal characteristics, hence, researching fungal features needs combining time and space, which can make researchers better understand fungal intrinsic traits.

2.3. Other microbes

The proportion of viruses and archaea in the detected results are at most 10% and at least 1% in total AM with low concentrations, but some of them own strong pathogenicity, which can generate bad influence on plants, livestock and even human through their low concentrations, so their existences should not be ignored.

2.3.1. Virus

Viral features, infectivity and survivability are effected by particle size, and virus distribution is represented by the particle volume distribution rather than the particle number distribution, therefore, investigating viral composition, concentration and other information over particles is useful (Zuo et al., 2013). For viral perniciousness and infection, more researchers have paid attention to airborne virus' investigations. Particle size can determine physical stability of aerosols, the sites of deposition and the degree of retention, and size of viral aerosols is an immense significance because they may cause human virus infections and affect viral personal size, survivability, pathogenicity rate and even meteorological conditions (Hogan et al., 2005; Sorrell et al., 2011). Small doses of respiratory viruses given by small particle aerosol were infective, and airborne viruses' transmission was most consistent with transmission of small particle aerosol, and these

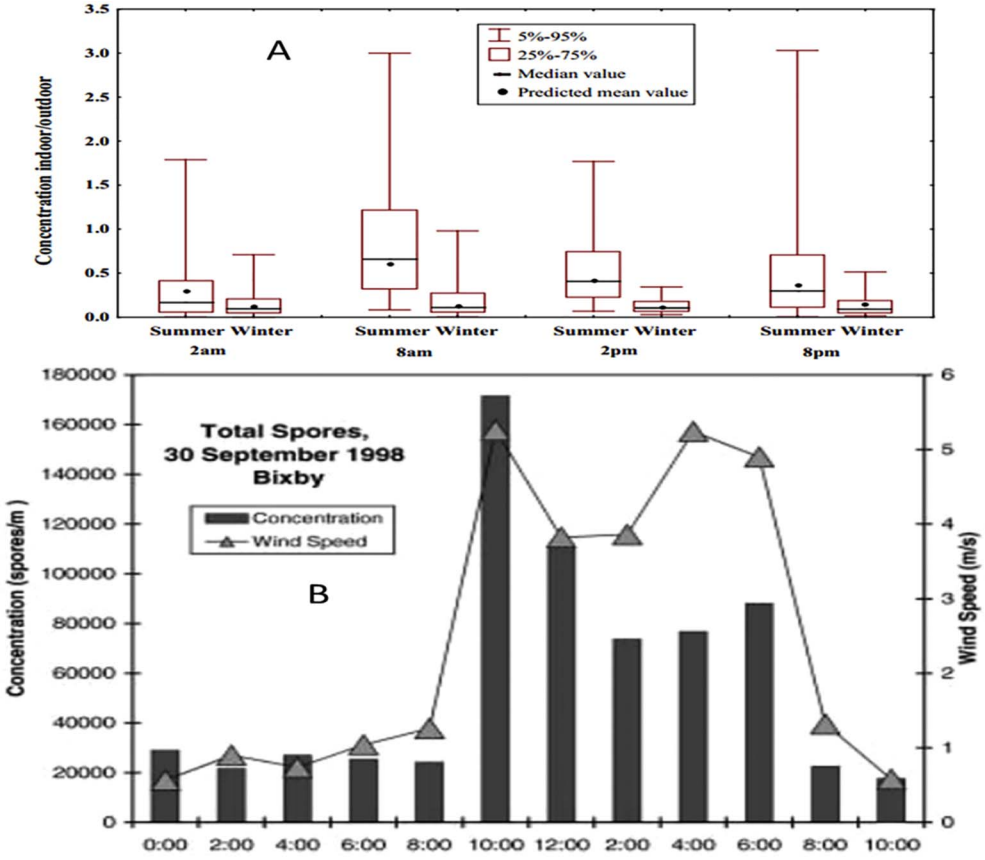

Fig. 6. Diurnal variations of airborne fungi concentrations, A) (Liao et al., 2004); B) (Burch and Levetin, 2002).

Table 4
Distribution by particle size of the quantity [geometric mean of RNA copies·m^{-3} (geometric standard deviation)] of influenza (IAV), porcine reproductive and respiratory syndrome (PRRSV) and porcine epidemic diarrhea (PEDV) viruses in air samples (Alonso et al., 2015).

