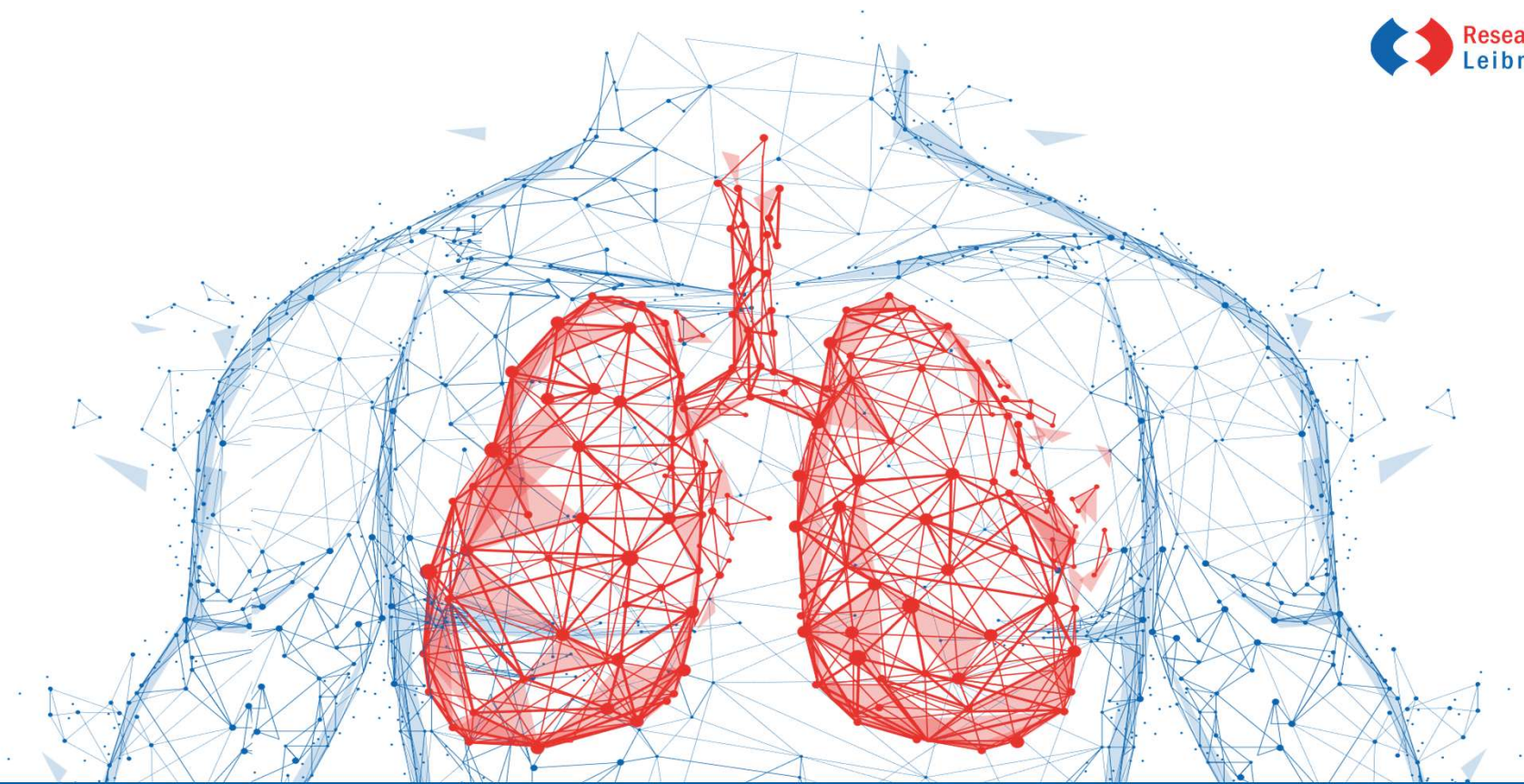


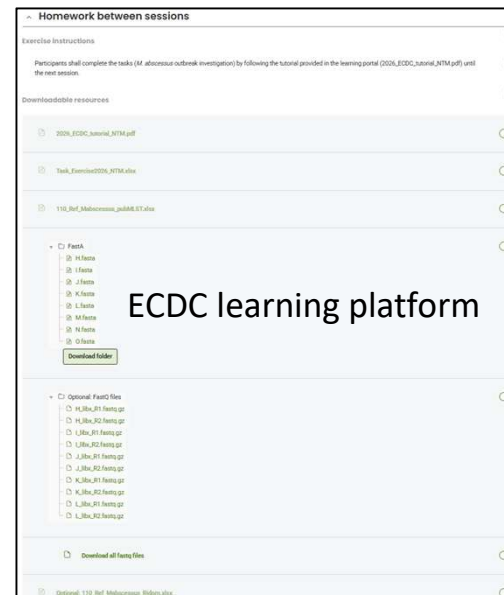


Genomic analysis of non-tuberculous mycobacteria (Tutorial) - Discussion

EXERCISE



- Analyse a skin infection outbreak of *M. abscessus*
 - Task: analyse WGS data from NTM isolated from patient and environmental samples → identify source of the outbreak
- Tutorial and WGS data can be found in the ECDC portal
 - Tutorial = Step-by-step instructions for analysis of WGS data using GUI-based tools
 - Pathogenwatch
 - pubMLST
 - NTM-Profiler
 - Ridom Typer



ECDC learning platform

**Forschungszentrum Borstel
Leibniz Lungenzentrum**

ecdc
EUROPEAN CENTRE FOR
DISEASE PREVENTION
AND CONTROL

Tutorial on
genomic analysis of non-tuberculous
mycobacteria
Analysis of a skin infection outbreak of *M. abscessus*

Trainer
Dr. ir. Margo Diricks (Research Center Borstel, Germany)
mdiricks@fz-borstel.de

Date:
05.11.2026

BioMed Research International

Research Article | [Open Access](#) | [CC BY](#)

Investigation of Two *Mycobacterium abscessus* Outbreaks in Quebec Using Whole Genome Sequencing

Michelle Wuzinski, Hafid Soualhine, Emilie Valliere, Pierre-Marie Akochy, Nancy Cloutier, Aaron Petkau, Brynn Kaplan, Maryse Duchesne, Jasmin Villeneuve, Meenu K. Sharma

First published: 09 November 2020 | <https://doi.org/10.1155/2020/7092053> | Citations: 1

Academic Editor: Luis Fernandes

WGS = whole genome sequencing data



M. ABSCESSUS



- Rapidly growing NTM
- Pulmonary and extra-pulmonary infections
- Notoriously difficult to treat
- 3 subspecies
 - massiliense
 - abscessus
 - bolletii
- 7 Dominant circulating clones
 - Most often found in patients (and the environment)
 - More virulent
 - Worse clinical outcomes
 - Lower mutation rate

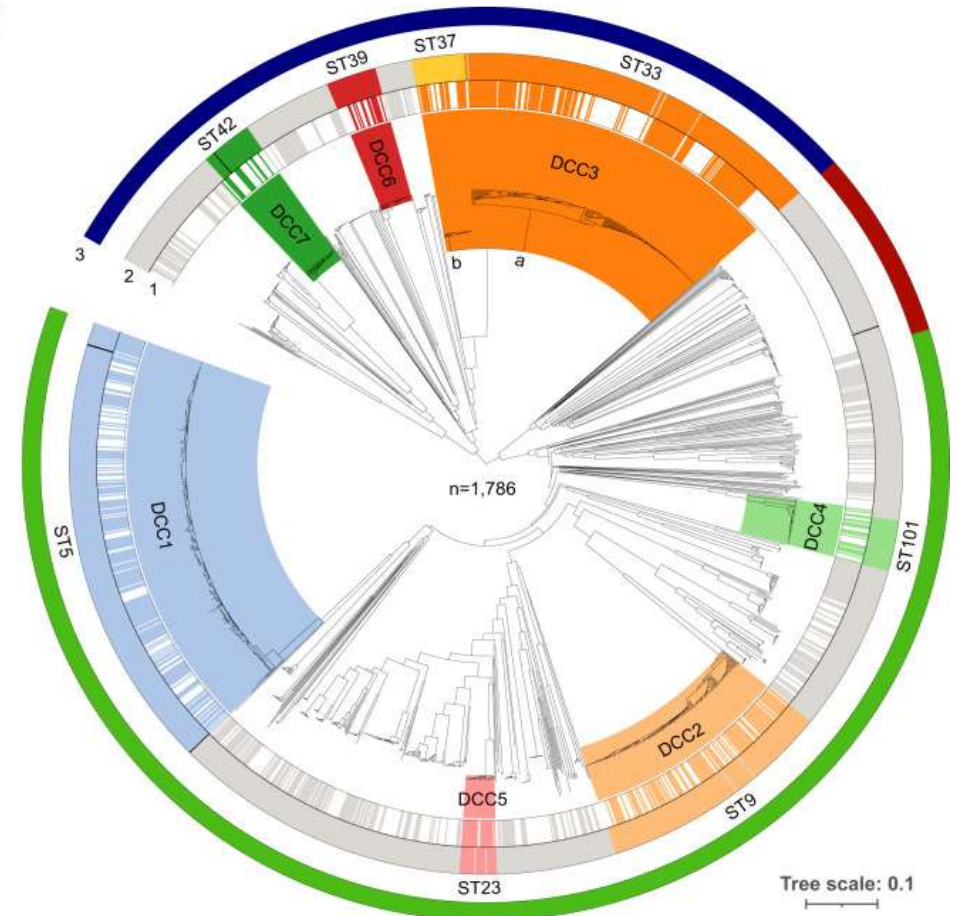
1. cgSNP (Ruis2021)



2. 7-loci MLST



3. Subspecies



Diricks et al 2022

CASE STUDY



- Within 6 weeks: 4 patients presented with skin infections around tattoo
- Biopsies: + for mycobacteria
- *M. abscessus subsp. abscessus* (MLST, 16S/hsp65)
- Same tattoo studio
- Public Health Laboratory in Quebec suspected outbreak
- Samples sent to National Microbiology Laboratory
- WGS: close genetic similarity (3-11 SNPs) → outbreak

BioMed Research International



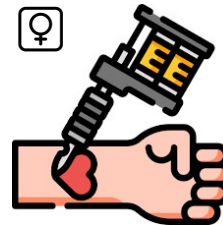
Research Article | [Open Access](#) |

Investigation of Two *Mycobacterium abscessus* Outbreaks in Quebec Using Whole Genome Sequencing

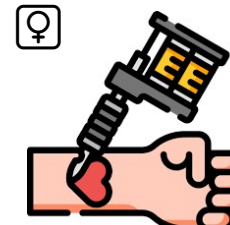
Michelle Wuzinski, Hafid Soualhine, Emilie Valliere, Pierre-Marie Akochy, Nancy Cloutier, Aaron Petkau, Brynn Kaplen, Maryse Duchesne, Jasmin Villeneuve, Meenu K. Sharma ✉

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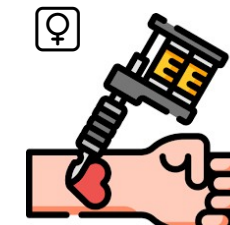
Academic Editor: Luis Fernandes



