Ultraviolet Rate Constants of Pathogenic Bacteria: A Database of Genomic Modeling Predictions

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Abstract

A database of bacterial ultraviolet (UV) susceptibilities is developed from an empirical model that correlates genomic parameters with UV rate constants. Software is used to count and evaluate potential ultraviolet photodimers and identifying hot spots in bacterial genomes. The method counts dimers that potentially form between adjacent bases that occur at specific genomic motifs such as TT, TC, CT, & CC. Hot spots are identified where clusters of three or more consecutive pyrimidines can enhance absorption of UV photons. The model incorporates nine genomic parameters into a single variable for each species that represents its relative dimerization potential. The bacteria model is based on a curve fit of the dimerization potential to the ultraviolet rate

constant data for 92 bacteria species represented by 216 data sets from published studies. There were 4 outliers excluded from the model resulting in a 98% Confidence Interval. The curve fit resulted in a Pearson correlation coefficient of 80%. All identifiable bacteria important to human health, including zoonotic bacteria, were included in the database and predictions of ultraviolet rate constants were made based on their specific genomes. This database is provided to assist healthcare personnel and researchers in the event of outbreaks of bacteria for which the ultraviolet susceptibility is untested and where it may be hazardous to assess due to virulence. Rapid sequencing of the complete genome of any emerging pathogen will now allow its ultraviolet susceptibility to be estimated with equal rapidity. Researchers are invited to challenge these predictions.

Importance

This research demonstrates the feasibility of using the complete genomes of bacteria to determine their susceptibility to ultraviolet light. Ultraviolet rate constants can now be estimated in advance of any laboratory test. The genomic methods developed herein allow for the assembly of a complete database of ultraviolet susceptibilities of pathogenic bacteria without resorting to laboratory tests. This UV rate constant information can be used to size effective ultraviolet disinfection systems for any specific bacterial pathogen when it becomes a problem.

Key Words: Genomics, ultraviolet, UVC, bacteria, pathogens, UV susceptibility, UV rate constant

Introduction

In spite of the widespread application of ultraviolet disinfection technologies in healthcare and other industries, less than 25% of pathogenic bacteria have been studied in laboratories to assess their UV rate constant. A complete database of bacteria UV rate constants would be useful for estimating the required UV dosage for bacteria when using UV disinfection equipment. Laboratory testing can be expensive, time-consuming, and even hazardous but the use of genomic modeling can enable rapid estimation of required UV dosage for any new or emerging pathogen once the genome is sequenced. Genomic predictions of UV rate constants can potentially be extremely accurate, more accurate than typical laboratory test results. The accuracy achievable by genomic modeling may be such that predictions could serve as a standard by which to judge the accuracy of laboratory testing, in much the same way as laws of physics are used to assess the efficiency of motors and the strength of structures. The present research is based on an empirical model that is fit to existing data and represents a step towards a fundamentals-based model of ultraviolet susceptibility that promises accuracy beyond six decimal places. The present research addresses bacteria because they have long been the largest and most persistent infection problem in healthcare. Although this view is being challenged by the current pandemic, the success of this bacteria genomic model will also lead to a model for predicting UV rate constants for viruses as well.

Methods

The methods used to develop the model and make predictions are purely analytical and empirical and involved firstly a compilation of UV rate constant studies for bacteria and

67 computation of the UV rate constants of k values. The measured UV rate constants are
68 averaged when there are multiple studies and are applied in an empirical model that
69 correlates the k values with a theoretical dimerization value, Dv, which quantifies a
70 series of genomic parameters into a single value. The dimerization value is computed
71 directly from the genomes for all subsequent bacteria to produce the predicted UV rate
72 constant. The details of these computations are discussed in the following subsections.

73 **Rate Constant Studies**

74 Studies on ultraviolet (254 nm) survival of bacteria on surfaces or in water were
75 reviewed. Criteria for selection included having interpretable results that would define
76 the first stage of exponential decay independent of any survival tail (the second stage)
77 or shoulder in the survival curve, since the presence of a tail can confuse interpretation
78 of the first stage rate constant. Table 1 summarizes the 92 bacteria that form the basis
79 of the model and the UV rate constants averaged from the indicated studies. Every
80 attempt was made to be inclusive of all available studies but invariably there were a few
81 studies that defied interpretation or for which a genome was lacking. Shown in the
82 columns of Table 1 are the UV rate constant k computed as the average of all studies,
83 the Mean Aerodynamic Diameter (MAD), the D90 values, and the genome identifier or
84 accession number. In some cases the identifier is the first in a series of shotgun
85 sequence identifiers. The number of data sets reflects the number of studies up to a
86 maximum of 3 beyond which no further weight is given to the species in the model. This
87 avoids bias for the small number of species that have a large number of studies and 3 is
88 an appropriate number of studies from which to obtain an average value. In cases
89 where an excessive number of studies exist many were omitted due to redundancy.

Four species formed outliers in this model and were excluded. *Nocardia asteroides* was also a low outlier and it is a bacteria that more resembles a fungus and may not belong to this data set, but more studies on *Nocardia* species are needed to resolve this issue. *Enterobacter cloacae* was a low outlier. *Mycobacterium abscessus, Burkholderia mallei*, and *B. pseudomallei* were all high outliers. These outliers were each single studies except for *B. pseudomallei* which had a second study which was not an outlier and which is included in the model in Table 1. *Micrococcus radiodurans* was expected to be a low outlier due to its unique ability to resist radiation and was excluded from consideration altogether except that it is shown for reference.

The Average UV Rate Constant k shown in Table 1 is computed from information provided in the referenced studies. If only a D90 value is provided and there is no significant shoulder or tail evident then the value is converted to a rate constant according to equation (1).

$$k = \frac{-\ln(0.10)}{D90} \qquad (1)$$

In most cases the original data is inspected to determine the UV rate constant separate from any shoulder or tail. The range of data points within which the value of k1 can be accurately computed is illustrated in Figure 2. Any points above and beyond the shoulder region, if any, and any points beyond the survival tail, if any, are suitable for use in computing the UV rate constant. In all case there are multiple studies available, the rate constant is computed as the average and not the D90 value.

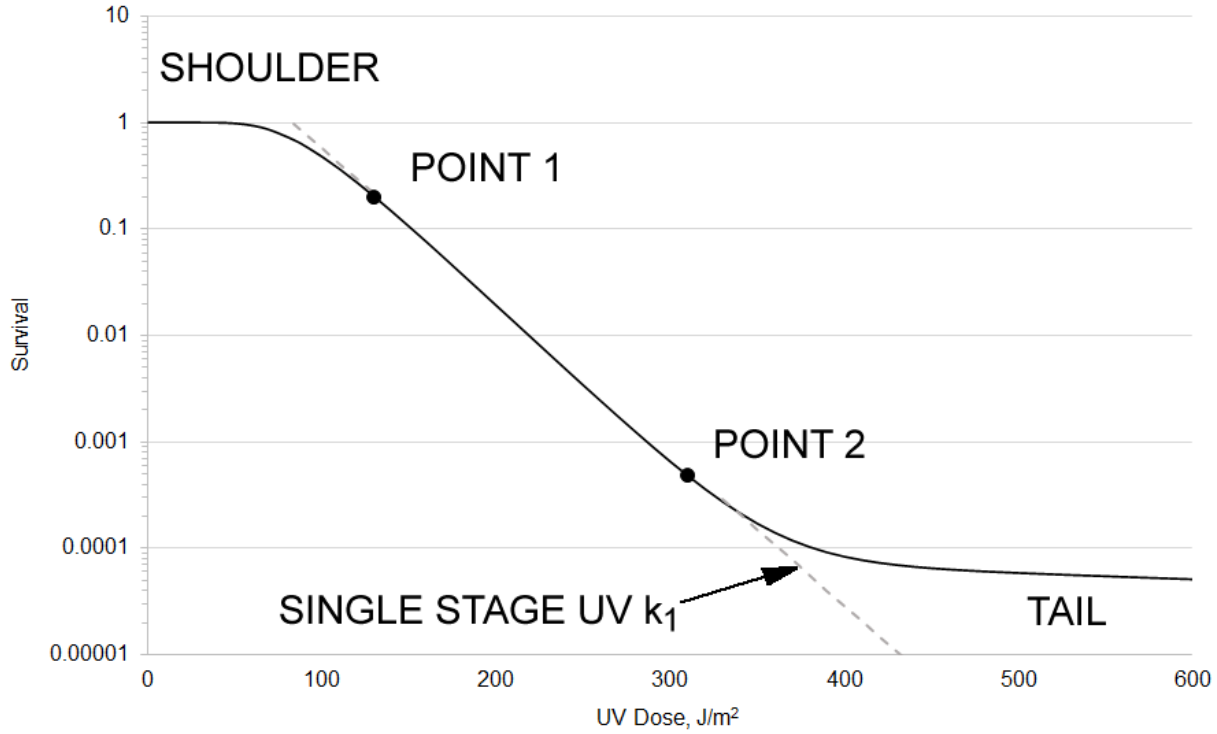

Figure 1: Figurative survival curve with a shoulder and a tail. The Single Stage UV rate constant k_1 must be computed between the data points beyond the shoulder region (Point 1) and the data points before the tail develops (Point 2). The UV Dose scale shown is arbitrary.

The Mean Diameter listed in Table 1 represents the logmean diameter of spherical cells and for rods or oblong cells it represents the logmean diameter computed with the Cauchy Theorem, which represents the average area of the profile of the rod. The profile area accounts for the area upon which the UV rays impinge and this determines the amount of UV scattering (Kowalski 2020). The mean diameter is used to compute the shielding constant Sc, which represents the amount of shielding a cell has from UV due to its physical size. The shielding constant is used in turn to compute the intrinsic UV rate constant which is the value correlated by the empirical model. The

advantage of using the intrinsic rate constant, however theoretical it may be, is seen in the fact that the MAD exponent in this model converged to zero and ceased to have any predictive value. This simplification separates the only physical parameter (MAD) from the genomic parameters and renders the core model purely genomic in nature.

Calculations of the UV rate constants from the studies in Table 1 will be made available as supplemental files online at XXXX.later.

