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Study on the Scavenging Effect of Steady-state Displacement Air Purification System on Indoor Bioaerosol

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ABSTRACT

Many types of microorganisms, including SARS-CoV-2, can spread through aerosols. Indoor medical environments are abundant in bioaerosols, which can cause infections among medical staff members and patients in hospitals. Given the ongoing COVID-19 pandemic, using a steady-state displacement air purification system may reduce the spread of SARS-CoV-2 and other microorganisms. In this study, we analyzed the purification effect of the steady-state displacement air purification system on bioaerosols in the bronchoscopy room of the hospital. In particular, bioaerosols were collected from the bronchoscopy room at different periods from April to May 2021. Among them, the microorganisms contained in the bioaerosol were identified using next-generation sequencing (NGS) and culture and strain identification. During the experiment, we took 5 sampling points to collect the bioaerosols. The total purification efficiency was 88.0% (NGS) and 87.5% (microbial culture count and identification). The results were significantly different between the purified and unpurified groups. In an occupant environment in the bronchoscopy room, the steady-state displacement air purification system exerted a favorable removal effect on the bioaerosols. Such purification efficiency may help prevent the in-hospital spread of COVID-19 and various infectious diseases.

Keywords: Bronchoscopy room, Indoor air

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1 INTRODUCTION

The spread of established infectious pathogens such as viruses has an important impact on human health (Judson and Munster, 2019). Indoor bioaerosols in hospitals and other medical establishments can cause infections among medical staff members and patients. SARS-CoV-2 can survive in indoor aerosols (Jarvis, 2020). Other indoor bioaerosols include Mycobacterium tuberculosis, measles virus, varicella-zoster virus (Tellier *et al.*, 2019), hand-foot-and-mouth disease–causing virus (Colenutt *et al.*, 2016), Ebola virus, and Middle East respiratory syndrome coronavirus. Reduction of indoor bioaerosol pollution may help prevent and control infection spread in public places, including medical environments.

High-throughput sequencing technologies, such as next-generation sequencing (NGS) technology, have been used to analyze the genome of microbes directly from various environmental samples (Madsen *et al.*, 2015; Segata *et al.*, 2013). Yooseph *et al.* (2013) used a wet cyclone portable air sampler to collect air samples at a flow rate of 450 L min^{-1}, each with a sampling volume of 54 000 L, and used whole-genome sequencing to study airborne microbial communities in various indoor

and outdoor environments in New York City. Barberán *et al.* (2014) applied high-throughput sequencing technology to characterize the atmospheric sedimentary microbial communities collected in northeastern Spain for 3 years. In the past few years, high-throughput sequencing technologies such as NGS have been used to characterize microbial communities in various environmental samples (Madsen *et al.*, 2015). Microbial culture-based identification and colony counting methods are simple and low-cost techniques. The microorganisms in the air are collected and cultured on a semi-solid medium. The results are expressed as the number of colonies in CFU (colony forming units). A single colony is often formed by a single microorganism; therefore, CFU provides information on the number of microorganisms present in the sample (Ghosh *et al.*, 2015). If we need to obtain information on the types of microorganisms, we can also further identify the species (Heidelberg *et al.*, 1997). Compared with Sanger sequencing (first-generation sequencing technology), NGS can sequence hundreds of thousands to millions of nucleic acid molecules at a time with high efficiency, thereby facilitating a detailed and comprehensive analysis of the transcriptome and genome of a species.

2 METHODS

2.1 Experimental Equipment and Experimental Materials

We used the following equipment: a steady-state replacement flow air purification system (Steady-State Displacement Flow Clean and Disinfection System; China Aoxiang), a circulating water vacuum pump (China Lichen), a 37-mm filter membrane sampling clip (US SKC), and a gelatin filtration membrane (Sartorius, Germany).

2.2 Introduction to the Steady-State Displacement Flow Air Purification System

The Aoxiang air purification system is characterized by a steady-state displacement flow field and high-efficiency air filtration technology, which is an energy-saving and efficient air cleaning technology. In this system, between the air outlet and inlet, a "vector flow"—one-way propelling airflow—is established to remove particles and aerosols with a minimum amount of diffusion from the indoor environment and form an air isolation barrier in the controlled area. Thus, it is a purely physical air purification technology. Fig. 1 presents the schematics of this system.

2.3 Grouping

We collected bioaerosol samples from the bronchoscopy room of the Second Hospital of Hebei Medical University during different periods from April to May 2021. The microorganisms in the bioaerosol samples were identified using NGS and culture-based microbial identification techniques with the purifier turned off (the unpurified group) and on (the purified group).

2.4 Sample Collection Method

Under the normal operating conditions of the bronchoscopy room, a gelatin filter membrane was used to collect indoor bioaerosols. The aerosol collection began half an hour after the patients or medical staff entered the bronchoscopy room. The sampling device is illustrated in Figs. 2(B) and 2(C).

