The spatial dispersion of infectious virus in a multi organism model of dental bioaerosols

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Introduction

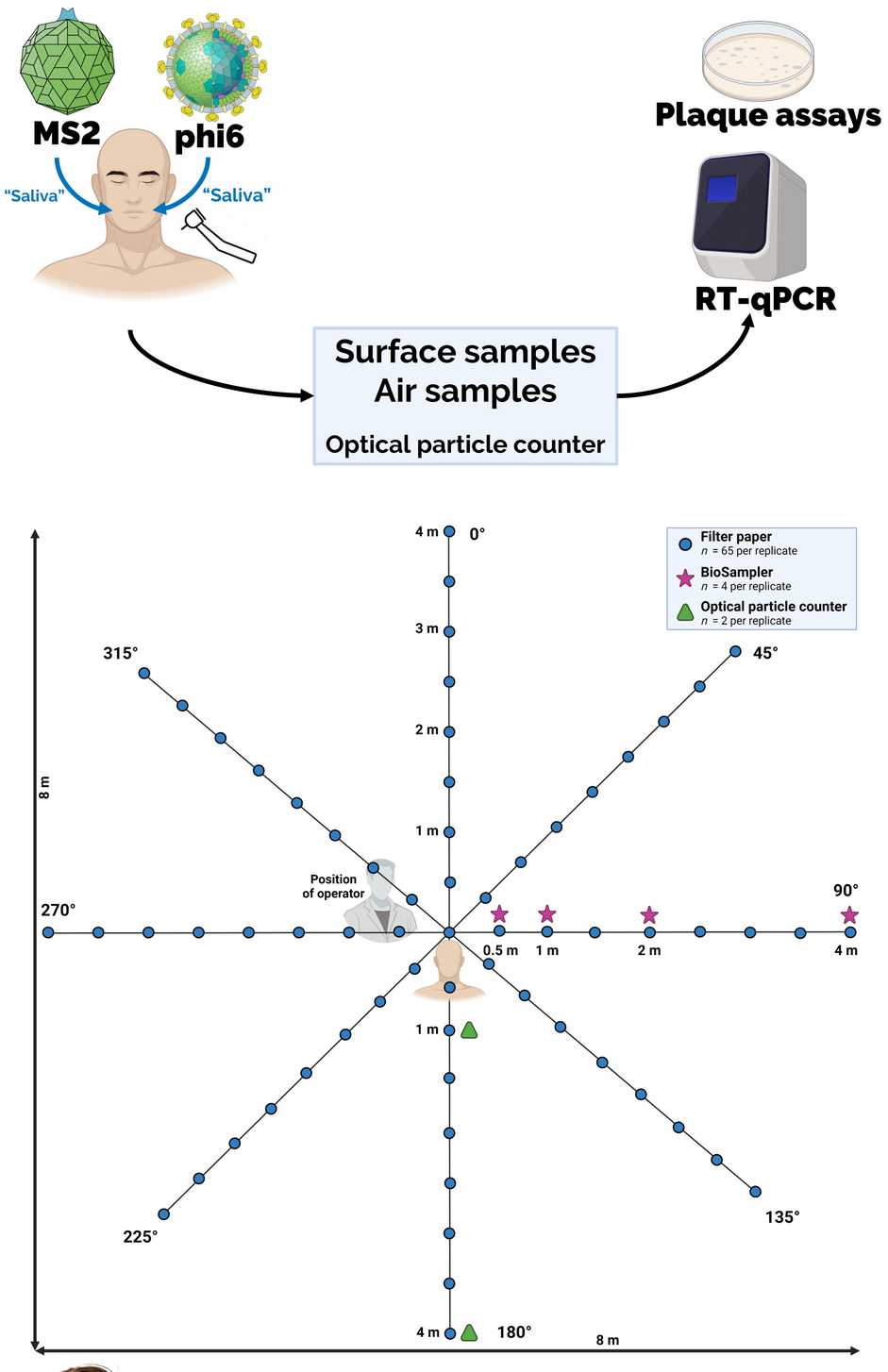
Bioaerosols generated during dental procedures contain microorganisms, risking occupational exposure and healthcare-associated infection. This study aimed to explore the spatial distribution of viruses in a simulation model of dental bioaerosols, using two bacteriophages (phages) as viral tracers to simulate human pathogens.

Methods

Simulated "saliva" containing the enveloped bacteriophage phi6 and non-enveloped MS2 (approx. 10^{10} Plaque-Forming Units [PFU]/mL) was infused into a dental mannequin's mouth. A 10-min dental procedure was performed with an air turbine dental handpiece (n=4 replicates). Filter papers, air samplers (BioSampler, SKC Inc), and optical particle counters (OPCs; 3016-IAQ, Lighthouse, USA) were used to sample aerosol as shown in fig. 1.

Plaque assays were used to measure infectious virus and reverse-transcription quantitative polymerase chain reaction (RT-qPCR) to measure viral RNA. Non-linear regression was used to describe the relationship between recovery and sample distance.