Particle size range (μm)	IAV	PRRSV	PEDV
0.4–0.7	8×10^2 (3.2)^a	6×10^2 (4.1)^a	1.3×10^6 (3.4)^a
0.7–1.1	6.1×10^2 (1.7)^a	† ≤ 5.1×10^2 (1)^a	3×10^5 (4.7)^a
1.1–2.1	5.5×10^2 (2.5)^a	† ≤ 3.6×10^2 (1)^a	1.6×10^6 (2.4)^a
2.1–3.3	1.4×10^3 (4)^{a,b}	7.8×10^2 (4.82)^a	5.2×10^5 (3.3)^{a,b}
3.3–4.7	7.8×10^3 (5.1)^{b,c}	1.8×10^3 (1.26×10^1)^a	4.5×10^7 (1.8)^c
4.7–5.8	2.3×10^4 (7.4)^c	1.7×10^3 (4.8)^a	5.5×10^7 (2.2)^{c,d}
5.8–9.0	1.5×10^4 (6)^c	1.1×10^2 (7)^a	3.1×10^7 (2)^{b,c}
> 9.0	4.3×10^5 (1.25×10^1)^d	5.1×10^4 (2.8×10^1)^b	3.5×10^8 (2.9)^d

^{a,b,c,d}Different superscripts between rows of the same column indicate statistically significant differences (Tukey's test, $p < 0.05$).
† LOD: Limit of q-PCR detection.

evidenced that particle size played a vital role in viral spread and infection, especially small size (Knight, 1970). Scott and Sydiskis (1976) reported airborne influenza virus had a high infectivity in small particle size (2 μm) than the larger-sized particles (10 μm) (Scott and Sydiskis, 1976). Yang et al. (2011) sampled virus in different sites and analyzed them with quantitative reverse transcriptase-polymerase chain reaction (qRT-PCR), the results showed the amounts of total virus found in each size fraction were 36, 28, 11, 10 and 15% on size which bigger than 2.5, 1.0–2.5, 0.5–1.0, 0.25–0.5 and < 0.25 μm, respectively, and 64% of the viral genome copies were associated with fine particles smaller than 2.5 μm as mentioned above (Yang et al., 2011). The majority of virus-containing particles ranged from 0.5 to 2 μm with the peak at around 1.1 μm, but the research objects most were inactivating viral strains in airborne (Agranovski et al., 2007; Pyankov et al., 2012). Sometimes the virus was evenly distributed in particles with different sizes, in some cases, it was found predominantly in the smallest and largest, or just the largest size fractions (Table 4). Zuo et al. (2013) researched four animal viruses' infectivity and survivability with its carrier particle size, and found that whether infectious virus or total virus were increased with carried particle size increasing (Zuo et al., 2013). These results testified that virus-laden particle size was one of the factors influencing viral properties and the virus distribution was found to be represented by the particle volume distribution. Viruses distribute in different particle size and change in different conditions, and these changes also include viral seasonal variation. Different viruses have disparate outbreak time, some concentrate on summer while others on winter or other time. These viral concentration, activity and negative/positive own diverse distribution with seasons. Boone and Gerba (2005) detected influenza viruses with 23 and 53% of the samples during autumn and spring, respectively (Boone and Gerba, 2005). Masclaux et al. (2014) detected airborne human adenovirus in WWTP and found that positive samples, exceeding the limit quantification (i.e. 2.72×10^3 genome equivalent copies·m^{-3}), were more in summer than in winter, and the mean concentration of airborne adenovirus was higher in summer than in winter, but two other viruses, norovirus and hepatitis E virus, scarcely appeared (Masclaux et al., 2014). Although virus has a great harm to humans, current understandings of virus aren't deeply enough. To get a better comprehension of airborne viral characteristics and to take preventive measures for viral harm, relevant researches about viral characters can be conducted step by step.

2.3.2. Archaea

Archaea, accounting for up to about 10% of the prokaryotes, have been thought to live in extreme environments, actually they have also

Table 5
Contribution of spores and the results of Spearman's rank correlation test between hourly and daily concentrations of fungal spores and meteorological parameters (Grinn-Gofroń et al., 2017).

