

# **BACTERIOLOGY PROFICIENCY TESTING PROGRAM**

## **General Category**

**September 20, 2005**

This report summarizes the results of the proficiency test administered September 20, 2005 to laboratories in the General Bacteriology category.

If you have any questions or comments, please contact either:

Mrs. Deborah Baker  
Dr. Wendy Archinal  
Dr. Ronald Limberger

Phone: (518) 474-4177  
Email: [bacti@wadsworth.org](mailto:bacti@wadsworth.org)



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# ***Bacteriology Proficiency Testing Program***

## ***GENERAL INFORMATION***

**The Bacteriology Proficiency Testing Program.** Three proficiency testing events are given annually, each consisting of a minimum of five specimens. In order to successfully complete a test event, participating laboratories must achieve a score of 80% or greater. Failure of the testing program is defined as a score of less than 80% on two of three consecutive test events.

**Authentication.** The presence and identity of the organism(s) in each specimen must be confirmed by at least 80% of the referee or participating laboratories. Referee laboratories are selected from New York State participating laboratories (located throughout the State) with acceptable and reproducible levels of performance. Sample vials are subjected to extensive quality control testing in our laboratory during preparation and storage.

**Grading System.** Laboratories are to process proficiency test specimens in the same manner as patient specimens. Thus, laboratories are responsible for identifying test isolates to the same level as performed on patient isolates. If your laboratory speciates an organism on special request, then you must also speciate it in the proficiency test; consider speciation to have been requested on all reportable isolates. In addition, laboratories are not responsible for culturing any test samples from specimen sources which they do not process. Information regarding your laboratory's reporting protocol was provided to us in the questionnaire previously distributed to all laboratories. Any changes in reporting protocol must be received by our office prior to the mailout date for proficiency testing for that information to be considered in grading.

Our testing format is in compliance with HCFA guidelines as specified in the regulations of CLIA '88. One-half of our samples require identification of all organisms present. The other half requires that only the pathogenic organism(s) be reported. We recognize the potential for any organism to be pathogenic depending on the clinical condition of the patient. However, our samples are designed so that only well-established pathogens should be reported.

Tests are graded in strict adherence to HCFA guidelines, as specified in the regulations of CLIA '88. Each of the specimens receives a score as determined by the following formula:

$$(a + b)/(c + d + e) \times 100\%$$

a = # correct identifications

b = # correct antibiotic susceptibility results (if applicable)

c = # possible identifications

d = # possible antibiotic susceptibility results (if applicable)

e = # additional organisms reported

Grades for each sample are then averaged to determine the final grade for this testing event. The minimum passing grade for each test event is 80%.

**Disclaimer**

The use of brand and/or trade names in this report does not constitute an endorsement of the products on the part of the Wadsworth Center or the New York State Department of Health.

## *Notes of Interest*

**Bacteriology Questionnaires** – please make sure that the information on your laboratory's Bacteriology Questionnaire is up to date. If you need a copy of your questionnaire for review, please contact our office at 518-474-4177 or email us at [bacti@wadsworth.org](mailto:bacti@wadsworth.org). Please note that proficiency test results are graded in accordance with information on the questionnaire.

**Recently, there have been several incidences where laboratories have lost credit on proficiency test results because of inaccuracies or outdated information on their Bacteriology Questionnaire. Grades will not be revised due to incorrect information on the questionnaire.**

### **New Director of Bacteriology Laboratory**

Robyn Atkinson, Ph.D. is the new director of the Wadsworth Center's Bacteriology Laboratory. Please find her letter of introduction on the following page.

## ***Letter of Introduction from New Bacteriology Director***

Dear Microbiology Laboratory Director:

Please allow me introduce myself. I recently joined the Wadsworth Center at the NYSDOH as Director of the Bacteriology Laboratory. One of my main goals is to improve communication between our laboratory and yours. We at the state level can better support your laboratory if there is an open dialogue about the challenges that you face and how we can help to address those challenges. If you need assistance regarding any laboratory-related matter, I encourage you to contact us. We are your reference center.

I hold an undergraduate degree in biochemistry, a graduate degree in pathology, and recently completed a fellowship in Medical and Public Health Microbiology at Washington University in St. Louis. My research experience includes identifying resistance and tolerance mechanisms in *Streptococcus pneumoniae*, molecular assay development for bacterial and viral targets, and epidemiology work related to the introduction of *Pandoraea apista* into a cystic fibrosis population. Now that I find myself in a public health laboratory, it is important that I maintain contact with NYS laboratory directors to stay up-to-date on issues that concern clinical laboratories.

My contact information is listed below. Please call or email me for consultations, questions regarding our procedures, or general comments regarding our laboratory. I hope to set up training sessions (some for CME credit) for technologists/interested directors regarding the identification of difficult-to-identify bacteria, including select agents; refreshers on proper laboratory technique; and sessions on PCR assay development and the Clinical Laboratory Evaluation Program (CLEP) approval process. I hope to develop a way to ensure regular communication with laboratory directors throughout the state to share experiences and knowledge and to discuss what tests you would like available through our laboratory.

Our doors are always open for tours. If you and/or your supervisory staff are interested in seeing what we do here, please don't hesitate to let me know. I look forward to hearing from you and hopefully meeting you in the near future.

Sincerely,  
Robyn M Atkinson, PhD

Wadsworth Center – New York State Department of Health  
120 New Scotland Ave., Albany NY 12208  
Phone: (518) 474-4177  
Email: [atkinson@wadsworth.org](mailto:atkinson@wadsworth.org)

**SEPTEMBER 20, 2005 TEST EVENT**

**Number of Participating Laboratories:**  
**Receiving specimens**           **236**  
**Returning results**           **236**   **(100%)**

Grade Distribution		
Score	Number	Percent
100	121	51.3
90 - 99	67	28.4
80 - 89	16	6.8
70 - 79	19	8.1
60 - 69	3	1.3
< 60	10	4.3

**BACTERIOLOGY - GENERAL**  
**SEPTEMBER 20, 2005**  
**ANSWER KEY**

**Specimen No. 1 - Stool (Pathogens Only)**

*Salmonella* serogroup B

**Specimen No. 2 – Abscess (All Organisms Reported)**

Beta-hemolytic *Streptococcus* group C

**Specimen No. 3 – Wound - Aerobic / Anaerobic (All Organisms Reported)**

*Fusobacterium necrophorum*

*Pasteurella multocida*

**Specimen No. 4 – Sputum (Pathogens Only) and Antibiotic Susceptibility**

*Haemophilus influenzae*

Susceptibility of *H. influenzae* to: Chloramphenicol - Resistant

Tetracycline - Resistant

**Specimen No. 5 – Blood (All Organisms Reported)**

*Corynebacterium jeikeium*

**Educational – Blood (All Organisms Reported)**

Rapidly-growing mycobacteria (*Mycobacterium brisbanense*)

***Chlamydia* Specimen**

Positive for *Chlamydia trachomatis*

**Direct Antigen Detection**

A (Throat)

Positive for Group A *Streptococcus*

C (Genital)

Positive for Group B *Streptococcus*

## REFEREE LABORATORY RESULTS

Specimen Number	Referee Laboratory Responses	Percent*
1	<i>Salmonella</i> serogroup B	80
	<i>Salmonella</i> serogroup D (not <i>typhi</i> )	10
	<i>Salmonella</i> species <sup>1</sup>	10
2	Beta-hemolytic <i>Streptococcus</i> group C	100
3	<i>Fusobacterium necrophorum</i>	80
	No anaerobic organisms	20
	<i>Pasteurella multocida</i>	100
4	<i>Haemophilus influenzae</i>	100
5	<i>Corynebacterium jeikeium</i>	100

\* Based on responses of 10 referee laboratories

<sup>1</sup> This laboratory does not perform serogrouping on *Salmonella* isolates.