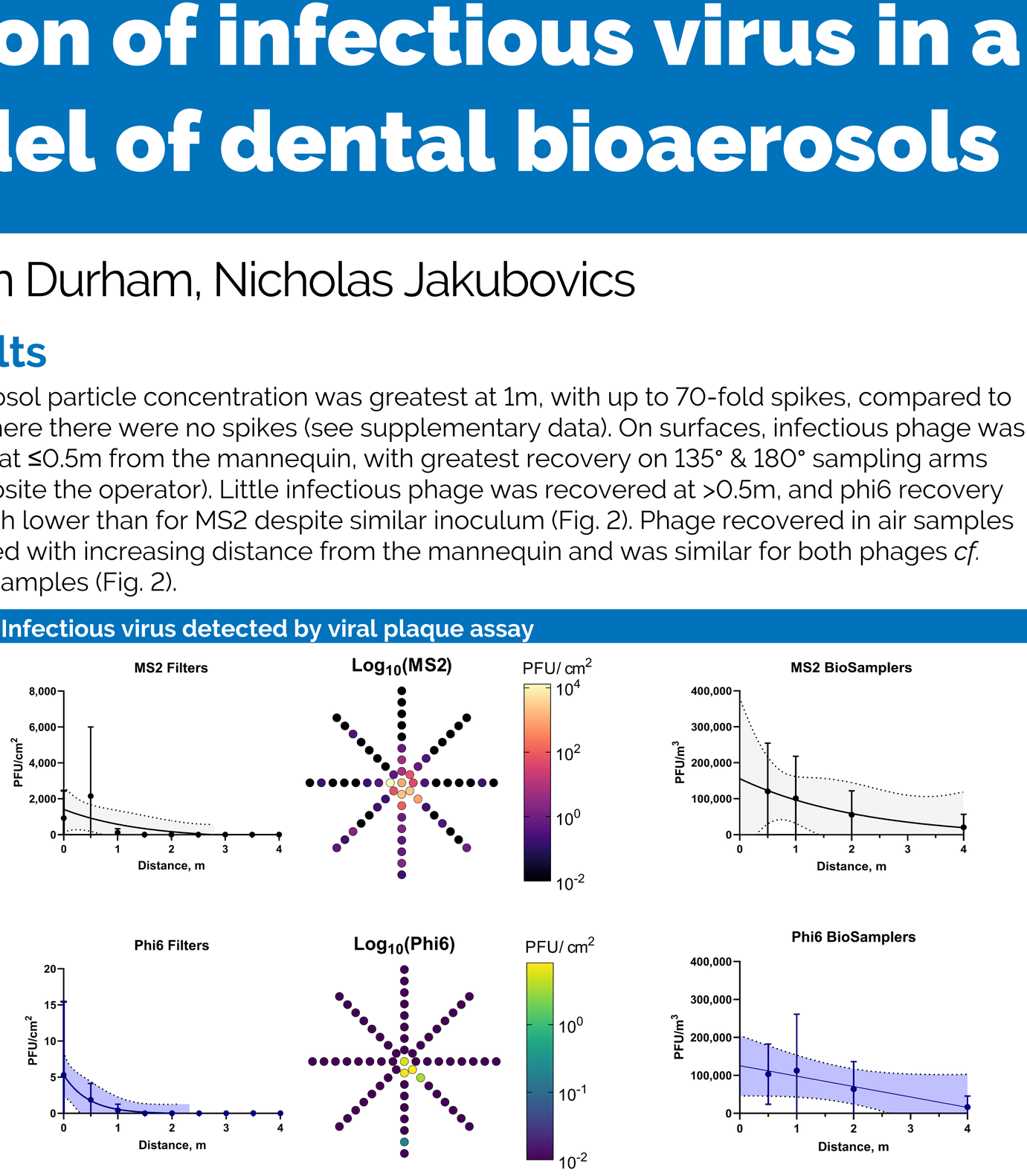
Figure 1. Overview of methods and sampling positions



Results

OPC aerosol particle concentration was greatest at 1m, with up to 70-fold spikes, compared to at 4m where there were no spikes (see supplementary data). On surfaces, infectious phage was greatest at ≤0.5m from the mannequin, with greatest recovery on 135° & 180° sampling arms (i.e., opposite the operator). Little infectious phage was recovered at >0.5m, and phi6 recovery was much lower than for MS2 despite similar inoculum (Fig. 2). Phage recovered in air samples decreased with increasing distance from the mannequin and was similar for both phages *cf.* surface samples (Fig. 2).