Taxon	Seasonal contribution		T		RH		WS		Precipitation	
	Count	%	Hourly	Daily	Hourly	Daily	Hourly	Daily	Hourly	Daily
Agrocybe	28	0.005	0.005	0.071	0.063*	0.165*	0.029	−0.224*	−0.024	−0.080
Alternaria	8648	1.586	0.359*	0.480*	−0.100*	−0.093	0.091*	−0.152	−0.078*	−0.200*
Chaetomium	108	0.020	0.049*	0.215*	0.085*	0.152	−0.026	−0.288*	−0.030	−0.048
Cladosporium	346,135	63,493	0.511*	0.601*	−0.075*	−0.072	0.121*	−0.152	−0.070*	−0.084
Coprinus	22	0.004	0.006	0.069	−0.013	−0.066	−0.012	−0.026	0.018	0.068
Curvularia	19	0.003	−0.009	−0.020	0.047*	0.262*	0.008	−0.123	0.041*	0.166*
Didymella	175,316	32,159	0.069*	0.268*	0.057*	−0.012	0.025	−0.072	0.002	0.051
Drechslera type	856	0.157	0.218*	0.525*	−0.099*	−0.172*	0.022	−0.066	−0.021	−0.106
Epicoccum	1413	0.260	0.162*	0.169*	−0.077*	−0.038	0.033*	−0.205*	−0.042*	−0.112
Fusarium	30	0.006	−0.083*	0.046	0.181*	0.294*	0.064*	−0.081	0.094*	0.205*
Ganoderma	3586	0.658	0.179*	0.529*	0.183*	−0.086	−0.032	−0.325*	−0.027	−0.201*
Leptosphaeria type	7112	1.305	0.110*	0.138	0.198*	0.130	−0.026	0.125	−0.025	0.416*
Periconia	28	0.005	0.086*	0.182*	−0.057*	−0.035	0.047*	0.014	−0.027	0.010
Phaeosphaeria	448	0.082	0.052*	0.082	0.164*	0.248*	0.005	−0.179	0.035*	0.205*
Pithomyces	76	0.014	0.074*	0.139	−0.026	−0.037	0.025	−0.078	−0.019	0.006
Pleospora	715	0.131	0.083*	0.217*	−0.011	0.183*	0.044*	−0.065	0.001	0.164*
Polythrincium	31	0.006	0.119*	0.398*	−0.066*	−0.146	0.037*	−0.117	−0.040*	−0.185*
Stachybotrys	11	0.001	−0.052*	−0.215*	0.020	0.138	−0.014	−0.056	0.022	0.025
Stemphylium	77	0.014	−0.037*	−0.095	0.011	−0.013	0.019	−0.015	0.019	0.300*
Tilletia	33	0.006	0.107*	0.321*	−0.066*	−0.350*	−0.031	−0.017	0.002	−0.210*
Torula	463	0.085	0.098*	0.301*	−0.083*	−0.400*	−0.016	0.031	−0.029	−0.194*

* $p < 0.05$.

been found in the atmospheric environment with low number. Generally, archaea have one main source - soil, but there also are other habitats like freshwater, freshwater sediment, estuarine sediment, marine water, marine sediment, geothermal system, and symbiosis (Fröhlichnowoisky et al., 2014). At present, abundance, diversity and dispersal of archaea are ill-informed in the atmosphere. However, they have research meaning in every sense, it is a remarkable thing that research their abundance and critical function in diverse natural environments, and that explore their quintessential role in shaping the evolutionary path of life on Earth and their pivotal role in the nitrification process (Cao et al., 2013; Cavicchioli, 2010). Fröhlichnowoisky et al. (2014) made a discussion of diversity and seasonal dynamics of airborne archaea, they detected 435 archaea species that grouped into 57 OTUs with the 16S rRNA gene. In addition, amoA gene was used to study diversity of archaea (Fröhlichnowoisky et al., 2014). *Euryarchaeota* and *Thaumarchaeota* were dominant, and *Thaumarchaeota* accounted for over four fifth which were widespread on Earth and detected in various environments (Pester et al., 2011). In different cities and sampling sites, the result of metagenomic reads of archaea were different, which showed archaea have special distribution and that the species composition was concerned with the airborne sources (Yooseph et al., 2013). Besides, archaea mostly appeared in all coarse samples (> 3 μm), only about one fifth in fine (< 3 μm), exactly, archaea were more susceptible to attach to coarse particles like soil dust particles (Jones and Harrison, 2004). Archaea inherent characteristics can be influenced by factors like RH, WS and temperature, and these factors cause archaea change with temporal variation, such as archaea species show various diversities in different seasons. Meanwhile, local environment is also a variable, the abundance and distribution of archaea in coastal environment owned special physiological types that little were described (DeLong, 1992). Generally, the archaea species richness has multiple linear correlations with these meteorological conditions. As on a long-term monthly basis, the normalized species richness negatively correlated with both temperature and WS, while the relative species richness showed a significant positive correlation with RH and WS. WS was found as the significant factors (negative correlation), although it played a secondary role in both cases. In different conditions, disparate combination of factors will exert unlike influence on archaea distribution, composition and diversity.

