A review of the emergence of antibiotic resistance in bioaerosols and its monitoring methods

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1 Introduction

Bioaerosols refer to airborne biological particles, including bacteria, fungal spores, pollen, viruses, and their derivatives, and these particles may result in adverse effects on human health (Douwes et al. 2003; Yoo et al. 2017). Bioaerosols are ubiquitous in the environment, and small microorganisms account for 30–80% of the particulate matter (PM); the remaining PM compositions include organic carbon, geological components, ions (nitrates and sulfates), elemental carbon, pollen, and atmospheric metals (Fröhlich-Nowoisky et al. 2016; Hyde and Mahalov et al. 2020). Because fragmented biological particles can move from the Earth’s surface into the air (Fröhlich-Nowoisky et al. 2016; Yoo et al. 2017), bioaerosols play an important role in atmospheric physical and chemical processes such as the global climate system (scattering and absorbing radiation) and cloud
microphysical processes (cloud droplets, ice crystals, and precipitation) through global transport (Fröhlich-Nowoisky et al. 2016; Gollakota et al. 2021). Particularly in pristine air over vegetated regions, bioaerosols are likely to be an essential factor regulating precipitation formation and vice versa (Fröhlich-Nowoisky et al. 2016). Interactions among ultraviolet (UV) radiation, photooxidants, pollen, and various air pollutants during bioaerosol transportation may lead to additional physicochemical transformations and the biological aging of bioaerosols (Yoo et al. 2017; Xie et al. 2021).

The emergence and spread of bioaerosols in indoor and outdoor environments have become worldwide public health issues that cause adverse events such as severe acute respiratory syndrome (SARS-CoV-2), the H1N1 influenza pandemic, and allergic reactions (Haig et al. 2016; Chen et al. 2019; Li et al. 2021a). According to previous studies (Heald and Spracklen 2009; Woo et al. 2018), bacterial and fungal species are predominant in bioaerosols, and estimated yearly amounts of 1.4–4.6 and 28–50 Tg are emitted into the Earth’s atmosphere, respectively. Thus, large levels of microbes can be present in bioaerosols and have the potential to greatly impact human health and the climate. Currently, impaction, liquid impingement, and filtration methods are commonly used for collecting bioaerosols from air, and their biological properties are identified using culture (liquid or solid culture media) and nonculture (captured suspended air using filtration)-based methods such as microarray, real-time qPCR, and sequencing technology (Fröhlich-Nowoisky et al. 2016; Yoo et al. 2017). Using these molecular approaches, bacteria such as *Bacillus, Pseudomonas, Staphylococcus, Micrococcus*, and *Acinetobacter* have been identified as predominant in bioaerosols (Mentese et al. 2009; Du et al. 2018; Gao et al. 2018b; Yu et al. 2021), and the dominant fungi are *Penicillium, Aspergillus, Candida, Cladosporium* and *Rhodotorula* (Mentese et al. 2009; Kumari et al. 2016; Frączek et al. 2017; Dai et al. 2020; Xie et al. 2021).

In recent years, antibiotic resistance has received considerable attention as an emerging cause of a global public health crisis (WHO 2019). The World Health Organization (WHO) declared that the emergence of antibiotic resistance is a complex problem driven by many interconnected factors (WHO 2019). The overuse and misuse of antibiotic drugs in human therapeutic and livestock settings have caused the development and dissemination of antibiotic resistance genes (ARGs) and bacteria (ARBs) in different environments, such as soil, wastewater, livestock, compost, lakes, oceans, and sediment (Ma et al. 2015; Tiedje et al. 2019; Yoo et al. 2020). The emergence of ARGs could significantly increase the spread of antibiotic resistance, particularly via mobile genetic elements (MGEs), such as plasmids, integrons and insertion sequences (Karkman et al. 2018). Therefore, obtaining baseline and background data for antibiotic resistance in the environment is needed to better understand the environmental behavior of ARGs and evaluate the potential risks that ARGs pose to human health (Yang et al. 2018b; Tiedje et al. 2019; Yoo et al. 2020).

Diverse antibiotics are used simultaneously in various industrial and environmental areas (Table 1). Tetracycline, macrolide-lincosamide-streptogramin (MLS), quinolone, beta-lactam, sulfonamide, and aminoglycoside antibiotics are widely used in hospitals (Wang et al. 2019; Ouyang et al. 2020; Li et al. 2021b), and the tetracycline, sulfonamide, quinolone, macrolide and aminoglycoside families are broadly used in farming areas such as agricultural and livestock farming (Song et al. 2021). This is because antibiotics such as beta-lactam, sulfonamide and tetracycline are widely used to treat diseases in humans and animals (Liang et al. 2020). In addition, ARGs such as sul1, sul2 (sulfonamide), tetA, tetG, tetW (tetracycline), mfpA (quinolone), ermB, ermG, ermF (MLS), blaTEM-1, blaAmpc, and blaOXA-1 (beta-lactam) are dominantly detected in wastewater treatment plants (WWTPs), but the underlying reasons are poorly understood because the characteristics and frequency of antibiotic use vary from region to country (Bylinski et al. 2019; Han et al. 2018; Han and Yoo 2020). According to the WHO report on the surveillance of antibiotic consumption (WHO 2018), the antibiotics most commonly used in Africa and the Americas are quinolone, MLS, sulfonamide, and beta-lactam. However, the European, Western Pacific, and Eastern Mediterranean regions exhibit high tetracycline and beta-lactam antibiotic consumption. Aminoglycoside-based antibiotics are usually used for infections with gram-negative bacteria, such as *Pseudomonas* spp., and a small number of gram-positive bacteria (Becker and Cooper 2013). Beta-lactam antibiotics have excellent efficacy for the treatment of bacterial
infections and are most widely used in clinical practice (Bush and Macielag 2010). MLS is mainly used for the treatment of skin and respiratory infections and patients with beta-lactam antibiotic allergies (Labro 2004). Tetracyclines have been used extensively to treat bacterial respiratory, urogenital tract and periodontal diseases and Lyme and rickettsial diseases in humans (Roberts 2002), and sulfonamide-based antibiotics are used to treat respiratory, skin, and central diseases and are also widely applied in veterinary medicine (Roberts 2002). The occurrence of antibiotic resistance is a natural phenomenon that is believed to be the result of the continuous evolution of bacteria to resist antibiotics (Allen et al. 2010; Blair et al. 2015). However, because antibiotic resistance produces relatively long-lasting residues due to naturally contained in liquid droplets, antibiotics used for the treatment of human and animal diseases have high potential for undergoing consistent accumulation, resulting in serious antibiotic pollution to environmental media, such as soil, water, and air (Prussin et al. 2017; Gwenzi et al. 2022).

Extensive studies have attempted to identify ARGs and ARBs in wastewater, soil, sediment, compost, and manure environments with the aim of obtaining a better understanding of the antibiotic contamination

Table 1 Antibiotic mechanism and target subject

| Antibiotic mechanism                  | Antibiotic    | Target                      |
|---------------------------------------|---------------|-----------------------------|
| Cell wall synthesis                   | Aminoglycoside| Cycloserine                 |
|                                       | Peptide       | Vancomycin                  |
|                                       |               | Bacitracin                  |
|                                       | Beta-lactam   | Penicillin                  |
|                                       |               | Cephalosporin               |
|                                       |               | Carbapenem                  |
| Cytoplasmic membrane structure        | Peptide       | Polymyxin                   |
| Protein synthesis                     | 50S inhibitors| MLS                         |
|                                       |               | Erythromycin                |
|                                       |               | Azithromycin                |
|                                       |               | Clindamycin                 |
|                                       |               | Lincomycin                  |
|                                       | Phenicol      | Chloramphenicol             |
|                                       | Tetracycline  | Tetracycline                |
|                                       |               | Doxycycline                 |
|                                       | Aminoglycoside| Spectinomycin               |
|                                       |               | Streptomycin                |
|                                       |               | Gentamicin                  |
|                                       |               | Kanamycin                   |
|                                       |               | Amikacin                    |
|                                       | tRNA Aminoglycoside | Mupirocin     |
|                                       |               | Puromycin                   |
| Folic acid metabolism                 | Trimethoprim  | Trimethoprim                |
|                                       | Sulfonamide   | Sulfonamides                |
| Inhibition of nucleic acid synthesis  | DNA gyrase    | Quinolone                   |
|                                       |               | Nalidixacin acid            |
| RNA elongation                        | Quinolone     | Ciprofloxacin               |
| DNA-directed RNA polymerase           | Anthracycline | Novobiocin                  |
|                                       | Ansamycin     | Actinomycin                 |
|                                       | MLS           | Rifampin                    |
|                                       |               | Streptovaricin              |
| Human and animal                      |               | Human and animal            |
| Human                                 |               | Human                       |
| Human and animal                      |               | Human and animal            |
of the environment (Xu et al. 2016; Chen et al. 2019; Yoo et al. 2020; Li et al. 2021a). Although air pollutants have attracted interest due to their direct effects on public health, the studies on the health-related effects of air pollution conducted to date have relied heavily on the PM mass concentrations without considering biological parameters such as ARGs or ARBs (Li et al. 2018). Airborne ARBs and ARGs exhibit markedly higher exposure through the respiratory tract than skin contact and can be inhaled into the respiratory tract through the human mouth as droplets and aerosols (Wang et al. 2019). In addition, antibiotic resistance can be caused by the short-term release of bioaerosols from coughing, sneezing, conversation, inhalation, and exhalation (Ian and Gerba 2015; McEacharan et al. 2015; Gao et al. 2018a; Gaviria-Figueroa et al. 2019; Han and Yoo 2020; Gwienzi et al. 2022; Xie et al. 2021). ARGs in bioaerosols may subsequently propagate or become further altered through MGEs and interaction with airborne microbes (Xie et al. 2021; Zhou et al. 2021). However, airborne microbial communities, unlike those in soil and aquatic environmental systems, have not been well characterized due to the difficulty in obtaining sufficient biomass. Additionally, the occurrences and diversities of ARGs, ARBs, and MGEs in the air environment remain to be extensively investigated (Gauthier-Levesque et al. 2016; Li et al. 2016, 2018; Yang et al. 2018a).

This review focuses on the current research trends in the field of antibiotic resistance in bioaerosols, including state-of-the-art technologies and advances in bioaerosol detection for effective monitoring and risk management. The present work provides information on the potential risk factors associated with antibiotic resistance in bioaerosols, their impact on human health, and appropriate methodological approaches.

2 Antibiotic resistance in bioaerosols

Most previous studies focused on aquatic and soil environments because these are regarded as important reservoirs of ARGs due to their direct relationship with human activities. Although airborne ARGs may be linked to a known source, previous studies have consistently suggested that the microbial community in the source is not the same as that in the air environment (Lin et al. 2018; Yoo et al. 2020). In particular, the proportions of species of microorganisms appear to differ greatly among different environments. A study of aerosols in compost facilities (Veillette et al. 2016) showed that the proportions of Methylobacterium species are higher in air samples than in compost samples. In addition, Legionella spp. are dominant in a carcass compost facility but have not been identified in compost samples. A recent study showed that aerosolized gram-negative (P. aeruginosa) and gram-positive (S. aureus, S. suis) bacteria can be viable and survive in harsh atmospheric environments (Gauthier-Levesque et al. 2016; Perrott et al. 2013). Pathogens and ARBs in bioaerosols are believed to interact with each other. It has been reported that potential pathogens such as Elizabethkingia, Klebsiella, Delftia, Pseudomonas, and Stenotrophomonas contain ARGs and can cause meningitis, pneumonia, bacteremia, corneal inflammation, and eye antibiotic resistance. In addition, potential pathogens such as E. coli, P. aeruginosa, P. mirabilis, S. aureus, S. sciuri, and S. xylosus, which are generally detected in the air, can contribute to the airborne propagation of ARBs, and the transition of antibiotic resistance through horizontal gene transfer (HGT) has also been observed (Kalwasińska and Burkowska 2013; Yu et al. 2021).

Highly aerosolized bacteria are thought to have multidrug-resistant capacities (Dijkshoorn et al. 2007), and the increase in human respiratory diseases is potentially linked to the prevalence of ARBs and ARGs arising through HGT (Wang et al. 2014). Although information on direct ARG infection through bioaerosols is limited, it has been continuously reported that inhalation through the respiratory tract is the main route through which ARGs enter the human body (Wei and Li 2016; Wang et al. 2019; Asadi et al. 2020). The detected airborne ARGs usually originate from the direct emission of ARB or their reaerolization due to natural winds or various human activities (Li et al. 2018). The inhalation of airborne ARGs is generally affected by the PM concentration, ARG HGT, and environmental deposition (Jin et al. 2021; Xie et al. 2021). Previous studies have suggested that airborne PM is a unique pathway for the environmental dissemination of ARGs, and the results show that multiresistant plasmids of pTAir-3 (containing 26 HGT and 10 ARGs), which promotes HGT, can potentially spread antibiotic
resistance via conjugative transfer-induced inhalable PM (Liang et al. 2013, Zhou et al. 2021). In addition, PM can selectively increase the pathogen levels, and such pathogens are more likely to rapidly spread antibiotic resistance. The daily intake (DI) of ARGs, such as those that induce resistance to beta-lactam (bla<sub>CTX</sub>, bla<sub>TEM-1</sub>), tetracycline (tetA, tetB, tetM), sulfonamide (sul1, sul2, sul3), and MLS (ermB, ermC), through PM is approximately 10<sup>2</sup>–10<sup>8</sup> copies/day, and a similar DI (10<sup>4</sup>–10<sup>7</sup> copies/day) of ARGs occurs through drinking water, indicating a high risk of ARG inhalation through PM in bioaerosols (Xie et al. 2018; Li et al. 2020a; Liang et al. 2020). ARGs in inhaled bacteria can be lost or decomposed due to growth or reduction, but their effects remain harmful if transferred to native human bacteria because HGT can cause resistance in other bacterial groups and pathogens (Liang et al. 2020; Zhou et al. 2021; Gwenzi et al. 2022).

