Assessment of Indoor Bioaerosols in Public Spaces by Real-time Measured Airborne Particles

Hsiao-Lin Huang*, Mei-Quei Lee, Hao-Wun Shih

Department of Occupational Safety and Health, Chia Nan University of Pharmacy and Science, Tainan City 71710, Taiwan

Abstract

Humans spend a considerable amount of time indoors, and indoor biological airborne pollutants may harm human health. Active bioaerosol samplers and conventional microbiological culture methods, which are widely applied in studies of airborne microbial contamination, are not only unable to perform continuous monitoring over long periods, but are also time-consuming and expensive. In order to rapid assess indoor airborne microbial contamination, multiple linear regression models were constructed by statistically analyzing the measured bioaerosol samples and the real-time measured mass and number concentrations of airborne particles using a direct reading instrument from 43 air-conditioned public spaces. There were significant positive correlations of indoor airborne bacterial and fungal concentrations with indoor size-segregated particle mass and number concentrations. The predictive power of the model was sufficient for predicting indoor bacterial concentrations from the indoor and outdoor size-segregated particle number concentrations as independent variables. Particle number concentration outperforms particle mass concentration as an independent variable in predicting indoor bioaerosol concentrations. The prediction model for indoor bacterial bioaerosol levels constructed in this study could facilitate a rapid assessment of potential airborne bacterial contamination via the simple and feasible measurement of particle number concentration, thus helping to improve the management and maintenance of indoor air quality.

Keywords: Suspended particulate; Biohazard; Aerosol; Indoor air; $PM_{2.5}$.

* Corresponding author. Tel: +886 6 2664911 ext. 6245; Fax: +886 6 2667320
E-*mail address*: hlhuang@mail.cnu.edu.tw

INTRODUCTION

Social patterns and lifestyles change over time. People spend nearly 90% of their time indoors, and hence indoor air quality (IAQ) has become an important environmental issue of concern to all (Sundell, 2004). Long-term exposure to indoor environments with inadequate air exchange and poor air quality may cause sick building syndrome (SBS), allergic reactions, respiratory tract infection, and lung cancer (Dales *et al.*, 2008; Joshi, 2008). Bioaerosols are suspended biological particles consisting of microorganisms or organism-derived materials (Brandl *et al.*, 2008; Douwes *et al.*, 2003). Indoor airborne biological pollutants have numerous sources, including outdoor air, human bodies, wallpaper, carpet, resuspended particles, air conditioning systems, and animal waste (Chao *et al.*, 2002; Hargreaves *et al.*, 2003; Hospodsky *et al.*, 2012; Kalogerakis *et al.*, 2005; Lindemann *et al.*, 1982, Pastuszka *et al.*, 2000; Tseng *et al.*, 2011). Exposure to indoor bioaerosols, such as bacteria, molds, viruses, pollen, pet allergens, mycotoxins, and bacterial endotoxins, may cause health effects, such as SBS, allergies, asthma, poisoning, infection, and even cancer (Bowers *et al.*, 2011; Douwes *et al.*, 2003; Schleibinger *et al.*, 2004).

The concentration of airborne bacteria or fungi was calculated by dividing numbers of colonies formed on the culture medium by air volume (m^3), therefore, the unit of bioaerosol concentration is expressed as the colony forming unit (CFU) m^{-3}. At present, there is rare direct reading instrument capable of rapidly determining the bioaerosol concentrations (CFU m^{-3}). Only a few instrument but expensive can detect the number concentrations and size distributions of airborne biological pollutants. To date, the most widely applied bioaerosol sampling method is still the inertial impaction method using culture media. However, the subsequent conventional microbiological cultivation takes 3–5 days to obtain biological pollutant concentrations at the sampling site, which may delay the response to poor IAQ. Although conventional microbiological culture methods are unable to measure the concentration of biological pollutants

in real time, there have been numerous studies investigating the correlation of indoor bioaerosols with indoor and outdoor air and environmental parameters, such as ventilation, house age, number of indoor personnel, temperature, relative humidity, wind speed, CO_2, and size-segregated particle number concentrations (total, ultrafine, and submicron particle number concentrations), and particle mass concentrations ($PM_{2.5}$ and PM_{10}) (Agranovski *et al.*, 2004; Bartlett *et al.*, 2004; Goh *et al.*, 2000; Hargreaves *et al.*, 2003; Luoma and Batterman, 2001; McDonagh *et al.*, 2014; Raval *et al.*, 2012; Tseng *et al.*, 2011; Zhu *et al.*, 2003).

In addition, some studies have established linear or non-linear statistical correlations between bioaerosol concentrations and different variables to predict the concentration of indoor airborne biological pollutants such as correlations between bacterial bioaerosols and particle number concentration in different indoor environments (Mirhoseini *et al.*, 2016; Parat *et al.*, 1999), fungal concentration and relative humidity in office buildings (Law *et al.*, 2001), fungal bioaerosols and building age, ambient temperature, relative humidity, CO_2, and ventilation in primary schools (Bartlett *et al.*, 2004), bacterial bioaerosols and particle size range in cabins with a controllable environment (Tham and Zuraimi, 2005), bacterial bioaerosols with temperature and relative humidity in air-conditioned offices (Mui *et al.*, 2008), and bacterial and fungal bioaerosols in office buildings with building monitoring and management data (Tseng *et al.*, 2011). These studies investigated one or more independent variables, and were confined to the same indoor space or type of space. Therefore, the constructed indoor bioaerosol prediction models are only applicable to a single space, building, or type of space in the geographical location where the study was performed.

Taiwan has conditions favorable for microbial growth due to a humid and warm subtropical climate throughout the year. Hence, many buildings may breed high concentrations of bioaerosols, and indoor air pollution has thus become an important issue in Taiwan. Currently, Tseng *et al.*

(2011) is the only research group in Taiwan that has constructed mathematical bioaerosol models to predict indoor bacterial and fungal bioaerosol concentrations in single and multiple office buildings in the metropolitan areas of Taipei. However, this study involved a large number of independent variables, including the number of floors, ventilation type, indoor personnel density, indoor and outdoor temperatures, relative humidity, and CO_2, PM_{10}, and $PM_{2.5}$ concentrations. The constructed model is inapplicable to other types of indoor spaces as it is limited to office buildings in Taipei. Furthermore, it involves too many variables for a rapid prediction of indoor bioaerosols and might be limited by the time resolution of the measurements for these variables or availability of these measurements.

In order to rapidly assess the potential of indoor bioaerosol pollution, such that management measures can be taken to prevent biohazards, real-time measurement of indoor and outdoor air parameters (particle mass and number concentrations) in multiple types of air-conditioned public spaces in southern Taiwan was performed using only a direct reading instrument. Then, multiple linear regression (MLR) models for bioaerosol concentrations in public spaces were constructed. The purpose of this study was that the prediction model can augment the conventional culture method and be used as a quick reference for IAQ management of biological pollutants through the indirect and rapid prediction of indoor bioaerosol concentrations.

MATERIALS AND METHODS

Sampling site

In this study, we focused on public spaces in southern Taiwan. Our sampling plan is outlined in Table 1. Bioaerosols and airborne particles were sampled from 43 sampling sites that can be classified into 9 types—government agencies, shopping malls, classrooms, hospitals, restaurants, gyms, libraries, convenience stores, and kindergartens—all of which had air conditioning systems

switched-on during the sampling period. Areas with high indoor personnel density and poor air ventilation were selected as sampling points. The sampling heights were about 1.2–1.5 meters above the ground. One sampling point was allocated for each outdoor location, while 1–4 sampling points were allocated for each indoor location, according to the room size at the sampling site. Our study allocated a total of 83 indoor sampling points and 43 outdoor sampling points.