Table 1: Average Rate Constant Summary from Studies

Bacteria	Source	Data Sets	Mean k_1 m^2/J	Avg D_{90} J/m^2	Mean Dia. μm	Genome ACC.# NCBI, Kegg	Genome kb
Acinetobacter baumannii	84,97	2	0.1527	15	1.31	NC_008801	3904
Aeromonas punctata (caviae)	56	1	0.1727	13	0.70	NZ_AP022254	4566
Aeromonas hydrophila	56101	2	0.1528	15	0.70	NC_008570	4744
Aeromonas salmonicida	55,66,88	3	0.1501	15	0.70	NC_009348	5041
Bacillus anthracis	46,57	2	0.1050	22	1.41	NC_007530	5504
Bacillus cereus	23,30	2	0.0582	40	1.28	NC_004722	5427
Bacillus megaterium	43	1	0.0540	43	1.79	NZ_CP009920	5747
Bacillus subtilis	40,68,69,85,100	3	0.0549	42	0.56	NC_000964	4215
Bacteroides fragilis	51,94,89	3	0.1020	23	1.15	NC_003228	5242
Brevundimonas diminuta	1	1	0.0311	74	0.27	NZ_UIGE01000002	3439
Brucella melitensis	87	1	0.0722	32	0.64	NZ_WUEE01000001	3291
Brucella suis	87	1	0.1057	22	0.64	NZ_CP007719	3297
Burkholderia cenocepacia	1	1	0.0397	58	0.76	NZ_MUTR01000001	9961
Burkholderia cepacia	1,15	2	0.0508	45	0.76	NZ_CP045235	8367
Burkholderia pseudomallei	49	1	0.0461	50	0.84	NC_006350	7248
Campylobacter jejuni	14,101	2	0.1375	17	0.63	NC_002163	1641
Citrobacter freundii	35,106	2	0.0525	44	1.28	NZ_AOMS01000001	4900
Citrobacter koseri	35	1	0.0461	50	1.28	NC_009792	4735
Clostridium perfringens	44	1	0.0600	38	5.00	NC_003366	3031
Corynebacterium diphtheria	92	1	0.0680	34	1.06	NZ_LN831026	2464
Coxiella burnetii	67,69	2	0.1036	22	0.32	NC_002971	2033
Enterobacter cloacae	106	1	0.0461	50	1.41	NZ_CP008823	5503
Enterococcus faecalis	1,19,20,38,40,58,77	3	0.0533	43	1.11	NZ_KE351595	2929
Enterococcus faecium	72,74,75	3	0.0639	36	1.11	NC_017958	3053
Escherichia coli	12,24,27,31,83,92,99,102	3	0.0973	24	0.94	NC_004431	5231
Fluoribacter bozemanae	36,57,103	3	0.1587	15	0.73	NZ_UGGY01000007	4232
Fluoribacter dumoffii	36,57	2	0.1039	22	0.73	NZ_LNXZ01000001	3817
Fluoribacter gormanii	36,57	2	0.1337	17	0.73	NZ_UGGV01000002	3873
Francisella tularensis	87	1	0.1708	13	0.22	NZ_KN046815	1818
Haemophilus influenzae	6,76	3	0.1265	18	0.33	NC_000907	1830
Helicobacter pylori	40	1	0.0971	24	0.94	NC_000921	1644
Klebsiella pneumoniae	35,106	2	0.0504	46	0.55	NC_009648	5315
Lactococcus lactis	85	1	0.0557	41	0.85	NZ_LT599049	2731
Legionella jordanis	57	1	0.0768	30	0.73	NZ_LR134383	3134
Legionella longbeachae	18,36	2	0.2022	11	0.73	NC_013861	4149
Legionella oakridgensis	57	1	0.0677	34	0.73	NZ_CP004006	2773
Legionella pneumophila	3,18,36,57,79,101,103	3	0.1447	16	0.73	NC_006369	3346
Legionella wadsworthii	57	1	0.1212	19	0.73	NZ_UGPB01000002	3603
Listeria monocytogenes	24,55,104	3	0.0771	30	0.71	NC_002973	4844
Lysinibacillus fusiformis	85	1	0.0763	30	0.56	NZ_CP010820	2905
Micrococcus luteus	4	1	0.0237	97	0.39	NC_012803	2501
Moraxella catarrhalis	85	1	0.0768	30	0.77	NC_014147	1863
Mycobacterium avium	41,73,93	3	0.0429	54	0.76	NC_008595	5475
Mycobacterium bovis BCG	24	1	0.1007	23	0.55	NZ_CP039850	4412
Mycobacterium gilvun	27	1	0.0285	81	0.78	NC_008595	5620
Mycobacterium intracellulare	27,41	2	0.0293	79	0.76	NC_016946	5402
Mycobacterium kansasii	27	1	0.0408	56	0.54	NC_022663	6577
Mycobacterium marinum	27	1	0.0468	49	0.55	NC_010612	6637
Mycobacterium smegmatis	11,27	3	0.0359	64	0.60	NC_008596	6988
Mycobacterium terrae	10	1	0.0461	50	0.64	CP002329	4644
Mycobacterium tuberculosis	11,24,25,27	3	0.0747	31	0.55	NC_009565	4424
Mycolicibacterium fortuitum	27	2	0.0542	42	0.80	NZ_CP011269	6255
Mycolicibacterium phlei	24,27	2	0.0549	42	0.50	NZ_CP014475	5350

Table 1: Average Rate Constant Summary from Studies

Bacteria	Source	Data Sets	Mean k_1 m^2/J	Avg D_{90} J/m^2	Mean Dia. μm	Genome ACC.# NCBI, Kegg	Genome kb
Mycoplasma arthritidis	32	1	0.1050	22	0.24	NC_011025	820
Mycoplasma fermentans	32	1	0.1163	20	0.31	NC_014921	1119
Mycoplasma hominis Type 1	32	1	0.1396	17	0.19	NC_013511	695
Mycoplasma orale Type 1	32	1	0.1308	18	0.24	NZ_LR214940	806
Mycoplasma pneumoniae	32	1	0.1396	17	0.31	NZ_CP010546	817
Mycoplasma salivarium	32	1	0.1308	18	0.32	NZ_LR214938	1737
Neisseria gonorrhoeae	16	1	0.0695	33	0.77	NZ_LT591897	2292
Proteus mirabilis	44	1	0.2890	8	0.63	NC_008806	4064
Proteus vulgaris	85	1	0.1085	21	0.63	NZ_LR590468	3925
Pseudomonas aeruginosa	1,9,13,31,35,39,74	3	0.0751	31	0.88	NC_002516	6588
Pseudomonas fluorescens	4,55,85	3	0.0919	25	0.69	NC_007492	6846
Raoultella terrigena	101	1	0.0700	33	0.70	NZ_LANE01000008	5717
Rickettsia prowazekii	2	1	0.1760	13	0.60	NC_008807	1112
Salmonella enterica subsp anatum	98	1	0.0384	60	1.12	NC_003197	4831
Salmonella enterica subsp derby	98	1	0.0636	36	1.12	CP029486	4885
Salmonella enteritidis	24,57,98	3	0.0671	34	1.12	CP032851	4680
Salmonella infantis	98	1	0.1151	20	1.12	CP038507	4728
Salmonella typhi	19,92,101	3	0.1122	21	1.12	NC_003198	5134
Salmonella typhimurium	19,48,54,62,98	3	0.1002	23	1.12	NC_003197	4951
Serratia marcescens	7,24,38,39,85,92,105	3	0.1111	21	0.72	NZ_HG326223	5114
Shewanella algae	82	1	0.2709	8	0.51	NZ_LN810009	5003
Shewanella putrefaciens	1,82	2	0.3587	6	0.51	NC_009438	4659
Shigella dysenteriae	48,92,101	3	0.1236	19	0.63	NC_009344	4369
Shigella sonnei	19	1	0.1486	15	0.63	NC_007384	4825
Staphylococcus aureus	1,19,23,28,33,74,92	3	0.0929	25	0.77	NC_010079	2873
Staphylococcus epidermis	24,92	2	0.0875	26	0.87	NC_004461	2617
Stenotrophomonas maltophilia	1,15	2	0.0447	52	0.60	NC_010943	4851
Streptococcus pyogenes	92	1	0.1084	21	1.02	NC_002737	1915
Streptococcus viridans	92	1	0.1134	20	1.00	NZ_UHHS01000002	1997
Streptomyces coelicolor	49	1	0.0384	60	1.00	NC_003888	8668
Streptomyces griseus	49,52	2	0.0281	82	0.71	NC_008802	8546
Tatlockia micdadei	35,56	1	0.1070	22	0.73	NZ_LN614830	3310
Vibrio anguillarum	56,65,88	3	0.1644	14	0.60	NC_015633	4052
Vibrio cholerae	5,101	3	0.1957	12	0.76	NZ_AP014524	4031
Vibrio ordalii	88	1	0.1256	18	0.60	NZ_AJYS02000001	3895
Vibrio parahaemolyticus	5,78	2	0.1797	13	0.77	NZ_CP031781	3289
Yersinia enterocolitica	14,127,23,101	3	0.1482	16	0.76	NC_008800	4616
Yersinia pestis	87	2	0.1645	14	0.73	NC_003143	4830
Yersinia ruckeri	65	1	0.1175	20	0.87	NZ_CP011078	3700
Burkholderia mallei	87	1	0.2111	11	0.87	NC_006348	5836
Burkholderia pseudomallei	87	1	0.1829	13	0.84	NC_006350	7248
Mycobacteroides abcessus	96	1	0.1727	13	0.55	NZ_AP018436	5080
Nocardia asteroides	22	1	0.0082	280	1.41	NZ_LR134352	6955
Deinococcus radiodurans	1,4,91	3	0.0039	593	1.41	NZ_CP031500	3283

The last five microbes shown in gray cells are the four outliers and *D. radiodurans*.

The Genomic Parameters

Theoretically, the exact sequence of adjacent base pairs are the primary determinants of the intrinsic UV sensitivity and the frequency of dimer formation is in the order TT>TC>CT>CC (Setlow 1966, Becker 1989, Khoe 2018). Specifically, adjacent pyrimidines have the potential to form dimers, and some purines flanked by pairs of pyrimidines may also form dimers (Pan 2011). Pyrimidine doublets, or pairs of pyrimidines, may have dimer formation suppressed when they are flanked by purines (Law 2013). Table 2 summarizes the genomic motifs that are likely to dimerize and those that are not.

Table 2: Potential Dimerization Sequences

Group	DNA Sequence				Dimer Production
Adjacent pyrimidines	TT	TC	CT	CC	Yes
Purines flanked by doublets	ATT	ATC	ACT	ACC	50% Yes
	GTT	GTC	GCT	GCC	50% Yes
	TTA	TCA	CTA	CCA	50% Yes
	TTG	CGT	CTG	CCG	50% Yes
Surrounded single pyrimidines	ATA	ATG	GTA	GTG	No
	ACA	ACG	GCA	GCG	No
Surrounded doublets	ATTA	ATCA	ACTA	ACCA	No
	GTTA	GTCA	GCTA	GCCA	No
	ATTG	ATCG	ACTG	ACCG	No
	GTTG	GTCG	GCTG	GCCG	No

There are five groups of potential dimers, TT, TC, CT, CC, and YR (where R represents purines and Y represents pyrimidines). The sites are counted inclusively, wherein, for example, the sequence TT counts as 2 dimer sites and the sequence CTC counts as 3 dimer sites. Where sequences overlap, dimers are categorized based on the priority TT>TC>CT>CC>YR.

When multiple pyrimidines occur sequentially they may create a hot spot where the likelihood of dimerization is increased by a factor of up to 2 (Becker 1989). This phenomenon is known as hyperchromicity. Not enough is known about the hyperchromic effect to quantify it precisely but a parameter is included to add to the sum of dimers of any doublet or triplet whenever 3 or more pyrimidines are found in sequence (Kowalski et al 2009). This factor, H, increases the probability of dimerization for doublets and triplets based on how many adjacent pyrimidines are present in the genome, up to a value of 8 in a row where the effect levels off. The value of H may typically double the value of an isolated doublet, based on studies by Becker and Wang (1989).

The value of TTh represents the additional effect from a local hotspot, a value from 0 – 1.0 which represents the increase in dimerization probability due to being part of a cluster. The increased photoreactivity is based on an assumed sigmoid function relating the hyperchromicity factors (TTh, etc.) to the number of pyrimidines in sequence, as shown in Table 3.

Table 3: Hyperprimer Values

Sequential # of Pyrimidines	TTh, TCh, CTh, CCh, or YRh
2	0
3	0.5
4	0.75
5	0.88
6	0.983
7	0.995
8	1
9+	1

166 It was found in the course of this research that the hyperprimers (labeled TTh,
167 TCh, CTh, CCh & YRh) were better predictors than the specific sequences of base pairs
168 (TT, TC, CT, CC & YR). This innovation marks a departure from previous genomic
169 models by the author (Kowalski 2009, 2009a, 2009b, 2009c). Since the hyperprimer
170 values represent hot spots where dimerization is amplified, this approach is called a Hot
171 Spot model. The values of the hyperprimers were simply substituted in place of the
172 dimer counts in the equation for computing the Dimerization value.

173

174 *The Dimerization Value*

175 The nine genomic parameters that proved most significant are identified in Table 3. The
176 Relative Dimerization Value Dv is computed by multiplying all parameters together, with
177 each having an adjustable exponent, as follows:

178

179 $$D_v = P^a Y^b TT_h{}^c TC_h{}^d CT_h{}^e CC_h{}^f YR_h{}^g bp^h \quad (2)$$

180

181 where a thru h are adjustable exponents

182

183 The exponents were adjusted through multiple iterations to maximize the least
184 squares curve fit of ki to Dv. If the exponent of a parameter is zero, then the dimer
185 contribution becomes unity, and the factor makes no contribution to the model. All
186 parameters except bp are fractions since they are individually normalized as a fraction

of the total bp. Since all the variables in equation (2) are dimensionless except bp, the dimerization value Dv has the units of bp.

Table 4 summarizes the final iterated values of the genomic parameter exponents after curve-fitting to maximize the Pearson Correlation coefficient.

