Reporting Comparative Genomic Data

Dr Courtney R Lane
Lead Epidemiologist, Centre for Pathogen Genomics
Doherty Institute, The University of Melbourne

A joint venture between The University of Melbourne and The Royal Melbourne Hospital

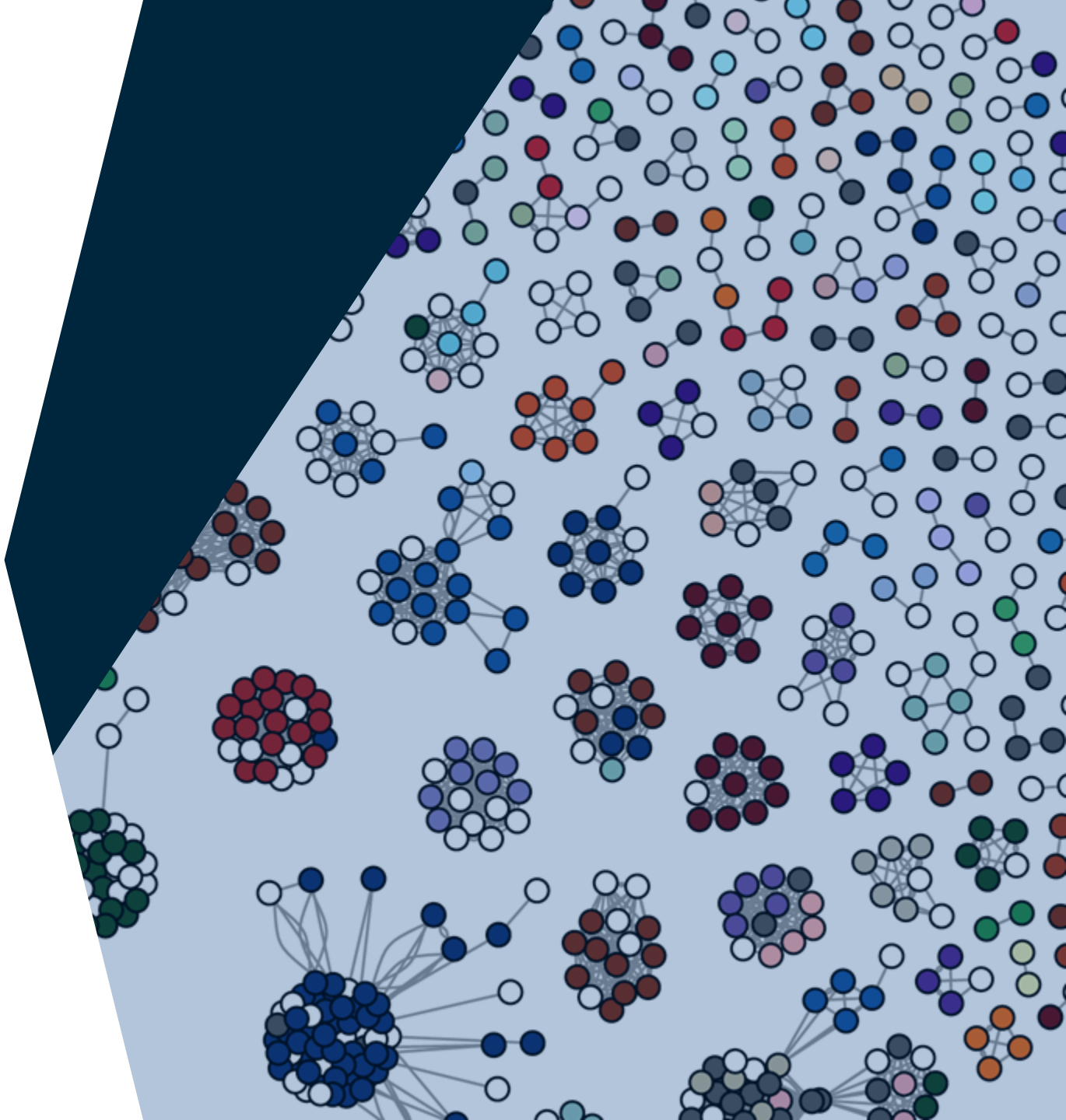
Webinar Overview

Recap: Reporting Comparative Genomics Results

How to write a report (step-by-step)

1. Consider your audience & purpose
2. Clearly outline methods
3. Report relevant sequence characteristics
4. Report comparative genomics results & metadata
5. Interpret results, draft narrative & risk assessment
6. Ensure limitations are clear
7. Enact appropriate approval processes

Summary



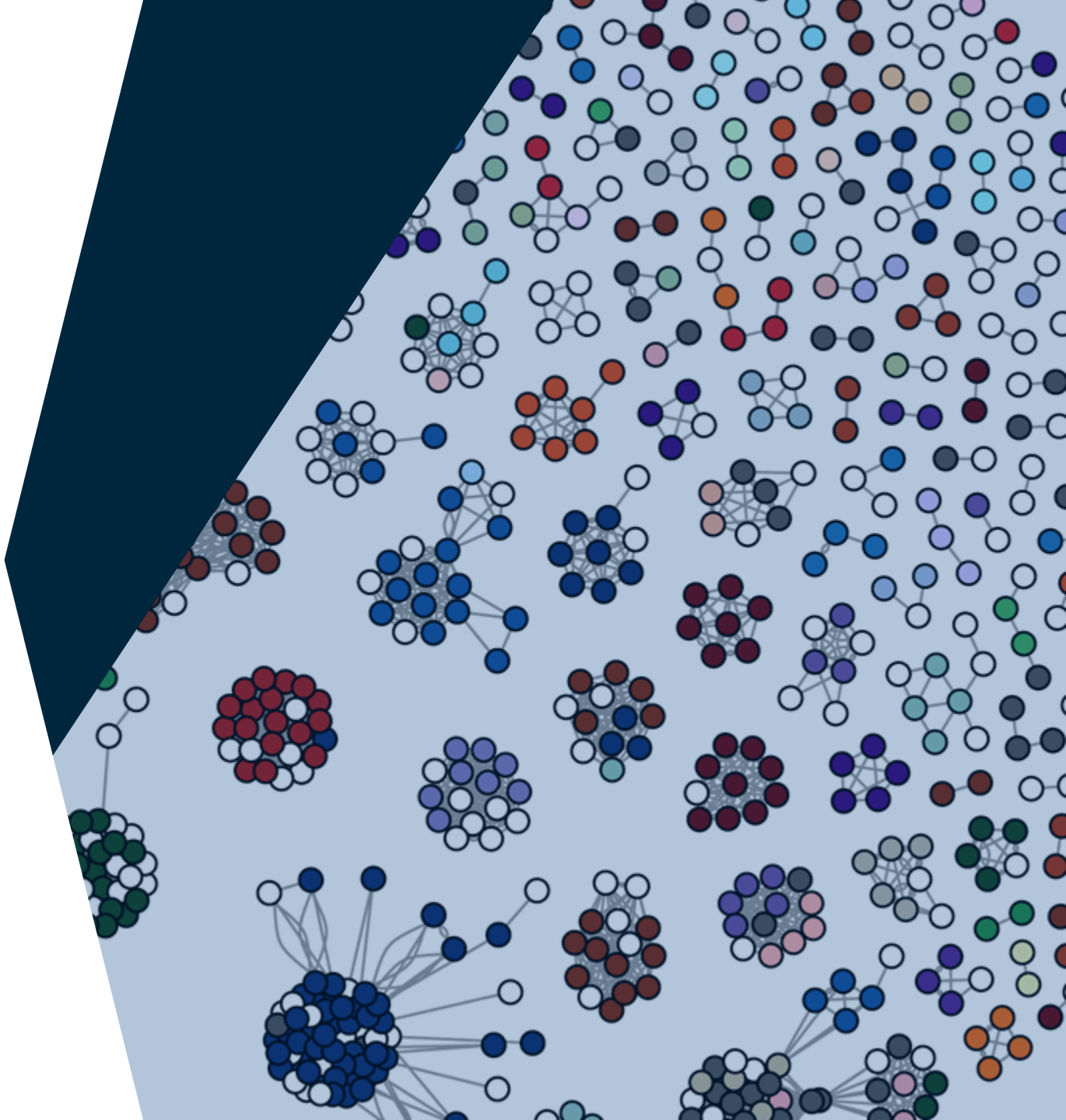
Webinar Overview

Recap: Reporting Comparative Genomics Results

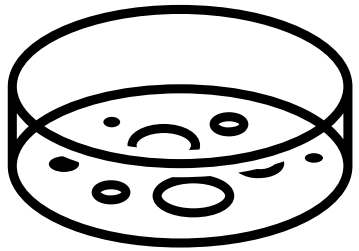
How to write a report (step-by-step)