In the air, microorganisms have already attracted researchers' attention with their self-characteristics, and their influences on nature and human. Combining with PM, the microbial concentration, size distribution, dominant species, diversity, temporal and spatial variation are point-cuts, through which researchers can have a more particular knowledge of AM and clearly know the relations between PM and AM.

3. Influence factors

3.1. Meteorological parameters

Microorganisms are not invariant in the air, and kinds of their features will change with many factors, to some extent, these factors decide microbial characteristics. Microorganisms live in the air with influence of meteorological parameters, these meteorological parameters have the most significant effect on AM, and multitudinous factors affect various species with different responses. To some degree, meteorological parameters lead the microbial communities and characteristics. Weather conditions have an impact on the production, release, dispersion and deposition of microbes, as well as influence the diversity and number of airborne bio-particles (Li et al., 2017; Şakiyan and Inceoğlu, 2003). The structures of airborne bacteria can show considerable temporal variability, and these shifts were likely to be driven by changes in meteorological conditions (Bertolini et al., 2013; Lighthart, 1997; Polymenakou and Mandalakis, 2013). In many studies, functional relationships between AM and meteorological factors were analyzed, and these factors generally include temperature, RH, WS, precipitation, solar radiation, air pressure (AP) and so on (Table 5).

3.1.1. Temperature

Temperature is assuredly the most important part of the meteorological parameters, because the span of temperature is so great in the earth and microbes have different distribution with their optimal living temperatures. For the influence mechanism of temperature on AM, researchers still haven't a much clear cognition, but through relevant articles, there is a preliminary comprehension. The effects generally include two main parts: i) directly, on microbes themselves, ii) indirectly, on other parameters. The former refers to that temperature promotes or restrains microbial release and growth, while the latter

says that temperature influences other parameters like cross-ventilation which decides the suspension and diffusion of microbes. Hoeksma et al. (2015) studied the effects of temperature on *E. coli*, *M. synoviae* and *E. mundtii* by observing bacterial decay and showed that temperature assuredly had influence on bacteria (Hoeksma et al., 2015). In many reports, temperature was thought having a significant positive correlation with bacteria and fungi, and high temperature was the optimal condition for fungal spores, while low temperature was a limiting factor for fungal development (Almaguer et al., 2014; Quintero et al., 2009; Rivera-Mariani and Bolaños-Rosero, 2012; Smets et al., 2016). Nonetheless, there was a viewpoint that cold air may facilitate the release and transportation of bacteria. The above conclusions manifested in different regions, for different microorganisms, temperature had inconsistent impacts on them, as temperature showed a negative correlation to archaea diversity, and temperature indirectly had a close relationship with archaea diversity by directly influencing soil conditions which were main sources of archaea (Fröhlichnowoisky et al., 2014; Sousa et al., 2008; Zhen et al., 2017). When $PM_{2.5} > 300$, a negative relationship was observed between AM and temperature, this result might because high temperature enhanced toxic compounds' release and promoted their chemical reactions which occurred on particulate surfaces (Alghamdi et al., 2014; Gao et al., 2016b). Generally, when temperature rose, viral survival rate decreased as temperature could affect viral proteins even genome, famously, high temperature could cause protein inactivation (Tang, 2009). Some microbes had high abundance at high temperature, some at low, but most of them occurred at moderate values of the air temperature, appropriate temperature facilitated the release and growth of microbes so that it could cause the increase of microbial concentration (Grinn-Gofroń et al., 2017). Therefore, the impact of temperature on AM can't be accurately summarized, it needs to take into account the different species and scale of AM and the interaction of other parameters. The linear correlations between AM and temperature alone are good, and in the researches of the multiple linear regressions between multiple parameters, temperature shows more influence.