## ***Specimen Number 1 - Stool (Pathogens Only)***

This simulated stool specimen contained *Salmonella* serogroup B (*Salmonella* serotype Typhimurium). Referee laboratory results are as follows: 80% reported *Salmonella* serogroup B, 10% incorrectly identified the isolate as *Salmonella* serogroup D (not *typhi*) and 10% reported *Salmonella* species and do not perform serogrouping. Among participating laboratories that process stool cultures, 62% correctly identified the isolate to the serogroup or serotype level while an additional 25% reported ‘*Salmonella* species’ and would forward the isolate to a reference laboratory for further identification.

We wish to clarify an issue with regard to identification of *Salmonella* and the interpretation of the Bacteriology Questionnaire. If the box under the heading of “species” is marked off on your laboratory’s questionnaire, this indicates that your laboratory would identify *Salmonella* beyond the genus level. *Salmonella* are unique in that most species cannot be distinguished biochemically, so this usually equates to a serogroup. Another example would be if your laboratory only identifies a particular species such as *Salmonella typhi*. In this case, all *Salmonella* isolates from proficiency tests should be reported as either *S. typhi* or *Salmonella* species, not *typhi*. Failure to provide the level of identification indicated on the questionnaire will result in a loss of credit on proficiency tests. If you have any questions about this or need to update your questionnaire to accurately reflect your current protocol, please contact us.

*Escherichia coli* and *Enterococcus faecalis* were included in this specimen as nonpathogenic flora.

### **Methods of identification used by laboratories reporting:**

#### ***Salmonella* serogroup B**

bioMerieux Vitek GNI +	52
Dade Behring MicroScan Gram Neg ID	38
bioMerieux Vitek API 20E	29
Two systems	7
BD BBL Crystal Enteric/Nonfermenter	4
bioMerieux Vitek API NH	1
bioMerieux Vitek GNI	1
BD BBL Enterotube II	1
Dade Behring MicroScan Rapid Gram Neg	1
Vitek 2 GN	1
Conventional biochemicals	1
<b>TOTAL</b>	<b>135</b>

#### ***Salmonella* species**

bioMerieux Vitek GNI +	24
Dade Behring MicroScan Gram Neg ID	16
bioMerieux Vitek API 20E	6
Two systems	6
BD BBL Crystal Enteric/Nonfermenter	2
BD BBL Enterotube II	1
Dade Behring MicroScan Rapid Gram Neg	1
<b>TOTAL</b>	<b>56</b>

<b>Do not process stool cultures</b>	<b>11</b>
<b><i>Salmonella</i> species, not typhi</b>	
Dade Behring MicroScan Gram Neg ID	4
bioMerieux Vitek GNI +	3
Conventional biochemicals	1
<b>TOTAL</b>	<b>8</b>
<b><i>Salmonella</i> serogroup D</b>	
Dade Behring MicroScan Gram Neg ID	5
BD Phoenix NID	1
<b>TOTAL</b>	<b>6</b>
<b>No enteric pathogens isolated</b>	<b>5</b>
<b><i>Salmonella</i> species Group D, not typhi</b>	
bioMerieux Vitek GNI +	2
bioMerieux Vitek API 20E	1
Two systems	1
<b>TOTAL</b>	<b>4</b>
<b><i>Salmonella enteritidis</i> group B</b>	
bioMerieux Vitek GNI +	2
Dade Behring MicroScan Gram Neg ID	1
<b>TOTAL</b>	<b>3</b>
<b><i>Escherichia coli</i></b>	
Remel RapID ONE	1
bioMerieux Vitek GNI +	1
<b>TOTAL</b>	<b>2</b>
<b><i>Salmonella</i> serotype Typhimurium</b>	
Conventional biochemicals	2
<b><i>Salmonella</i> Group</b>	
bioMerieux Vitek GNI +	1
<b><i>Salmonella</i> serogroup C</b>	
bioMerieux Vitek GNI +	1
<b><i>Salmonella</i> species; A-I-Pos; Vi-Neg</b>	
bioMerieux Vitek GNI +	1
<b><i>Salmonella</i> species, not group D</b>	
Dade Behring MicroScan Gram Neg ID	1

## ***Specimen No. 2 – Abscess (All Organisms)***

This simulated abscess contained a single organism, Beta-hemolytic *Streptococcus* group C (*S. dysgalactiae* ssp. *equisimilis*). This organism was correctly identified by all referee laboratories and by 91% of participants that process abscess specimens. An additional 4% reported that the organism was a beta-hemolytic *Streptococcus* not group A or B while 1% reported it as not group A, B or D.

### **Methods of identification used by laboratories reporting:**

#### **Beta-hemolytic *Streptococcus*, group C**

BD BBL Streptocard	57
Murex Streptex	55
DPC PathoDx Strep Grouping	42
Two systems	19
Boule Diagnostics Phadebact Streptococcus	5
bioMerieux Vitek GPI	5
Conventional biochemicals	4
bioMerieux Vitek Slidex Strepto	4
Dade Behring MicroScan Gram Pos ID	3
bioMerieux Vitek API 20 Strep	2
Hardy Diagnostics Strep Pro	2
bioMerieux Vitek API Rapid 32A	1
Hardy Diagnostics Strep PRO Grouping Kit	1
Meridian Diagnostics Meritec Strep	1
Oxoid Strep Grouping Kit	1
Remel BactiCard Strep	1
Remel RapID STR	1
Strep Pro Serogrouping Hardy Diagnostics	1
Not given	1
Hardy Diagnostics Strep Pro kit	1
<b>TOTAL</b>	<b>206</b>

#### **Beta-hemolytic *Streptococcus* not A or B**

Conventional biochemicals	3
Dade Behring MicroScan Gram Pos ID	3
DPC PathoDx Strep Grouping	2
BD BBL Streptocard	1
Murex Streptex	1
<b>TOTAL</b>	<b>10</b>

#### ***Streptococcus dysgalactiae***

bioMerieux Vitek GPI	2
bioMerieux Vitek API Rapid 32A	1
Two systems	1
<b>TOTAL</b>	<b>4</b>