1. Consider your audience & purpose
2. Clearly outline methods
3. Report relevant sequence characteristics
4. Report comparative genomics results & metadata
5. Interpret results, draft narrative & risk assessment
6. Ensure limitations are clear
7. Enact appropriate approval processes

Summary

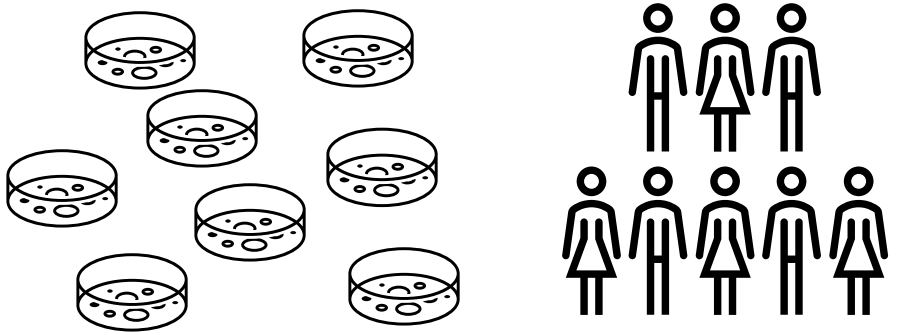


Recap: What types of genomic results do we report?



SINGLE ISOLATES

- **Speciation**
- **Typing**
  - Generic e.g. MLST, cgMLST
  - Species-specific typing schemes
    - *In silico* serotypes, capsule types
    - Others e.g. NG-MAST, *emm* typing
- **AMR**
  - Resistance mechanisms, inferred phenotype
- **Virulence factors**



MULTIPLE ISOLATES

- **Line list reports** – multiple independent results
  - Usually for surveillance/public health

- **Comparative genomics**
  - Compares multiple genomes to each other to establish genomic relationships

Slide courtesy of A/Prof Norelle Sherry

Recap: What do we report?

Single sample reports

Microbiological Diagnostic Unit - Public Health Laboratory

	MIC (mg/L)	Interpretation
Amikacin	>32	Resistant
Aztreonam	>32	Resistant
Cefepime	>16	Resistant
Ceftaz-Avibactam	>16	Resistant
Ceftazidime	>16	Resistant
Ceftoloz-Tazobactam	>16	Resistant
Ceftriaxone	>32	Resistant
Colistin	≤0.5	Susceptible
Ertapenem	>8	Resistant
Gentamicin	>8	Resistant
Imipenem-Relebactam	>8	Resistant
Meropenem	>16	Resistant
Meropenem-Vaborbactam	>16	Resistant
Piper-Tazo	>128	Resistant
Tigecycline	≤0.5	Susceptible
Tobramycin	>8	Resistant

Service 7035 Bacterial isolates: antimicrobial susceptibility testing (Etest)

	MIC (mg/L)	Interpretation
Aztreonam-Avibactam	8	Resistant

Service 7039 Bacterial isolates: antimicrobial susceptibility testing (Disc Diffusion)

	Zone size (mm)	Interpretation
Cefiderocol	18	Resistant

Service 6200 Bacterial antimicrobial resistance: characterisation

	Result
Resistance genes (alleles) detected	OXA-181,NDM-5,rmtB1
MLST type	2851

MICs interpreted according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) methods and clinical breakpoints (2025 ver 15).

For systemic infections, aminoglycosides must be used in combination with other active therapy. A 'susceptible' result indicates the isolate most likely does not harbour acquired resistance mechanisms. A result of 'resistant' indicates the isolate harbours resistance mechanisms.

For systemic infections, colistin must be used in combination with other active therapy. A 'susceptible' result indicates the isolate most likely does not harbour acquired resistance mechanisms. A 'resistant' results indicates the isolate harbours resistance mechanisms.

NATA/RCPA accreditation does not cover the performance of SOP ATS006.

MMS118 is the detection of acquired antimicrobial resistance genes from whole genome sequencing. Presence of antimicrobial resistance genes does not necessarily infer phenotypic resistance and the absence of resistance genes do not imply susceptibility. Please contact the Medical Microbiologist at MDU PHL if further information is required.

The MLST and resistance gene alleles are predicted from *in silico* analysis of the genome sequence data.

rmtB1 is a 16S rRNA methyltransferase gene.

This report constitutes a diagnosis of a notifiable infectious disease that must be notified to the Victorian Department of Health by the requesting doctor and the pathology service in accordance with the Victorian Public Health and Wellbeing Regulations 2019.

MDU PHL will submit this result to the National Alert System for Critical Antimicrobial Resistances (CARAlert).

Routine surveillance reports

Sample ID	Date collected	Sample type	2x2	DOB	MLST	cgT	2 SNP	5 SNP	10 SNP	New	Report ID	Analysis Date
	24/12/2024	Human		01/12/1993	19	2938	UC	UC	1		R2025-001704	24/01/2025
	24/08/2024	Human		01/08/1999	19	2938	UC	UC	1		R2025-001704	24/01/2025
	11/08/2024	Human		01/03/2005	19	2938	UC	UC	1		R2025-001704	24/01/2025
	02/08/2024	Human		01/04/1952	19	2938	UC	UC	1		R2025-001704	24/01/2025
	30/09/2024	Non-human			19	2938	UC	2.1	2		R2025-001704	24/01/2025
	07/08/2024	Human		01/04/2020	19	2938	UC	2.1	2		R2025-001704	24/01/2025
	17/12/2024	Human		01/08/1948	19	2938	UC	UC	2		R2025-001704	24/01/2025
	01/10/2024	Non-human			19	2938	UC	UC	2		R2025-001704	24/01/2025
	15/11/2024	Human		01/12/1991	19	2938	UC	3.1	3		R2025-001704	24/01/2025
	30/08/2024	Human		01/08/2004	19	2938	UC	3.1	3		R2025-001704	24/01/2025
	16/11/2024	Human		01/09/2022	19	2938	4.1.1	4.1	4		R2025-001704	24/01/2025
	28/10/2024	Human		01/05/1958	19	2938	4.1.1	4.1	4		R2025-001704	24/01/2025
	03/01/2025	Human		01/12/1988	19	2938	5.1.1	5.1	5	New	R2025-001704	24/01/2025
	05/01/2025	Human		01/11/1979	19	2938	5.1.1	5.1	5	New	R2025-001704	24/01/2025
	30/12/2024	Human		01/01/2023	19	2938	5.1.1	5.1	5	New	R2025-001704	24/01/2025
	01/01/2025	Human		01/04/1989	19	2938	5.1.1	5.1	5	New	R2025-001704	24/01/2025
	30/12/2024	Human		01/06/2002	19	2938	5.1.1	5.1	5	New	R2025-001704	24/01/2025
	14/12/2024	Human		01/06/1942	19	2938	UC	UC	UC		R2025-001704	24/01/2025
	30/10/2024	Human		01/01/1958	19	2938	UC	UC	UC		R2025-001704	24/01/2025
	31/07/2024	Non-human			19	2938	UC	UC	UC		R2025-001704	24/01/2025

Ad hoc investigations / analyses

Phylogenetic analysis report:
OXA-72 producing *Acinetobacter baumannii* novel ST

To:

Copied to:

Report ID: R2024-021821
Issue Date: 31/10/2024
Prepared By: Catherine Glover, Himal Shrestha, Mathilda Wilmot
Authorised By: A/Prof Norelle Sherry (Deputy Director)

1. ANALYSIS SUMMARY

As part of the combined epidemiological and genomic surveillance of carbapenemase-producing organisms (CPO) in Victoria, phylogenetic analyses are conducted where the potential for local transmission exists among groups of isolates of the same species, sequence type (ST), and carbapenemase gene combination.