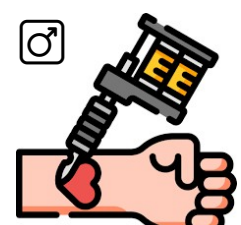
Patient 1
Sample H



Patient 2
Sample I



Patient 3
Sample J



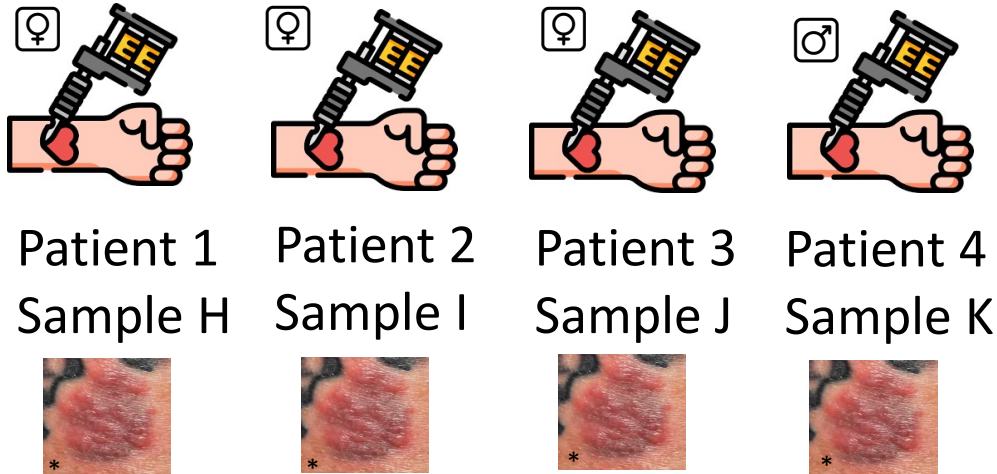
Patient 4
Sample K



*Wu 2017



CASE STUDY (WUZINSKI ET AL. 2020)



Hypothetical environmental investigation in tattoo shop and patient environment

Ink tattoo shop



Negative

Tap water tattoo shop



Isolate M

Aquarium patient 1



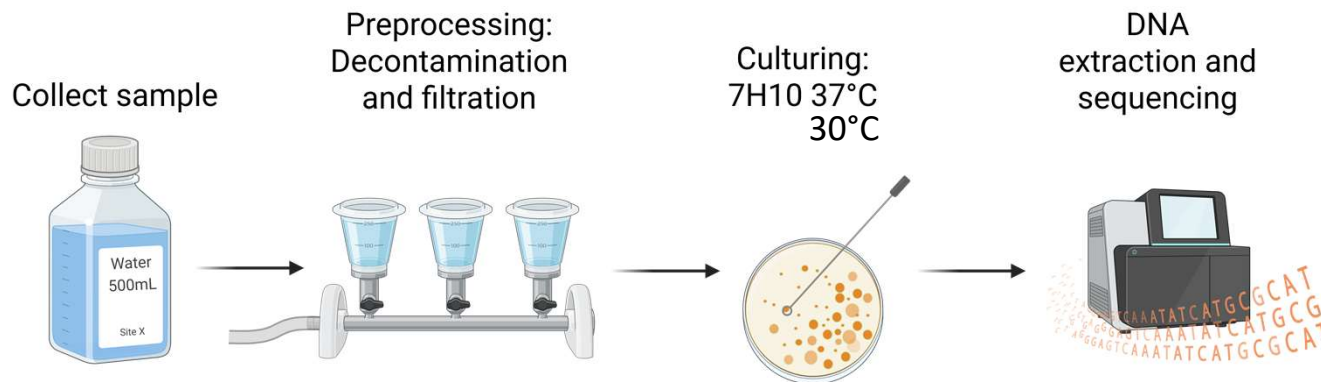
Sample O

Shower patient 1



Sample L (SGM)
Sample N (RGM)

What is the source of the outbreak?



TASKS



- Goal: identify the source of the skin infection outbreak
 - Task 1: Determine which NTM (sub)species were isolated from the environmental samples (L-O)
 - Task 2: Determine the 7-loci MLST Sequence Type (ST) of the *M. abscessus* isolates
 - Task 3: Determine the genetic distance (expressed as allele differences) between outbreak isolates
 - Task 4: Determine whether the *M. abscessus* isolates belong to known dominant circulating clones (DCCs)
 - Task 5: Determine the genetic resistance profiles of the isolates

→ Complete all results in **Task_Exercise2026_NTM.xlsx**

Task 6: Formulate a hypothesis regarding the transmission route

A	B	C	D	E	F	G	H	I	J	K	L
Sample ID	Reference	Isolation Source	Country of Isolation	Species	Subspecies	MLST ST	DCC	Amikacin resistance	Macrolide resistance	Fluoroquinolone resistance	Part of outbreak?
H	Wuzinski 2020	Patient 1	Canada	abscessus	abscessus						
I	Wuzinski 2020	Patient 2	Canada	abscessus	abscessus						
J	Wuzinski 2020	Patient 3	Canada	abscessus	abscessus						
K	Wuzinski 2020	Patient 4	Canada	abscessus	abscessus						
L	Hypothetical investigation	Shower	Canada								
M	Hypothetical investigation	Tap water	Canada								
N	Hypothetical investigation	Shower	Canada								
O	Hypothetical investigation	Aquarium	Canada								

TASKS - NTMPROFILER



- Goal: identify the source of the skin infection outbreak
 - **Task 1: Determine which NTM (sub)species were isolated from the environmental samples (L-O)**
 - Task 2: Determine the 7-loci MLST Sequence Type (ST) of the *M. abscessus* isolates
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 - **Task 5: Determine the genetic resistance profiles of the isolates**

→ Complete all results in **Task_Exercise2026_NTML.xlsx**

Task 6: Formulate a hypothesis regarding the transmission route

A	B	C	D	E	F	G	H	I	J	K	L
Sample ID	Reference	Isolation Source	Country of Isolation	Species	Subspecies	MLST ST	DCC	Amikacin resistance	Macrolide resistance	Fluoroquinolone resistance	Part of outbreak?
H	Wuzinski 2020	Patient 1	Canada	abscessus	abscessus						
I	Wuzinski 2020	Patient 2	Canada	abscessus	abscessus						
J	Wuzinski 2020	Patient 3	Canada	abscessus	abscessus						
K	Wuzinski 2020	Patient 4	Canada	abscessus	abscessus						
L	Hypothetical investigation	Shower	Canada								
M	Hypothetical investigation	Tap water	Canada								
N	Hypothetical investigation	Shower	Canada								
O	Hypothetical investigation	Aquarium	Canada								

- **Web-based:** <https://bioinformatics.lshtm.ac.uk/ntm-profiler/>



Jody Phelan

NTM-Profiler
Home
Upload

Welcome to the webserver of NTM-Profiler - a pipeline which allows users to analyse *Mycobacterial* whole genome sequencing data to predict lineage and drug resistance. Follow the instructions below to upload a new sample or view analysed runs.

How does it work?

The pipeline searches for small variants and big deletions associated with drug resistance. It will also report the lineage. By default it uses Trimmomatic to trim the reads, BWA (or minimap2 for nanopore) to align to the reference genome and GATK (open source v4) to call variants.

Step 1

Profile your sample

Upload your next generation sequencing data in **fastQ** format. You can upload one or two (forward and reverse) fastq files. When you upload your data, the run will be assigned a unique ID. Please take a note of this ID as you will need to find your results later. Batch upload of samples is also

Upload

Step 2

View the results

Find your results by entering you unique run ID directly into the search box below.

Sample ID

Submit

NTM-Profiler
Home
Upload

Upload your next generation sequencing data in **fastq or fastq** format. Files will be processed using the NTM-Profiler pipeline with default parameters. You may select the technology used to generate the data (Illumina or Oxford Nanopore). Samples will be processed with a first in first out policy so please be patient as there may be runs waiting to be processed before yours.

Please note: at the moment we can only accommodate uploads of files under 4GB. If you have files which are larger or you require many isolates to be processed and have access to a linux or macOS operating system then it might be worthwhile to run the commandline version of NTM-Profiler. For more information on this please visit the [github repository](#).

Please drop your files in here and click submit when done.

5.1 MB

5.1 MB

5.1 MB

5.1 MB

6.5 MB

5.1 MB

5.3 MB

6.3 MB

Platform:

☒ Illumina
☐ Nanopore

Filetype:

☐ Paired fastq
☐ Single fastq
☒ Fastq

File suffix:

Read suffix. Use this option to change the default suffix of files. For example if your fastq file is named **sample1.fastq** then your suffix should be **.fast**

File suffix:

fastq

Submit

NTM-Profiler Home Upload

Summary QC Species Drug resistance Genome browser Log Download

Run ID: 3b45c8b5-c449-4894-a717-8fbe17273f4b
Species: Mycobacterium abscessus subsp. abscessus

NTM-Profiler Home Upload

Summary QC Species Drug resistance Genome browser Log Download

Run ID: 574af4d8-4630-46ba-9062-0abb113291d4
Species: Mycobacterium abscessus subsp. massiliense

- Resistance

Sample H, I, J, K and M

M. abscessus subsp. abscessus

- Typically have a full length erm(41) gene
- Inducible resistant against macrolides
- But p.Trp10Arg = loss of function variant
- Likely phenotypically susceptible

NTM-Profiler Home Upload

Summary QC Species Drug resistance Genome browser Log Download

Overview
The drug resistance analysis is performed using the genome variants found in the sample. The resistance is determined by the presence of known resistance mutations and genes in the genome. This table shows the resistance to the drugs tested and the supporting genetic determinants.

Drug	Resistance	Supporting variants
macrolides	Susceptible	
amikacin	Susceptible	
fluoroquinolones		

Drug resistance genes
The following table lists resistance-associated genes found in your sample.

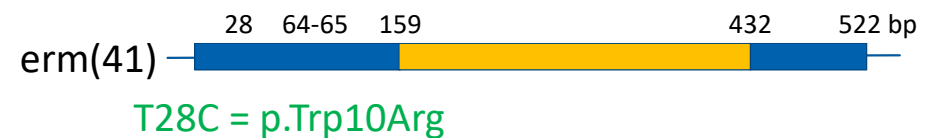
Gene	Type	Drugs

Drug resistance variants
The following table lists resistance-associated variants found in your sample.

Gene	Genome position	Mutation	Type	Estimated fraction	Drugs

Other variants
The following table lists variants that are not resistance-associated but are found in candidate genes.

