

Sharpening the hospital infection control toolset with genomic sequencing

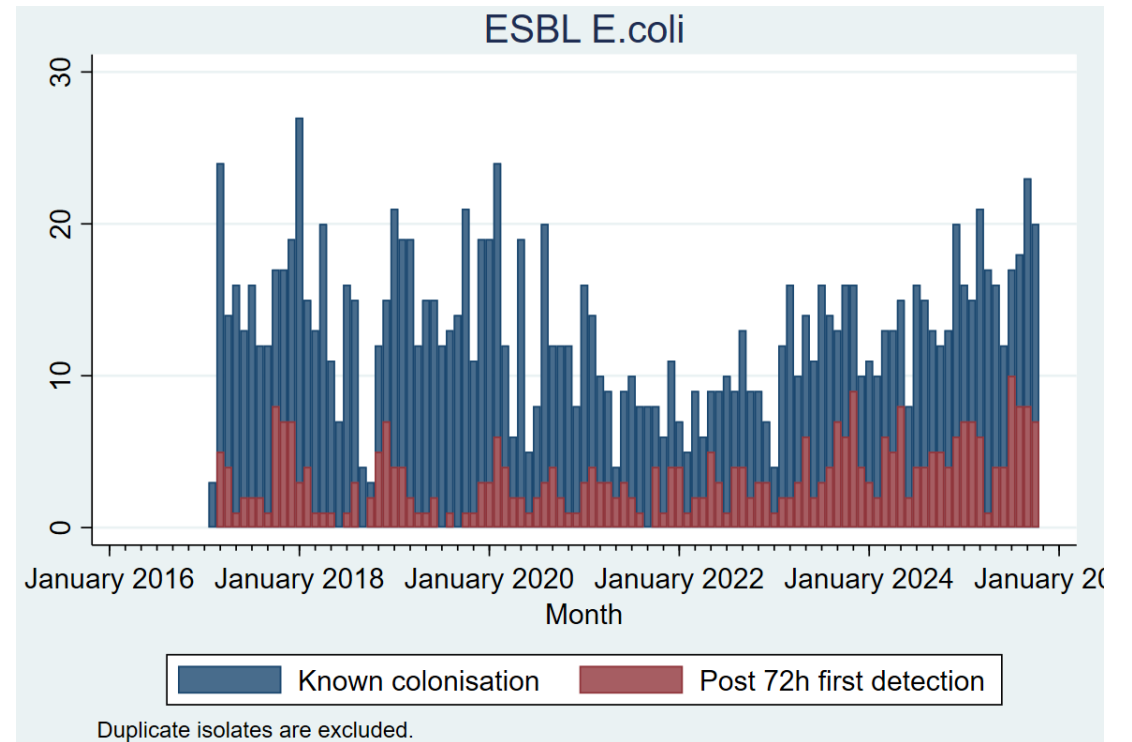
Dr Max Bloomfield

Clinical Microbiologist, Awanui Labs Wellington

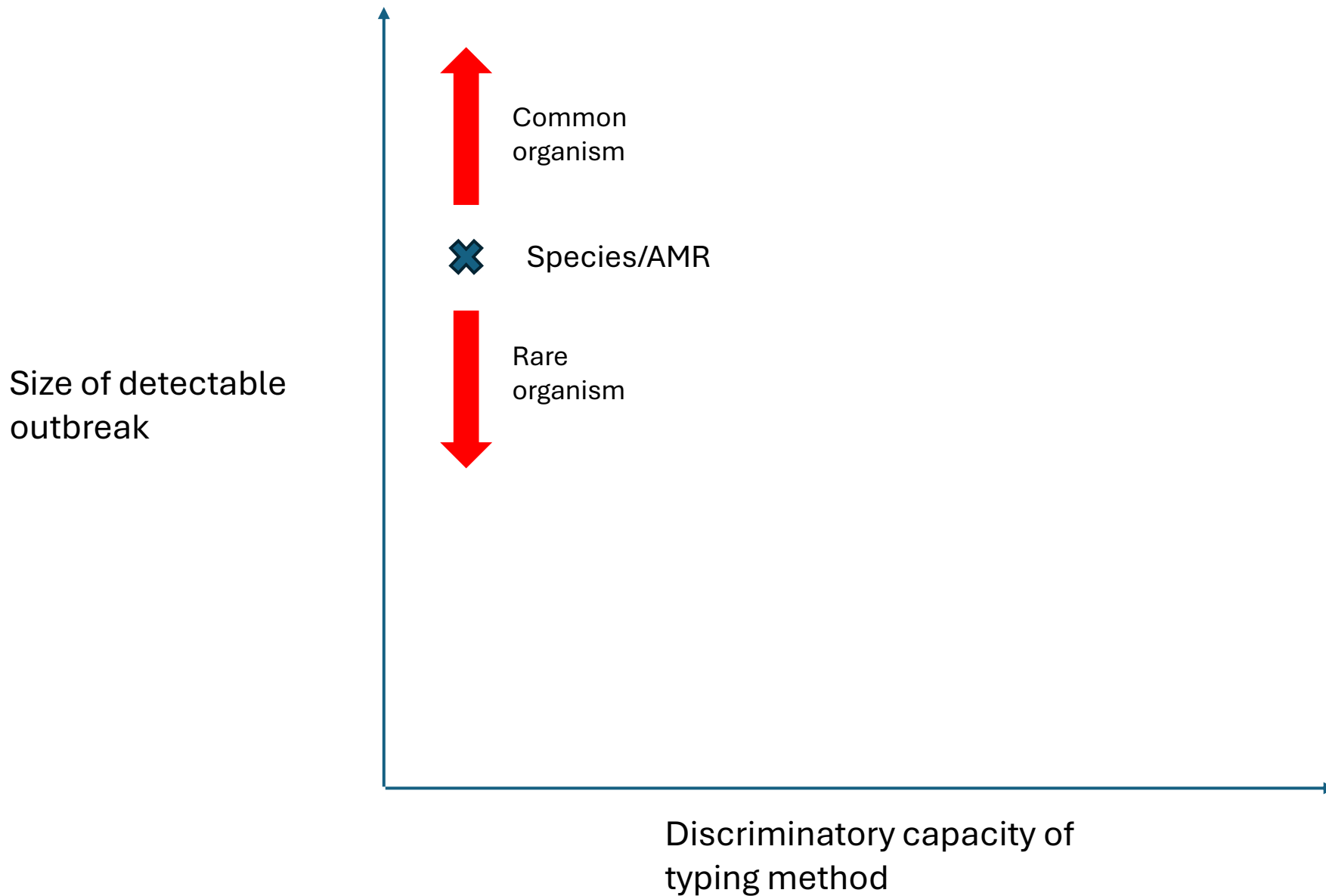
Infectious Diseases Physician, Te Whatu Ora – Capital, Coast and Hutt Valley