A phylogenetic analysis was conducted following the recent identification of an OXA-72 producing *Acinetobacter baumannii* novel ST isolate from a patient with admission to Health.

2. RESULTS

On phylogenetic analysis, the recent OXA-72 producing *Acinetobacter baumannii* novel ST isolate from patient (Lab ID was found to be closely related to an isolate from patient (Lab ID Table 1). No other samples of this species, gene and novel ST combination were identified in the dataset at MDU PHL.

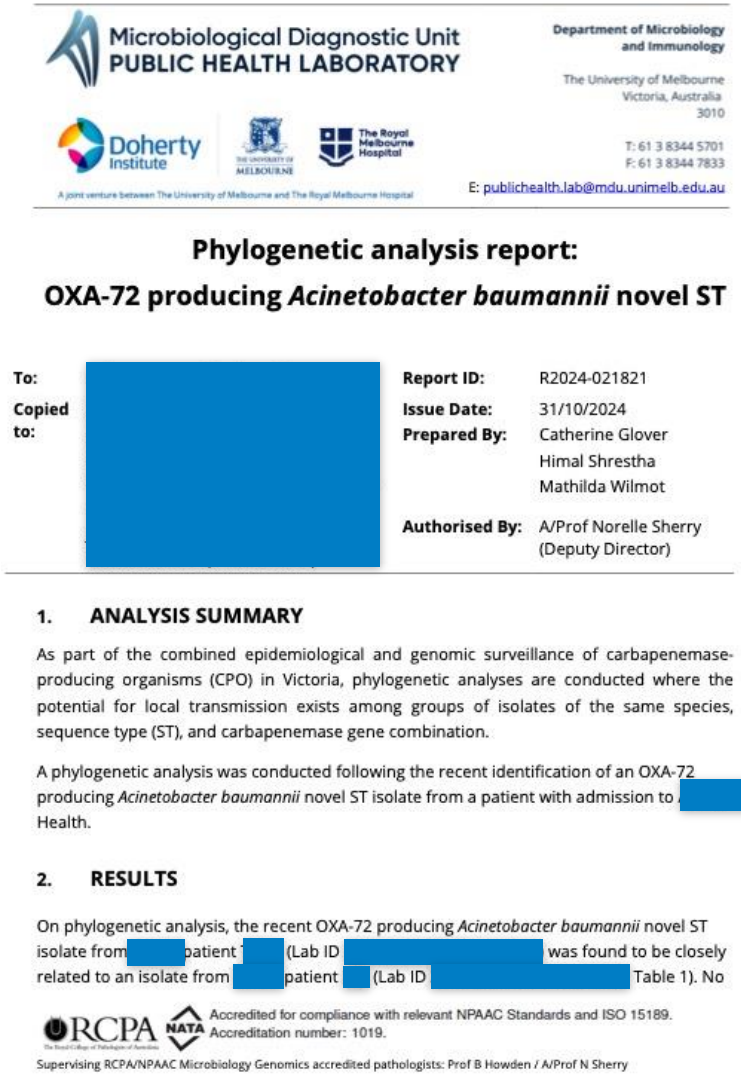
This is consistent with transmission between patients or acquisition from a common source (environmental or person) but should be considered within the context of epidemiological evidence. Additional epidemiological data, including details of patient's hospital admissions would assist in the interpretation and understanding of these genomic relationships.

Table 1 List of closely *Acinetobacter baumannii* novel ST isolates

Name	Sex	Date of Birth	UR	Lab ID	Date of Collection	MDU sample ID
	Female				07/10/2024	
	Male				30/09/2024	

Recap: What do we report?

Ad hoc investigations / analyses



Microbiological Diagnostic Unit
PUBLIC HEALTH LABORATORY

Department of Microbiology and Immunology
The University of Melbourne
Victoria, Australia
3010

Doherty Institute
A joint venture between The University of Melbourne and The Royal Melbourne Hospital

T: 61 3 8344 5701
F: 61 3 8344 7833
E: publichealth.lab@mdu.unimelb.edu.au

Phylogenetic analysis report:

OXA-72 producing *Acinetobacter baumannii* novel ST

To: [redacted]
Copied to:

Report ID: R2024-021821
Issue Date: 31/10/2024
Prepared By: Catherine Glover, Himal Shrestha, Mathilda Wilmot
Authorised By: A/Prof Norelle Sherry (Deputy Director)

1. ANALYSIS SUMMARY

As part of the combined epidemiological and genomic surveillance of carbapenemase-producing organisms (CPO) in Victoria, phylogenetic analyses are conducted where the potential for local transmission exists among groups of isolates of the same species, sequence type (ST), and carbapenemase gene combination.

A phylogenetic analysis was conducted following the recent identification of an OXA-72 producing *Acinetobacter baumannii* novel ST isolate from a patient with admission to [redacted] Health.

2. RESULTS

On phylogenetic analysis, the recent OXA-72 producing *Acinetobacter baumannii* novel ST isolate from [redacted] patient [redacted] (Lab ID [redacted] was found to be closely related to an isolate from [redacted] patient [redacted] (Lab ID [redacted] Table 1). No

RCPA NATA Accredited for compliance with relevant NPAAC Standards and ISO 15189. Accreditation number: 1019.

Supervising RCPA/NPAAC Microbiology Genomics accredited pathologists: Prof B Howden / A/Prof N Sherry

other samples of this species, gene and novel ST combination were identified in the dataset at MDU PHL.

This is consistent with transmission between patients or acquisition from a common source (environmental or person) but should be considered within the context of epidemiological evidence. Additional epidemiological data, including details of patient's hospital admissions would assist in the interpretation and understanding of these genomic relationships.

Table 1 List of closely *Acinetobacter baumannii* novel ST isolates

Name	Sex	Date of Birth	[redacted] UR	[redacted] Lab ID	Date of Collection	MDU sample ID
[redacted]	Female	[redacted]			07/10/2024	[redacted]
	Male				30/09/2024	

3. DISCLAIMER:

Results should be interpreted in conjunction with available epidemiological data and used for epidemiological purposes only. Epidemiological links should be investigated to support genomic clusters identified by phylogenetic analysis.

- Defined list of sequences, based on set criteria
  - e.g. Species, resistance gene, location
- OR *ad hoc*, based on suspicion OR surveillance findings

- **<u>Investigate</u>** putative outbreaks
- Phylogenetic analysis & interpretation

Recap: What do we report?

Routine surveillance reports

Microbiological Diagnostic Unit
PUBLIC HEALTH LABORATORY

Department of Microbiology and Immunology
The University of Melbourne
Victoria, Australia
3010

Doherty Institute
A joint venture between The University of Melbourne and The Royal Melbourne Hospital

T: 61 3 8344 5701
F: 61 3 8344 7833
E: publichealth.lab@mdu.unimelb.edu.au

Phylogenetic analysis report:
***Salmonella* Typhimurium Surveillance**

To: [redacted]
Copy to:

Report ID: [redacted]
Issue Date:
Prepared By:

Authorised By: A Prof Norelle Sherry (Deputy Director)

1. Analysis Summary

Here we present data on Victorian human and food samples of *Salmonella* Typhimurium (STm) for the period **16/07/2025 to 16/01/2026** (6 month rolling window). When a collection date is not available, the received date is used to determine inclusion in the reporting period.

- There are 19 new isolates available for this report.
- Phylogenetic analysis is performed on cgT groups (excluding cgT UC) containing more than three isolates, where one or more new isolates were added since last report.
- Phylogenetic analysis and single linkage clustering of isolates in the reporting period is shown in Section 2 and Appendix A.

Table 1. Count of observed cgT groups with new isolates over the reported period. UC = unclustered.

cgT	Added since the last report	Total in cgT (6 months)
169	1	5
220	1	3
226	1	1
323	1	1
1313	1	1
1668	1	8
2168	7	145
2411	1	7
3268	2	12
3302	1	4
UC	2	10

2.6 cgT3268

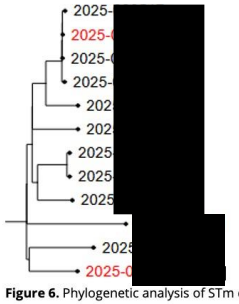


Figure 6. Phylogenetic analysis of STm cgT3268 based on core genome SNPs of cases received in MDU PHL for 6 month reporting period ending 16/01/2026. Sample ID highlighted in red is new to this report.