<b>Do not process abscess specimens</b>	<b>4</b>
<b>Beta-hemolytic <i>Streptococcus</i> not group A, B, D</b>	
Dade Behring MicroScan Gram Pos ID	1
bioMerieux Vitek GPI	1
Conventional biochemicals	1
<b>TOTAL</b>	<b>3</b>
<b><i>Streptococcus constellatus</i></b>	
Two systems	1
Remel RapID STR	1
<b>TOTAL</b>	<b>2</b>
<b>Beta-hemolytic <i>Streptococcus</i>, group B</b>	
Murex Streptex	1
Hardy Diagnostics Strep Kit	1
<b>TOTAL</b>	<b>2</b>
<b>Beta-hemolytic <i>Streptococcus</i> not group A</b>	
Conventional biochemicals	1
Dade Behring MicroScan Gram Pos ID	1
<b>TOTAL</b>	<b>2</b>
<b><i>Streptococcus dysgalactiae</i> ssp. <i>equisimilis</i></b>	
Conventional biochemicals	1
<b>Beta-hemolytic <i>Streptococcus</i> Group C/Group G</b>	
bioMerieux Vitek GPI	1
<b>Beta-hemolytic <i>Streptococcus</i> group A</b>	
Boule Diagnostics Phadebact Streptococcus	1
<b>Additional organism reported in Specimen 2:</b>	
<i>Streptococcus constellatus</i>	1

### **Specimen No. 3 – Wound - Aerobic/Anaerobic (All Organisms)**

This simulated wound culture contained *Fusobacterium necrophorum* and *Pasteurella multocida*.

*Fusobacterium necrophorum* was identified by 80% of the referee laboratories and by 52% of participating laboratories that process wound cultures for anaerobic organisms. An additional 6% of participants reported this organism as *Fusobacterium species*. Surprisingly, 20% of the referee laboratories and 35% of the participants failed to isolate this organism. Since the *Pasteurella multocida* in this sample also grew anaerobically, a media selective for anaerobes (such as PEA) was necessary to recover *F. necrophorum*. For optimal recovery of anaerobes, laboratories should incorporate a variety of media including those that are enriched, selective and differential. After inoculation, media should be placed into anaerobic conditions immediately and should be held for 5-7 days before specimens are reported as negative.<sup>1</sup> Laboratories who had difficulty in isolating this organism from the proficiency sample are encouraged to contact us for a replacement sample to investigate sources of error in their laboratory. To date, several replacement samples have been provided and most laboratories have been successful in isolating this organism after incorporating some procedural changes.

*Pasteurella multocida* was identified by all referee laboratories and by 98% of participating laboratories that process wound cultures.

<sup>1</sup> Isenberg, Henry D. 2004. *Clinical Microbiology Procedures Handbook*, 2<sup>nd</sup> edition. ASM Press, Washington, DC.

#### **Methods of identification used by laboratories reporting:**

##### ***Fusobacterium necrophorum***

Remel RapID ANA II	60
bioMerieux Vitek ANI	19
bioMerieux Vitek API 20A	17
Dade Behring MicroScan Rapid Anaerobe	12
BD BBL Crystal Anaerobe	2
Remel RapID NH	2
16s rDNA sequencing	1
bioMerieux Vitek API An-ident	1
bioMerieux Vitek API Rapid 32A	1
Conventional biochemicals	1
Remel MicroID	1
Not given	1
<b>TOTAL</b>	<b>118</b>

**No anaerobic organisms isolated 80**

##### ***Fusobacterium species***

Remel RapID ANA II	9
bioMerieux Vitek ANI	2
bioMerieux Vitek API 20A	1
Conventional biochemicals	1
<b>TOTAL</b>	<b>13</b>

<b>Do not culture for anaerobes</b>	<b>7</b>
<i>Fusobacterium varium</i>	
bioMerieux Vitek ANI	4
Two or more systems	1
<b>TOTAL</b>	<b>5</b>
<b>Anaerobic gram negative bacilli</b>	<b>3</b>
<b>Do not process wound cultures</b>	
<b>3</b>	
<i>Fusobacterium nucleatum</i>	
Remel RapID ANA II	2
Conventional biochemicals	1
<b>TOTAL</b>	<b>3</b>
<b>No Bifidobacterium isolated</b>	<b>2</b>
<i>Propionibacterium acnes</i>	
Remel RapID ANA II	1
<i>Veillonella species</i>	
Conventional biochemicals	1
<b>Methods of identification used by laboratories reporting:</b>	
<i>Pasteurella multocida</i>	
bioMerieux Vitek GNI +	79
Dade Behring MicroScan Gram Neg ID	51
bioMerieux Vitek API 20E	32
Two systems	16
Remel RapID NH	15
bioMerieux Vitek API 20NE	7
Conventional biochemicals	6
BD BBL Crystal Enteric/Nonfermenter	6
bioMerieux Vitek API Rapid 20E	2
BD BBL Oxi-Ferm II	2
Dade Behring MicroScan Rapid Gram Neg	2
bioMerieux Vitek GNI	2
Remel RapID NF Plus	2
bioMerieux Vitek API NH	1
Not given	1
BD Phoenix NID	1
bioMerieux Vitek API ZYM	1
Vitek 2 GN	1
Test method not indicated	1
<b>TOTAL</b>	<b>228</b>

<b>Do not process wound cultures</b>	<b>3</b>
<b>Gram negative bacillus</b>	<b>2</b>
<i>Haemophilus influenzae</i> Remel RapID NH	1
<i>Haemophilus</i> species bioMerieux Vitek API NH	1
<b>Non-fermenting gram negative bacillus</b> bioMerieux Vitek GNI +	<b>1</b>
<b>Additional organisms reported in Specimen 3:</b>	
<i>Propionibacterium acnes</i>	1
<i>Streptococcus</i> , group C	1

## ***Specimen No. 4 – Sputum (Pathogens Only) and Antibiotic Susceptibility***

The pathogenic organism included in this simulated sputum specimen was *Haemophilus influenzae*. All referee laboratories and 98% of participating laboratories that process sputum specimens successfully isolated and identified this organism.

Antimicrobial susceptibility testing was indicated using chloramphenicol and tetracycline. This isolate was reported as resistant to both antibiotics by all referee laboratories that tested these antibiotics. Of the participating laboratories that tested these antibiotics, 93% reported chloramphenicol as resistant and 96% reported tetracycline as resistant.

CLSI guidelines for disk diffusion testing of *Haemophilus* sp. specify the following conditions:

- Use of *Haemophilus* Test Medium
- Inoculation with a direct colony suspension equivalent to a 0.5 McFarland
- Incubation conditions: 35°C (± 2°) in 5% CO<sub>2</sub> for 16-18 hours

Surprisingly, 22 laboratories reported an incubation time of between 20-24 hours. In addition, 10 laboratories are utilizing CLSI guidelines dated 2003 and earlier. It is extremely important that clinical laboratories have a recent version of the CLSI guidelines for susceptibility testing available for reference. Each year, important revisions are made to these documents and it is imperative that laboratories are familiar with the most recent information.

Clinical and Laboratory Standards Institute/NCCLS, 2005. Performance Standards for Antimicrobial Susceptibility Testing; Fifteenth Informational Supplement, M100-S15. Clinical and Laboratory Standards Institute, Wayne, PA.