Air sampling parameters

In this study, we selected independent variables to estimate the indoor bioaerosol concentration (dependent variable), and primarily considered important factors affecting indoor bioaerosol and other air parameters that can be measured in real time using direct reading instruments. Indoor bioaerosols—biological particles suspended in the air—may be derived from human respiration, skin or shed material from the body, indoor activities that resuspend deposited particles, outdoor air, etc. Microorganisms in the air are able to survive both as individual cells and through particle or intercellular adhesion. The selected air sampling parameters only included indoor and outdoor particle mass and number concentrations based on the kind of thinking that biological particles suspended in the air are also aerosols. The bioaerosol sampling included both bacteria and fungi.

Sampling period and frequency

The sampling process conducted between October 2014 and February 2015. All air samples were collected during standard business hours. The sampling of bacterial and fungal bioaerosols at each sampling point was repeated twice, at 30 seconds each. The bioaerosol sampling was completed within 5 minutes, and the bacterial and fungal bioaerosol concentrations were

measured twice to obtain the mean values. Both particle number and mass concentrations were automatically recorded every minute. To coordinate the bioaerosol sampling times and facilitate subsequent comparative analysis, we set the total measurement time to 5 minutes, and the 5-minute average values were used.

Bioaerosol measurements

Airborne bacteria and fungi were sampled onto tryptone soya agar (HiMedia Laboratories Pvt. Ltd., Mumbai, India) and malt extract agar (HiMedia Laboratories Pvt. Ltd., Mumbai, India) using the MAS-100 bioaerosol sampler (Merck Inc., USA) at a flow rate of 100 L/min. Cultures were incubated at 30±1°C for 48±2 hours (bacterial) and 25±1°C for 4±1 days (fungal). Bioaerosol concentrations were calculated from the colony forming units (CFU) and adjusted using the positive hole conversion table. During the measurement of bioaerosols, CO_2 was also measured using an indoor IAQ monitoring instrument (IAQ-Calc, Model 7545, TSI Inc., USA). Zero and span calibrations for CO_2 were performed on a monthly basis.

Particle concentration measurements

Airborne particle mass and number concentrations were measured using the particle size analyzer (Grimm, Model 1.109, Germany), which was returned to the manufacturer for calibration annually. The measuring principle of the analyzer is to use a semiconductor laser as light source to detect the light scattering of single particle. The scattering light pulse of every single particle is counted while a particle is passing through the laser beam. The intensity of its scattering light signal is classified to a certain particle size. Therefore, the particle size distribution can be measured and it also provides the basis for calculating the particle mass. Finally, the particle number concentration and mass concentration can be calculated based on the

151 sampling volume of 1.2 L min^{-1}. The analyzer can detect particles over a wide size range from
152 0.25 μm up to 32 μm. The particle mass concentration (MC) measurement included
153 size-segregated mass concentration intervals of <1.0, 1–2.5, 2.5, 2.5–10, and >10 μm ($PM_{1.0}$,
154 $PM_{1\text{-}2.5}$, $PM_{2.5}$, $PM_{2.5\text{-}10}$, and PM_{10}). The cutoff diameter for bioaerosols sampled with the
155 MAS-100 was 1.62 μm (Engelhart et al., 2007) or 1.7 μm (Li and Lin, 1999; Yao and Mainelis,
156 2006). Therefore, the particle size measurement range for particle number concentration (NC)
157 was 1.6–>32 μm and the size-segregated particle number concentrations included 18 particle size
158 intervals of 1.6–2, 2–2.5, 2.5–3, 3–3.5, 3.5–4, 4–5, 5–6.5, 6.5–7.5, 7.5–8.5, 8.5–10, 10–12.5,
159 12.5–15, 15–17, 17–20, 20–25, 25–30, 30–32, and >32 μm ($PN_{1.6\text{-}2}$, $PN_{2\text{-}2.5}$, $PN_{2.5\text{-}3}$, $PN_{3\text{-}3.5}$,
160 $PN_{3.5\text{-}4}$, $PN_{4\text{-}5}$, $PN_{5\text{-}6.5}$, $PN_{6.5\text{-}7.5}$, $PN_{7.5\text{-}8.5}$, $PN_{8.5\text{-}10}$, $PN_{10\text{-}12.5}$, $PN_{12.5\text{-}15}$, $PN_{15\text{-}17}$, $PN_{17\text{-}20}$, $PN_{20\text{-}25}$,
161 $PN_{25\text{-}30}$, $PN_{30\text{-}32}$, and $PN_{>32}$).
162
163 ***Data analysis***
164 *Descriptive and test statistics*
165 Descriptive statistics were taken for the measured data, including the mean and standard
166 deviation of each variable. Mann-Whitney U tests were performed on indoor and outdoor
167 bacterial and fungal bioaerosols, as well as on the five size-segregated particle mass
168 concentrations, to compare differences between indoor and outdoor concentrations. All related
169 statistical analysis was performed using IBM SPSS Statistics software (SPSS, Inc., Chicago, IL,
170 USA) in this study.
171
172 *Spearman's correlation coefficients*
173 Spearman's correlation coefficients were calculated to explore the correlation of indoor
174 bacterial and fungal bioaerosol concentrations with MC and NC. Parameters with significant

correlations (p-value<0.05) were selected as independent variables in the subsequent MLR analysis. The dependent variables in this study were the indoor bacterial and fungal bioaerosol concentrations, which were divided into two conditions based on the independent variables, namely MC (Case I) and NC (Case II).

Bioaerosol prediction models

In this study, the prediction model for bioaerosol concentration was constructed using the MLR method, as follows:

$$Y=\beta_0+\beta_1X_1+\beta_2X_2+\beta_3X_3+\ldots+\beta_nX_n+\varepsilon \quad (1)$$

where Y represents the dependent variables (bacterial and fungal bioaerosol concentrations), X_1, X_2, X_3,…X_n represent the independent variables (air parameters; principal components or factors), β_0 represents the intercept coefficients, β_1…β_n represent regression coefficients, and ε represents random errors.

Because the MC in Case I only includes 5 size-aggregated concentrations (5 parameters), we performed a stepwise MLR directly to obtain the prediction model. However, the NC in Case II includes 18 size-aggregated concentrations (18 parameters). Therefore, in addition to prediction models obtained by MLR (Case II-1), we also used the principle component analysis method (Case II-2) and factor analysis method (Case II-3) to simplify the NC into fewer parameters for subsequent MLR.

Assessment of the predictive power of models

The first method to evaluate the predicting capability of the regression model in this study was

to randomly select 90% of the total samples in order to obtain a regression line and subsequently apply the regression model to the remaining 10% samples (Xue et al., 2011). This study also uses the standard statistical forecasting method for total samples to obtain the mean absolute percentage error (MAPE), which assesses the predictive power of MLR models in predicting the indoor bioaerosol concentration. MAPE is defined as follows (Lewis, 1982):

$$\mathrm{MAPE} = \frac{1}{n}\sum_{t}^{n}\frac{|e_t|}{y_t} \times 100\% \qquad (2)$$

where n represents the sample size, y_t represents the measured bioaerosol concentration, and e_t represents the deviation between the measured and predicted values. MAPE values <10%, 10–20%, 20–50% and >50% indicate a highly accurate prediction, a good prediction, a fair prediction, and an inaccurate prediction, respectively.

RESULTS AND DISCUSSION

Concentration and distribution of bioaerosols and airborne particles

The indoor and outdoor bioaerosol concentrations and particle concentrations measured in public spaces are shown in Fig. 1. The indoor bacterial bioaerosol concentration (1044±1088 CFU m^{-3}) was significantly higher than the outdoor concentration (649±464 CFU m^{-3}) (Mann-Whitney U test, P=0.005), with an indoor/outdoor (I/O) ratio of 2.18±2.13. Since indoor environments are air-conditioned with doors and windows kept closed, the indoor-outdoor air exchange rate was low, leading to the accumulation of CO_2 generated from the metabolism of people indoors (Tseng *et al.*, 2011). Hence, CO_2 concentrations were significantly higher indoors (853±393 ppm) than outdoors (492±128 ppm) (Mann-Whitney U test, p=0.000), with an I/O ratio of 1.84±0.83. These results were similar to the trend obtained by Kalogerakis *et al.* (2005). We

223 thus speculated that people indoors are primary contributors of bacteria, based on changes in
224 indoor CO_2 concentrations (Hospodsky *et al.*, 2012; Pastuszka *et al.*, 2000).