Table 6. Clustering of new STm cgT3268 isolates at the 2, 5, and 10 SNP single linkage clustering thresholds for reporting period ending 16/01/2026. Full line listed clustering data (n=12) shown in appendix A.

Sample ID	PHESS ID	Date collected	Sample type	MLST	cgT	2 SNP	5 SNP	10 SNP
[redacted]	[redacted]	20/08/2025	Human	19	3268	UC	2.1	2
		28/07/2025	Human	19	3268	UC	2.1	2
		22/12/2025	Human	19	3268	3.1.1	3.1	3
		13/12/2025	Human	19	3268	3.1.1	3.1	3
		03/12/2025	Human	19	3268	3.1.1	3.1	3
		23/09/2025	Human	19	3268	3.1.1	3.1	3
		22/12/2025	Human	19	3268	UC	UC	UC
		21/12/2025	Human	19	3268	UC	UC	UC
		25/11/2025	Human	19	3268	UC	UC	UC
		08/11/2025	Human	19	3268	UC	UC	UC
		28/10/2025	Human	19	3268	UC	UC	UC
		16/09/2025	Human	19	3268	UC	UC	UC

- All isolates meeting a surveillance criteria
  - e.g. Species, resistance gene, location
- **Detect** putative outbreaks
- Isolate characterization, phylogenetic analysis, clustering & interpretation

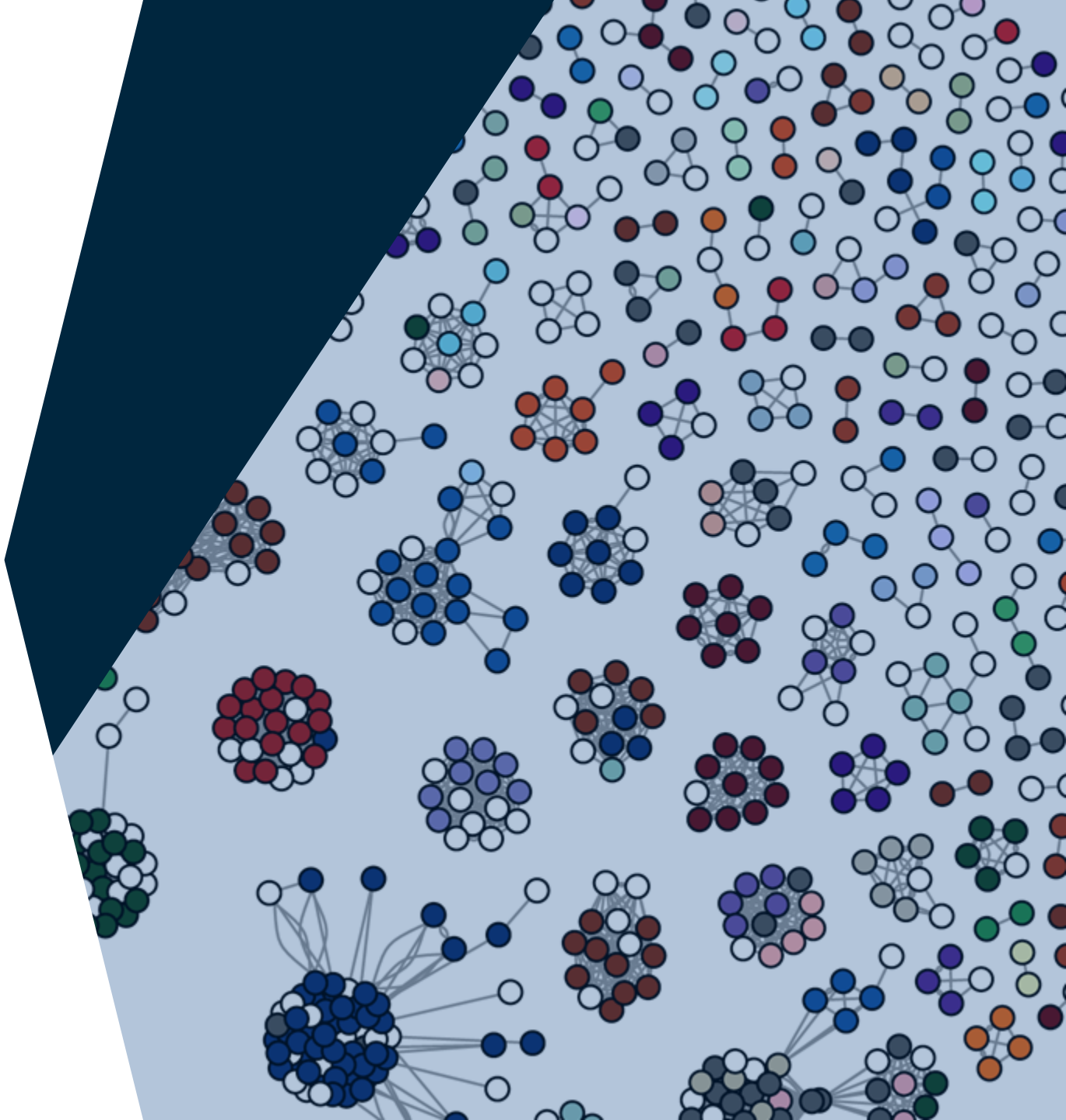
Webinar Overview

Recap: Reporting Comparative Genomics Results

How to write a report (step-by-step)

1. Consider your audience & purpose
2. Clearly outline methods
3. Report relevant sequence characteristics
4. Report comparative genomics results & metadata
5. Interpret results, draft narrative & risk assessment
6. Ensure limitations are clear
7. Enact appropriate approval processes

Summary



Example report

Microbiological Diagnostic Unit
Public Health Laboratory
Department of Microbiology & Immunology
University of Melbourne, Victoria 3010
Telephone: 61 3 8344 5713
Facsimile: 61 3 8344 7833
Email: publichealth.lab@mdu.unimelb.edu.au

Listeria monocytogenes Surveillance REPORT

REPORTING PERIOD TO: 11/01/2026

To: OzFoodNet_Epidemiologists

Copy to: [redacted]

Report ID: R[redacted]

Issue Date: 14/01/2026

Prepared By: [redacted]

Authorised By: A Prof Norelle Sherry (Deputy Director)

1. ANALYSIS SUMMARY

A total of 40 isolates; 19 human cases and 21 non-human sample isolates were received in the 24-week reporting period ending 11/01/2026. All isolates where whole genome sequencing data is available were included in the phylogenetic analysis to provide a more comprehensive representation.

- The phylogenetic tree of all isolates is shown in Section 2. MLST is annotated on the tip labels.
- There are 6 new isolates available for this report.
- There are no new recommendations for this reporting period.

Table 1. New isolates added in this report.

Isolate	Primary Lab ID	State	NELSS ID	Source	MLST
[redacted]	[redacted]	[redacted]	[redacted]	Human	1
[redacted]	[redacted]	[redacted]	[redacted]	Human	1
[redacted]	[redacted]	[redacted]	[redacted]	Food	3
[redacted]	[redacted]	[redacted]	[redacted]	Human	87
[redacted]	[redacted]	[redacted]	[redacted]	Human	91
[redacted]	[redacted]	[redacted]	[redacted]	Food	204

1. Consider your audience & purpose

1. What is the purpose of sequencing and reporting?
2. Who is the audience/client (and how much knowledge)?
3. What are the main question/s to be answered?
4. How long will they have to read the report?

Iterative co-design of reporting with end-users wherever possible

What do end-users want in a genomics-based report?

Clinicians

- Reporting presence/absence of resistance genes or mutations in most cases
- Most clinicians can't infer resistance from a given AMR gene (name or description)
- Specify antibiotic class/antibiotic – need to make sense clinically – **interpret for audience**
- Rapid information transfer

Epidemiologists

- Reporting presence/absence of resistance genes or mutations in most cases
- Generally like **more information** rather than less information
- Have more domain specific knowledge, likely to be integrated into PH databases

What don't they want to know?