Five sampling membranes (1–5) were used to sample the unpurified group for 1–3 h. Subsequently, the purifier was turned on for 40 min, during which no sampling was performed. After 40 min, with the purifier still on, five sampling membranes (A–E) were used to sample the aerosols of the purified group for 1–3 h. The sampling times of the purified and unpurified groups were consistent. The sampling flowchart is illustrated in Fig. 2(D). The samplings were conducted during regular working hours, and each sampling membrane contained a total sampling of 39.5 h. NGS detection was undertaken by Shanghai Bingyuan Medical Technology. According to Shanghai Bingyuan Medical Technology., this technology can detect 560 types of clinically common microorganisms—including bacteria, fungi, viruses, and parasites, particularly bacteria and fungi—and 70 types of viruses. Culture-based microbial identification was performed at the clinical laboratory of the Second Hospital of Hebei Medical University. After sampling, sampling membranes 1 and 3–5

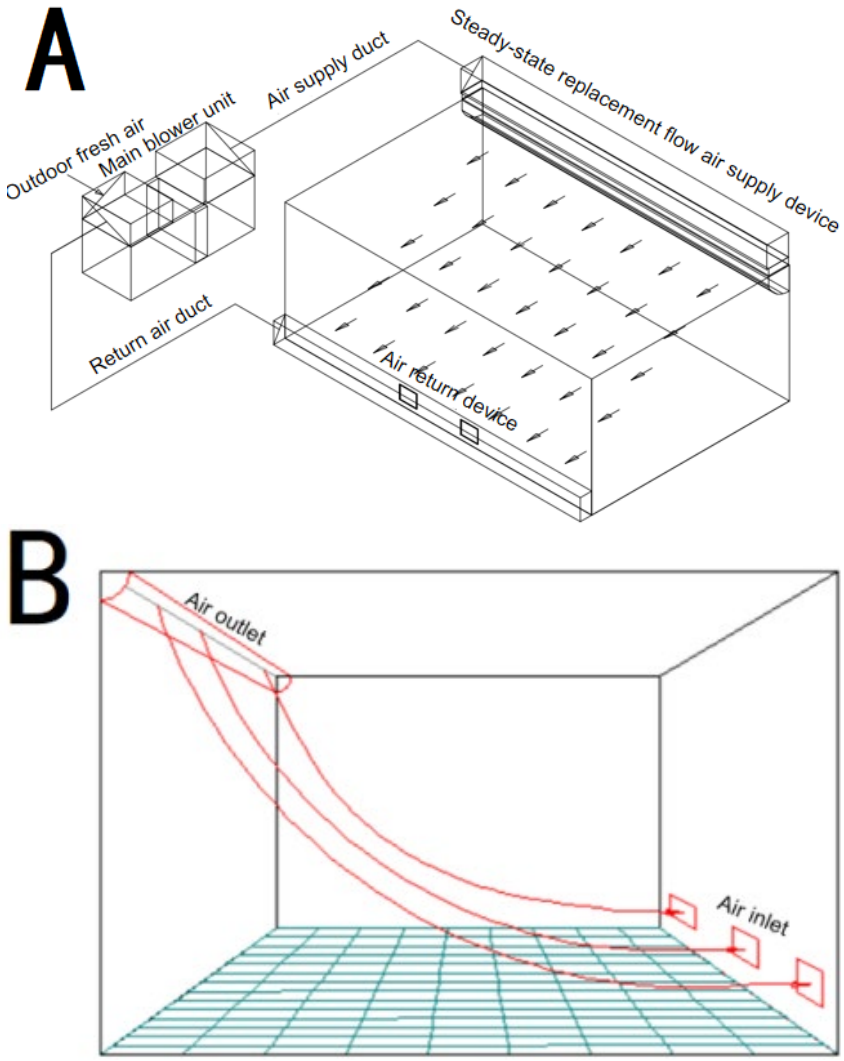

Fig. 1. (A) Schematic of the steady-state replacement flow air supply system. (B) Schematic of its working principle.

(the unpurified group) as well as A and C-E (the purified group) were dissolved separately in 4 mL of the NGS special specimen storage solution, followed by a 7-min water bath at 37°C. The solutions obtained in this step were tested with NGS (total air volume: 94 800 L). Sampling membranes 2 and B were dissolved separately in 2 mL of the normal saline, followed by a 7-min water bath at 37°C. Next, 1 mL of each specimen was extracted, inoculated by streaking on both nutrient agar medium and Sabouraud medium, and then cultivated in a CO_2 incubator (Thermo Fisher) under the following conditions: nutrient agar medium, 35°C for 48 h; Sabouraud medium, 26°C for 72 h (total air volume: 23 700 L).

To overcome the confounders of uncertainty in the number of patients, type of disease, and time of visit; insufficiency of air collection to reach the lower limit of detection; and other multivariable problems, a long-duration (39.5 h) and large-volume (118 500 L) method was used to more comprehensively compare the purification efficiency of a single microorganism. The samplings were conducted for 16 working days over 1 month. The amount of air collected was sufficiently large to represent the average purification efficiency of the bioaerosol in the bronchoscopy room, thus reflecting more statistical power than studies with shorter sampling times or lower air volumes.

