Mycobacterium chelonae-abscessus Complex Associated with Sinopulmonary Disease, Northeastern USA

Technical Appendix

Technical Appendix Table 1. Study isolates and sequevar group for the 16S rRNA, rpoB, sodA, hsp65 genes and ITS region of the

Mycobacterium chelonae-abscessus complex *

Isolate no.	16S rRNA sequevar	rpoB sequavar	sodA sequevar	hsp65 sequevar	ITS sequevar group
	group	group	group	group	
M. abscessus isolates					
A001	ABS[A]	ABS[C]	ABS[A]	ABS[A]	ABS[C]
A003	ABS[A]	ABS[A]	ABS[A]	ABS[A]	ABS[C]
A004	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A005	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A006	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A007	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A010	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A011	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A014	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A015	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A017	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A020	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A021	ABS[B]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A023	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A024	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A029	ABS[A]	ABS[C]	ABS[A]	ABS[A]	ABS[C]
A030	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A032	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A033	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A034	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A035	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A036	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A039	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A041	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A042	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A043	ABS[A]	ABS[C]	ABS[A]	ABS[A]	ABS[C]
A044	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A046	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A047	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A048	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A049	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A050	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A051	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A052	ABS[A]	ABS[C] ABS[C]	ABS[B]	ABS[B]	ABS[D]
A053	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
A054	ABS[A]	ABS[B]	ABS[B]	ABS[B]	ABS[D] ABS[A]
A056 A057	ABS[A]	ABS[C]	ABS[B]	ABS[B] ABS[A]	ABS[D]
	ABS[A]	ABS[C]	ABS[A]		ABS[C]
A058	ABS[A]	ABS[C]	ABS[A]	ABS[A]	ABS[C]
A059	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A060	ABS[A]	ABS[C]	ABS[A]	ABS[A]	ABS[C]
A061	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A063	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[B]
A064	ABS[A]	ABS[C]	ABS[C]	ABS[B]	ABS[D]

4005	ADOIAI	ADOIOI	ADOIOI	A DOID!	A DOID!
A065	ABS[A]	ABS[C]	ABS[C]	ABS[B]	ABS[D]
A066	ABS[A]	ABS[C]	ABS[C]	ABS[B]	ABS[D]
A067	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
A068	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
A069	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A070	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
A071	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
A072	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
A073	ABS[A]	ABS[C]	ABS[D]	ABS[C]	ABS[D]
A074	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[A]
A075	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[A]
A076	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[A]
A077	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
A078	ABS[A]	ABS[D]	ABS[C]	ABS[B]	ABS[A]
A079	ABS[A]	ABS[C]	ABS[C]	ABS[B]	ABS[D]
A080	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
A081	ABS[B]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
A082	ABS[B]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
A083	ABS[B]	ABS[D]	ABS[C]	ABS[B]	ABS[D]
M. abscessus CIP 104536 ^T	ABS[A]	ABS[C]	ABS[B]	ABS[B]	ABS[D]
M. bolletii isolates					
M. bolletii CIP 108541 [™]	ABS[A]	BOL	BOL	BOL	ABS[D]
M. chelonae isolates					
C001	CHE[A]	CHE[G]	CHE[E]	CHE[C]	CHE[G]
C002	CHE[A]	CHE[A]	CHE[B]	CHE[A]	CHE[E]
C003	CHE[A]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C004	CHE[A]	CHE[B]	CHE[A]	CHE[A]	CHE[F]
C005	CHE[A]	CHE[E]	CHE[C]	CHE[A]	CHE[H]
C006	CHE[A]	CHE[A]	CHE[B]	CHE[A]	CHE[E]
C009	CHE[A]	CHE[G]	CHE[E]	CHE[C]	CHE[G]
C010	CHE[A]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C011	CHE[A]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C012	CHE[A]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C013	CHE[A]	CHE[F]	CHE[D]	CHE[A]	CHE[C]
C014	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C015	CHE[A]	CHE[G]	CHE[E]	CHE[C]	CHE[G]
C016	CHE[D]	CHE[H]	CHE[E]	CHE[C]	CHE[I]
C017	CHE[A]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C018	CHE[A]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C019	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C020	CHE[A]	CHE[E]	CHE[C]	CHE[B]	CHE[J]
C021	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C022	CHE[D]	CHE[I]	CHE[G]	CHE[C]	CHE[I]
C023	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C024	CHE[A]	CHE[A]	CHE[B]	CHE[A]	CHE[E]
C025	CHE[B]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C026	CHE[A]	CHE[H]	CHE[E]	CHE[D]	CHE[D]
C027	CHE[A]	CHE[E]	CHE[C]	CHE[A]	CHE[H]
C029	CHE[A]	CHE[G]	CHE[C]	CHE[E]	CHE[G]
C031	CHE[A]	CHE[A]	CHE[B]	CHE[A]	CHE[E]
C032	CHE[C]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C033	CHE[A]	CHE[G]	CHE[C]	CHE[E]	CHE[G]
C034	CHE[B]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C035	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C038	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C039	CHE[A]	CHE[A]	CHE[B]	CHE[A]	CHE[B]
C040	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C040	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C041 C042	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C042 C043	CHE[A]	CHE[A]	CHE[H]	CHE[A]	CHE[F]
C043	CHE[D]	CHE[I]		CHE[C]	CHE[I]
			CHE[G]		
C045	CHE[A]	CHE[E]	CHE[C]	CHE[A]	CHE[H]
C047	CHE[A]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C048	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C050	CHE[A]	CHE[D]	CHE[C]	CHE[E]	CHE[G]
C051	CHE[D]	CHE[I]	CHE[G]	CHE[C]	CHE[I]