### **Methods of identification used by laboratories reporting:**

#### ***Haemophilus influenzae***

Remel RapID NH	58
Conventional biochemicals	54
bioMerieux Vitek NHI	31
bioMerieux Vitek API NH	24
Dade Behring MicroScan HNID	24
BD BBL <i>Haemophilus</i> ID Quad	18
BD BBL Crystal <i>Neisseria</i> / <i>Haemophilus</i>	2
Dade Behring MicroScan Gram Neg ID	2
Remel RapID NF Plus	2
Two systems	2
Remel RapID ANA II	1
bioMerieux Vitek GPI	1
Remel <i>Haemophilus</i> ID Quad	1
Remel <i>Haemophilus</i> Triplate	1
<b>TOTAL</b>	<b>221</b>

**Do not process sputum specimens 10**

<b><i>Haemophilus influenzae</i> type b</b>	
Two or more methods	1
<b><i>Haemophilus</i> species</b>	
Test method not indicated	1
<b>No pathogens isolated</b>	1
<b><i>Pasteurella multocida</i></b>	
bioMerieux Vitek GNI +	1
<b><i>Streptococcus</i> species</b>	
Murex Streptex	1
<b>Additional organism reported in Specimen 4:</b>	
<i>Fusobacterium necrophorum</i>	1

**Results of Antimicrobial Susceptibility Testing – *H. influenzae* with Chloramphenicol**

<b>Result</b>	<b>Method</b>	<b>MIC - µg/ml</b>	<b>Zone - mm</b>		
<b>Resistant (89)</b>	AB Biodisk E-test (4)	8 (1)			
		16 (1)			
		24 (1)			
		32 (1)			
	Sensititre (1)	16 (1)			
	PML Fastidious Panel (1)	≥4 (1)			
	TREK (2)	4 (1)			
		16 (1)			
	Disk diffusion (81)				8 (1)
					9 (2)
					11 (2)
					12 (2)
					13 (3)
					14 (3)
					15 (4)
					16 (8)
					17 (4)
					18 (7)
					19 (5)
					20 (8)
			21 (8)		
			22 (8)		
	23 (6)				
	Not indicated (2)				
<b>Intermediate (3)</b>	Agar Dilution (1)	4 (1)			
	Disk diffusion (2)		26 (1)		
			27 (1)		
<b>Susceptible (4)</b>	Disk diffusion (4)		20 (1)		
			26 (1)		
			30 (1)		
			36 (1)		
<b>Chloramphenicol not tested (130)</b>					
<b>Sputum cultures not performed (10)</b>					

Number of laboratories reporting each result indicated in ( )

**Results of Antimicrobial Susceptibility Testing – *H. influenzae* with Tetracycline**

<b>Result</b>	<b>Method</b>	<b>MIC (µg/ml)</b>	<b>Zone (mm)</b>		
<b>Resistant (93)</b>	Frozen panels (1)	8 (1)			
	Agar dilution (1)	>4 (1)			
	Sensititre (1)	>8 (1)			
	PMC Microtiter/Fastidious Panel (2)	≥8 (2)			
	AB Biodisk E-test (3)	8 (1)			
		32 (1)			
	TREK (2)	>4 (1)			
		>8 (1)			
	Disk diffusion (84)				10 (1)
					12 (1)
					13 (2)
					15 (2)
					16 (3)
					17 (4)
			18 (14)		
			19 (10)		
			20 (11)		
			21 (14)		
			22 (9)		
			23(4)		
24 (5)					
25 (2)					
26 (1)					
Not indicated (1)					
<b>Intermediate (1)</b>	AB Biodisk E-test (1)	6 (1)			
<b>Susceptible (3)</b>	Disk diffusion (3)		27 (1)		
			31 (2)		
<b>Tetracycline not tested (129)</b>					
<b>Sputum cultures not performed (10)</b>					

Number of laboratories reporting each result indicated in ( )

Antibiotic Susceptibility Results - Participating & Referee Labs <i>Haemophilus influenzae</i>				
	Chloramphenicol		Tetracycline	
	Referee <sup>a</sup>	Participant <sup>b</sup>	Referee <sup>a</sup>	Participant <sup>b</sup>
Susceptible	0	4	0	3
Intermediate	0	3	0	1
Resistant	7	82	7	86
Not Tested <sup>c</sup>	0	22	0	21
Do not process source <sup>d</sup>	0	10	0	10
No result reported	0	0	0	0
Not performed on organism <sup>e</sup>	3	94	3	94
Not performed on source <sup>f</sup>	0	11	0	11
No susceptibility testing done <sup>g</sup>	0	0	0	0

<sup>a</sup>Referee Laboratories (10 labs total)

<sup>b</sup>Other Participating Laboratories (236 labs total)

<sup>c</sup>Antibiotic not tested / reported for this organism

<sup>d</sup>Do not process specimen source

<sup>e</sup>Do not perform antimicrobial susceptibility testing on this organism

<sup>f</sup>Do not perform susceptibility testing on specimen source

<sup>g</sup>No antimicrobial susceptibility testing performed

## ***Specimen No. 5 – Blood (All Organisms)***

This simulated blood culture contained *Corynebacterium jeikeium*. All referee laboratories correctly identified this organism. Of the participating laboratories that process blood cultures, 74% identified *C. jeikeium* while an additional 17% reported ‘*Corynebacterium* species’.

*Corynebacterium jeikeium* is a well-documented pathogen most often associated with nosocomial sepsis. This organism colonizes the skin of hospitalized patients and infection often results from medical procedures involving breaches in the skin. Factors that predispose patients to infection include neutropenia, prolonged hospitalization, treatment with broad-spectrum antibiotics and insertion of medical devices such as intravenous catheters. Although infections have most commonly occurred in neutropenic patients, there have been reports of infections in both immunocompetent patients as well as outpatients. *C. jeikeium* is often resistant to multiple antibiotics and therapy is usually with vancomycin. However, recent studies show that newer antibiotics such as linezolid, daptomycin, quinupristin-dalfopristin and teicoplanin are also effective against this organism.

Brown, A.E. Other Corynebacteria and *Rhodococcus*. 2000. pp. 2198 – 2208. In G.L. Mandell, J.E. Bennett and R. Dolin (eds.) Mandell, Douglas, and Bennett’s Principles and Practice of Infectious Diseases. Churchill Livingstone, Philadelphia.

Coyle, M.B. 1990. Coryneform bacteria in infectious diseases: clinical and laboratory aspects. *Clinical Microbiology Reviews*. 3(3):227-246.

Goldstein, E. et al. 2003. In vitro activities of daptomycin, vancomycin, quinupristin-dalfopristin, linezolid, and five other antimicrobials against 307 gram-positive anaerobic and 31 *Corynebacterium* clinical isolates. *Antimicrobial Agents and Chemotherapy*. 47(1):337-341.