- Reporting QC, % gene identity and coverage is usually not a reasonable option
- Make a call – is the gene/mutation likely to be there or not?
  - (Not going to go into this – been covered in previous webinars)
- Users unlikely to want to know about QC results – trust you only report is QC is good
- **Extraneous information not** usually wanted and can confuse reports (clinicians >> epis) e.g. intrinsic resistance mechanisms

Slide courtesy of A/Prof Norelle Sherry

Reporting comparative genomics to healthcare facilities

Focus group participants wanted:

- Simplified results (very limited time to view)
- ‘Traffic light’ system to classify likelihood of transmission
- Directions on where to focus infection control investigation
- Generally discouraged phylogenetic trees (until high level of genomic proficiency)

Multi-site implementation of whole genome sequencing for hospital infection control: A prospective genomic epidemiological analysis

Norelle L. Sherry,[a,b,c] Claire L. Gorrie,[a,c] Jason C. Kwong,[b,c,d] Charlie Higgs,[c] Rhonda L. Stuart,[e,f,g] Caroline Marshall,[h,i] Susan A. Ballard,[a] Michelle Sait,[a] Tony M. Korman,[e,f,j] Monica A. Slavin,[k,l] Robyn S. Lee,[c,2] Maryza Graham,[e,f,j] Marcel Leroi,[b,m] Leon J. Worth,[k,l] Hiu Tat Chan,[n,3] Torsten Seemann,[a,c] M. Lindsay Grayson,[b,d,m,1] and Benjamin P. Howden [a,b,c,1], on behalf of the Controlling Superbugs Study Group*

Phylogenetic Analysis Report
vanA Enterococcus faecium, Network A, July 2020

ANALYSIS SUMMARY

Six new *vanA* VRE isolates from four patients were submitted for WGS and analysis in this reporting period: four ST80 isolates and two ST203 isolates (full details in Table 4).

- Two new ST203 isolates are **very closely-related** to isolates from three patients in the last four months (Ward W and ICU), and should be investigated for possible in-hospital transmission.
- Multiple isolates from one patient (ST80) are **closely-related** to isolates from three other patients over the last 12 months from three different wards; suggest correlation with epidemiology given isolates detected over a prolonged time period.

Table 1. New isolates in this report and genomic relationships to previous isolates from Network A

	ST	New patient isolates	Collection date	Links to previous patients (year last isolated)	Details in section
	203	PatientB UR64825921 PatientA UR64825851	12/6/20 13/6/20	PatientE UR60020052 (2020) PatientF UR63822546 (2020) PatientG UR64447847 (2020)	2A
	80	PatientC UR56321120	9-11/6/20	PatientH UR65932125 (2019) PatientJ UR65832623 (2019) PatientK UR62221253 (2020)	2B
	80	PatientD UR61132522	5/4/20	None	2B

Key: Genomic relationship between isolates

Very closely related | Closely related | Unlikely related

Reporting comparative genomics to public health authorities

Most public health reports: Line listed characterization/clustering of related isolates, sometimes with tree, and with interpretation in text

- Categorical data is needed to be combined with other data / databases (e.g. notifiable diseases)
- Happy to receive longer/more detailed reports, but highlight key findings

Not a one-way street, ideally genomics epidemiologists are included in outbreak, incident management & response teams

- Allows understanding of emerging public health threats and potential uses of genomic data
- Reduces risk of misinterpretation

- Need to be careful to keep a traceable history of results from when a decision made
  - If databases are updated, how will you make sure data is up to date to compare with future results, but also keep track of when a result became known or available.

1. Consider your audience & purpose

1. What is the purpose of sequencing and reporting?

2. Who is the audience/client (and how much knowledge)?

3. What are the main question/s to be answered?

4. How long will they have to read the report?

Microbiological Diagnostic Unit
Public Health Laboratory
Department of Microbiology & Immunology
University of Melbourne, Victoria 3010
Telephone: 61 3 8344 5713
Facsimile: 61 3 8344 7833
Email: publichealth.lab@mdu.unimelb.edu.au

Listeria monocytogenes Surveillance REPORT

REPORTING PERIOD TO: 11/01/2026

To: OzFoodNet_Epidemiologists
Copy to: [redacted]

Report ID: R[redacted]
Issue Date: 14/01/2026
Prepared By: [redacted]
Authorised By: A Prof Norelle Sherry (Deputy Director)

1. ANALYSIS SUMMARY

A total of 40 isolates; 19 human cases and 21 non-human sample isolates were received in the 24-week reporting period ending 11/01/2026. All isolates where whole genome sequencing data is available were included in the phylogenetic analysis to provide a more comprehensive representation.

- The phylogenetic tree of all isolates is shown in Section 2. MLST is annotated on the tip labels.
- There are 6 new isolates available for this report.
- There are no new recommendations for this reporting period.

Table 1. New isolates added in this report.

Isolate	Primary Lab ID	State	NELSS ID	Source	MLST
[redacted]	[redacted]	[redacted]	[redacted]	Human	1
[redacted]	[redacted]	[redacted]	[redacted]	Human	1
[redacted]	[redacted]	[redacted]	[redacted]	Food	3
[redacted]	[redacted]	[redacted]	[redacted]	Human	87
[redacted]	[redacted]	[redacted]	[redacted]	Human	91
[redacted]	[redacted]	[redacted]	[redacted]	Food	204

1. Consider your audience & purpose

1. **What is the purpose of sequencing and reporting?**
   - Prospective surveillance of *Listeria monocytogenes*
   - Detect outbreaks and/or link human cases and potential food sources
2. **Who is the audience/client (and how much knowledge)?**
   - Department of Health epidemiologists
   - Routine report, high familiarity & knowledge
3. **What are the main question/s to be answered?**
   - Are the new cases (patients) closely related to any previous cases and/or potential food sources
4. **How long will they have to read the report?**
   - Relatively long, results may need to be incorporated into surveillance databases

Microbiological Diagnostic Unit
Public Health Laboratory
Department of Microbiology & Immunology
University of Melbourne, Victoria 3010
Telephone: 61 3 8344 5713
Facsimile: 61 3 8344 7833
Email: publichealth.lab@mdu.unimelb.edu.au

Listeria monocytogenes Surveillance REPORT

REPORTING PERIOD TO: 11/01/2026

To: OzFoodNet_Epidemiologists
Copy to: [redacted]

Report ID: R[redacted]
Issue Date: 14/01/2026
Prepared By: [redacted]
Authorised By: A Prof Norelle Sherry (Deputy Director)

1. ANALYSIS SUMMARY

A total of 40 isolates; 19 human cases and 21 non-human sample isolates were received in the 24-week reporting period ending 11/01/2026. All isolates where whole genome sequencing data is available were included in the phylogenetic analysis to provide a more comprehensive representation.

- The phylogenetic tree of all isolates is shown in Section 2. MLST is annotated on the tip labels.
- There are 6 new isolates available for this report.
- There are no new recommendations for this reporting period.

Table 1. New isolates added in this report.

Isolate	Primary Lab ID	State	NELSS ID	Source	MLST
[redacted]	[redacted]	[redacted]	[redacted]	Human	1
[redacted]	[redacted]	[redacted]	[redacted]	Human	1
[redacted]	[redacted]	[redacted]	[redacted]	Food	3
[redacted]	[redacted]	[redacted]	[redacted]	Human	87
[redacted]	[redacted]	[redacted]	[redacted]	Human	91
[redacted]	[redacted]	[redacted]	[redacted]	Food	204

2. Clearly outline methods

What do I need to include to ensure:

- The reader can interpret the results
- You can re-trace analysis steps and troubleshoot
- Results are comparable across reports, where required

2. Clearly outline methods

Ensure you cover:

- Inclusion/Exclusion criteria, included sequences
  - QC parameters (not in detail)
- How samples & metadata were obtained
- Analysis methods
- Don't forget, if relevant:
  - Cluster definitions
  - Reference genomes
  - Interpretation definitions
  - Tool/database names & version numbers
- Place methods at the end or in technical appendix for routine reports

1. ANALYSIS SUMMARY

A total of 40 isolates; 19 human cases and 21 non-human sample isolates were received in the 24-week reporting period ending 11/01/2026. All isolates where whole genome sequencing data is available were included in the phylogenetic analysis to provide a more comprehensive representation.