C052	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C053	CHE[A]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C054	CHE[A]	CHE[A]	CHE[B]	CHE[A]	CHE[E]
C055	CHE[A]	CHE[E]	CHE[C]	CHE[A]	CHE[H]
C056	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C057	CHE[A]	CHE[A]	CHE[A]	CHE[A]	CHE[A]
C058	CHE[A]	CHE[C]	CHEIBI	CHE[A]	CHE[F]
C059	CHE[A]	CHE[A]	CHE[B]	CHE[A]	CHE[E]
C060	CHE[A]	CHE[G]	CHE[F]	CHE[E]	CHE[H]
C061	CHE[A]	CHE[E]	CHE[C]	CHE[A]	CHE[F]
C062	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[H]
C063	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
C064	CHE[A]	CHE[E]	CHE[C]	CHE[A]	CHE[H]
C065	CHE[A]	CHE[H]	CHE[I]	CHE[E]	CHE[K]
C066	CHE[A]	CHE[C]	CHE[B]	CHE[A]	CHE[F]
M. chelonae ATCC 35758 ^T	CHE[E]	CHE[J]	CHE[J]	CHE[F]	CHE[L]
M.immunogenum isolates	CHLL	CHE[J]	Cric[0]	CIIL[I]	CHELL
M. immunogenum CIP 106684 ^T	IMM	IMM	IMM	IMM	IMM
M. massiliense isolates	IIVIIVI	IIVIIVI	IIVIIVI	IIVIIVI	IIVIIVI
M001	MAS[B]	MAS[A]	ABS[A]	ABS[A]	ABS[C]
M002					ABS[C]
M003	MAS[B]	MAS[A]	ABS[A]	ABS[A]	
	ABS[A]	MAS[B]	ABS[A]	ABS[A]	ABS[C]
M004	ABS[A]	MAS[B]	ABS[A]	ABS[A]	ABS[C]
M005	MAS[B]	MAS[A]	ABS[A]	ABS[A]	ABS[C]
M. massiliense CCUG 48898 [™]	ABS[A]	MAS[C]	ABS[A]	ABS[A]	ABS[C]
Novel species	0115751	O) (TD)	O) (TD)	0) ([D]	0) (50)
CV002	CHE[E]	CV[B]	CV[B]	CV[B]	CV[B]
CV004	CHE[E]	CV [A]	CV [A]	CV [A]	CV [A]
CV005	CHE[E]	CV[B]	CV[B]	CV[B]	CV[B]
CV006	CHE[E]	CV [A]	CV [A]	CV [A]	CV [A]
CV007	CHE[E]	CV[B]	CV[B]	CV[B]	CV[B]
CV008	CHE[E]	CV[B]	CV[B]	CV[B]	CV[B]
CV010	CHE[E]	CV[B]	CV[B]	CV[B]	CV[B]
CV012	CHE[E]	CV[B]	CV[B]	CV[B]	CV[B]
CV013	CHE[E]	CV [A]	CV [A]	CV [A]	CV [A]
CV014	CHE[E]	CV [A]	CV [A]	CV [A]	CV [A]
CV015	CHE[E]	CV [A]	CV [A]	CV [A]	CV [A]
CV021	NA	CV[B]	NA	NA	NA
CV022	NA	CV[D]	NA	NA	NA
CV023	NA	CV[D]	NA	NA	NA
CV024	NA	CV [A]	NA	NA	NA
CV025	NA	CV[C]	NA	NA	NA
CV026	NA	CV[D]	NA	NA	NA
CV027	NA	CV [A]	NA	NA	N/
CV028	NA	CV[B]	NA	NA	NA
CV030	NA	CV[B]	NA	NA	NA
CV031	NA	CV[C]	NA	NA	NA
CV032	NA	CV[C]	NA	NA	NA
CV033	NA	CV[B]	NA	NA	NA
CV034	NA	CV[B]	NA	NA	NA
CV035	NA	CV[B]	NA	NA	NA
CV036	NA	CV[A]	NA	NA	NA
*ITS_internal transcribed spacer: CID					