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### **Methods of identification used by participating laboratories reporting:**

#### ***Corynebacterium jeikeium***

bioMerieux Vitek API CORYNE	75
Conventional biochemicals	46
Remel RapID CB Plus	27
bioMerieux Vitek ANI	7
Remel RapID ANA II	4
Two systems	2
bioMerieux Vitek GPI	2
BD BBL Crystal Rapid Gram Positive	1
BD BBL Crystal Gram Positive	1
16s rDNA sequencing	1
bioMerieux Vitek API Staph	1
<b>TOTAL</b>	<b>167</b>

<b><i>Corynebacterium</i> species</b>	
Conventional biochemicals	30
Test method not indicated	3
Two systems	1
Remel RapID CB Plus	1
Gram stain	1
bioMerieux Vitek ANI	1
bioMerieux Vitek API CORYNE	1
Dade Behring MicroScan Gram Pos ID	1
<b>TOTAL</b>	<b>39</b>
<b>Do not process blood cultures</b>	<b>9</b>
<b>Diphtheroids</b>	
Conventional biochemicals	3
<b>Gram positive bacillus</b>	<b>3</b>
<b><i>Corynebacterium</i> species, not <i>diphtheriae</i></b>	
Conventional biochemicals	2
<b><i>Corynebacterium afermentans ssp. lipophilum</i></b>	
bioMerieux Vitek API CORYNE	1
<b><i>Corynebacterium bovis</i></b>	
MIDI Sherlock Microbial ID System	1
<b><i>Corynebacterium</i> species not <i>jeikeium</i> or <i>xerosis</i></b>	
bioMerieux Vitek GPI	1
<b><i>Corynebacterium</i> species resembling JK</b>	
Conventional biochemicals	1
<b><i>Corynebacterium</i> species, presumptive JK</b>	
Conventional biochemicals	1
<b><i>Corynebacterium</i>, presumptive JK group</b>	
Conventional biochemicals	1
<b>Coryneform gram positive bacilli</b>	<b>1</b>
<b>Gram positive bacillus - not <i>Listeria</i> and not <i>C. jeikeium</i></b>	
Conventional biochemicals	1
<b><i>Kocuria rosea</i></b>	
bioMerieux Vitek GPI	1
<b><i>Micrococcus</i> species</b>	
Conventional biochemicals	1

**Possible *Corynebacterium jeikeium***

Conventional biochemicals

**1**

***Staphylococcus aureus***

BD BBL Staphyloslide

**1**

***Streptococcus constellatus***

Remel RapID ANA II

**1**

## ***Educational Specimen – Blood (All Organisms)***

This simulated blood culture contained *Mycobacterium brisbanense*. The inclusion of this organism as an educational sample was a collaborative effort with the Wadsworth Center Mycobacteriology Laboratory and represents the actual clinical situation described below. This organism was sent as an educational specimen to highlight the fact that bacteriology laboratories need to be aware that non-tuberculous mycobacteria (NTM) are increasing in frequency and are often times found in routine bacterial cultures. Without proper recognition and testing, organisms such as this may be misidentified and/or dismissed as non-pathogens or contaminants.

This blood culture isolate was recovered from a 69 year-old male who underwent heart surgery to remove/replace a previously transplanted bovine aortic valve. This organism was also cultured from the removed valve. The primary laboratory reported an initial blood culture as positive for diptheroids and no further work up was performed. Once the patient was sent to a tertiary care facility, this facility forwarded the isolates from the blood culture and the valve to the Wadsworth Center's Clinical Mycobacteriology Laboratory. The Wadsworth Center initially identified the isolate as *Mycobacterium spp.* mostly closely resembling *M. wolinski* and *M. fortuitum* based on DNA sequence information. Subsequently, Brown et. al. from the CDC Meningitis and Special Pathogens Branch published a report concerning the identification and re-classification of a species named *M. brisbanense* whose published sequence matched the results from the isolates above.<sup>1</sup> The isolates were forwarded to the CDC and their DNA sequence analysis on both isolates showed 99.7% homology establishing them as *Mycobacterium brisbanense*.

Blood stream infections are one of the most serious problems in infectious disease. It has been estimated that 200,000 to 300,000 cases of bacteremia occur annually, with mortality rates reported from 20% to 50%. Therefore, the timely detection and identification of positive blood cultures are among the most important functions of the microbiology laboratory.<sup>2</sup> This is especially true with the emergence of non-tuberculous mycobacteria as a significant source of bacteremia in both immunocompromised and immunocompetent patients. However, when these organisms are isolated from a blood sample, the clinical significance of each isolate needs to be addressed, since NTM are ubiquitous in the environment and may represent a contaminant. NTM are not considered to be a threat to public health, as is *Mycobacterium tuberculosis*, and person-to-person transmission is rare, yet laboratories need to be aware that these organisms may cause serious morbidity and mortality.

Twenty-five years ago, the *Mycobacterium* genus was comprised of 30 species. At present, it encompasses more than 110 species. In the past, the identification of the NTM was feasible using an algorithm of culture growth characteristics, including colony morphology and color, in conjunction with a panel of biochemicals. However, the recent plethora of newly described species isolated from an increasing number of sources poses a challenge for the clinical microbiology laboratory to provide accurate and timely services since the conventional tests are time-consuming, require special expertise, and often do not lead to a definitive identification of the organism in question. As a result, laboratories will either send acid-fast bacilli to a reference laboratory for identification or use probe technology to identify the more common NTM (such as *M. avium*). Some have implemented DNA sequencing technology.

With the knowledge that this organism was isolated from a blood culture, it should have been plated on blood, chocolate and MacConkey agar. After 2 to 3 days, the blood and chocolate agar should have demonstrated small white to beige mucoid colonies when grown at 35°C; the MacConkey agar should have shown no growth. After prolonged incubation, the colonies remain mucoid; they do not develop aerial hyphae. On Gram stain, these organisms are long, sometimes filamentous, gram-positive rods. They do not demonstrate branching and may be pleomorphic. The rods are about 2 to 3 times the size of typical *Corynebacterium spp.* and do not appear coryneform or diphtheroid (i.e. no pointed or elongated ends). Based on these gram-stain and colony characteristics, one should suspect *Nocardia spp.* or a *Mycobacterium spp.* and a modified or full acid-fast stain should be performed. This organism is acid-fast positive. At this time, biochemicals and/or DNA sequencing should be set-up to identify a mycobacterial species. If the laboratory is not equipped to this, it should be reported as acid-fast bacilli and sent to a reference laboratory for full identification.

Given the recent focus on the importance of NTM, we recommend that laboratories who do not perform mycobacterial identification implement the following protocol: in wound and blood cultures where the predominant organism is a gram-positive rod that appears elongated or branching, modified acid fast stains be performed along with an arylsulfatase test. An arylsulfatase test is a good screen to detect rapidly-growing NTM; rapidly-growing mycobacterial species will be positive in 3 days where as other organisms will be negative.<sup>3</sup>

A great deal of variety was seen in the answers submitted for this organism's identification raising some points for concern. Many of the erroneous identifications resulted from an incorrect Gram stain result. It is essential to keep laboratory staff proficient at reading stains, especially those technicians that read stains on limited occasions. Gram stains are a key starting point on the path toward an organism identification and misinterpretation of the stain will ultimately result in an incorrect identification. In the case of automated identification systems, the use of an inappropriate system based on an incorrectly read gram stain will result in an erroneous identification. Also, colony morphology is a key clue. Some of the identifications reported were organisms that are pink or yellow/orange in color and some were for organisms that produce hyphae. This *Mycobacterium* species possesses none of these characteristics. Ultimately, it is good quality laboratory practice to confirm any unusual results to the extent possible and determine if the identification corresponds with the clinical picture of the patient.

