Report on the Performance of the Arcalux Health Risk Management System



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Executive Summary

The superior performance of the Arcalux Health Risk Management System will enable high levels of air disinfection to be achieved as well as a consequent reduction in the risk of airborne nosocomial infection in any health care environment. This report evaluates the performance of the Arcalux Health Risk Management System in terms of the removal rates of known airborne nosocomial or hospital-acquired pathogens, including bacteria, viruses, and fungi. Removal rates due to filtration and UV irradiation are evaluated using computer models and tabulated for various operating conditions. These removal rates, which will reduce concentrations of airborne pathogens, are used to estimate the risk of infection to occupants and this risk is presented in terms of the Zonal Protection Factor (ZPF). The ZPF is a measure of the percentage of occupants protected form infection. Removal rates for most pathogens are in excess of 90% in the primary configurations. At the nominal design airflow of 50 cfm, and with a **MERV 6** filter and a UV lamp with **15 W** of UV output, the Health Risk Management System provides overall single pass removal rates of approximately 97% on the average for the 44 airborne nosocomial pathogens in the database. For the nominal design floor area of 100 ft², the unit will provide Zonal Protection Factors that exceed 91% for most of the pathogens in the database, with an average ZPF of 90%. ZPF data is provided for alternate airflows ranging from 50 ft² to 300 ft² as shown in Table 6. Both the single pass removal rates and the ZPFs are close to the limits of what can be achieved with a combined UV and filtration system, and this unit should outperform other similar units while consuming the least amount of energy as it has been optimized for both high performance and low power consumption. Quiet operation also makes this unit suitable for any hospital environment and it can be used in general wards, procedure rooms, hallways, laboratories, and other facilities.

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Introduction

The Arcalux Health Risk Management System is a UV air disinfection system incorporated into a ceiling light fixture such that it has no visible profile. It is intended to disinfect the air of bacteria, viruses, and fungi in hospital environments. The system includes an ultraviolet (UV) lamp, a filter, and a fan that will recirculate air locally, such as in a hallway or procedure room. Light baffles ensure that no hazardous levels of UV will escape into the local area. The system is designed to operate quietly while delivering air of the highest purity, with disinfection rates approaching 100%. Targeted microorganisms include MRSA, VRE, Acinetobacter, Streptococcus species, Influenza, VZV, Pseudomonas, Clostridium difficile, and other causative agents of hospitalacquired infections (HAIs). This report summarizes the predicted performance of the unit in terms of UV dose, filter removal rates, and overall disinfection or kill rates of pathogenic nosocomial microbes. Comparative predictions are provided for reductions of airborne concentrations of microbes for particular floor areas and room volumes. These airborne reductions are related to the risk of reduced infections. This unit will also remove fungal and bacterial spores at rates that are specified in this report.

System Description

The Arcalux Health Risk Management System consists of a ceiling light fixture that includes a UV lamp, a filter, light baffles, and a UV irradiation chamber. Air is drawn into the unit, filtered and disinfected, and then exhausted back into the local airspace. A MERV 6 filter is included to keep dust off the UV lamp, but this filter also serves to remove a percentage of airborne pathogens. Figure 1 shows a partially exploded view of the major components of the system. From top to bottom are shown the UV irradiation chamber, the lighting components, and the bottom grille.

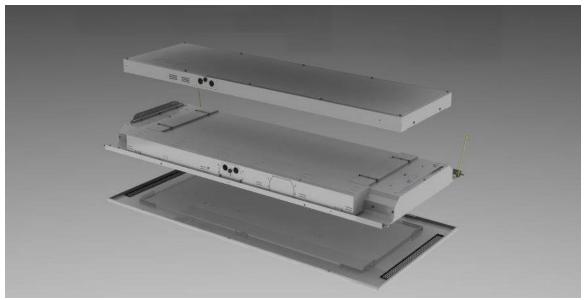


Figure 1: Partially exploded view of the Health Risk Management System showing major components.

Figure 2 shows the internal arrangement of the UV irradiation chamber, including the UV lamps and the fans at the outlet. The irradiation chamber is lined or coated with reflective materials to increase the total irradiance.



Figure 2: Schematic image of Arcalux Health Risk Management System showing internal UV lamps and irradiation chamber.

The properties of the reflective material were provided in the manufacturer's documents. The reflectivity of the aluminum surface is approximately 75-85% in the UV spectrum. Dimensions and design specifications are summarized in Table 1. These dimensions have been adjusted from those shown in the previous figure. The two configurations represent two different UV lamp sizes. The nominal airflow is 50 cfm. The airflow affects the air velocity and the exposure time (Et). Lamp dimensions and coordinates are unchanged from Table 1. At the nominal airflow of 50 scfm the air velocity is approximately 252 fpm. This is an acceptable airflow and will not decrease filter performance – in fact, filter performance will be slightly improved over the results given in the tables. The normal operating design airflow for a UV lamp is about 400-600 fpm.