Gene	Genome position	Mutation	Type	Estimated fraction
rrl	1464841	n.634C>T	non_coding_transcript_exon_variant	1.0
rrl	1465142	n.935T>C	non_coding_transcript_exon_variant	1.0
erm(41)	2345982	p.Trp10Arg	loss_of_function_variant	1.0
erm(41)	2346113	c.139T>C	synonymous_variant	1.0
erm(41)	2346192	p.Ile80Val	missense_variant	1.0
erm(41)	2346284	c.330A>C	synonymous_variant	1.0

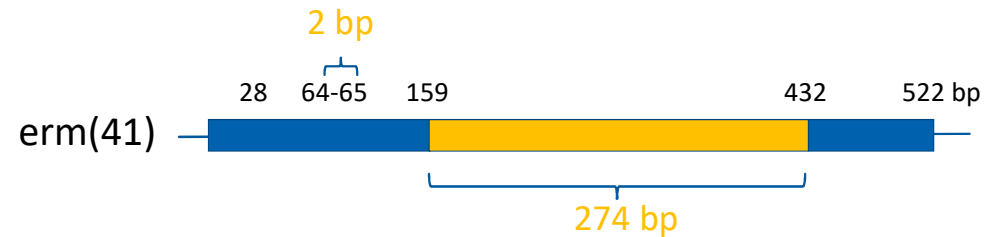


- Examples when resistances are detected

Summary	QC	Species	Drug resistance	Genome browser	Log	Download
Overview						
The drug resistance analysis is performed using the genome variants found in the sample. The resistance is determined by the presence of known resistance mutations and genes in the genome. This						
Drug			Resistance	Supporting variants		
macrolides			erm(41)	functionally_normal		
amikacin						
fluoroquinolones						

Summary	QC	Species	Drug resistance	Genome browser	Log	Download
Overview						
The drug resistance analysis is performed using the genome variants found in the sample. The resistance is determined by the presence of known resistance mutations and genes in the genome. Th						
Drug			Resistance	Supporting variants		
macrolides			rrl	n.2270A>C		
amikacin			rrs	n.1375A>G		
fluoroquinolones						

- Sample N (subsp. massiliense)



erm(41)	2345951	c.-4C>T	upstream_gene_variant	1.0
erm(41)	2345995	p.Pro14Gln	missense_variant	1.0
erm(41)	2346000	p.Thr16Ala	missense_variant	1.0
erm(41)	2346017	c.64_65delCG	frameshift_variant	1.0
erm(41)	2346039	p.Val29Phe	missense_variant	1.0
erm(41)	2346044	c.90C>T	synonymous_variant	1.0
erm(41)	2346063	p.Asp37Asn	missense_variant	1.0
erm(41)	2346077	c.123A>G	synonymous_variant	1.0
erm(41)	2346112	c.159_432del	frameshift_variant	1.0
erm(41)	2346392	c.438A>C	synonymous_variant	1.0
erm(41)	2346420	p.Ala156Thr	missense_variant	1.0

TASKS - PATHOGENWATCH



- Goal: identify the source of the skin infection outbreak
 - **Task 1: Determine which NTM (sub)species were isolated from the environmental samples (L-O)**
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→ Complete all results in **Task_Exercise2026_NTML.xlsx**

Task 6: Formulate a hypothesis regarding the transmission route

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I	Wuzinski 2020	Patient 2	Canada	abscessus	abscessus						
J	Wuzinski 2020	Patient 3	Canada	abscessus	abscessus						
K	Wuzinski 2020	Patient 4	Canada	abscessus	abscessus						
L	Hypothetical investigation	Shower	Canada								
M	Hypothetical investigation	Tap water	Canada								
N	Hypothetical investigation	Shower	Canada								
O	Hypothetical investigation	Aquarium	Canada								

The screenshot displays the Pathogenwatch web application interface. At the top, a navigation bar includes links for GENOMES, COLLECTIONS, UPLOAD, and DOCUMENTATION. The main content area is divided into several sections:

- Left Sidebar:** Displays "8 genomes completed" with a list of Mycobacteroides species and their metrics (QUAST).
- Central Circular Chart:** A donut chart labeled "VIEW GENOMES" showing the progress of genome completion. A red box highlights the "VIEW GENOMES" button in the center.
- World Map:** Titled "Genomic Surveillance", showing a map of Europe with data points representing genomic surveillance locations.
- File Upload Section:** Includes a "Drop files here" area and a list of uploaded files (H.fasta to O.fasta).
- Bottom Section:** Contains buttons for "Upload" and "Analyze", along with text describing the upload process and the analysis results.



<https://pathogen.watch/>



Not displayed like this anymore in current version (29.04.2026)!

Same 7 loci MLST sequence type → first indication strains might be part of same outbreak/transmission chain

Old version

✓ H	Patient 1	<i>Mycobacteroides abscessus</i>	222	MLST
✓ I	Patient 2	<i>Mycobacteroides abscessus</i>	222	MLST
✓ J	Patient 3	<i>Mycobacteroides abscessus</i>	222	MLST
✓ K	Patient 4	<i>Mycobacteroides abscessus</i>	222	MLST
✓ L	Shower (SGM)	<i>Mycobacterium chimaera</i>	81	MLST
✓ M	Tap water	<i>Mycobacteroides abscessus</i>	222	MLST
✓ N	Shower (RGM)	<i>Mycobacteroides abscessus</i>	33	MLST
✓ O	Aquarium	<i>Mycobacterium marinum</i>	22	MLST

New version

Pathogenwatch

My folders > Untitled folder - Created 29 April 2026 18:36

Status ▾

Name	Organism	Country	Date
Aquarium patient 1	<i>Mycobacterium marinum</i>		
Shower (RGM) patient 1	<i>Mycobacteroides abscessus</i>		
Tap water tattoo shop	<i>Mycobacteroides abscessus</i>		
Shower (SGM) patient 1	<i>Mycobacterium chimaera</i>		
Patient 4	<i>Mycobacteroides abscessus</i>		
Patient 3	<i>Mycobacteroides abscessus</i>		
Patient 2	<i>Mycobacteroides abscessus</i>		
Patient 1	<i>Mycobacteroides abscessus</i>		

= *M. intracellulare* subsp. *chimaera*

Front Microbiol. 2018 Aug 22;9:2007. doi: [10.3389/fmicb.2018.02007](https://doi.org/10.3389/fmicb.2018.02007)

Genome-Based Taxonomic Classification of the Phylum *Actinobacteria*

Imen Nouioui^{1,2}, Lorena Carro^{1,2}, Marina García-López^{2,3}, Jan P Meier-Kolthoff², Tanja Woyke³, Nikos C Kyrpides³, Rüdiger Pukall², Hans-Peter Klenk¹, Michael Goodfellow¹, Markus Göker^{2,*}

Author information Article notes Copyright and License information

PMCID: PMC6113628 PMID: 30186281

Description of *Mycobacterium intracellulare* subsp. *Chimaera*, subsp. nov.

M. in.tra.cel.lu.la're subsp. *chi.mae'ra* (L. n. *chimaera*, the chimaera, the mythological being made up of parts of three different animals).

The description is as given for *Mycobacterium chimaera* (Tortoli et al., 2004) with the following addition. The G+C content of the type-strain genome is 67.7%, its approximate size 6.09 Mbp, its GenBank deposit [SAMN04216918](https://www.ncbi.nlm.nih.gov/nuclseq/SAMN04216918). The type strain is FI-01069 = CCUG 50989 = CIP 107892 = DSM 44623 = JCM 14737.

No subspecies information!!

NTM-Profiler Home Upload

Summary	QC	Species	Drug resistance	Genome browser	Log	Download
Run ID: 297e869a-7336-4ff1-b7ea-63f8c854126e Species: <i>Mycobacterium intracellulare</i> HCU_outbreak_strain, L2.2, subsp. <i>chimaera</i>						

Pathogenwatch

My folders > Untitled folder - Created 29 April 2026 18:36

Status ▾

☐ Name	Organism	Country	Date
☐ Aquarium patient 1	<i>Mycobacterium marinum</i>		
☐ Shower (RGM) patient 1	<i>Mycobacteroides abscessus</i>		
☐ Tap water tattoo shop	<i>Mycobacteroides abscessus</i>		
☐ Shower (SGM) patient 1	<i>Mycobacterium chimera</i>		
☐ Patient 4	<i>Mycobacteroides abscessus</i>		
☐ Patient 3	<i>Mycobacteroides abscessus</i>		
☐ Patient 2	<i>Mycobacteroides abscessus</i>		
☐ Patient 1	<i>Mycobacteroides abscessus</i>		

H

Mycobacteroides abscessus

Pathogenwatch

Metadata

No metadata defined

Typing

MLST - Multilocus sequence typing

Sequence type: 222

argH	cya	gnd	murC	pta	purH	rpoB
1	2	3	2	2	25	4

Core genome clustering

Source: M. abscessus cgMLST v1.0 - PubMLST

Clusters have not been calculated for this genome

RUN CLUSTERING

QC & Stats

QC	Genome length	No. contigs
Passed	5,004,181	25
Largest contig	Average contig length	N50
1,551,651	200,167	354,864

cgMLST: higher resolution, more reliable for outbreak analysis!

PATHOGENWATCH



H

Mycobacteroides abscessus

Metadata

No metadata defined

Typing

MLST - Multilocus sequence typing

Sequence type **222**

argH	cya	gnd	murC	pta	purH	rpoB
1	2	3	2	2	25	4

Core genome clustering

Source: M. abscessus cgMLST v1.0 - PubMLST

Cluster of 6 at threshold of 10

Pick a threshold by clicking on the chart below

VIEW CLUSTER

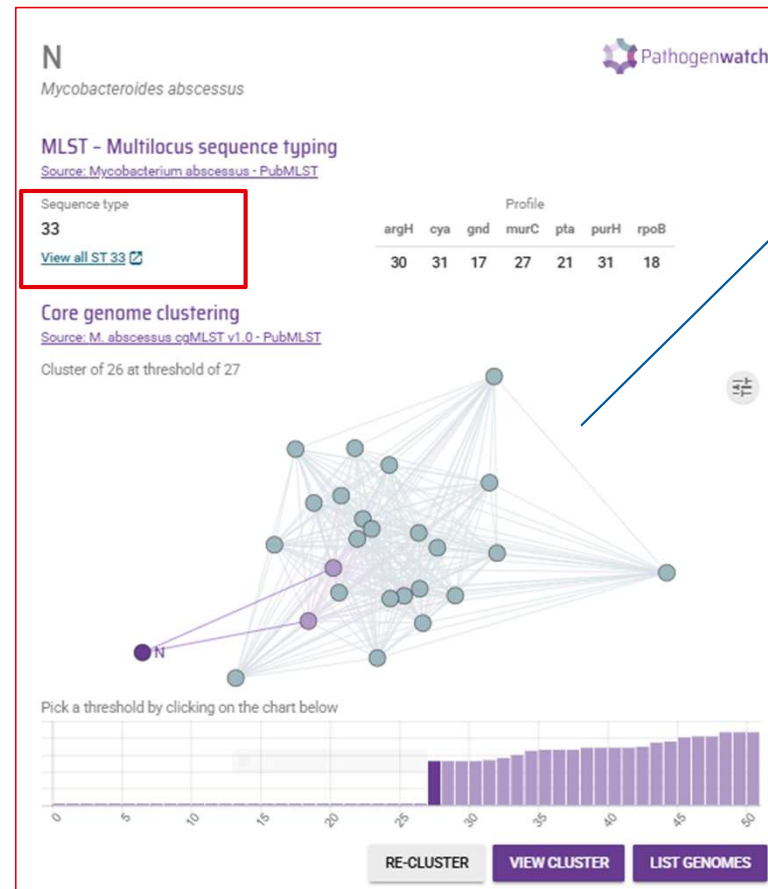
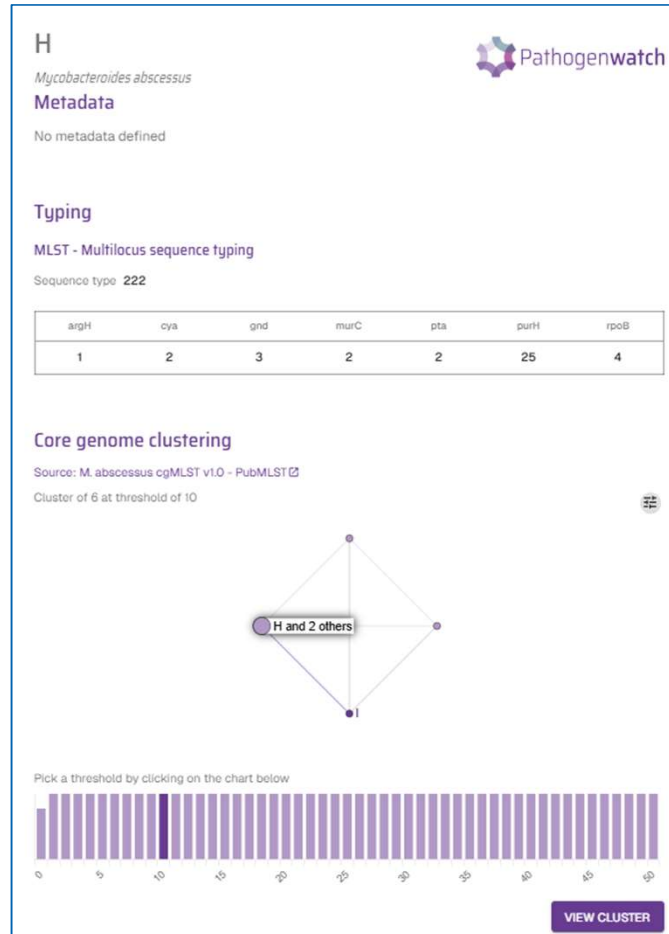
Cluster threshold = 10