225 Conversely, outdoor fungal bioaerosol concentrations (2412±2155 CFU m^{-3}) were
226 significantly higher than those indoors (572±601 CFU m^{-3}) (Mann-Whitney U test, p=0.000),
227 with an I/O ratio of 0.37±0.76. The relative humidity of air-conditioned indoor environments was
228 less than 60%, a condition unfavorable for fungal growth. Moreover, there was no obvious indoor
229 source of fungi, thus we speculated that indoor fungi originated mainly from the outdoors, which
230 corroborates findings by Chao *et al.* (2002).

231 Table 2 shows the suspended PM MC in indoor and outdoor air. The outdoor MC at different
232 sizes ($PM_{1.0}$, $PM_{1\text{-}2.5}$, $PM_{2.5}$, $PM_{2.5\text{-}10}$, and PM_{10}) were significantly higher than those indoors
233 (Mann-Whitney U test, P=0.000), with an I/O ratio of less than 1, indicating a higher quantity of
234 airborne particles outdoors than indoors. Additionally, we investigated the particle concentration
235 percentages at different sizes within PM_{10} and found that the percentages of submicron particles
236 ($PM_{1.0}$), fine particles ($PM_{2.5}$), and coarse particles ($PM_{2.5\text{-}10}$) were significantly higher indoor
237 than outdoors (Mann-Whitney U test, $P<0.05$). These results indicate that suspended particles in
238 the indoor and outdoor air are mainly fine particles. Coarse particles have fewer indoor than
239 outdoor sources due to the indoor-outdoor barrier, thereby leading to a higher ratio of small-sized
240 particles in indoor environments. Furthermore, the particle size distribution in Fig. 2 shows that
241 the NC for particle sizes of less than 1 μm were significantly higher than those of particles greater
242 than 1 μm in size, and particles between 0.2–0.3 μm had the highest NC, which further confirmed
243 the MC distribution results that airborne particles mainly consist of small particles.

244

245 ***Correlation between bioaerosols and MC of suspended particles***

246 The correlation between indoor bioaerosol concentrations and MC at different particle sizes is

247 shown in Table 3. There were significant moderate and weak positive correlations between indoor
248 airborne bacterial concentrations with indoor $PM_{1\text{-}2.5}$, $PM_{2.5}$, $PM_{2.5\text{-}10}$, and PM_{10}. The greatest
249 correlation was with indoor coarse particles ($PM_{2.5\text{-}10}$). Indoor aerosols include both viable and
250 nonviable particles. Agranovski *et al.* (2004) indicated that about 95% of total particulate matter
251 (TPM) and viable particles in the air of agricultural buildings are inhalable (<7 μm) and 50% of
252 viable particles are fine particles (<2.5 μm). Qian *et al.* (2012) indicated that about 18% of
253 microorganisms with particle sizes between 3–5 μm are closely associated with human skin.
254 Boreson *et al.* (2004) indicated that the total biomass in the air is positively proportional to the
255 MC of coarse particles. These studies suggest that bacterial bioaerosols are mostly distributed on
256 coarse particles, while only a proportion is distributed on fine particles, which is consistent with
257 the results in this study.

258 In this study, we also found that there was no significant correlation between indoor bacteria
259 and submicron particles ($PM_{1.0}$), as bioaerosols are mainly distributed on coarse particles and the
260 MAS-100 bioaerosol sampler used in this study primarily collects bioaerosols with aerodynamic
261 diameters greater than 1.6 μm (Engelhart *et al.*, 2007; Li and Lin, 1999; Yao and Mainelis, 2006).
262 There was therefore no significant correlation between $PM_{1.0}$ at particle sizes <1.0 μm and
263 bacterial bioaerosol concentrations. Since all public spaces sampled were air-conditioned indoor
264 environments, we expected the indoor personnel and their activities that lift deposited particles to
265 be the main bacterial source, and that indoor bacterial concentrations would be only slightly
266 affected by external air since there was little indoor-outdoor air exchange. However, the results
267 showed no significant correlation between indoor bacterial bioaerosols and outdoor MC, which
268 might be due to the small number of outdoor bacteria affecting indoor bioaerosols distributed on
269 particles within a certain size range. Hence, their correlations could not be observed using the
270 existing size-segregated MC.

Indoor fungal bioaerosol concentrations have moderate and weak positive correlations with indoor $PM_{1\text{-}2.5}$, $PM_{2.5\text{-}10}$, and PM_{10}, respectively, and have no significant correlation with outdoor MC at any size. Indoor fungi mainly originate from the outdoors, and although they could flow inside through the gap openings of doors, windows, or the air conditioning system (Tseng *et al.*, 2011), fungal bioaerosols enter in a limited amount and are distributed on particles within a certain size range, so that no significant correlation was observed. Qian *et al.* (2012) indicated that, in the presence of ordinary indoor personnel, the aerodynamic diameters of typical unicellular and multicellular fungal spores at peak concentrations were 2–5 μm and >10 μm, respectively. Hargreaves *et al.* (2003) indicated that fungi in houses have no significant correlation with $PM_{2.5}$, which is consistent with the results of this study. Based on the results of this study, which showed that there were significant moderate and weak positive correlations of indoor fungi to fine particles ($PM_{1\text{-}2.5}$) and coarse particles ($PM_{2.5\text{-}10}$), respectively, we speculated that fungal bioaerosols in these air-conditioned indoor spaces are mainly present in the air as unicellular and multicellular spores.

Correlation between bacterial bioaerosols and NC

Indoor bioaerosols are particles suspended in the air. In this study, we therefore investigated the correlation between NC (including viable and nonviable particles) and indoor bioaerosol concentrations. The correlations between indoor bacterial bioaerosol concentrations and NC at particle sizes >1.6 μm are shown in Table 4. The results indicate that there were significant weak to strong positive correlations of bacterial concentrations to size-segregated NC at particle sizes of 1.6–17.5 μm and 25–32 μm (R=0.233–0.625, p=0.000–0.049), indicating that bacteria are widespread on fine and coarse particles. Our study produced similar results as other related studies (Batterman, 2001; Parat *et al.*, 1999; Tham and Zuraimi, 2005; Oxborrow *et al.*, 1975).

In addition, relevant studies have explored the particle size range of bacterial bioaerosol distribution. For instance, Qian *et al.* (2012) found that the peak concentration of indoor airborne bacteria is distributed on particles with aerodynamic diameters of 3–5 μm. McDonagh and Noakes (2014) indicated that bacterial bioaerosols in offices are mainly distributed on particles 1.1–2.1 μm in size. Bhangar *et al.* (2016) indicated that each person generates 0.9–0.3 million coarse particle bioaerosols (2.5–10 μm) per hour, of which walking, sitting, physical activities of upper limbs, clothing, or the contact between clothing and skin are main sources. Tham and Zuraimi (2005) indicated that indoor viable bacteria with particle sizes of 1–2 μm exist alone, viable bacteria with particle sizes of 3–7.5 μm exist as aggregates, and viable bacteria with particle sizes >7.5 μm originate from the shedding of human skin. Taking the results from other literature and our study together, there were significant weak to strong positive correlations of indoor airborne bacterial concentrations to size-segregated NC at particle sizes of 1.6–17.5 μm and 25–32 μm, respectively. In particular, the correlation coefficient of the NC at particle sizes 7.5–17.5 μm to bacterial bioaerosol concentrations was greater than 0.5. The results indicate that indoor bacterial aerosols may not only exist as single cells, but that most of them adhere to each other or adhere to small organisms or non-biological particles. Hence, the distribution contains a wide range of particle sizes.