Table 4: Genomic Constants of the Model and Correlations

Parameter	Description	Exponent	Final Value
P	Total Primer Sites	a	1
Y	Total Pyrimidine Sites	b	0.068
TTh	TT Hot Spots	c	-1.19
TCh	TC Hot Spots	d	1
CTh	CT Hot Spots	e	-0.02
CCh	CC Hot Spots	f	-0.128
YRh	YR Hot Spots	g	-3.1
bp	Total Base Pairs	h	0.124
	Pearson Correlation		80
Statistical	Maximum CI Range		98%
Data	Minimum CI Range		-100%
	Logarithmic R2		65.5%

In this model, as opposed to previous models by the author, the intrinsic UV rate constant is used as the predictor (Kowalski 2020). The intrinsic UV rate constant is theorized as a parameter that depends solely on the genomic sequences and not on any physical parameter. The physical size of a microorganism plays a role in determining its ultraviolet sensitivity via Mie scattering effects. The intrinsic UV rate constant is defined as:

$$k_i = \frac{k_1}{S_c} \qquad (3)$$

Where k_1 = first stage UV rate constant, m^2/J

S_c = shielding constant

The shielding constant is computed as the complement of the ratio of the scattering cross-section to the extinction cross-section per Kowalski (2020):

$$S_c = 1 - \frac{C_{sca}}{C_{ext}} \quad (4)$$

Computations of the shielding constants are provided in the supplementary materials. UV rate constants from Table 1 are converted to intrinsic rate constants for use in the genomic model. The resulting predictions are then converted back to first stage rate constants in the final summary.

The Empirical Model

The final empirical model correlating measured UV rate constants with those predicted by the model is summarized by the parameters in Table 3 and plotted in Figure 2.

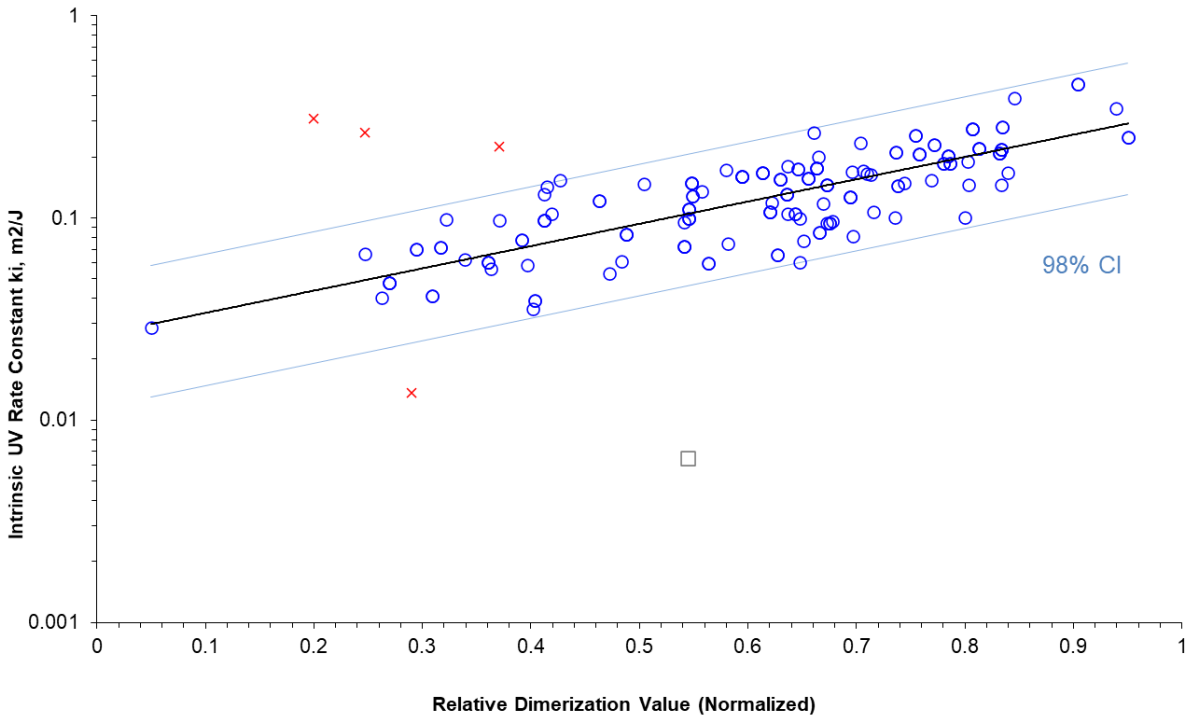

Figure 2: Plot of the 92 tested bacteria (blue circles) and the genomic model (dark line) with the 98% Confidence Interval (CI) high and low limits shown in light blue. Four outliers are shown as red X's. *D. radiodurans* (hollow square) is not a pathogen but is shown for perspective since it is the most radiation resistant microbe.

The complete equation for the intrinsic rate constant ki can be written as follows:

$$k_i = 0.026284e^{2.536438D_v} \quad (5)$$

Equations (2) and (3) can then be combined into a complete closed form equation to determine k_i.

The Bacteria Database

Table 5 presents a summary of all human pathogens and zoonotic pathogens that could be identified that have a published genome. The Type of microbe (H=Human, Z =

Zoonotic) is specified for each pathogen. The “Genome RefSeq/NCBI#” shows either the complete genome number or in some cases it shows the first chromosome or segment identification number from a shotgun sequence. The UV k is given along with the D90 range (for a 98% Confidence Interval) and the Mean D90 is computed based on the UV k. No account is taken for shoulders in this summary and therefore the UV k value and the D90 value represent the absence of any shoulder.

Table 5: Bacterial Pathogen Ultraviolet Susceptibility Predictions

Bacteria	Type	Genome RefSeq/NCBI #	Predicted UV k m^2/J	D90 Range J/m^2	Mean D90 J/m^2
Achromobacter xylosoxidans	H	NZ_CP043820	0.0723	16 - 72	32
Acinetobacter baumannii	H	NC_008801	0.1819	6 - 29	13
Acinetobacter lwoffii	H	NZ_CP046296	0.1138	10 - 46	20
Acinetobacter sp. VT-511	H	NZ_LFRE01000001	0.1236	9 - 42	19
Actinobacillus pleuropneumoniae	Z	NZ_CP030753	0.0984	12 - 53	23
Actinomyces bovis	Z	NZ_UAPQ01000012	0.0847	14 - 62	27
Actinomyces gerencseriae	H	NZ_KE386871	0.0282	41 - 186	82
Actinomyces israelii	H	NZ_LR134357	0.0914	13 - 57	25
Actinomyces naeslundii	H	NZ_CP066049	0.0324	36 - 162	71
Aerococcus viridans	Z	NZ_CP014164	0.0648	18 - 81	36
Aeromonas caviae punctata	H	NZ_AP022254	0.0940	12 - 56	24
Aeromonas hydrophila	H	NC_008570	0.1242	9 - 42	19
Aeromonas salmonicida	H	NC_009348	0.1308	9 - 40	18
Aeromonas veronii biovar sobria	H	NC_015424	0.1261	9 - 42	18
Anaerococcus tetradius	Z	NZ_CP027793	0.0761	15 - 69	30
Anaplasma marginale	Z	NC_012026	0.0575	20 - 91	40
Anaplasma phagocytophilum	H	NC_007797	0.0743	16 - 70	31
Arachnia propionica	H	NZ_LR134406	0.0382	31 - 137	60
Arcanobacterium haemolyticum	H	NC_014218	0.0401	29 - 131	57
Arcobacter butzleri	Z	NC_017187	0.1260	9 - 42	18
Arcobacter cibarius	Z	NZ_JABW01000001	0.1168	10 - 45	20
Arcobacter cryaerophilus	Z	NZ_LRUS01000011	0.1203	10 - 43	19
Arcobacter skirrowii	Z	NZ_LRUY010000006	0.1349	9 - 39	17
Arcobacter thereius	Z	NZ_LCUJ010000001	0.0915	13 - 57	25
Austwickia chelonae	Z	NZ_FOJD01000007	0.0286	41 - 183	81
Avibacterium paragallinarum	Z	NZ_CBMK010000001	0.0952	12 - 55	24
Bacillus anthracis	H	NC_007530	0.0798	15 - 66	29
Bacillus cereus	H	NC_004722	0.0885	13 - 59	26
Bacillus megaterium	H	NZ_CP009920	0.0575	20 - 91	40
Bacillus obstructivus	H	NZ_MPHG01000001	0.0922	13 - 57	25
Bacillus subtilis	H	NC_000964	0.0775	15 - 68	30
Bacteroides fragilis	H	NC_003228	0.0741	16 - 71	31
Bartonella alsatica	Z	NZ_CP058235	0.0667	18 - 78	35
Bartonella australis	Z	NC_020300	0.0540	22 - 97	43
Bartonella bacilliformis	H	NC_008783	0.0685	17 - 76	34
Bartonella bovis	Z	NZ_CM001844	0.0539	22 - 97	43
Bartonella capreoli	Z	NZ_CADEAD010000001	0.0694	17 - 75	33
Bartonella chomelii	Z	NZ_JACJIR010000001	0.0598	20 - 88	39
Bartonella clarridgeiae	H	NC_014932	0.0781	15 - 67	29
Bartonella elizabethae	H	NZ_LR134527	0.0601	19 - 87	38
Bartonella grahamii	H	NC_012846	0.0720	16 - 73	32
Bartonella henselae	H	NZ_HG965802	0.0638	18 - 82	36
Bartonella koehlerae	H	NZ_KL407334	0.0630	19 - 83	37
Bartonella phoceenis	Z	NC_011852	0.0876	13 - 60	26
Bartonella quintana	H	NC_005955	0.0565	21 - 93	41
Bartonella rochalimae	H	NZ_KL407337	0.0704	17 - 74	33
Bartonella vinsonii	Z	NC_020301	0.0660	18 - 79	35
Bartonella washoensis	H	NZ_JH725022	0.0682	17 - 77	34
Bifidobacterium longum	H	NZ_AP010888	0.0356	33 - 147	65
Bilophila wadsworthia	H	NZ_KE150238	0.0432	27 - 121	53
Blautia producta	Z	NZ_KQ955244	0.0726	16 - 72	32
Bordetella avium	Z	NZ_CP025522	0.0991	12 - 53	23
Bordetella bronchiseptica	Z	NZ_LR134326	0.0769	15 - 68	30
Bordetella parapertussis	H	NZ_CP025070	0.0703	17 - 74	33
Bordetella pertussis	H	NC_018518	0.0703	17 - 74	33
Borrelia afzelii	H	NC_018887	0.0515	23 - 102	45
Borrelia burgdorferi	H	NZ_CP019767	0.0904	13 - 58	25