Table 1: Specifications for Health Risk Management System

Long Type	T5
Lamp Type	15
# Lamps	·
Lamp UV Output, W	15
Width, in	14.5
Length, in	30.979
Height, in	1.97
Width, ft	1.21
Length, ft	2.58
Height, ft	0.16
Width, cm	36.83
Length, cm	78.69
Height, cm	5.0038
Nominal Airflow, Q, cfm	50
Nominal Airflow, Q, m ³ /min	1.42
Velocity, fpm	252
Velocity, fps	4.20
Velocity, cm/s	128.04
Velocity, m/s	1.28
Face Area, in ²	28.57
Face Area, ft ²	0.1984
Face Area, cm ²	184.29
Face Area, m ²	0.0184
Exposure Time, Et, s	0.6145
lamp end coordinate, x1, cm	18.42
lamp end coordinate, x2, cm	18.42
lamp end coordinate, y1, cm	2.50
lamp end coordinate, y2, cm	2.50
lamp end coordinate, z1, cm	10.77
lamp end coordinate, z2, cm	67.92
lamp arc length, arcl, cm	57.15
lamp radius, r, cm	0.79

A MERV 6 filter is included in the unit and a representative filter performance curve is adapted from Kowalski and Bahnfleth (2002). Figure 3 shows the filter performance curve. The removal efficiency at any microbial particle size can be estimated from this curve.

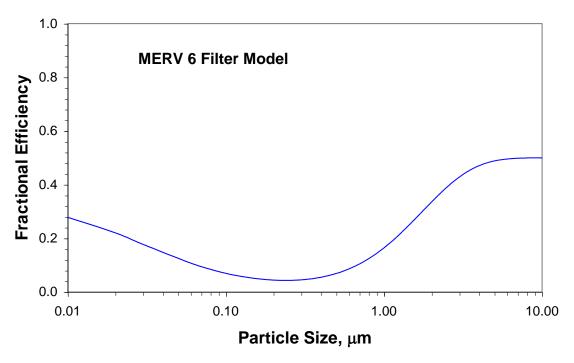


Figure 3: Performance of a generic MERV 6 filter. Based on modeling per Kowalski & Bahnfleth (2002).

Fan Pressure Loss and Noise

One of the design criteria for the Arcalux Health Risk Management System is that it must have quiet operation and produce the lowest possible level of noise. Noise is produced by the airflow as it moves through the fan and from turbulence inside the unit. The higher the pressure drop through the system the higher the fan static pressure and noise level. The unit includes smooth baffles to reduce turbulence inside the unit and fans have been selected for quiet operation. In order to minimize pressure losses a low pressure drop MERV 6 filter has been selected.

Analysis Results

Table 2 lists all nosocomial or HAI microbes that are known or suspected of having an airborne opponent in their transmission cycle. These include bacteria, viruses, fungal spores, and bacterial spores. Table 2 identifies the predicted filter removal rate for all these microbes based on the Figure 3 filter model. These filter removal rates will be combined with the UV disinfection rates to develop the overall removal rates of the pathogens. The filter removal rates are computed based on the log mean diameter of each pathogen. The size range of any microbe in nature will have a lognormal distribution, or a normal distribution (bell curve) on a logarithmic scale. The log mean diameter is an adequate representation of the mean size of any microbial population (Kowalski et al 1999). The log mean diameter will therefore be an adequate predictor of removal rates through any filter with a known performance curve.