References:

<sup>1</sup>Schinsky, M.F. et al. 2004. Taxonomic variation in the *Mycobacterium fortuitum* third biovariant complex: description of *Mycobacterium boenickei* sp. nov., *Mycobacterium houstonense* sp. nov., *Mycobacterium neworleansense* sp. nov. and *Mycobacterium brisbanense* sp. nov. and recognition of *Mycobacterium porcinum* from human clinical isolates. International Journal of Systematic & Evolutionary Microbiology 54(pt. 5):1653-1667.

<sup>2</sup>Magadia, R.R. and Weinstein, M.P. 2001. Laboratory diagnosis of bacteremia and fungemia. Infectious Disease Clinics of North America. 15:1009-1024.

<sup>3</sup>Vincent V, Brown-Elloit B, Jost, K Jr., and Wallace, R, Jr. *Mycobacterium: Phenotypic and Genotypic Identification*. In: Murray PR, Baron E, Jorgensen J, Pfaller M, and Tenover FC (eds). *Manual of Clinical Microbiology*, 8<sup>th</sup> ed. Washington, DC: ASM Press, 2003:560-584.

**Laboratory responses for educational specimen:**

***Rhodococcus* species**

bioMerieux Vitek API CORYNE	16
Conventional biochemicals	7
bioMerieux Vitek API NH	1
Two systems	1
<b>TOTAL</b>	<b>25</b>

**No report** 21

**Gram positive bacillus** 17

***Rhodococcus equi***

Remel RapID CB Plus	6
bioMerieux Vitek API CORYNE	4
Conventional biochemicals	3
Two systems	1
Remel RapID ANA II	1
<b>TOTAL</b>	<b>15</b>

***Nocardia* species**

Conventional biochemicals	10
Two systems	1
Not given	1
bioMerieux Vitek API CORYNE	1
<b>TOTAL</b>	<b>13</b>

**Acid fast bacillus / Acid fast gram positive bacillus /  
Acid fast organism / Presumptive acid fast bacilli** 12

**Aerobic Actinomycete / Aerobic Actinomycetes species /  
Possible aerobic Actinomycetes / Presumptive  
Actinomycetes / Actinomycete group**

Conventional biochemicals	7
Test method not indicated	5
<b>TOTAL</b>	<b>12</b>

***Tsukamurella* species**

Conventional biochemicals	8
Remel RapID CB Plus	1
<b>TOTAL</b>	<b>9</b>

**Do not process blood cultures** 9

**Rapid growing *Mycobacterium* species**

Conventional biochemicals	7
16S rDNA sequencing	1
<b>TOTAL</b>	<b>8</b>

<b><i>Capnocytophaga</i> species</b>	
Remel RapID ANA II	3
bioMerieux Vitek ANI	2
Conventional biochemicals	1
<b>TOTAL</b>	<b>6</b>
<b><i>Mycobacterium</i> species</b>	
Conventional biochemicals	6
<b>Rapid growing acid fast bacilli / organism</b>	
<b>5</b>	
<b><i>Brevibacterium</i> species</b>	
Remel RapID CB Plus	2
Not given	1
bioMerieux Vitek API CORYNE	1
<b>TOTAL</b>	<b>4</b>
<b><i>Actinomyces</i> species</b>	
Conventional biochemicals	2
bioMerieux Vitek ANI	1
<b>TOTAL</b>	<b>3</b>
<b><i>Bacillus</i> species</b>	
Conventional biochemicals	3
<b><i>Gordonia</i> species</b>	
bioMerieux Vitek API CORYNE	1
Conventional biochemicals	1
Two or more systems	1
<b>TOTAL</b>	<b>3</b>
<b>Gram negative bacillus</b>	
<b>3</b>	
<b>Gram variable rod</b>	
<b>3</b>	
<b><i>Mycobacterium fortuitum</i></b>	
Conventional biochemicals	2
MIDI Sherlock Microbial ID System	1
<b>TOTAL</b>	<b>3</b>
<b><i>Arthrobacter</i> species</b>	
Conventional biochemicals	1
bioMerieux Vitek API CORYNE	1
<b>TOTAL</b>	<b>2</b>
<b><i>Corynebacterium auris</i></b>	
Remel RapID CB Plus	2

<b>Coryneform aerobic gram positive bacillus / Coryneform gram positive rod</b>	
Two or more test methods	2
<b><i>Mycobacterium fortuitum</i> complex</b>	
Conventional biochemicals	1
HPLC	1
<b>TOTAL</b>	<b>2</b>
<b>Partial acid fast bacilli</b>	<b>2</b>
<b><i>Turicella otitidis</i></b>	
Conventional biochemicals	1
Dade Behring MicroScan Gram Pos ID	1
<b>TOTAL</b>	<b>2</b>
<b>Acid fast bacillus, possible <i>Tsukamurella</i> sp</b>	<b>1</b>
<b>Acid fast gram positive pleomorphic bacilli</b>	
bioMerieux Vitek API CORYNE	1
<b><i>Actinomyces</i></b>	<b>1</b>
<b><i>Actinomyces odontolyticus</i></b>	
Remel RapID NH	1
<b><i>Actinomyces viscosus</i></b>	
Conventional biochemicals	1
<b>Aerobic <i>Actinomyces</i> group</b>	
Conventional biochemicals	1
<b><i>Amycolatopsis (Nocardia) orientalis</i></b>	
Two systems	1
<b><i>Arthrobacter cummingsii</i></b>	
Test method not indicated	1
<b><i>Bacillus</i> species, unable to rule out <i>anthracis</i></b>	
Conventional biochemicals	1
<b><i>Burkholderia cepacia</i> complex</b>	
bioMerieux Vitek GNI +	1
<b><i>Capnocytophaga sputigena</i></b>	
Conventional biochemicals	1
<b><i>Cardiobacterium hominis</i></b>	
bioMerieux Vitek NHI	1

<i>Corynebacterium jeikeium</i>	
Remel RapID CB Plus	1
<i>Corynebacterium</i> species	
Conventional biochemicals	1
<i>Corynebacterium</i> species, not <i>diphtheriae</i>	
bioMerieux Vitek API CORYNE	1
<i>Dermabacter hominis</i>	
Conventional biochemicals	1
<b>Filamentous gram variable rods</b>	
bioMerieux Vitek API 20 Strep	1
<b>Gram positive branching bacilli</b>	1
<b>Gram positive Corynebacteria-like organism</b>	1
<b>Gram positive nonsporeforming bacilli</b>	1
<b>Gram variable bacillus</b>	1
<i>Kurthia bessonii</i>	
Conventional biochemicals	1
<i>Legionella</i> species	
Conventional biochemicals	1
<b>Modified acid fast bacilli</b>	1
<i>Mycobacterium abscessus</i>	
Conventional biochemicals	1
<i>Mycobacterium brisbanense</i>	
16s rDNA sequencing	1
<i>Mycobacterium fortuitum</i> group	
HPLC	1
<i>Mycobacterium fortuitum</i> group; genotype <i>M. brisbanense</i>	
16S rDNA sequencing	1
<i>Mycobacterium fortuitum</i> species group	
HPLC	1
<i>Mycobacterium fortuitum/chelonae</i> complex	
Conventional biochemicals	1