Table 5: Bacterial Pathogen Ultraviolet Susceptibility Predictions

Bacteria	Type	Genome RefSeq/NCBI #	Predicted UV k m^2/J	D90 Range J/m^2	Mean D90 J/m^2
Borrelia garinii	H	NZ_CP018744	0.0665	18 - 79	35
Borrelia japonica	Z	NZ_FMTE01000048	0.0644	18 - 81	36
Borrelia recurrentis	H	NZ_CP000993	0.0818	14 - 64	28
Brachyspira hyodysenteriae	Z	NZ_MAOY01000001	0.0949	12 - 55	24
Brachyspira pilosicoli	Z	NZ_SAXY01000001	0.1184	10 - 44	19
Brevundimonas diminuta	H	NZ_UIGE01000002	0.0637	18 - 82	36
Brucella abortus	Z	NZ_CP008774	0.0501	23 - 104	46
Brucella canis	Z	NZ_CP016975	0.0508	23 - 103	45
Brucella ceti	Z	NZ_BLZI01000001	0.0532	22 - 98	43
Brucella melitensis	H	NZ_WUEE01000001	0.0494	24 - 106	47
Brucella neotomae	Z	NZ_UAQU01000037	0.0505	23 - 104	46
Brucella ovis	Z	NZ_UFUD01000002	0.0508	23 - 103	45
Brucella pinnipedalis	Z	NZ_CP061816	0.0504	23 - 104	46
Brucella suis	H	NZ_CP007719	0.0554	21 - 94	42
Burkholderia cenocepacia	H	NZ_MUTR01000001	0.0479	24 - 109	48
Burkholderia cepacia	H	NZ_CP045235	0.0424	28 - 123	54
Burkholderia contaminans	H	NZ_AP018360	0.0486	24 - 108	47
Burkholderia mallei	Z	NC_006348	0.0305	38 - 172	76
Burkholderia mallei	H	NC_006348	0.0302	39 - 174	76
Burkholderia pseudomallei	H	NC_006350	0.0344	34 - 152	67
Campylobacter coli	H	NZ_CP028187	0.1555	8 - 34	15
Campylobacter fetus	H	NZ_CP043435	0.2410	5 - 22	10
Campylobacter jejuni	H	NC_002163	0.1390	8 - 38	17
Campylobacter lari	H	NC_012039	0.1705	7 - 31	14
Campylobacter mucosalis	Z	JHQQ01000001	0.3448	3 - 15	7
Campylobacter rectus	H	NZ_ACFU01000089	0.1092	11 - 48	21
Campylobacter upsaliensis	H	NZ_JHZN01000001	0.1229	10 - 43	19
Candidatus Mycoplasma haemolamae	Z	NC_021283	0.0800	15 - 65	29
Capnocytophaga canimorsus	Z	NZ_PGTV01000001	0.0909	13 - 58	25
Chlamydia pneumoniae	H	NC_007429	0.0679	17 - 77	34
Chlamydia trachomatis	H	NC_005043	0.0623	19 - 84	37
Chlamydophila abortus	Z	NZ_CP021996	0.0593	20 - 88	39
Chlamydophila caviae (C.psittaci)	Z	NC_003361	0.0627	19 - 83	37
Chlamydophila felis	Z	NC_007899	0.0591	20 - 89	39
Chlamydophila muridarum	Z	NZ_CP007276	0.0632	18 - 83	36
Citrobacter amalonaticus	H	NZ_CP011132	0.0790	15 - 66	29
Citrobacter freundii	H	NZ_AOMS01000001	0.0886	13 - 59	26
Citrobacter koseri	H	NC_009792	0.0711	16 - 74	32
Citrobacter rodentium	H	NC_013716	0.0906	13 - 58	25
Clostridium perfringens	H	NC_003366	0.0707	17 - 74	33
Clostridium ventriculi	H	NZ_BCMV01000001	0.0846	14 - 62	27
Corynebacterium bovis	Z	NZ_PQNX01000001	0.0135	87 - 389	171
Corynebacterium diphtheria	H	NZ_LN831026	0.0490	24 - 107	47
Corynebacterium jeikeum	H	NC_007164	0.0415	28 - 126	56
Corynebacterium kutscheri	Z	NZ_CP011312	0.0889	13 - 59	26
Corynebacterium macginleyi	H	NZ_REGE01000001	0.0418	28 - 125	55
Corynebacterium minutissimum	H	NZ_LS483460	0.0392	30 - 133	59
Corynebacterium pseudotuberculosis	Z	NC_017301	0.0566	21 - 92	41
Corynebacterium ulcerans	H	NZ_LT906443	0.0543	22 - 96	42
Corynebacterium urealyticum	H	NC_010545	0.0322	36 - 162	71
Coxiella burnetii	H	NC_002971	0.0711	16 - 74	32
Cronobacter sakazakii	H	NZ_CP011047	0.0909	13 - 58	25
Deinococcus radiodurans	Non	NZ_CP031500	0.0633	18 - 83	36
Dermatophilus congolensis	Z	NZ_LT906453	0.0448	26 - 117	51
Edwardsiella tarda	H	NC_013508	0.0856	14 - 61	27
Eggerthela lenta	Z	NC_013204	0.0323	36 - 162	71
Ehrlichia canis	Z	NC_007354	0.0959	12 - 55	24

Table 5: Bacterial Pathogen Ultraviolet Susceptibility Predictions

Bacteria	Type	Genome RefSeq/NCBI #	Predicted UV k m^2/J	D90 Range J/m^2	Mean D90 J/m^2
Ehrlichia chaffeensis	H	NC_007799	0.0933	13 - 56	25
Ehrlichia ruminantium	Z	NZ_CP040111	0.1015	12 - 52	23
Elizabethkingia anophelis	H	NZ_CP007547	0.1149	10 - 46	20
Enterobacter cloacae	H	NZ_CP008823	0.0828	14 - 63	28
Enterococcus avium	Z	NZ_KE136500	0.0919	13 - 57	25
Enterococcus casseliflavus	H	NC_020995	0.0751	16 - 70	31
Enterococcus cecorum	Z	NZ_LS483306	0.0763	15 - 69	30
Enterococcus durans	Z	NZ_JAAMRZ010000001	0.0618	19 - 85	37
Enterococcus faecalis	H	NZ_KE351595	0.0565	21 - 93	41
Enterococcus faecium	H	NC_017958	0.0658	18 - 80	35
Enterococcus gallinarum	H	NZ_CP014067	0.0800	15 - 65	29
Enterococcus hirae	Z	NZ_CP023011	0.0707	17 - 74	33
Enterococcus raffinosus	H	NZ_KB946255	0.0922	13 - 57	25
Erysipelothrix rhusiopathiae	Z	NC_021354	0.0442	26 - 118	52
Escherichia albertii	H	NZ_CP007025	0.1059	11 - 49	22
Escherichia coli	H	NC_004431	0.0976	12 - 54	24
Eubacterium rectale	H	NZ_FR890957	0.0626	19 - 84	37
Finegoldia magna	Z	NZ_NDYD01000032	0.0464	25 - 113	50
Fluoribacter bozemanae	H	NZ_UGGY01000007	0.1476	8 - 35	16
Fluoribacter dumoffii	H	NZ_LNXZ01000001	0.1217	10 - 43	19
Fluoribacter gormanii	H	NZ_UGGV01000002	0.1381	8 - 38	17
Francisella tularensis	H	NZ_KN046815	0.1793	7 - 29	13
Fusobacterium necrophorum	H	NZ_AJSY01000001	0.0342	34 - 153	67
Fusobacterium nucleatum	H	NZ_LN831027	0.0905	13 - 58	25
Glaesserella (Haemophilus) parasuis	Z	NZ_LR698957	0.1018	11 - 51	23
Grimontia hollisae	H	NZ_CP014056	0.1047	11 - 50	22
Haemophilus aegyptius	H	NZ_LS483429	0.0796	15 - 66	29
Haemophilus ducreyi	H	NZ_CP015425	0.1334	9 - 39	17
Haemophilus haemolyticus	H	NZ_LS483458	0.0799	15 - 65	29
Haemophilus influenzae	H	NC_000907	0.0891	13 - 59	26
Haemophilus parahaemolyticus	H	NZ_CP069510	0.0915	13 - 57	25
Haemophilus parainfluenzae	H	NZ_GL872339	0.0823	14 - 64	28
Hafnia alvei	H	NZ_CP009706	0.1022	11 - 51	23
Helicobacter canadensis	Z	NC_014810	0.1456	8 - 36	16
Helicobacter cinaedi	H	NZ_AP012344	0.1287	9 - 41	18
Helicobacter felis	Z	NZ_CDMK01000001	0.1605	7 - 33	14
Helicobacter fennelliae	H	UGIB01000002	0.1116	10 - 47	21
Helicobacter heilmannii	Z	NZ_LS483446	0.2044	6 - 26	11
Helicobacter mustelae	Z	NZ_FZPI01000013	0.0579	20 - 90	40
Helicobacter pametensis	Z	NZ_MAJG01000001	0.0417	28 - 125	55
Helicobacter pullorum	Z	NZ_CP046672	0.1189	10 - 44	19
Helicobacter pylori	H	NC_000921	0.1434	8 - 37	16
Kingella kingae	H	NZ_HG427488	0.1071	11 - 49	21
Klebsiella aerogenes	H	NZ_LR134475	0.0805	15 - 65	29
Klebsiella oxytoca	H	NZ_CP011636	0.0926	13 - 57	25
Klebsiella pneumoniae	H	NC_009648	0.0997	12 - 52	23
Kluyvera intestini	H	MKZW03000008	0.0991	12 - 53	23
Kytococcus schroeteri	H	NZ_PKIZ01000001	0.0306	38 - 171	75
Lactobacillus acidophilus	H	NZ_CP005926	0.1316	9 - 40	17
Lactococcus lactis	H	NZ_CP066300	0.1015	12 - 52	23
Lawsonia intracellularis	Z	NZ_CP030241	0.0976	12 - 54	24
Legionella jordanis	H	NZ_LR134383	0.1152	10 - 45	20
Legionella longbeachae	H	NC_013861	0.1565	7 - 33	15
Legionella oakridgensis	H	NZ_CP004006	0.1037	11 - 50	22
Legionella pneumophila	H	NC_006369	0.1374	9 - 38	17
Legionella wadsworthii	H	NZ_UGPB01000002	0.1091	11 - 48	21
Listeria monocytogenes	H	NC_002973	0.0904	13 - 58	25

Table 5: Bacterial Pathogen Ultraviolet Susceptibility Predictions

Bacteria	Type	Genome RefSeq/NCBI #	Predicted UV k m^2/J	D90 Range J/m^2	Mean D90 J/m^2
Lysinibacillus fusiformis	H	NZ_CP010820	0.1111	11 - 47	21
Mannheimia haemolytica	Z	NZ_UGTB01000005	0.1246	9 - 42	18
Micrococcus luteus	H	NC_012803	0.0243	48 - 215	95
Mobiluncus curtisii	H	NZ_CP001992	0.0431	27 - 121	53
Moraxella bovis	Z	NC_015758	0.3239	4 - 16	7
Moraxella catarrhalis	H	NC_014147	0.1459	8 - 36	16
Morganella morganii	H	NC_020418	0.0758	15 - 69	30
Mycobacterium avium	H	NC_008595	0.0474	25 - 110	49
Mycobacterium avium subsp hominissuis	Z	NZ_CP033688	0.0545	21 - 96	42
Mycobacterium avium subsp paratuberculos	Z	NZ_CP039850	0.0508	23 - 103	45
Mycobacterium bovis BCG	H	NZ_CP039850	0.0586	20 - 89	39
Mycobacterium chimaera	H	NZ_CP015278	0.0498	23 - 105	46
Mycobacterium gilvun	H	NC_008595	0.0363	32 - 144	63
Mycobacterium intracellulare	H	NC_016946	0.0413	28 - 127	56
Mycobacterium kansasii	H	NC_022663	0.0688	17 - 76	33
Mycobacterium leprae	H	NZ_AP014567	0.0760	15 - 69	30
Mycobacterium lepraemurium	Z	NZ_LR882497	0.0469	25 - 111	49
Mycobacterium lepromatosis	H	NZ_JRPY01000026	0.0776	15 - 67	30
Mycobacterium marinum	H	NC_010612	0.0702	17 - 74	33
Mycobacterium parafortuitum	H	NZ_AP022598	0.0409	29 - 128	56
Mycobacterium simiae	Z	NZ_NCXM01000100	0.0521	22 - 101	44
Mycobacterium smegmatis	H	NC_008596	0.0396	29 - 132	58
Mycobacterium terrae	H	CP002329	0.0469	25 - 112	49
Mycobacterium tuberculosis	H	NC_009565	0.0586	20 - 89	39
Mycobacterium tuberculosis var. africanum	Z	NZ_AP020326	0.0582	20 - 90	40
Mycobacterium tuberculosis var. bovis	Z	NZ_CP021238	0.0586	20 - 89	39
Mycobacterium tuberculosis var. microti	Z	NZ_AP022568	0.0587	20 - 89	39
Mycobacterium ulcerans	H	NC_008611	0.0646	18 - 81	36
Mycobacterium vulneris	Z	NZ_FWXE01000039	0.0633	18 - 83	36
Mycobacteroides abcessus	H	NZ_AP018436	0.0520	22 - 101	44
Mycobacteroides chelonae	H	NZ_CP007220	0.0507	23 - 103	45
Mycolicibacterium fortuitum	H	NZ_CP011269	0.0504	23 - 104	46
Mycolicibacterium phlei	H	NZ_CP014475	0.0440	27 - 119	52
Mycoplasma agassizii	Z	NZ_ADNC01000033	0.1055	11 - 50	22
Mycoplasma alligatoris	Z	NZ_LR214970	0.1397	8 - 37	16
Mycoplasma arthritidis	H	NC_011025	0.1119	10 - 47	21
Mycoplasma bovigenitalium	Z	NZ_LR214972	0.0586	20 - 89	39
Mycoplasma bovirhinis	Z	NZ_CP005933	0.1107	11 - 47	21
Mycoplasma bovis	Z	NZ_CP007154	0.1150	10 - 46	20
Mycoplasma bovoculi	Z	NZ_CP011368	0.0959	12 - 55	24
Mycoplasma canis	Z	NC_014014	0.0665	18 - 79	35
Mycoplasma crocodyli	Z	NZ_LR214974	0.0774	15 - 68	30
Mycoplasma cynos	Z	NZ_LS991951	0.0767	15 - 68	30
Mycoplasma edwardii	Z	NZ_JHXU01000001	0.0714	16 - 73	32
Mycoplasma elephantis	Z	NZ_AP022325	0.0448	26 - 117	51
Mycoplasma felis	Z	NZ_KB199571	0.0841	14 - 62	27
Mycoplasma feriruminatoris	Z	NZ_JHZE01000001	0.1357	9 - 39	17
Mycoplasma fermentans	H	NC_014921	0.0912	13 - 57	25
Mycoplasma gallinarum	Z	NC_018406	0.0698	17 - 75	33
Mycoplasma gallisepticum	Z	NC_016638	0.0871	13 - 60	26
Mycoplasma genitalium	H	NC_000908	0.1006	12 - 52	23
Mycoplasma haemocanis	Z	NC_014970	0.0515	23 - 102	45
Mycoplasma haemofelis	Z	NC_018219	0.0694	17 - 75	33
Mycoplasma hominis Type 1	H	NC_013511	0.0696	17 - 75	33
Mycoplasma hyopneumoniae	Z	NZ_KB911485	0.0528	22 - 99	44
Mycoplasma hyorhinis	Z	NZ_CP008748	0.0962	12 - 54	24
Mycoplasma hyosynoviae	Z	NZ_CP001668	0.0657	18 - 80	35