Table 4 shows that there were significant weak and moderate positive correlations of indoor bacterial bioaerosols to outdoor size-segregated NC at particle sizes of 10–20 μm, 25–30 μm, and >32 μm ($R=0.230–0.319$, $p=0.000–0.046$), indicating that microorganisms affecting indoor airborne bacterial concentrations adhered mainly to particles with a larger size. The result differs from that of the previous section, which indicated that there was no correlation between bioaerosols and outdoor MC, mainly because some outdoor suspended particles still could come indoors by way of doors, humans, and air conditioning systems. At the measured particle size

319 >1.6 μm, NC had a greater number of sizes (18) than MC (5). The measurement of
320 size-segregated NC, with its smaller particle size interval, therefore reflects the actual particle
321 size range containing bacteria. In contrast, size-segregated MC is unable to highlight the effect of
322 certain particle sizes on bacteria due to the greater particle size intervals.
323
324 ***Correlation between fungal bioaerosols and NC***
325 Table 4 shows that there were significant weak and moderate positive correlations of fungal
326 concentration to size-segregated NC at particle sizes of 1.6–10 μm and 17.5–20 μm (R=0.253–
327 0.436, p=0.000–0.031), indicating that fungal bioaerosols are widespread among multiple particle
328 size ranges. This result is different from Batterman (2001), who found no significant correlation
329 between indoor fungal bioaerosol concentrations and NC in offices, which could be due to the
330 geographical environment, air conditioning system, or particle sampling at only 5 size intervals.
331 In this study, we were able to measure a greater number of particle size intervals with smaller
332 particle size ranges. Therefore, we were able to better elucidate the correlation between fungal
333 bioaerosols and NC. In the presence of general indoor personnel, the aerodynamic diameters of
334 typical unicellular and multicellular fungal spores at peak concentrations were 2–5 μm and >10
335 μm, respectively (Qian *et al.*, 2012). There were significant weak and moderate positive
336 correlations of size-segregated NC at particle size ranges of 1.6–10 μm and 17.5–20 μm to fungal
337 concentrations, which was similar to results obtained in previous studies (Hargreaves *et al.*, 2003;
338 Qian *et al.*, 2012). Our study confirmed that both unicellular and multicellular fungal spores
339 co-exist in public spaces. There were significant moderate and weak positive correlations of
340 indoor airborne fungal concentrations to size-segregated NC of outdoor particles at 12.5–17.5 μm
341 (R=0.335, 0.251, p=0.004, 0.029), which was mainly due to the difference in the measured
342 particle size intervals between NC and MC, as described previously.

343

344 ***MLR prediction models for indoor bacterial bioaerosol concentration***

345 *Case I: Indoor bacterial bioaerosol concentration versus MC*

346 Four size-segregated MC bins (indoor $PM_{1\text{-}2.5}$, $PM_{2.5}$, $PM_{2.5\text{-}10}$, and PM_{10}) that correlated
347 significantly to indoor airborne bacterial concentrations were selected through the correlation
348 analysis, after the collinearity diagnosis. $PM_{1\text{-}2.5}$, $PM_{2.5\text{-}10}$, and PM_{10} were selected as independent
349 variables. After that, an MLR prediction model for indoor bacterial bioaerosol concentration (C_b)
350 was constructed via the stepwise MLR analysis, as shown in Table 5. Although there were
351 moderate and weak positive correlations between the four MC parameters and indoor bacterial
352 bioaerosol concentrations at the beginning, only indoor $PM_{2.5\text{-}10}$ could significantly explain the
353 unique variance of indoor bacterial bioaerosol concentration, with 27.6% of the explanatory
354 power.

355

356 *Case II: Indoor bacterial bioaerosol concentrations versus NC*

357 Case II-1: Stepwise MLR analysis

358 A total of 15 indoor and 6 outdoor size-segregated NC that correlated significantly to indoor
359 airborne bacterial concentrations were selected through the correlation analysis, after the
360 collinearity diagnosis. $PN_{8.5\text{-}10}$, $PN_{30\text{-}32}$, $PN_{out10\text{-}12.5}$, and $PN_{out>32}$ were selected as the independent
361 variables for regression analysis. After that, the MLR prediction models for indoor bacterial
362 bioaerosol concentrations were constructed via the stepwise MLR analysis as shown in Table 5.
363 There were initially 21 parameters with significant weak to strong positive correlations to indoor
364 bacterial bioaerosol concentrations, but ultimately, only $PN_{8.5\text{-}10}$, $PN_{30\text{-}32}$, $PN_{out10\text{-}12.5}$, and $PN_{out>32}$
365 could significantly explain the unique variance of indoor bacterial bioaerosol concentrations, with
366 an explanatory power of 86.0%. Based on the MLR analysis results, we learned that coarse

367 particles (particle sizes of 2.5–10 μm) and ultramicro particles (particle sizes of >10 μm) are the
368 indoor and outdoor suspended particles that significantly affect indoor bioaerosol concentrations,
369 indicating that most indoor airborne bacteria adhere to coarse (or even larger) particles. The
370 standardized regression coefficients showed that indoor coarse particles with sizes of 8.5–10 μm
371 ($PN_{8.5\text{-}10}$) exhibit the greatest effect on indoor bacterial bioaerosol concentrations.
372
373 Case II-2: Combination of principal component analysis (PCA) with MLR analysis (PCA+MLR)
374 PCA is a multivariate statistical technique to reduce the dimensionality of a data set. PCA uses
375 linear transformation to extract a smaller number of orthogonal variables called principal
376 components from a larger set of data. The new variables (components) are uncorrelated and
377 explain most of variance in the original data set (Abdi and Williams, 2010). PCA was used to
378 reduce the number of independent variables from an excessive number of independent
379 variables—the 21 indoor and outdoor size-segregated NC. A total of 3 new indoor variables
380 ($PCA1_{1.6\text{-}7.5}$, $PCA2_{7.5\text{-}17.5}$, and $PCA3_{25\text{-}32}$) and one new outdoor variable ($PCA4_{Out}$) were extracted
381 from the PCA, as shown in Table 6. The first principal component, $PCA1_{1.6\text{-}7.5}$, was primarily
382 based on the particle concentration at particles sizes of 1.6–7.5 μm, and its maximum explained
383 variance of the original data was 63.1%. The second principal component, $PCA2_{7.5\text{-}17.5}$, was
384 primarily based on the particle concentration particle sizes of 7.5–17.5 μm, and its maximum
385 explained variance of the original data was 13.4%. The third principal component, $PCA3_{25\text{-}32}$,
386 was primarily based on the particle concentration at particle sizes of 25–32 μm, and its maximum
387 explained variance of the original data was 8.3%. The fourth principal component, $PCA4_{Out}$, was
388 primarily based on the outdoor particle concentration at particle sizes of 10–20 μm, 25–30 μm,
389 and >32 μm, and its maximum explained variance of the original data was 44.9%.
390 These four principal components were taken as new independent variables for an MLR