3.1.2. RH

RH is the ratio of the partial pressure of water vapor to the equilibrium vapor pressure of water at a given temperature. With analogous function as temperature, RH has a significant impact on airborne microbial concentration, diversity, composition and so on, and the bonding effects combining with temperature are most likely to be produced and are more obvious (Yan et al., 2016). In previous studies, single or several microorganisms were researched to explore the relation of RH, and most reports found that microbial release level increased with decreasing RH. *Alternaria alternata*, *Cladosporium*, *Drechslera type*, *Epicoccum*, *Pithomyces*, *Polythrincium*, *Sphaerotheca pannosa*, *Erysiphe pisi*, *Erysiphe graminis*, influenza A virus and other AM were reported had negative correlation with RH (Ianovici, 2016; Sadys et al., 2015; Schaffer et al., 1976; Zhen et al., 2017). There was a conclusion that the conidia were released when RH decreased and the largest peaks in spore release were achieved when RH reduced in the range of 60 to 40% (Jones and Harrison, 2004). However, the discrepancies of the conclusions were found, a high humidity values, about 70–80%, particularly assisted the release of basidiospores and ascospores, high RH could trigger spore release thus increases the abundance of spores and improve archaea diversity (Fröhlichnowoisky et al., 2014; Gabey et al., 2010; Leyronas and Nicot, 2012; Tang, 2009). Despite high RH was benefit to bacterial release and growth, it might also reduce the viability of bacteria (Mouli et al., 2005). By this token, the influence of RH on microbial release is not clear, and different microbes have diverse reactions even no reaction on RH (Knudsen et al., 2017). Through these data, the conclusion that RH can affect microbial release and concentration in the air is true, and negative effect is a main part considered to be convincing. High RH levels postponed anther dehiscence and pollen dispersion as well as prevented dust rising from wet surfaces, as mentioned above, microbes entranced into the atmosphere depending on attaching on the dust and particles, thus decreasing dust reduced microbial suspension (Sousa et al., 2008). Besides, high RH will augment the probability of deposition because suspended particles absorb ambient moisture leading increasing particle weight and size (Zhen et al., 2017). These reasons may illuminate why the majority of microbes are existing in the air at low RH.

3.1.3. WS

As an important parameter of meteorological parameters, WS plays an indispensable role in affecting ambient microbial characteristics. The average WS, maximum and minimum WS have different impacts, in which the former operates over a longer period while the latter over a short. Average WS was more important than maximum WS on the whole, while maximum WS may signally influence release and resuspension of dry spore (Li and Kendrick, 1995). High WS can bring more microbes into the near surface atmosphere and favor the suspension of microorganisms which will lead a high concentration of microorganisms (Jones and Harrison, 2004; Savage et al., 2012). Nevertheless, in another aspect, high WS has a quite strong atmospheric dilution effect that will decrease ambient microbial levels even though it can bring in exogenous microbes (Sabariego et al., 2000; Stennett and Beggs, 2004; Zhong et al., 2016). In these studies, author didn't found linear correlations and/or significant relation of WS with AM (Li et al., 2011; Sousa et al., 2008), while the different results of significant relations were found in some reports might due to study regions, microbial sources, inhibitory effect of microbial internal components and other factors' cooperation (Crandall and Gilbert, 2017; Grinn-Gofron and Strzelczak, 2011; Harrison et al., 2005; Ma et al., 2011; Mouli et al., 2005; Raisi et al., 2010; Wu et al., 2012). In multiple linear regression, two variable sets, average temperature and RH with WS, WS just played a secondary role in archaea diversity (Fröhlichnowoisky et al., 2014). From these relevant articles, WS has different or no impacts on microbial concentration, composition and other characteristics. In addition to WS itself, other factors, such as microbial types, study region etc., can influence the effect on it, so the effect mechanism of WS on microbes individually should more further researches.

3.1.4. Others

Except for the main three factors mentioned above, there are some other parameters play a role in influencing microbes. Meteorological parameters as the part of microbial living environments, they inevitably affect AM. Rain is widely known to clearing ambient environments by removing aerosol particles which are microbial carriers, in that sense, precipitation theoretically will reduce the concentration of AM, but in many researches precipitation increase airborne microbial concentration. Raindrops were significant for dispersal of slimy spores, which resisted wind dislodgement and made a dramatic increase in some spores, and due to the hit and shake of the air and leaves caused by the droplet, the chance of lifting spores from the surface into air was enhanced (Jones and Harrison, 2004; Li and Kendrick, 1995). Rain could enrich air humidity which may be a sufficient condition for the growth of microorganisms, and the vibrations caused by droplets may facilitate the aerosolization of ground microorganisms, meanwhile, rain could enhance ambient moisture, which enhancing production and release of some AM, so precipitation played a promoting role in the concentration and release of AM (Crandall and Gilbert, 2017; Heo et al., 2014). Different from precipitation, solar radiation mostly has a negative relation with AM because it may provide an unfavorable condition for the growth and survival of airborne microorganisms, and it can kill these microbes with microbicidal efficacy of UV. When solar radiation became strong, the UV generally strengthened which would enhance microbicidal ability (Li et al., 2017; Noakes et al., 2004; Raisi et al., 2012). Besides, there is another common meteorological parameter, AP. Increasing AP reflected there was cold air entrance which could improve air diffusion conditions. Cold air can facilitate the release and