^{*}ITS, internal transcribed spacer; CIP, Collection of Institut Pasteur; NA, not applicable.

Technical Appendix Table 2. Gene designations and corresponding GenBank accession numbers of study isolates and reference sequences from *Mycobacterium abscessus**

sequences from Mycobacterium abscessus*				
Gene name	Alignment	M. abscessus	M. abscessus	GenBank accession nos.
	gene length,	ORF designation	(NC_010397)	for study isolates
	bp		Protein ID#	
Translation initiation factor IF-3 (infC)	531	MAB_2321	YP_001703056	HQ661899- HQ661904
S-adenosyl-methyltransferase (<i>mraW</i>)	1014	MAB_1998	YP_001702734	HQ661905- HQ661910
Phosphatidate cytidylyltransferase (cdsA)	879	MAB_3186c	YP_001703917	HQ661911- HQ661916
Phosphoribosylaminoimidazole carboxylase (<i>purE</i>)	501	MAB_3619c	YP_001704347	HQ661917- HQ661922
Preprotein translocase subunit (secY)	1260	MAB_3784c	YP_001704513	HQ661923- HQ661928
(HSP-70 cofactor (grpE)	753	MAB_4272c	YP_001704999	HQ661929- HQ661934
Recombination protein (recR)	609	MAB_0320	YP_001701073	HQ661935-HQ661940
Ribonuclease P protein component (rnpA)	384	MAB_4954c	YP_001705676	HQ661941-HQ661946
Elongation factor Ts (tsf)	834	MAB_3195c	YP_001703926	HQ661947-HQ661952
Hypothetical protein Lactamase_B	1692	MAB_3083c	YP_001703815	HQ661953-HQ661958
50S ribosomal protein L7/L12 (rplL)	390	MAB_3876c	YP_001704604	HQ661959-HQ661964
50S ribosomal protein L13 (<i>rplM</i>)	444	MAB_3752c	YP_001704480	HQ661965-HQ661970
Co-chaperonin GroES (groES)	300	MAB_3732c	YP_001704460	HQ661971-HQ661976
30S ribosomal protein S1 (rpsA)	1446	MAB_2296	YP_001703031	HQ661977-HQ661982
Phosphoribosylformylglycinamidine synthase II (purL)	2286	MAB_0707	YP_001701457	HQ661983-HQ661988
Putative Mrp homolog protein	1137	MAB 1366c	YP 001702106	HQ661989-HQ661994
Putative metalloprotease	513	MAB 1669	YP 001702408	HQ661995-HQ662000
50S ribosomal protein L20 (<i>rplT</i>)	390	MAB 2323	YP 001703058	HQ662001-HQ662006
ABC transporter ATP-binding protein	720	MAB 2747c	YP 001703038	
Guanylate kinase	501	MAB 2823c	YP_001703460 YP_001703556	HQ662007–HQ662012 HQ662013–HQ662018
Elongation factor P (efP)	564		YP_001703536 YP_001703570	
Deoxyuridine 5'-triphosphate nucleotidohydrolase	453	MAB_2837c	YP_001703570	HQ662019-HQ662024
(dut)	455	MAB_3003c	1P_001703735	HQ662025-HQ662030
30s ribosomal protein S2 (rpsB)	849	MAB_3196c	YP 001703927	HQ662031-HQ662036
Aspartyl/glutamyl-tRNA amidotransferase, B	1482	MAB_3334c	YP 001704064	HQ662037-HQ662042
subunit (gatB)		_	_	
30s ribosomal protein S9 (rpsl)	534	MAB_3751c	YP 001704479	HQ662043-HQ662048