Traditional Hospital Organism Surveillance is a Blunt Tool

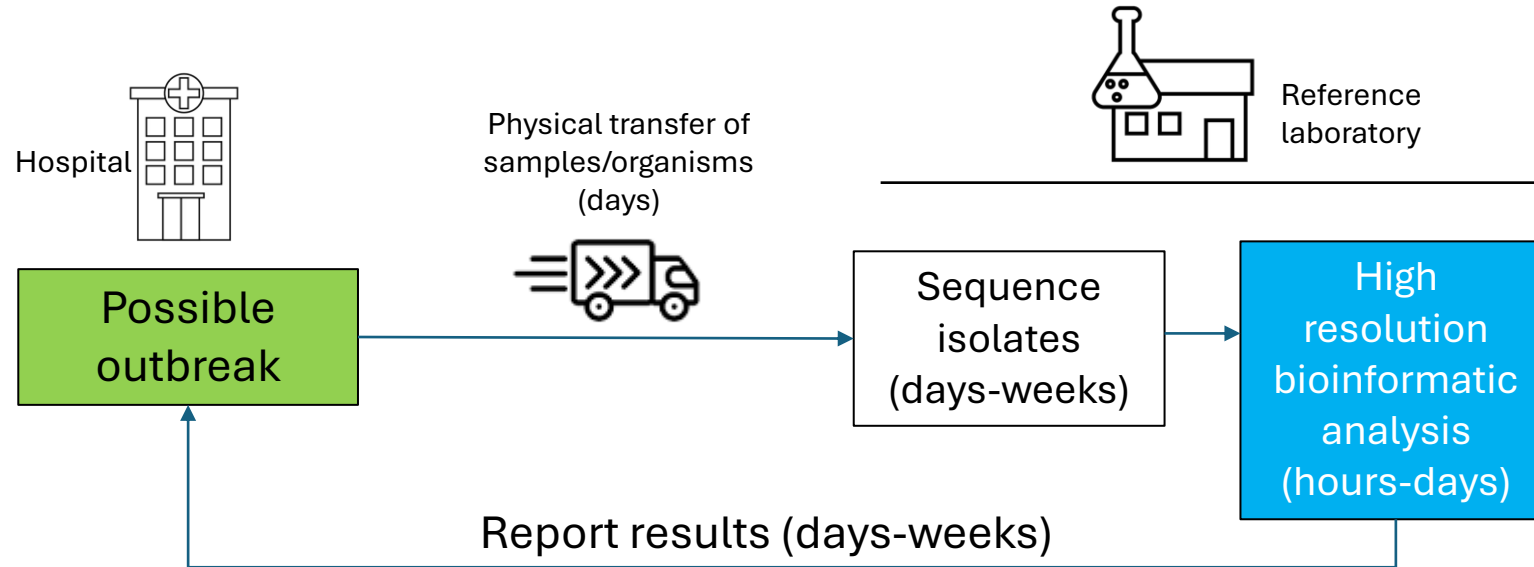
- Counting organisms
- Differentiate based on species and resistance phenotype
- Will spot problems if:
 - Rare organism/phenotype
 - Problem gets very large



