**Supplemental Information for**

**Experimental and Numerical Study of the Performance of Upper-Room Ultraviolet Germicidal Irradiation with the Effective Z-Value of Airborne Bacteria**

Yi Yanga, Alvin CK Laib, R.Y.C. Kongc and Qihong Denga[[1]](#footnote-1)\*

a*School of Energy Science and Engineering,* *Central South University, Changsha,* *Hunan, China*

b*Department of Architecture and Civil Engineering,* *City University of Hong Kong, Tat Chee Avenue, Kowloon, Hong Kong*

c*Department of Biology and Chemistry, City University of Hong Kong, Tat Chee Avenue, Kowloon, Hong Kong*

**S1 Simulation Methodologies**

**S1.1 Air flow**

The Renormalization Group (RNG) *k*-*ε* turbulence model was employed in this study because it is one of the most reliable models for simulating air flow in full-scale indoor environments (**Chen, 1995; Mui et al., 2009; Yang et al., 2016**). The fraction of bacteria was sufficiently small; hence, airflow was independent of bacteria movement. Enhanced wall treatment was applied for near-wall treatment because the maximal *y*+ was 8.4 in this simulation. The boundary conditions were identical to those in our recent study; the settings can be found elsewhere (**Yang et al., 2016**). The inlet boundary condition was set with the velocity magnitude and direction, respectively. The velocity magnitude was calculated from the ACH and the direction was set to 45°in four sector regions. The outlet boundary condition was set to zero diffusion flux. No-slip condition was applied for all solid wall boundary conditions.

**S1.2 Transport of airborne bacteria**

The drift flux model based on the Eulerian approach was developed to numerically describe the transport of airborne bacteria in the indoor environment (**Murakami et al., 1992**). It has been adopted and modified to model the airborne bacteria inactivation by UR-UVGI (**Yang et al., 2012; Yang et al., 2016**). The transport equations considering the removal mechanisms as turbulence diffusion, the deposition rate and the UVGI inactivation of airborne microorganisms can be written as:

 (S1)

where *Ci* is the concentration of bacteria *i*, ***vs,i***is the airborne bacteria settling velocity, *εp,i* is the airborne bacteria eddy diffusivity, *Di* is the Brownian diffusion coefficient, and *Sd,i* is the sink term for the deposition of bacteria *i* and it is expressed as:

 (S2)

where the summation in parentheses is over all wall faces of the first layer grids near the wall; **v***d,i* is the local deposition velocity, which was evaluated using the method suggested by **Lai and Nazaroff (2000)**; **A***w* is the face normal vector; *Vcell,i* is the grid cell volume; and *Cw,i* is the local concentration of the near-wall cell. *Suv,i* is the sink term for the bacteria *i* inactivation of UVGI and is expressed as Eq. (4) in manuscript. The boundary conditions of Eq. (S1) are non-diffusive fluxes in the outlet and wall boundary for all tested bacteria. Fresh air (*Ci*=0.0 CFU/m3) enters from the ceiling inlet. The deposition of bacteria onto the wall surface has been included in the deposition sink term (Eq. (S2)).

In this study, the fraction of bacteria is low enough that airflow pattern is independent of the bacteria movement. Hence, the residence time of air is equal to the time bacteria remains in the room. The air age equation can be described as (**Li et al., 2003;** **Sandberg and Sjöberg, 1983**):

 (S3)

where *tr* is the bacteria residence time in the ventilated room, *μeff* is the effective viscosity, *ρa* is the air density, *tr* is zero in the inlet boundary and is a non-diffusive flux in the outlet and wall boundary.

The percentage of bacteria disinfected or removed by different mechanisms is defined in **Yang et al. (2012**) and summarized as:

 (S4)

where *ti* is the integral time (720 s in this study), *V* is the chamber volume, *η* denotes the disinfection or removal mechanisms, *γ* is the field of integration, *ζ* is the variable of integration and *φ* is the quantity of airborne bacteria that was disinfected or removed by different mechanisms per unit time. The expressions for *η* and *φ* are shown in Table S1.

**Table S1** The variables of Eq. (S4).

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| --- | --- | --- | --- | --- |
| *η* | *φ* | *γ* | *ζ* | Mechanism |
| *uv* | *-Suv,i* | *Vr* | *V* | UV disinfection |
| *v* | *voCo,i* | *Ao* | *A* | Ventilation |
| *d* | *-Sd,i* | *Vr* | *V* | Deposition |

Note: *uv*, *v* and *d* are the abbreviation of ultraviolet, ventilation and deposition, respectively. *Suv,i* is the UV inactivation sink term of bacteria transport equation (Eq. (S1)) and it is expressed as Eq. (4) in manuscript, *vo* is velocity at the outlet, *Co,i* is the concentration of bacteria *i* in the first grid cell near the outlet, *Sd,i* is the sink term of deposition in bacteria transport equation (Eq. (S1)) and is expressed as Eq. (S2), *Ci* is the spatial concentration of bacteria *i*, *γ* represents the field of integration, *ζ* is the variable of the integration for Eq. (S4), *Vr* is the volume of room, *Ao* is the outlet area, *V* is volume and *A* is area.