391 analysis and after the collinearity diagnosis, MLR models of indoor bacterial bioaerosol
392 concentrations were constructed via the stepwise MLR analysis as shown in Table 5. The results
393 showed that only $PCA1_{1.6\text{-}7.5}$, $PCA3_{25\text{-}32}$, and $PCA4_{Out}$ could significantly explain the unique
394 variance of indoor bacterial bioaerosol concentrations, with explanatory power of 43.3%. The
395 standardized regression coefficients showed that $PCA4_{Out}$ has a similar effect to $PCA1_{1.6\text{-}8.5}$ on
396 indoor bioaerosol concentrations, and were greater than that for $PCA3_{25\text{-}32}$.
397
398 Case II-3: Combination of factor analysis (FA) and MLR analysis (FA+MLR)
399 FA divided the 15 indoor variables and 6 outdoor variables into three ($FACTOR1_{1.6\text{-}7.5}$,
400 $FACTOR2_{7.5\text{-}17.5}$, and $FACTOR3_{25\text{-}32}$) and one ($FACTOR4_{Out}$) factors, respectively (Table 7).
401 After that, these four new variables were subjected to collinearity diagnosis and then MLR
402 prediction models of indoor bacterial bioaerosol concentrations were constructed via the stepwise
403 MLR analysis, as shown in Table 5. Only $FACTOR2_{7.5\text{-}17.5}$ and $FACTOR4_{Out}$ could significantly
404 explain the unique variance of indoor bacterial bioaerosol concentrations, with an explanatory
405 power of 82.9%. Besides, the standardized regression coefficients showed that the indoor NC at
406 particle sizes of 7.5–17.5 μm had similar effects to the outdoor NC on indoor bacterial bioaerosol
407 concentrations.
408 A total of three methods were used in Case II to construct the model and the results indicate
409 that models constructed using different methods result in different independent variables for the
410 regression model, but all of them include the indoor and outdoor NC. Among these, the stepwise
411 MLR (Case II-1) and FA+MLR (Case II-3) yielded similar coefficients of determination (R^2),
412 which were significantly higher than that of the PCA+MLR (Case II-2).
413
414 ***MLR prediction models for indoor fungal bioaerosol concentrations***

MLR prediction models for indoor fungal bioaerosol concentrations were constructed using the same procedure as for bacterial bioaerosols. MLR prediction models for indoor fungal bioaerosol concentrations (C_f) constructed in Cases I and II are shown in Table 5. In Case I, only the indoor $PM_{1\text{-}2.5}$ could significantly explain the unique variance in indoor bioaerosol concentrations, with an explanatory power of just 14.9%. In Case II-1, only $PN_{1.6\text{-}2}$ and $PN_{Out12.5\text{-}15}$ could significantly explain the unique variance of indoor bioaerosol concentrations, with an explanatory power of 67.7%. Indoor and outdoor suspended particles that significantly affect indoor fungal bioaerosol concentrations have particle sizes of 1.6–2 μm and >10 μm, respectively, indicating that most indoor airborne fungi are unicellular fungi while most outdoor fungi are multicellular fungal spores or fungi adhered to large particles. Of these, indoor particles with sizes of 1.6–2 μm ($PN_{1.6\text{-}2}$) exhibit the greatest effect on indoor fungal bioaerosol concentrations. For Case II-2, three new independent variables ($PCA1_{1.6\text{-}10}$, $PCA2_{17.5\text{-}20}$, and $PCA3_{Out}$) were extracted via PCA and are shown in Table 6. The regression prediction model indicated that PCA_{Out} is solely dominated by outdoor NC, and could explain the indoor fungal bioaerosol concentration with an explanatory power of only 10%, indicating a low predictive power on indoor fungal bioaerosols. For Case II-3, three new independent variables ($FACTOR1_{1.6\text{-}10}$, $FACTOR2_{17.5\text{-}20}$ and $FACTOR3_{Out}$) were extracted via FA and are shown in Table 7. The regression prediction model indicated that ultimately, only $FACTOR1_{1.6\text{-}10}$ and $FACTOR3_{Out}$ could significantly explain the unique variance of indoor fungal bioaerosol concentrations, with an explanatory power of 66.1%. In addition, the standardized regression coefficients indicated that indoor NC at particle sizes of 1.6–10 μm had a greater effect than outdoor NC on indoor fungal bioaerosol concentrations. Similar to the results from the MLR prediction model for indoor bacterial bioaerosol concentrations, R^2 values for Cases II-1 and II-3 were similar and significantly higher than that of Case II-2.

Comparison and validation of prediction models

In Case II-1, the direct regression model (R^2=0.860) that took indoor size-segregated NC as the independent variables had the best performance in predicting indoor airborne bacterial concentrations. In Case I, the regression model (R^2=0.276) that took indoor size-segregated MC as independent variables was the worst. Hence, NC significantly outperforms MC in predicting bacterial bioaerosol concentrations. R^2 of the regression prediction models obtained from different public spaces in this study was higher than that of MLR model constructed by Tseng et al.[12], which used multiple and complex independent variables to predict bacterial bioaerosol concentrations in 37 single-type office buildings. The results indicated that it is feasible to predict indoor bacterial bioaerosol concentrations by measuring only the NC and without having to measure an excessive number of air parameters.

The regression prediction model of fungal bioaerosol concentrations also indicated that size-segregated NC (Cases II-1 and II-3) had a significantly better predictive power than size-segregated MC (Case I). The R^2 value of the regression prediction model for different public spaces obtained in this study was higher than that of models constructed by Tseng *et al.* (2011) and Bartlett *et al.* (2004), which used multiple and complex independent variables to predict fungal concentrations in office buildings and primary school buildings, respectively. The regression results of Case II indicated that indoor and outdoor NC are the best independent variables in predicting indoor fungal bioaerosol concentrations, but their explanatory power for indoor airborne fungal concentrations was lower than 70%, indicating that NC alone is still insufficient for predicting indoor fungal concentrations.

In order to evaluate the predicting capability of the regression model, the first method randomly selected 90% of the total of 83 samples to obtain a regression equation for case II-1

(C_b=0.120$PN_{8.5-10}$+11.123PN_{30-32}+0.099$PN_{Out10-12.5}$+0.755$PN_{Out>32}$, R^2=0.865). Subsequently, the regression equation was applied to the remaining 10% samples to calculate the bias between the measured bacteria concentration and predicted concentration. The average bias was less than 206 CFU/m^3. The result indicates that the linear regression equation using four variables ($PN_{8.5-10}$, PN_{30-32}, $PN_{Out10-12.5}$, $PN_{Out>32}$) still can be accepted to assess the approximate indoor bacteria distribution based on the indoor air quality standard for bacteria (1500 CFU/m^3) set by Taiwan Environmental Protection Administration (Taiwan EPA, 2012). Furthermore, MAPE is a standard statistical method to measure forecast accuracy. The higher the MAPE value, the better the regression equation predicts. In order to better comprehend the predictive accuracy of these regression models listed in Table 5, the second method used MAPE value was calculated from equation (2) (Lewis, 1982), which has been frequently applied in different areas (Chang *et al.*, 2007; Chen *et al.*, 2012; Chou and Telaga, 2014; Pao, 2009; Wei and Lee, Yang *et al.*, 2012) to assess the fitness of prediction models. MAPE values for the bacterial bioaerosol concentration prediction models in Cases II-1 and II-3 with the highest R^2 values were 40.0% and 49.1% (20–50%), respectively. The results indicate that both models could reasonably predict indoor airborne bacterial concentrations, and that the Case II-1 model obtained via MLR is the most favorable model. Fig. 3 also demonstrates that the measured airborne bacteria concentrations can be reasonably predicted by the established regression model with the highest R^2 (case II-1) except for a few samples marked in circles. Through the case study of Case II-1 model for indoor bacteria, it shows that both the methods can be applied to evaluate the predicting capability of regression model. MAPE values for the fungal bioaerosol concentration prediction models in Cases II-1 and II-3 with the highest R^2 values were 112.8% and 126.4% (>50%), respectively. The results indicate that neither model could reasonably predict indoor airborne fungal concentrations, and that they need other parameters to improve their predictive power. In

conclusion, the developed prediction model can be applied for the self-management of indoor bacterial bioaerosols in public spaces.