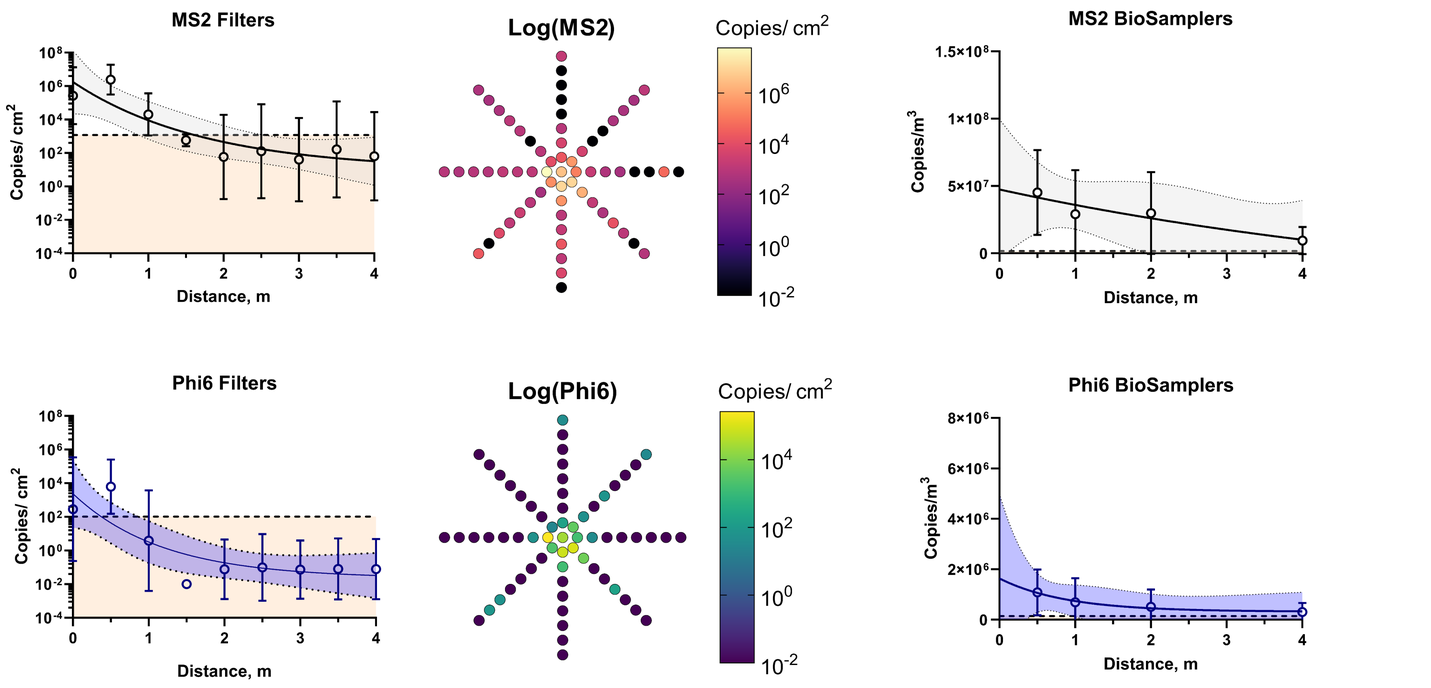
Figure 2. Infectious virus detected by viral plaque assay



Infectious MS2 (upper panels) and phi6 (lower panels) bacteriophage recovered from surface samples (filter paper samples) and air samples (BioSamplers). Data from 4 replicates. Left panels show recovery from surface samples grouped at each distance from the procedure with 65 samples per replicate. Centre panels show heatmaps of recovery from surface samples, with each circle representing the mean of 4 replicates at each sample location (see fig. 1). Right panels show recovery in air samples with 4 samples per replicate. Curves in left and right panels are non-linear regression curves and 95% confidence intervals using a one-phase decay model (except lower right panel which uses a straight-line model due to better curve fit). PFU: Plaque forming units.

Phage RNA recovered from surface samples was greatest at ≤0.5m. Low levels also seen in distant sites where infectious phage was not detectable (Fig. 3). Viral RNA in air samples was greater for MS2 than for phi6 and decreased with increasing distance from the mannequin.

Figure 3. Viral copies detected by RT-qPCR



MS2 (upper panels) and phi6 (lower panels) RNA recovered from surface samples (filter paper samples) and air samples (BioSamplers). Data from 4 replicates. Left panels show recovery from surface samples grouped at each distance from the procedure with 65 samples per replicate. Centre panels show heatmaps of recovery from surface samples, with each circle representing the mean of 4 replicates at each sample location (see Fig. 1). Right panels show recovery in air samples with 4 samples per replicate. Curves in left and right panels are non-linear regression curves and 95% confidence intervals using a one-phase decay model. The dashed line enclosing the orange shaded area denotes the limit of detection of the RT-qPCR assay.

Conclusion

Infective virus was dispersed during simulated dental procedures. Surface contamination was mostly within 0.5m, but airborne phage was detected up to 4m. The pattern of distribution was similar for both viruses, being greatest opposite the operator, but recovery was lower for phi6. These findings should inform infection prevention & control practices in dentistry. Careful selection of microorganisms is important in future studies due to recovery differences.

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Supplementary Data

Abstract #31

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