<b><i>Mycobacterium mucogenicum</i></b>	
Conventional biochemicals	1
<b><i>Mycobacterium</i> sp not tuberculosis - rapid growing</b>	
Conventional biochemicals	1
<b><i>Mycobacterium</i> species chelonae/abseous group</b>	
Conventional biochemicals	1
<b><i>Mycobacterium</i> species, fast grower (possible <i>M. septicum</i>)</b>	
Conventional biochemicals	1
<b>No growth</b>	1
<b><i>Nocardia asteroides</i> complex</b>	
Conventional biochemicals	1
<b>Pleomorphic gram + branching rods</b>	1
<b>Presumptive <i>Streptobacillus moniliformis</i></b>	
bioMerieux Vitek API 20E	1
<b><i>Pseudomonas stutzeri</i></b>	
BD BBL Crystal Enteric/Nonfermenter	1
<b>Rapid growing AFB or Actinomycete</b>	
bioMerieux Vitek NHI	1
<b>Resembles Actinomycetes sp.</b>	
Conventional biochemicals	1
<b><i>Rhodococcus/Gordonia</i> species</b>	
bioMerieux Vitek API CORYNE	1
<b><i>Streptococcus constellatus</i></b>	
Remel RapID ANA II	1
<b>Unable to identify</b>	1

## ***Chlamydia – cervical swab for direct testing***

This simulated cervical swab was provided to laboratories that test for *Chlamydia* using direct detection methods. However, this sample contains non-viable organisms and is not suitable for laboratories performing *Chlamydia* culture.

This sample was positive for *Chlamydia* and was reported as such by 98% of the participating laboratories that tested this specimen.

### **Test kits used by laboratories reporting this specimen as:**

#### **Positive for *Chlamydia trachomatis***

Gen-Probe PACE 2 CT OR CT/GC	57
BD ProbeTec <i>C. trachomatis</i> assay	12
Roche Diagnostics COBAS Amplicor CT/NG	11
Gen-Probe Aptima Combo 2	9
bioMerieux Vitek VIDAS	6
Abbott LCx <i>C. trachomatis</i> assay	5
Roche Diagnostics Amplicor CT/NG	4
Beckman Coulter Access Chlamydia EIA	3
Digene Hybrid Capture hc2 CT/NG	1
BioRad Chlamydia Microplate EIA	1
Wampole MicroTrak <i>Chlamydia</i>	1
Thermo Biostar Chlamydia OIA	1
Real-time PCR	1
Two or more test methods	1
<b>TOTAL</b>	<b>113</b>

#### **Positive for *C. trachomatis*/ *N. gonorrhoeae***

Gen-Probe PACE 2 CT OR CT/GC	1
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#### **Negative for *Chlamydia trachomatis***

bioMerieux Vitek VIDAS	1
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<b>No report</b>	<b>1</b>
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## ***Direct Antigen Detection***

All participating laboratories which perform direct antigen testing received either a simulated throat swab to be tested for Group A *Streptococcus* or a genital swab to be tested for Group B *Streptococcus*. Information provided in the Bacteriology Questionnaire was used to determine which type of specimen to send to each laboratory.

### **Specimen A - Source: Throat for Group A *Streptococcus***

This specimen was positive for Group A *Streptococcus*. All of the participating laboratories that processed this specimen reported it as positive.

#### **Test kits used by laboratories reporting Specimen A as:**

##### **Positive for Group A *Streptococcus*:**

Thermo BioStar Acceava Strep A	14
BD Q Test Strep	14
Abbott Signify Strep A	11
Quidel QuickVue + Strep A	8
Fisher Healthcare Sure-Vue Strep A	6
Genzyme OSOM Ultra Strep A	6
Thermo BioStar Strep A OIA Max	5
BD Link 2 Strep A	4
Quidel QuickVue Inline Strep A	3
Test method not indicated	3
BD Directigen Grp A Strep	2
Cardinal Health SP Brand Rapid Strep A	2
LifeSign Status Accustrep A	2
Meridian Diagnostics ImmunoCard Stat Strep A	2
Remel PathoDx Strep A	2
Applied Biotech SureStep Strep A	1
BD Directigen EZ Strep	1
Gen-Probe Group A Strep	1
Polymedco Poly Stat Strep A	1
Remel RIM A.R.C. Strep A	1
<b>TOTAL</b>	<b>89</b>

**Specimen C – Source: Genital for Group B *Streptococcus***

This specimen was positive for Group B *Streptococcus*. All laboratories that tested this sample reported it as positive.

**Test kits used by laboratories reporting Specimen C as:**

**Positive for Group B *Streptococcus***

BioStar Strep B OIA

**5**

**BACTERIAL IDENTIFICATION BY PARTICIPATING LABORATORIES**

	<u>Number Reported</u>	<u>%</u>
<b>SPECIMEN NUMBER 1</b>		
<i>Salmonella</i> serogroup B	135	57.2
<i>Salmonella</i> species	56	23.7
Do not process stool cultures	11	4.7
<i>Salmonella</i> species, not <i>typhi</i>	8	3.4
<i>Salmonella</i> serogroup D	6	2.5
No enteric pathogens isolated	5	2.1
<i>Salmonella</i> species Group D, not <i>typhi</i>	4	1.7
<i>Salmonella enteritidis</i> group B	3	1.3
<i>Escherichia coli</i>	2	0.8
<i>Salmonella</i> serotype Typhimurium	2	0.8
<i>Salmonella</i> Group	1	0.4
<i>Salmonella</i> serogroup C	1	0.4
<i>Salmonella</i> species; A-I-Pos; Vi-Neg	1	0.4
<i>Salmonella</i> species, not group D	1	0.4
*****		

<b>SPECIMEN NUMBER 2</b>		
Beta-hemolytic <i>Streptococcus</i> , group C	206	87.3
Beta-hemolytic <i>Streptococcus</i> not A or B	10	4.2
<i>Streptococcus dysgalactiae</i>	4	1.7
Do not process abscess specimens	4	1.7
Beta-hemolytic <i>Streptococcus</i> not group A, B, D	3	1.3
<i>Streptococcus constellatus</i>	2	0.8
Beta-hemolytic <i>Streptococcus</i> , group B	2	0.8
Beta-hemolytic <i>Streptococcus</i> not group A	2	0.8
<i>Streptococcus dysgalactiae</i> ssp. <i>equisimilis</i>	1	0.4
Beta-hemolytic <i>Streptococcus</i> Group C/Group G	1	0.4
Beta-hemolytic <i>Streptococcus</i> group A	1	0.4
*****		