The real-time percentage of suspended bacteria (*Ps*) in the chamber room is defined in **Yang et al. (2012**) and is calculated as

 (S5)

The average bacteria concentration in the breathing zone was calculated for the room volume under the 1.68 m breathing level (**Yang et al., 2016**):

 (S6)

where *Cb* is the average bacteria concentration in the breathing zone and *Vb* is the room volume below the breathing level (*w* ≤ 1.68m in this study).

**S1.3 Numerical procedure**

The bacteria transport equations were defined as scalar equation. The view factor mathematical model, the bacteria transport equations (Eq. (S1)) and the bacteria residence time equation (Eq. (S3)) were coded into the commercial CFD software ANSYS FLUENT version 14.0 through user-defined subroutines. The PISO algorithm was employed to decouple the pressure and velocity fields. The body force weighted scheme was applied for pressure interpolation and the second-order upwind scheme was used to discretize the convective terms of the transport equations (except the bacteria transport equations, were discretized with QUICK scheme). In the simulation, the steady flow field was obtained by first solving the fluid equations. Next, the irradiance was calculated and stored in the grid cell memory before solving the bacteria transport equations, and a uniformly spatial concentration was initially set in the computational zone at this stage. Finally, the airborne bacteria transport equations (Eq. (S1)) and the air age equation (Eq. (S3)) were simultaneously solved with the fluid equations when the airflow reached steady state. The partial derivative of *tr,uv* was calculated with *tr* in the irradiated zone at the end of each time step and the values was stored in the grid cell to solve for the UVGI sink term (Eq. (4) in manuscript) in the subsequent time step. The UR-UVGI fixture-off cases were resolved synchronously with the corresponding UR-UVGI fixture-on cases without considering the UVGI sink term in the bacteria transport equations. The time step was set to 0.1 s when solving the equations. The bacteria transport equations were solved in 720 s. The volumes of rod-shaped bacteria (*S. marcescens* and *P. alcaligenes*) were calculated initially with the cylinder volume formula. Then, spherical shape was assumed for all tested bacteria and their diameters were calculated from their volumes. The diameters for *S. marcescens,* *P. alcaligenes,* *M. luteus* and *S. epidermidis* used in this study are 0.8μm, 0.8μm, 0.7μm and 0.9μm, respectively. Their densities were assumed to be 1000 kg/m3. Non-uniform structure grid and grid-independent tests were performed with 512,400 and 988,320 grid cells, respectively. The difference from the predicted *Cb* that was obtained with both types of grids was less than 5%. Therefore, the simulation using 512,400 grid cells was selected for all simulation cases to save computational time and resources.

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| **Fig. S1** The comparison of the measured and predicted irradiance (*Ir*) of UR-UVGI fixture used in experiment at *w*=2.05 m plane. |

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| (a) 3 ACH | (b) 6 ACH |
|  |  |
| (c) 10 ACH |  |
| **Fig. S2** The contour of air velocity (*v*) in the center plane ( *x*=1.125 m) for three ACHs. | |

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| (a) 3 ACH | (b) 6 ACH |
|  |  |
| (c) 10 ACH |  |
| **Fig. S3** The contour of the bacteria residence time (*tr*) in the room in the center plane (*x*=1.125 m) for *t*=720 s. | |

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| --- | --- |
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| (a) 3 ACH | (b) 6 ACH |
|  |  |
| (c) 10 ACH |  |
| **Fig. S4** The contour of the concentration of *s. marcescens* (*C**s.* *marcescens*) represented with colors and the contour of the inactivation rate per unit time (*Suv,s. marcescens*) represented with black lines and values in the center plane (*x*=1.125 m) for *t*=720 s. | |

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| --- | --- |
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| (a) 3 ACH | (b) 6 ACH |
|  |  |
| (c) 10 ACH |  |
| **Fig. S5** The contour of the concentration of *s. marcescens* (*Cs. marcescens*) represented with colors and the contour of the inactivation rate per unit time (*Suv,s. marcescens*) represented with black lines and values at *w*=2.05 m plane for *t*=720 s. | |

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| **Fig. S6** The comparison of the percentage of bacteria suspended in air (*Ps*), removed by ventilation (*Pv*), inactivated by UR-UVGI (*Puv*) and removed by deposition (*Pd*) for different tested bacteria and ACHs after *t*=720 s. |

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1. \* Corresponding author. School of Energy Science and Engineering, Central South University, Changsha 410083, Hunan, China. Tel.:+86 731 8887 7175.

   *E-mail address*: [qhdeng@csu.edu.cn](mailto:qhdeng@csu.edu.cn) (Q. Deng). [↑](#footnote-ref-1)