Counting bugs is a blunt tool



Traditional 'centralised' sequencing model



- Turnaround time often slow
- Lack of agility/flexibility to local needs

} Problematic with rapidly evolving hospital outbreaks

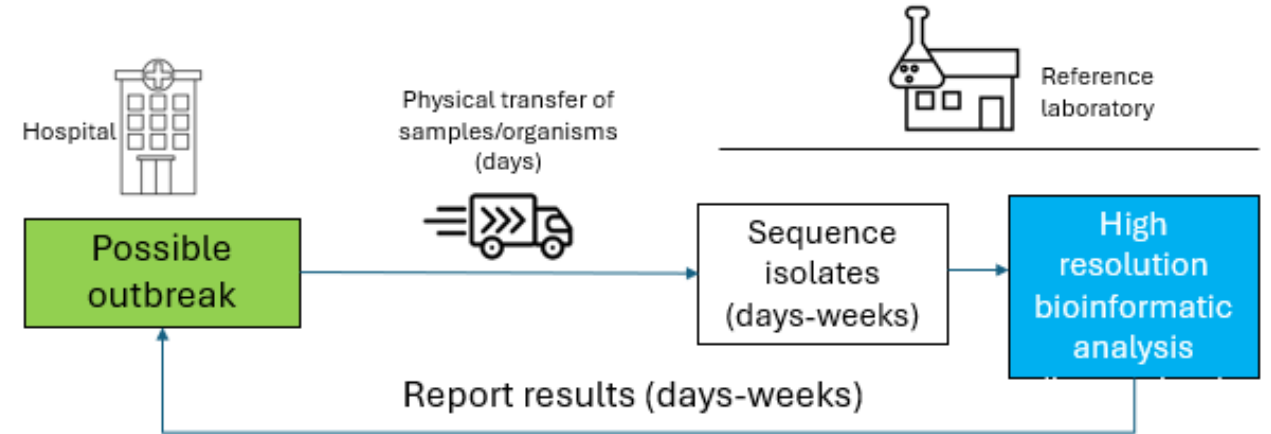
Bringing genomics to the front line

- Prospective genomic surveillance

‘early warning’

- Rapid sequencing of possible transmission events

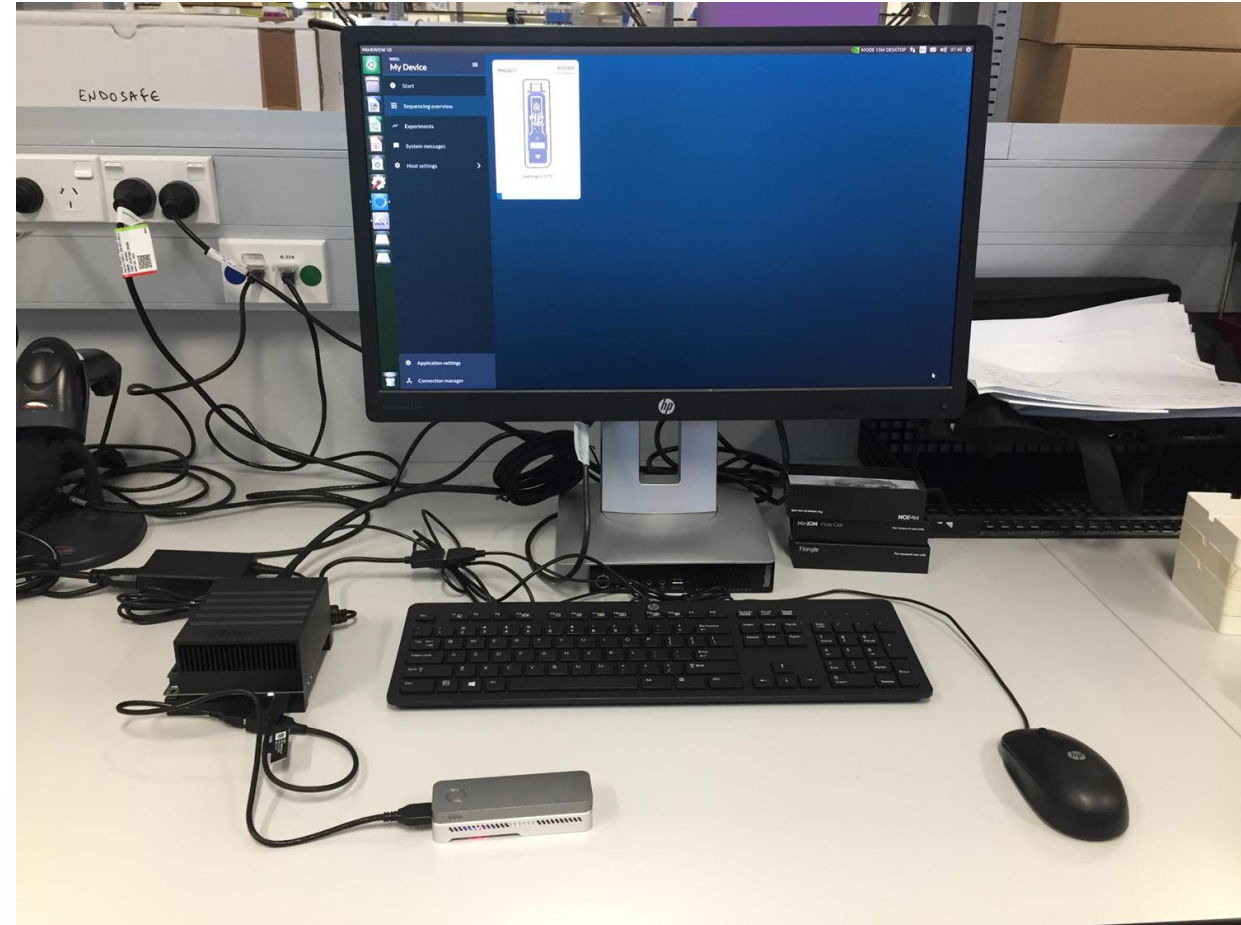
‘rapid response’



- Reduce turnaround time
- Local flexibility/agility

2022

- ‘Prospective/proactive’ surveillance
 - Weekly sequencing run
 - When key organisms isolated from hospital patients -> forwarded for sequencing
- Rapid ‘reactive’ sequencing
 - Ability to sequence ‘surprise’ organisms at short notice
- No prior experience of next generation sequencing or bioinformatics