50S ribosomal protein L6 (rplF)	540	MAB 3797c	YP 001704526	HQ662049-HQ662054
Transcription antitermination protein NusG (nusG)	804	MAB_3894c	YP 001704622	HQ662055-HQ662060
Adenylosuccinate synthetase (purA)	1296	MAB 4249c	YP 001704976	HQ662061-HQ662066
Cell division protein FtsZ (ftsZ)	1164	MAB_2009	YP_001702745	HQ662067-HQ662072
Recombinase A (recA)	1041	MAB 3060c	YP 001703792	HQ662073-HQ662078
Tyrosyl-tRNA synthetase (tyrS)	1293	MAB 2354	YP 001703089	HQ662079-HQ662084
UDP-N-acetylglucosamine pyrophosphorylase	1452	MAB_1148c	YP_001701890	HQ662085-HQ662090
(glmU)		_	_	
Valyl-tRNA synthetase (valS)	2643	MAB_1603	YP_001702342	HQ662091-HQ662096
Crossover junction endodeoxyribonuclease (<i>ruvC</i>)	510	MAB_2884c	YP 001703617	HQ662097-HQ662102
DNA-directed RNA polymerase subunit beta (rpoC)	3960	MAB_3868c	YP_001704596	HQ662103-HQ662108
DNA repair protein RecN (recN)	1770	MAB_2361	YP_001703096	HQ662109-HQ662114
GTP-dependent nucleic acid-binding protein (ychF)	1074	MAB 1266	YP_001702008	HQ662115-HQ662120
GTP-binding protein Era (era)	915	MAB_1672	YP 001702411	HQ662121-HQ662126
Hypothetical protein MAB2781c	978	MAB_2781c	YP 001703514	HQ662127-HQ662132
Nicotinate-nucleotide adenylyltransferase (nadD)	638	MAB 1621	YP 001702360	HQ662133-HQ662138
50S ribosomal protein L10 (<i>rplJ</i>)	531	MAB_3877c	YP 001704605	HQ662139-HQ662144
50S ribosomal protein L35 (<i>rpml</i>)	195	MAB_2322	YP 001703057	HQ662145-HQ662150
Putative Holliday junction resolvase	522	MAB_2850c	YP_001703583	HQ662151-HQ662156
- I I I I I I I I I I I I I I I I I I I	, <u></u>			

^{*}ORF, open reading frame; ID, identification

Technical Appendix Table 3. Similarity table of the average (range) of percent identity between concatenated DNA sequences of 43 genes of the *Mycobacterium chelonae-abscessus* complex type strains and CV002*

gones or the myse	Average % identity (range)								
	M. abscessus	M. bolletii	M. chelonae	CV002	M. massiliense	M. immunogenum			
Strains	CIP 104536 ^{Ta}	CIP 108541 ^T	ATCC 35752 ^T	(M. chelonae variant)	CCUG 48898 [™]	CIP 106684 ^T			
M. abscessus		98.3	89.1	90.0	98.2	91.4			
CIP 104536 ^{Ta}	_	(94.4–99.8)	(80.7–97.3)	(83.5–97.3)	(92.2-100)	(83.9-98.0)			
M. bolletii			89.3	90.1	98.2	91.5			
CIP 108541 ^T		_	(80.7-98.0)	(83.8–98.0)	(95.1-100)	(84.1-98.3)			
M. chelonae _				90.0	89.3	89.6			
ATCC 35752 [™]			_	(82.2–98.3)	(81.0-97.7)	(81.0-98.0)			
CV02					90.1	90.5			
				_	(83.8-97.7)	(83.4-99.7)			
M. massiliense		_				91.7			
CCUG 48898 [™]					_	(83.9-99.2)			

^{*}Sequences derived from GenBank accession no. NC_010397. CIP, Collection of Institut Pasteur.