Table 2: MERV 6 Filter Removal Rates of Airborne Nosocomial Pathogens

Nienele		MERV 6 Removal Rate			
Microbe	Туре	Size			
	 	μm	fraction	%	
Acinetobacter	Bacteria	1.225	0.2089	20.9	
Adenovirus	Virus	0.079	0.0853	8.5	
Aspergillus spores	Fungi	3.354	0.4476	44.8	
Blastomyces dermatitidis spores	Fungi	12.649	0.5000	50.0	
Bordetella pertussis	Bacteria	0.245	0.0431	4.3	
Clostridium difficile spores	Bacteria	2	0.3353	33.5	
Clostridium perfringens spores	Bacteria	1	0.1643	16.4	
Coronavirus (SARS)	Virus	0.11	0.0643	6.4	
Corynebacterium diphtheriae	Bacteria	0.698	0.1040	10.4	
Coxsackievirus	Virus	0.027	0.1886	18.9	
Cryptococcus neoformans spores	Fungi	4.899	0.4872	48.7	
Enterobacter cloacae	Bacteria	1.414	0.2442	24.4	
Enterococcus	Bacteria	1.414	0.2442	24.4	
Fusarium spores	Fungi	11.225	0.5000	50.0	
Haemophilus influenzae	Bacteria	0.285	0.0443	4.4	
Haemophilus parainfluenzae	Bacteria	1.732	0.2973	29.7	
Influenza A virus	Virus	0.098	0.0709	7.1	
Klebsiella pneumoniae	Bacteria	0.671	0.0988	9.9	
Legionella pneumophila	Bacteria	0.52	0.0721	7.2	
Measles virus	Virus	0.158	0.0493	4.9	
Mucor spores	Fungi	7.071	0.4983	49.8	
Mumps virus	Virus	0.164	0.0483	4.8	
Mycobacterium avium	Bacteria	1.118	0.1879	18.8	
Mycobacterium tuberculosis	Bacteria	0.637	0.0925	9.3	
Mycoplasma pneumoniae	Bacteria	0.177	0.0464	4.6	
Neisseria meningitidis	Bacteria	0.775	0.1190	11.9	
Nocardia asteroides	Bacteria	1.118	0.1879	18.8	
Norwalk virus	Virus	0.029	0.1809	18.1	
Parainfluenza virus	Virus	0.194	0.0447	4.5	
Parvovirus B19	Virus	0.022	0.2104	21.0	
Proteus mirabilis	Bacteria	0.494	0.0680	6.8	
Pseudomonas aeruginosa	Bacteria	0.494	0.0680	6.8	
Reovirus	Virus	0.075	0.0892	8.9	
RSV	Virus	0.19	0.0450	4.5	
Rhinovirus	Virus	0.023	0.2057	20.6	
Rhizopus spores	Fungi	6.928	0.4981	49.8	
Rotavirus	Virus	0.073	0.0913	9.1	
Rubella virus	Virus	0.061	0.1062	10.6	
Serratia marcescens	Bacteria	0.632	0.0916	9.2	
Staphylococcus aureus	Bacteria	0.866	0.1372	13.7	
Staphylococcus epidermis	Bacteria	0.866	0.1372	13.7	
Streptococcus pneumoniae	Bacteria	0.707	0.1057	10.6	
Streptococcus pyogenes	Bacteria	0.894	0.1428	14.3	
Chiopicocodo pyogorios	Daotona	0.007	U. 172U	1-7.0	

Appendix A reproduces the information in Table 2 but arranges the microbes in order of decreasing removal rates. Figure 4 illustrates how the pathogen removal rates correlate with the microbe size. This chart essentially duplicates Figure 4, the performance curve for a MERV 6 filter.

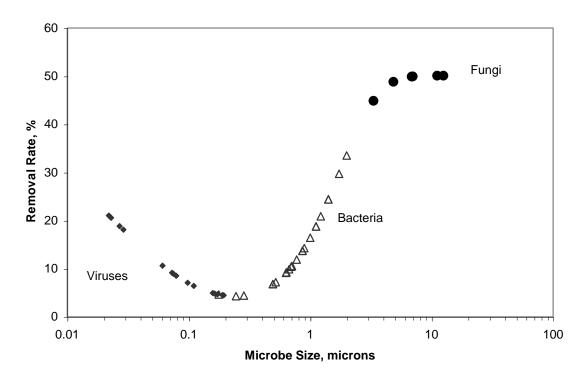


Figure 4: Removal rates for nosocomial pathogens arranged in a MERV 6 filter performance curve format (see Figure 3).

Table 3 lists the disinfection rates for airborne nosocomial pathogens based on the dose produced by the UV lamp. The 15 W lamp has been modeled (using the methods from Kowalski 2009) and found to produce a UV dose of 198 J/m² at 50 cfm. This dose is used to compute the disinfection rate based on the indicated UV rate constants listed in Table 3. Table 3 is reproduced in Appendix B where the pathogens are listed in order of decreasing removal rates.

Table 3: UV Disinfection Rates of Airborne Nosocomial Pathogens

Microbe	Table 3: UV DISINTED				
Acinetobacter	Microbe	Туре	_		Disinfection Rate, %
Adenovirus Virus 0.054 43 100 Aspergillus spores Fungi 0.00894 258 83 Blastomyces dermatitidis spores Fungi 0.00864 140 96 Bordetella pertussis* Bacteria 0.0364 63 100 Clostridium perfringens spores Bacteria 0.0385 60 100 Coronavirus (SARS) Virus 0.377 6 100 Corynebacterium diphtheriae Bacteria 0.0701 33 100 Coxsackievrus Virus 0.111 21 100 Coxypeococus neoformans spores Fungi 0.0167 138 96 Enterobacter cloacae Bacteria 0.03598 64 100 Enterococcus* Bacteria 0.0322 28 100 Enterococcus* Bacteria 0.03598 64 100 Enterococcus* Bacteria 0.0325 269 82 Haemophilus influenzae Bacteria 0.11845 19 100			m²/J	J/m ²	15 W
Aspergillus spores	Acinetobacter	Bacteria	0.16	14	100
Blastomyces dermatitidis spores	Adenovirus	Virus	0.054	43	100
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	Streptococcus pneumoniae	Bacteria	0.00492	468	62
VZV (Varicella surrogate k) Virus 0.1305 18 100	Streptococcus pyogenes	Bacteria	0.8113	3	100
		Virus	0.1305	18	100
UV Dose, J/m ² 198	UV Dose, J/m ²		198		

Note: Asterisk means the UV rate constant is a predicted value based on the complete genome.

