SAFESTART
ENVIRONMENTAL

SOURCES OF ACTINOMYCETES ENVIRONMENTAL BACTERIA IN HOMES AND METHODS OF CONTROLLING THEIR PROLIFERATION AND LEVELS

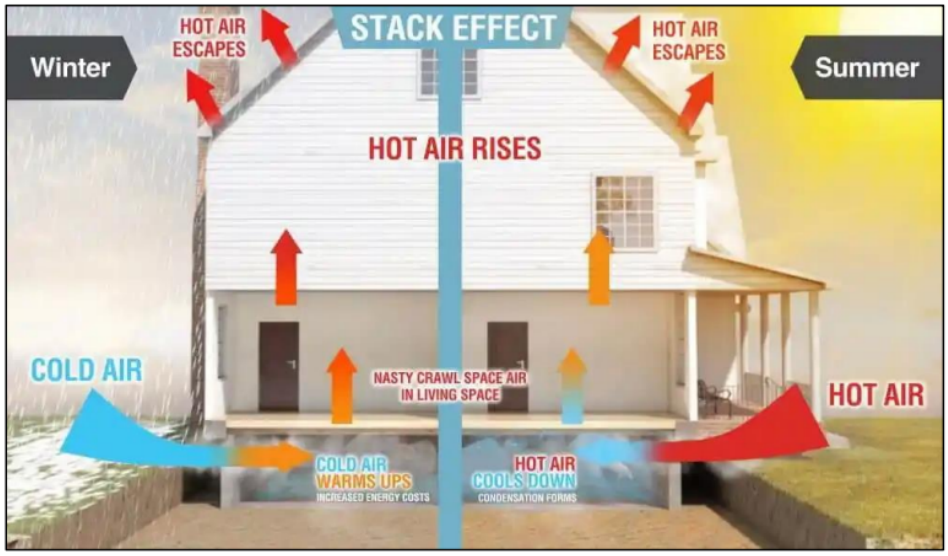
Larry Schwartz, BSME, MBA, CIEC, President, Safestart Environmental Co-chairman, Indoor Environmental Professional Committee of the International Society for Environmentally Acquired Illness (ISEAI) Member,Surviving Mold Indoor Environmental Professional Panel Consensus for Microbial Remediation 2020 September 26,2021

ABSTRACT: Environmental bacteria and their shedding of endotoxins play a major role in both symptoms and levels of contaminants in patients with inflammatory illnesses such as CIRS,Lyme disease, Mast Cell ActivationSyndrome, among others. This has been evidenced by those in our group and others,based on Gene Expression: Inflammation Explained (GENIE) testing results,research papers and curren medical testing of patients. (1,2)

So far as we know currently,the sources of their entry or creation in the home area result of interior water events, intrusion into the home from above-ground air outdoors,air mixed in soils, and from those on and in our bodies, not to mention possibilities from pets

All buildings have negative pressure that allows the ingress of outdoor air through doors and door frames and other paths of least resistance, such as coming and going, around windows and window frames, electrical outlets and switch plates, uncovered pits in belowground levels, foundation cracks, among others.

When we run bath and kitchen fans, clothes dryers, and the stack effect of rising air, we are pushing air out of the home (egress). The home is therefore always trying to replace that air being pushed out by this suction. The highest level of this suction is the lowest surface in the home due to the stack effect. (3,4)



This paper is an attempt to prove my hypothesis that we can test where and how the majority of Human Habitat (HH) bacteria are created and stored in the home. I'll discuss how to minimize the creation and levels of these bacteria in the home using this knowledge, as well as how to minimize soil-based bacteria entry into the home. Another major hypothesis I attempt to prove is via a testing protocol I have created and performed that measures the cleaning efficacy of various cleaning solutions for removal of bacteria on paper drywall that is painted with flat paint.

So far, data from Actinomycetes Next Generation Sequence (NGS) testing from Envirobiomics, Inc., with newer Prevalence and Dominance indices, finds data showing many more Human Habitat Prevalence indices greater than 2.0, than soil-based bacteria.

I believe the major areas of the home where generation and proliferation of HH bacteria are maximized are in the "inner-sancta" — bedrooms and bathrooms and levels of the home populated the greatest amount of time.

Using my testing protocol, the cleaning formula and methods described in the latest Surviving Mold Environmental Consensus document (5) performed better than other cleaning products tested. I also saw an improvement of the Surviving Mold cleaning solution by lowering its pH to between 3.5 and 4.0, via the addition of a small, measured amount of vinegar and testing the pH with litmus paper.