High threshold for clustering in this cluster

Name	Profile	ST
M	1_2_3_2_2_...	222
K	1_2_3_2_2_...	222
J	1_2_3_2_2_...	222
I	1_2_3_2_2_...	222
H	1_2_3_2_2_...	222

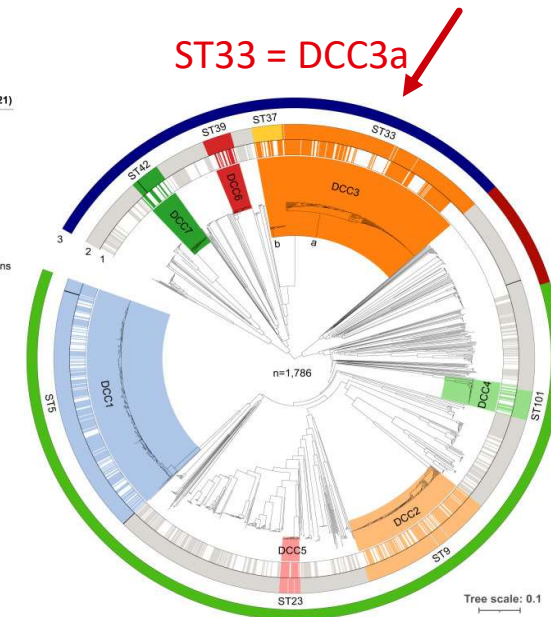
You can choose a **cluster threshold**

PATHOGENWATCH



25 other (public)
genomes clustering at
threshold of 27 alleles

- cgSNP (Ruis2021)**
 - DCC1
 - DCC2
 - DCC3
 - DCC4
 - DCC5
 - DCC6
 - DCC7
 - Non-DCC strains
 - Unknown
- 7-loci MLST**
 - ST5
 - ST9
 - ST33
 - ST37
 - ST101
 - ST23
 - ST39
 - ST42
 - No ST
 - Other ST
- Subspecies**
 - massiliense*
 - bolletii*
 - abscessus*



Note: No other (public) genomes within 50 allele distance

Diricks et al. 2022



TASKS - PUBMLST



- Goal: identify the source of the skin infection outbreak
 - Task 1: Determine which NTM (sub)species were isolated from the environmental samples (L-O)
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→ Complete all results in **Task_Exercise2026_NTM.xlsx**

Task 6: Formulate a hypothesis regarding the transmission route

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K	Wuzinski 2020	Patient 4	Canada	abscessus	abscessus						
L	Hypothetical investigation	Shower	Canada								
M	Hypothetical investigation	Tap water	Canada								
N	Hypothetical investigation	Shower	Canada								
O	Hypothetical investigation	Aquarium	Canada								

- Goal: identify the source of the skin infection outbreak
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→ Complete all results in **Task_Exercise2026_NTML.xlsx**

Task 6: Formulate a hypothesis regarding the transmission route

A	B	C	D	E	F	G	H	I	J	K	L
Sample ID	Reference	Isolation Source	Country of Isolation	Species	Subspecies	MLST ST	DCC	Amikacin resistance	Macrolide resistance	Fluoroquinolone resistance	Part of outbreak?
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J	Wuzinski 2020	Patient 3	Canada	abscessus	abscessus						
K	Wuzinski 2020	Patient 4	Canada	abscessus	abscessus						
L	Hypothetical investigation	Shower	Canada								
M	Hypothetical investigation	Tap water	Canada								
N	Hypothetical investigation	Shower	Canada								
O	Hypothetical investigation	Aquarium	Canada								

PubMLST

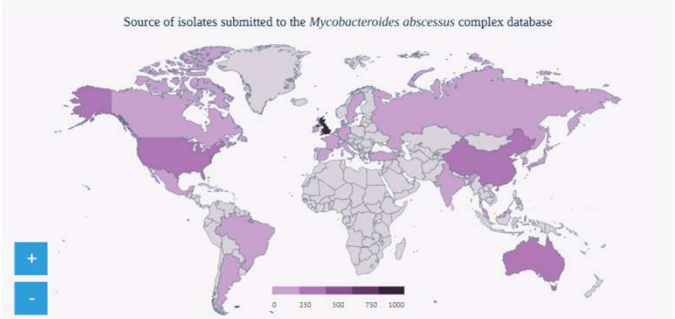
Public databases for molecular typing and microbial genome diversity

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[UPDATES](#)

[Home](#) > [Organisms](#)

Mycobacteroides abscessus complex

Source of isolates submitted to the *Mycobacteroides abscessus* complex database



[SUBMIT](#)

This MLST scheme was developed by Song Yee Kim and colleagues at the Yonsei University College of Medicine, Seoul, Korea. It is described in Kim et al. 2013 *Diagn Microbiol Infect Dis* 77:143-9.

Database curated by Margo Diricks.

The separate scheme for *M. massiliense* has been removed since this was leading to confusion with the *M. abscessus* scheme as they used the same loci with different allele numbers. Allele and profile definitions for the legacy *M. massiliense* scheme are available for download here.

The preferred citation for this website is:
Jolley et al. *Wellcome Open Res* 2018, 3:124 [version 1; referees: 2 approved]

Typing

The typing database contains nomenclature - allele definitions that provide an identifier for every unique allele sequence, and MLST profiles that index each unique combination of alleles with a sequence type (ST).

Allele sequences: 191,947
Last updated: 2026-04-22

Isolate collection

The isolate database consists of isolate records containing provenance and phenotype information linked to molecular typing information. These records may also include genome assemblies.

Isolates: 2,233
Last updated: 2026-04-28

Genome collection

A subset of records within the isolate database may contain genomes assemblies. You can access these from the isolate database by filtering on sequence bin size in a query.

Genomes: 2,189
Last updated: 2026-04-22

Sequence query

Please paste in your sequence to query against the database. Query sequences will be checked first for an exact match against the chosen (or all) loci - they do not need to be trimmed. The nearest partial matches will be identified if an exact match is not found. You can query using either DNA or peptide sequences.

Please select locus/scheme

Order results by

MLST

locus

Enter query sequence (single or multiple contigs up to whole genome in size)

Alternatively upload FASTA file

Select FASTA file:

Click to select or drag and drop...

RESET

SUBMIT

Uploaded file: H.fasta

7 exact matches found.

Locus	Allele	Length	Contig	Start position	End position
argH	1	510	contig00001_len=1551651_cov=62.3_corr=0_origname=Contig_11_62.3438_pilon_sw=showill-skese/1.1.0_date=20211201	430151	430660
cya	2	540	contig00002_len=769008_cov=65.6_corr=0_origname=Contig_23_65.5755_pilon_sw=showill-skese/1.1.0_date=20211201	490649	491188
gnd	3	506	contig00001_len=1551651_cov=62.3_corr=0_origname=Contig_11_62.3438_pilon_sw=showill-skese/1.1.0_date=20211201	505859	506364
murC	2	445	contig00001_len=1551651_cov=62.3_corr=0_origname=Contig_11_62.3438_pilon_sw=showill-skese/1.1.0_date=20211201	45742	46186
pta	2	520	contig00008_len=189718_cov=68.3_corr=0_origname=Contig_19_68.252_pilon_sw=showill-skese/1.1.0_date=20211201	128141	128660
purH	25	497	contig00004_len=318344_cov=63.5_corr=0_origname=Contig_18_63.4806_pilon_sw=showill-skese/1.1.0_date=20211201	224905	225401
rpoB	4	503	contig00009_len=155652_cov=65.9_corr=0_origname=Contig_2_65.8717_pilon_sw=showill-skese/1.1.0_date=20211201	139878	140380

Only exact matches are shown above. If a locus does not have an exact match, try querying specifically against that locus to find the closest match.

Text

Excel

MLST

Matching profile

ST: 222

Should be the same result as Pathogenwatch!!

- Goal: identify the source of the skin infection outbreak
 - Task 1: Determine which NTM (sub)species were isolated from the environmental samples (L-O)
 - Task 2: Determine the 7-loci MLST Sequence Type (ST) of the *M. abscessus* isolates
 - **Task 3: Determine the genetic distance (expressed as allele differences) between outbreak isolates**
 - Task 4: Determine whether the *M. abscessus* isolates belong to known dominant circulating clones (DCCs)
 - Task 5: Determine the genetic resistance profiles of the isolates

→ Complete all results in **Task_Exercise2026_NTML.xlsx**

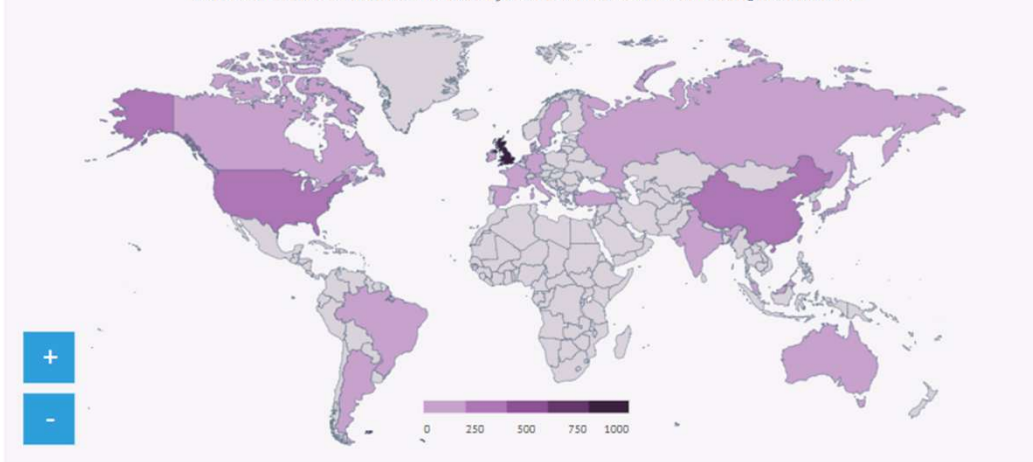
Task 6: Formulate a hypothesis regarding the transmission route

A	B	C	D	E	F	G	H	I	J	K	L
Sample ID	Reference	Isolation Source	Country of Isolation	Species	Subspecies	MLST ST	DCC	Amikacin resistance	Macrolide resistance	Fluoroquinolone resistance	Part of outbreak?
H	Wuzinski 2020	Patient 1	Canada	abscessus	abscessus						
I	Wuzinski 2020	Patient 2	Canada	abscessus	abscessus						
J	Wuzinski 2020	Patient 3	Canada	abscessus	abscessus						
K	Wuzinski 2020	Patient 4	Canada	abscessus	abscessus						
L	Hypothetical investigation	Shower	Canada								
M	Hypothetical investigation	Tap water	Canada								
N	Hypothetical investigation	Shower	Canada								
O	Hypothetical investigation	Aquarium	Canada								

Mycobacteroides abscessus complex

<https://pubmlst.org/>

Source of isolates submitted to the *Mycobacteroides abscessus* complex database



[SUBMIT](#)

This MLST scheme was developed by Song Yee Kim and colleagues at the Yonsei University College of Medicine, Seoul, Korea. It is described in Kim *et al.* 2013 *Diagn Microbiol Infect Dis* **77**:143-9 [et](#).