3. METHODS

3.1 Procedure No(s)

Procedure No.	Service
MMS103	Whole genome sequencing
MMS109	Multilocus sequence typing (MLST)
MMS126	*In silico* analysis and reporting guidelines for *Listeria monocytogenes*
MMS147	SNP detection and interpretation of genomic relatedness

3.2 Determination of pair-wise SNP distances and cluster analysis

Phylogenetic trees were generated using a maximum-likelihood method, based on core genome alignment of all isolates analysed in this report. Pairwise SNP distances were also calculated from this alignment. The core genome alignments and clustering presented in this report are specific to this analysis and may change in subsequent analyses depending on the choice of reference, methodological approach employed and isolates included. Potential clusters were detected based on pairwise SNP distance thresholds current for *Listeria monocytogenes* analyses only. Criteria for relatedness is as follows:

- Highly related clusters consist of isolates that were collected during the reporting period are linked at ≤ 5 SNP threshold.
- Potentially related clusters consist of isolates that that were collected during the reporting period are linked at >5 and ≤ 20 SNP threshold.
- Unrelated isolates do not cluster with other isolates that were collected during the reporting period at a threshold >20 SNPs.

Maximum likelihood phylogenies, generated from core alignments, were annotated with clusters determined as described above. Recommendations regarding the degree of genomic relatedness are based only on the SNP distance matrix using a single-linkage analysis.

The following genomic references were used in the analyses presented in this report:

Sequence ID	Description
AE017262.2	Genome used as reference for Full phylogeny
AE017262.2	Genome used as reference for ST1

3.3 Bioinformatic Tools

The following bioinformatics tools were used in the analysis:

Tool	Version
Bohra	1.2.12
Snippy	4.4.5

2.3 Re-analysis of potential clusters

Potential clusters identified in Figure 1 containing cases within the current reporting period are re-analysed with historical isolates of the same sequence types to determine whether any further investigation is required.

Cases are colour coded as follows:

Red	Recent cases are highly likely to be linked to other cases and further investigation is recommended to confirm these links. Highly related clusters consist of isolates that were collected during the reporting period are linked at ≤ 5 SNP threshold.
Orange	Recent cases that are potentially linked to one or more cases and further investigation is recommended to confirm or reject the cluster. Potentially related clusters consist of isolates that that were collected during the reporting period are linked at ≤ 20 SNP threshold.
Green	Recent cases that are not linked to any other cases therefore no further investigation is recommended. Unrelated isolates do not cluster with other isolates that were collected during the reporting period at a threshold >20 SNPs
Blue	Cases identified with the last 12 months.
Black	Historical cases.

3. Report relevant sequence characteristics

- Generally, individual sequence characteristics still reported, most commonly:
  - Sequence type (see weeks 31/32)
  - Species specific typing results (see weeks 31/32)
  - Key resistance genes (see weeks 33/34)

These were previously discussed in week 36/37 – “Single isolate reporting”

Table 2. All isolates of *Listeria* from HUMAN sources received in the past 24 weeks for the reporting period ending 11/01/2026.

MDU ID	State	Date Collected	NELSS ID	Molecular Serotype	MLST
[redacted]	[redacted]	2025-12-26	[redacted]	4b, 4d, 4e	1
		2025-12-12		1/2a/3a	91
		2025-11-23		4b, 4d, 4e	1
		2025-10-31		1/2a, 3a	321
		2025-10-31		1/2b, 3b, 7	87
		2025-10-27		1/2b, 3b, 7	59
		2025-10-13		4b, 4d, 4e	4
		2025-10-10		1/2a, 3a	321
		2025-09-30		1/2a, 3a	321
		2025-09-29		4b, 4d, 4e	1
		2025-09-25		4b, 4d, 4e	1
		2025-09-20		4b, 4d, 4e	1
		2025-08-27		1/2b, 3b, 7	3
		2025-08-27		1/2b, 3b, 7	3
		2025-08-24		4b, 4d, 4e	1
		2025-08-15		1/2a, 3a	321
		2025-08-15		4b, 4d, 4e	1
		2025-08-13		4b, 4d, 4e	308
		2025-08-13		4b, 4d, 4e	308

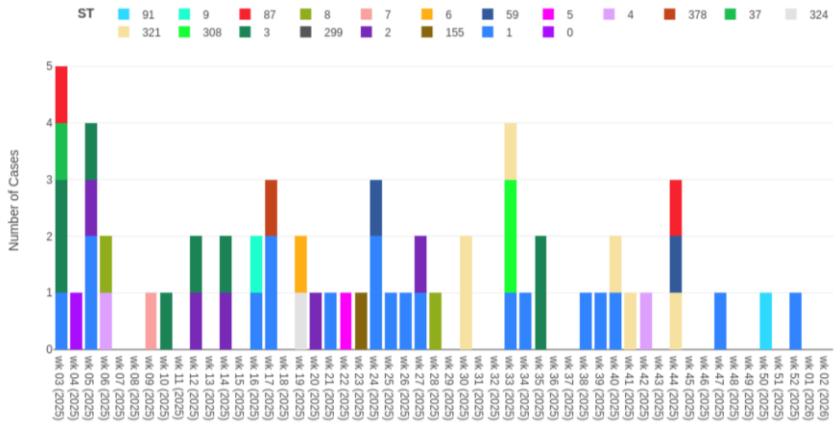


Figure 1. MDU PHL 12 month Listeriosis cases epicurve by sample collection date and multi-locus sequence type as determined from whole genome sequence data. Note, where sample collection date is not available sample submission date to MDU PHL is used. Isolates from non-sterile sample sites are not included.

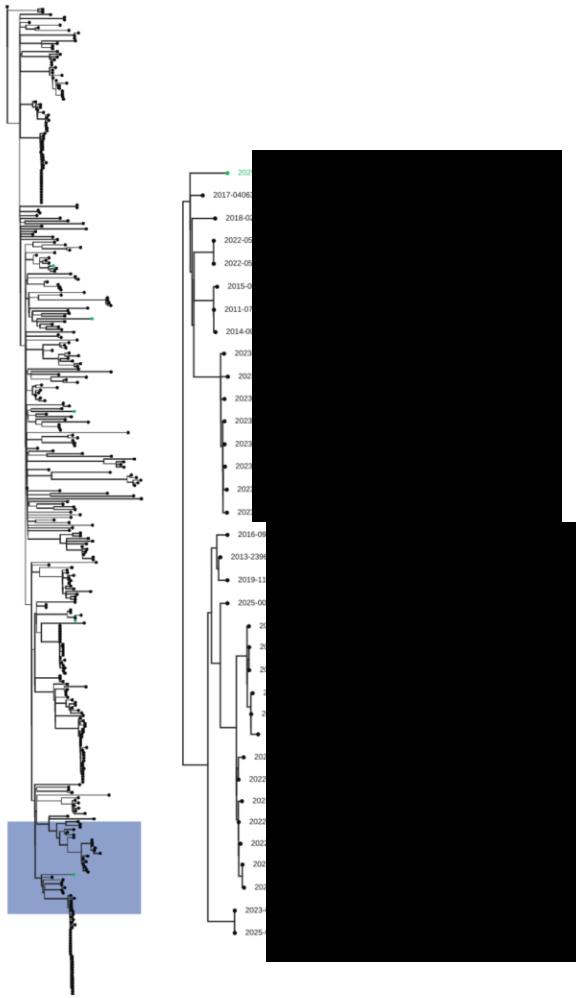
4. Report comparative genomics results & metadata

- Results as required to answer your analysis questions
- Most commonly includes:
  - Phylogenetic analysis (see weeks see weeks 40 / 41)
  - Clustering (various methods, see weeks 42 / 43)
  - Integration with epidemiological data (see week 44)

- Information communication & visualization is key
  - Trees can show relatedness, but can be difficult to interpret
  - Integration of meta/epi data is needed to make data actionable
  - Timelines & exposure diagrams can show spatio-temporal spread
  - Use visualization to highlight new/critical findings (e.g. placement of new cases)
  - Don't forget clear, descriptive legends and figure captions!