CONCLUSIONS

Numerous studies have investigated the correlation between indoor bioaerosol concentrations with various indoor and outdoor air and environmental parameters, but those studies used multiple and complex parameters to construct linear and non-linear regression models for the prediction of indoor bioaerosol concentrations. Additionally, the R^2 of the developed models vary widely. In contrast to previous studies, we used only simple bioaerosol-related air parameters—MC and NC—to construct MLR prediction models of indoor bioaerosol concentrations. The results indicate that the direct regression models (Case II-1) that took indoor and outdoor size-segregated NC as the independent variables yielded the best performance in predicting indoor bacterial and fungal bioaerosol concentrations. MAPE validated that models obtained via MLR in Case II-1 and FA+MLR in Case II-3 could reasonably predict indoor bacterial bioaerosol concentrations, but that they are unable to reasonably predict fungal bioaerosol concentrations. We recommend that other parameters or regression models can be included in the future to improve prediction models for fungal bioaerosol concentrations. Through this study, we learned that NC outperforms MC as a parameter for the construction of MLR prediction models for bioaerosol concentrations, as they have a better prediction result. At present, cheap and rapid inspection instruments for indoor airborne biological pollutants are still rarely available, thus we recommend that the potential distribution of bacterial bioaerosols in an indoor air-conditioned environment can be assessed at a preliminary level via a simple measurement of indoor and outdoor size-segregated NC in combination with the prediction model constructed in this study. The preliminary proposed prediction model can be seen as a potential

complementary method for the pre-assessment of indoor microbiological air quality before we use the conventional culture-based method in public spaces.

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621

622 **Table 1.** Bioaerosol and airborne particle sampling plan in public spaces.

Public space	Indoor sampling point	Outdoor sampling point	Sampling site	Air conditioning system
Hospital (n=5)	14	5	Registration area, medicine receiving area, waiting area	Central air conditioning system
Government agency (n=4)	12	4	Administrative area	Central air conditioning system, packaged air conditioner
Library (n=5)	11	5	Reading area, collection area, lobby	Central air conditioning system, packaged air conditioner, window-type air conditioner
Shopping mall (n=5)	15	5	Fresh food area, grocery area, cashier area	Central air conditioning system
Classroom (n=7)	10	7	Seating area	Window-type air conditioner
Restaurant (n=6)	6	6	Dining area	Packaged air conditioner
Gym (n=2)	2	2	Customer service area	Packaged air conditioner
Convenience store (n=6)	6	6	Seating area	Packaged air conditioner, Split-type air conditioner
Kindergarten (n=3)	7	3	Teaching area, service area	Central air conditioning system, window-type air conditioner, split-type air conditioner

623

Table 2. Mass concentrations and distribution ratios of suspended particles in indoor and outdoor environments.

		PM_1 ($\mu g\ m^{-3}$)	$PM_{1-2.5}$ ($\mu g\ m^{-3}$)	$PM_{2.5}$ ($\mu g\ m^{-3}$)	$PM_{2.5-10}$ ($\mu g\ m^{-3}$)	PM_{10} ($\mu g\ m^{-3}$)
Indoor PM (n=83)	Min	6.43	0.27	8.18	0.57	18.38
	Max	59.47	18.30	61.70	135.90	188.82
	Mean	30.32	3.21	33.52	15.09	48.62
	SD	10.78	2.68	11.63	17.19	23.23
	PM/PM_{10}(%) (Mean±SD)	66.10±17.27	6.17±2.54	72.27±15.52	27.73±15.52	
Outdoor PM (n=43)	Min	20.36	2.30	24.83	8.35	33.59
	Max	73.18	20.83	84.19	80.25	131.61
	Mean	44.06	9.05	53.11	27.40	80.51
	SD	13.12	3.26	14.11	12.23	20.40
	PM/PM_{10}(%) (Mean±SD)	57.40±10.49	10.93±2.66	68.33±9.05	31.67±9.05	
Mann-Whitney U Test	P-value	0.000	0.000	0.000	0.000	0.000
I/O Ratio	Mean	0.73	0.41	0.67	0.64	0.65
	SD	0.30	0.29	0.27	0.62	0.30

Min: minimum; Max: maximum; SD: standard deviation.

Table 3. Correlation coefficients between bioaerosol concentrations and size-segregated particle mass concentrations.

		Indoor bacteria(CFU m^{-3})		Indoor fungi(CFU m^{-3})	
		R	p-value	R	p-value
Indoor PM ($\mu g\ m^{-3}$)	$PM_{1.0}$	0.015	0.889	0.088	0.431
	$PM_{1-2.5}$	0.534*	0.000	0.549*	0.000
	$PM_{2.5}$	0.125	0.260	0.163	0.142
	$PM_{2.5-10}$	0.644*	0.000	0.483*	0.000
	PM_{10}	0.434*	0.000	0.346*	0.001
Outdoor PM ($\mu g\ m^{-3}$)	$PM_{1.0}$	-0.002	0.988	-0.005	0.963
	$PM_{1-2.5}$	0.154	0.164	-0.061	0.584
	$PM_{2.5}$	-0.039	0.724	0.011	0.921
	$PM_{2.5-10}$	0.202	0.066	0.112	0.313
	PM_{10}	0.177	0.108	0.074	0.504

*p-value<0.05

Table 4. Correlation coefficients between bioaerosol concentrations and size-segregated particle number concentrations.

Indoor or Outdoor PN (# m^{-3})	Indoor bacteria (CFU m^{-3})		Indoor fungi (CFU m^{-3})	
	R_{indoor}	$R_{outdoor}$	R_{indoor}	$R_{outdoor}$
$PN_{1.6-2}$	0.364*	0.029	0.436*	-0.057
$PN_{2-2.5}$	0.495*	0.048	0.356*	0.046
$PN_{2.5-3}$	0.440*	0.087	0.307*	0.038
$PN_{3-3.5}$	0.359*	0.166	0.325*	0.082
$PN_{3.5-4}$	0.387*	0.086	0.335*	0.013
PN_{4-5}	0.301*	0.088	0.294*	0.041
$PN_{5-6.5}$	0.371*	0.079	0.340*	0.126
$PN_{6.5-7.5}$	0.388*	0.091	0.253*	0.101
$PN_{7.5-8.5}$	0.567*	0.146	0.311*	0.146
$PN_{8.5-10}$	0.625*	0.182	0.262*	0.213
$PN_{10-12.5}$	0.596*	0.391*	0.222	0.135
$PN_{12.5-15}$	0.557*	0.391*	0.185	0.335*
$PN_{15-17.5}$	0.592*	0.292*	0.085	0.251*
$PN_{17.5-20}$	0.219	0.257*	0.266*	-0.095
PN_{20-25}	0.227	0.179	0.146	0.094
PN_{25-30}	0.339*	0.230*	0.096	0.029
PN_{30-32}	0.233*	0.000	0.103	0.000
$PN_{>32}$	0.158	0.347*	-0.010	-0.096

*p-value<0.05

Table 5. Prediction models of indoor bioaerosol concentrations in public spaces.

Bioaerosol	Case	Method	Regression model	R^2 (Adj R^2)	R(p-value)
Bacteria	I	MLR	$C_b(\text{CFU m}^{-3}) = 33.368PM_{2.5\text{-}10}(\mu\text{g m}^{-3})+364.329$	0.276 (0.265)	0.525 (0.000)
	II-1	MLR	$C_b(\text{CFU m}^{-3}) = 0.126PN_{8.5\text{-}10}(\text{\# m}^{-3})+11.166PN_{30\text{-}32}(\text{\# m}^{-3})$ $+0.094PN_{Out10\text{-}12.5}(\text{\# m}^{-3})+0.707PN_{Out>32}(\text{\# m}^{-3})$	0.860 (0.851)	0.928 (0.000)
	II-2	PCA+MLR	$C_b(\text{CFU m}^{-3}) = 50.410PCA1_{1.6\text{-}7.5}+112.399PCA3_{25\text{-}32}$ $+95.993PCA4_{Out}+698.710$	0.433 (0.403)	0.658 (0.000)
	II-3	FA+MLR	$C_b(\text{CFU m}^{-3}) = 0.037FACTOR2_{7.5\text{-}17.5}(\text{\# m}^{-3})+0.064FACTOR4_{Out}(\text{\# m}^{-3})$	0.829 (0.823)	0.911 (0.000)
Fungi	I	MLR	$C_f(\text{CFU m}^{-3}) = 101.169PM_{1\text{-}2.5}(\mu\text{g m}^{-3})+166.255$	0.149 (0.136)	0.385(0.001)
	II-1	MLR	$C_f(\text{CFU m}^{-3}) = 0.003PN_{1.6\text{-}2}(\text{\# m}^{-3})+0.131PN_{Out12.5\text{-}15}(\text{\# m}^{-3})$	0.677 (0.666)	0.823(0.000)
	II-2	PCA+MLR	$C_f(\text{CFU m}^{-3}) = 82.160PCA3_{Out}(\text{\# m}^{-3})+387.213$	0.100 (0.084)	0.316(0.013)
	II-3	FA+MLR	$C_f(\text{CFU m}^{-3}) = 0.001FACTOR1_{1.6\text{-}10}(\text{\# m}^{-3})+0.092FACTOR3_{Out}(\text{\# m}^{-3})$	0.661 (0.650)	0.813(0.000)