HYPOTHESIS OF PRIMARY LOCATIONS OF HUMAN HABITAT (HH) PRODUCTION:

It stands to reason that where we gather the most in our homes for the longest time will have the greatest amount of HH bacteria. From what I have learned, bacteria are on our skin and in mucus membranes in the nose, mouth, digestive, and reproductive tracts, etc. Additionally, we are always shedding dried skin via exfoliation.

Consider: When we are in bed 6-8 hours a day or more, we are generally under covers with little to no ventilation, the air in the space heats up to near body temperature, we exfoliate skin, we perspire. We may discharge saliva into the pillows, and other body fluids, like sweat, into the bedding. I hypothesize that this is the primary HH bacteria factory in the home.

In the bathroom, we shower or bathe and remove skin particles that travel in the air and may stick to shower tiles, drains, mirrors, and walls. There is a thin to larger coating of condensation created on these surfaces from the shower and water use. HH bacteria grow on these surfaces on the skin particles. Our bath towels and racks are reservoirs of bacteria.

HYPOTHESIS OF PRIMARY LOCATIONS OF ENTRY OF SOIL HABITAT (SH) BACTERIA:

There is air mixed in soils as well as molds, bacteria, gases such as radon and more. Soils are known to be at least 25% microbial growth, which comes from decaying dead organic material such as twigs, leaves, plant matter, etc.

In areas where basements and below ground levels such as crawl spaces, and partial basements exist, there are often drainage systems installed (such as a sump pit) to collect water and pump it to the outdoors. If installed correctly, the pit has a tubing known as drain tile connected to it. The drain tile rests on gravel underground, around the exterior foundation of the home. This piping has slits in it to allow water to enter and directs it into the sump pit in the home. Now recall, as mentioned above, that the greatest level of negative pressure in the home is the home's lowest level. If this pit is not air sealed, that negative pressure pulls air mixed in soils into and through the drain tile piping and into the pit, where the stack effect pushes it into the house.

Some basements have windows above and/or below ground as well as doors to patios, etc. Many basements' window wells don't drain properly, there are window air leaks, there may be algae and microbial growth on the surface of the window well surfaces, etc.

Domestic animals may bring in outdoor bacteria as well as emit exfoliated skin. We bring in outdoor bacteria on our shoes and our clothing.

There are HH bacteria as well as other bacteria and more growing in the upper drain pipes in showers and sinks, and the negative pressure in the home may pull these airborne as well as sewer gases on occasion into the air of the home.

TEST DESCRIPTION AND RESULTS PRESENTING HH BACTERIA SOURCES IN A TEST HOME:

A. In our first test, the main bed linens have been changed weekly. And each time, for years, the mattress cover has been HEPA vacuumed, as well as the pillows.

   In July 2021, a new filter was installed in the vacuum and the dust collected from the mattress cover and bedding was sent to Envirobiomics for Actinomycetes test processing. Note the following results in the attached lab report:

   Actino Score: 8

   Dominance Index: 8.7
   Prevalence Index: 52.2

   Actino Abundance: 28.4%

   Note the unusually high level of the Prevalence Index.

B. Actinomycetes testing was performed on multiple levels of a 100-year-old Evanston, Illinois home, currently being lived in. This home has a basement, a main and second level, and a finished bedroom on the 3rd floor attic level. Actinomycete tests were performed in the basement, a combination of the first and second levels, and in the attic bedroom. The test results are as follows:

   Basement:
   Score 26
   Dominance Index 0.9

Prevalence Index 2.6
Abundance: 30%

1st and 2nd Floors:
Score 21
Dominance Index 1.3
Prevalence Index 7.7
Abundance 22.1%

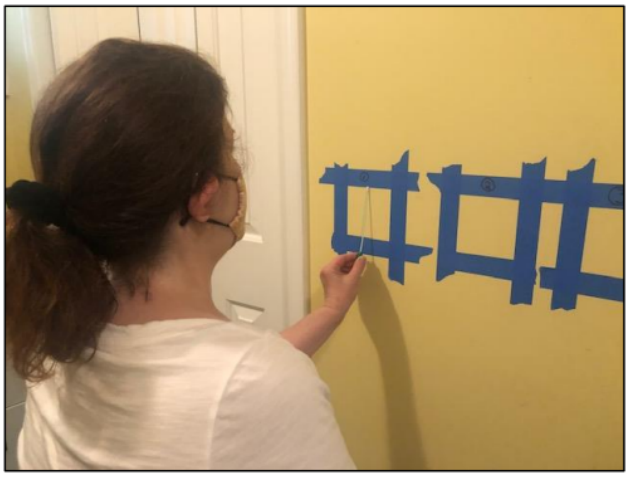
Attic Bedroom:
Score 21
Dominance 2.2
Prevalence 15.9
Abundance 30%

Note that the levels occupied the longest have the highest PI, and that the level of the PI in the attic bedroom is 5-6 times higher than the basement level, which is not occupied frequently.