Rapid reactive sequencing: local flexibility/agility

Rapid response to rise in *Klebsiella variicola* bloodstream infection on neonatal unit

Neonatal Unit Clinical Meeting Monday PM

- Notified of four *Klebsiella pneumoniae* bloodstream infections over preceding month
- Clear rise above baseline incidence
- Wild-type organisms, so not part of routine surveillance



Neonatal Unit Outbreak Investigation Timeline

Afternoon of Day 0

K. pneumoniae
isolates retrieved
from frozen storage
and sub cultured

Day 1

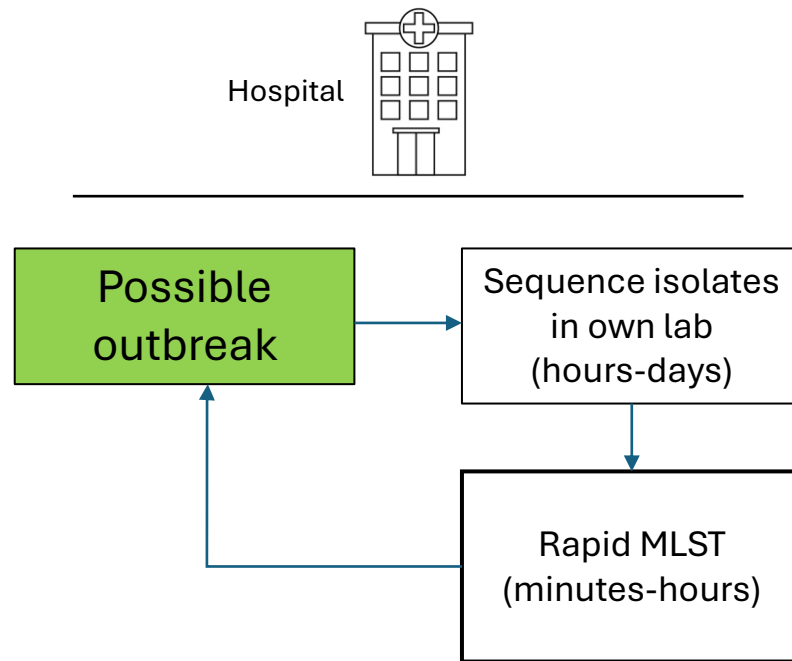
Isolates added to