MLR: stepwise multiple linear regression; PCA: principle component analysis; FA: factor analysis; Adj R^2: adjusted coefficient of determination; PN: indoor particle number concentration; PN_{Out}: outdoor particle number concentration

Table 6. Principle components extracted from variables of size-segregated particle number concentrations.

Bioaerosol	Principle component	Principle component equation
Bacteria	$PCA1_{1.6\text{-}7.5}$	$0.220Z_{1.6\text{-}2}+0.285Z_{2\text{-}2.5}+0.307Z_{2.5\text{-}3}+0.303Z_{3\text{-}3.5}+0.302Z_{3.5\text{-}4}+0.302Z_{4\text{-}5}+0.299Z_{5\text{-}6.5}+0.295Z_{6.5\text{-}7.5}+0.298Z_{7.5\text{-}8.5}+0.280Z_{8.5\text{-}10}+0.260Z_{10\text{-}12.5}+0.209Z_{1.25\text{-}15}+0.197Z_{15\text{-}17.5}+0.090Z_{25\text{-}30}+0.005Z_{30\text{-}32}$
	$PCA2_{7.5\text{-}17.5}$	$-0.390Z_{1.6\text{-}2}-0.227Z_{2\text{-}2.5}-0.146Z_{2.5\text{-}3}-0.214Z_{3\text{-}3.5}-0.205Z_{3.5\text{-}4}-0.165Z_{4\text{-}5}-0.103Z_{5\text{-}6.5}+0.088Z_{6.5\text{-}7.5}+0.148Z_{7.5\text{-}8.5}+0.245Z_{8.5\text{-}10}+0.352Z_{10\text{-}12.5}+0.409Z_{1.25\text{-}15}+0.392Z_{15\text{-}17.5}+0.137Z_{25\text{-}30}-0.309Z_{30\text{-}32}$
	$PCA3_{25\text{-}32}$	$0.211Z_{1.6\text{-}2}+0.155Z_{2\text{-}2.5}-0.041Z_{2.5\text{-}3}-0.065Z_{3\text{-}3.5}-0.122Z_{3.5\text{-}4}-0.171Z_{4\text{-}5}-0.18Z_{5\text{-}6.5}-0.155Z_{6.5\text{-}7.5}-0.023Z_{7.5\text{-}8.5}-0.024Z_{8.5\text{-}10}+0.089Z_{10\text{-}12.5}+0.220Z_{1.25\text{-}15}+0.078Z_{15\text{-}17.5}+0.623Z_{25\text{-}30}+0.611Z_{30\text{-}32}$
	$PCA4_{Out}$	$0.483Z_{Out10\text{-}12.5}+0.428Z_{Out12.5\text{-}15}+0.472Z_{Out15\text{-}17.5}+0.347Z_{Out17.5\text{-}20}+0.286Z_{Out25\text{-}30}+0.398Z_{Out>32}$
Fungi	$PCA1_{1.6\text{-}10}$	$0.262Z_{1.6\text{-}2}+0.323Z_{2\text{-}2.5}+0.332Z_{2.5\text{-}3}+0.329Z_{3\text{-}3.5}+0.329Z_{3.5\text{-}4}+0.331Z_{4\text{-}5}+0.327Z_{5\text{-}6.5}+0.309Z_{6.5\text{-}7.5}+0.306Z_{7.5\text{-}8.5}+0.290Z_{8.5\text{-}10}+0.103Z_{17.5\text{-}20}$
	$PCA2_{17.5\text{-}20}$	$-0.343Z_{1.6\text{-}2}-0.178Z_{2\text{-}2.5}-0.108Z_{2.5\text{-}3}-0.154Z_{3\text{-}3.5}-0.111Z_{3.5\text{-}4}-0.092Z_{4\text{-}5}-0.011Z_{5\text{-}6.5}+0.253Z_{6.5\text{-}7.5}+0.213Z_{7.5\text{-}8.5}+0.278Z_{8.5\text{-}10}+0.780Z_{17.5\text{-}20}$
	$PCA3_{Out}$	$0.707Z_{12.5\text{-}15}+0.707Z_{15\text{-}17.5}$

Z : numerical value through standardization of particle number concentration

Table 7. Factors extracted from variables of size-segregated particle number concentrations.

Bioaerosol	Factor	Principle component equation
Bacteria	$FACTOR1_{1.6\text{-}7.5}$	$PN_{1.6\text{-}2}+PN_{2\text{-}2.5}+PN_{2.5\text{-}3}+PN_{3\text{-}3.5}+PN_{3.5\text{-}4}+PN_{4\text{-}5}+PN_{5\text{-}6.5}+PN_{6.5\text{-}7.5}$
	$FACTOR2_{7.5\text{-}17.5}$	$PN_{7.5\text{-}8.5}+PN_{8.5\text{-}10}+PN_{10\text{-}12.5}+PN_{12.5\text{-}15}+PN_{15\text{-}17.5}$
	$FACTOR3_{25\text{-}32}$	$PN_{25\text{-}30}+PN_{30\text{-}32}$
	$FACTOR4_{out}$	$PN_{Out10\text{-}12.5}+PN_{Out12.5\text{-}15}+PN_{Out15\text{-}17.5}+PN_{Out17.5\text{-}20}+PN_{Out25\text{-}30}+PN_{Out>3}$
Fungi	$FACTOR1_{1.6\text{-}10}$	$PN_{1.6\text{-}2}+PN_{2\text{-}2.5}+PN_{2.5\text{-}3}+PN_{3\text{-}3.5}+PN_{3.5\text{-}4}+PN_{4\text{-}5}+PN_{5\text{-}6.5}+PN_{6.5\text{-}7.5}+PN_{7.5\text{-}8.5}+PN_{8.5\text{-}10}$
	$FACTOR2_{17.5\text{-}20}$	$PN_{17.5\text{-}20}$
	$FACTOR3_{out}$	$PN_{Out12.5\text{-}15}+PN_{Out15\text{-}17.}$