Table 4 lists the combined single pass removal rates for the array of nosocomial pathogens in the previous tables. This table is shown again in Appendix C where they have been rearranged in order of most susceptible to least susceptible.

Given the removal rates as listed in Table 4, the Zonal Protection Factor (ZPF) can be computed assuming the floor area coverage is 100 ft² and the zone has 15% outside air (from the normal ventilation system). The ZPF (aka BPF or Building Protection Factor) represents the theoretical protection offered to occupants by the Health Risk Management System. It must be computed for each individual pathogen since each pathogen has a different removal rate (RR). The ZPF is computed by transient analysis of the airborne concentrations in the zone and is based on eight hours of breathing air in the occupied zone. The ZPF is the percentage of occupants likely to be protected from infection. The converse of the ZPF (1-ZPF) represents the number of likely infections. It is computed by assuming that the baseline condition has no air cleaning. The baseline condition assumes a release rate of pathogens sufficient to cause 99% infections. See Kowalski (2009) or Kowalski (2006) for more specific details on the computation of the BPF or ZPF.

Table 5 summarizes the predicted ZPF for each of the nosocomial pathogens under consideration and it indicates that very high protection factors are possible with the Health Risk Management System, which could be expected since the removal rates are high for most pathogens and the airflow rate (50 cfm) is appropriate for the subject floor area (100 ft²). The maximum ZPF is 93% and this cannot be increased further without increasing airflow. The minimum acceptable ZPF for any system is about 50%, which means that half the occupants are protected from infection. Based on the results in Table 5, the ZPF is above the minimum for all pathogens, including bacterial and fungal spores.

The results in Table 5 are based on the nominal airflow rate of 50 cfm. The results will be proportionally lower for lower airflow rates, since the combined removal rates (filters plus UV) are largely maxed out. Table 5 is reproduced in Appendix C but rearranged in order of decreasing ZPF.

Table 4: Combined Single Pass Removal Rates

Microbe Component Removal Rates Overall Removal Rates						
Microbe			Overall Removal Rates			
	MERV 6	15 W	MERV 6 + 15 W			
	fraction	fraction	%			
Acinetobacter	0.2089	1.0000	100.0			
Adenovirus	0.0853	1.0000	100.0			
Aspergillus spores	0.4476	0.8297	90.6			
Blastomyces dermatitidis spores	0.5000	0.9615	98.1			
Bordetella pertussis	0.0431	0.9993	99.9			
Clostridium difficile spores	0.3353	0.9995	100.0			
Clostridium perfringens spores	0.1643	0.9995	100.0			
Coronavirus (SARS)	0.0643	1.0000	100.0			
Corynebacterium diphtheriae	0.1040	1.0000	100.0			
Coxsackievirus	0.1886	1.0000	100.0			
Cryptococcus neoformans spores	0.4872	0.9634	98.1			
Enterobacter cloacae	0.2442	0.9992	99.9			
Enterococcus	0.2442	1.0000	100.0			
Fusarium spores	0.5000	0.8160	90.8			
Haemophilus influenzae	0.0443	1.0000	100.0			
Haemophilus parainfluenzae	0.2973	0.9974	99.8			
Influenza A virus	0.0709	1.0000	100.0			
Klebsiella pneumoniae	0.0988	0.9998	100.0			
Legionella pneumophila	0.0721	1.0000	100.0			
Measles virus	0.0493	1.0000	100.0			
Mucor spores	0.4983	0.8652	93.2			
Mumps virus	0.0483	1.0000	100.0			
Mycobacterium avium	0.1879	0.9998	100.0			
Mycobacterium tuberculosis	0.0925	1.0000	100.0			
Mycoplasma pneumoniae	0.0464	1.0000	100.0			
Neisseria meningitidis	0.1190	1.0000	100.0			
Nocardia asteroides	0.1879	1.0000	100.0			
Norwalk virus	0.1809	0.8994	91.8			
Parainfluenza virus	0.0447	1.0000	100.0			
Parvovirus B19	0.2104	1.0000	100.0			
Proteus mirabilis	0.0680	1.0000	100.0			
Pseudomonas aeruginosa	0.0680	1.0000	100.0			
Reovirus	0.0892	0.9444	94.9			
RSV	0.0450	1.0000	100.0			
Rhinovirus	0.2057	0.9399	95.2			
Rhizopus spores	0.4981	0.8182	90.9			
Rotavirus	0.0913	0.9903	99.1			
Rubella virus	0.1062	0.5193	57.0			
Serratia marcescens	0.0916	1.0000	100.0			
Staphylococcus aureus	0.1372	1.0000	100.0			
Staphylococcus epidermis	0.1372	1.0000	100.0			
Streptococcus pneumoniae	0.1057	0.6225	66.2			
Streptococcus pyogenes	0.1428	1.0000	100.0			
VZV	0.0469	1.0000	100.0			

