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A Genomic Approach to Quantify UV-C Sensitivity of *Coxiella burnetii* Strains

Coxiella burnetii (*C. burnetii*), a pathogenic microorganism of the family Coxiellaceae, is the causative agent of Q fever. Despite extensive research, *C. burnetii* remains of great interest due to its obligate intracellular lifestyle, extreme infectivity, challenges in genetic manipulation, and the limitations of small animal models in replicating human Q fever. A major Q fever outbreak in the Netherlands (2007–2010) notably affected dairy farms, resulting in over 4,000 confirmed human infections. Ultraviolet-C (UV-C) irradiation has emerged as a promising method for disinfecting and decontaminating a wide range of microorganisms, including fungi, bacteria, viruses, and spores. UV photons damage nucleic acids—primarily through the formation of pyrimidine dimers—thereby disrupting microbial replication. However, handling highly infectious organisms such as *C. burnetii* requires specialized training and containment in high-level biosafety laboratories, which can complicate direct experimental UV-C sensitivity assessments. In this study, we aim to quantify the pyrimidine dinucleotide frequency values (PyNNFV) to estimate UV-C sensitivity in three *C. burnetii* strains: the virulent Nine Mile phase I (NMII or RSA 493), the less virulent Nine Mile phase II (NMII or RSA 439), and a milk isolate strain (CMSC1). The genomes of these strains are approximately 1,995,500 base pairs in length. Among the NMI, NMII, and CMSC1 genomes, the frequencies of TT, TC, CT, and CC dimers were used to calculate PyNNFV values of 1.001858e-5, 1.018742e-5, and 1.007166e-5, respectively (probability functions). Experimental data (collimated beam test) revealed a D_{10} value of 4.1 ± 0.04 mJ/cm^2 for the NMII strain; the model subsequently predicted D_{10} values of 4.03 mJ/cm^2 for NMI and 4.05 mJ/cm^2 for CMSC1. These findings underscore the utility of predictive genomic modeling for estimating UV-C susceptibility of risk group 3 pathogens. In the future, we plan to conduct bioassays to experimentally determine the D_{10} values for RSA 493 and CMSC1 strains and compare them with our model predictions.