Technical Appendix Table 4. Similarity table of the average (range) of percent identity between concatenated amino acid sequences of 43 genes of the *Mycobacterium chelonae-abscessus* complex type strains and CV002*

or to genes or the	Average % identity (range)									
	M. abscessus	M. bolletii	M. chelonae_	CV002	M. massiliense	M. immunogenum				
Strains	CIP 104536 ^T	CIP 108541 ^T	ATCC 35752 [™]	(M. chelonae variant)	CCUG 48898 [™]	CIP 106684 ^T				
M. abscessus CIP 104536 [™]	-	99.6 (97.6–100)	95.6 (83.7–100)	95.9 (87.3–100)	99.5 (97.8—100)	97.2 (88.3–100)				
M. bolletii CIP 108541 [™]		-	95.7 (84.5–100)	95.9 (88.0–100)	99.5 (98.2–100)	97.2 (88.3–100)				
M. chelonae ATCC 35752 ^T			-	95.8 (84.1–100)	95.6 (84.5–100)	95.9 (84.1–100)				
CV002				_	95.9 (88.0–100)	96.1 (86.5–100)				
M. massiliense CCUG 48898 ^T					-	97.2 (88.3–100)				

^{*}CIP, Collection of Institut Pasteur.

Technical Appendix Table 5. Comparison of DNA-DNA hybridization results of patient isolates and phylogenetically related type strains of *the Mycobacterium chelonae-abscessus* complex*

Unlabeled DNA	% similarity to rac	liolabeled CV002	% similarity to radiolabeled CV005		
	RBR at 70°C	% Divergence	RBR at 70°C	% Divergence	
CV002	100	0.0	100	0.5	
CV004	80	1.5			
CV005	66	0.0	100	0.0	
CV006	96	2.0			
CV015	94	2.0			
M. abscessus CIP 104536 ^T	66	6.0			
M. bolletii CIP 108541 ^T	15	6.0			
M. chelonae ATCC 35752 [™]	42	8.0			
M. immunogenum CIP 1066841	65	5.0			
M. massiliense CCUG 488981	69	6.5			
M. salmoniphilum ATCC 13758	41	6.5			

^{*}RBR, relative binding ratio (see text for full definition); CIP, Collection of Institut Pasteur.