Table 5: Zonal Protection Factors for Nosocomial Pathogens

l able 5: Zonal Protection	Туре	MERV6+15W	FA 100 ft ²
Pathogen		Removal %	ZPF %
Acinetobacter	Bacteria	100.0	91
Adenovirus	Virus	100.0	91
Aspergillus spores	Fungi	90.6	89
Blastomyces dermatitidis spores	Fungi	98.1	90
Bordetella pertussis	Bacteria	99.9	91
Clostridium difficile spores	Bacteria	100.0	91
Clostridium perfringens spores	Bacteria	100.0	91
Coronavirus (SARS)	Virus	100.0	91
Corynebacterium diphtheriae	Bacteria	100.0	91
Coxsackievirus	Virus	100.0	91
Cryptococcus neoformans spores	Fungi	98.1	90
Enterobacter cloacae	Bacteria	99.9	91
Enterococcus	Bacteria	100.0	91
Fusarium spores	Fungi	90.8	89
Haemophilus influenzae	Bacteria	100.0	91
Haemophilus parainfluenzae	Bacteria	99.8	91
Influenza A virus	Virus	100.0	91
Klebsiella pneumoniae	Bacteria	100.0	91
Legionella pneumophila	Bacteria	100.0	91
Measles virus	Virus	100.0	91
Mucor spores	Fungi	93.2	89
Mumps virus	Virus	100.0	91
Mycobacterium avium	Bacteria	100.0	91
Mycobacterium tuberculosis	Bacteria	100.0	91
Mycoplasma pneumoniae	Bacteria	100.0	91
Neisseria meningitidis	Bacteria	100.0	91
Nocardia asteroides	Bacteria	100.0	91
Norwalk virus	Virus	91.8	89
Parainfluenza virus	Virus	100.0	91
Parvovirus B19	Virus	100.0	91
Proteus mirabilis	Bacteria	100.0	91
Pseudomonas aeruginosa	Bacteria	100.0	91
Reovirus	Virus	94.9	90
Rhinovirus	Virus	100.0	91
Rhizopus spores	Virus	95.2	90
Rotavirus	Fungi	90.9	89
RSV	Virus	99.1	91
Rubella virus	Virus	57.0	73
Serratia marcescens	Bacteria	100.0	91
Staphylococcus aureus	Bacteria	100.0	91
Staphylococcus epidermis	Bacteria	100.0	91
Streptococcus pneumoniae	Bacteria	66.2	79
Streptococcus pyogenes	Bacteria	100.0	91
VZV	Virus	100.0	91
Average Protection Factor %			90

Table 6 provides the Zonal Protection Factors for a range of alternate airflows from 50 ft² to 300 ft², arranged in order of descending ZPF.

Table 6: Zonal Protection Factors for Nosocomial Pathogens at Alternate Room Areas

Table 6: Zonai Protectioi	MERV6+15W				rotection			
Pathogen	Removal	Area	Area	Area	Area	Area	Area	Area
	%	50 ft ²	75 ft ²	100 ft ²	125 ft ²	150 ft ²	200 ft ²	300 ft ²
Coronavirus (SARS)	100.0	93	92	91	90	88	85	80
Legionella pneumophila	100.0	93	92	91	90	88	85	80
Mycobacterium tuberculosis	100.0	93	92	91	90	88	85	80
Mycoplasma pneumoniae	100.0	93	92	91	90	88	85	80
Proteus mirabilis	100.0	93	92	91	90	88	85	80
Pseudomonas aeruginosa	100.0	93	92	91	90	88	85	80
Serratia marcescens	100.0	93	92	91	90	88	85	80
Staphylococcus aureus	100.0	93	92	91	90	88	85	80
Streptococcus pyogenes	100.0	93	92	91	90	88	85	80
Acinetobacter	100.0	93	92	91	90	88	85	80
VZV	100.0	93	92	91	90	88	85	80
Influenza A virus	100.0	93	92	91	90	88	85	80
Haemophilus influenzae	100.0	93	92	91	90	88	85	80
Coxsackievirus	100.0	93	92	91	90	88	85	80
Parainfluenza virus	100.0	93	92	91	90	88	85	80
Neisseria meningitidis	100.0	93	92	91	90	88	85	80
Measles virus	100.0	93	92	91	90	88	85	80
Staphylococcus epidermis	100.0	93	92	91	90	88	85	80
Parvovirus B19	100.0	93	92	91	90	88	85	80
Rhinovirus	100.0	93	92	91	90	88	85	80
Enterococcus	100.0	93	92	91	90	88	85	80
Nocardia asteroides	100.0	93	92	91	90	88	85	80
Mumps virus	100.0	93	92	91	90	88	85	80
Corynebacterium diphtheriae	100.0	93	92	91	90	88	85	80
Adenovirus	100.0	93	92	91	90	88	85	80
Mycobacterium avium	100.0	93	92	91	90	88	85	80
Klebsiella pneumoniae	100.0	93	92	91	90	88	85	80
Clostridium difficile spores	100.0	93	92	91	90	88	85	80
Clostridium perfringens spores	100.0	93	92	91	90	88	85	80
Enterobacter cloacae	99.9	93	92	91	90	88	85	80
Bordetella pertussis	99.9	93	92	91	90	88	85	80
Haemophilus parainfluenzae	99.8	93	92	91	90	88	85	79
RSV	99.1	93	92	91	89	88	85	79
Cryptococcus neoformans spores	98.1	93	92	90	89	88	85	79
Blastomyces dermatitidis spores	98.1	93	92	90	89	88	85	79
Rhizopus spores	95.2	92	91	90	88	87	84	78
Reovirus	94.9	92	91	90	88	87	84	78
Mucor spores	93.2	92	91	89	88	86	83	77
Norwalk virus	91.8	92	90	89	87	86	83	76
Rotavirus	90.9	91	90	89	87	86	82	76
Fusarium spores	90.8	91	90	89	87	86	82	76
Aspergillus spores	90.6	91	90	89	87	86	82	76
Streptococcus pneumoniae	66.2	83	81	79	77	74	69	61
Rubella virus	57.0	78	75	73	70	67	62	53
Average Protection Factor %		92.2	91.1	90.0	88.8	86.9	83.8	78.3