Database curated by Margo Diricks.

The separate scheme for *M. massiliense* has been removed since this was leading to confusion with the *M. abscessus* scheme as they used the same loci with different allele numbers. Allele and profile definitions for the legacy *M. massiliense* scheme are available for download [here](#).

The preferred citation for this website is:

Jolley *et al.* *Wellcome Open Res* 2018, **3**:124 [version 1; referees: 2 approved] [et](#).

In case you want to analyse your own samples

Typing

The typing database contains nomenclature - allele definitions that provide an identifier for every unique allele sequence, and MLST profiles that index each unique combination of alleles with a sequence type (ST).

Allele sequences: **191,889**

Last updated: 2026-02-10

Isolate collection

The isolate database consists of isolate records containing provenance and phenotype information linked to molecular typing information. These records may also include genome assemblies.

Isolates: **2,123**

Last updated: 2026-02-28

Genome collection

A subset of records within the isolate database may contain genomes assemblies. You can access these from the isolate database by filtering on sequence bin size in a query.

Genomes: **2,079**

Last updated: 2025-05-27

PubMLST

Public databases for molecular typing and microbial genome diversity

HOME

ORGANISMS

SPECIES ID

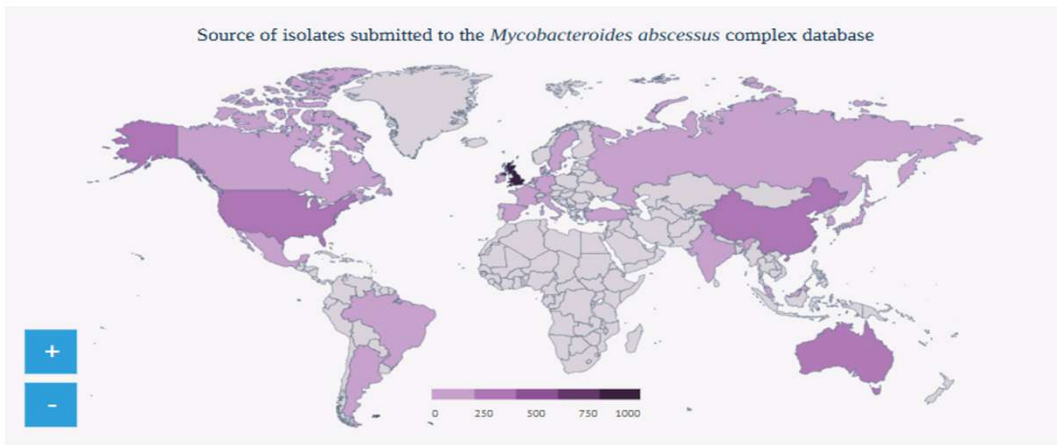
ABOUT US

UPDATES

Home > Organisms

Mycobacteroides abscessus complex

Source of isolates submitted to the *Mycobacteroides abscessus* complex database



SUBMIT

This MLST scheme was developed by Song Yee Kim and colleagues at the Yonsei University College of Medicine, Seoul, Korea. It is described in Kim *et al.* 2013 *Diagn Microbiol Infect Dis* **77**:143-9 *et al.*

Database curated by Margo Diricks.

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Jolley *et al.* *Wellcome Open Res* 2018, **3**:124 [version 1; referees: 2 approved] *et al.*

Typing

The typing database contains nomenclature - allele definitions that provide an identifier for every unique allele sequence, and MLST profiles that index each unique combination of alleles with a sequence type (ST).

Allele sequences: 191,947

Last updated: 2026-04-22

Isolate collection

The isolate database consists of isolate records containing provenance and phenotype information linked to molecular typing information. These records may also include genome assemblies.

Isolates: 2,233

Last updated: 2026-04-28

Genome collection

A subset of records within the isolate database may contain genomes assemblies. You can access these from the isolate database by filtering on sequence bin size in a query.

Genomes: 2,189

Last updated: 2026-04-22

Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance/primary metadata fields

isolate contains ECDC-FZB_training_2025

Sequence bin

total length (Mbp) >= 1

Display/sort options

Order by: id ascending

Display: 25 records per page

Action

RESET

SEARCH

Isolate count

6

0 [month]

Genome count

6

0 [month]

Continent



Subspecies



Year



6 records returned. Click the hyperlinks for detailed information.

Bookmark query

Bookmark

Isolate fields													
id	isolate	aliases	country	subspecies	year	source	argH	cya	gnd	murC	pta	purH	rpoH
2111	H	ECDC-FZB_training_2025_1	Canada	abscessus	2018	human	1	2	3	2	2	25	4
2112	I	ECDC-FZB_training_2025_2	Canada	abscessus	2018	human	1	2	3	2	2	25	4
2113	J	ECDC-FZB_training_2025_3	Canada	abscessus	2018	human	1	2	3	2	2	25	4
2114	K	ECDC-FZB_training_2025_4	Canada	abscessus	2018	human	1	2	3	2	2	25	4
2115	M	ECDC-FZB_training_2025_5	Canada	abscessus	2018	environmental	1	2	3	2	2	25	4
2116	N	ECDC-FZB_training_2025_6	Canada	massiliense	2018	environmental	30	31	17	27	21	31	18

Analysis tools

Breakdown: Fields Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence GeneScanner Genome Comparator BLAST rMLST species id PCR

Export: Dataset Contigs Sequences

Third party: GrapeTree ITOL Microreact PhyloViz PlasmidFinder ReporTree SNPsites

Home > Organisms > *Mycobacteroides abscessus* complex > *Mycobacteroides abscessus* complex isolates > Plugins > GrapeTree

Logged in Help Tooltips

GrapeTree: Visualization of genomic relationships



This plugin generates a minimum-spanning tree and visualizes within GrapeTree:

GrapeTree is developed by: Zhemín Zhou (1), Nabil-Fareed Alikhan (1), Martin J. Sergeant (1), Nina Luhmann (1), Cátia Vaz (2,5), Alexandre P. Francisco (2,4), João André Carriço (3) and Mark Achtman (1)

1. Warwick Medical School, University of Warwick, UK
2. Instituto de Engenharia de Sistemas e Computadores: Investigação e Desenvolvimento (INESC-ID), Lisboa, Portugal
3. Universidade de Lisboa, Faculdade de Medicina, Instituto de Microbiologia and Instituto de Medicina Molecular, Lisboa, Portugal
4. Instituto Superior Técnico, Universidade de Lisboa, Lisboa, Portugal
5. ADEETC, Instituto Superior de Engenharia de Lisboa, Instituto Politécnico de Lisboa, Lisboa, Portugal

Publication: Zhou *et al.* (2018) GrapeTree: Visualization of core genomic relationships among 100,000 bacterial pathogens. *Genome Res* 28:1395-1404.

This tool will generate minimum spanning trees from allelic profiles. Please check the loci that you would like to include. Alternatively select one or more schemes to include all loci that are members of the scheme.

Analysis is limited to 50,000 records.

Isolates	Loci	Schemes	Include fields
2111 2112 2113 2114 2115 2116 Clear List all	Select options All None Paste list	All loci MLST Ribosomal MLST cgMLST	Select additional fields to include in GrapeTree metadata. Select options
Parameters / options ☐ Rescan undesignated loci ⓘ Method: MSTreeV2 ⓘ		Action SUBMIT	

PubMLST

Public databases for molecular typing and microbial genome diversity

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[Home](#) > [Organisms](#) > [Mycobacteroides abscessus complex](#) > [Mycobacteroides abscessus complex isolates](#) > Job status viewer

[Logged in](#)
[Expand](#)

Job status viewer



Status

Job id: BIGSdb_2518788_8924264597_69673
 Submit time: 2026-05-07 15:26:45
 Status: finished
 Start time: 2026-05-07 15:26:52
 Progress: 100%
 Stop time: 2026-05-07 15:26:54
 Total time: 2 seconds

Output

[Launch GrapeTree](#)

Files


[Profiles \(TSV format\)](#)


[Tree \(Newick format\)](#)


[Metadata \(TSV format\)](#)


[Tar file containing all output files](#)

Please note that job results will remain on the server for 7 days.

Number on branches = cgMLST-based allele distances

isolate

- H [1]
- I [1]
- J [1]
- K [1]
- M [1]
- N [1]

PUBMLST – DISTANCE MATRIX



Home > Organisms > *Mycobacteroides abscessus* complex > *Mycobacteroides abscessus* complex isolates > Search or browse database

Search or browse database

Enter search criteria or leave blank to browse all records. Modify form parameters to filter or enter a list of values.

Isolate provenance/primary metadata fields: Isolate contains ECDC +

Sequence bin: total length (Mbp) >= 1 +

Display/sort options: Order by: id ascending Display: 25 records per page

Action: [RESET](#) [SEARCH](#)

Isolate count: 6 (0 [month])

Genome count: 6 (0 [month])

Continent:

Subspecies:

Year:

6 records returned. Click the hyperlinks for detailed information.

Bookmark query: [Bookmark](#)

Id	Isolate	aliases	country	subspecies	year	source	arrH	oia	gnd	murC	pta	putH	ipoB	ST	clonal complex
2111	H	ECDC-FZB_training_2025_1	Canada	abscessus	2018	human	1	2	3	2	2	25	4	222	
2112	I	ECDC-FZB_training_2025_2	Canada	abscessus	2018	human	1	2	3	2	2	25	4	222	
2113	J	ECDC-FZB_training_2025_3	Canada	abscessus	2018	human	1	2	3	2	2	25	4	222	
2114	K	ECDC-FZB_training_2025_4	Canada	abscessus	2018	human	1	2	3	2	2	25	4	222	
2115	M	ECDC-FZB_training_2025_5	Canada	abscessus	2018	environmental	1	2	3	2	2	25	4	222	
2116	N	ECDC-FZB_training_2025_6	Canada	massiliense	2018	environmental	30	31	17	27	21	31	18	33	3

Analysis tools: Breakdown: Fields Two Field Combinations Polymorphic sites Publications Sequence bin

Analysis: BURST Codons Gene Presence GeneScanner **Genome Comparator** BLAST rMLST species id PCR

Export: Dataset Contigs Sequences

Third party: GrapeTree iTOL Microreact PhylorViz PlasmidFinder ReportTree SNPsites

Home > Organisms > *Mycobacteroides abscessus* complex > *Mycobacteroides abscessus* complex isolates > Plugins > Genome comparator

Genome Comparator

Please select the required isolate ids and loci for comparison. In addition to selecting individual loci, you can choose to include all loci defined in schemes by selecting the appropriate scheme description. Alternatively, you can enter the accession number for an annotated reference genome and compare using the loci defined in that.

Isolates: 2111, 2112, 2113, 2114, 2115, 2116

User genomes: Optionally include data not in the database. Upload assembly FASTA file (or zip/tar.gz/tar file containing multiple FASTA files - one per genome).