MinION sequencing
run

Morning of Day 2

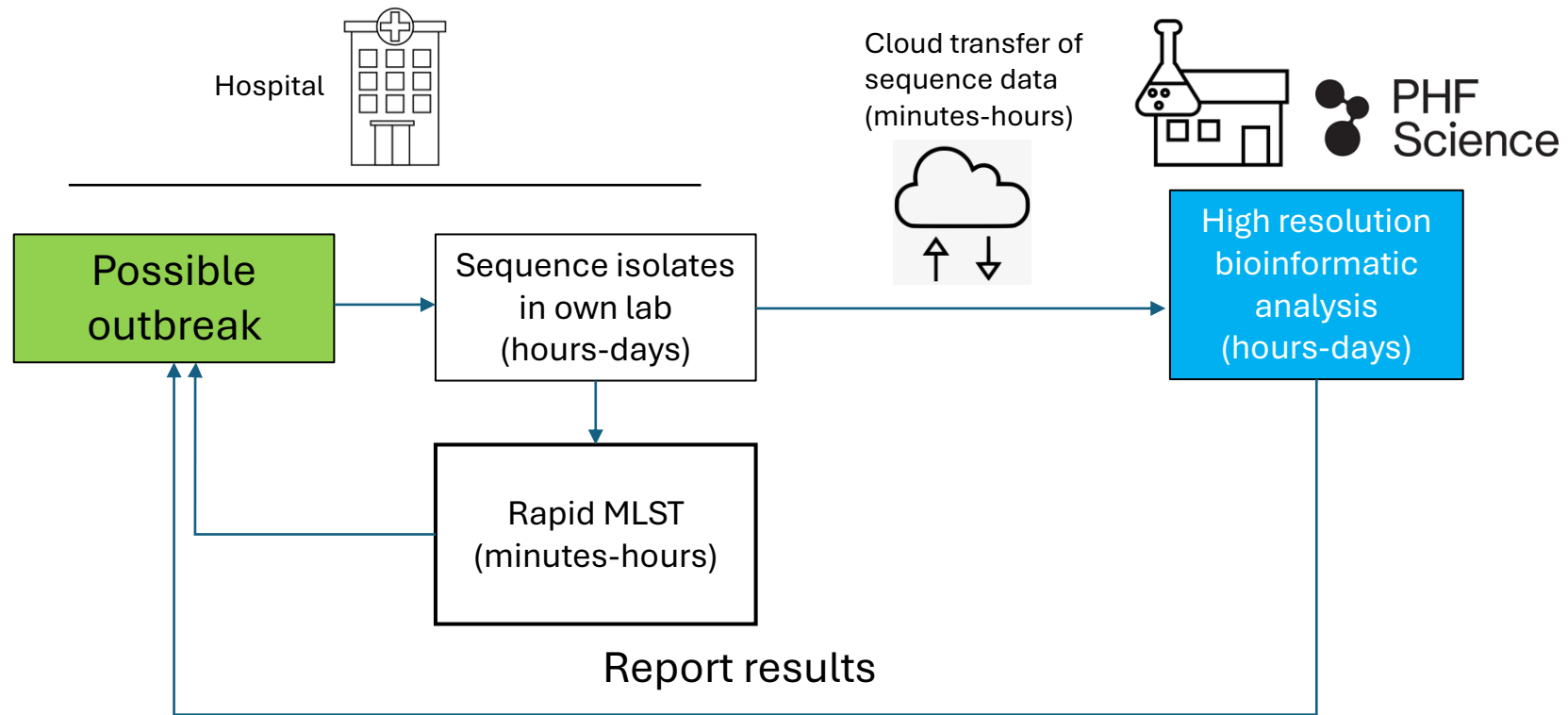
Sequencing results
and MLST available

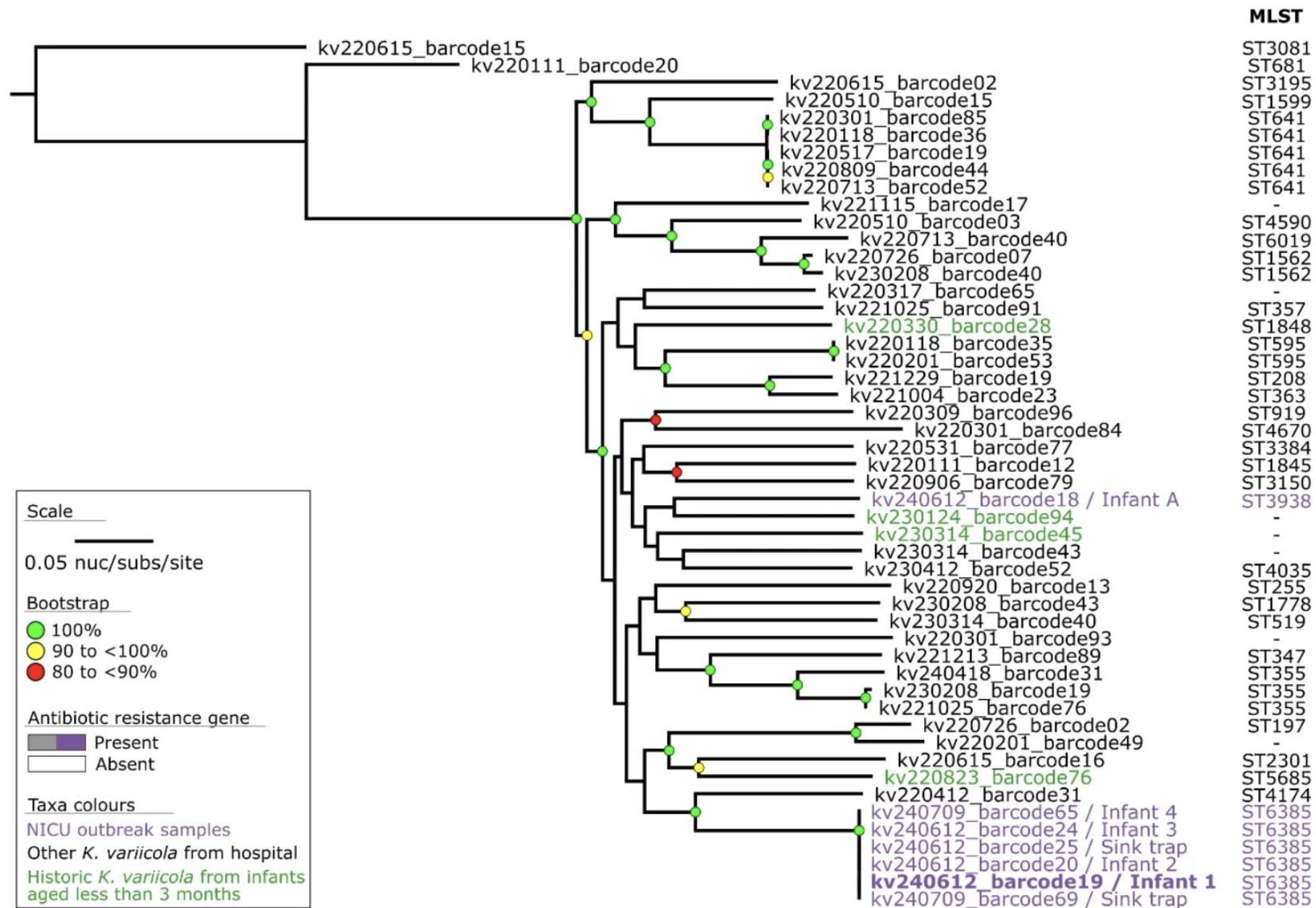
- Three of four isolates actually *K. variicola* (misidentified by routine lab methods)
- Two of the *K. variicola* isolates were ST6385 (rare ST)
- **Epi + sequencing data = transmission highly likely**
 - (Only had MLST at this stage)
- Further investigation found two further colonised infants and two environmental reservoirs (sinks) for the organism
- Containment measures implemented and outbreak controlled