Unfortunately, there remain gaps in our knowledge of the airborne ARG pollution profiles and their inhalation-related health impacts because obtaining sufficient amounts of bioaerosols for ARG identification and further quantification is challenging (Usachev and Agranovski 2012). Therefore, in this review, studies of antibiotic resistance in indoor and outdoor environments were comprehensively analyzed and summarized. Although research on antibiotic resistance in the atmospheric environment remains in its infancy, this review attempts to provide overall information on the status, indicators and types of antibiotic contamination in various indoor and outdoor atmospheric environments.

2.1 Indoor environments

Anthropogenic antimicrobial chemicals and airborne microbes interact with each other in indoor buildings or their occupants. Despite the existence of multiple sources of indoor ARBs and ARGs, the increasing use of antibiotics for personal care is suspected of being responsible for the spread of antibiotic resistance in indoor environments. Human activities such as salivary discharge, sneezing, dermal contact, and inhalation processes (Gilbert et al. 2010; Zhao et al. 2021) can also strongly affect the airborne ARG composition and thus lead to potential mutual exposure among different individuals. Previous studies have also suggested that tetracycline resistance gene-carrying microbes are concentrated in different human organs (e.g., skin, oral, urogenital, and gastrointestinal organs) and can easily spread into atmospheric environments through skin contact, respiratory, and sternutation processes (Adams et al. 2015; Pal et al. 2016). The predominant ARGs in indoor environments primarily confer beta-lactam, multidrug, and tetracycline resistance, whereas those conferring multidrug, aminoglycoside, and tetracycline resistance are the most predominant ARGs in outdoor environments. The indoor environment is usually affected by the air and floor dust supplied by ventilation (Hospodsky et al. 2012). Due to ventilation, indoor and outdoor air and suspended matter exhibit a mutual exchange, and the ARG abundances in indoor air account for an average of 52% of outdoor air (Zhou et al. 2021). However, one thing to note in indoor environments is that ARGs can be strongly produced under the influence of HGT, which can be increased by various stresses, including malnutrition in indoor environments, DNA damage, and exposure to human-used antibiotics (Ghosh et al. 2015; Gwenzi et al. 2022). Interestingly, stressors such as halogenated organic chemicals (e.g., antimicrobials), metals or nanoparticles are likely to trigger HGT and the dissemination of resistance to multiple chemicals, including antibiotics, through MGEs (Chen et al. 2022; Gwenzi et al. 2022). In contrast, some other stressors, such as desiccation, are unlikely to trigger HGT.

The research on ARGs in indoor environments remains insufficient, and ARGs need to be analyzed by considering various indoor environmental factors in the future. Temperature and humidity are currently considered major factors, but their interaction with the indoor microbiome and their impact on heavy metals limit the effects of these factors.

In this study, hospitals, laboratory buildings, healthcare facilities, and downtown facilities, such as offices, homeless shelters, wet markets, kindergartens, and university campuses (Table 2), were considered indoor environments.

2.1.1 Hospitals and healthcare facilities

Hospitals and healthcare facilities are the most common places in which antibiotics are applied, and the use of antibiotics may be the main reason for the high rate of ARGs in these settings (Wang
| Target environment      | Country | Method | Antibiotics                                      | Type of ARGs                                      | References       |
|-------------------------|---------|--------|--------------------------------------------------|--------------------------------------------------|------------------|
| Indoor Urban Hospital   | Canada  | PCR    | Tetracycline, Macrolide                          | tetG, ermF, ermX, sul1, sul2, sul3, tetA, tetC, tetT, tetQ, tetW, qnrS, ermA, ermB, ermC, blaTEM, blaDHA, blaOXA | Gilbert et al. (2010) |
|                         | China   | RT-qPCR| Sulfonamide, Tetracycline, Quinolone, Macrolide, β-lactam | blacTX-M, mecA, blaTEM, blaOXA-23, blaOXA-24, mecA | Wang et al. (2019) |
|                         | Iran    | PCR    | β-lactam                                         | blacTX-M, mecA, blacTX-M, mecA, blacOXA-23, mecA | Mirhoseini et al. (2016a) |
|                         | Iran    | PCR    | β-lactam                                         | blacTX-M, mecA, blacTX-M, mecA, blacOXA-23, mecA | Mirhoseini et al. (2016a) |
| Laboratory              | China   | RT-qPCR| Sulfonamide, β-lactam, Tetracycline, Multidrug, Aminoglycoside, MLSB | blacOXA-23, blacOXA-24, blacOXA-51 | Shamsizadeh et al. (2017) |
|                         | China   | HT-qPCR| Sulfonamide, β-lactam, Tetracycline, Multidrug, Aminoglycoside, MLSB, Multidrug, β-lactam, Vancomycin | blacOXA-23, blacOXA-24, blacOXA-51 | Tao et al. (2021) |
|                         | China   | RT-qPCR| Sulfonamide, Tetracycline, Quinolone, Macrolide, β-lactam | blacOXA-23, blacOXA-24, blacOXA-51 | Wang et al. (2019) |
| Healthcare facilities   | Poland  | PCR    | MLS                                              | msrA, msrA1, msrB, mphC, lnuA, ermB, ermB | Lenart-Boroń et al. (2016) |
| Homeless shelter and clinics | United states | qPCR   | Tetracycline                                     | tetW, tetX | Ling et al. (2013) |
| Wet Market              | China   | qPCR   | Sulfonamide, Tetracycline, Macrolide             | sul2, tetC, tetG, ermC | Gao et al. (2016)) |
| Target environment                  | Country    | Method               | Antibiotics                                | Type of ARGs                                                    | References |
|------------------------------------|------------|----------------------|--------------------------------------------|----------------------------------------------------------------|------------|
| Bathroom                           | China      | RT-qPCR              | Sulfonamide, Tetracycline, Quinolone, Macrolide, β-lactam | sul1, sul2, sul3, tetA, tetC, tetG, tetM, tetQ, tetW, qnrS, ermA, ermB, ermC, bla\textsubscript{Ampc}, bla\textsubscript{DHA-1}, bla\textsubscript{OXA-1} | Wang et al. (2019) |
| Kindergarten                       | Hong Kong  | qPCR                 | Sulfonamide, Tetracycline, Aminoglycoside, Macrolide, β-lactam, Amphenicol | sul1, sul2, tetM, tetO, tetW, tetS, tetQ, aac, ermA, ermB, ermC, ermF, mecA, floR, cat2 | Li et al. (2020b) |
| Pig farm                           | China      | Metagenomic sequencing analysis | Tetracycline, Aminoglycoside, Macrolide, Multidrug, β-lactam, Vancomycin | tetA, tetZ, tetP, acrA, mdtL, smeF, oprA, mdtP, opcM, cmeA, qacA, mexC, mcr-1.2, mcr-1.6, mcr-1.7, mphB, mphC, mcrA, erm (TR), etc. | Yan et al. (2021) |
| University Dormitory and Office    | China      | HT-qPCR              | β-lactam, Tetracycline, Multidrug, Aminoglycoside | The 62–67 ARGs detection | Zhao et al. (2021) |
| Rural Laboratory                   | China      | RT-qPCR              | Sulfonamide, Tetracycline, Aminoglycoside, MLSB, Multidrug, β-lactam, Vancomycin | bla\textsubscript{TEM}, floR, sul2, aadA, aac(6’)-II, ermA, qnrS, bla\textsubscript{OXA-1}, mphA1, mphA2, qnrS, acrA, sul2, tetG, tetW, vanA, vanB | Tao et al. (2021) |
| Pig farm                           | China      | RT-qPCR              | Sulfonamide, Tetracycline, Quinolone, Aminoglycoside, Macrolide | sul1, sul2, tetM, tetG, tetO, qnrA, strA, ermA, ermB | Song et al. (2021) |
| Outdoor WWTP (Wastewater treatment plant) | China | PCR                  | Sulfonamide                                | sul1, sul2 | Li et al. (2016) |
|                                    | China      | RT-qPCR              | Sulfonamide, Tetracycline, Quinolone, Macrolide, β-lactam | sul1, sul2, sul3, tetA, tetC, tetG, tetM, tetQ, tetW, ermA, ermB, ermC, bla\textsubscript{TEM-1}, bla\textsubscript{Ampc}, bla\textsubscript{DHA-1}, bla\textsubscript{OXA-1} | Wang et al. (2019) |
| Target environment            | Country          | Method                  | Antibiotics                                      | Type of ARGs                                                                 | References                  |
|-------------------------------|------------------|-------------------------|--------------------------------------------------|------------------------------------------------------------------------------|-----------------------------|
| South Korea                   | Metagenomic     | Sulfonamide, Tetracycline, MLS | sul1, sul2, tetA, tetG, tetQ, tetW, ermB, ermG, ermF etc. | Han and Yoo (2020)                                                         |
| Public building               | Turkey           | qPCR                    | Sulfonamide, Quinolone, β-lactam                 | sul1, qnrS, MecA                                                             | Lang-Yona et al. (2020)     |
| China                         | Real-Time PCR    | Sulfonamide, Tetracycline, Macrolide, β-lactam | sul3, tetW, tetQ, tetM, tet32, tetO, ermB, blaTEM etc. | Zhang et al. (2019)                                                          |
| 19 Global city                | HT-qPCR          | Sulfonamide, Tetracycline, Macrolide, β-lactam, vancomycin, aminoglycoside | The 30 ARGs detection | Li et al. (2018)                                                              |
| Urban park                    | United states    | qPCR                    | Sulfonamide, β-lactam                            | sul1, bla<sub>SHV</sub>                                                      | Echeverria-Palencia et al. (2017) |
| Rooftop of school             | China            | qPCR                    | Sulfonamide, Tetracycline, Quinolone, Aminoglycoside, Macrolide, Multidrug, β-lactam | sul1, tetW, qnrS, ermB, ermG, aadd, mexF, bla<sub>SHV</sub>-M1 | Sun et al. (2020)            |
| Municipal solid waste treatment system | China | RT-qPCR                 | Sulfonamide, Tetracycline, Quinolone, Aminoglycoside, Macrolide, β-lactam | sul1, sul2, sul3, tetW, tetM, tetQ, tetA, qepA, qnrA, qnrS, aacC2, aacC3, ermB, ermC, bla<sub>TEM-1</sub>, bla<sub>OXA-1</sub>, bla<sub>OXA-2</sub>, bla<sub>OXA-3</sub>, bla<sub>AMPC</sub>, bla<sub>TEM</sub>-1, bla<sub>SHV</sub>-1 | Li et al. (2020a)            |
| Composting plants             | China            | ddPCR                   | Sulfonamide, Tetracycline, Macrolide, β-lactam | sul1, sul2, sul3, dfrA1, tetQ, tetM, tetS, tetT, tetW, tetA/P, tetG, tetL, tetZ, tetX, ermB bla<sub>ARB-4</sub>, bla<sub>OXA-1</sub>, bla<sub>OXA-2</sub>, bla<sub>OXA-3</sub>, bla<sub>OXA</sub>, bla<sub>OXAB-1</sub>, bla<sub>OXAB-2</sub>, bla<sub>OXAB-3</sub>, bla<sub>PSE</sub>, bla<sub>TEM</sub> | Gao et al. (2018a)           |
| Target environment | Country     | Method  | Antibiotics                          | Type of ARGs                                                                 | References                  |
|-------------------|-------------|---------|--------------------------------------|------------------------------------------------------------------------------|-----------------------------|
| Laboratory area   | China       | RT-qPCR | Sulfonamide, Tetracycline, Aminoglycoside, MLSB, Multidrug, β-lactam, Vancomycin | blaTEM, floR, sul2, aadA, aac(6’)-II, ermA, qnrS, blaOXA1, mphA1, mphA2, qnrS, acrA, sul2, tetG, tetW, vanA, vanB | Tao et al. (2021)           |
| University area   | China       | RT-qPCR | Sulfonamide, Tetracycline, Quinolone, Macrolide, β-lactam | sul1, sul2, sul3, tetA, tetC, tetG, tetM, tetQ, tetW, qnrS, ermB, ermC, blaCMY-2, blaTEM-1, blaAmpc, blaDHA-1, blaOXA-1 | Wang et al. (2019)          |
| China             | qPCR        |         | Tetracycline, Aminoglycoside, Macrolide | tetM, tetO, tetW, aph(3’)-IIIa, ermB, ermQ, mphE etc.                         | Ouyang et al. (2020)       |
| China             | HT-qPCR     |         | β-lactam, Tetracycline, Multidrug, Aminoglycoside | The 46 ARGs detection                                                        | Zhou et al. (2021)         |
| Yangtze river area| China       | RT-qPCR | Sulfonamide, Tetracycline, Quinolone, β-lactam, MLS | sul1, tetW, qnrS, blaTEM-1, ermB, lnuA                                      | Xie et al. (2019)          |
| Pearl river area  | China       | RT-qPCR | Sulfonamide, Tetracycline, Quinolone, β-lactam, MLS | sul1, tetW, qnrS, blaTEM-1, ermB, lnuA                                      | Xie et al. (2019)          |
| China             | qPCR        |         | Sulfonamide, Tetracycline, Aminoglycoside, MLSB, Multidrug, β-lactam | sul1, sul2, sul3, tetA, tetB, tetC, tetD, tetG, tetL, tetM, tetO, tetQ, tetS, tetT, tetX, tetW, aadA, aadE aacA/ aphD, str, sat, ereA, ermB, ermC, ermT, lnuA, lnuB, vatE, mefA, acrA, mexF, blaTEM-1, blaCTX-M | Liang et al. (2020)        |
| Rural Yangtze river rural area | China | RT-qPCR | Sulfonamide, Tetracycline, Quinolone, β-lactam, MLS | sul1, tetW, qnrS, blaTEM-1, ermB, lnuA                                      | Xie et al. (2019)          |
et al. 2019). Research on ARGs in bioaerosols in hospitals has been conducted in indoor hospital spaces (such as operating rooms and outpatient clinics). Genes conferring resistance to beta-lactam antibiotics and beta-lactam-resistant bacteria, such as Staphylococcus spp. and A. baumannii, have been widely detected. Staphylococcus spp. often develops antibiotic resistance mechanisms via the enzymatic initiation of antibiotic particles (Mirhoseini et al. 2016a, b; Gao et al. 2018a, b), such as hydrolases and transfers and efflux pumps (Table 1). The blaOXA-23, blaCTX-M, and mecA genes are major ARGs in hospital settings. Another study identified ARGs such as those that confer resistance to tetracycline, macrolide, and sulfonamide, and the occurrence of the tetG gene is common in both Canada and China. Through RT–qPCR, Wang et al. (2019) found that the most frequently detected ARGs are blaTEM-1, blaAmpc, blaOXA-1, ermA, ermC, qnrS, and tetG, and the quantitative levels of the detected genes ranged from $8.8 \times 10^2$ to $1.4 \times 10^5$ copies/m$^3$. In addition, ARBs such as S. maltophilia, Enterobacter, and S. aureus and the resistance genes ermA, ermX, mecA, tetA, tetC, and tetG were detected in hospital environments by PCR (Gilbert et al. 2010). A recent study (Zhou et al. 2021) showed that hospitals are hotspots for airborne ARGs and detected a total of 95–151 ARGs, including macrolides, cephalosporins, and penicillin antibiotics, by high-throughput qPCR (HT-qPCR) (Table 2). In hospital environments, beta-lactam resistance genes are detected at particularly high frequencies, and this result was obtained because beta-lactam antibiotics are generally used for the treatment of inpatients and account for approximately 50–70% of the total antibiotic use (Mirhoseini et al. 2016a, b). In addition, ARGs are differentially detected among the various indoor spaces in the hospital, and the abundance of ARGs increases during a patient’s long stay because antibiotics are continuously used for patient treatment, which can produce resistance genes in the patient’s body, and HGT can potentially occur due to high exposure to antibiotics (Huddleston 2014; Gao et al. 2018a, b). It is understood that the discharge of ARBs and ARGs due to the patients breathing, speaking, coughing, and sneezing affects the contamination of ARGs in hospitals (Xie et al. 2021; Zhou et al. 2021, 2022). Additionally, variations in indoor air parameters, such as
temperature, humidity, and location, and ventilation systems directly or indirectly affect the dissemination of ARBs and ARGs in hospitals and healthcare facilities (Chen et al. 2022).