Table 5: Bacterial Pathogen Ultraviolet Susceptibility Predictions

Bacteria	Type	Genome RefSeq/NCBI #	Predicted UV k m^2/J	D90 Range J/m^2	Mean D90 J/m^2
Mycoplasma mycoides	Z	NZ_AGRE01000010	0.118818011	10 - 44	19
Mycoplasma orale Type 1	H	NZ_LR214940	0.0822516	14 - 64	28
Mycoplasma ovipneumoniae	Z	NC_023062	0.070089322	17 - 75	33
Mycoplasma ovis	Z	NZ_CP033058	0.055707664	21 - 94	41
Mycoplasma phocacerebrale	Z	NC_002771	0.095927496	12 - 55	24
Mycoplasma pneumoniae	H	NZ_CP010546	0.13710651	9 - 38	17
Mycoplasma pulmonis	Z	NZ_JHVF01000001	0.094669023	12 - 55	24
Mycoplasma salivarium	H	NZ_LR214938	0.158026065	7 - 33	15
Mycoplasma spumans	Z	NZ_CP029258	0.055446645	21 - 94	42
Mycoplasma synoviae	Z	NZ_LR134313	0.074122762	16 - 71	31
Mycoplasma zalophi	H	NZ_JAHMHI010000001	0.068562782	17 - 76	34
Neisseria canis	Z	NZ_CP007481	0.087061963	13 - 60	26
Neisseria gonorrhoeae	H	NZ_LT591897	0.041792025	28 - 125	55
Neisseria meningitidis	H	NZ_LR134525	0.043739612	27 - 120	53
Neorickettsia helminthoeca	Z	NC_013009	0.039887094	29 - 131	58
Neorickettsia risticii	Z	NC_007798	0.04774405	24 - 110	48
Neorickettsia sennetsu	Z	NZ_LYMA01000001	0.046866263	25 - 112	49
Nocardia asteroides	H	NZ_LR134352	0.033464175	35 - 156	69
Nocardia brasiliensis	H	NC_018681	0.042193165	28 - 124	55
Nocardia cyriacigeorgica	H	NC_016887	0.032769437	36 - 160	70
Nocardia farcinica	H	NZ_LN868938	0.031663048	37 - 165	73
Nocardia nova	H	NZ_CP006850	0.032649201	36 - 160	71
Ochrobactrum anthropi	H	NC_009667	0.06635168	18 - 79	35
Orientia tsutsugamushi	Z	NZ_AXDE01000001	0.150851281	8 - 35	15
Ornithobacterium rhinotracheale (ORT)	Z	NZ_WUMP01000001	0.086750482	13 - 60	27
Pantoea agglomerans	H	NZ_CP077366	0.075722847	15 - 69	30
Pantoea ananatis	H	NC_016816	0.104952589	11 - 50	22
Pantoea dispersa	H	NZ_AVSS01000001	0.088526576	13 - 59	26
Pasteurella canis	Z	NZ_LT906448	0.120858302	10 - 43	19
Pasteurella dagmatis	Z	NC_021883	0.106940633	11 - 49	22
Pasteurella multocida	H	NZ_CP008918	0.082303476	14 - 64	28
Peptostreptococcus anaerobius	Z	NZ_CP039126	0.121931825	10 - 43	19
Photobacterium damselae	H	NZ_CP035780	0.137555548	8 - 38	17
Plesiomonas shigelloides	H	NZ_LT575468	0.105914152	11 - 49	22
Porphyromonas gingivalis	H	NC_010729	0.057272941	20 - 91	40
Prevotella intermedia	H	NZ_CP019300	0.070820038	17 - 74	33
Prevotella melaninogenica	H	NC_014370	0.074898973	16 - 70	31
Proteus mirabilis	H	NC_008806	0.167680442	7 - 31	14
Proteus vulgaris	H	NZ_LR590468	0.149922149	8 - 35	15
Providencia alcalifaciens	H	NZ_CP023536	0.215012614	5 - 24	11
Providencia rettgeri	H	NZ_CP017671	0.172681021	7 - 30	13
Providencia stuartii	H	NC_017731	0.156590278	7 - 33	15
Pseudomonas aeruginosa	H	NC_002516	0.072077771	16 - 73	32
Pseudomonas fluorescens	H	NC_007492	0.113766473	10 - 46	20
Pseudomonas putida	H	NC_021505	0.139650143	8 - 37	16
Raoultella orthinolytica	Z	NZ_JH603143	0.075383984	16 - 69	31
Raoultella planticola	Z	NC_020127	0.074134143	16 - 71	31
Raoultella terrigena	H	NZ_LANE01000008	0.107261761	11 - 49	21
Rhodococcus hoagii	Z	NZ_LANQ01000001	0.028453899	41 - 184	81
Rhodospirillum rubrum	H	NC_017584	0.047270549	25 - 111	49
Rickettsia akari	H	NC_009881	0.120438692	10 - 43	19
Rickettsia felis	Z	NZ_CM001467	0.101915482	11 - 51	23
Rickettsia helvetica	Z	NZ_LN794217	0.107236286	11 - 49	21
Rickettsia monacensis	Z	AUYQ02000001	0.096812826	12 - 54	24
Rickettsia prowazekii	H	NC_008807	0.11759588	10 - 45	20
Rickettsia rickettsii	H	NC_010263	0.119397737	10 - 44	19
Rickettsia typhi	H	NC_006142	0.109597439	11 - 48	21

Table 5: Bacterial Pathogen Ultraviolet Susceptibility Predictions

Bacteria	Type	Genome RefSeq/NCBI #	Predicted UV k m^2/J	D90 Range J/m^2	Mean D90 J/m^2
Salmonella abortusovis	Z	NC_010067	0.086688558	13 - 60	27
Salmonella bongori	Z	NZ_AZLC01000153	0.083863231	14 - 62	27
Salmonella bovis morbificans	Z	NC_006905	0.088074398	13 - 59	26
Salmonella choleraesuis	Z	NC_011205	0.090733551	13 - 58	25
Salmonella enterica subsp anatum	H	NC_003197	0.087595498	13 - 60	26
Salmonella enterica subsp derby	H	CP029486	0.087365854	13 - 60	26
Salmonella enterica subsp. Arizonae	Z	NZ_CP053416	0.08351672	14 - 63	28
Salmonella enterica subsp. Dublin	Z	JSWQ01000001	0.088850364	13 - 59	26
Salmonella enterica subsp. Gallinarum	Z	NZ_JZWK01000001	0.083529949	14 - 63	28
Salmonella enteritidis	H	CP032851	0.086475482	14 - 61	27
Salmonella heidelberg	H	NZ_ABEL01000048	0.083266545	14 - 63	28
Salmonella infantis	H	CP038507	0.08504933	14 - 62	27
Salmonella Livingstone	Z	NZ_CP012347	0.0931305	13 - 56	25
Salmonella pullorum	Z	NZ_CP027770	0.094179372	12 - 56	24
Salmonella typhi	H	NC_003198	0.090969955	13 - 58	25
Salmonella typhimurium	H	NC_003197	0.089190977	13 - 59	26
Serratia ficaria	H	NZ_LT906479	0.103750468	11 - 50	22
Serratia fonticola	H	NZ_CP011254	0.149088478	8 - 35	15
Serratia liquifaciens	H	NC_021741	0.125310268	9 - 42	18
Serratia marcescens	H	NZ_HG326223	0.094949724	12 - 55	24
Serratia odorifera	H	NZ_LR134117	0.118879715	10 - 44	19
Serratia plymuthica	H	NZ_LS483469	0.117235635	10 - 45	20
Serratia quinivorans	H	NZ_LR134494	0.136264015	9 - 38	17
Serratia rubidaea	H	NZ_CP014474	0.112868822	10 - 46	20
Shewanella algae	H	NZ_LN810009	0.225716032	5 - 23	10
Shewanella putrefaciens	H	NC_009438	0.207113617	6 - 25	11
Shigella boydii	H	NZ_CP026731	0.095270641	12 - 55	24
Shigella dysenteriae	H	NC_009344	0.09302565	13 - 56	25
Shigella flexneri	H	NZ_CP026788	0.105673178	11 - 50	22
Shigella sonnei	H	NC_007384	0.106301247	11 - 49	22
Staphylococcus aureus	H	NC_010079	0.093159533	13 - 56	25
Staphylococcus capitis	H	NZ_CP007601	0.078509822	15 - 67	29
Staphylococcus epidermis	H	NC_004461	0.07158352	16 - 73	32
Staphylococcus felis	Z	NZ_CP008747	0.080240027	15 - 65	29
Staphylococcus haemolyticus	H	NC_007168	0.097129641	12 - 54	24
Staphylococcus hyicus	Z	NZ_MWRT01000035	0.078573661	15 - 67	29
Staphylococcus intermedius	Z	NC_014925	0.075391335	16 - 69	31
Staphylococcus lugdunensis	H	NC_013893	0.104472493	11 - 50	22
Staphylococcus pseudintermedius	Z	NZ_JABMKT010000100	0.075526544	15 - 69	30
Staphylococcus saprophyticus	H	NZ_CP031196	0.122208534	10 - 43	19
Staphylococcus warneri	H	NZ_LR134269	0.091773648	13 - 57	25
Staphylococcus xylosus	H	NZ_CP008724	0.106823296	11 - 49	22
Stenotrophomonas maltophilia	H	NC_010943	0.084359194	14 - 62	27
Streptobacillus felis	Z	NC_013515	0.078902592	15 - 66	29
Streptobacillus moniliformis	Z	NZ_BEWZ01000001	0.06133855	19 - 85	38
Streptococcus agalactiae	H	NZ_CP026082	0.098866859	12 - 53	23
Streptococcus anginosus	H	NC_022239	0.063867667	18 - 82	36
Streptococcus canis	Z	NZ_JAUA01000048	0.103484201	11 - 51	22
Streptococcus constellatus	H	NC_022238	0.065245581	18 - 80	35
Streptococcus dysgalactiae	H	NZ_AP023394	0.111235355	11 - 47	21
Streptococcus equi	Z	NZ_UHFP01000002	0.143740822	8 - 36	16
Streptococcus equinus	H	NZ_JNLO01000001	0.06972037	17 - 75	33
Streptococcus gordonii	H	NC_009785	0.095835119	12 - 55	24
Streptococcus infantarius	Z	NZ_CP024843	0.075073232	16 - 70	31
Streptococcus iniae	Z	NZ_UYIP01000002	0.095826568	12 - 55	24
Streptococcus intermedius	H	NZ_LS483436	0.075916693	15 - 69	30
Streptococcus mitis	H	NZ_CP014326	0.086741858	13 - 60	27