transportation of bacteria, and can also quickly dilute bacterial concentrations, so the eventual results, negative or positive relation, are decided by the stronger one of the two. AP was the dominant factor shaping bacterial communities in winter and detected the correlation was negative between AP and bacterial abundance (Zhen et al., 2017). On the contrary, *Exiguobacterium*, *Citricoccus*, *Nesterenkonia*, *Mycoplana*, *Bacterium*, *Maris* were positively related with AP (Ma et al., 2011). Therefore, different conditions bring diverse effects. Actually, the effects of meteorological conditions on microbes are additive, not independent. Hence, considering the impact of meteorological parameters on AM, the synergistic effect of many factors is more meaningful.

3.2. PM

AM mostly exist in the form of aerosol and rarely of individual, so they generally attach on PM. As microbial carriers, particles are considered as one of the important influence factors that decide microbial traits. However, in some reports, relations between AM and PM were not found, and the reason might be that some microbial weights were too light to detected by the quantification method, and the big discrepancy of shapes between PM and AM was also one of the reasons (Raisi et al., 2010; Sousa et al., 2008). Under certain conditions, a constant relationship between biological and total PM would be found, in fact, these conditions were unstable thus the correlations were not strong. Nevertheless, researchers found a positive relation between protein and coarse PM fraction, not in the fine fraction, and the positive relation existed between PM_{10} and Gram-negative rods (Boreson et al., 2004; Degobbi et al., 2011; Wu et al., 2012). Different AM have diverse abundance and size-distribution in different size PM, therefore many different AM show significant difference among samples of PM which mirror the different correlation with PM. *Malassezia*, *Fusarium* and *Alternaria* were more abundant in $PM_{2.5}$, PM_{10} and TSP samples, respectively, which showed microbial types might play an important role in associating microbial composition and diversity with PM, and the main proportion of fungi (aerodynamic diameters between 2.1 and 3.3 μm) increased with increasing mass concentration of all three inhalable sizes of PM (PM_1, $PM_{2.5}$, PM_{10}) (Raisi et al., 2012; Yan et al., 2016). A unanimously negative correlation between cultivable bioaerosols with $PM_{2.5}$ was observed and the reason of that was $PM_{2.5}$ usually contained soot, metals, and secondary inorganic components which were harmful to bioaerosol (Gao et al., 2016a). However, at the low-haze station, different from above conclusion, PM_{10} was positively related to bioaerosol showing that particles indeed could carry microbes and affect them under suitable conditions. Particulate characteristics in some degree decide the relationship between PM and microbes, but the definite mechanisms are certainly not clear, this could be caused by that the effects of other parameters are great thus the influence of PM on microorganisms is not obvious.

3.3. Sources

To some extent, sources of microbes, both local air mass and long distance air masses, decide the airborne microbial communities (Innocente et al., 2017). AM are mainly derived from local source, so the sampling sites are important influence factors of microbial communities, which cause the bioclimatic characteristics of the sampling environment becoming one of the hot research points. AM almost come from other environments, because atmosphere just is a temporary residence not origin, this characteristic lead to air microbial communities greatly depend on microbial sources, and relative contribution from these sources may determine the airborne microbial composition and temporal variability (Bertolini et al., 2013). Local sources played a leading role in shaping airborne bacterial communities and had a larger impact than those caused by meteorological conditions. Besides, local sources influenced microbial seasonal variation, because in different seasons, local sources always were dominant among the changed dominant sources which affected temporal variability of airborne microbial communities (Bowers et al., 2011; Gandolfi et al., 2015; Zhen et al., 2017). Also like in the built environments, there are several kinds of the sources of microbes, and the intensities of these sources are different leading to different indoor microbial communities (Prussin and Marr, 2015). As mentioned above, the characteristics of microbes have some discrepancies in different environments, and this can account for the importance of sources on affecting air microbes. Every environment has their particular and primary sources, like indoors, the dominant source may be the human skin and oral cavity (Blais-Lecours et al., 2015; Stetzenbach et al., 2006), outdoors be the vegetation and soil, inland be the dust (Kellogg and Griffin, 2006; Prospero and Lamb, 2003), and in the marine may be the sea water, these diversities of sources provide discrepant proportions for AM, and the ultimate communities certainly have differences.