TESTING DESCRIPTION AND EFFICACY RESULTS OF CLEANING AGENTS OF BACTERIA ON PAINTED DRYWALL IN A BASEMENT OFFICE OF AN 80-YEAR-OLD HOME IN OAK PARK, IL.:

On July 24th, 2021, we performed the following testing stated above (see cleaning and collection methods used below).

We taped off 5 sections of 4-inch by 4-inch squares for a total of square inches of area, on drywall in a basement office of the property. We used 4 of the squares for testing.



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We first performed an initial sterile swabbing of each area with a sterile swab supplied by Prestige EnviroMicrobiology, Inc., in Voorhees, New Jersey. Each square surface was swabbed by the same person (the homeowner) under my direction, vertically, horizontally, and again vertically. Each wipe of the swab was turned 1/3rd turn.

Cleaning solutions were prepared and put into new never-used spray bottles. The bottles were used to spray the solution onto new microfiber cloths which had been sealed until use for this purpose. We then wiped each surface once with a different cloth and solution. The surfaces were allowed to dry for 30 minutes.

The surfaces were then swabbed a second time with new sterile swabs, following the same collection protocol.

The tests on each wipe were labeled 1 A and B, 2 A and B, 3 A and B, and 4 A and B. The A wipes were the pre-cleaning wipes, and B wipes were the post-cleaning wipes.

The swabs were sealed and sent to Prestige EnviroMicrobiology, Inc., where the samples were then cultured on Malt Extract Agar (MEA) and Tryptic Soy Agar (TSA). The results were speciated microscopically and sent to me on the attached report form.

Test number 3 on this report had used the cleaning solution described in the newest Surviving Mold Environmental Consensus Document. (5) The test number 4 was the same solution with a reduction of pH by using a vinegar additive

The other tests of products and solutions had reductions from bacteria at 100% to 7.8% and 24.6% respectively. The Surviving Mold formula had a reduced 100% of the bacteria down to 0.12%, and with the vinegar additive, to 0.08%. Both are excellent results.

CONCLUSIONS:

Of the 60 Actinomycetes lab test reports I have seen processed by Envirobiomics, Inc., there hasn't been one home that doesn't have them. In fact, more than 95% of those had abundances >20%.

Considering that inflammatory patients have different levels of sensitivities to types of contaminants, and that all homes have levels of Actinomycetes, we need to reach an ongoing level of less than or equal to 2.0 scores of HH and SH indices that will be the safest for the most patients.

I believe further NGS testing will repeat the same pattern of results that I have received from the testing I have performed and noted in this paper. Therefore, I recommend that patients make ongoing efforts to control and minimize the sources and concentrations of these bacteria in the home by implementing sound principles of personal hygiene and housecleaning methods.

Although I have created protocols that involve methods incorporating specialized HEPA vacuuming of source areas, laundering methods, cleaning methods, personal hygiene habits, air purification and ventilation as may be needed, each case may need detailed information and data to tailor a plan for maximum efficacy. I recommend that experienced Indoor Environmental Professionals in this paradigm be used to assess and to develop effective treatment plans

Although GENIE testing may indicate, at a point in time, indoor environmental conditions of a patient's symptoms being "triggered" by Actinomycetes, Endotoxins, mycotoxins, not all patients have the same sensitivity triggering levels; therefore, we cannot generalize these specific outcomes, but strive to create and keep the indoor levels as low as possible.

I believe information in Surviving Mold's latest Environmental Consensus Document is a major element in this process.