Technical Appendix Table 6. Case histories of patients with CV recovered during study*									
		Patient							
Isolate	Year	age,							
no.	isolated	y/sex	State	Source	Underlying condition	Symptoms	Treatment	Outcome	
CV002	2005	9/M	NY	Skin lesion	Unknown	Unknown	Unknown	Unknown	
CV004	2007	5/M	PA	Central line	Medulloblastoma,	Erythema and purulent	Levofloxacin,	Infection resolved	
				port	chemotherapy	discharge at central	cefoxitin,		
CV005	2007	2/F	PA	Propobiol	Eastronia vasal sard	line site	clarithromycin Unknown	Infection resolved	
CV005	2007	2/୮	PA	Bronchial wash	Esotropia, vocal cord paralysis, and gastro-	Cough	Ulknown	intection resolved	
				wasii	duodenal fistula				
CV006	2007	10/F	PA	Liver	Relapsed acute	Biopsy-confirmed	Clindamycin,	Infection resolved	
				biopsy	lymphoblastoma	granulomatous liver	ceftazidime		
				, ,	leukemia	lesions			
CV007	2007	41/F	PA	Sputum	Primary ciliary	Dyspnea and	Intravenous	Symptoms	
					dyskinesia,	increased sputum for	cefepime for 3	improved	
					bronchiectasis and	several months	weeks		
					prior Mycobacterium				
					avium-intracellulare and M. abscessus				
					infection				
CV008	2007	64/F	PA	Sputum	Prednisone therapy,	Dyspnea and	10-d course of	Respiratory	
]			bronchiectasis,	increased sputum	fluoroquinolone	function	
					multiple episodes of	production for 3 weeks	·	subjectively and	
					pneumonia and			radiographically	
					autoimmune hepatitis			improved	
CV010	2007	72/F	PA	Sputum	Unknown	Unknown	Unknown	Unknown	
CV012	2007	63/F	PA	Maxillary	Unknown	Unknown	Unknown	Unknown	
0) (040	0007	45/5	- DA	sinus	O ti- filmii	M/	A 4 4	0	
CV013	2007	45/F	PA	Sputum	Cystic fibrosis and prior Mycobacterium	Worsening cough, sputum production and	At time of presentation,	Symptoms subjectively	
					avuim infection	dyspnea. Chest CT	receiving	improved and	
					avaiiii iiiicctioii	scan showed bilateral	azithromycin,	follow up cultures	
						bronchiectasis and tree	ethambutol and	were repeatedly	
						in bud opacities	rifampin for M.	negative for M.	
						·	avium;	avium and rapidly	
							continued on	growing	
							same regimen	mycobacteria	
							for several		
CV014	2007	74/F	PA	Sputum	Unknown	Three isolates	months Unknown	Unknown	
CV014	2007	74/1	FA	Sputum	OTIKITOWIT	recovered over 3- year	Olikilowii	OTIKITOWIT	
						period			
CV015	2008	10/M	PA	Sputum	Eczema	power	Acyclovir	Lost to follow-up	
						Fever, sore throat,	,	'	
						stomatitis, and			
						drooling. HSV-1 PCR			
0) (00 (2222					sputum/saliva positive			
CV021	2008	76/M	NJ	Bronchial	Unknown	Unknown	Unknown	Unknown	
CV022	2008	58/F	MN	wash Sputum	Unknown	Unknown	Unknown	Unknown	
CV022	2009	69/M	VA	Respiratory	Unknown	Unknown	Unknown	Unknown	
CV023	2009	78/F	ME	Respiratory	Unknown	Unknown	Unknown	Unknown	
CV025	2009	73/F	OR	Body fluid	Unknown	Unknown	Unknown	Unknown	
CV026	2009	18/M	CO	Sputum	Unknown	Unknown	Unknown	Unknown	
CV027	2009	18/M	PA	Sputum	Diabetes	Lung injury following	Unknown	Patient died	
						smoke inhalation from			
						house fire. Diagnosed			
						with pulmonary			
						mucormycosis by BAL.			
						Weeks later developed			
						respiratory failure and pulmonary hemorrhage			
CV028	2009	38/F	ME	Sputum	Unknown	Unknown	Unknown	Unknown	
CV020	2009	48/F	ME	Sputum	Unknown	Unknown	Unknown	Unknown	
CV030	2009	53/F	ND	Bronchial	Unknown	Unknown	Unknown	Unknown	
		50.1		lavage		2			
			•						

CV032	2009	1/M	NJ	Blood	Unknown	Unknown	Unknown	Unknown
CV033	2009	73/M	PA	Maxillary	Unknown	Unknown	Unknown	Unknown
				sinus				
CV034	2009	44/F	PA	Maxillary	Maxillary sinus	Two weeks	None	Nasal drainage
				sinus	surgery for chronic	postoperatively had		resolved over
					sinusitis	routine follow-up and		several weeks
						complained of nasal		without
						drainage.		antimicrobial
								therapy
CV035	2010	66/F	PA	Thigh	Diabetes	Erythematous 2-cm	Unknown	Unknown
				lesion		indurated plaque to a		
						3.5- x 3.5-cm lesion.		
						First skin biopsy		
						showed granulomatous		
						reaction. Subsequent		
						biopsies showed		
						abscess and adjacent		
						leukocytoclastic		
21/222						vasculitis		
CV036	2010	47/M	PA	Maxillary	Unknown	Unknown	Unknown	Unknown
				sinus				

^{*}CV, Mycobacterium chelonae variant; CT, computed tomography; HSV-1, herpes simplex virus 1.