### 2.1.2 Laboratory buildings

Biological and biochemical laboratories provide good conditions for airborne ARGs because antibiotics and ARGs are widely used in cloning, protein production, gene therapy, and disease models. However, research on ARGs in the laboratory is limited (Hamdy et al. 2018; Tao et al. 2021). Tao et al. (2021) and Wang et al. (2019) investigated ARGs in biology and biochemical labs. In these studies, the most commonly detected ARGs were blaTEM, blaOXA1, blaAmpc, and blaDHA-1 (beta-lactam resistance), sul1 and sul2 (sulfonamide resistance), aadA, aac(6’)-II (aminoglycoside), qnrS (quinolone resistance), and vanA and vanB (vancomycin resistance) (Table 2), and the sul1 gene was not detected or was detected at a low level (5.5×10^0–3.0×10 copies/m^3). The most frequently detected genes were blaTEM, blaTEM-1, blaAmpc, and blaOXA-1, and beta-lactam resistance was dominant. In addition, the comparison of urban and natural environments revealed that the floR, sul2, and aadA1 genes were commonly detected in laboratory buildings. According to Wang et al. (2019), ARGs were detected in samples from a biochemistry laboratory and the balcony outside the laboratory. The results revealed that the ARGs detected in the two locations were similar, and the largest cause of this result was air circulation due to ventilation. Biological laboratories include plants, animals, and cell biology labs. In particular, animal-derived antibiotics may be the main source of the ARGs detected in the laboratory due to frequent animal testing and the high correlation between ARGs from livestock and ARGs in animal laboratories. These results suggest that it is necessary to identify antibiotic usage and antibiotic hotspots in the surrounding environment.

### 2.1.3 Downtown facilities

Elderly people and young children are relatively vulnerable to pathogens and ARB compared to healthy adults, and indoor spaces with a large floating population or a large number of people are also suspected to be potentially high exposed to ARB and ARGs. Therefore, we selected homeless shelters, clinics, kindergartens, wet market, university campus as downtown facilities in this study (Table 2).

Both tetX and tetW genes were detected in the clinic, indicating that the air was conducive to carrying ARGs. TetM, blaAmpc, and blaOXA-1 genes were detected in the bathroom, and tetW was also detected in the homeless shelter, suggesting that ARGs exist in various indoor environments (Ling et al. 2013; Wang et al. 2019). Because airborne ARGs are detected in various environments and are a known risk factor for humans, studies of ARGs have been conducted in indoor spaces such as kindergartens. In a study by Li et al. (2020b), ARGs were evaluated in 17 kindergartens in Hong Kong. Sulfonamide resistance genes were the most frequently detected genes, and macrolides, tetracyclines, aminoglycosides, beta-lactams, and amphenicols resistance genes were also identified through metagenomic methods (Table 2). According to previous study (Li et al. 2018), these antibiotic resistance genes are the most commonly detected genes in urban atmospheres around the world (Li et al. 2018). It is known that airborne ARGs generally travel through PM. However, because the current studies of ARGs in the atmosphere have not investigated the spread of ARGs and only included point-based studies with samplers, research on the spread of spatial ARGs is needed in the future. In addition, research should be conducted to clearly identify the source of ARGs detected in indoor environments.

Wet markets are popular multiuse facilities. Wet markets in China are indoor multiuse facilities that trade poultry, live fish, pork, and vegetables and are also an environment in which livestock, poultry, and humans are in close proximity; for this reason, these wet markets are attracting attention as a new source of ARGs as well as harmful microorganisms (Zhang et al. 2015; Gao et al. 2016). Antibiotics widely used in animal farms, such as tetracycline, sulfonamide, and macrolide, have been identified at wet markets, and the sul2, ermC, tetG, and tetC genes are dominant (Table 2). In a wet market, ARGs are likely to have been aerosolized and released from livestock and poultry manure in an environment in which livestock and poultry are in close contact with humans, and manure may be a major source contributing to the spread of ARGs.

With respect to university campuses, 67 and 62 ARGs were detected by HT-qPCR in a dormitory
and an office, respectively, and beta-lactam (19.23%), tetracycline (17.95%), multidrug systems (16.67%), and aminoglycosides (12.82%) antibiotics were dominantly identified. This result may be due to airborne bacterial communities in university campus environments because they are more easily spread by human activities and thereby contribute to a high abundance of antibiotics. Our results suggested that human density or activities may play a dominant role in the transmission of airborne ARGs in indoor environments because human commensal microbiota are actually carriers of airborne ARGs. Usually, blaTEM genes inactivate antibiotics for gram-negative pathogens, such as Pseudomonas, Klebsiella, and Escherichia spp., that can disseminate among microbes via MGEs (Chen et al. 2022; Gwenzi et al. 2022) and the global threat of antimicrobial-resistant gram-negative bacteria is increasing (Zhao et al. 2021). Therefore, the high abundance of blaTEM genes in indoor aerosols of laboratory buildings should be given more attention.

These previous studies showed that ARGs are prevalent in air in indoor environments and that many types of ARGs are present (Zhao et al. 2021). Because downtown facilities are not facilities that use antibiotics, such as hospitals and laboratories, external factors should be considered important. The indoor environment is a space where humans live 90% of the day, and because human commensal microbiota can potentially carry ARGs in the air, the population density and human activity may be important factors in the spread of ARGs (Zhao et al. 2021; Zhou et al. 2021). Thus, the dissemination of airborne ARGs by human activities in indoor public buildings needs to be further elucidated.

2.2 Outdoor environments

The source of ARGs is most important in outdoor environments. To date, the ARG hotspots are WWTPs, pharmaceutical manufacturing sites, food and animal production sites related to architecture and aquaculture, and hospital and clinical areas (Kunhikannan et al. 2021). ARGs generated from hotspots are greatly influenced by the atmospheric environment (wind speed and direction, relative humidity, atomic pollutants, temperature, and rain condition). In particular, the relative humidity and atmospheric pollutants such as PM10 and PM2.5 directly affect the growth and spread of airborne microorganisms, ARBs, and ARGs (Gao et al. 2018a, b; Wang et al. 2019). As the concentration of heavy metal pollutants in the atmosphere, such as Mn and Pb, increases, the abundance of ARGs increases. Temperature is highly related to the season; in the summer, the growth of bacteria is delayed due to the high temperature, and the abundance of ARGs also tends to decrease (Liang et al. 2020; Kathiriya et al. 2021). To understand ARGs in outdoor environments, it is necessary to comprehend the relationship among different natural environments and to consider the presence or absence of antibiotic hotspots and the direction of wind around these hotspots.

ARGs have been detected in outdoor environments (urban, rural, farm, coastal, agriculture, and forest). In study, airborne ARGs have been investigated in areas such as WWTPs, composting plants, public buildings and parks, and farm area (Table 2).

2.2.1 WWTPs

WWTPs are known to be a major source of antibiotic and ARG contamination (Karkman et al. 2018; Yoo et al. 2020). In addition, studies on antibiotics and ARGs under aerobic and anaerobic conditions and in inflow and discharge water related to WWTPs have been widely conducted worldwide, and various ARGs have been identified (Table 2). However, few studies have investigated airborne ARGs in WWTPs. Recent studies have revealed that the most commonly detected antibiotics are macrolides, sulfonamides, and tetracyclines. In previous studies, this observation appeared to be related to the frequent detection of sulfonamides and MLS in WWTPs (Table 2). In addition, sulfonamides and tetracycline are most commonly used to prevent and treat diseases in humans and animals, and genes such as sul1, sul2, tetA, tetQ, and tetG are also spread in the air surrounding WWTPs and have been detected in various studies (Li et al. 2016; Wang et al. 2019; Yoo et al. 2020). Gaviria-Figueroa et al. (2019) detected ARGs upwind and downwind from WWTPs through HT-qPCR. Both upwind and downwind analyses revealed the presence of blaOXA-60, ermB, ermC, qnrB-5 group, and aadA1 genes, and studies have confirmed that more diverse ARGs are detected downwind than upwind. These results suggest that the transport of ARGs may vary depending on the factors affecting the physio/
chemical environment or the mechanism through which ARGs diffuse into the atmosphere, and more complex mechanisms exist. Therefore, future studies on the effect of weather factors on ARGs are needed. In addition, the presence of intI1 genes in the atmosphere at high concentrations in WWTPs is potentially highly likely to result in the HGT of ARGs, but information on the interaction between the ARG profile and bacterial composition is currently very limited (Forsberg et al. 2014). Therefore, field-based research should be conducted considering the composition of ARGs during the entire wastewater treatment process and the amount and geographical characteristics of antibiotics used in animals and humans in the region.

In WWTPs, the bioaerosol levels depend on the treatment process and phase, and bioaerosols are detected at a high level during the aeration process in the bioreactor (Li et al. 2016; Han et al. 2019a; Jin et al. 2021). Previous studies have shown that bioaerosols released during the aeration of activated sludge can transmit ARGs and pathogens through the upper respiratory tract of WWTP workers (Han et al. 2018; Zielinski et al. 2020, 2021). In addition, genes such as tet36, tetQ, sul2, ermG, and ermF are detected in bioaerosols generated during the activated sludge dewatering process (Han and Yoo 2020). ARGs present in activated sludge, such as blaTEM, sul1, and mefA, have been simultaneously detected in the upper respiratory system of WWTP workers through throat and nasal swabs (Zielinski et al. 2021). In addition, some studies (Han et al. 2019b; Jin et al. 2021) have found that WWTPs can produce bioaerosols with a particle size under 1 μm, which can penetrate human lungs (<2.1 μm). These findings show that bioaerosols in WWTPs may have a harmful effect on WWTP workers (Han et al. 2019a; Zielinski et al. 2021).