3.4. Othersc

AM have influences on humans, in turn, anthropic activities as well as decide microbial communities and other features. Human epidermis and alimentary tract carry 10^{12}–10^{14} microorganisms, thus in the indoor environments human might be the greatest sources of bioaerosol (Luckey, 1972). In indoors environments, some microbial species were brought in by heavy traffic and increased human activities, and the flux of the crowd and human occupancy might be the most crucial factors affecting the total number and community structure of bioaerosol, especially in poorly ventilated or heavily occupied environments (Adams et al., 2015; Bogomolova and Kirtsideli, 2009; Fang et al., 2007). In outdoor environments, the more pedestrian volume is, the more bioaerosol are observed. Therefore, human activity is one of the crucial factors.

Besides, air pollutions are the influence factors which worth mentioning. Common air pollutions include SO_2, O_3, NO_x and so on, though there is a view that air pollutions' effect is smaller than other factors, they still have different effects on AM. Ozone is notoriously difficult to control and famous for its oxidation, in high concentrations ozone, AM may be killed by the oxidation of ozone, and these processes can completely inhibit or effectively reduce the growth of fungi, but low O_3 concentration has no evident effect on the AM (Whangchai et al., 2006). Ozonic germicidal properties let it be toxic to AM, so ozone was found showing a negative effect on AM (Gao et al., 2016b; Ho et al., 2005). But *Cladosporium* and *Alternaria* spore abundance was observed having a positive dependence on O_3, and positive statistically significant correlation coefficients between O_3 and *Aspergillaceae* and the total fungal spores were found (Adhikari et al., 2006; Grinngofroń et al., 2011). However, Sousa et al. (2008) didn't discover ozone have significant influence on the concentration of fungal spores (Sousa et al., 2008). The difference may be caused by the neutralization of other factors and the distinction of microbial types. SO_2 and NO_2 usually were considered as toxic pollutants to microorganisms (Abdel Hameed et al., 2012), theoretically playing an obvious negative relation with AM, but according to research by Grinngofroń et al. (2011), they thought there were no or weak negative significant relation between SO_2, NO_2 concentrations and the fungal spore concentrations (Grinngofroń et al., 2011). And Gao et al. (2016b) observed that at different times, the effects on bioaerosol were changed with a positive relationship in the morning and evening, but a negative relationship at mid-day (Gao et al., 2016b). SO_2 and NO_2 and other air pollution generally have no direct impact on the AM, and they have more interactions with other factors thus affect bioaerosol.

According to influence factors discussed above, the correlation between them and airborne microbial characteristics are concluded in Table 6. Except for the above factors, there are other factors of AM that can be researched with their impact types and mechanisms. These factors are not independent but interactive which may be interoperable or antagonistic. Because of effects of these parameters, the AM own

Table 6
Correlation between influence factors and airborne microbial characteristics.

Influence factors	Concentration		Size distribution		Diversity		Variation		Type	
	Correlation	Reference	Correlation	Reference	Correlation	Reference	Correlation	Reference	Correlation	Reference
Temperature	⊕	(Dong et al., 2016)	⊖	(Dybwad et al., 2014)	⊖	(Agabou et al., 2013)	⊕	(Gao et al., 2016a)	⊖	(Seifried et al., 2015)
RH	⊕	(Almaguer et al., 2014)	⊖	(Li et al., 2017)	⊖	(Abdel Hameed et al., 2012)	⊕	(Alghamdi et al., 2014)	⊕	(Sousa et al., 2008)
WS	⊕	(Jones and Harrison, 2004)	⊗	–	⊖	(Fröhlich-Nowoisky et al., 2014)	⊖	(Sabariego et al., 2000)	⊖	(Gandolfi et al., 2015)
Solar radiation	⊖	(Lee et al., 2007)	⊖	(Li et al., 2017)	⊗	–	⊖	(Raisi et al., 2012)	⊗	–
Precipitation	⊖	(Heo et al., 2014)	⊗	–	⊗	–	⊖	(Quintero et al., 2009)	⊖	(Crandall and Gilbert, 2017)
PM	⊖	(Degobbi et al., 2011)	⊗	(Yamamoto et al., 2012)	⊖	(Kumari et al., 2016)	⊕	(Yan et al., 2016)	⊖	(Bertolini et al., 2013)
Sources	⊖	(Goudarzi et al., 2014)	⊕	(Bowers et al., 2013)	⊖	(Bowers et al., 2012)	⊕	(Fang et al., 2016)	⊕	(Bowers et al., 2011)
Air pollutions	⊖	(Gao et al., 2015)	⊖	(Liu et al., 2017a)	⊗	–	⊖	(Gandolfi et al., 2015)	⊖	(Grinnogfroń et al., 2011)

"⊕": have significant correlation.
"⊖": have correlation.
"⊗": no correlation.
"–": no data.
PS: the correlation described in the table is primary, not absolute.

variability and diversity. These factors can give researchers study orientations, if they want to clearly know the AM, these factors with their effects should be researched.

