Contribution ID: **104** Type: **Poster**

The influence of ventilation conditions on the spread of human respiratory aerosols in indoor spaces: an experimental aerobiological study

The transmission of pathogens between humans in indoor environments has been recognized for a long time. The SARS-CoV-2 pandemic showed the significance of expiratory aerosols as a source of virus transmission indoors. A concern particularly in elderly care homes. Since then, studies have explored indoor distribution patterns through modeling or experimental investigations using artificial aerosol sources. However, the reliability of these methods for real-life conditions remains uncertain.

To address this gap, we examined how different ventilation conditions affect the dispersion of human respiratory emissions by human volunteers within a room under realistic conditions in a large-scale test facility. By including various airflow scenarios, we aimed to explore how ventilation can influence the distribution and concentration of human respiratory excreta within an indoor environment.

In a large-scale test facility of approximately 70m², we replicated the furniture setup and ventilation conditions typical of common rooms in long-term elderly care facilities. Five healthy human volunteers were seated in the room to simulate residents. To minimize the impact of non-respiratory aerosols, participants wore coveralls, hairnets, and galoshes during the experiments. They engaged in activities such as playing games and reciting a play to ensure regular aerosol production from speaking over the 1.5 hours session. This was repeated three times per research day with randomly assigned ventilation conditions (150 m³/hr, 400 m³/hr, or 150 m³/hr with a mobile air cleaner) Incoming air was HEPA filter treated. The distribution of human expiratory aerosols was measured at various distances (<1.5m, 3m, and <6m) from the participants. The experiment was repeated over three independent days.

During each 1.5-hour session, the following data was collected:
• Active air sampling of bio-aerosols using a NIOSH BC215 sampler and inhalable dust using a GSP sampler at six locations. Samples were analyzed for common bacterial biomarkers (16S rRNA gene, S. Salivarius, S. epidermidis) by qPCR, and total bacteria by culture for NIOSH samples.
• Particulate matter size distribution in 31 size fractions using GRIMM samplers, and indoor air quality parameters (CO2, temperature and relative humidity) measured by sensors at 1 minute intervals at seven locations.
• Passive total bacterial aerosol samples were collected at 11 locations in the room by exposing tryptone soy agar plates.

Data collection has just been completed, and sample analysis in the laboratory is ongoing. We expect to present a full analysis of the results at the conference. These kinds of experiments will add to the body of evidence in addition to modeling and artificial experimental studies to improve future risk assessments.

Primary author: WOUTERS, Inge (Utrecht University)

Co-authors: KRITSI, Effy (Utrecht University); LOOMANS, Marcel (Eindhoven university of Technology (TU/e)); TRAVERSARI, Roberto (Netherlands Organisation for Applied Scientific Research (TNO)); SMIT, Lidwien (Utrecht University)

Presenter: WOUTERS, Inge (Utrecht University)