### 2.2.2 Composting plants

Animal excrement is a major source of ARGs recognized as environmental pollutants, and some studies have shown that composting can potentially reduce ARGs (Selvam et al. 2012; Wang et al. 2015); however, other studies have shown that the ARG levels are similar or increased in these environments, causing significant aerosolization. For this reason, an ARG study on composting plants was conducted by Gao et al. (2018a). During the composting process, bioaerosol can be produced from shredding, composite file turning, and composite screening (Mbareche et al. 2017a). By ddPCR, 4 sulfonamide resistance genes, 10 tetracycline resistance genes, 7 beta-lactam resistance genes, and erythromycin resistance genes were detected (Table 2).

### 2.2.3 Public buildings and parks

Public buildings and parks were spaces with a large floating population considerably influenced by weather conditions. The urban downtown areas included school, building, laboratory, park and university areas in downtown (Table 2). In this study, public buildings and parks bioaerosol was regarded as generated in a typical urban environment and as air affected by artificial activities.

Sun et al. (2020) showed that ARGs differ depending on the weather in a downtown school area. Eight ARGs (sul1, tetW, qnrS, ermB, aadd, mexF, and blaCTX-M1) were detected in the PM2.5 sample. More ARG types were detected on hazy days and on days with high levels of air pollution than on clear days, and on hazy days, qnrS, aadd, and sul1 were detected in greater amounts than blaCTX-M1, mexF, ermB, tetW, and ermB. In addition to comparisons between hazy and clear environments, studies have been conducted during rainfall, and genes including tetM, tetO, tetW, aph(3’)-IIIa, ermB, ermQ and mphE were detected on the university rooftop. The bioaerosol samples collected before and after rain were different, and ARG levels were approximately 22% lower after rain than before. This result appears to be due to the washing effect of rain, and a strong washing effect on aminoglycosides (28.81%), tetracyclines (21.89%) and macrolides (19.34%) was observed. In a study by Zhao et al. (2021), ARGs were detected in different locations of university buildings, and 46 ARGs were detected less often outdoors than in dormitory and office areas. These findings are believed to have been obtained because indoor environments is less affected by the wind direction and wind speed than outdoor environments and contain ARGs in the bioaerosol emitted from the mouth and nose due to microbial growth and human activity in a static environment. In addition, 36 ARGs were shared between indoor and outdoor spaces, and 6 ARGs were detected only in the outdoor buildings. Many common ARGs were found in indoor and outdoor.
airs, which indicated that indoor and outdoor environments affect each other. Outdoor air is the source of an average of 52% of the indoor air environment, and many common ARGs have been detected due to the circulation between indoor and outdoor air through ventilation and humans (Zhou et al. 2021). In a study by Li et al. (2018), ARGs were evaluated in automobile AC filters from several international mega-cities in eight different climatic regions with different antibiotic usage patterns. This study minimized the effect of major sources of ARGs because AC filters were collected from cars away from sources of ARGs, such as agricultural land, WWTPs, and animal facilities, which are major sources of ARGs. Thirty ARGs were detected in 39 samples, and ARGs such as blaCMY2, ermT, tetK, vanB, qnrB, and tet32 accounted for 50% of the total. A study conducted by Lang-Yona et al. (2020) identified sul1, mecA, and qnrS in downtown bioaerosols collected from the roof of a city government building with little local industry activities in Turkey. The detection of ARGs in cities is associated with human activity and the migration of bioaerosols, and it has been shown that the antibiotic usage pattern in cities and the amount of ARGs in bioaerosols are significantly correlated (Li et al. 2018). In particular, multidrug or quinolone resistance was detected in PM near the hospital, and in contrast, aminoglycoside, tetracycline, and trimethoprim resistance tends to migrate from the city to the hospital, indicating the possibility of two-way ARG propagation (He et al. 2020). These findings suggest that antibiotic use in cities can affect atmospheric ARGs and thereby affect people and the environment (Zhou et al. 2021).

2.2.4 Farm areas

Over 70% of antibiotics are administered to livestock worldwide. The livestock used for food include chicken, pig and cattle, and pig farms have 50% higher levels of antimicrobial compounds and are thus recognized as hotspots of antibiotic use (Van Boeckel et al. 2019). The livestock industry commonly uses antibiotics. ARGs derived from livestock can be transported to humans through air downwind of animal feeding and transportation operations, retail deliveries and pollution (Sanchez et al. 2016). Because ARGs derived from livestock can travel in air, studies of ARGs have been conducted at various farms. Tests of the sensitivity of Staphylococcus aureus to 15 types of antibiotics have been conducted at chicken farms because this bacterium is a known environmental pathogen in this environment. It is believed that the ventilation facilities of various farms spread ARGs while accelerating the air circulation between the breeding grounds and the external environment. Another study (Liu et al. 2012) also showed that the sulfamethoxazole, penicillin, tetracycline and erythromycin resistance rates at six chicken farms are approximately 94%, 78.5%, 75.2%, and 66.4%, respectively. This study showed that most of the airborne bacteria in six chicken farms exhibit severe antibiotic resistance, and many of these were resistant to methicillin. Only approximately 15% of antibiotics are metabolized and absorbed—the remaining drug is released into the environment through excretion (Pei et al. 2019). ARGs have been detected in pig feces, and it has been reported that these ARGs in feces can be introduced into the surrounding environment through agricultural fertilizers or volatilized into the air, from which they spread in the form of bioaerosols (McEachran et al. 2015).

3 Detection of ARGs in bioaerosols

3.1 Sampling methods

No standard sampling method has yet been established for the detection of ARGs in the atmosphere, and most previous studies have used existing aerosol sampling methods (Gwenzi et al. 2022). A previous study reported that bacteria can be under extreme stress during air sampling, which could result in severe membrane impairment and lead to the release of DNA as free molecules (Zhen et al. 2013). When DNA is damaged and broken, it fails to use the currently used molecular microbiology techniques and eventually makes it difficult to analyze ARGs. Due to this problem, the impaction, impingement, and filtration methods are commonly used to detect ARGs in the atmospheric environment (Ghosh et al. 2015; Yoo et al. 2017; Mainelis 2020).

The bioaerosol sampling methods commonly used in previous studies can be classified into culture-based and nonculture-based methods. The impaction method is a widely used culture-based methods, and the impingement and filtration methods are the most commonly used nonculture-based methods.
### Table 3  Summary of bioaerosols sampling method in target atmospheric environment

| Target environment          | Sampling method | Sampling material                        | Flow rate | Total sampling time | Total volume | References                 |
|-----------------------------|----------------|------------------------------------------|-----------|---------------------|--------------|---------------------------|
| Indoor Hospital             | Filtration     | Quartz microfiber filter                 | 100 L min⁻¹ | 24 h                | 144 m³       | Zhou et al. (2021)        |
|                             | Filtration     | Filter dirt                              | –         | –                   | –            | Li et al. (2021b)         |
|                             | Impingement    | Phosphate buffer solution                | 12.5 L min⁻¹ | 3 h                 | 2.5 m³       | Mirhoseini et al. (2016a) |
|                             | Impingement    | Phosphate buffer solution                | 10.0 L min⁻¹ | 4 h                 | 2.4 m³       | Shamsizadeh et al. (2017) |
|                             | Impaction      | Trypticase soy agar                      | 28.3 L min⁻¹ | 20 min              | 0.566 m³     | Gilbert et al. (2010)     |
|                             |                | Blood Agar                               | 28.3 L min⁻¹ | 20 min              | 0.566 m³     | Gao et al. (2018b)        |
|                             |                | Red blood agar                           | 28.3 L min⁻¹ | 5 min               | 0.142 m³     | Mao et al. (2019)         |
|                             | Filtration     | Glass fiber filter                       | 1050 L min⁻¹ | 20 h               | ~1200 m³     | Wang et al. (2019)        |
|                             | Filtration     | Glass microfiber filter                  | 100 L min⁻¹ | 12 h                | 72 m³        | He et al. (2017)          |
|                             | Impingement    | Saline solution (0.85% NaCl)             | 300 L min⁻¹ | 10 min              | 3 m³         | He et al. (2017)          |
| Office and Experiment building | Impaction      | Trypticase soy Agar                      | 28.3 L min⁻¹ | 10 min              | 0.283 m³     | Bragoszewska and Biedron (2018) |
|                             | Impaction      | Tryptic soy agar, Malt extract agar       | 15 L min⁻¹  | 5 min               | 0.075 m³     | Mirhoseini et al. (2016a) |
|                             | Impingement    | Endotoxin free water                     | 12.5 L min⁻¹ | 60 min              | 0.75 m³      | Mao et al. (2019)         |
|                             | Impaction      | Nutrient Agar                            | 28.3 L min⁻¹ | 10 min              | 0.283 m³     | Mirhoseini et al. (2016a) |
| Laboratory                  | Impaction      | Tryptic soy agar, Malt extract agar       | 15 L min⁻¹  | 5 min               | 0.075 m³     | Mirhoseini et al. (2016a) |
|                             | Impingement    | Endotoxin free water                     | 12.5 L min⁻¹ | 60 min              | 0.75 m³      | Mirhoseini et al. (2016a) |
|                             | Filtration     | Glass microfiber filter                  | 100 L min⁻¹ | 12 h                | 72 m³        | Tao et al. (2021)         |
|                             | Filtration     | Aluminum foil (covered with 500 µl mineral oil) | 1000 L min⁻¹ | 30 min              | 30 m³        |                            |
| Healthcare facilities       | Impaction      | Lysogeny broth agar                      | 1000 L min⁻¹ | 1 min               | 1 m³         | Lenart-Boroń et al. (2016) |
| Homeless shelter and clinics | Impaction      | Chapman medium mannitol salt agar        | 100 L min⁻¹ | 1 min               | 0.1 m³       | Ling et al. (2013)        |
|                             | Impingement    | Phosphate buffer solution                | 277 L min⁻¹ | 30 min              | 8.31 m³      |                            |
| Target environment                  | Sampling method | Sampling material                  | Flow rate | Total sampling time | Total volume | References                  |
|------------------------------------|----------------|------------------------------------|-----------|--------------------|--------------|-----------------------------|
| Wet Market                         | Filtration     | Glass fiber filter                 | 1050 L min⁻¹ | 4-23 h             | 250–1500 m³  | Gao et al. (2016)           |
| Bathroom                           | Filtration     | Glass microfiber filter            | 100 L min⁻¹  | 12 h               | 72 m³        | Wang et al. (2019)          |
| Kindergarten Pig farm              | Filtration     | AC filter                          | -         | 1 h                 | -            | Li et al. (2020b)           |
| Pig farm                           | Filtration     | Glass microfiber filters           | 100 L min⁻¹  | 6 h                | 36 m³        | Song et al. (2021)          |
| University Dormitory, Classroom and Office | Filtration    | Phosphate buffer solution          | 200 L min⁻¹  | 48 h               | 576 m³       | Zhao et al. (2021)          |
| Filter                             | Filtration     | Cellulose ester filter             | 4 L min⁻¹   | 8 h                 | 1.92 m³      | Meadow et al. (2014)        |
| Impaction                          | Tryptic soy agar, Malt extract agar | 15 L min⁻¹  | 5 min              | 0.075 m³      | Mirhoseini et al. (2016a)   |
| Impingement                        | Endotoxin free water | 12.5 L min⁻¹  | 60 min             | 0.75 m³       |               |                            |
| Childcare facility (day-care center & elementary school) | Filtration | Cellulose ester filter             | 24 L min⁻¹  | 10 h               | 14.4 m³      | Shin et al. (2015)          |
| Impaction                          | Tryptic soy agar, Sabaroud dextrose agar | 180 L min⁻¹ | 2 min              | 0.36 m³       | Hussin et al. (2011)        |
| Impaction                          | Tryptic soy agar, Malt extract agar | 15 L min⁻¹  | 5 min              | 0.075 m³      | Mirhoseini et al. (2016a)   |
| Impingement                        | Endotoxin free water | 12.5 L min⁻¹  | 60 min             | 0.75 m³       |               |                            |
| Apartment                          | Impaction      | Tryptic soy agar, Malt extract agar | 15 L min⁻¹  | 5 min              | 0.075 m³      | Mirhoseini et al. (2016a)   |
| Impingement                        | Endotoxin free water | 12.5 L min⁻¹  | 60 min             | 0.75 m³       |               |                            |
| Subway station                     | Filtration     | Polytetrafluoroethylene (PTFE) filter | 38 L min⁻¹  | 5–5.5 h           | 11.4–12.54 m³ | Grydaki et al. (2021)       |
| Swine confinement building WWTP (Wastewater treatment plant) | Filtration | Glass fiber filter                 | 2 L min⁻¹   | 12 h               | 1.44 m³      | Yan et al. (2021)           |
| Outdoor                            | Filtration     | Glass microfiber filter            | 100 L min⁻¹  | 12 h               | 72 m³        | Wang et al. (2019)          |
| Sampling method  | Sampling material                  | Flow rate  | Total sampling time | Total volume | References                      |
|------------------|------------------------------------|------------|---------------------|--------------|---------------------------------|
| Filtration       | Polytetrafluoroethylene (PTFE) filter | 56 L min⁻¹ | 90 min              | 5.04 m³      | Gaviria-Figueroa et al. (2019)  |
| Impaction        | Gelatin membrane filter            | 125 L min⁻¹| 30 min              | 3.75 m³      | Li et al. (2016)                |
| Impingement      | Trypticase soy agar, Malt extract agar | 100 L min⁻¹| 1 min               | 0.1 m³       |                                 |
| Filtration       | Distillation (DI) water            | 12.5 L min⁻¹| 30 min              | 0.375 m³     |                                 |
| Public building  | Glass fiber filter                 | 1000 L min⁻¹| 48 h                | 2,880 m³     | Yang et al. (2018a)             |
| Filtration       | Polycarbonate filter               | 1500 L min⁻¹| 24 h                | 2160 m³      | Han and Yoo (2020)              |
| Filtration       | AC filter, Quartz fiber filter     | 5 L min⁻¹  | 24 h                | 7.2 m³       | Li et al. (2018)                |
| Filtration       | Quartz filter                      | 1180 L min⁻¹| 24 h                | 1700 m³      | Lang-Yona et al. (2020)         |
| Filtration       | Quartz microfiber filter           | 1000 L min⁻¹| 24 h                | 1,440 m³     | Xie et al. (2018)               |
| Hospital         | Tissuquartz filters                | 1130 L min⁻¹| 23 h                | 1,559.4 m³   | Cao et al. (2014)               |
| Urban park       | Quartz microfiber filter           | 100 L min⁻¹| 24 h                | 144 m³       | Zhou et al. (2021)              |
| Filtration       | Polycarbonate filter, Glass fiber filter | 2 L min⁻¹ | 4 h                 | 0.48 m³      | Echeverria-Palencia et al. (2017) |
| Rooftop of school| Quartz filter                      | 1050 L min⁻¹| 24 h                | 1,512 m³     | Sun et al. (2020)               |
| Municipal solid waste treatment system | Quartz fiber filter | 100 L min⁻¹| 20 h                | 120 m³       | Li et al. (2020a)               |
| Composting plants| Quartz fiber filter                | 100 L min⁻¹| 24 h                | 144 m³       | Gao et al. (2018a)              |
| Laboratory area  | Aluminum foil (covered with 500 µl mineral oil) | 1000 L min⁻¹| 30 min              | 30 m³        | Tao et al. (2021)               |
| Impaction        | Lysogeny broth agar                | 1 min      |                     | 1 m³         |                                 |
| University area  | Glass microfiber filter            | 100 L min⁻¹| 12 h                | 72 m³        | Wang et al. (2019)              |
| Filtration       | Aluminum membrane coated with 600 µl mineral oil | 1000 L min⁻¹| 20 min              | 20 m³        | Zhang et al. (2019)             |
The impaction method is used to directly collect microorganisms from the captured air using a solid medium, and agar, including tryptic soy agar, malt extract agar, nutrient broad agar and rose Bengal agar, is widely used. This method usually involves a flow rate of 15–28.5 L min\(^{-1}\), and the total sampling time ranges from 1 to 20 min. Because short sampling times are possible, many previous studies, such as those conducted in hospitals, offices, and school classrooms, have used this approach to investigate ARGs in indoor places (Gilbert et al. 2010; Hussein et al. 2011; Lenart-Boróń et al. 2016; Mirhoseini et al. 2016b; Bragoszewska and Biedron 2018; Mao et al. 2019; Tao et al. 2021). The impaction method has the advantages of easy manipulation and capture of living microorganisms (Yoo et al. 2017), but because it is a culture-based sampling method, only specific microorganisms in the air can be cultured, which makes it difficult to efficiently identify the bioaerosol microbiome (Ghosh et al. 2015; Mainelis 2020; Mbareche et al. 2017a; Yoo et al. 2017). Due to these shortcomings, nonculture-based methods are preferred, and the use of nonculture-based methods that can effectively understand microbial communities continues to increase due to the spread of high-throughput sequencing technology (Mbareche et al. 2017b). The impaction method can be used for antimicrobial susceptibility testing (AST) by utilizing the advantage of being able to capture living microorganisms in a real atmosphere environment (Mao et al. 2019). The wells of each AST plate are covered with common antibiotics for gram-positive and gram-negative bacteria, indicating resistance to antibiotics (Mao et al. 2019). ARBs can also be identified using