4. Perspectives

According to the above summarized in this review, advance has already been made for the understanding of microbial composition and their influence factors, but there are many other information waiting to be found and understood. Based on the general consideration above, several research gaps are listed below:

(1) Size decides the inhalation and deposition of particles, which is a key factor causing diseases and influence climate. With kinds of AM in particles, the potential hazard and influence are more worth exploring, hence, on size-segregated particles, airborne microbial compositions and traits can be subsequent research objects. Multi-stage sampler can achieve particulate separation, and the right sampler should be chosen for the experiment based on the sampling environment and conditions. About detection of AM, culture-independent method is a better choice because the vast majority of AM are non-cultivable. Molecular biological techniques, such as high-throughput sequencing technology like 16S rRNA sequencing, metagenomics sequencing and Illumina MiSeq sequencing (Gao et al., 2017a), and electrophoresis technology can be used for analysis for their high efficiency accuracy.

(2) AM are not invariable on PM, many factors influence their characteristics, and relationships between the two are necessary to study clearly. At present, the influence mechanisms of these factors are ill-defined, researches just measured temporary relationship at a certain circumstance. In order to take better defense and monitoring measures for AM, stable relations should be established between influence factors and AM, and influence mechanisms should be understood. Further studies can adopt control variable method and appropriate simulation to research influence mechanisms, and create optimal multivariate linear regression model to synthesize multi-factors' effects.

(3) PM can cause a wide range of diseases that reduce human life, and some AM with pathogenicity also affect human health, so detailed knowledge of impact of AM on human health is of primary significance. Nowadays, health risk assessment of exposure to PM and other pollutions in particles are hot research points (Balwant et al., 2015; Huang et al., 2014; Wang et al., 2017; Zhai et al., 2016), but less attention about AM. The relevant research contents about AM can combine with PM because particles as carriers will affect microbial traits. Getting the accurate risk level can provide a basis for people to better take protective measures and plan solutions. Researchers generally just get several sets of microbial data in one study, which are not enough to do health risk assessment, so we can choose simulation methods to do this. As a statistical test method, Monte Carlo simulation method is applied in many experiments and simulation with its advantages that can deal with non-linear, large-wave problems, get more accurate and reliable results by a lot of path simulation scenarios and so on (Safadi et al., 2015; Smid et al., 2010). Hence, Monte Carlo simulation method is a choice for health risk assessment of AM over PM.

(4) Like some researchers study patience and resistance for some matters of microbes in soil and/or water, the similar contents also can extend to the AM. Through source apportionments we can confirm some AM experience long-distance transportation and long-time suspension, but they still maintain survivability evidencing AM own resistibility to some hazardous substances in the air. These properties can be used to protect environment rehabilitating damaged ecosystems and utilized for biological monitoring and biological purification. Relevant researches can start from one or two dominant and representative species then conducted follow-up

studies.

These research contents talked above which are expanded beyond AM themselves are prolongable, there are other contents, like systematic source apportionments and applications of AM in circulation of S/N in nature, still waiting to be researched.

5. Conclusion

Microbes are pervasive in atmosphere, taking into consideration that the effects of AM on biological health and natural climate, their various characteristics should be observed thoroughly. In this review, we summarized airborne microbial composition, concentration, size distribution, diversity and so on, and found bacteria were the most widely studied components. Besides, influence factors of microbes were also discussed because they could largely affect airborne microbial integral structure. Nevertheless, detection methods of microbes were most culture-dependent methods with limited capability, though molecular biological technique already has been used, it don't be extensively used, so in later studies, the optimal ways should be considered first. The influence mechanisms of above factors are not completely clear, so more relative researches should be conducted about AM in future which can bring us more information. Present research contents are just some parts of AM, besides, the development of research methods, the health risk assessment of exposure to AM, and the utilization of some AM are also the contents with potential and value, and future researches of AM can be based on these. Although current studies are not adequate, now more focuses are concentrated on airborne microbes, so we can gradually get a more comprehensive acknowledgement about them.

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