Make sure to include an executive summary ("inverted pyramid" approach, where the most critical findings are up front, can work well)

4. Report comparative genomics results & metadata



Cases are colour coded as follows:

Red	Recent cases are highly likely to be linked to other cases and further investigation is recommended to confirm these links. Highly related clusters consist of isolates that were collected during the reporting period are linked at ≤ 5 SNP threshold.
Orange	Recent cases that are potentially linked to one or more cases and further investigation is recommended to confirm or reject the cluster. Potentially related clusters consist of isolates that that were collected during the reporting period are linked at ≤ 20 SNP threshold.
Green	Recent cases that are not linked to any other cases therefore no further investigation is recommended. Unrelated isolates do not cluster with other isolates that were collected during the reporting period at a threshold >20 SNPs
Blue	Cases identified with the last 12 months.
Black	Historical cases.

Figure 4. Phylogenetic re-analysis of **ST3** as identified in the initial full analysis – Full tree shown on left, highlighted region zoomed on the right.

- From a more recent supplementary report:

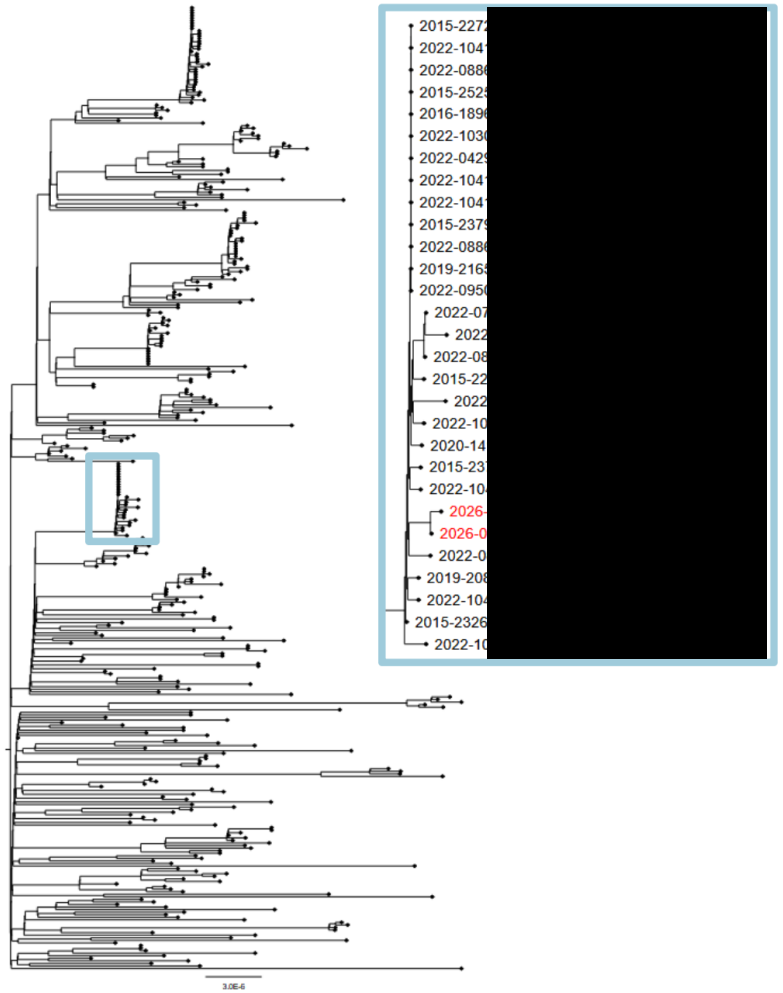


Figure 1. Phylogenetic analysis of **ST3** – Full tree shown on left, highlighted region zoomed on the right. Recent isolates are shown in red.

5. Interpret results, draft narrative & risk assessment

- You are the expert – Reader is reliant on your interpretation of the results

- How do they:
  - Answer the stated question?
  - Support/refute a given hypothesis?
  - Correlate with other data (e.g. epidemiological)?
  - Support the provided recommendations?

5. Interpret results, draft narrative & risk assessment

1.1 New Recommendations:

There are no new recommendations for:

- **ST1**
  - Sample [redacted] is **not likely related** to other isolates.
  - Sample [redacted] is **not likely related** to other recent isolates.
    - The sample above is **potentially related** to historical samples [redacted]
- **ST3**
  - Sample [redacted] is **not likely related** to other isolates.
- **ST87**
  - Sample [redacted] is **not likely related** to other recent isolates.
- **ST91**
  - Sample [redacted] is **not likely related** to other recent isolates.
- **ST204**
  - Sample [redacted] is **not likely related** to other recent isolates.

- Some other examples
  - **ST2**
    - Samples [redacted] are **highly related** to each other.
      - The samples above are **potentially related** to historical samples [redacted]

1. ANALYSIS SUMMARY

As part of the combined epidemiological and genomic surveillance of carbapenemase-producing organisms (CPO) in Victoria, phylogenetic analyses are conducted where the potential for local transmission exists among groups of isolates of the same species, sequence type (ST), and carbapenemase gene combination.

A phylogenetic analysis was conducted following the recent identification of an OXA-72 producing *Acinetobacter baumannii* novel ST isolate from a patient with admission to [redacted] Health.

2. RESULTS

On phylogenetic analysis, the recent OXA-72 producing *Acinetobacter baumannii* novel ST isolate from [redacted] patient [redacted] (Lab ID [redacted] was found to be closely related to an isolate from [redacted] patient [redacted] (Lab ID [redacted] Table 1). No other samples of this species, gene and novel ST combination were identified in the dataset at MDU PHL.

This is consistent with transmission between patients or acquisition from a common source (environmental or person) but should be considered within the context of epidemiological evidence. Additional epidemiological data, including details of patient's hospital admissions would assist in the interpretation and understanding of these genomic relationships.

Table 1 List of closely *Acinetobacter baumannii* novel ST isolates

Name	Sex	Date of Birth [redacted] UR [redacted] Lab ID	Date of Collection	MDU sample ID
[redacted]	Female	[redacted]	07/10/2024	[redacted]
[redacted]	Male	[redacted]	30/09/2024	

6. Ensure limitations are clear

- Genomic data alone is generally only ”consistent with” and not conclusive

- In particular:
  - Changes in **included isolates**, methods and/or tools can alter results
  - Testing practices and/or sample selection for sequencing can introduce biases
  - Direct transmission, and direction of transmission, cannot be “proven” without epidemiological evidence

- Ensure your reader is aware of the limitations of your analyses.

6. Ensure limitations are clear

3.2 Determination of pair-wise SNP distances and cluster analysis

Phylogenetic trees were generated using a maximum-likelihood method, based on core genome alignment of all isolates analysed in this report. Pairwise SNP distances were also calculated from this alignment. The core genome alignments and clustering presented in this report are specific to this analysis and may change in subsequent analyses depending on the choice of reference, methodological approach employed and isolates included. Potential clusters were detected based on pairwise SNP distance thresholds current for *Listeria monocytogenes* analyses only. Criteria for relatedness is as follows:

- Some other common disclaimers include:

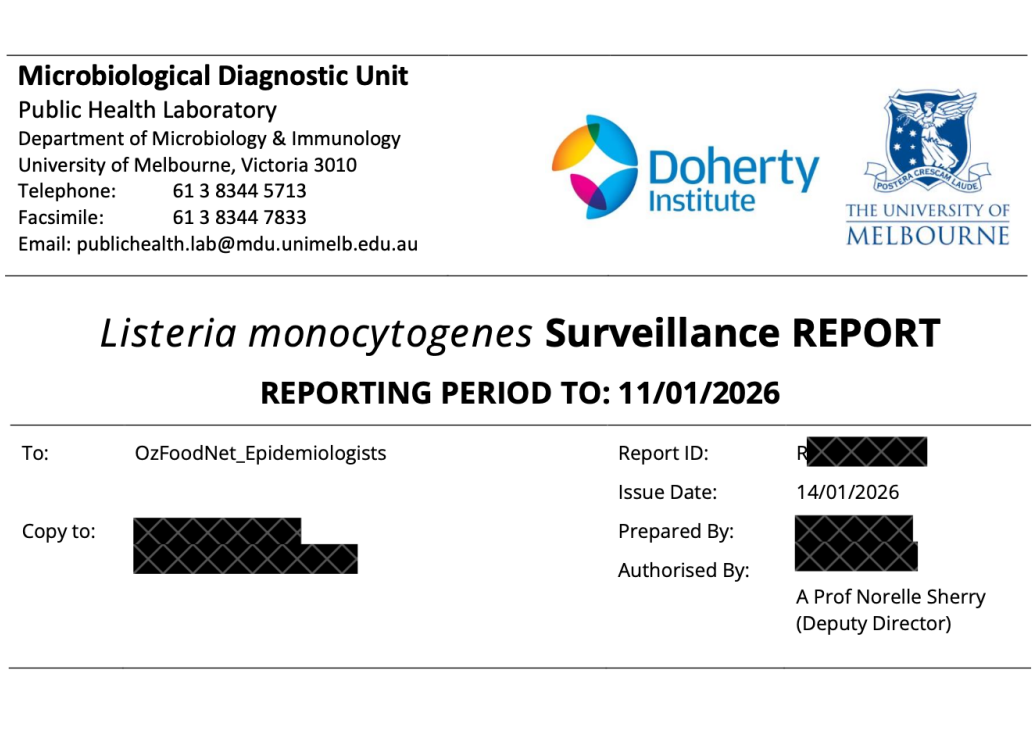
3. DISCLAIMER

Results should be interpreted in conjunction with available epidemiological data and used for epidemiological purposes only. Epidemiological links should be investigated to support genomic clusters identified by phylogenetic analysis.

This may be consistent with transmission between patients or acquisition from a common source (environmental or person) but should be considered within the context of further epidemiological evidence. Additional epidemiological data, including details of patient's hospital admissions would assist in the interpretation and understanding of these genomic relationships.

7. Enact appropriate approval processes

- Follow setting and context specific approval processes
- Reporting may be governed by:
  - Laboratory accreditation requirements
  - Professional responsibilities
- Record, store and archive all reports for traceabilit



Microbiological Diagnostic Unit
Public Health Laboratory
Department of Microbiology & Immunology
University of Melbourne, Victoria 3010
Telephone: 61 3 8344 5713
Facsimile: 61 3 8344 7833
Email: publichealth.lab@mdu.unimelb.edu.au

Doherty Institute

THE UNIVERSITY OF MELBOURNE

Listeria monocytogenes **Surveillance REPORT**

REPORTING PERIOD TO: 11/01/2026

To: OzFoodNet_Epidemiologists

Copy to: [redacted]

Report ID: R[redacted]

Issue Date: 14/01/2026

Prepared By: [redacted]

Authorised By: A Prof Norelle Sherry (Deputy Director)

RCPA The Royal College of Pathologists of Australasia NATA Accredited for compliance with relevant NPAAC Standards and ISO 15189. Accreditation number: 1019.

Supervising RCPA/NPAAC Microbiology Genomics accredited pathologists: Prof B Howden / A/Prof N Sherry

This report is intended solely for the named addressee, is confidential and may contain legally privileged information. The copying or distribution of this document or any information it contains, by anyone other than the addressee, is prohibited. If you have received this document in error, please contact MDU on 03 8344 5713.

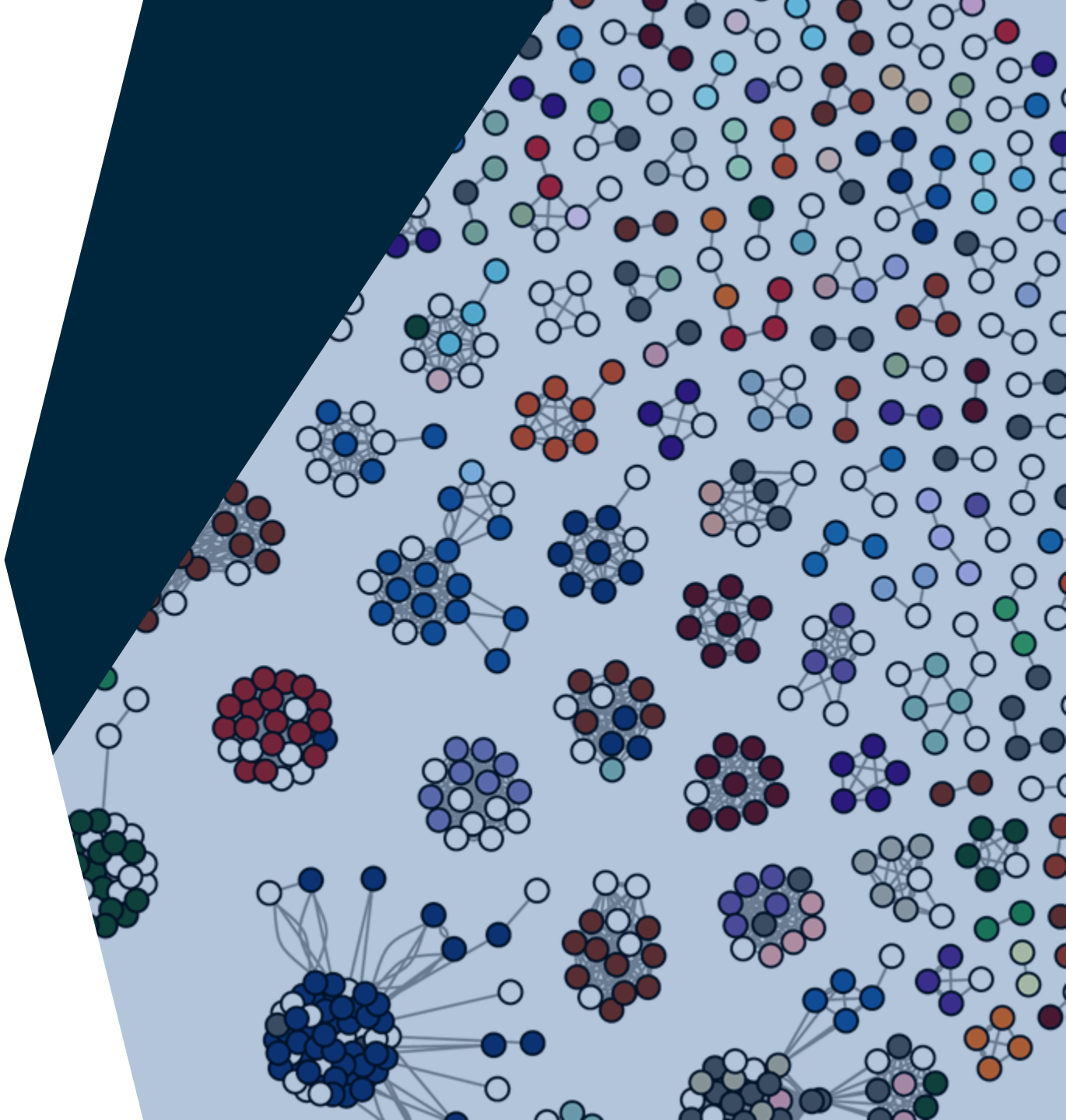
Webinar Overview

Recap: Reporting Comparative Genomics Results

How to write a report (step-by-step)

1. Consider your audience & purpose
2. Clearly outline methods
3. Report relevant sequence characteristics
4. Report comparative genomics results & metadata
5. Interpret results, draft narrative & risk assessment
6. Ensure limitations are clear
7. Enact appropriate approval processes

Summary



Summary

Reporting comparative genomics data requires clear, concise & purposeful communication

While all reports will require similar components, how you present these depends on:

- Who is your audience?
- What is the purpose of your report?

In general, routine reporting needs to be:

- Quickly interpretable – you're the expert, tell them what it means
- Tailored to highlight key results
- Easily integrated with other databases/data

Comparative genomic data can be complex – explore data visualisation and narratives to make your data understandable

Work with your end-user to define reports that work for them!

Next week:

Exercise on reporting comparative genomic data

Then: Reporting aggregate data
(e.g. incorporating genomics into annual surveillance reports)

E: centre-pathogen@unimelb.edu.au

W: bit.ly/CentreforPathogenGenomics

CENTRE FOR PATHOGEN GENOMICS

Dr. Courtney Lane
Lead, Genomic Epidemiology
Centre for Pathogen Genomics

E: C.Lane@unimelb.edu.au