2.5 Distribution of Sampling Points

The bioaerosol sampling point distribution is illustrated in Fig. 2(A). Four of 5 sampling points were placed at the height of 1.5 m from the ground, and the distance from the patient to the

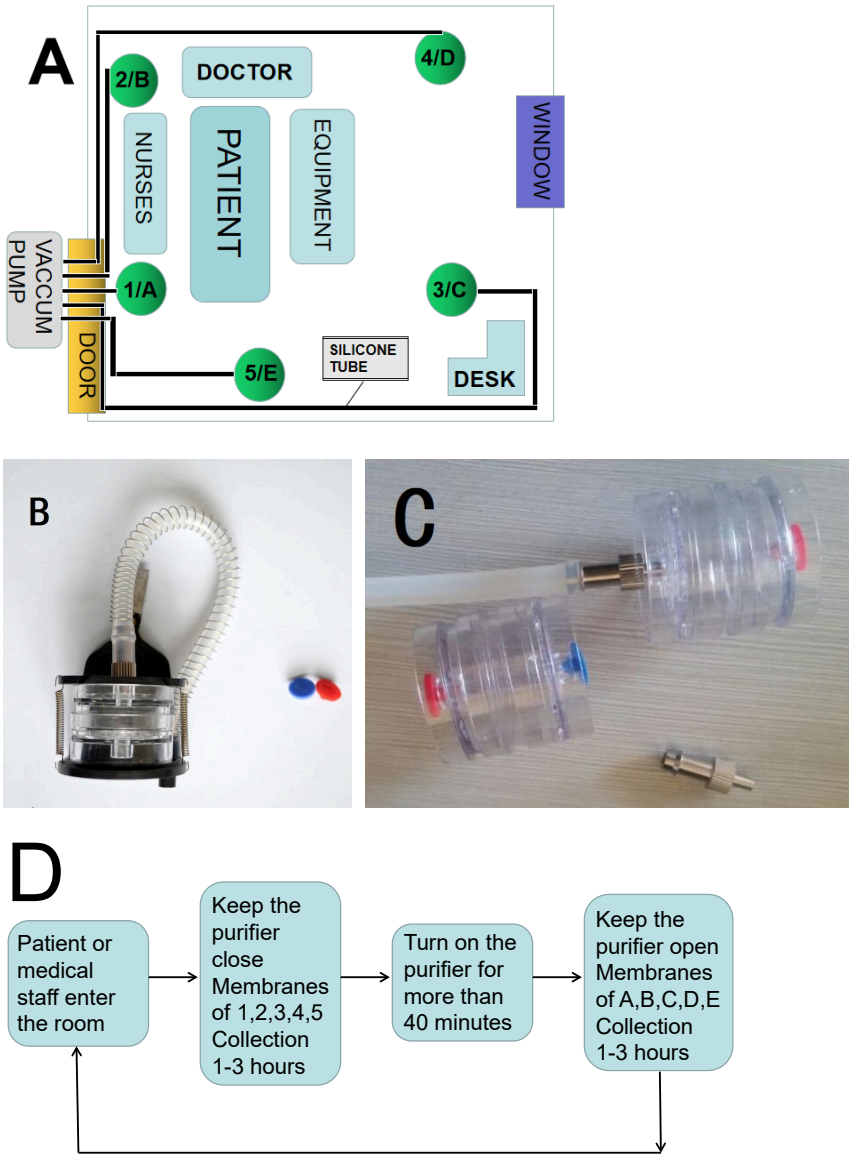

Fig. 2. (A) Placement of the sampling membranes in the bronchoscopy room; (B, C) Equipment for installing the membrane: the sampling clamp; (D) Sampling flowchart.

sampling points was greater than 2 m. The sampling point 2/B was approximately 1 m from the ground. The dimensions of the bronchoscopy room were 5 m × 6 m × 3 m (volume = 90 m^3). Moreover, 0–20 procedures a day were conducted during the study period, and the total working time was 8–12 h a day. Conventional disinfection measures comprised a spray disinfector and ultraviolet radiation regularly during nonworking hours. During the sampling process, the staff wore surgical masks. On most working days during the sampling period, approximately 3–20 patients and 7–10 physicians and nurses were on duty each day to execute operations; all staff members wore hats and masks, and the surgeons wore a hat, a mask, gloves, and a surgical gown. The experimental conditions were as follows: temperature of 23–26°C and humidity of 40%–65%.

2.6 Detection Method

2.6.1 NGS detection steps

2.6.1.1 Nucleic acid extraction

First, 2 mL of sample solution was centrifuged at 13000 rpm for 10 min. The supernatant was discarded to obtain a sample volume of 500 μL in the tube. The centrifuged sample was

resuspended and transferred to a grinding tube with preinstalled glass beads (0.1 and 0.5 mm). The tube cover was sealed tight, after which the tube was fixed to the adapter of a fully automatic sample rapid grinding machine (jxfstprp-48 l, Shanghai Jingxin) that was operated at 60 Hz for 10 min.

The ground sample was used for extracting and purifying DNA/RNA (zymoBIOMICS DNA/RNA Miniprep Kit, R2002). The extracted DNA/RNA products could be directly used for downstream multiplex amplification and library building.

2.6.1.2 Library preparation

Reverse transcription reagent (MonScript) purchased from Mona Biotechnology (Rtiii all-in-one mixture, mr05001) was used to reverse transcribe the RNA product into cDNA. Furthermore, multiplex PCR amplification was performed using the pathogen-targeted sequencing Library Building Kit (Pathogeno One standard edition, sj0005; Bingyuan Medical Technology Co., Ltd.), with the cDNA obtained from the reverse transcription reaction and the previously extracted DNA products serving as the reaction templates; subsequently, the pathogen target gene sequences in the samples were enriched. The PCR amplification process was executed in two rounds. The products obtained in the first round of PCR amplification were sorted using DNA purification magnetic beads; thus, pure target fragment products were obtained. After the second round of PCR amplification, a sequencing linker and a barcode sequence used for sample identification were added. The derived products were again purified using DNA, after which the library for pathogen sequencing was obtained.