| Target environment      | Sampling method | Sampling material                  | Flow rate | Total sampling time | Total volume | References               |
|-------------------------|-----------------|------------------------------------|-----------|---------------------|--------------|--------------------------|
| River area (Yangtze/pearl) | Filtration     | Polycarbonate membrane filter      | 300–500 L min\(^{-1}\) | 24 h       | 432–720 m\(^3\)  | Yoo et al. (2018)         |
|                         | Filtration     | Tissuquartz filter                 | 1130 L min\(^{-1}\)  | 23 h       | 1560 m\(^3\)     | Ouyang et al. (2020)      |
|                         | Filtration     | Quartz microfibre filter           | 1000 L min\(^{-1}\) | 24 h       | 1,440 m\(^3\)   | Xie et al. (2019)         |
| Impaction               | Nutrient broth Agar | Rose Bengal Agar               | 28.5 L min\(^{-1}\) | 5 min      | 0.143 m\(^3\)    | Liang et al. (2020)       |
| Filtration              | Polycarbonate membrane filter | 28.3 L min\(^{-1}\) | 30 min     | 0.849 m\(^3\) |              |                          |
| Industrial area         | Filtration     | Quartz microfiber filter           | 1000 L min\(^{-1}\) | 24 h       | 1,440 m\(^3\)   | Xie et al. (2018)         |
| Botanic garden          | Filtration     | Quartz microfiber filter           | 1000 L min\(^{-1}\) | 24 h       | 1,440 m\(^3\)   | Xie et al. (2018)         |
| Farm area (Chicken/Beef cattle/Pig) | Filtration | Glass fiber filter                | 1000 L min\(^{-1}\) | 48 h       | 2,880 m\(^3\)   | Yang et al. (2018a)       |
| Impaction               | Baird-park Agar |                                | 28.3 L min\(^{-1}\) | 1-15 min   | 0.0283–0.4245 m\(^3\) | Liu et al. (2012)         |
| Filtration              | Glass fiber filter |                                 | 2 L min\(^{-1}\)   | 4 h        | 0.48 m\(^3\)    | Sanchez et al. (2016)     |
| Impingement             | Liquid medium of 10% glycerol |                     | 12.5 L min\(^{-1}\) | 3 m\(^3\)  |              |                          |
the culture method by adding specific antibiotics to the solid medium used (Mirhoseini et al. 2016a, b). This method has been used more frequently in the past than it is today, particularly in hospitals to check for antibiotic resistance in pathogens (Gilbert et al. 2010; Shamsizadeh et al. 2017). A faster wind speed makes it more difficult to capture the aerosol through the inlet of the impactor (Ghosh et al. 2015; Mainelis 2020; Chen et al. 2022). Therefore, the impaction method is more suitable for indoor environments than outdoor environments because this method is highly affected by the wind speed. However, due to the selective culturing characteristics, there is a clear limit to capturing whole microbiome information and entire genes (Ghosh et al. 2015; Mainelis 2020).

Impingement, a nonculture-based method, can reduce overloading by reducing physical stress on microorganisms using liquid buffer-based sampling (Ghosh et al. 2015). Sterilized 1 × phosphate-buffered saline (PBS) buffer, saline solution (0.85% NaCl), endotoxin-free water, and distortion (DI) water are the main liquids used for sampling, and the flow rate is generally 12.5–300 L min⁻¹ (Ling et al. 2013; Li et al. 2016; Mirhoseini et al. 2016a; Sancheza et al. 2016; Zhao et al. 2021). The total sampling time ranges from 10 min to 4 h, and the total volume is approximately 0.375–8 m³ (Yoo et al. 2017). However, because the postcollection process needed for quantification is difficult and liquid is lost due to evaporation, the filtration method is preferred over the impingement method.

As shown in Table 3, among the nonculture-based methods, the method most commonly used in recent studies is the filtration method, which collects airborne microorganisms by passing air through quartz fiber, glass fiber, polycarbonate, cellulose ester, polytetrafluoroethylene, and gelatin filters (Ghosh et al. 2015). Filtration methods can be divided into three categories: buffer wash, preheating and bead beating (Fig. 1). Buffer wash is mainly used for filter samples captured by quartz fiber filter, glass fiber filter, and aluminum membrane (foil) (covered with 500–600 µl mineral oil), and the wash is performed by centrifugation and sonication (Xie et al. 2018, 2019; Zhou et al. 2021). Filtration is currently the most commonly used method due to the greatest advantage of being nonselective. However, PM can block the air gap and cause equipment overload; in addition, the ability of bioaerosol to collect may decrease due to the inability to pass air, or the survival environment of extreme bacteria may occur (King et al. 2020). Nevertheless, filtration method is preferred by bioaerosol study because the area where bioaerosols are collected using filtration method is large, and this is useful for detecting target ARGs by qPCR and HT-qPCR after extracting DNA (King et al. 2020). A cyclone-based sampler is recently used in bioaerosol study. Although the cyclone method is known to have excellent collection efficiency, there is a problem of loss due to evaporation because a liquid medium, such as an impingement method, is used (Ghosh et al. 2015; Mainelis 2020; Chen et al. 2022). Due to the high capture efficiency of small aerosols, they are currently actively used in more diverse viral studies than relatively large bacteria (Coleman et al. 2018; Yadana et al. 2019; Lane et al. 2020).

Because dead cell or low levels of biomass are common in the collected filter or remain attached to the filter after pretreatment it is necessary to develop an advanced pretreatment and sampling method to effectively analyze the ARGs and ARB attached to the filter in the near future (King et al. 2020).

3.2 Pretreatment method for DNA extraction

A review of previous studies and methods revealed that most of the impaction and impingement methods involved DNA extraction within a short period after sampling without pretreatment, and pretreatment is performed only with the filtration method. There are two main methods for extracting DNA from bioaerosols collected by the filtration method (Luhung et al. 2021; Yoo et al. 2017). The main reason for the pretreatment of filters is to increase the yield and purity of DNA, and if the sampled filter is used immediately, the efficient extraction of DNA is difficult because the filter absorbs a large amount of lysis buffer (Ouyang et al. 2020; Xie et al. 2018, 2019; Zhou et al. 2021). The pretreatment methods are largely divided into three categories: buffer wash, preheating and bead beating (Fig. 1). Buffer wash is mainly used for filter samples captured by quartz fiber filter, glass fiber filter, and aluminum membrane (foil) (covered with 500–600 µl mineral oil), and the wash is performed using centrifugation and sonication (Xie et al. 2018, 2019; Zhang et al. 2019; Ouyang et al. 2020; Tao et al. 2021; Zhou et al. 2021). Quartz fiber and glass fiber filters are placed in a 50-mL conical tube filled with esterified 1 × PBS buffer. The samples are then
vortexed and subsequently centrifuged for approximately 2–3 h at 200 g, which is a low speed, and 4 °C. Aluminum membranes (foil) are incubated for 30 min or centrifuged immediately after the addition of 1–1.5 mL of Tween-20 (0.05%). Twenty-five milligrams of magnetite nanoparticles (MNPS) are then added, and the sample is sonicated for 30 s or at 120 W for 5 min. After the buffer wash, gentle vortexing is performed, and this step is followed by subsequent filtering through a PES membrane (disc) to capture the biomass. The preheating method is mainly used for polycarbonate membrane filters and PES filters (Cao et al. 2014; Liang et al. 2020). Before preheating, the filter is cut, lysed at 65 °C for 30 min, and vortexed every 5 min. After preheating, DNA is extracted using a DNA extraction kit according to the manufacturer’s protocol. Bead beating for 10 min with silicon carbide beads in a conical tube is used for polytetrafluoroethylene filters, and this step is followed by freezing for 1 min with liquid nitrogen and a subsequent 5-min freeze–thaw cycle. Subsequently, DNA is extracted (Gaviria-Figueroa et al. 2019).
pretreatment differs depending on the filter, and due to the lack of a standard pretreatment method, there are slight differences based on the research study design and objective.

3.3 Molecular and biotechnological methods for the identification of ARGs

Because air environmental conditions are extremely dynamic and complex in natural ecosystems, investigation of the occurrence and diversity of ARGs is very difficult (Liu et al. 2019). Most previous studies utilized widely employed molecular and biotechnological methods, such as quantitative real-time PCR (qPCR), amplicon targeted next-generation sequencing (16S rRNA), and microarray (GeoChip and PhyloChip)-based techniques, to evaluate the prevalence and levels of antibiotic resistance genes in environmental samples (Ju and Zhang 2015; Zhou et al. 2015; Yoo et al. 2017). The use of molecular and biotechnological methods in environmental microbiology studies is primarily focused on detecting genetic information in various types of environmental samples. In addition, high-resolution microbial community information can be obtained to better understand the ecological roles and environmental systems of microbes. Currently, high-throughput qPCR (HT-qPCR) and metagenomic approaches are regarded as the most useful methods to understand ARG occurrence, diversity, and profiling in environmental ARG monitoring (Port et al. 2014; Ju and Zhang 2015; Su et al. 2017; Yang et al. 2018b; Waseem et al. 2019; Yoo et al. 2020). Compared with previous ARG profiling methods, both HT-qPCR and metagenomic approaches can provide high-resolution ARG and MGE information and information on a greater number of ARG subtypes and HGT profiles with reliable accuracy and optimal time periods (Su et al. 2017; Waseem et al. 2019).