Moving away from the centralised model

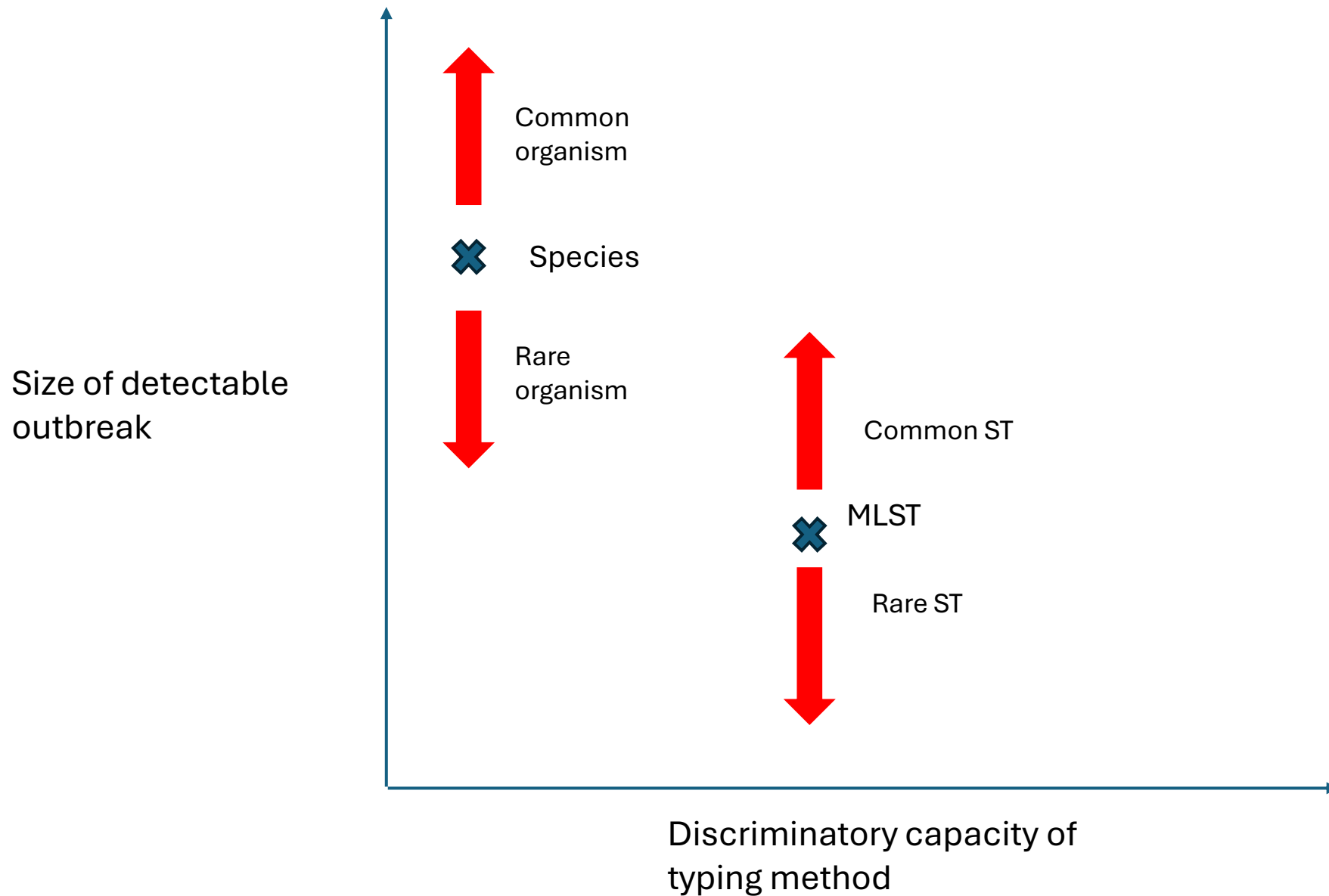


Moving away from the centralised model

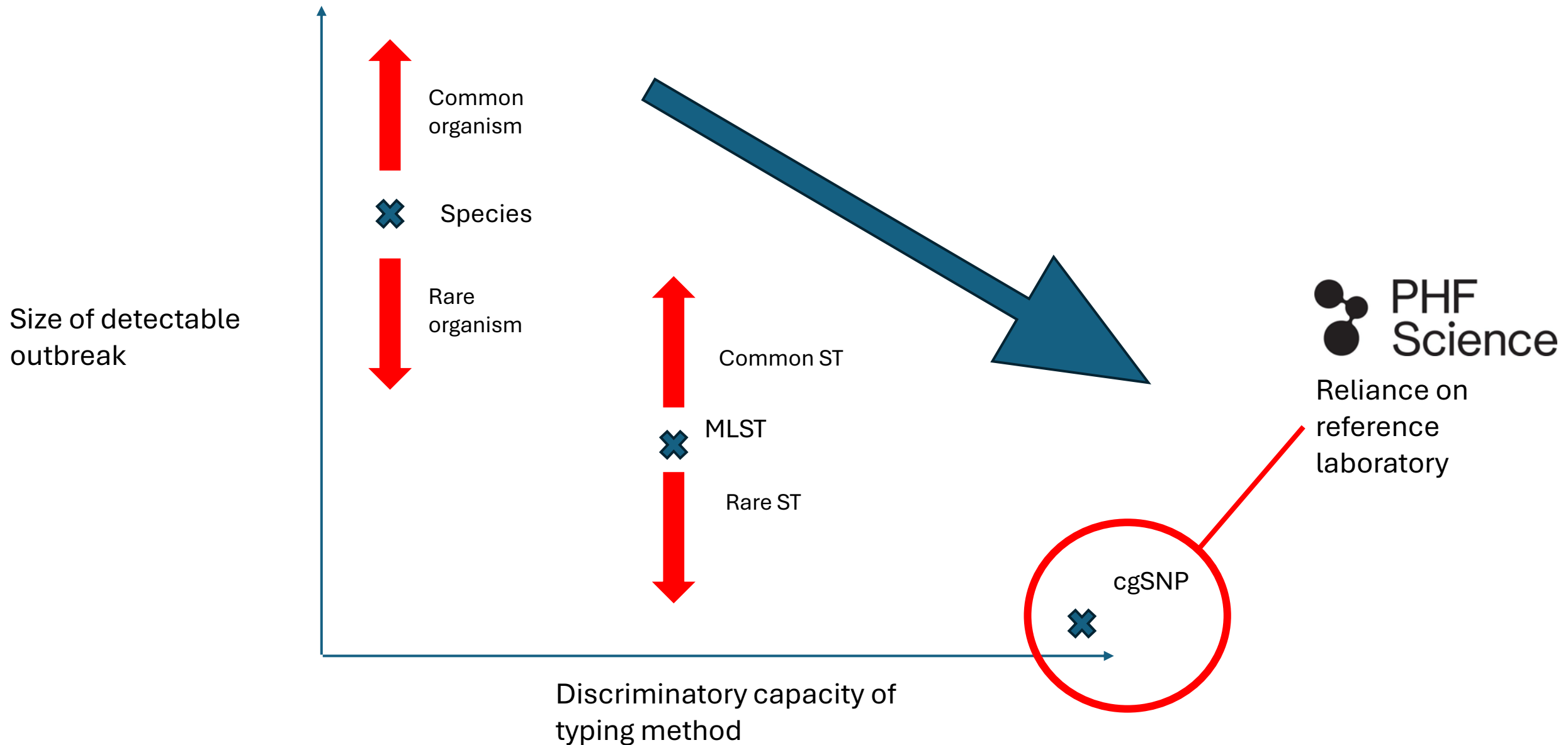




MLST was good, but...



MLST was good, but...



2025: a game changer for us



Journal of Hospital Infection 168 (2026) 48–57

Available online at www.sciencedirect.com



Journal of Hospital Infection

journal homepage: www.elsevier.com/locate/jhin



The need for speed: ultra-rapid high-resolution outbreak analysis in a front-line hospital microbiology laboratory