2.6.1.3 Library quality inspection and mixing

The prepared library was tested through agarose gel electrophoresis. The normal library fragment size was approximately 350 bp, and no detailed dimers or nonspecific bands were observed. Subsequently, a Qubit 4.0 fluorometer (Invitrogen) was used to quantify the library concentration, and the constituents of the library were mixed according to the quantification results.

2.6.1.4 High-throughput sequencing

A Qubit 4.0 fluorometer was used to quantify the concentration of the mixed library. Subsequently, the library was diluted to a final concentration of 4 nm, and 5 μL of the diluted library was mixed with 5 μL of freshly prepared 0.2 N NaOH. The mixture was next shaken in a vortex mixer, centrifuged at 280 g for 1 min, and then placed at room temperature for 5 min to denature the library. The denatured library was subjected to high-throughput sequencing by using the Illumina Miseq Reagent Nano Kit. The average data volume of the library was determined to be 0.03–0.05 m reads, and the sequencing read length was pe60.

2.6.1.5 Data filtration and analysis

The original data were first identified using the connector. The identified reads were cut off and then sequenced, after which low-quality filtering was performed to retain high-quality data. The high-quality data were analyzed for primer identification, and reads with correct alignment at both ends were maintained. The maintained reads were then aligned with pathogen sequences in databases such as RefSeq and GenBank, which are available on the NCBI website. Finally, after the alignment process, the pathogen species and content in the samples could be determined.

The efficiency of the removal of bioaerosol pollutants was derived using the following equation: purification efficiency = (copy number of the unpurified group − copy number of the purified group)/copy number of the unpurified group.

2.6.2 The steps of culture-based microbial identification are as follows

Sampling membranes 2 and B were dissolved separately in 2 mL of the normal saline, followed by a 7-min water bath at 37°C. Next, 1 mL of each specimen was extracted, inoculated by streaking on both nutrient agar medium and Sabouraud medium, and then cultivated in a CO_2 incubator (Thermo Fisher) under the following conditions: nutrient agar medium, 35°C for 48 h; Sabouraud medium, 26°C for 72 h (total air volume: 23 700 L). For culture-based microbial identification, after the culture process, the culture medium was photographed and preserved,

and each colony was identified using various species identification methods such as physical morphology and biochemistry. VITEK 2 AST-GN09 (France) and VITEK 2 AST-GP67 (France) kits were used to identify specific microbial species. The microbial identification machine used was the Vitek2 Compact Automatic Biological Analyzer. Its technical indicators: 997 kinds of bacterial resistance phenotype identification, rapid bacterial identification, drug sensitivity report, fully automatic operation, and 99% accuracy of bacterial identification. Its main function is to identify G + bacteria, G-bacteria, yeast and anaerobic bacteria and conduct drug sensitivity test.

The total colony count was compared between the 2 groups by using the following formula: Efficiency of removing bioaerosol pollution = purification efficiency = (colony count in the unpurified group − colony count in the purified group)/colony count in the unpurified group.

2.6.3 Statistical analysis

The researchers used SPSS statistics 26 for nonparametric tests.

2.6.4 Case study

We retrieved information on patients undergoing bronchoscopy during the sampling period and recorded their clinical microbiological test results, such as sputum culture, blood culture, respiratory pathogen antibody detection, bronchoalveolar lavage fluid culture, and bronchoalveolar lavage fluid NGS.

3 RESULTS

3.1 NGS Detection

Efficiency of removal of bioaerosol pollution = 88.0%.

The results are illustrated in Fig. 3.

