Seminar

Viral UV Inactivation and Microbiome of Drinking Water Distribution Systems

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Abstract:

The following provides a summary on viral inactivation of viruses in different culture media and microbiome of drinking water and Prevalence of *Legionella*, *Mycobacterium*, and *Pseudomonas* Species.

Exposure to germicidal ultraviolet (UV-C) light damages viral nucleic acid rendering them non-infectious. Most of the recent viral inactivation studies have not considered potential artifacts caused by interactions between UV-C light and culture media used to suspend and deposit virus on surfaces. We show that the reactive oxygen and nitrogen species (ROS and RNS) form when commonly used virus culture media is exposed to 265 nm irradiation. Surface viral inactivation values were enhanced from 0.49 to 2.92 log10 of viruses in DMEM, EMEM or EMEM-F as compared to absence of culture media (only suspended in Tris-buffer). The mechanisms responsible for the enhanced surface inactivate is hypothesized to involve photo-activation of vitamins and dyes present in the culture media, which produce ROS and RNS. Given the rapidly growing research and commercial markets for UV-C disinfecting devices, there is a need to establish surface disinfecting protocols that avoid viral inactivation enhancement artifacts associated with selection and use of common cell culture media in the presence of UV-C light. This study addresses this weak link in the literature and highlights that inadequate selection of virus suspension media may cause a bias (i.e., over-estimation) for the UV-C dosages required for virus inactivation on surfaces.

In drinking water distribution systems (DWDSs), pipe material and water temperature are some of the critical factors affecting the microbial flora of water. Six model DWDSs consisting of three pipe materials (galvanized steel, copper, and PEX) were constructed. The temperature in three systems was maintained at 22◦C and the other 3 at 32◦C to study microbial and elemental contaminants in a 6-week survey using 16S rRNA next-generation sequencing (NGS) and inductively coupled plasma-optical emission spectrometry (ICP-OES). Proteobacteria was the most dominant phylum across all water samples ranging from 60.9% to 91.1%. Species richness (alpha diversity) ranking was PEX < steel ≤ copper system and elevated temperature resulted in decreased alpha diversity. Legionellaceae were omni-prevalent, while Mycobacteriaceae were more prevalent at 32 ◦C (100% vs. 58.6%) and Pseudomonadaceae at 22 ◦C (53.3% vs. 62.9%). The elevated temperature resulted in well-defined microbial clusters (high pseudo-F index) in all systems, with the highest impact in PEX (10.928) followed by copper (9.696) and steel (5.448). Legionellaceae and Mycobacteriaceae are preferentially prevalent in warmer waters. The results suggest that the water temperature has a higher magnitude of impact on the microbiome than the pipe material.