184-AGR

The First Report on the UV-C sensitivity Human metapneumovirus (hMPV) using omics approach.

Human metapneumovirus (hMPV) is a negative-sense, single-stranded RNA virus within the Pneumoviridae family, which also includes respiratory syncytial virus (RSV). Commonly causing mild upper respiratory infections (i.e., the common cold), hMPV was first identified in 2001 and has likely been circulating for several decades. Following a recent viral outbreak in China, its critical to evaluate the UV-C sensitivity of hMPV to develop effective UV-C disinfection systems. Ultraviolet (UV-C) treatments are known to be effective against a broad spectrum of microorganisms on surfaces, in air and fluid systems. In our previous studies, we designed a pyrimidine dinucleotide frequency (PyNNFV)-based genomic model to calculate the UV-C sensitivity of various enveloped and non-enveloped viruses. The goal of this study was to determine hMPV's UV-C sensitivity by applying the same PyNNFV approach. Analysis of the hMPV genome (13,350 nucleotides) revealed 728 TT dimers, 498 TC dimers, 285 CT dimers, and 239 CC dimers, 100% probability of dimer formation. The PyNNFV value for hMPV was found to be 5.64×10^{-4} which is similar to that of SARS-CoV-2. Based on the obtained PyNNFV value the UV-C sensitivity of for hMPV is 2.16 $mJ/cm^2/log_{10}$, a predicted dose of 10.8 mJ/cm^2 should yield 5 log reduction of hMPV in buffer systems. The model predicted data indicates that hMPV is sensitive to UV-C photons. These findings aid in identifying non-pathogenic (to humans) surrogate viruses useful for studying UV-C inactivation kinetics and validating UV-C disinfection systems. This approach also helps minimize the number of surrogate viruses needed for testing UV-C treatment of other human and animal –(ss) RNA viral pathogens, ultimately saving time, labor, and resources.