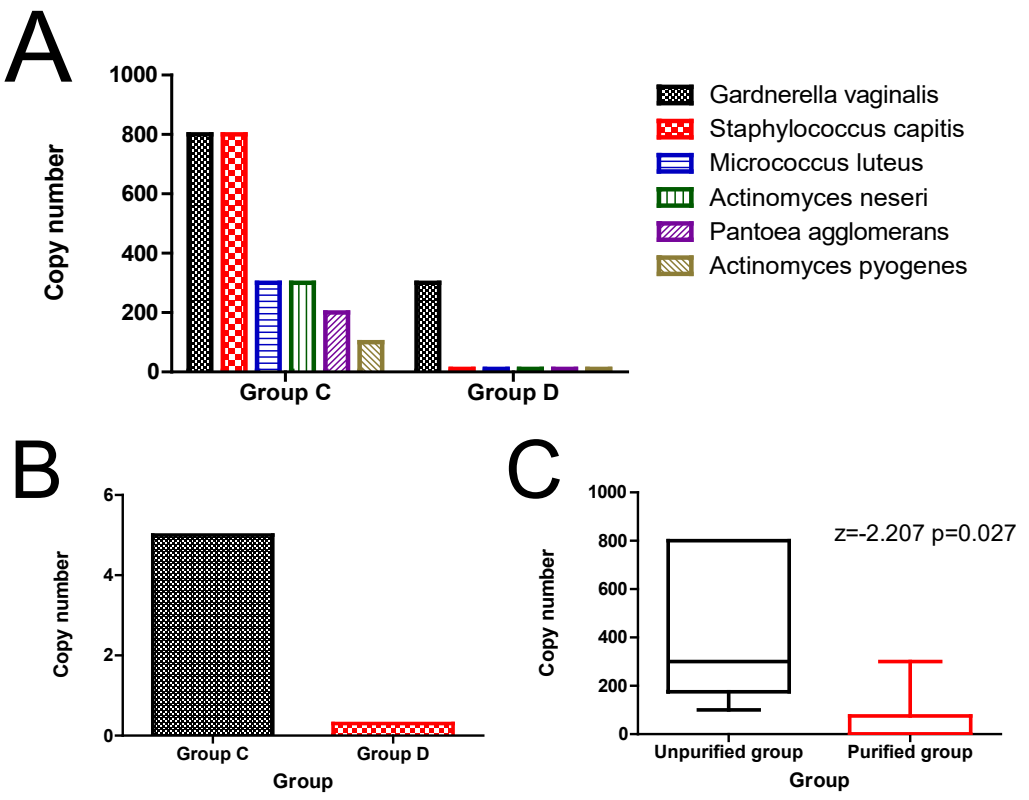

Fig. 3. Mild-to-high copy number results of NGS test: (A) NGS comparison results of the unpurified group and purified group. (B) Total copy number results of NGS comparison results of the unpurified group and purified group. (C) Statistical results of the unpurified group and purified group.

The purification efficiencies of individual microorganisms are as follows: *Gardnerella vaginalis:* 62.5%, *Staphylococcus capitis:* 100%, *Micrococcus luteus:* 100%, *Actinomyces naevitii:* 100%, *Pantoea agglomerans:* 100%, and purulent actinomycetes bacteria: 100%.

A significant difference was noted between the NGS-derived copy numbers of different microorganisms between the unpurified and purified groups ($\alpha = 0.05$ and $P = 0.027$).

Efficiency of removing bioaerosol pollution = 88.0%.

3.2 Results of Microbial Culture and Identification

3.2.1 Colony count results

Efficiency of removing bioaerosol pollution = 87.5%.

The results are illustrated in Fig. 4.

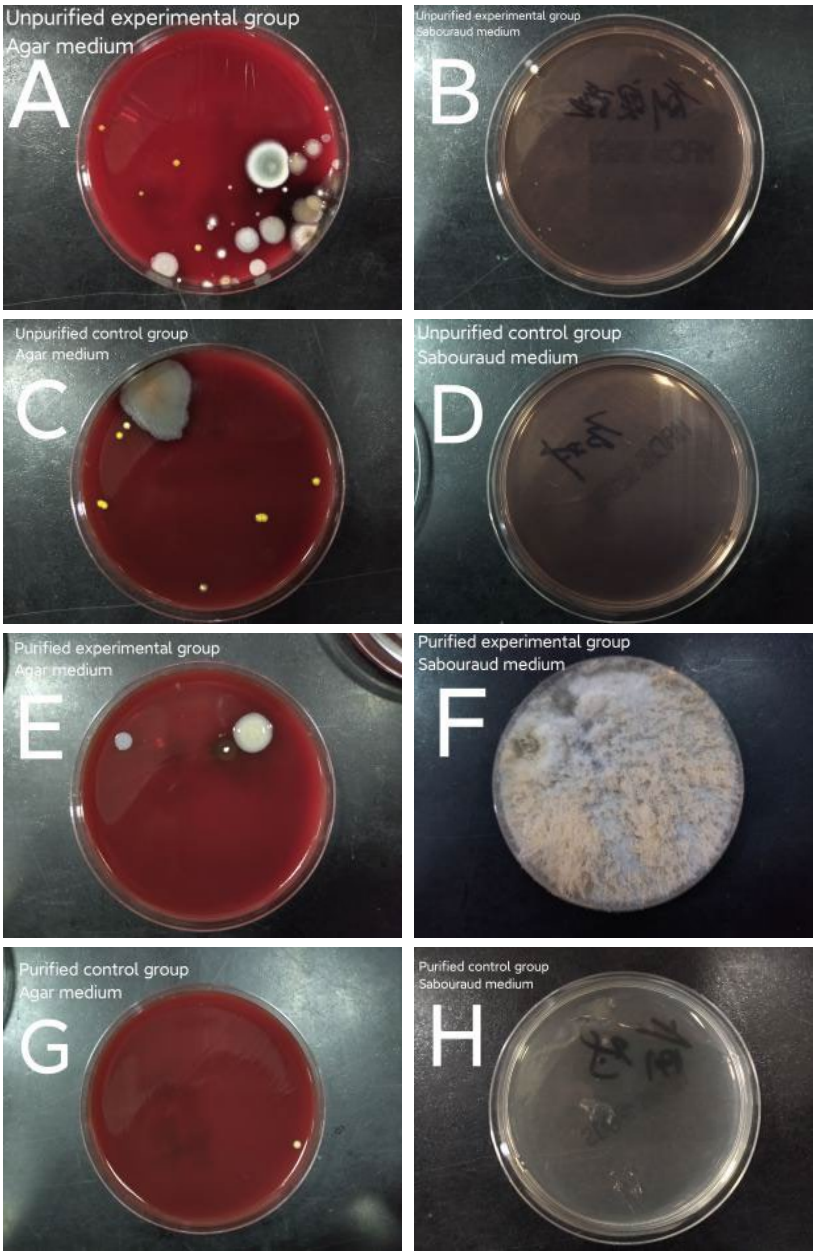

Fig. 4. Results of microbial culture and colony count. (A, B) Unpurified test group. Number of colonies: 32. (C, D) Unpurified control group. Number of colonies: 9. (E, F) Purified test group. Number of colonies: 4. (G, H) Purified control group. Number of colonies: 1. (A, C, E, G) Agar medium. (B, D, F, H) Sabouraud medium.

