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# SARS Coronavirus UV Susceptibility

Severe Acute Respiratory Syndrome (SARS) virus is an emerging respiratory infection that has caused outbreaks in health care settings (Ho et al 2003, HWFB 2003). SARS virus is a new variant of the Coronavirus family and transmits by the airborne route and by direct contact or contact with fomites on surfaces. Transmission is believed to be by droplet spray from coughing and sneezing and by direct contact but airborne transmission can also occur (He et al 2003, CDC 2003). SARS has been transmitted to HCWs during high-risk exposure associated with aerosolization of respiratory secretions.

Coronaviruses are members of the Coronaviridae group and contain a single-stranded, positive-sense RNA genome surrounded by a corona-like helical envelope (Ryan 1994). The SARS virus genome consists of 29,751 base pairs. Approximately 41% of the genome is GC base pairs while 59% is TA base pairs. Coronaviruses have a size range of 0.08-0.15 microns; with a mean size of 0.11 microns (see Figure 1). Common Coronaviruses are responsible for colds and can transmit by the airborne route as well as through direct contact.

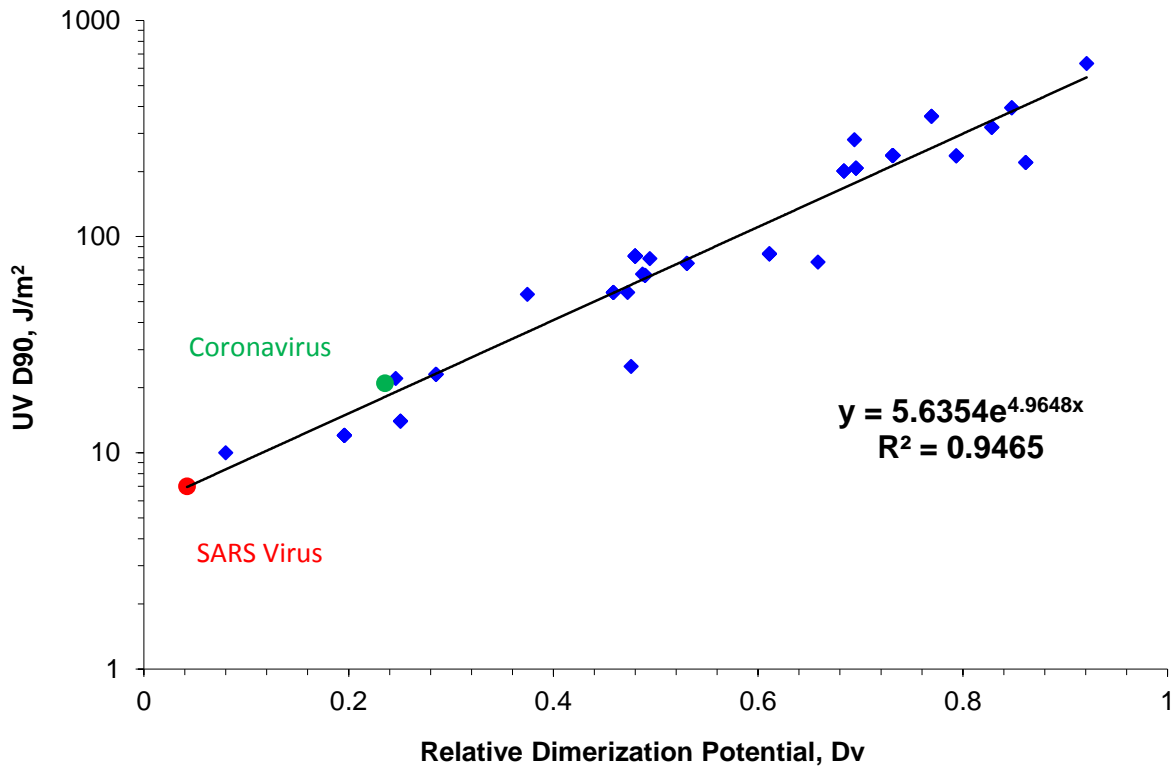
NOTE: SARS is not to be confused with Influenza A viruses (i.e. Influenza AH1N1) which are members of the Orthomyxovirus group and contain a single-stranded RNA genome enclosed in a helical envelope. The genome consists of 13,588 base pairs. Influenza viruses are responsible for flus and can transmit by the airborne route as well as through direct contact.

SARS coronavirus is one of the most hazardous infections for hospital personnel. In a study by He et al (2003) it was found that index patients were the first generation source of transmission and they infected inpatients and medical staff, creating second generation patients. The major transmission routes were close proximity airborne droplet infection and close contact infection. There was also evidence for the likelihood of aerosol transmission of infections through the ventilation system, which spread the infection to other hospital floors. A similar report comes from Ho et al (2003), who found that Hospital outbreaks of SARS typically occurred within the first week after admission of the first SARS cases before recognition and before isolation measures were implemented. In the majority of hospital infections, there was close contact with a SARS patient, and transmission occurred via large droplets, direct contact with infectious fluids or by contact with fomites from infectious fluids. In some instances, potential airborne transmission was reported in association with endotracheal intubation, nebulised medications and non-invasive positive pressure ventilation of SARS patients. Nosocomial transmission was effectively halted by enforcement of standard routines, contact and droplet precautions in all clinical areas, and additional airborne precautions in high-risk areas.

**Table 1: Summary of Ultraviolet Studies on Coronaviruses**

Microbe	D <sub>90</sub> J/m <sup>2</sup>	UVGI k m <sup>2</sup> /J	Media	RH %	Dia. µm	Base Pairs kb	Source
Coronavirus	3	0.37700	Air	50	0.113	30.738	Walker 2007
Coronavirus	7	0.32100	W	Wat	0.113	30.738	Weiss 1986
Coronavirus (SARS)	9	0.25340	W	Wat	0.113	29.751	Duan 2003
Coronavirus (SARS)	226	0.01000	W	Wat	0.113	29.751	Kariw a 2004
Coronavirus (SARS)	3046	0.00076	W	Wat	0.113	29.751	Darnell 2004
Genomic Prediction	7	0.3289	W	Wat	0.113	29.751	Kowalski 2015

Table 1 summarizes the studies that have been performed on Coronaviuses under UV exposure and also shows the genomic prediction of the UV rate constant in the final row. The last two studies (Kariwa 2004 and Darnell 2004) seem to be anomalous but it is unclear from the data why these results indicate such an unusually high UV resistance, but have been included for completeness. All the data in Table 1 except for the Duan (2003) study were used in the development of the genomic model of ssRNA viruses shown in Figure 2. Based on the ssRNA genomic model the UV rate constant for SARS Coronavirus computes to be 0.3289 m<sup>2</sup>/J and this gives a D90 value of 7 J/m<sup>2</sup>, which is in fairly good agreement with the first three studies shown in Table 1.



**Figure 2:** Genomic model of 27 ssRNA viruses representing 62 data sets (Kowalski et al 2009). The SARS virus (NC\_004718) is highlighted in red and the average of the four Coronavirus studies are highlighted in green.

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