M. Bloomfield^{a,b}, S. Bakker^c, M. Burton^a, K. Dyet^c, A. Eustace^c, S. Hutton^a, J. Jeram^a, D. Macartney-Coxson^c, D.J. Winter^c, R.T. White^{c,*}

^a Awanui Labs Wellington, Department of Microbiology and Molecular Pathology, Wellington 6021, New Zealand

^b Te Whatu Ora/Health New Zealand, Infection Prevention and Control, Capital, Coast & Hutt Valley, Wellington 6021, New Zealand

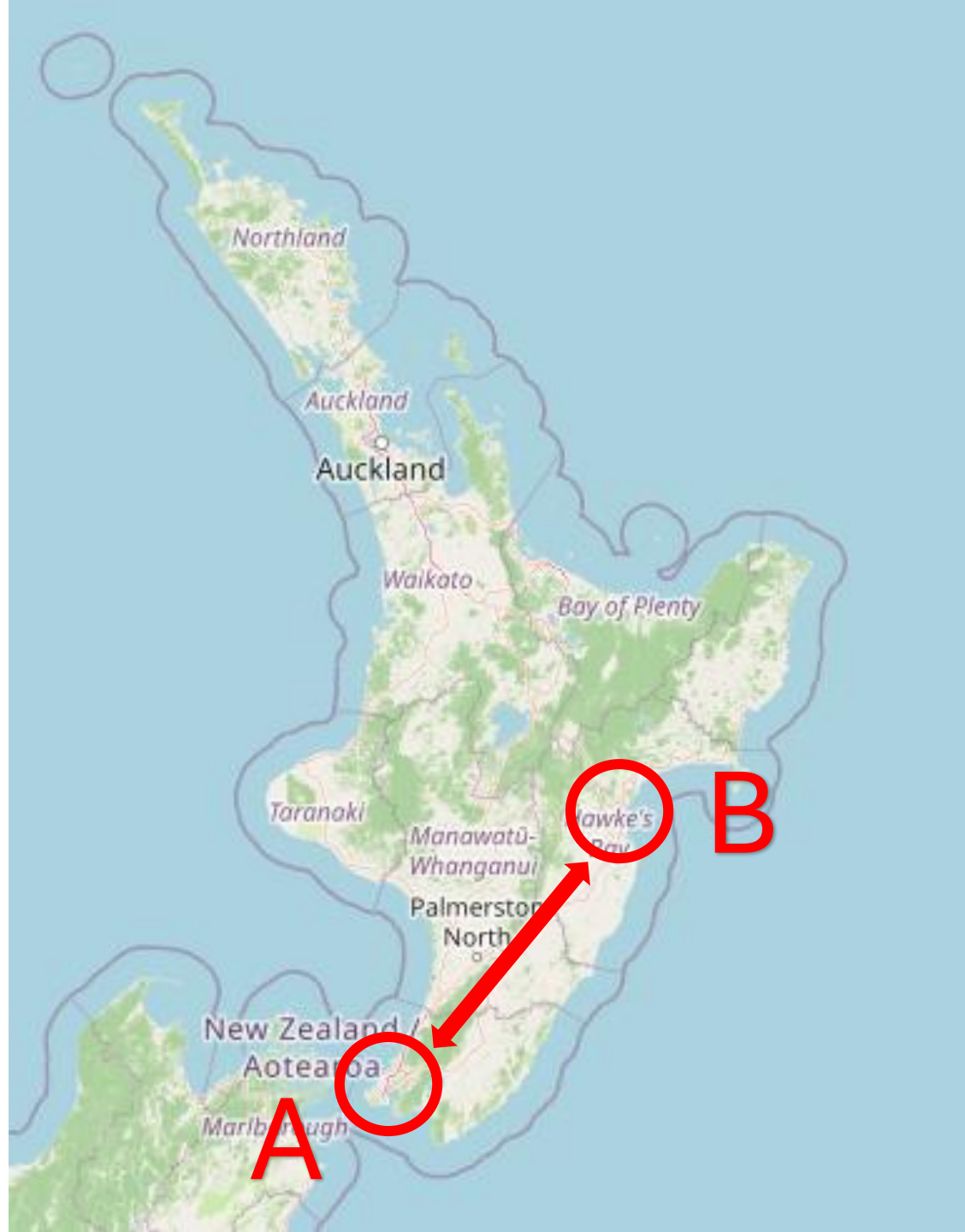
^c New Zealand Institute for Public Health and Forensic Science, Health Security, Porirua 5022, New Zealand