REFERENCES:

1. Shoemaker R, Neil V, Heyman A, van der Westhuizen M, McMahon S, Lark D. Newer Molecular Methods Bring New Insights into Human - and Building - Health Risk Assessments from Water-Damaged Buildings: Defining Exposure and Reactivity, the Two Sides of Causation of CIRS-WDB Illness. Med. Res. Arc; 2021; 9(3):1-36.
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3. U.S. Environmental Protection Agency. Moisture Control Guidance for Building Design, Instruction and Maintenance. American Society of Heating, Refrigeration, and AirConditioning Engineers (ASHRAE); December 2013;17-18.
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5. The CIRS Academy of www.survivingmold.com. The Indoor Environmental Professional Panel of Surviving Mold Consensus Statement for Microbial Remediation 2020; Med. Res. Arc; January 2021;9(1).

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5 ACTINO INDEX

Human Habitat (HH)

Species	BE/mg
Actinomadura chibensis	ND
Actinomyces canis	ND
Actinomyces europaeus	ND
Actinomyces meyeri	6,948
Actinomyces neuii	41,648
Actinomyces odontolyticus	ND
Actinomyces turicensis	884
Corynebacterium accolens	7,369
Corynebacterium amycolatum	7,454
Corynebacterium argentoratense	2,316
Corynebacterium coyleae	ND
Corynebacterium falsenii	ND
Corynebacterium glucuronolyticum	4,969
Corynebacterium hansenii	1,137
Corynebacterium imitans	ND
Corynebacterium jeikeium	1,727
Corynebacterium kroppenstedtii	1,011
Corynebacterium matruchotii	10,780
Corynebacterium minutissimum	5,727
Corynebacterium propinquum	1,811
Corynebacterium resistens	ND
Corynebacterium riegelii	ND
Corynebacterium simulans	26,993
Corynebacterium striatum	3,495
Corynebacterium sundsvallense	4,422
Corynebacterium tuberculostearicum	56,724
Corynebacterium ureicelerivorans	8,254
Corynebacterium xerosis	ND
Dermatophilus congolensis	ND
Propionibacterium acnes	45,185
Propionibacterium avidum	3,495
Propionibacterium granulosum	1,558
Rothia mucilaginosa	2,527

Soil Habitat (SH)

Species	BE/mg
Arthrobacter creatinolyticus	ND
Arthrobacter crystallopoietes	ND
Brevibacterium mcbrellneri	ND
Brevibacterium paucivorans	ND
Clavibacter michiganensis	ND
Curtobacterium flaccumfaciens	ND
Gordonia terrae	ND
Nocardia higoensis	ND
Rathayibacter tritici	ND
Rhodococcus equi	ND
Rhodococcus fascians	2,611
Saccharopolyspora rectivirgula	ND
Sanguibacter suarezii	ND

BE = Bacteria Equivalents
BE/mg = BE/milligrams of sample
ND = None Detected

Dominance Index (DI)	**8.7**
Prevalence Index (PI)	**52.2**

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Human Habitat (HH)		Soil Habitat (SH)	
Species	**BE/mg**	**Species**	**BE/mg**
Actinomadura chibensis	ND	Arthrobacter creatinolyticus	ND
Actinomyces canis	ND	Arthrobacter crystallopoietes	1,333
Actinomyces europaeus	ND	Brevibacterium mcbrellneri	328
Actinomyces meyeri	ND	Brevibacterium paucivorans	219
Actinomyces neuii	ND	Clavibacter michiganensis	ND
Actinomyces odontolyticus	ND	Curtobacterium flaccumfaciens	874
Actinomyces turicensis	ND	Gordonia terrae	ND
Corynebacterium accolens	284	Nocardia higoensis	ND
Corynebacterium amycolatum	940	Rathayibacter tritici	ND
Corynebacterium argentoratense	1,005	Rhodococcus equi	ND
Corynebacterium coyleae	1,049	Rhodococcus fascians	306
Corynebacterium falsenii	ND	Saccharopolyspora rectivirgula	219
Corynebacterium glucuronolyticum	2,797	Sanguibacter suarezii	1,049
Corynebacterium hansenii	459		
Corynebacterium imitans	874		
Corynebacterium jeikeium	634		
Corynebacterium kroppenstedtii	ND		
Corynebacterium matruchotii	ND		
Corynebacterium minutissimum	809		
Corynebacterium propinquum	ND		
Corynebacterium resistens	437		
Corynebacterium riegelii	3,081		
Corynebacterium simulans	ND		
Corynebacterium striatum	ND		
Corynebacterium sundsvallense	699		
Corynebacterium tuberculostearicum	2,032		
Corynebacterium ureicelerivorans	2,557		
Corynebacterium xerosis	ND		
Dermatophilus congolensis	ND		
Propionibacterium acnes	1,552		
Propionibacterium avidum	197		
Propionibacterium granulosum	ND		
Rothia mucilaginosa	ND		