Table 5: Bacterial Pathogen Ultraviolet Susceptibility Predictions

Bacteria	Type	Genome RefSeq/NCBI #	Predicted UV k m^2/J	D90 Range J/m^2	Mean D90 J/m^2
Streptococcus mutans	H	NZ_LS483349	0.102087168	11 - 51	23
Streptococcus oralis	H	NZ_LR134336	0.064086445	18 - 82	36
Streptococcus pneumoniae	Z	NZ_LR594050	0.065053642	18 - 80	35
Streptococcus porcinus	Z	NZ_LR134341	0.09628205	12 - 54	24
Streptococcus pseudoporcinus	Z	NZ_CP021246	0.104577316	11 - 50	22
Streptococcus pyogenes	H	NC_002737	0.103156327	11 - 51	22
Streptococcus salivarius	H	NZ_LR134274	0.086489082	14 - 61	27
Streptococcus sanguis	H	NZ_LS483385	0.10724565	11 - 49	21
Streptococcus suis	H	NZ_LS483418	0.064263383	18 - 81	36
Streptococcus viridans	H	NZ_UHHS01000002	0.074000124	16 - 71	31
Streptomyces coelicolor	H	NC_003888	0.047541043	25 - 110	48
Streptomyces griseus	H	NC_008802	0.052811551	22 - 99	44
Sutterella wadsworthensis	H	NZ_KE150480	0.050916935	23 - 103	45
Tatlockia micdadei	H	NZ_LN614830	0.123864346	9 - 42	19
Taylorella equigenitalis	Z	NZ_CP009770	0.136821618	9 - 38	17
Trueperella pyogenes	Z	NZ_CP007519	0.027438377	43 - 191	84
Ureaplasma diversum	Z	NZ_CP031781	0.122016424	10 - 43	19
Ureaplasma urealyticum	H	NC_011374	0.110201901	11 - 47	21
Veillonella parvula	H	NZ_LT906445	0.090550665	13 - 58	25
Vibrio alginolyticus	H	LOSN02000001	0.103404691	11 - 51	22
Vibrio anguillarum	H	NC_015633	0.165095456	7 - 32	14
Vibrio cholerae	H	NZ_AP014524	0.145286705	8 - 36	16
Vibrio fluvialis	H	NZ_CP014034	0.095638106	12 - 55	24
Vibrio furnisii	H	NZ_CP040990	0.178053419	7 - 29	13
Vibrio metschnikovii	H	NZ_CP046793	0.15125094	8 - 35	15
Vibrio ordalii	H	NZ_AJYS02000001	0.167734227	7 - 31	14
Vibrio parahaemolyticus	Z	NZ_LR134373	0.172587609	7 - 30	13
Vibrio vulnificus	H	NZ_CP014636	0.1518112	8 - 34	15
Yersinia enterocolitica	H	NC_008800	0.156378449	7 - 33	15
Yersinia pestis	H	NC_003143	0.135175545	9 - 39	17
Yersinia pseudotuberculosis	H	NZ_LR134373	0.131933095	9 - 40	17
Yersinia ruckeri	Non	NZ_CP011078	0.109287372	11 - 48	21

The genomic parameters used in the model were further studies to evaluate their relative contribution to the model. The contributions were analyzed as stand-alone correlations and the results are shown in Figure 3. Only the Hot Spots were used for this model and no correlations can be made for the individual dimers. The results indicate that the combined Hot Spots (TTh+TCh+CTh+CCh+YRh) were the single strongest predictor with a 70% Pearson correlation coefficient.

A graph of the Hot Spots was made and the results are presented as a circular genome for the bacteria *Borrelia afzeli* in Figure 4. In this graph only the highest

hyperprimer values for the first 4000 bp are shown for simplicity. Figure 4 shows the pyrimidine hot spots in red and the purine hot spots in yellow. It is worth noting that of the hundreds of indicated Hot Spots only a few would be necessary to inactivate the pathogen. The purine hot spots are significant because photoreactivation enzymes may repair pyrimidine dimers but they cannot repair purine dimers. Purine dimers may therefore be more fatal to the pathogen than pyrimidine dimers.

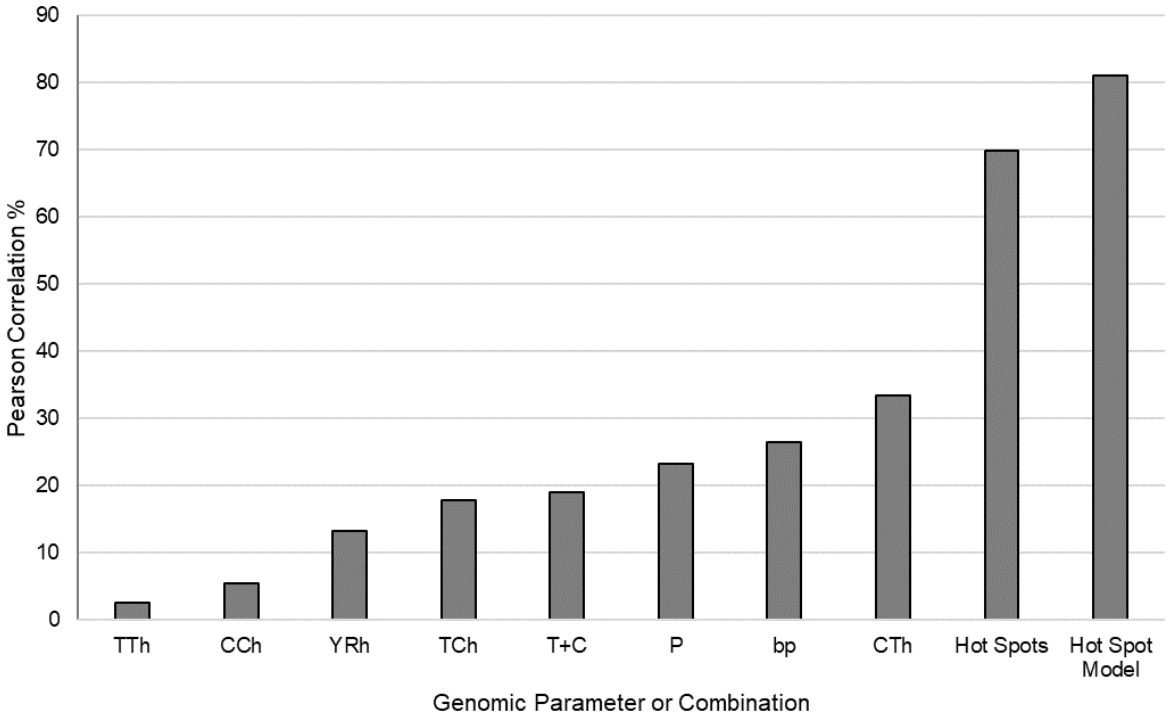

Figure 3: Pearson Correlation coefficients for genomic parameters in isolation and in combinations of parameters. Hot Spots are the sum of all hot spots (TTh+TCh+CTh+CCh+YRh).

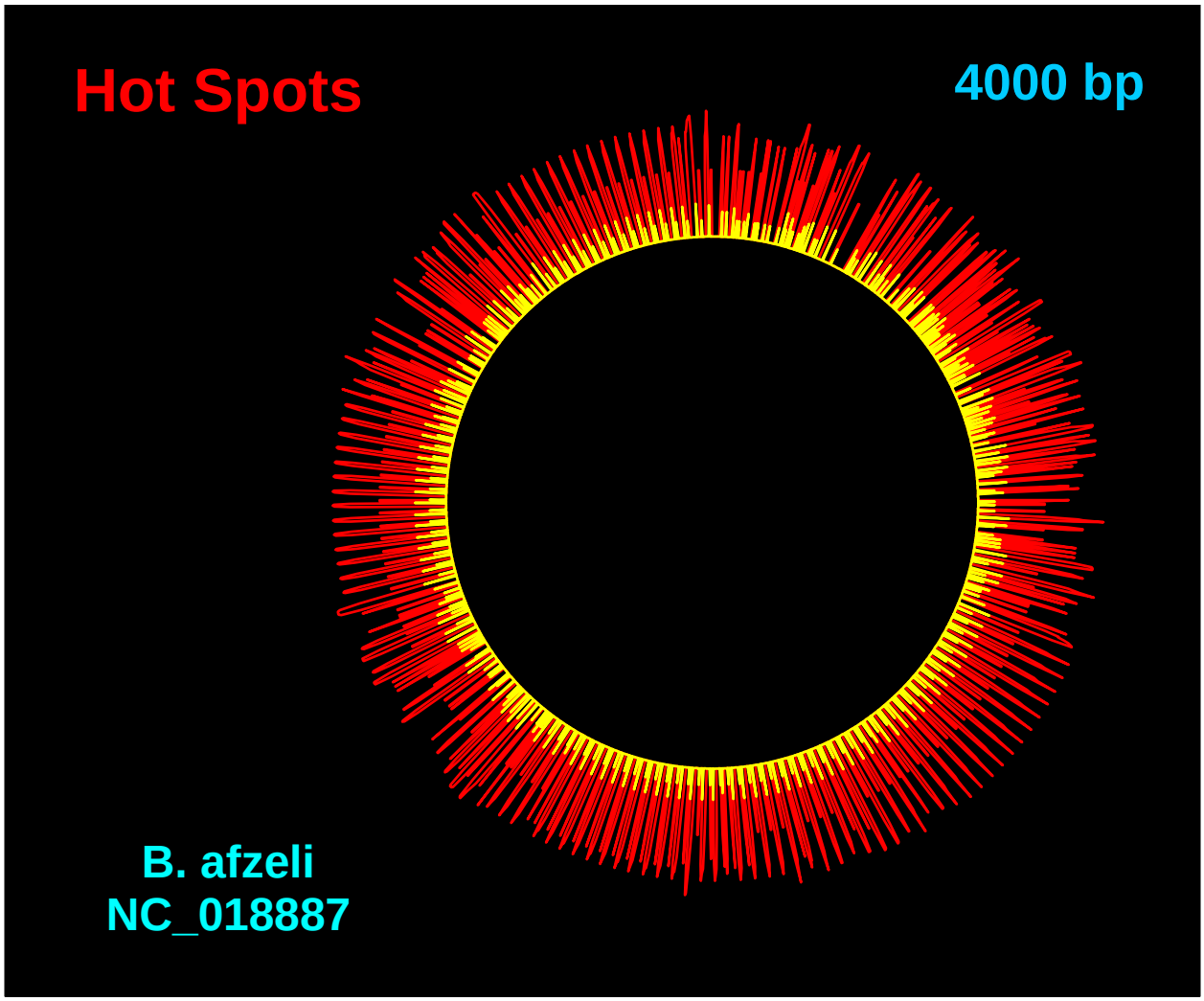

Figure 4: Example of hot spots highlighted on the circular genome of *Borrelia afzeli*. Red signifies pyrimidine hot spots where three or more pyrimidines are clustered. Yellow signifies hot spots at purine bases.

Discussion

The present genomic model improves upon the results presented previously by the author (Kowalski 2009, 2009a, 2009b, 2009c). The current Hot Spot bacteria model incorporates many more studies than previous models and more scrutiny was placed on

calculating the UV rate constants but the results are not drastically different from previous attempts. While there are clearly a great many variations possible in the modeling approach and in the selection and adjustment of parameters, the final predictions of UV rate constants have changed little, suggesting they limited sensitivity to the approach.

Other attempts to develop genomic models for viruses have been published and these have employed much the same genomic motifs as specified in the current model and have also produced similar predictions of UV rate constants (or D90 values) as the author's virus genomic models (Rockey 2021, Pendyala 2020). Although a fundamentals-based genomic model has been elusive, it appears that empirically based genomic models are adequate to generate predictions of UV sensitivity for all types of pathogens. Genomic modeling has also been used by the author to successfully predict the UV sensitivity of individual antibiotic resistant genes (Destiani 2017).