Summary and Discussion of Analysis Results

The analysis presented herein indicates that the Arcalux Health Risk Management System will produce high removal rates of all nosocomial pathogens including bacteria, fungi, and viruses. Analysis also shows that the risk of infection in areas where the unit is installed will be considerably reduced, based on predicted reduction in airborne concentrations of microbes. The combination of a 15 W UV lamp, a MERV 6 filter, and an airflow rate of 50 cfm will produce an average removal rates in excess of 97%, in a single pass, for all but two of the pathogens listed in Table 5. Table 7 provides a comparison of unitary UV systems operating between 30-100 cfm arranged in order of UV dose. The Arcalux Health Risk Management System provides a higher UV dose than most of these systems and has more efficient filtration than all but one of these systems.

Table 7: Comparison of Unitary UV Systems between 30-100 cfm

Manufacturer	Model	Airflov	v/CADR	Prefilter	Primary	UVP	Dose	URV	Notes
		cfm	m³/min		Filter	W	J/m ²		
Virobuster	Steritube	44	1.25	G4	none	57	592	23	multispeed
Virobuster	Steritube	59	1.67	G4	none	57	443	22	multispeed
Virobuster	Steritube	74	2.083	G4	none	57	355	21	multispeed
sterilAir AG	LSK2036-U	29.2	0.83	none	none	30	315	21	
Arcalux	HR Mgt System	50	1.42	Yes	MERV6	15	198	19	
sterilAir AG	UVR2250-1	88	2.50	optional	none	27	190	19	
sterilAir AG	LSK2018	11.8	0.33	none	none	7	173	19	
Holmes Group	BAP920-U	100	2.83	none	MERV15	22	69.2	17	PCO
Sanuvox	P-900	35	0.99	Yes	none	4.76	48	15	multispeed
Amcor	AM-45	30	0.85	none	none	1.96	26.9	13	
Amcor	AM-45C	31	0.88	Yes	none	25	23.2	13	PCO, carbon
Amcor	AM-45C	40	1.13	Yes	none	25	17.8	12	PCO, carbon
Amcor	AM-45C	45	1.27	Yes	none	25	15.9	12	PCO, carbon
Amcor	AM-45	60	1.70	none	none	1.96	13.5	11	

NOTE: CADR is approximately equal to the airflow for all systems.

References & Bibliography

- Kowalski, W. J., W. P. Bahnfleth, T. S. Whittam (1999). "Filtration of Airborne Microorganisms: Modeling and prediction." *ASHRAE Transactions* 105(2), 4-17. http://www.engr.psu.edu/ae/wjk/fom.html.
- Kowalski, W. J., and Bahnfleth, W. P. (2000). "UVGI Design Basics for Air and Surface Disinfection." *HPAC* 72(1), 100-110.
- Kowalski, W. J., and Bahnfleth, W. P. (2002). "MERV filter models for aerobiological applications." *Air Media* Summer, 13-17.
- Kowalski, W. J., and Bahnfleth, W. P. (2004). "Proposed Standards and Guidelines for UVGI Air Disinfection." *IUVA News* 6(1), 20-25.
- Kowalski, W. J., Bahnfleth, W. P., and Mistrick, R. G. (2005). "A specular model for UVGI air disinfection systems." *IUVA News* 7(1), 19-26.
- Kowalski, W. J. (2006). Aerobiological Engineering Handbook: A Guide to Airborne Disease Control Technologies. McGraw-Hill, New York.
- Kowalski, W. J. (2007). "Air-Treatment Systems for Controlling Hospital-Acquired Infections." HPAC Engineering 79(1), 28-48.
- Kowalski, W. J. (2009). *Ultraviolet Germicidal Irradiation Handbook: UVGI for Air and Surface Disinfection*. Springer, New York.
- Kowalski, W. J. (2011). *Hospital Airborne Infection Control.* Taylor & Francis/CRC Press, New York.