BE = Bacteria Equivalents
BE/mg = BE/milligrams of sample
ND = None Detected

Dominance Index (DI)	**0.9**
Prevalence Index (PI)	**2.6**

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Human Habitat (HH)		Soil Habitat (SH)	
Species	**BE/mg**	**Species**	**BE/mg**
Actinomadura chibensis	ND	Arthrobacter creatinolyticus	ND
Actinomyces canis	784	Arthrobacter crystallopoietes	1,333
Actinomyces europaeus	ND	Brevibacterium mcbrellneri	ND
Actinomyces meyeri	ND	Brevibacterium paucivorans	ND
Actinomyces neuii	ND	Clavibacter michiganensis	1,176
Actinomyces odontolyticus	ND	Curtobacterium flaccumfaciens	1,411
Actinomyces turicensis	ND	Gordonia terrae	ND
Corynebacterium accolens	1,803	Nocardia higoensis	ND
Corynebacterium amycolatum	3,763	Rathayibacter tritici	862
Corynebacterium argentoratense	2,195	Rhodococcus equi	ND
Corynebacterium coyleae	6,428	Rhodococcus fascians	941
Corynebacterium falsenii	ND	Saccharopolyspora rectivirgula	ND
Corynebacterium glucuronolyticum	9,563	Sanguibacter suarezii	2,979
Corynebacterium hansenii	1,646		
Corynebacterium imitans	12,385		
Corynebacterium jeikeium	4,468		
Corynebacterium kroppenstedtii	1,176		
Corynebacterium matruchotii	ND		
Corynebacterium minutissimum	3,371		
Corynebacterium propinquum	784		
Corynebacterium resistens	1,097		
Corynebacterium riegelii	14,815		
Corynebacterium simulans	1,646		
Corynebacterium striatum	ND		
Corynebacterium sundsvallense	5,409		
Corynebacterium tuberculostearicum	13,796		
Corynebacterium ureicelerivorans	12,934		
Corynebacterium xerosis	ND		
Dermatophilus congolensis	ND		
Propionibacterium acnes	5,565		
Propionibacterium avidum	1,019		
Propionibacterium granulosum	ND		
Rothia mucilaginosa	ND		

BE = Bacteria Equivalents
BE/mg = BE/milligrams of sample
ND = None Detected

Dominance Index (DI)	**1.3**
Prevalence Index (PI)	**7.7**

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Human Habitat (HH)

Species	BE/mg
Actinomadura chibensis	ND
Actinomyces canis	ND
Actinomyces europaeus	ND
Actinomyces meyeri	271
Actinomyces neuii	ND
Actinomyces odontolyticus	ND
Actinomyces turicensis	ND
Corynebacterium accolens	1,564
Corynebacterium amycolatum	3,594
Corynebacterium argentoratense	1,007
Corynebacterium coyleae	601
Corynebacterium falsenii	ND
Corynebacterium glucuronolyticum	481
Corynebacterium hansenii	1,007
Corynebacterium imitans	12,240
Corynebacterium jeikeium	3,519
Corynebacterium kroppenstedtii	ND
Corynebacterium matruchotii	ND
Corynebacterium minutissimum	3,925
Corynebacterium propinquum	195
Corynebacterium resistens	451
Corynebacterium riegelii	2,195
Corynebacterium simulans	1,368
Corynebacterium striatum	421
Corynebacterium sundsvallense	5,143
Corynebacterium tuberculostearicum	12,075
Corynebacterium ureicelerivorans	3,940
Corynebacterium xerosis	ND
Dermatophilus congolensis	256
Propionibacterium acnes	3,714
Propionibacterium avidum	436
Propionibacterium granulosum	ND
Rothia mucilaginosa	391

Soil Habitat (SH)

Species	BE/mg
Arthrobacter creatinolyticus	ND
Arthrobacter crystallopoietes	ND
Brevibacterium mcbrellneri	752
Brevibacterium paucivorans	571
Clavibacter michiganensis	ND
Curtobacterium flaccumfaciens	556
Gordonia terrae	ND
Nocardia higoensis	ND
Rathayibacter tritici	ND
Rhodococcus equi	ND
Rhodococcus fascians	ND
Saccharopolyspora rectivirgula	ND
Sanguibacter suarezii	466

BE = Bacteria Equivalents
BE/mg = BE/milligrams of sample
ND = None Detected

Dominance Index (DI)	**2.2**
Prevalence Index (PI)	**15.9**

Prestige EnviroMicrobiology, Inc.