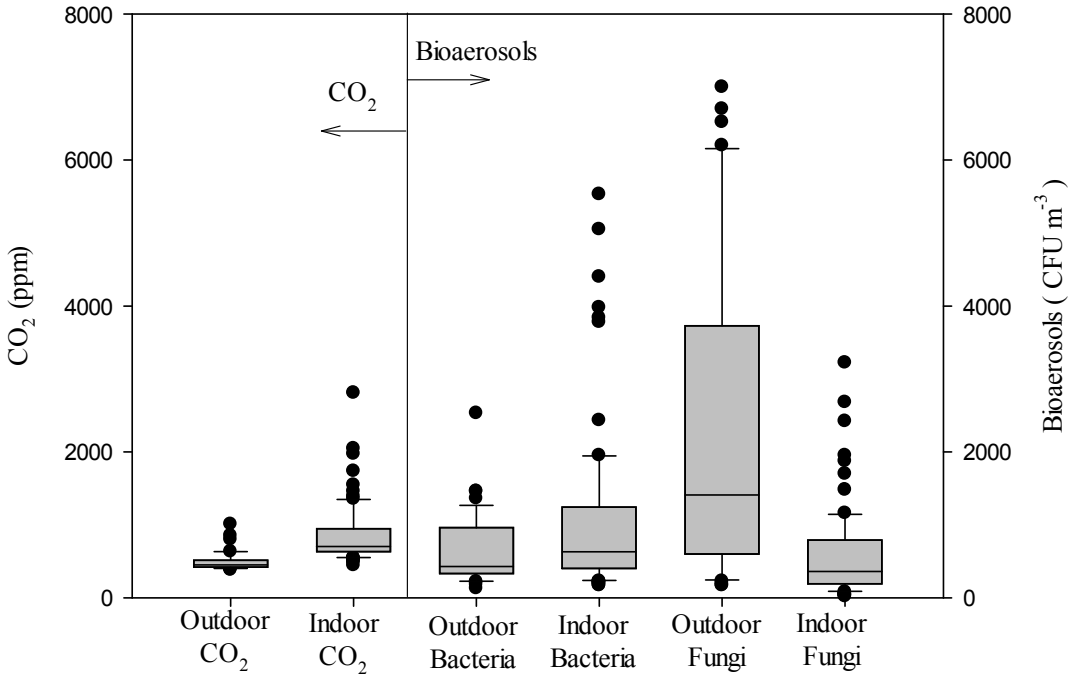
Figure Captions

Fig. 1. Indoor and outdoor bioaerosol and CO_2 concentrations in public spaces (Top and bottom of box indicates the 75th and 25th percentiles. Solid line across the box indicates median. The whiskers extend from the box to the 90th and 10th percentiles. Outliers are displayed as solid circles).

Fig. 2. Particle size distributions in indoor and outdoor environments.

Fig. 3. Comparison of predicted bacterial bioaerosol concentrations using regression model (Case II-1) with measured bacterial bioaerosol concentrations.

19 **Fig. 1.**



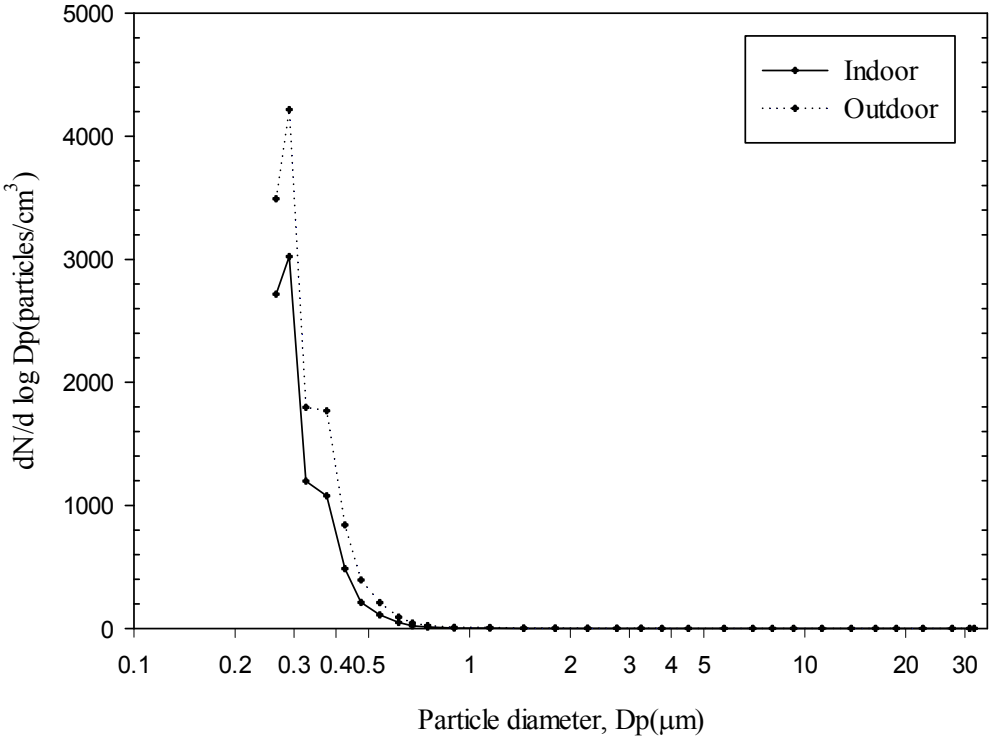
20

21 **Fig. 1.** Indoor and outdoor bioaerosol and CO_2 concentrations in public spaces (Top and bottom
22 of box indicates the 75th and 25th percentiles. Solid line across the box indicates median. The
23 whiskers extend from the box to the 90th and 10th percentiles. Outliers are displayed as solid
24 circles).

25

26

27 **Fig. 2.**



28

29 **Fig. 2.** Particle size distributions in indoor and outdoor environments.

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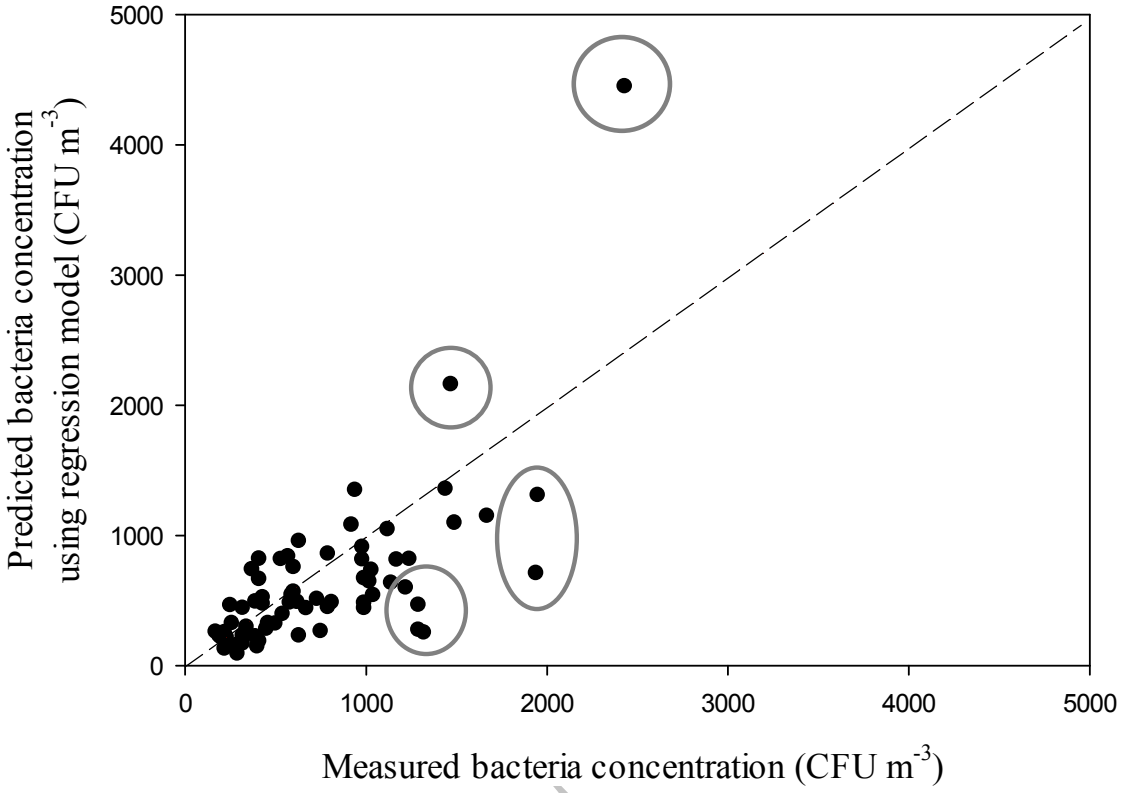
31
32

33 **Fig. 3.**



34
35
36 **Fig. 3.** Comparison of predicted bacteria bioaerosol concentrations using regression model (Case
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38