Appendix A: Filter Removal Rates of Airborne Nosocomial Pathogens

Appendix A: Filter Remova	al Rates of Airbo	Pathogens			
Microbe	Туре	Size	Removal Rate %		
		μm	MERV 6		
Blastomyces dermatitidis spores	Fungi	12.649	50.0		
Fusarium spores	Fungi	11.225	50.0		
Mucor spores	Fungi	7.071	49.8		
Rhizopus spores	Fungi	6.928	49.8		
Cryptococcus neoformans spores	Fungi	4.899	48.7		
Aspergillus spores	Fungi	3.354	44.8		
Clostridium difficile spores	Bacteria	2	33.5		
Haemophilus parainfluenzae	Bacteria	1.732	29.7		
Enterobacter cloacae	Bacteria	1.414	24.4		
Enterococcus	Bacteria	1.414	24.4		
Acinetobacter	Bacteria	1.225	20.9		
Mycobacterium avium	Bacteria	1.118	18.8		
Nocardia asteroides	Bacteria	1.118	18.8		
Clostridium perfringens spores	Bacteria	1	16.4		
Streptococcus pyogenes	Bacteria	0.894	14.3		
Staphylococcus aureus	Bacteria	0.866	13.7		
Staphylococcus epidermis	Bacteria	0.866	13.7		
Neisseria meningitidis	Bacteria	0.775	11.9		
Streptococcus pneumoniae	Bacteria	0.707	10.6		
Corynebacterium diphtheriae	Bacteria	0.698	10.4		
Klebsiella pneumoniae	Bacteria	0.671	9.9		
Mycobacterium tuberculosis	Bacteria	0.637	9.3		
Serratia marcescens	Bacteria	0.632	9.2		
Legionella pneumophila	Bacteria	0.52	7.2		
Proteus mirabilis	Bacteria	0.494	6.8		
Pseudomonas aeruginosa	Bacteria	0.494	6.8		
Haemophilus influenzae	Bacteria	0.285	4.4		
Bordetella pertussis	Bacteria	0.245	4.3		
Parainfluenza virus	Virus	0.194	4.5		
RSV	Virus	0.19	4.5		
Mycoplasma pneumoniae	Bacteria	0.177	4.6		
VZV	Virus	0.173	4.7		
Mumps virus	Virus	0.164	4.8		
Measles virus	Virus	0.158	4.9		
Coronavirus (SARS)	Virus	0.11	6.4		
Influenza A virus	Virus	0.098	7.1		
Adenovirus	Virus	0.079	8.5		
Reovirus	Virus	0.075	8.9		
Rotavirus	Virus	0.073	9.1		
Rubella virus	Virus	0.061	10.6		
Norwalk virus	Virus	0.029	18.1		
Coxsackievirus	Virus	0.027	18.9		
Rhinovirus	Virus	0.023	20.6		
Parvovirus B19	Virus	0.022	21.0		