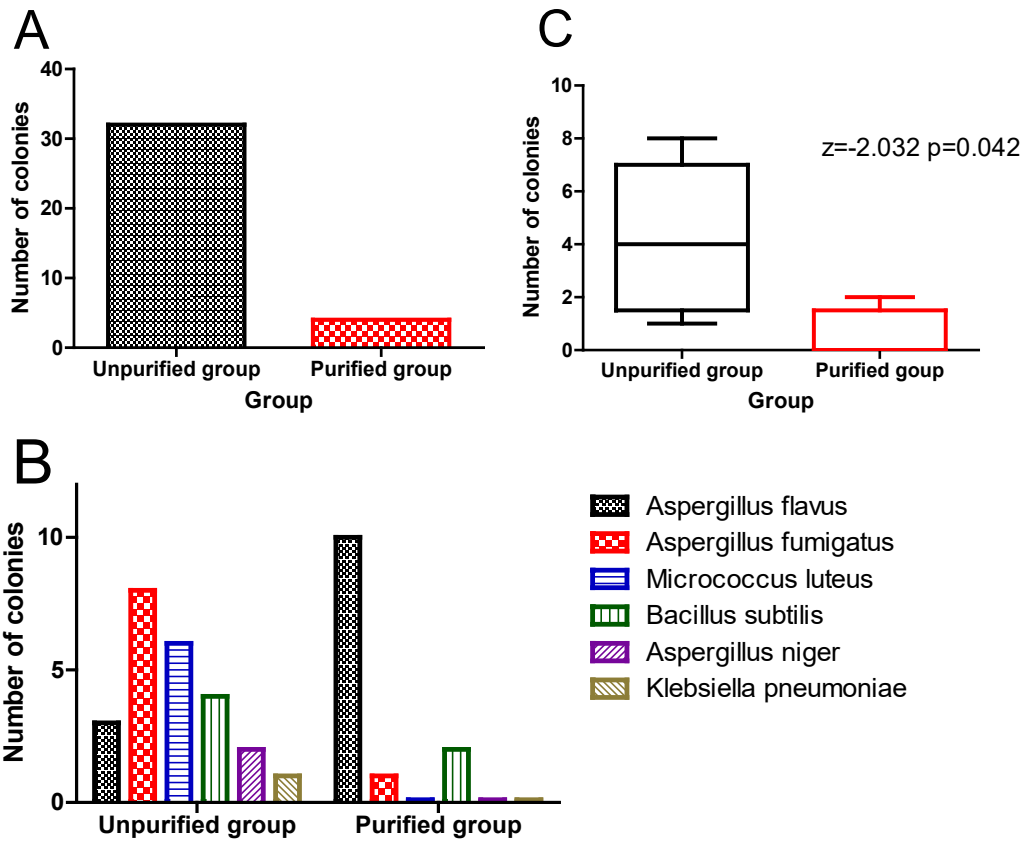

Fig. 5. Results of culture-based microbial identification analysis: (A) Total number of colonies. (B) Microorganisms identified in the unpurified and purified groups. (C) Statistical results of the 2 groups.

3.2.2 Identification results of bacterial and fungal species

The researchers identified the dominant colonies in the culture medium. The results are illustrated in Fig. 5.

Among them, *Aspergillus flavus* was a special case and is discussed separately in the Discussion section. The purification efficiencies of the other 5 microorganisms were as follows: *Aspergillus fumigatus*: 87.5%, *Aspergillus niger*: 100%, *Klebsiella pneumoniae*: 100%, *Micrococcus luteus*: 100%, and *Bacillus subtilis*: 50%.

We conducted nonparametric tests for the remaining 5 microorganisms by using SPSS statistics 26, and the results are as follows:

The difference in the number of colonies of different types of microorganisms between the 2 groups was significant ($\alpha = 0.05$, $P = 0.042$).

3.3 Case Study

During the sampling period of the unpurified group, the corresponding microorganisms that were consistent with the experimental results were as follows: Klebsiella pneumoniae, Actinomyces neisseria, Staphylococcus capitis, Gardnerella vaginalis, Pseudomonas aeruginosa spp., Stenotrophomonas maltophilia, and Fusarium spp., whereas the only corresponding microbe in the purified group was Aspergillus flavus. The information are illustrated in Table 1.

4 DISCUSSION

Luongo *et al.* (2017) obtained samples from the filter for microbiological testing, which indirectly confirmed the purifying effect of the filter. However, the microorganisms on the filter may reproduce

Table 1. Comparison of microbiological detection results obtained in this study with those obtained in patients undergoing bronchoscopy during the study period.