The HT-qPCR approach can simultaneously quantify thousands of nanoliter reactions in parallel in one run (Waseem et al. 2019). This technique can provide a large number of ARGs, MGEs, and gene-specific quantification of certain bacterial species in environmental samples. HT-qPCR has a high processing rate and acceptably high sensitivity/accuracy for the simultaneous evaluation of multiple ARGs (Lamas et al. 2016; Waseem et al. 2020; Yang et al. 2018b). In addition, the volume of reagents and chemicals is significantly lower in HT-qPCR than in traditional qPCR assays. Therefore, the HT-qPCR approach has been developed to determine ARG contamination and is an efficient method for monitoring antimicrobial resistance dissemination. Currently, four types of HT-qPCR platforms (WaferGen SmartChip, Biomark Dynamic Array Platform, Bio-Rad CFX384, and Applied Biosystem Open Array) have been used to profile ARGs and MGEs, as shown in Fig. 2 (Waseem et al. 2019). Among these platforms, the WaferGen SmartChip is most widely used to profile ARG occurrence and abundance because of its relatively large reaction volume (approximately 100 nL) and high analytical sensitivity compared to other HT-qPCR platforms (Table 4). WaferGen SmartChip systems also have a clear advantage in that they allow for the profiling of more than 1000 genes in a single run and in quadruplicate (Waseem et al. 2019). This technique allows the user to screen genes closer to the amplitude of microarray technologies than that achieved with other platforms (Waseem et al. 2019). However, HT-qPCR has some limitations. First, a large sample size is necessary for analysis as only one run is performed, and the cost of establishing the HT-qPCR platform is high, which makes it difficult to set up. In addition, reactions at the nanoliter scale make it difficult to recover and sequence amplified products (Waseem et al. 2019). This disadvantage may be overcome by applying a multiplex PCR step with a low number of cycles to specifically amplify the target DNA sequences. Second, the HT-qPCR array system requires qPCR arrays with appropriate specific primers. This parameter is most important because the specific binding of primers is dependent on annealing temperatures (Liu et al. 2019; Waseem et al. 2020).

Metagenomic approaches and developed bioinformatics tools can provide a rapid and economically feasible platform for identifying and characterizing ARGs from various environmental samples (Hendriksen et al. 2019; Nowrotek et al. 2019). Furthermore, these approaches have enhanced the study of phylogenetic characteristics and allowed the functional resolution of large numbers of environmental samples and clinical isolates, furthering understanding of ARG contamination and novel ARG evolution (Torres-Cortés et al. 2011; Kleinheinz et al. 2014). The metagenomic approach can profile identified resistance genes in unassembled reads or assembled sequences from the whole
genome of target organisms or environmental samples using ARG databases, such as the antibiotic resistance genes database (ARDB) (Liu and Pop 2009), ResFinder (Zankari et al. 2012), ARG-ANNOT (Gupta et al. 2014), The Comprehensive Antibiotic Resistance Database (CARD) (McArthur et al. 2013), and the structured ARG reference database (SARG) (Yang et al. 2016; Yin et al. 2018). Moreover, metagenomics provides information regarding the bacterial species, pathogens and virulence genes present. On the other hand, microbial genomes can be constructed through assembly and binning approaches that can provide the phylogeny and genetic location of the genes (Albertsen et al. 2013; Ju and Zhang 2015; Karkman et al. 2018). The sequences obtained from assembly or binning can then be compared with a reference database for annotation, shedding new light on the complex

**Fig. 2** Reaction volume and running time of various HT-qPCR platforms

| Platform                        | Reaction volume | Limit of detection | Reaction chamber | Running time |
|--------------------------------|-----------------|--------------------|------------------|--------------|
| Biomark Dynamic Array™         | 7 - 9 nl        | 88.1–98.41%*       | 4,608/2,304/9,216| 1 h + 2 h    |
| Wafergen SmartChip             | 100 nl          | 99.23–100%*        | 5,130            | 1 h + 2 h    |
| Bio-rad CFX384™ Real-Time PCR Detection System | 3000 nl         | 96%**              | 384              | 10 min + 2 h |
| Applied Biosystem OpenArray Platform | 33 nl           | 77.78–94.44%*      | 384              | 15 min + 4.5 h |

*Farr et al. (2015)

**Gough et al. (2019)
microbial communities and functions within environmental samples.

Metagenomic approaches also have some disadvantages. Metagenomic sequencing generally requires high DNA concentration and purity. In addition, the sequencing depth may have serious impacts on the completeness of ARG identification using the similarity search method (Zhang et al. 2015). According to Liu et al. (2019), approximately 10 Gb of high-quality metagenomic sequencing data (approximately $7 \times 10^7$ pairs of sequencing reads 150 bp in length) is suitable to provide sufficient sequencing depth. Furthermore, metagenomic analysis requires greater computational resources and data processing power. A previous study (Liu et al. 2019) revealed that the HT-qPCR approach is currently less time and cost-intensive for obtaining ARG profiles of the same samples than metagenomics analysis. However, since the advantages of the metagenomics method outweigh the disadvantages, many current studies still use the metagenomics method to profile ARGs and MGEs. Metagenomic approaches can be a good choice for general and comprehensive surveys of environmental ARGs. Therefore, it is necessary to conduct an antibiotic contamination study by making good use of the advantages and disadvantages of HT-qPCR and metagenomics.

4 Future perspectives

The acquisition and intake of airborne bacteria and associated ARGs by humans from the surrounding environments have been poorly reported. ARGs in water or soil can enter the atmosphere by aerosolization, resulting in a wider propagation range than in water or soil. Hence, the control of ARG pollution in air is inseparable from the control of ARGs in water and soil. However, most researchers currently focus on the generation and transmission of ARGs in bioaerosols and do not connect these with ARGs in soil and water (Gwenzi et al. 2022). In studies of regional and even global ARG management, the atmosphere, water and soil should be regarded as a whole, particularly the ARGs in bioaerosols, to comprehensively understand ARG contamination. Studies on bioaerosols consider the relationship with environmental factors important, but studies that analyze the relationship between ARGs and environmental factors are insufficient. Studies of airborne ARGs have found that the relationship with PM is highest, and research considering heavy metal pollutants, seasonal changes, and relative humidity is underway but remains insufficient. Various sampling methods have been used to detect ARGs in the atmosphere in several studies, but air environmental factors are most important during sampling period. In addition, because most methods for the detection of ARGs in the air developed thus far performed sampling in the local range, the spatial movement of ARGs and the ARGs according to seasonal changes and patterns of air pollution over time are unknown, and further research is absolutely needed in the future.

Reducing the production of ARGs at the source is also very important for controlling ARG contamination in air. Evaluating the viability and metabolic activity of detected ARB, the ability to transmit mobile genetic factors, and the phenotypic status are also important parameters for predicting the potential propagation path of ARGs. These efforts can be significantly contributed to expand the understanding of the ARGs propagation mechanism through the air environment. To date, DNA-based methods are useful for detecting the possibility of ARG propagation within indoor and outdoor environment because genes contained in dead bacteria can still form a repository for ARGs of surviving bacteria.

With the advancement of high-throughput techniques and bioinformatics tools such as HT-qPCR and metagenomics approaches, the knowledge gaps regarding the prevalence of ARGs in environmental systems has narrowed. However, despite researchers’ efforts, large knowledge gaps remain in the bioaerosol area. Bioaerosol studies are multidisciplinary, and resistance genes are found universally in diverse environments. Since data interpretation may vary depending on the scientific background of researchers, it is difficult to assess whether ARG quantitative differences in specific environments are relevant. To find the optimal methodology, it is essential to set up standard high-throughput methods to identify ARGs and MGEs, which may contribute to deeper insight into antibiotic resistance in bioaerosols because many technical details need to be studied for longer time periods to obtain reliable results. To gain a better understanding of ARG dissemination in bioaerosols, it is necessary to characterize entire bioaerosol communities, which requires the careful selection of
detection methods. Currently used protocols need to be reconsidered at every experimental stage to verify the optimal conditions for each particular situation. Depending on the target genes and/or airborne microorganisms, modifications to the sampling strategy and processes are necessary. It is also necessary to interpret and translate these data across various disciplines of bioaerosol research to better understand the impact of bioaerosols on human health.

The combination of high-throughput-based metagenomic analysis with HT-qPCR approaches would be relatively powerful for studying the fate and dynamics of ARGs in bioaerosols. The combination method provides the possibility of customization because metagenomics provides details regarding ARG occurrences and abundances in bioaerosols, and HT-qPCR provides quantitative information regarding the change in specific ARGs using the metagenomic results. The combined powers of high-throughput sequencing and qPCR can improve the detection of specific target microorganisms and ARGs in a complex and dynamic bioaerosol background. Bioaerosols are a research area of relatively high interest, and studies are needed to compare the differences in detected types and abundances of ARGs with metagenomics to verify HT-qPCR results. This advanced concept will also contribute to the development of advanced detection technologies and equipment in the near future to efficiently set up environmental monitoring systems.

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**Declarations**

**Conflict of interest.** The authors declare no competing financial interests.

**References**

Adams RI, Bhangar S, Pasut W, Arens EA, Taylor JW, Lindow SE, Nazaroff WW, Bruns TD (2015) Chamber bioaerosol study: outdoor air and human occupants as sources of indoor airborne microbes. PLoS ONE 10(5):e0128022

Albertsen M, Hugenholtz P, Skarszewski A, Nielsen KL, Tyson GW, Nielsen PH (2013) Genome sequences of rare, uncultured bacteria obtained by differential coverage binning of multiple metagenomes. Nat Biotechnol 31(6):533–538

Allen HK, Donato J, Wang HH, Cloud-Hansen KA, Davies J, Handelsman J (2010) Call of the wild: antibiotic resistance genes in natural environments. Nat Rev Microbiol 8(4):251–259

Asadi S, Bouvier N, Wexler AS, Ristenpart WD (2020) The coronavirus pandemic and aerosols: Does COVID-19 transmit via expiratory particles? Aerosol Sci Technol 54(6):635–638

Becker B, Cooper MA (2013) Aminoglycoside antibiotics in the 21st century. ACS Chem Biol 8(1):105–115

Blair JM, Webber MA, Baylay AJ, Ogoblu DO, Piddock LJ (2015) Molecular mechanisms of antibiotic resistance. Nat Rev Microbiol 13(1):42–51

Bragoszewska E, Biedron I (2018) Indoor air quality and potential health risk impacts of exposure to antibiotic resistant bacteria in an office rooms in Southern Poland. Int J Environ Res Public Health 15(11):2604

Bush K, Macielag MJ (2010) New β-lactam antibiotics and β-lactamase inhibitors. Expert Opin Ther Pat 20(10):1277–1293

Bylinski H, Gebicki J, Namiesnik J (2019) Evaluation of health hazard due to emission of volatile organic compounds from various processing units of wastewater treatment plant. Int J Environ Res Public Health 16(10):1712

Cao C, Jiang W, Wang B, Fang J, Lang J, Tian G, Jiang J, Zhu TF (2014) Inhalable microorganisms in Beijing’s PM2.5 and PM10 pollutants during a severe smog event. Environ Sci Technol 48(3):1499–1507

Chen Y, Su QJ, Zhang J, Li P, Chen H, Zhang B, Gin KYH, He Y (2019) High-throughput profiling of antibiotic resistance gene dynamic in a drinking water river-reservoir system. Water Res 149:179–189

Chen P, Guo X, Li F (2022) Antibiotic resistance genes in bioaerosols: Emerging, non-ignorable and pernicious pollutants. J Clean Prod 348:131094

Coleman KK, Nguyen TT, Yadana S, Hansen-Estruch C, Lindsley WG, Gray GC (2018) Bioaerosol sampling for respiratory viruses in singapore's mass rapid transit network. Sci Rep 8(1):17476

Dai P, Shen D, Tang Q, Huang K, Li C (2020) PM2.5 from a broiler breeding production system: the characteristics and microbial community analysis. Environ Pollut 256:113368

Dijkshoorn L, Nemec A, Seifert H (2007) An increasing threat in hospitals: multidrug-resistant Acinetobacter baumannii. Nat Rev Microbiol 5(12):939–951

Douroes J, Thorne P, Pearce N, Heederik D (2003) Bioaerosol health effects and exposure assessment: progress and prospects. Ann Occup Hyg 47(3):187–200

Du P, Du R, Ren W, Lu Z, Fu P (2018) Seasonal variation characteristic of inhalable microbial communities in PM2.5 in Beijing city. China Sci Total Environ 610–611:308–315

Echeverria-Palencia CM, Thulsiraj V, Tran N, Erickson CA, Melendez I, Sanchez MG, Walpert D, Yuan T, Ficara E, Senthilkumar N (2017) Disparate antibiotic resistance gene quantities revealed across 4 major cities in
California: a survey in drinking water, air, and soil at 24 public parks. ACS Omega 2(5):2255–2263