We invite researchers to challenge these predictions, especially those bacteria that have no prior studies, and also for the four outlying bacteria. The predicted values for UV rate constants can act as a target for the experimental design and should enable researchers to seek more accurate results. Because of the fact that the UV rate constant must be absolutely defined by the species genome, the predictions provided here may act as a standard by which to gauge results from future experiments.

It was clear from reviewing all studies that there was a lack of consistency in the test methods and this surely resulted in scattering of the results and reduced predictive performance of the model. Problems were observed in many studies related to how the UV dose was established. Researchers should take care to use photosensors properly.

In general, if a collimated beam apparatus is not used, the distance from the photosensor to the lamp should be on the order of one lamp length. In addition, many studies used low levels of UV irradiance and this produced a shoulder in the survival curve. The shoulder will distort any D90 value estimated from the data. It is suggested that researchers use irradiance levels of at least 1 W/m^2 (100 $\mu W/cm^2$) to avoid shoulders in the results and allow more accurate determination of the first stage rate constant.

A standardized test for UV rate constant evaluation is needed. Genomic modeling makes it possible to compute UV rate constants to six decimal places for bacteria, which have genomes on the order of 1M bp. A standard test capable of resolving UV rate constants to six decimal places, which represents six logs of reduction, may require the use of bacteria monolayers to avoid tailing in the survival curve, which reduces measurement accuracy.

The current method makes it possible to quickly evaluate the UV susceptibility of any emerging pathogen once the genome is published. The calculations could conceivably be incorporated into the NCBI Genome database to provide instant results once a genome is sequenced. Future research will address improved genomic modeling of viruses and fungi and investigation will be conducted into whether the Hot Spot model may have applications in predicting susceptibility to skin cancer.

References

1. Abshire R.L., Dunton H. 1981. Resistance of selected strains of *Pseudomonas aeruginosa* to low-intensity ultraviolet radiation. Appl Envir Microb 41,1419-1423.
2. Allen EG, Bovarnick MR, Snyder JC. 1954. The effect of irradiation with ultraviolet light on various properties of typhus rickettsiae. J Bacteriol 67,718-23.
3. Antopol SC, Ellner PD. 1979. Susceptibility of *Legionella pneumophila* to ultraviolet radiation. Appl & Environ Microb 38,347-348.
4. Arrage AA, Phelps TJ, Benoit RE, White DC. 1993. Survival of subsurface microorganisms exposed to UV radiation and hydrogen peroxide. Appl Environ Microbiol 59,3545-50.
5. Banerjee SK, Chatterjee SN. 1977. Sensitivity of the vibrios to ultraviolet-radiation. Int J Radiat Biol Relat Stud Phys Chem Med 32,127-33.
6. Barnhart DJ, Cox SH. 1970. Recovery of *Haemophilus influenzae* from ultraviolet and x-ray damage. Photochem Photobiol 11,147-62.
7. Bayliss CE, Waites WM. 1981. Resistance of *Serratia marcescens* to hydrogen peroxide. J Appl Bacteriol 50,131-7.
8. Becker, M. M. and Z. Wang 1989. "Origin of ultraviolet damage in DNA." J Mol Biol 210: 429-438.
9. Blatchley ER, 3rd, Dumoutier N, Halaby TN, Levi Y, Laine JM. 2001. Bacterial responses to ultraviolet irradiation. Water Sci Technol 43,179-86.
10. Bohrerova Z, Linden KG. 2006. Assessment of DNA damage and repair in *Mycobacterium terrae* after exposure to UV irradiation. J Appl Microbiol 101,995-1001.

11. Boshoff HI, Reed MB, Barry CE, 3rd, Mizrahi V. 2003. DnaE2 polymerase contributes to in vivo survival and the emergence of drug resistance in *Mycobacterium tuberculosis*. Cell 113,183-93.
12. Bowker C, Sain, A. Shatalov, M. Ducoste, J. 2011. Microbial UV fluence-response assessment using a novel UV-LED collimated beam system. Water Research 45,2011-2019.
13. Brahmi M, Belhadi NH, Hamdi H, Hassen A. 2010. Modeling of secondary treated wastewater disinfection by UV irradiation: effects of suspended solids content. J Environ Sci China 22,1218-24.
14. Butler RC, Lund, V., and Carlson, D. A. 1987. Susceptibility of *Campylobacter jejuni* and *Yersinia enterolitica* to UV radiation. Zbl Vet Med B 29,129-136.
15. Cairns G, Kerr KG, Beggs CB, Sleigh PA, Mooney L, Keig P, Donnelly JK. 2001. Susceptibility of *Burkholderia cepacia* and other pathogens of importance in cystic fibrosis to u.v. light. Lett Appl Microbiol 32,135-8.
16. Campbell, L. A. and R. E. Yasbin 1979. "Deoxyribonucleic acid repair capacities of *Neisseria gonorrhoeae*: absence of photoreactivation." J Bacteriol 1403: 1109-1111.
17. Carlson D, Seabloom R, DeWalle F, Wetzler T, Engeset J, Butler R, Wangsuphachart S, Wang S. 1985. Ultraviolet disinfection of water for small water supplies. EPA, EPA Report No. EPA/600/S2-85/092.
18. Cervero-Aragó S, Sommer R, Araujo RM. 2014. Effect of UV irradiation 253.7 nm on free *Legionella* and *Legionella* associated with its amoebae hosts. Water Research, 67,299-309.

19. Chang JCH, Ossoff SF, Lobe DC, Dorfman MH, Dumais CM, Qualls RG, Johnson JD. 1985. UV inactivation of pathogenic and indicator microorganisms. Appl & Environ Microbiol 49,1361-1365.
20. Chen PY, X C, J H. 2015. Effects of Salinity and Temperature on Inactivation and Repair Potential of *Enterococcus Faecalis* following Medium- and Low-Pressure Ultraviolet Irradiation. JAM 120,816-825.
21. Chen RZ, Craik SA, JR B. 2009. Comparison of the action spectra and relative DNA absorbance spectra of microorganisms: information important for the determination of germicidal fluence UV dose in an ultraviolet disinfection of water. Wat Res 43,5087-5096.
22. Chick EW, A.B. Hudnell J, Sharp DG. 1963. Ultraviolet sensitivity of fungi associated with mycotic keratitis and other mycoses. Sabouviad 2,195-200.
23. Clauss M. 2006. Higher effectiveness of photoinactivation of bacterial spores, UV resistant bacteria and mold spores with 222 nm compared to 254 nm wavelength. Acta hydrochim hydrobiol 34,525-532.
24. Collins FM. 1971. Relative susceptibility of acid-fast and non-acid fast bacteria to ultraviolet light. Appl Microbiol 21,411-413.
25. Darwin KH, C N. 2005. Role for Nucleotide Excision Repair in Virulence of *Mycobacterium tuberculosis*. Infection & Immunity 73,4581-4587.
26. David H. 1973. Response of mycobacteria to ultraviolet radiation. Am Rev Resp Dis 108,1175-1184.
27. David HL, Jones WD, Newman CM. 1971. Ultraviolet light inactivation and photoreactivation in the mycobacteria. Infect and Immun 4,318-319.

383 28. Destiani, R, Michael R. Templeton, and Wladyslaw Kowalski. 2017.
384 Environmental Engineering Science.Jul 2018.770-
385 774.http://doi.org/10.1089/ees.2017.0179
386 29. Dolman, P. J. and M. J. Dobrogowski 1989. "Contact lens disinfection by
387 ultraviolet light." Am J Opthalmol 1086: 665-669.
388 30. Drobnik J, Krekulova A. 1969. UV sensitivity of germinating culture of *B. cereus*.
389 Folia Microbiol Praha 14,104-111.
390 31. Eischeid AC, Linden KG. 2007. Efficiency of pyrimidine dimer formation in
391 *Escherichia coli* across UV wavelengths. J Appl Microbiol 103,1650-1656.
392 32. Elasri MO, Miller RV. 1999. Response of a biofilm bacterial community to UV
393 Radiation. Appl & Environ Microbiol 65,2025-2031.
394 33. Furness G. 1969. Differential responses of single cells and aggregates of
395 mycoplasmas to ultraviolet irradiation. Appl Microbiol 18,360-4.
396 34. Gates F. 1929. A study of the bactericidal action of ultraviolet light. J Gen Physiol
397 13,231-260.
398 35. Giese N, Darby J. 2000. Sensitivity of microorganisms to different wavelengths of
399 UV light: Implications on modeling of medium pressure UV systems. Wat Res
400 34,4007-4013.
401 36. Gilpin RD, Dillon SB, Keyser P, Androkites A, Berube M, Carpendale N, Skorina
402 J, Hurley J, Kaplan AM. 1985. Disinfection of circulating water systems by
403 ultraviolet light and halogenation. Water Res 19,839-848.
404 37. Gritz DC, Lee TY, McDonnell PJ, Shih K, Baron N. 1990. Ultraviolet radiation for
405 the sterilization of contact lenses. CLAO J 16,294-298.

406 38. Harris GD, Adams VD, Sorenson DL, Curtis MS. 1987. Ultraviolet inactivation of
407 selected bacteria and viruses with photoreactivation of the bacteria. Water Res
408 21,687-692.
409 39. Harris MG, Fluss L, Lem A, Leong H. 1993. Ultraviolet disinfection of contact
410 lenses. Optom Vis Sci 70,839-842.
411 40. Hassen A, Mahrouk M, Ouazari H, Cherif M, Boudabous A, Damelincourt JJ.
412 2000. UV Disinfection of treated wastewater in a large-scale pilot plant and
413 inactivation of selected bacteria in a laboratory UV device. Bioresource Technol
414 74,141-150.
415 41. Hayes SL, Sivaganesan M, White KM, Pfaller SL. 2008. Assessing the
416 effectiveness of low-pressure ultraviolet light for inactivating *Mycobacterium*
417 *avium* complex MAC micro-organisms. Lett Appl Microbiol 47,386-92.
418 42. Hayes SL, White KM, Rodgers MR. 2006. Assessment of the effectiveness of
419 low-pressure UV light for inactivation of *Helicobacter pylori*. Appl Environ
420 Microbiol 72,3763-5.
421 43. Hercik F. 1937. Action of ultraviolet light on spores and vegetative forms of *B.*
422 *megatherium* sp. J Gen Physiol 20,589-594.
423 44. Hijnen WAM, van der Veer AJ, Beerendonk EF, Medema GJ. 2004. Increased
424 resistance of environmental anaerobic spores to inactivation by UV. Water Sci.
425 Technol.:Water Supply 4,54-61.
426 45. Hofemeister J, Bohme H. 1975. DNA repair in *Proteus mirabilis*. III. Survival,
427 dimer excision, and UV reactivation in comparison with Escherichia coli K12. Mol
428 Gen Genetic 141,147-161.

429 46. Hollaender A. 1942. Abiotic and sublethal effects of ultraviolet radiation on
430 microorganisms. Aerobiol. 17,156-165.
431 47. Hollaender, A. 1955. Radiation Biology, Volume II: Ultraviolet and Related
432 Radiations. New York, McGraw-Hill.
433 48. Howard K, TJJ I. 2005. Disinfection of *Burkholderia pseudomallei* in potable
434 water. Wat Res 39,1085-1092.
435 49. Hu XX, Geng S, Hu C. 2012. Inactivation and Photorepair of Enteric Pathogenic
436 Microorganisms with Ultraviolet Irradiation. Environ Eng Sci 29,549-553.
437 50. Jagger J, Takebe H, Snow JM. 1970. Photoreactivation of killing in
438 *Streptomyces*: Action spectra and kinetic studies. Photochem Photobiol 12,185-
439 196.
440 51. Jones, D. T., F. T. Robb and D. R. Woods 1980. "Effect of oxygen on
441 *Bacteroides fragilis* survival after far-ultraviolet irradiation." J Bacteriol 1443:
442 1179-1181.
443 52. Keller, L. C., T. L. Thompson and R. B. Macy 1982. "UV light-induced survival
444 response in a highly radiation-resistant isolate of the *Moraxella-Acinetobacter*
445 group." Appl & Environ Microb 432: 424-429.
446 53. Kelner A. 1949. Effect of visible light on the recovery of *Streptomyces griseus*
447 conidia from ultraviolet irradiation injury. Proc Nat Acad Sci 35,73-79.
448 54. Khoe, C. V., L. H. Chung and V. Murray 2018. "The sequence specificity of UV-
449 induced DNA damage in a systematically altered DNA sequence." J Photochem
450 Photobiol B 183: 88-100.