Sampling days	Microbes detected in the unpurified group	Microbes detected in the purified group
Day 3	*Klebsiella pneumoniae*	
Day 4		*Micrococcus luteus*
Day 5	*Pseudomonas aeruginosa*, Actinomycetes, *Gardnerella vaginalis*, *Fusarium*	
Day 6	*Klebsiella pneumoniae*	*Pseudomonas aeruginosa*
Day 7	*Staphylococcus capitis*, *Klebsiella pneumoniae*	Actinomycetes, *Aspergillus flavus*, *Pseudomonas aeruginosa*
Day 8	*Pseudomonas aeruginosa*, *Stenotrophomonas maltophilia*	
Day 9	*Pseudomonas aeruginosa*, *Klebsiella pneumoniae*	
Day 11	*Klebsiella pneumoniae*	
Day 13	*Stenotrophomonas maltophilia*	
Day 14	*Pseudomonas aeruginosa*	
Day 15	*Klebsiella pneumoniae*	
Day 16	*Pseudomonas aeruginosa*	

or die and decompose; thus, the data obtained could not directly reflect the microorganisms in the air. Some studies have proven that air purifiers can reduce the concentration of allergens, improve the clinical performance of patients with allergic rhinitis, and reduce the need for antiallergic drugs (Park *et al.*, 2017; Park *et al.*, 2020). Chen *et al.* (2018) demonstrated that air purifiers can reduce the total colony count on the fungal culture medium. However, they did not test for bacterial species, and their method did not allow the purification effect to be assessed for each microorganism. Lee *et al.* (2019) used aerosol generators to artificially make certain types of microorganisms into aerosols and verified the purifying effect of air purifiers in the ideal environment of a closed experimental chamber. Although all these approaches can intuitively reflect the purification effect, none have evaluated the purification effect of the microorganisms that actually exist in the environment under a dynamic clinical environment. Dee *et al.* (2019) investigated whether air purifiers can reduce the pathogenicity of a certain virus to animals by detecting the infection rate of animals to a certain virus; however, this method cannot directly reflect the direct purification effect of the purifier on biological aerosol.

Our results indicated a considerable reduction in the total number of copies of microorganisms and the total number of colonies in the dynamic clinical environment of the bronchoscopy room through the use of the purifier used in this study. The overall purification efficiency was 88.0% and 87.5% through NGS and rapid culture-based microbial identification, respectively. Moreover, species and quantity of single specific microorganism identified using NGS and microbial culture also has dropped a lot; the purification efficiency ranged from 50% to 100% but was 100% for most strains. This implies that the new purifier has good purification efficiency for indoor biological aerosols. The long-term, large-capacity sampling method used in this experiment conforms to statistical laws. Some related studies have confirmed the purification effect of several types of air purifiers. The results obtained from our comparison of the total number of copies with the number of colonies are similar to those of previous studies (Yang *et al.*, 2018); however, unlike those studies, we collected data from an actual dynamic working clinical environment.

Our data also indicate that the purification effect for a single microorganism varies somewhat. This may be related to the different times of entering the bronchoscopy room and the different number of coughs by the different patients, which were uncontrollable factors in this study. However, this also implies that even in the dynamic clinical environment, the steady-state displacement air purification system maintains high bioaerosol removal efficiency.

The purifier system used in this study considerably reduced the total amount of microbes of most species, except Aspergillus flavus. We found that only one patient was positive for Aspergillus flavus on microbiological examination; this patient entered the bronchoscopy room during the sampling period of the purified group. The positive samples were obtained from sampling

membranes 2/B, which was 2 m away from the patient and was, thus, the closest to the patient among all the sampling membranes. The purifier's indoor air flow is gentle and cannot normally be detected by humans. The 2/B sampling point was determined to be closest to the patient's mouth and nose; this thus afforded sufficient time and opportunity to collect the aerosols generated by the patient when coughing, talking, or breathing. The aerosols containing Aspergillus flavus was eliminated by the purifier after it was produced by the patient and collected by the sampling membranes. Aspergillus flavus was not detected on NGS because sampling membranes 1 and 3–5 were positioned further away from the patient, the sampling time was short, and the aerosols generated by the patient were not detected using the sampling membranes in time. This situation is unavoidable in the dynamic environment of this experiment. This explains why the number of colonies of Aspergillus flavus in the purified group was greater than that in the unpurified group. Nevertheless, the overall microbial clearance remained unaffected. Both NGS and culture-based microbial detection had surprisingly similar results, indicating that in the dynamic diagnosis and treatment environment, the purification efficiency of the new purifier for indoor bioaerosol was relatively stable, ranging from 87.5% to 88%.