Farr RJ, Januszewski AS, Joglekar MV, Liang H, McAuley AK, Hewitt AW, Thomas HE, Loudovaris T, Kay TWM, Jenkins A (2015) A comparative analysis of high-throughput platforms for validation of a circulating microRNA signature in diabetic retinopathy. Sci Rep 5(1):1–11

Forsberg KJ, Patel S, Gibson MK, Lauber CL, Knight R, Fierer N, Dantas G (2014) Bacterial phylogeny structures soil resistomes across habitats. Nature 509(7520):612–616

Fröhlich-Nowoisky J, Kampf CJ, Weber B, Huffman JA, Pöhlker C, Andreae MO, Lang-Yona N, Burrows SN, Gunthe SS, Elbert W (2016) Bioaerosols in the earth system: climate, health, and ecosystem interactions. Atmos Res 182:346–376

Frączek K, Kozdrój J, Górny RL, Cyprowski M, Golofit-Szymczak M (2017) Fungal air contamination in distinct sites within a municipal landfill area. Int J Environ Sci Technol 14(12):2637–2648

Gao XL, Shao MF, Luo Y, Dong YF, Ouyang F, Dong WY, Li J (2016) Airborne bacterial contaminations in typical Chinese wet market with live poultry trade. Sci Total Environ 572:681–687

Gao M, Qiu T, Sun Y, Wang X (2018a) The abundance and diversity of antibiotic resistance genes in the atmospheric environment of composting plants. Environ Int 116:229–238

Gao XL, Shao MF, Wang Q, Wang LT, Fang WY, Ouyang F, Li J (2018b) Airborne microbial communities in the atmospheric environment of urban hospitals in China. J Hazard Mater 349:10–17

Gauthier-Levesque L, Bonfait L, Turgeon N, Veillette M, Perrrot P, Grenier D, Duchaine C (2016) Impact of serotype and sequence type on the preferential aerosolization of Streptococcus suis. BMC Res Notes 9(1):1–7

Gaviria-Figueroa A, Preisner EC, Hoque S, Feigley CE, Norman RS (2019) Emission and dispersal of antibiotic resistance genes through bioaerosols generated during the treatment of municipal sewage. Sci Total Environ 686:402–412

Ghosh B, Lal H, Srivastava A (2015) Review of bioaerosols in indoor environment with special reference to sampling, analysis and control mechanisms. Environ Int 85:254–272

Gilbert Y, Veillette M, Duchaine C (2010) Airborne bacteria and antibiotic resistance genes in hospital rooms. Aerobiologia 26(3):185–194

Gollakota ARK, Gautam S, Santosh M, Sudan HA, Gandhi R, Jebadurai VS, Shu C (2021) Bioaerosols: characterization, pathways, sampling strategies, and challenges to geo-environment and health. Gondwana Res 99:178–203

Gough R, Ellis J, Stark D (2019) Comparison and recommendations for use of Dientamoeba fragilis real-time PCR assays. J Clin Microbiol 57(5):e01466-e01518

Grydaki N, Colbeck I, Mendes L, Eleftheriadis K, Whitby C (2021) Bioaerosols in the Athens Metron: metagenetic insights into the PM10 microbiome in a naturally ventilated subway station. Environ Int 146:106186

Gupta SK, Padmanabhan BR, Diene SM, Lopez-Rojas R, Kempf M, Landraud L, Rolain JM (2014) ARG-ANNOT, a new bioinformatic tool to discover antibiotic resistance genes in bacterial genomes. Antimicrob Agents Chemother 58(1):212–220

Gwenzi W, Shamsizadeh Z, Gholiopour S, Nkaeem M (2022) The airborne antibiotic resistome: occurrence, health risks, and future directions. Sci Total Environ 804:150154

Haig CW, Mackay WG, Walker JT, Williams C (2016) Bioaerosol sampling: sampling mechanisms, bioefficiency and field studies. J Hosp Infect 93(3):242–255

Hamdy AM, El-Massry M, Kashef MT, Amin MA, Aziz RK (2018) Toward the drug factory microbiome: micro-bial community variations in antibiotic-producing clean rooms. OMICS J Integr Biol 22(2):133–144

Han Y, Wang Y, Li L, Xu G, Liu J, Yang K (2018) Bacterial population and chemicals in bioaerosols from indoor environment: sludge dewatering houses in nine municipal wastewater treatment plants. Sci Total Environ 618:469–478

Han Y, Yang K, Yang T, Zhang M, Li L (2019a) Bioaerosols emission and exposure risk of a wastewater treatment plant with A(2)O treatment process. Ecotoxicol Environ Saf 169:161–168

Han Y, Yang T, Chen T, Li L, Liu J (2019b) Characteristics of submicron aerosols produced during aeration in wastewater treatment. Sci Total Environ 696:134019

Han II, Yoo K (2020) Metagenomic profiles of antibiotic resistance genes in activated sludge, dewatered sludge and bioaerosols. Water 12(6)

He C, Mackay IM, Ramsay K, Liang Z, Kidd T, Knibbs LD, Johnson G, McNeale D, Stockwell R, Coulthard MG, Long DA, Williams TJ, Duchaine C, Smith N, Wainwright C, Morawska L (2017) Particle and bioaerosol characteristics in a paediatric intensive care unit. Environ Int 107:89–99

He P, Wu Y, Huang W, Wu X, Lv J, Liu P, Bu L, Bai Z, Chen S, Feng W (2020) Characteristics of and variation in airborne ARGs among urban hospitals and adjacent urban and suburban communities: a metagenomic approach. Environ Int 139:105625

Heald CL, Spracklen DV (2009) Atmospheric budget of primary biological aerosol particles from fungal spores. Geophys Res Lett 36(9)

Hendriksen RS, Munk P, Njage P, Bunnik BV, McNally L, Lukjancenko O, Röder T, Nieuwenhuijse D, Pedersen SK, Kjeldgaard J (2019) Global monitoring of antimicrobials in aerosols from indoor environments. Nat Commun 10(1):1–12

Hospodsky D, Qian J, Nazaroff WW, Yamamoto N, Bibby K, Hendriksen RS, Rismani-Yazdi H, Peccia J (2012) Human occupancy and field studies. J Hosp Infect 93(3):242–255

Hussin NHM, Sann LM, Shamsudin MN, Hashim Z (2011) Antimicrobial resistance genes in hospital rooms. OMICS J Integr Biol 22(2):133–144

Jin L, Xie J, He T, Wu D, Li X (2021) Airborne transmission of Staphylococcus aureus and sewage. Nat Commun 10(1):1–12

Jin L, Xie J, He T, Wu D, Li X (2012) Airborne transmission of Dientamoeba fragilis. Environ Int 146:106186

Johnson G, McNeale D, Stockwell R, Coulthard MG, Long DA, Williams TJ, Duchaine C, Smith N, Wainwright C, Morawska L (2017) Particle and bioaerosol characteristics in a paediatric intensive care unit. Environ Int 107:89–99

