

Contribution ID: 62

Type: Oral presentation

Dynamics of Airborne Epidemics Are Strongly Determined by Heterogeneity in Ventilation: Insights from Hybrid Air-Dynamic Disease Models

Wednesday, May 7, 2025 3:00 PM (15 minutes)

Background: While the areas of study of indoor air and infectious disease epidemiology both emphasize the use of modeling for understanding disease transmission systems, siloing of disciplines, different model assumptions, and different vocabulary have limited the emergence of transdisciplinary science around airborne infectious diseases. Here we show that integration of simple air and epidemic models provides useful and policy-relevant insights that can be used to protect population health.

Methods: The Wells-Riley (WR) model is a simple, widely used model for estimation of cross-sectional risk of transmission of infection from an infectious case. The Reed-Frost (RF) model is a disease transmission model used to simulate transmission over time as a discrete process in relatively small populations. Both models treat infection transmission as a binomial process, which allows hybridization whereby WR is used as the RF transmission coefficient (a "WRRF"model). We simulate disease dynamics for a disease similar to Wuhanvariant SARS-CoV-2 which dominated in the early months of the recent pandemic. Cases may either be a minority "aerosolizers", who are highly infective in poorly ventilated environments, or "non-aerosolizers", who are less infectious but equally infective in all environments, regardless of ventilation efficiency. We used a meta-population structure and modeled transmission both within and between three sub-populations with poor, intermediate, and good ventilation respectively. We performed both deterministic and stochastic model runs with the initial outbreak seeded with an "aerosolizer" in one of the three linked populations.

Results: Final total outbreak size was strongly influenced by which sub-population was seeded with the first case; final outbreak size was approximately 3-fold larger when initial seeding occurred in the poorly ventilated sub-population than when seeded in better-ventilated subpopulations due to large initial case numbers. For outbreaks seeded in the poorly ventilated population, improvement in ventilation in that population slowed epidemic emergence in the other two subpopulations more effectively than further improvements in ventilation in already well-ventilated environments. In stochastic model runs, the probability of stochastic extinction was inversely related to ventilation rate in the population in which the initial case was seeded.

Conclusions: Ventilation can easily be incorporated into epidemic models, and evaluation of heterogeneity in ventilation provides important insights into the dynamics of emerging infectious diseases. In particular, outbreak size, rapidity of spread between populations, and the likelihood of stochastic extinction in the population as a whole are driven by ventilation quality in the worst-ventilated environments. This supports the importance of universal ventilation standards as an important element of population health protection.

Primary authors: FISMAN, David (University of Toronto); Ms WILSON, Natalie (University of Toronto)

Presenter: FISMAN, David (University of Toronto)

Session Classification: SESSION 4b - Mathematical Modeling and Risk Assessment, Oral Presentations