The main limitation of culture-based microbial identification is that only a fraction of the microorganisms present in the environment can be cultured and identified (Heidelberg *et al.*, 1997). Pillai and Ricke (2002) have demonstrated that culture conditions limit the growth of viable and culturable microorganisms: mesophilic bacteria such as Bacillus subtilis exhibit adequate colony formation at temperatures between 5 and 55°C, whereas thermophilic microorganisms are best cultured at temperatures above 50°C. In our study, Gardnerella vaginalis was detected using NGS; it is an anaerobic bacterium that is difficult to cultivate. Similarly, not all the microorganisms identified using NGS were suitable for culture; the culture conditions set were the most commonly used conditions for microbial culture and may not be suitable for detecting microorganisms that cannot survive outside the human body. Furthermore, because NGS can detect both live and dead bacteria, some of those detected using NGS may be dead bacteria that could not form colonies. Nevertheless, NGS can only detect the microorganisms above the detection limit of 2 copies mL^{-1} and within its detection range. Thus, both NGS and culture-based microbial identification methods have their advantages and disadvantages. Although NGS is more sensitive, the culture-based microbial identification methods can distinguish between dead and alive microorganisms. Whether it is the result of colony counting or identification of bacterial species, they are all microorganisms in the living state of the reaction. Therefore, the combination of these 2 methods could objectively reflect the true reliability of the data.

The purification time in the current study was set to 40 min. According to our pre-experimental results, when the steady-state displacement air purification system was turned on for approximately 10 min, a relatively obvious particle purification effect could be observed; this was confirmed in the closed experimental chamber. However, during the normal operation of the bronchoscopy room, a more stable particle purification effect can be achieved 40 min after the purifier is turned on. Compared with traditional disinfection methods, the new purifier can be used in the medical environment at any time, which can maximize the safety of medical personnel and patients and decrease the risk of nosocomial infection.

The COVID-19 pandemic has caused serious casualties and economic losses. Many outbreaks have been closely related to bioaerosols in indoor environments (Kirtipal *et al.*, 2020). Studies have indicated that infection in the endoscopic room is related to cross-infection of endoscopic instruments (Kong *et al.*, 2021), but our results imply that infection in the bronchoscopy room may also have a certain relationship with bioaerosols. However, numerous bioaerosols exist in the hospital, which can cause drug resistance after repeated infections by patients, making treatment more difficult. The new type of purifiers can reduce the spread of nosocomial infections and the emergence of drug-resistant bacterial infections. The steady-state displacement air purification system used in the present study had a removal efficiency of approximately 85%, which may be useful for epidemic control and reduction of nosocomial infections.

The current 222-nm "light vaccine," which belongs to the ultraviolet range of light, can kill SARS-CoV-2 in the air without causing harm to the human body. The light vaccine can emit radiation energy with a wavelength of 222 nm. Once the light is substantially absorbed by a novel coronavirus, it destroys the helical structure of the ribonucleic acid (RNA) of the virus, thus preventing the replicability of the virus and achieving disinfection and sterilization effects. Accordingly, light

irradiated at a specific spectral wavelength can have disinfection and sterilization effects against viruses, bacteria, and fungi. Because the short wavelength of 222 nm cannot penetrate the skin or eyes, it is harmless to the human body; hence, the corresponding light can be used for disinfection even in environments occupied by people. Therefore, this light vaccine solves a challenging problem in the field of disinfection: how to realize human–machine coexistence and real-time disinfection. After the light vaccine instrument is turned on, its krypton chloride excimer lamp can emit light under the excitation of high-frequency and high-voltage current. After passing through the nanoscale high-precision optical interference membrane filter, pure light that is harmless to the human body can be emitted at 222 nm to disinfect the air and object surface. The disinfection and sterilization process is direct and does not produce any harmful substances or chemical residues to which humans are sensitive (Kitagawa *et al.*, 2021). By contrast, although the conventional ultraviolet disinfection protocol has a wider range of sterilization, it can harm the human body. Conventional disinfectant spraying can also regularly disinfect bioaerosols floating in the air. Steady-state displacement air cleaning systems clean and replace indoor air anytime. Combined with the use of light vaccines and regular disinfectant sprays, this purification system can minimize the spread of pathogenic microorganisms, reduce nosocomial infections, and ensure the safety of medical staff members and patients.

5 CONCLUSION

1. In the dynamic environment of the bronchoscopy room, the steady-state displacement air purification system has a strong bioaerosol removal effect.
2. The microorganisms involved in this study may be spread through aerosols.

ADDITIONAL INFORMATION AND DECLARATIONS

Ethical Approval and Consent to Participation (Human Ethics, Animal Ethics, or Plant Ethics)

Not applicable.

Agree to Publish

Author confirms: The work described has not been published before and has not been considered for publication elsewhere; preprint exists: link: Lijuan Wu, XIXIN YAN. Under the dynamic environment of normal diagnosis and treatment in the bronchoscopy room, the study of the removal efficiency of the new air purifier on microbial aerosols, 25 August 2021, PREPRINT (Version 1) available at Research Square https://doi.org/10.21203/rs.3.rs-812319/v1

The publication has been approved by all co-authors. Its publication has been approved by the competent authority of the institution in which the work was conducted.

Availability of Data and Materials

Not applicable.

Competing Interests

The authors have no conflicts of interest or financial relationships that affect this manuscript.

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Author Contributions

Lijuan Wu: Methods, Software, Writing, Data Management, Editing; Zhigang Cai: Method; Jihong Li: Method; Jingwen Li: Method; Hao Pu: Method; Xianghong Liu: Methods, Data Management; Xixin Yan: Methods, Supervision.

The manuscript was drafted by Wu Lijuan and reviewed by Yan Xixin. Both authors have contributed to, reviewed, and approved the final version of the manuscript.

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