Loci: Select options Paste list

Include in identifiers: isolate

Schemes: All loci, MLST, Ribosomal MLST, cgMLST

Annotated reference genome: Enter accession number: or choose annotated genome: or upload Genbank/EMBL/FASTA file: Datei auswählen Keine ausgewählt

Parameters / options: Min % identity: 70 Min % alignment: 50 BLASTN word size: 20 Rescan undesignated loci

Distance matrix calculation: ☐ Disable distance matrix calculation ☐ With incomplete loci: ☐ Completely exclude from analysis ☐ Treat as distinct allele ☒ Ignore in pairwise comparison ☒ Exclude pairwise missing loci ☒ Exclude loci paralogous in all ☒ Exclude pairwise paralogous loci

Alignments: ☐ Produce alignments ☒ Include ref sequences in alignment ☐ Align all loci (not only variable) ☐ Create alignment stats Aligner: MAFFT

Core genome analysis: Core threshold (%): 90 Sequence method: [RESET](#) [SUBMIT](#)

☐ Calculate mean distances

Files

Scroll down to end of the page

Text output file

Excel format output

Distance matrix (Nexus format) - Suitable for loading in to SplitsTree. Distances between taxa are calculated as the number of loci with different allele sequences.

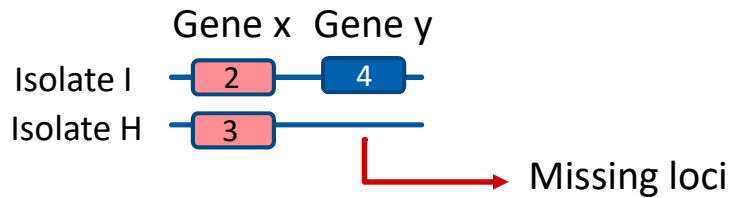
Locus presence frequency (text)

Tar file containing all output files

Splits graph (Neighbour-net; SVG format)

(click to enlarge)

PUBMLST – DISTANCE MATRIX



Home > Organisms > Mycobacteroides abscessus complex > Mycobacteroides abscessus complex isolates > Plugins > Genome comparator

Genome Comparator

Please select the required isolate ids and loci for comparison. In addition to selecting individual loci, you can choose to include all loci defined in schemes by selecting the appropriate scheme description. Alternatively, you can enter the accession number for an annotated reference genome and compare using the loci defined in that.

Isolates

2111
2112
2113
2114
2115
2116

User genomes

Optionally include data not in the database.

Upload assembly FASTA file (or zip/tar.gz/tar file containing multiple FASTA files - one per genome):

[Datei auswählen] Keine ausgewählt

Loci

Select options

Include in identifiers

Isolate

Schemes

All loci
MLST
Ribosomal MLST
cgMLST

Annotated reference genome

Enter accession number:

or choose annotated genome:

or upload Genbank/EMBL/FASTA file:

[Datei auswählen] Keine ausgewählt

Parameters / options

Min % identity: 70

Min % alignment: 50

BLASTN word size: 20

Rescan undesignated loci

Distance matrix calculation

Disable distance matrix calculation

With incomplete loci:

Completely exclude from analysis

Treat as distinct allele

Ignore in pairwise comparison

☒ Exclude pairwise missing loci

Exclude loci paralogous in all

Exclude pairwise paralogous loci

Alignments

Produce alignments

Include ref sequences in alignment

Align all loci (not only variable)

Create alignment stats

Aligner: MAFFT

Core genome analysis

Core threshold (%): 90

Sequence method:

Calculate mean distances

RESET **SUBMIT**

With option „Exclude pairwise missing loci“ not checked (default)

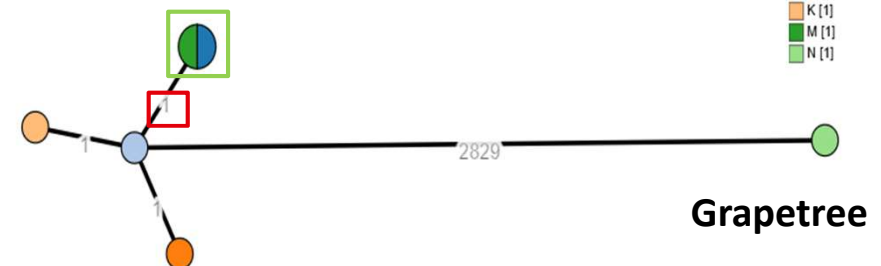
MATRIX

2111 H Tattoo_lesion	0						
2112 I Tattoo_lesion	2	0					
2113 J Tattoo_lesion	3	1	0				
2114 K Tattoo_lesion	6	6	7	0			
2115 M Tab_water_hypothetical_	0	2	3	6	0		
2116 N Shower_hypothetical_	2875	2875	2875	2875	2875	0	

With option „Exclude pairwise missing loci“ checked → most similar to grapetree distances

MATRIX

2111 H Tattoo_lesion	0						
2112 I Tattoo_lesion	1	0					
2113 J Tattoo_lesion	2	1	0				
2114 K Tattoo_lesion	0	1	2	0			
2115 M Tab_water_hypothetical_	0	1	2	0	0		
2116 N Shower_hypothetical_	2827	2828	2828	2823	2827	0	



Recommendation: exclude missing loci (to avoid inflated distances due to technical errors e.g. low coverage, assembly errors)

DISTANCE MATRICES COMPARISON

pubMLST - cgMLST with Genome comparator - With option „Exclude pairwise missing loci“ checked

```
MATRIX
2111|H|Tattoo_lesion    0
2112|I|Tattoo_lesion    1    0
2113|J|Tattoo_lesion    2    1    0
2114|K|Tattoo_lesion    0    1    2    0
2115|M|Tab_water__hypothetical_ 0    1    2    0    0
2116|N|Shower__hypothetical_ 2827 2828 2828 2823 2827 0
```

Different methods might result in slightly different distance matrices
(mainly depends on filter steps – e.g. removal of recombination)

Original publication – cgSNP with SNVphyl

Table 3. SNV matrix of tattoo isolates representing nucleotide differences between isolates.

Strain	H	I	J	K	G	F	Reference
H	0	3	4	7	45715	45909	45701
I	3	0	3	10	45714	45908	45700
J	4	3	0	11	45715	45909	45701
K	7	10	11	0	45714	45908	45700
G	45715	45714	45715	45714	0	1270	36
F	45909	45908	45909	45908	1270	0	1256
Reference	45701	45700	45701	45700	36	1256	0

Single nucleotide variations between study isolates as determined by SNVPhyl. Reference is *M. abscessus* ATCC19977.

cgSNP with MTBseq

H_libx					
I_libx	3				
J_libx	4	3			
K_libx	0	3	4		
M_libx	0	3	4	0	

CGSNP ANALYSIS WITH MTBSEQ



https://github.com/ngs-fzb/MTBseq_source

Code:

```
$ conda install -c bioconda mtbseq
```

```
$ conda activate mtbseq
```

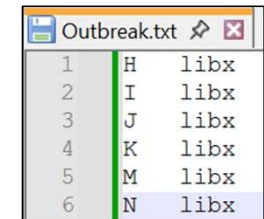
```
$ cd path/to/FastQ
```

```
$ MTBseq --step TBfull --ref M._abscessus_CIP-104536T_2014-02-03 --threads 1 --continue --sample Outbreak.txt
```

Comparative analysis

(i.e. Strain ID and lib ID if your fastq file is named like StrainID_libID_run_date_xbp_R*.fastq.gz).

In this case, 6 samples will be compared.



1	H	libx
2	I	libx
3	J	libx
4	K	libx
5	M	libx
6	N	libx

- Goal: identify the source of the skin infection outbreak
 - Task 1: Determine which NTM (sub)species were isolated from the environmental samples (L-O)
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→ Complete all results in **Task_Exercise2026_NTML.xlsx**

Task 6: Formulate a hypothesis regarding the transmission route

A	B	C	D	E	F	G	H	I	J	K	L
Sample ID	Reference	Isolation Source	Country of Isolation	Species	Subspecies	MLST ST	DCC	Amikacin resistance	Macrolide resistance	Fluoroquinolone resistance	Part of outbreak?
H	Wuzinski 2020	Patient 1	Canada	abscessus	abscessus						
I	Wuzinski 2020	Patient 2	Canada	abscessus	abscessus						
J	Wuzinski 2020	Patient 3	Canada	abscessus	abscessus						
K	Wuzinski 2020	Patient 4	Canada	abscessus	abscessus						
L	Hypothetical investigation	Shower	Canada								
M	Hypothetical investigation	Tap water	Canada								
N	Hypothetical investigation	Shower	Canada								
O	Hypothetical investigation	Aquarium	Canada								

DOES MY ISOLATE BELONG TO A DCC?

1. Does my isolate has an ST that has been related with known DCCs?

E.g. DCC3a strains → most often ST33

2. Does my isolate cluster closely with known DCC isolates on the whole-genome level?

→ Use **reference** set (e.g. ECDC learning portal)

Homework between sessions		
Participants shall complete the tasks by following the tutorial provided in the learning portal (2026_ECDC_tutorial_NTM.pdf) until the next session.		
 2026_ECDC_tutorial_NTM.pdf		☐
 Task_Exercise2026_NTM.xlsx		☐
 110_Ref_Mabscessus_pubMLST.xlsx		☐

1. cgSNP (Ruis2021)

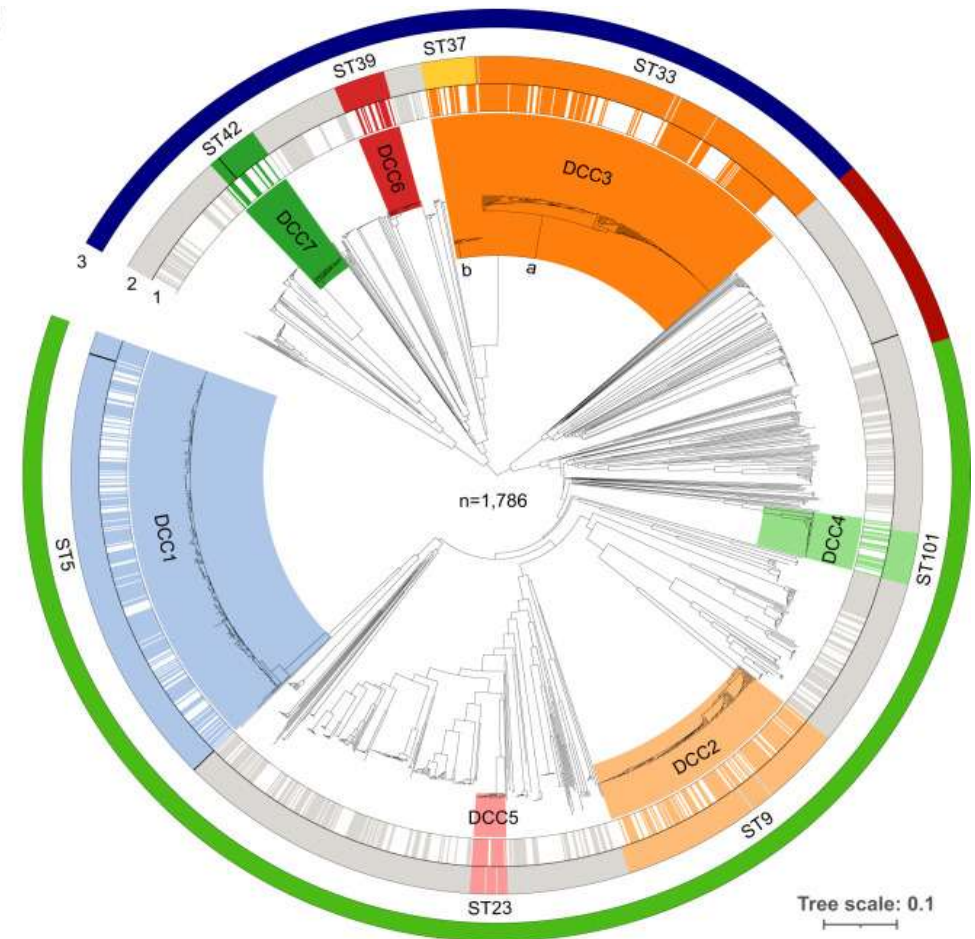
- DCC1
- DCC2
- DCC3
- DCC4
- DCC5
- DCC6
- DCC7
- Non-DCC strains
- Unknown