Appendix B: UV Disinfection Rates of Airborne Nosocomial Pathogens

Appendix B: UV Disinfection Rates of Airborne Nosocomial Pathogens							
Microbe	Type	UV k	UV D90	Disinfection Rate, %			
		m²/J	J/m²	15 W			
Coronavirus (SARS)	Virus	0.377	6	100			
Legionella pneumophila	Bacteria	0.2024	11	100			
Mycobacterium tuberculosis	Bacteria	0.4721	5	100			
Mycoplasma pneumoniae	Bacteria	0.2791	8	100			
Proteus mirabilis	Bacteria	0.289	8	100			
Pseudomonas aeruginosa	Bacteria	0.5721	4	100			
Serratia marcescens	Bacteria	0.221	10	100			
Staphylococcus aureus	Bacteria	0.5957	4	100			
Streptococcus pyogenes	Bacteria	0.8113	3	100			
Acinetobacter	Bacteria	0.16	14	100			
VZV (Varicella surrogate k)	Virus	0.1305	18	100			
Influenza A virus	Virus	0.119	19	100			
Haemophilus influenzae	Bacteria	0.11845	19	100			
Coxsackievirus	Virus	0.111	21	100			
Parainfluenza virus*	Virus	0.1086	21	100			
Neisseria meningitidis*	Bacteria	0.1057	22	100			
Measles virus	Virus	0.1051	22	100			
Staphylococcus epidermis	Bacteria	0.09703	24	100			
Parvovirus B19	Virus	0.092	25	100			
RSV*	Virus	0.0917	25	100			
Enterococcus*	Bacteria	0.0822	28	100			
Nocardia asteroides	Bacteria	0.0822	28	100			
Mumps virus*	Virus	0.0766	30	100			
Corynebacterium diphtheriae	Bacteria	0.0701	33	100			
Adenovirus	Virus	0.054	43	100			
Klebsiella pneumoniae	Bacteria	0.04435	52	100			
Mycobacterium avium	Bacteria	0.04387	52	100			
Clostridium difficile spores	Bacteria	0.0385	60	100			
Clostridium perfringens spores	Bacteria	0.0385	60	100			
Bordetella pertussis*	Bacteria	0.0364	63	100			
Enterobacter cloacae	Bacteria	0.03598	64	100			
Haemophilus parainfluenzae*	Bacteria	0.03398	77	100			
Rotavirus	Virus	0.02342	98	99			
Cryptococcus neoformans spores	Fungi	0.02342	138	96			
Blastomyces dermatitidis spores	Fungi	0.01645	140	96			
Reovirus	Virus	0.01043	158	94			
Rhinovirus*	Virus	0.01439	162	94			
Norwalk virus*	Virus	0.0142	198	90			
	Fungi	0.01012	228	87			
Mucor spores Aspergillus spores							
	Fungi	0.00894	258	83			
Rhizopus spores	Fungi	0.00861	267	82			
Fusarium spores	Fungi	0.00855	269	82			
Streptococcus pneumoniae	Bacteria	0.00492	468	62			
Rubella virus*	Virus	0.0037	622	52			
UV Dose, J/m ²		198	<u> </u>	1			

Note: Asterisk means the UV rate constant is a predicted value based on the complete genome.

Appendix C: Combined Single Pass Removal Rates

Appendix C: Combined Single Pass Removal Rates						
Microbe	Component	Removal Rates	Overall Removal Rates			
	MERV 6	15 W	MERV 6 + 15 W			
	fraction	fraction	%			
Coronavirus (SARS)	0.0643	1.0000	100.0			
Legionella pneumophila	0.0721	1.0000	100.0			
Mycobacterium tuberculosis	0.0925	1.0000	100.0			
Mycoplasma pneumoniae	0.0464	1.0000	100.0			
Proteus mirabilis	0.0680	1.0000	100.0			
Pseudomonas aeruginosa	0.0680	1.0000	100.0			
Serratia marcescens	0.0916	1.0000	100.0			
Staphylococcus aureus	0.1372	1.0000	100.0			
Streptococcus pyogenes	0.1428	1.0000	100.0			
Acinetobacter	0.2089	1.0000	100.0			
VZV	0.0469	1.0000	100.0			
Influenza A virus	0.0709	1.0000	100.0			
Haemophilus influenzae	0.0443	1.0000	100.0			
Coxsackievirus	0.1886	1.0000	100.0			
Parainfluenza virus	0.0447	1.0000	100.0			
Neisseria meningitidis	0.1190	1.0000	100.0			
Measles virus	0.0493	1.0000	100.0			
Staphylococcus epidermis	0.1372	1.0000	100.0			
Parvovirus B19	0.2104	1.0000	100.0			
RSV	0.0450	1.0000	100.0			
Enterococcus	0.2442	1.0000	100.0			
Nocardia asteroides	0.1879	1.0000	100.0			
Mumps virus	0.0483	1.0000	100.0			
Corynebacterium diphtheriae	0.1040	1.0000	100.0			
Adenovirus	0.0853	1.0000	100.0			
Mycobacterium avium	0.1879	0.9998	100.0			
Klebsiella pneumoniae	0.0988	0.9998	100.0			
Clostridium difficile spores	0.3353	0.9995	100.0			
Clostridium perfringens spores	0.1643	0.9995	100.0			
Enterobacter cloacae	0.2442	0.9992	99.9			
Bordetella pertussis	0.0431	0.9993	99.9			
Haemophilus parainfluenzae	0.2973	0.9974	99.8			
Rotavirus	0.0913	0.9903	99.1			
Cryptococcus neoformans spores	0.4872	0.9634	98.1			
Blastomyces dermatitidis spores	0.5000	0.9615	98.1			
Rhinovirus	0.2057	0.9399	95.2			
Reovirus	0.0892	0.9444	94.9			
Mucor spores	0.4983	0.8652	93.2			
Norwalk virus	0.1809	0.8994	91.8			
Rhizopus spores	0.4981	0.8182	90.9			
Fusarium spores	0.5000	0.8160	90.8			
Aspergillus spores	0.4476	0.8297	90.6			
Streptococcus pneumoniae	0.1057	0.6225	66.2			
Rubella virus	0.1062	0.5193	57.0			