Hyde P, Mahalov A (2020) Contribution of bioaerosols to airborne particulate matter. J Air Waste Manag Assoc 70(1):71–77
resistance through the “One Health” lens. Crit. Rev Environ Sci Technol 1–22
Ju F, Zhang T (2015) Bacterial assembly and temporal dynamics in activated sludge of a full-scale municipal wastewater treatment plant. ISME J 9(3):683–695
Kalwasinska A, Burkowski A (2013) Municipal landfill sites as sources of microorganisms potentially pathogenic to humans. Environ Sci Process Impacts 15(5):1078–1086
Karkman A, Do TT, Walsh F, Virta MJP (2018) Antibiotic resistance genes in waste water. Trends Microbiol 26(3):220–228
Kathiriya T, Gupta A, Singh NK (2021) An opinion review on sampling strategies, enumeration techniques, and critical environmental factors for bioaerosols: an emerging sustainability indicator for society and cities. Environ Technol Innov 21:101287
King MD, Lacey RE, Pak H, Fearing A, Ramos G, Baig T, Smith B, Kousta A (2020) Assays and enumeration of bioaerosols-traditional approaches to modern practices. Aerosol Sci Technol 54(5):611–633
Kleinheinz KA, Joensen KG, Larsen MV (2014) Applying the ResFinder and VirulenceFinder web-services for easy identification of acquired antibiotic resistance and E. coli virulence genes in bacteriophage and prokaryote nucleotide sequences. Bacteriophage 4(2):27943
Kumari P, Woo C, Yamamoto N, Choi H (2016) Variations in abundance, diversity and community composition of airborne fungi in swine houses across seasons. Sci Rep 6(1):1–11
Labro MT (2004) Macrolide antibiotics: current and future uses. Expert Opin Pharmacother 5(3):541–550
Lamas A, Franco CM, Regal P, Miranda JM, Vázquez B, Cepeda A (2016) High-throughput platforms in real-time PCR and applications. Polymerase chain reaction for biomedical applications:15
Lane MA, Brownswod EA, Morgan JS, Babiker A, Vanairsdale SA, Lyon GM, Mehta AK, Ingersoll JM, Lindsley WG, Kraft CS (2020) Bioaerosol sampling of a ventilated patient with COVID-19. Am J Infect Control 48(12):1540–1542
Lang-Yona N, Ozturk F, Gat D, Akturk M, Dikmen E, Mihalopoulos N, Birgul A, Kurt-Karakus PB, Rudich Y (2020) Links between airborne fungi as sources of microorganisms potentially pathogenic to humans. Environ Sci Process Impacts 15(5):1078–1086
Li N, Chai Y, Ying GG, Jones KC, Deng WJ (2020b) Antibiotic resistance genes in Hong Kong kindergartens. Environ Pollut 260:114009
Li B, Li X, Yan T (2021a) A quantitative metagenomic sequencing approach for high throughput gene quantification and demonstration with environmental antibiotic resistance genes. Appl Environ Microbiol 87(16):e0087121
Li X, Wu Z, Dang C, Zhang M, Zhao B, Cheng Z, Chen L, Zhong Z, Ye Y, Xia Y (2021b) A metagenomic-based method to study hospital air dust resistance. Chem Eng J 406:126854
Liang Z, Yu Y, Ye Z, Li G, Wang W, An T (2020) Pollution profiles of antibiotic resistance genes associated with airborne opportunistic pathogens from typical area, Pearl River Estuary and their exposure risk to human. Environ Int 143:105934
Lin W, Zeng J, Wan K, Lv L, Guo L, Li X, Yu X (2018) Reduction of the fitness cost of antibiotic resistance caused by chromosomal mutations under poor nutrient conditions. Environ Int 120:63–71
Ling AL, Pace NR, Hernandez MT, LaPara TM (2013) Tetacycline resistance and Class 1 integron genes associated with indoor and outdoor aerosols. Environ Sci Technol 47(9):4046–4052
Liu B, Pop M (2009) ARDB—antibiotic resistance genes database. Nucleic Acids Res 37(suppl_1):D443–D447
Liu D, Chai T, Xia X, Gao Y, Cai Y, Li X, Miao Z, Sun L, Hao H, Roesler U, Wang J (2012) Formation and transmission of Staphylococcus aureus (including MRSA) aerosols carrying antibiotic-resistant genes in a poultry farming environment. Sci Total Environment 426:139–145
Liu X, Xiao P, Guo Y, Liu L, Yang J (2019) The impacts of different high-throughput profiling approaches on the understanding of bacterial antibiotic resistance genes in a freshwater reservoir. Sci Total Environment 693:133585
Luhung I, Uchida A, Lim SBY, Gaultier NE, Kee C, Lau KJX, Guasareva ES, Heinle CE, Wong A, Premkhrishnan BNV (2021) Experimental parameters defining ultra-low biomass bioaerosol analysis. NPJ Biofilms Microbiomes 7(1):1–11
Ma X, Zhang Q, Zhu Q, Liu W, Chen Y, Qiu R, Wang B, Yang Z, Li H, Lin Y (2015) A robust CRISPR/Cas9 system for convenient, high-efficiency multiplex genome editing in monocot and dicot plants. Mol Plant 8(8):1274–1284
Mainelis G (2020) Bioaerosol sampling: classical approaches, advances, and perspectives. Aerosol Sci Technol 54(5):496–519
Mao Y, Ding P, Wang Y, Ding C, Wu L, Zheng P, Zhang X, Li X, Wang L, Sun Z (2019) Comparison of cultivable antibiotic-resistant bacteria in polluted and non-polluted air in Beijing. China Environ Int 131:104936
Mbareche H, Brisebois E, Veillette M, Duchaine C (2017a) Bioaerosol sampling and detection methods based on molecular approaches: No pain no gain. Sci Total Environment 599–600:2095–2104
Mbareche H, Veillette M, Bonfait L, Dubuis ME, Benard Y, Marchand G, Bilodeau GJ, Duchaine C (2017b) A next generation sequencing approach with a suitable
bioinformatics workflow to study fungal diversity in bioaerosols released from two different types of composting plants. Sci Total Environ 601–602:1306–1314
McArthur AG, Waglechner N, Nizam F, Yan A, Azad MA, Baylay AJ, Bhullar K, Canova MJ, Pascale GD, Ejim J (2013) The comprehensive antibiotic resistance database. Antimicrob Agents Chemother 57(7):3348–3357
McEachran AD, Blackwell BR, Hanson JD, Wooten KJ, Mayer GD, Cox SB, Smith PN (2015) Antibiotics, bacteria, and antibiotic resistance genes: aerial transport from cattle feed yards via particulate matter. Environ Health Perspect 123(4):377–343
Meadow JF, Altrecht AE, Kembel SW, Kline J, Mhureche R, Moriyama M, Northcutt D, O’Connor TK, Womack AM, Brown GZ, Green JL, Bohannan BJ (2014) Indoor airborne bacterial communities are influenced by ventilation, occupancy, and outdoor air source. Indoor Air 24(1):41–48
Mentese S, Arisoy M, Rad AY, Güllü G (2009) Bacteria and fungi levels in various indoor and outdoor environments in Ankara. Turkish Clean (weinh) 37(6):487–493
Mirhoseini SH, Nikaeeen M, Shamsizadeh Z, Khamanahad H (2016a) Hospital air: a potential route for transmission of infections caused by beta-lactam-resistant bacteria. Am J Infect Control 44(8):898–904
Mirhoseini SH, Nikaeeen M, Satoh K, Makimura K (2016b) Assessment of airborne particles in indoor environments: applicability of particle counting for prediction of bioaerosol concentrations. Aerosol Air Qual Res 16(8):1903–1910
Nowrotek M, Jawoiewicz L, Harnisz M, Plaza GA (2019) Cultureomics and metagenomics: in understanding of environmental resistome. Front Environ Sci Eng 13(3):1–12
Ouyang W, Gao B, Cheng H, Zhang L, Wang Y, Lin C, Chen J (2020) Airborne bacterial communities and antibiotic resistance gene dynamics in during rainfall. Environ Int 134:105318
Pal C, Bengtsson-Palme J, Kristiansson E, Larsson DG (2016) The structure and diversity of human, animal and environmental resistomes. Microbiome 4(1):54
Pei M, Zhang B, He Y, Su J, Gin K, Lev O, Shen G, Hu S (2019) State of the art of tertiary treatment technologies and controlling antibiotic resistance in wastewater treatment plants. Environ Int 131:105026
Perrott P, Turgeon N, Veillette M, Duchaine C (2013) Preferential aerosolisation of respiratory pathogens. American Association for Aerosol Research 32nd Annual Conference
Port JA, Cullen AC, WallaceJCE SMN, Faustman EM (2014) Metagenomic frameworks for monitoring antibiotic resistance in aquatic environments. Environ Health Perspect 122(3):222–228
Prussin AJ II, Schwake DO, Marr LC (2017) Ten questions concerning the aerosolization and transmission of Legionella in the built environment. Build Environ 123:684–695
Roberts MC (2002) Resistance to tetracycline, macrolide-lincosamide-streptogramin, trimethoprim, and sulfonamide drug classes. Mol Biotechnol 20(3):261–283
Sanchez HM, Echeverria C, Thulsiraj V, Zimmer-Faust A, Flores A, Laitz M, Healy G, Mahendra S, Paulson SE, Zhu Y, Jay JA (2016) Antibiotic resistance in airborne bacteria near conventional and organic beef cattle farms in California, USA. Water Air Soil Pollut 227(8)
Selvam A, Xu D, Zhao Z, Wong JW (2012) Fate of tetracycline, sulfonamide and fluoroquinolone resistance genes and the changes in bacterial diversity during composting of swine manure. Bioresour Technol 126:383–390
Shamsizadeh Z, Nikaeeen M, Esfahani BN, Mirhoseini SH, Hatamzadeh M, Hassanzadeh A (2017) Detection of antibiotic resistant Acinetobacter baumannii in various hospital environments: potential sources for transmission of Acinetobacter infections. Environ Health Prev Med 22(1):44
Shin SK, Kim J, Ha SM, Oh HS, Chun J, Sohn J, Yi H (2015) Metagenomic insights into the bioaerosols in the indoor and outdoor environments of childcare facilities. PLoS ONE 10(5):e0126960
Song L, Wang C, Jiang G, Ma J, Li Y, Chen H, Guo J (2021) Bioaerosol is an important transmission route of antibiotic resistance genes in pig farms. Environ Int 154:106559
Su H, Liu S, Hu X, Xu X, Xu W, Xu Y, Li Z, Wen G, Liu Y, Cao Y (2017) Occurrence and temporal variation of antibiotic resistance genes (ARGs) in shrimp aquaculture: ARGs dissemination from farming source to reared organisms. Sci Total Environ 607:357–366
Sun X, Li D, Li B, Sun S, Yabo SD, Geng J, Ma L, Qi H (2020) Exploring the disparity of inhalable bacterial communities and antibiotic resistance genes between hazy days and non-hazy days in a cold megacity in Northeast China. J Hazard Mater 398:122984
Tao Y, Yue Y, Wang J (2021) Abundance and diversity of antibiotic resistance genes possibly released to ambient air by experiments in biology laboratories. Sci Total Environ 797:149147
Tiedje JM, Fang W, Manaa CM, Virta M, Sheng H, Liping MA, Zhang T, Edward TOPP (2019) Antibiotic resistance genes in the human-impacted environment: a one health perspective. Pedosphere 29(3):273–282
Torres-Cortés G, Millán V, Ramírez-Saad HC, Nisa-Martínez R, Toro N, Martínez-Abarca F (2011) Characterization of novel antibiotic resistance genes identified by functional metagenomics on soil samples. Environ Microb 13(4):1101–1114
Usachev EV, Agranovskiy IE (2012) Internally controlled PCR system for detection of airborne microorganisms. J Environ Monit 14(6):1631–1637
Van Boeckel TP, Pires J, Silvester R, Zhao C, Song J, Criscuolo NG, Gilbert M, Bonhoeffer S, Laxminarayan R (2019) Global trends in antimicrobial resistance in animals in low-and middle-income countries. Science 365(6459):44
Veillette M, Bonifait M, Marchand G, Duchaine C (2016) Bioaerosols exposure in indoor composting installations: classical and molecular approaches and preferential aerosolization. In: Paper read at 4th workplace and indoor aerosols conference 20–22 April 2016 Barcelona, Spain
WHO (2018) WHO Report in surveillance of antibiotic consumption. World Health Organisation, Geneva
WHO (2019) Global antimicrobial resistance surveillance system (GLASS) report. World Health Organisation, Geneva
Wang FH, Qiao M, Su JQ, Chen Z, Zhou X, Zhu YG (2014) High throughput profiling of antibiotic resistance genes in urban park soils with reclaimed water irrigation. Environ Sci Technol 48(16):9079–9085

Wang J, Ben W, Zhang Y, Yang M, Qiang Z (2015) Effects of thermophilic composting on oxystercycline, sulfamethazine, and their corresponding resistance genes in swine manure. Environ Sci Processes Impacts 17(9):1654–1660

Wang Y, Wang C, Song L (2019) Distribution of antibiotic resistance genes and bacteria from six atmospheric environments: exposure risk to human. Sci Total Environ 694:133750

Waseem H, Jameel S, Ali J, Rehman HSU, Tauseef I, Farooq U, Jamal A, Ali MI (2019) Contributions and challenges of high throughput qPCR for determining antimicrobial resistance in the environment: a critical review. Molecules 24(1):163

Waseem H, Ur Rehman HS, Ali J, Iqbal MJ, Ali MI (2020) Global trends in ARGs measured by HT-qPCR platforms. In Antibiotics and Antimicrobial Resistance Genes in the Environment. Elsevier

Wei J, Li Y (2016) Airborne spread of infectious agents in the indoor environment. Am J Infect Control 44(9):S102–S108

Woo C, An C, Xu S, Yi SM, Yamamoto N (2018) Taxonomic diversity of fungi deposited from the atmosphere. ISME J 12(8):2051–2060

Xie J, Jin L, Luo X, Zhao Z, Li X (2018) Seasonal Disparities in Airborne Bacteria and Associated Antibiotic Resistance Genes in PM2.5 between Urban and Rural Sites. Environ Sci Technol Lett 5(2):74–79

Xie J, Jin L, He T, Chen B, Luo X, Feng B, Huang W, Li J, Fu P, Li X (2019) Bacteria and antibiotic resistance genes (ARGs) in PM2.5 from China: implications for human exposure. Environ Sci Technol 53(2):963–972

Xie W, Li Y, Bai W, Hou J, Ma T, Zeng X, Zhang L, An T (2021) The source and transport of bioaerosols in the air: a review. Front Environ Sci Eng 15(3):44

Xu Y, Guo C, Luo Y, Lv J, Zhang Y, Lin H, Wang L, Xu J (2016) Occurrence and distribution of antibiotics, antibiotic resistance genes in the urban rivers in Beijing, China. Environ Pollut 213:833–840

Yadana S, Coleman KK, Nguyen TT, Hansen-Estruch C, Kalimuddin S, Thoon KC, Low JGH, Gray GC (2019) Monitoring for airborne respiratory viruses in a general pediatric ward in Singapore. J Public Health Res 8(3):1407

Yang Y, Jiang X, Chai B, Ma L, Li B, Zhang A, Cole JR, Tiedje JM, Zhang T (2016) ARGs-OAP: online analysis pipeline for antibiotic resistance genes detection from metagenomic data using an integrated structured ARG-database. Bioinformatics 32(15):2346–2351

Yang Y, Zhou R, Chen B, Zhang T, Hu L, Zou S (2018a) Characterization of airborne antibiotic resistance genes from typical bioaerosol emission sources in the urban environment using metagenomic approach. Chemosphere 213:463–471

Yang Y, Song W, Lin H, Wang W, Du L, Xing W (2018b) Antibiotics and antibiotic resistance genes in global lakes: a review and meta-analysis. Environ Int 116:60–73

Yin X, Jiang XT, Chai B, Li L, Yang Y, Cole JR, Tiedje JM, Zhang T (2018) ARGs-OAP v2. 0 with an expanded SARG database and Hidden Markov Models for enhancement characterization and quantification of antibiotic resistance genes in environmental metagenomes. Bioinformatics 34(13):2263–2270

Yoo K, Lee TK, Choi EJ, Yang J, Shukla SK, Hwang SI, Park J (2017) Molecular approaches for the detection and monitoring of microbial communities in bioaerosols: a review. J Environ Sci 51:234–247

Yoo K, Yoo H, Lee JM, Shukla SK, Park J (2018) Classification and regression tree approach for prediction of potential hazards of urban airborne bacteria during Asian dust events. Sci Rep 8(1):11823

Yoo K, Yoo H, Lee J, Choi EJ, Park J (2020) Exploring the antibiotic resistome in activated sludge and anaerobic digestion sludge in an urban wastewater treatment plant via metagenomic analysis. J Microbiol 58(2):123–130

Yu Y, Liang Z, Liao W, Ye Z, Li G, An T (2021) Contributions of meat waste decomposition to the abundance and diversity of pathogens and antibiotic-resistance genes in the atmosphere. Sci Total Environ 784:147128

Zankari E, Hasman H, Cosentino S, Vestergaard M, Rasmussen S, Lund O, Aarestrup FM, Larsen MV (2012) Identification of acquired antimicrobial resistance genes. J Antimicrob Chemother 67(11):2640–2644

Zhang T, Li X, Wang M, Chen H, Yang Y, Chen QL, Yao M (2019) Time-resolved spread of antibiotic resistance genes in highly polluted air. Environ Int 127:333–339

Zhang T, Yang Y, Pruden A (2015) Effect of temperature on removal of antibiotic resistance genes by anaerobic digestion of activated sludge revealed by metagenomic approach. Appl Microbiol Biotechnol 99(18):7771–7779

Zhao Y, Wang Q, Chen Z, Mao D, Luo Y (2021) Significant higher airborne antibiotic resistance genes and the associated inhalation risk in the indoor than the outdoor. Environ Pollut 268(Pt B):115620

Zhou H, Han T, Fennell DE, Mainelis G (2013) Release of free DNA by membrane-impaired bacterial aerosols due to aerosolization and air sampling. Appl Environ Microbiol 79(24):7780–7789

Zhou J, He Z, Yang Y, Deng Y, Tringe SG, Alvarez-Cohen L (2015) High-throughput metagenomic technologies for complex microbial community analysis: open and closed formats. Mbio 6(1):e02288-e2314

Zhou Z, Liu Y, Lin ZJ, Shuai XY, Zhu L, Xu L, Meng LX, Sun YJ, Chen H (2021) Spread of antibiotic resistance genes and microbiota in airborne particulate matter, dust, and human airways in the urban hospital. Environ Int 153:106501

Zhou Z, Shuai X, Lin Z, Meng L, Ba X, Holmes MA, Chen H (2022) Short-term inhalation exposure evaluations of airborne antibiotic resistance genes in environments. J Environ Sci 122:62–71
Zielinski W, Korzeniewska E, Harnisz M, Hubeny J, Buta M, Rolbiecki D (2020) The prevalence of drug-resistant and virulent Staphylococcus spp. in a municipal wastewater treatment plant and their spread in the environment. Environ Int 143:105914

Zielinski W, Korzeniewska E, Harnisz M, Drzymala J, Felis E, Bajkacz S (2021) Wastewater treatment plants as a reservoir of integrase and antibiotic resistance genes: an epidemiological threat to workers and environment. Environ Int 156:106641

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