2. 7-loci MLST

- ST5
- ST9
- ST33
- ST37
- ST101
- ST23
- ST39
- ST42
- No ST
- Other ST

3. Subspecies

- massiliense*
- bolletii*
- abscessus*

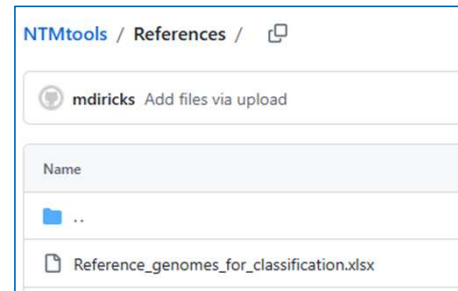


Diricks et al. 2022

M. ABSCCESSUS DCC CLASSIFICATION



Alternative source to get the reference list: <https://github.com/ngs-fzb/NTMtools/tree/main/References>



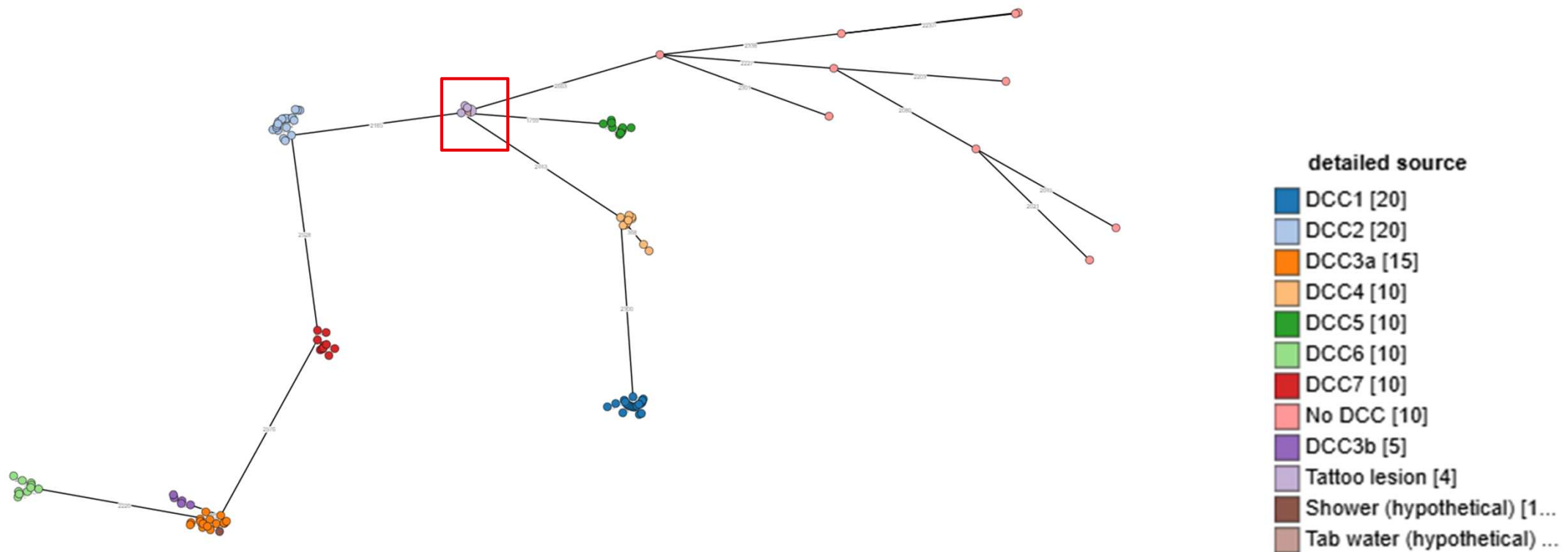
Compare your *M. abscessus* genome with this reference set to confirm subspecies and to determine whether it belongs to a DCC

List of ~100 genomes with known DCC classification

SeqSphere ID	cgMLST cluster (Diricks 2021)	FastBAPS cluster (Ruis2021)	ST	CF states	Continent	Country	Location	Sample Date	Run accession number	Patient	Biosample	BioProject	Reference
ABA-NC_010337.1-Ripoll201	DCC1	DCC1	5	Non-CF	Europe	France	Unknown	Unknown	Unknown	Public_abscessus4	SAMEA31382	PRJNA6161	Ripoll 2003
GCF-300138775.1	DCC1	DCC1	5	Non-CF	Europe	UK	Grampian	Unknown	ERR340511	SMRL_BT	SAMEA20715	PRJEB2773	Bryant 2016
GCF-300134335.1	DCC1	DCC1	5	CF	Europe	UK	Grampian	2011	ERR340526	SMRL_CY	SAMEA20715	PRJEB2773	Bryant 2016
GCF-300137325.1	DCC1	DCC1	5	CF	Europe	UK	Manchester	2013	ERR340573	AHL_J	SAMEA20716	PRJEB2773	Bryant 2016
GCF-300133025.1	DCC1	DCC1	5	CF	NorthAmerica	USA	UNC_Chapel_Hill	2005	ERR343268	UNC_I	SAMEA21622	PRJEB2773	Bryant 2016
GCF-300133085.1	DCC1	DCC1	5	Non-CF	NorthAmerica	USA	UNC_Chapel_Hill	2006	ERR343274	UNC_CS	SAMEA21486	PRJEB2773	Bryant 2016
GCF-300137365.1	DCC1	DCC1	5	CF	Europe	UK	Leeds	2013	ERR363410	RVL_AB	SAMEA21606	PRJEB2773	Bryant 2016
GCF-300133745.1	DCC1	DCC1	5	Non-CF	NorthAmerica	USA	UNC_Chapel_Hill	2012	ERR363425	UNC_CB	SAMEA21427	PRJEB2773	Bryant 2016
GCF-300140135.1	DCC1	DCC1	5	CF	Europe	Denmark	Copenhagen	Unknown	ERR363146	DEN_E	SAMEA21567	PRJEB2773	Bryant 2016
GCF-300140265.1	DCC1	DCC1	5	Non-CF	NorthAmerica	USA	UNC_Chapel_Hill	2011	ERR363167	UNC_BU	SAMEA21576	PRJEB2773	Bryant 2016
GCF-300140675.1	DCC1	DCC1	5	CF	Europe	Denmark	Skejby	Unknown	ERR373344	DEN_C	SAMEA21525	PRJEB2773	Bryant 2016
GCF-300140685.1	DCC1	DCC1	5	Non-CF	NorthAmerica	USA	UNC_Chapel_Hill	2006	ERR373372	UNC_BV	SAMEA21565	PRJEB2773	Bryant 2016
GCF-300133515.1	DCC1	DCC1	5	CF	Europe	Holland	Holland	2009	ERR453733	HOL_A	SAMEA22535	PRJEB2773	Bryant 2016
GCF-300132205.1	DCC1	DCC1	5	CF	Oceania	Australia	TPCH	2006	ERR453732	AUS_M	SAMEA22535	PRJEB2773	Bryant 2016
GCF-300132315.1	DCC1	DCC1	5	Non-CF	Oceania	Australia	TPCH	2008	ERR453854	AUS_AL	SAMEA22536	PRJEB2773	Bryant 2016
GCF-300135825.1	DCC1	DCC1	5	Non-CF	Oceania	Australia	GPH	2011	ERR453855	AUS_AN	SAMEA22536	PRJEB2773	Bryant 2016
GCF-300137115.1	DCC1	DCC1	5	CF	Oceania	Australia	RCH	2012	ERR453922	AUS_AE	SAMEA22536	PRJEB2773	Bryant 2016
GCF-300132605.1	DCC1	DCC1	5	Non-CF	Oceania	Australia	GPH	2007	ERR453966	AUS_AW	SAMEA22536	PRJEB2773	Bryant 2016
GCF-300133115.1	DCC1	DCC1	5	CF	Europe	UK	Leicester	2008	ERR453986	LEL_C	SAMEA22537	PRJEB2773	Bryant 2016
GCF-300133175.1	DCC1	DCC1	5	Non-CF	Oceania	Australia	GPH	2008	ERR484380	AUS_AY	SAMEA22758	PRJEB2773	Bryant 2016
GCF-017183335.1	DCC2	DCC2	3	CF	Oceania	Australia	NSW	2013	Unknown	DED_1	SAMN168287	PRJNA6690	Dedrick 2021
GCF-300130255.1	DCC2	DCC2	3	CF	Europe	UK	Lothian	2001	ERR337807	SMRL_U	SAMEA20704	PRJEB2773	Bryant 2016
GCF-300135015.1	DCC2	DCC2	3	Non-CF	Europe	UK	Lothian	2011	ERR340437	SMRL_BA	SAMEA20706	PRJEB2773	Bryant 2016

Diricks et al. 2022; PMID: 35999208

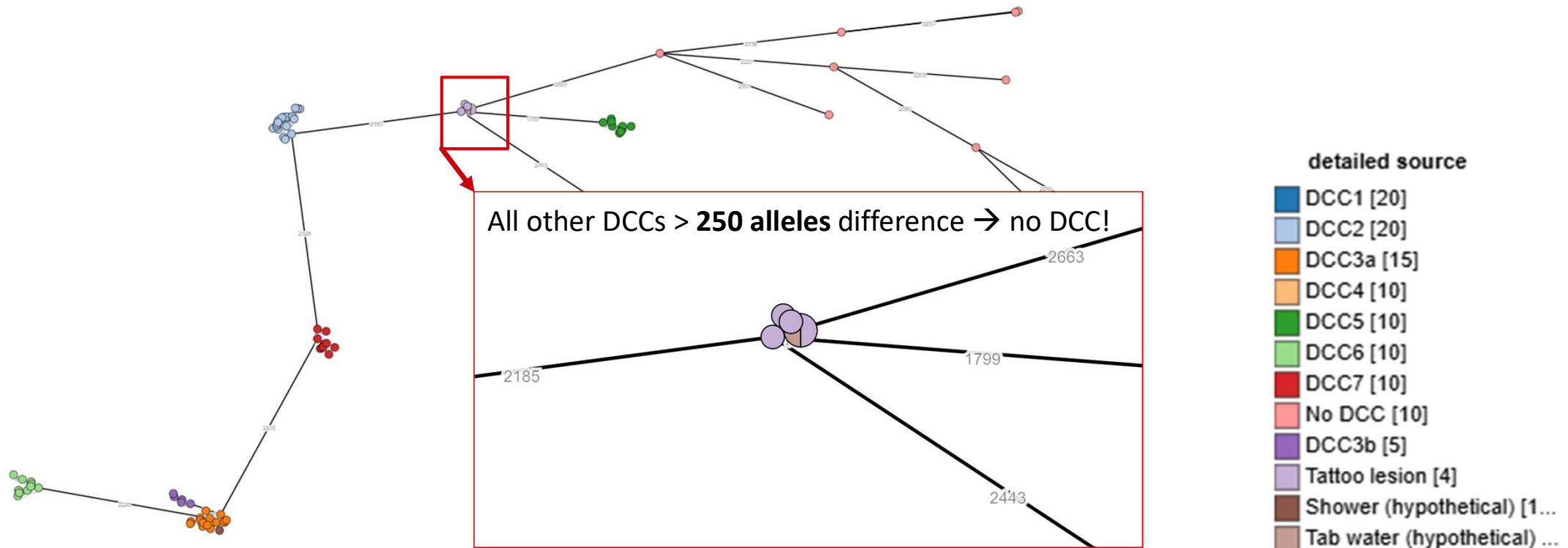
- Does my isolate cluster closely with known DCC isolates on the whole-genome level?
 - Compare your isolates with an available **reference** set (see tutorial)



DOES MY ISOLATE BELONG TO A DCC?