451 55. Kim T, Silva JL, Chen TC. 2002. Effects of UV irradiation on selected pathogens
452 in peptone water and on stainless steel and chicken meat. J Food Prot 65,1142-
453 1145.
454 56. Kimura T, M. Yoshimizu, K. Tajima, Y. Ezura, and M., Sakia. 1976. Disinfection
455 of hatchery water supply by ultraviolet UV irradiation, I. Susceptibility of some
456 fish-pathogenic bacterium and microorganisms inhabiting pond waters. Bulletin of
457 the Japanese Society of Scientific Fisheries 42,207-211.
458 57. Knudson GB. 1986. Photoreactivation of ultraviolet-irradiated, plasmid-bearing,
459 and plasmid-free strains of *Bacillus anthracis*. Appl & Environ Microbiol 52,444-
460 449.
461 58. Koivunen J, Heinonen-Tanski H. 2005. Inactivation of enteric microorganisms
462 with chemical disinfectants, UV irradiation and combined chemical/UV
463 treatments. Water Res 39,1519-26.
464 59. Kowalski W, Bahnfleth W, Hernandez M. 2009a. A Genomic Model for Predicting
465 the Ultraviolet Susceptibility of Bacteria and Viruses. In IUVA. IUVA, ed.
466 International Ultraviolet Association, Amsterdam.
467 60. Kowalski W, Bahnfleth W, Hernandez M. 2009b. A Genomic Model for Predicting
468 the Ultraviolet Susceptibility of Viruses. IUVA News 11,15-28.
469 61. Kowalski W, Bahnfleth W, Hernandez M. 2009c. A Genomic Model for the
470 Prediction of Ultraviolet Inactivation Rate Constants for RNA and DNA Viruses. In
471 IUVA. International Ultraviolet Association, Boston, MA.
472 62. Kowalski WJ, Bahnfleth WP, Raguse M, Moeller R. 2020. The cluster model of
473 ultraviolet disinfection explains tailing kinetics. J Appl Microbiol 128,1003-1014.

63. Kowalski WJ. 2009. Ultraviolet Germicidal Irradiation Handbook: UVGI for Air and Surface Disinfection. Springer, New York.

64. Kuo F, Carey J, Ricke S. 1997. UV irradiation of shell eggs: Effect on populations of aerobes, molds, and inoculated *Salmonella typhimurium*. J Food Prot 60,639-643.

65. Law, Y. K., R. A. Forties, X. Liu, M. G. Poirier and B. Kohler 2013. "Sequence-dependent thymine dimer formation and photoreversal rates in double-stranded DNA." Photochem Photobiol Sci 128: 1431-1439.

66. Liltved H, Hektoen H, Efraimsen H. 1995. Inactivation of bacterial and fish pathogens by ozonation or UV irradiation in water of different salinity. Aquacult Eng 14,107-122.

67. Liltved, H. and B. Landfald 1996. "Influence of liquid holding recovery and photoreactivation on survival of ultraviolet-irradiated fish pathogenic bacteria." Wat Res 305: 1109-1114.

68. Little JS, Kishimoto RA, Canonico PG. 1980. In vitro studies of interaction of rickettsia and macrophages: Effect of ultraviolet light on *Coxiella burnettii* inactivation and macrophage enzymes. Infect Immun 27,837-841.

69. Liu W-J, Zhang Y-J. 2006. Effects of UV intensity and water turbidity on microbial indicator inactivation. J Environ Sci 18,650-653.

70. Lojo MM. 1995. Thymine auxotrophy is associated with increased UV sensitivity in *Escherichia coli* and *Bacillus subtilis*. Mutation Research 347,25-30.

71. Luhrmann, A. and C. R. Roy 2007. "*Coxiella burnetii* inhibits activation of host cell apoptosis through a mechanism that involves preventing cytochrome c release from mitochondria." Infect Immun 7511: 5282-5289.

72. Martin, E., R. Reinhardt, L. Baum, M. Becker, J. Shaffer and T. Kokjohn 2000. "The effects of ultraviolet radiation on the moderate halophile *Halomonas elongata* and the extreme halophile *Halobacterium salinarum*." Can J Microbiol 462: 180-187.

73. Martiny H, Wlodavezyk K, Ruden H. 1988. Use of UV rays for the disinfection of water. II. Microbiological studies of surface water. Zentralbl Bakteriol Mikrobiol Hyg B 186,344-359.

74. McCarthy C, Schaefer J. 1974. Response of *Mycobacterium avium* to ultraviolet irradiation. Appl Environ Microbiol 28,151-153.

75. McKinney C, Pruden A. 2012. Ultraviolet Disinfection of Antibiotic Resistant Bacteria and Their Antibiotic Resistance Genes in Water and Wastewater. Environ Sci & Technol 46,13393-13400.

76. Mitchell JB, Sifuentes LY, Wissler A, Abd-Elmaksoud S, Lopez GU, Gerba CP. 2019. Modelling of ultraviolet light inactivation kinetics of methicillin-resistant *Staphylococcus aureus*, vancomycin-resistant *Enterococcus, Clostridium difficile* spores and murine norovirus on fomite surfaces. J Appl Microbiol 126,58-67.

77. Mongold J. 1992. DNA repair and the evolution of transformation in *Haemophilus influenzae*. Genetics 132,893-898.

78. Moreno-Andrés J R-ML, Acevedo-Merino A, Nebot E. 2016. Determining disinfection efficiency on *E. Faecalis* in saltwater by photolysis of H2O2: implications for ballast water treatment. Chem Eng J 283,1339-1348.
79. Nozu K, Ohnishi T. 1977. Ultraviolet sensitivity of *Vibrio parahaemolyticus*, a causative bacterium of food poisoning. Photochem Photobiol 26,483-486.
80. Oguma K, Katayama H, Ohgaki S. 2004. Photoreactivation of *Legionella pneumophila* after inactivation by low- or medium-pressure ultraviolet lamps. Wat Res 38,2757-2763.
81. Pan, Z., Hariharan, M., Arkin, J. D., Jalilov, A. S., McCullagh, M., Schatz, G. C., & Lewis, F. D. 2011. Electron donor-acceptor interactions with flanking purines influence the efficiency of thymine photodimerization. Journal of the American Chemical Society, 13351, 20793-20798. https://doi.org/10.1021/ja205460f
82. Pendyala, B., A. Patras, B. Pokharel and D. D'Souza 2020. "Genomic Modeling as an Approach to Identify Surrogates for Use in Experimental Validation of SARS-CoV-2 and HuNoV Inactivation by UV-C Treatment." Front Microbiol 11: 572331.
83. Qiu X, Sundin GW, Chai B, Tiedje JM. 2004. Survival of *Shewanella oneidensis* MR-1 after UV radiation exposure. Appl Environ Microbiol 70,6435-43.
84. Quek PH, Hu J. 2008. Indicators for photoreactivation and dark repair studies following ultraviolet disinfection. J Ind Microbiol Biotechnol 35,533-541.
85. Rastogi VK, Wallace L, Smith LS. 2007. Disinfection of *Acinetobacter baumanii*-contaminated surfaces relevant to medical treatment facilities with ultraviolet C light. Mil Med 172,1166-1169.

539 86. Rentschler HC, Nagy R, Mouromseff G. 1941. Bactericidal effect of ultraviolet
540 radiation. J Bacteriol 42,745-774.
541 87. Rockey, N. C., J. B. Henderson, K. Chin, L. Raskin and K. R. Wigginton 2021.
542 "Predictive Modeling of Virus Inactivation by UV." Environ Sci Technol 555: 3322-
543 3332.
544 88. Rose LJ, O'Connell H. 2009. UV Light Inactivation of Bacterial Biothreat Agents.
545 Appl Environ Microbiol 75,2987-2900.
546 89. Sako H, and Sorimachi, M. 1985. Susceptibility of fish pathogenic viruses,
547 bacteria and fungus to ultraviolet radiation and the disinfectant effect of U.V.-
548 ozone water sterilise on the pathogens in water. Bull Nat Res Inst Aquacult 8,51-
549 58.
550 90. Schumann, J. P., D. T. Jones and D. R. Woods 1984. "Effect of UV irradiation on
551 macromolecular synthesis and colony formation in *Bacteroides fragilis*." J Gen
552 Microbiol 1304: 771-777.
553 91. Setlow, R. B. and W. L. Carrier 1966. "Pyrimidine dimers in ultraviolet-irradiated
554 DNA's." J Mol Biol 17: 237-254.
555 92. Setlow JK, Duggan DE. 1964. The resistance of *Micrococcus radiodurans* to
556 ultraviolet radiation. I. Ultraviolet-induced lesions in the cell's DNA. Biochim
557 Biophys Acta 87,664-668.
558 93. Sharp G. 1939. The lethal action of short ultraviolet rays on several common
559 pathogenic bacteria. J Bact 37,447-459.
560 94. Shin G. 2008. Inactivation of *Mycobacterium avium* complex by UV irradiation.
561 Appl Environ Microbiol 74,7067-7069.

562 95. Slade, H. J., D. T. Jones and D. R. Woods 1981. "Effect of oxygen radicals and
563 peroxide on survival after ultraviolet irradiation and liquid holding recovery of
564 *Bacteroides fragilis*." J Bacteriol 1472: 685-687.
565 96. Sommer R, Haider T, Cabaj A, Pribil W, Lhotsky M. 1998. Time dose reciprocity
566 in UV disinfection of water. Wat Sci Technol 38,145-150.
567 97. Sullivan PK, Conner-Kerr T. 2000. A comparative study of the effects of UVC
568 irradiation on select procaryotic and eucaryotic wound pathogens. Ostomy
569 Wound Manage 46,28-34.
570 98. Templeton M, Antonakaki M, Rogers M. 2009. UV dose-response of
571 *Acinetobacter baumanii* in water. Environ Sci Eng 26,697-701.
572 99. Tosa K, Hirata T. 1998. Photoreactivation of *Salmonella* following UV
573 disinfection. Proc IAWQ 19th Biennial Int Conf. 10, Health-Related Water
574 Microbiology.
575 100. Tyrrell RM, Moss SH, Davies DJG. 1972. The variation in UV sensitivity of
576 four K12 strains of *Escherichia coli* as a function of their stage of growth. Mutat
577 Res 16,1-12.
578 101. Wassmann M, R Moeller, Reitz G, Rettberg P. 2010. Adaptation of *Bacillus*
579 *subtilis* Cells to Archean-Like UV Climate: Relevant Hints of Microbial Evolution
580 to Remarkably Increased Radiation Resistance. ASTROBIOLOGY 10.
581 102. Wilson BR, Roessler, P.F., Van Dellen, E., Abbaszadegan,, M. and Gerba
582 CP. 1992. Coliphage MS-2 as a UV water disinfection efficacy test surrogate for
583 bacterial and viral pathogens. In Water Quality Technology Conference, Nov 15-
584 19, 1992. Amer. Wat. Works Assoc. D, CO., ed. AWWA, Toronto, Canada.

585 103. Wu Y, Clevenger, T. and Deng, B. 2005. Impacts of goethite particles on
586 UV disinfection of drinking water, 717: 4140-4143. Appl Environ Microbiol
587 71,4140-4143.
588 104. Yamamoto H, Urakami I, Nakano K, Ikedo M, Yabuuchi E. 1987. Effects of
589 Flonlizer, ultraviolet sterilizer, on *Legionella* species inhabiting cooling tower
590 water. Microbiol Immunol 31,745-752.
591 105. Yousef A, Marth E. 1988. Inactivation of *Listeria monocytogenes* by
592 Ultraviolet Energy. J Food Sci 53,571-573.
593 106. Zelle MR, Hollaender A. 1955. Radiation Biology Volume II. McGraw-Hill,
594 New York.
595 107. Zemke V, Podgorsek L, Schoenen D. 1990. Ultraviolet disinfection of
596 drinking water. 1. Communication: Inactivation of *E. coli* and coliform bacteria.
597 Zentralbl Hyg Umweltmed 190,51-61.