<b>SPECIMEN NUMBER 3</b>		
<i>Fusobacterium necrophorum</i>	118	50.0
No anaerobic organisms isolated	80	33.9
<i>Fusobacterium</i> species	13	5.5
Do not culture for anaerobes	7	3.0
<i>Fusobacterium varium</i>	5	2.1
Anaerobic gram negative bacilli	3	1.3
Do not process wound cultures	3	1.3
<i>Fusobacterium nucleatum</i>	3	1.3
No <i>Bifidobacterium</i> isolated	2	0.8
<i>Propionibacterium acnes</i>	1	0.4
<i>Veillonella</i> species	1	0.4
 <i>Pasteurella multocida</i>	 228	 96.6
Do not process wound cultures	3	1.3

Gram negative bacillus	2	0.8
<i>Haemophilus influenzae</i>	1	0.4
<i>Haemophilus</i> species	1	0.4
Non-fermenting gram negative bacillus	1	0.4

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#### **SPECIMEN NUMBER 4**

<i>Haemophilus influenzae</i>	221	93.6
Do not process sputum specimens	10	4.2
<i>Haemophilus influenzae</i> type b	1	0.4
<i>Haemophilus</i> species	1	0.4
No pathogens isolated	1	0.4
<i>Pasteurella multocida</i>	1	0.4
<i>Streptococcus</i> species	1	0.4

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#### **SPECIMEN NUMBER 5**

<i>Corynebacterium jeikeium</i>	167	70.7
<i>Corynebacterium</i> species	39	16.5
Do not process blood cultures	9	3.8
Diphtheroids	3	1.3
Gram positive bacillus	3	1.3
<i>Corynebacterium</i> species, not <i>diphtheriae</i>	2	0.8
<i>Corynebacterium afermentans</i> ssp. <i>lipophilum</i>	1	0.4
<i>Corynebacterium bovis</i>	1	0.4
<i>Corynebacterium</i> species not <i>jeikeium</i> or <i>xerosis</i>	1	0.4
<i>Corynebacterium</i> species resembling JK	1	0.4
<i>Corynebacterium</i> species, presumptive JK	1	0.4
<i>Corynebacterium</i> , presumptive JK group	1	0.4
Coryneform gram positive bacilli	1	0.4
Gram positive bacillus - not <i>Listeria</i> and not <i>C. jeikeium</i>	1	0.4
<i>Kocuria rosea</i>	1	0.4
<i>Micrococcus</i> species	1	0.4
Possible <i>Corynebacterium jeikeium</i>	1	0.4
<i>Staphylococcus aureus</i>	1	0.4
<i>Streptococcus constellatus</i>	1	0.4

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#### **EDUCATIONAL SPECIMEN**

<i>Rhodococcus</i> species	25	10.6
No report	21	8.9
Gram positive bacillus	17	7.2
<i>Rhodococcus equi</i>	15	6.4
<i>Nocardia</i> species	13	5.5
Acid fast bacillus/Acid fast gram positive bacillus/Acid fast organism/Presumptive acid fast bacilli	12	5.1
Aerobic Actinomycete/Aerobic Actinomycetes sp./Possible aerobic Actinomycetes/Presumptive Actinomycetes/Actinomycete group	12	5.1
<i>Tsukamurella</i> species	9	3.8

Do not process blood cultures	9	3.8
Rapid growing <i>Mycobacterium</i> species	8	3.4
<i>Capnocytophaga</i> species	6	2.5
<i>Mycobacterium</i> species	6	2.5
Rapid growing acid fast bacilli / organism	5	2.1
<i>Brevibacterium</i> species	4	1.7
<i>Actinomyces</i> species	3	1.3
<i>Bacillus</i> species	3	1.3
<i>Gordonia</i> species	3	1.3
Gram negative bacillus	3	1.3
Gram variable rod	3	1.3
<i>Mycobacterium fortuitum</i>	3	1.3
<i>Arthrobacter</i> species	2	0.8
<i>Corynebacterium auris</i>	2	0.8
Coryneform aerobic gram positive bacillus/Coryneform gram pos rod	2	0.8
<i>Mycobacterium fortuitum</i> complex	2	0.8
Partial acid fast bacilli	2	0.8
<i>Turicella otitidis</i>	2	0.8
Acid fast bacillus, possible <i>Tsukamurella</i> sp	1	0.4
Acid fast gram positive pleomorphic bacilli	1	0.4
<i>Actinomyces</i>	1	0.4
<i>Actinomyces odontolyticus</i>	1	0.4
<i>Actinomyces viscosus</i>	1	0.4
Aerobic <i>Actinomyces</i> group	1	0.4
<i>Amycolatopsis (Nocardia) orientalis</i>	1	0.4
<i>Arthrobacter cumminsii</i>	1	0.4
<i>Bacillus</i> species, unable to rule out <i>anthracis</i>	1	0.4
<i>Burkholderia cepacia</i> complex	1	0.4
<i>Capnocytophaga sputigena</i>	1	0.4
<i>Cardiobacterium hominis</i>	1	0.4
<i>Corynebacterium jeikeium</i>	1	0.4
<i>Corynebacterium</i> species	1	0.4
<i>Corynebacterium</i> species, not <i>diphtheriae</i>	1	0.4
<i>Dermobacter hominis</i>	1	0.4
Filamentous gram variable rods	1	0.4
Gram positive branching bacilli	1	0.4
Gram positive Corynebacteria-like organism	1	0.4
Gram positive nonsporeforming bacilli	1	0.4
Gram variable bacillus	1	0.4
<i>Kurthia bessonii</i>	1	0.4
<i>Legionella</i> species	1	0.4
Modified acid fast bacilli	1	0.4
<i>Mycobacterium abscessus</i>	1	0.4
<i>Mycobacterium brisbanense</i>	1	0.4
<i>Mycobacterium fortuitum</i> group	1	0.4
<i>Mycobacterium fortuitum</i> group; genotype <i>M. brisbanense</i>	1	0.4
<i>Mycobacterium fortuitum</i> species group	1	0.4
<i>Mycobacterium fortuitum/chelonae</i> complex	1	0.4
<i>Mycobacterium mucogenicum</i>	1	0.4

<i>Mycobacterium</i> sp not <i>tuberculosis</i> - rapid growing	1	0.4
<i>Mycobacterium</i> species <i>chelonae/absceus</i> group	1	0.4
<i>Mycobacterium</i> species, fast grower (possible <i>M. septicum</i> )	1	0.4
No growth	1	0.4
<i>Nocardia asteroides</i> complex	1	0.4
Pleomorphic gram + branching rods	1	0.4
Presumptive <i>Streptobacillus moniliformis</i>	1	0.4
<i>Pseudomonas stutzeri</i>	1	0.4
Rapid growing AFB or Actinomycete	1	0.4
Resembles Actinomycetes sp.	1	0.4
<i>Rhodococcus/Gordonia</i> species	1	0.4
<i>Streptococcus constellatus</i>	1	0.4
Unable to identify	1	0.4

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**CHLAMYDIA SPECIMEN**

Positive for <i>Chlamydia trachomatis</i>	113	97.4
Positive for <i>C. trachomatis/ N. gonorrhoeae</i>	1	0.9
Negative for <i>Chlamydia trachomatis</i>	1	0.9
No report	1	0.9

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**DIRECT ANTIGEN SPECIMEN**

A. Positive for Group A <i>Streptococcus</i>	89	100.0
C. Positive for Group B <i>Streptococcus</i>	5	100.0