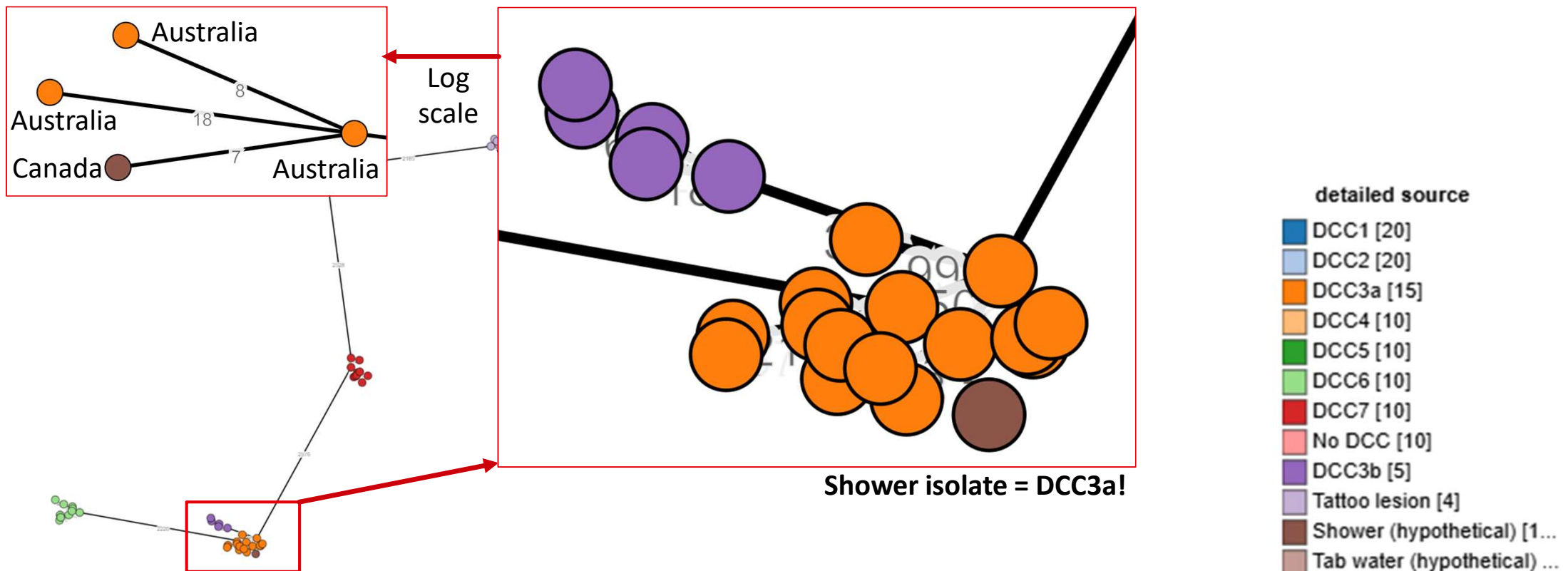


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DOES MY ISOLATE BELONG TO A DCC?

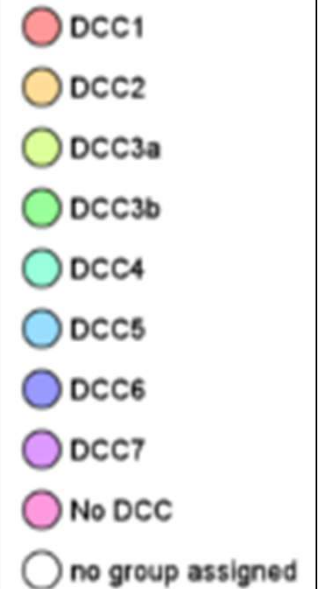
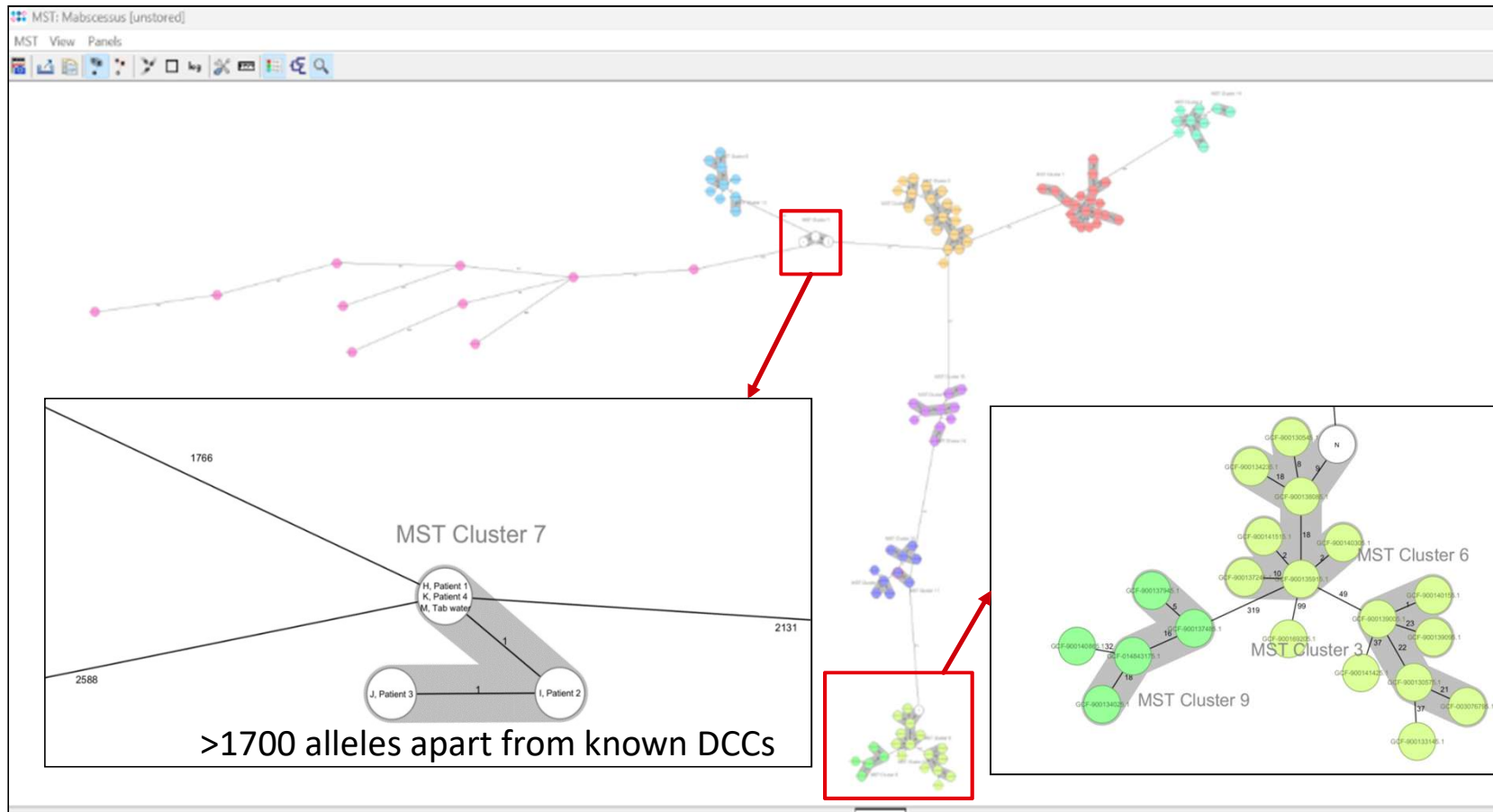
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RIDOM TYPER



<https://www.ridom.de/ridom-typer>



RESULTS



A	B	C	D	E	F	G	H	I	J	K	L
Sample ID	Reference	Isolation Source	Country of Isolation	Species	Subspecies	DCC	MLST ST	Amikacin resistance	Macrolide resistance	Fluoroquinolone resistance	Part of outbreak?
H	Wuzinski 2020	Patient 1	Canada	abscessus	abscessus	/	222	No known mutation - S	erm(41) p.Trp10Arg - S	No known mutation	Yes
I	Wuzinski 2020	Patient 2	Canada	abscessus	abscessus	/	222	No known mutation - S	erm(41) p.Trp10Arg - S	No known mutation	Yes
J	Wuzinski 2020	Patient 3	Canada	abscessus	abscessus	/	222	No known mutation - S	erm(41) p.Trp10Arg - S	No known mutation	Yes
K	Wuzinski 2020	Patient 4	Canada	abscessus	abscessus	/	222	No known mutation - S	erm(41) p.Trp10Arg - S	No known mutation	Yes
L	Hypothetical investigation	Shower	Canada	intracellulare	chimaera	/	81	No known mutation - S	No known mutation	#N/A	No
M	Hypothetical investigation	Tap water	Canada	abscessus	abscessus	/	222	No known mutation - S	erm(41) p.Trp10Arg - S	No known mutation	Yes
N	Hypothetical investigation	Shower	Canada	abscessus	massiliense	DCC 3a	33	No known mutation - S	Truncated erm(41) - S	No known mutation	No
O	Hypothetical investigation	Aquarium	Canada	marinum	/	/	22	#N/A	#N/A	#N/A	No

What is the most likely transmission route?

Ink tattoo shop



Negative

Tap water tattoo shop



Isolate M

Aquarium patient 1



Sample O

Shower patient 1



Sample L (SGM)
Sample N (RGM)

RESULTS



Sample ID	Reference	Isolation Source	Country of Isolation	Species	Subspecies	DCC	MLST ST	Amikacin resistance	Macrolide resistance	Fluoroquinolone resistance	Part of outbreak?
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N	Hypothetical investigation	Shower	Canada	abscessus	massiliense	DCC 3a	33	No known mutation - S	Truncated erm(41) - S	No known mutation	No
O	Hypothetical investigation	Aquarium	Canada	marinum	/	/	/	#N/A	#N/A	#N/A	No
/	Hypothetical investigation	Ink tattoo shop	Canada	No growth	/	/	/	/	/	/	/

What is the most likely transmission route?

BioMed Research International



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Investigation of Two *Mycobacterium abscessus* Outbreaks in Quebec Using Whole Genome Sequencing

Michelle Wuzinski, Hafid Soualhine, Emilie Valliere, Pierre-Marie Akochy, Nancy Cloutier, Aaron Petkau, Brynn Kaplen, Maryse Duchesne, Jasmin Villeneuve, Meenu K. Sharma

First published: 09 November 2020 | <https://doi.org/10.1155/2020/7092053> | Citations: 1

Academic Editor: Luis Fernandes

- Source of infection could not be identified in tattoo outbreak
- Hypothesized that tap water bottle was likely a cause since it was routinely used for tattoo ink dilution at the parlour
- Drastic infection control measures were put into place including equipment disinfection and replacements, disposal material, and reagent changes and disinfection → no further cases