Analytical Test Report

Client: Safestart Environmental, 1608 Sienna Ct, Indian Creek, IL 60061

Client Project/Name: BB Cleaning Test

Sample date: 7-24-2021

Submittal date: 7-26-2021

Date samples received: 7-27-2021

Date of inoculation: 7-27-2021 (Swab)

Samples submitted by: Larry Schwartz

Date analysis completed: August 3, 2021

Prestige Report number: 210727-06

Culture Method (P028): Culture Analysis of Swab Samples for Fungi with Full Speciation and Bacteria

Prestige # Client sample ID Location	Area ($inch^2$)	Medium used	Dilution factor	Fungal/Bacterial Identification	Colony counts	Conc. ($CFU/inch^2$)	Percentage
210727-06-018 1-A Wall in Basement Office	16	MEA TSA	100x 1,000x	No fungal colony detected gram (-) bacteria gram (+) bacteria *Micrococcus luteus* *Staphylococcus* spp.	ND 30 15 12 10	<6 Total <6 1,900 940 750 630 Total 4,200	NA 45% 22% 18% 15%
210727-06-019 1-B Wall in Basement Office	16	MEA TSA	100x 100x	No fungal colony detected gram (-) bacteria gram (+) bacteria *Micrococcus luteus*	ND 33 17 1	<6 Total <6 210 110 6 Total 330	NA 65% 33% 2%
210727-06-020 2-A Wall in Basement Office	16	MEA TSA	100x 10,000x	No fungal colony detected gram (-) bacteria gram (+) bacteria *Micrococcus luteus*	ND 143 25 75	<6 Total <6 89,000 16,000 47,000 Total 150,000	NA 59% 10% 31%
210727-06-021 2-B Wall in Basement Office	16	MEA TSA	100x 10,000x	No fungal colony detected gram (-) bacteria gram (+) bacteria *Micrococcus luteus*	ND 29 16 15	<6 Total <6 18,000 10,000 9,400 Total 37,000	NA 48% 27% 25%

210727-06-022 3-A Wall in Basement Office	16	MEA TSA	100x 10,000x	No fungal colony detected gram (-) bacteria gram (+) bacteria	ND 135 18	<6 Total <6 84,000 11,000 Total 95,000	NA 88% 12%
210727-06-023 3-B Wall in Basement Office	16	MEA TSA	100x 100x	No fungal colony detected gram (-) bacteria gram (+) bacteria	ND 16 3	<6 Total <6 100 19 Total 120	NA 84% 16%
210727-06-024 4-A Wall in Basement Office	16	MEA TSA	100x 10,000x	No fungal colony detected Bacteria overloaded *Bacillus* spp. gram (-) bacteria gram (+) bacteria *Micrococcus luteus*	ND >500	<6 Total <6 >310,000 Total >310,000	NA NA
210727-06-025 4-A Wall in Basement Office	16	MEA TSA	100x 100x	No fungal colony detected gram (-) bacteria gram (+) bacteria	ND 36 4	<6 Total <6 230 25 Total 260	NA 90% 10%

Report approved: Theresa Lehman
Theresa Lehman, MPH, Lab Director

Technical Manager:
Chin S Yang, Ph.D.

Analyst: Ching-Yi Tsai, Ph.D.

1. The samples in this report were received in good, acceptable conditions. Prestige EnviroMicrobiology has not performed sample collection for the sample items listed in this report. Results relate only to the items tested.
2. Percentage is for each group in total population.
3. Concentrations and percentages are rounded. Total percentage may not add up to 100% due to rounding.
4. Abbreviations where applicable: CMA = cornmeal agar, DG18 = Dichloran 18% glycerol agar, MEA = 2% malt extract agar, PCA = plate count agar, TSA = tryptic soy agar, ND = not detected, NA = not applicable.
5. All culture samples are incubated at 25± 1ºC unless otherwise indicated.
6. Field blank, if submitted with the project, has not been used to adjust data.
7. The detection limit of this analysis is one fungal colony, one bacterial colony or one fungal structure. The analytical sensitivities vary from analysis to analysis or by air volume. For calculation of your analytical sensitivities, please visit our webpage http://prestige-em.com/index-tech.htm or contact us by calling 856-767-8300 or by email info@Prestige-em.com.