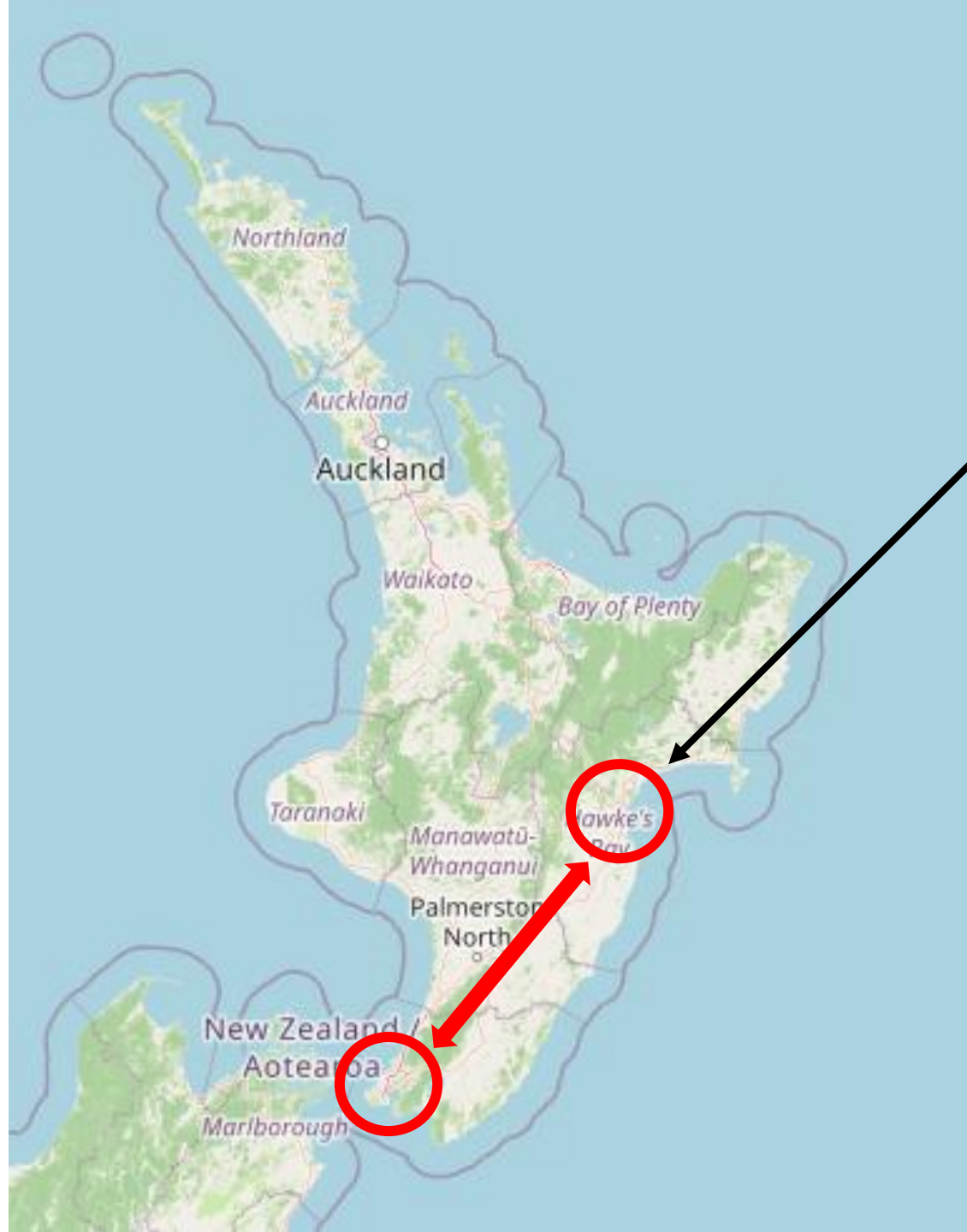
- We can now do our own high-resolution typing
- Two key advantages:
 - High-resolution results within minutes
 - Cloud based – facilitates data sharing/transfer

Decentralised genomics in action

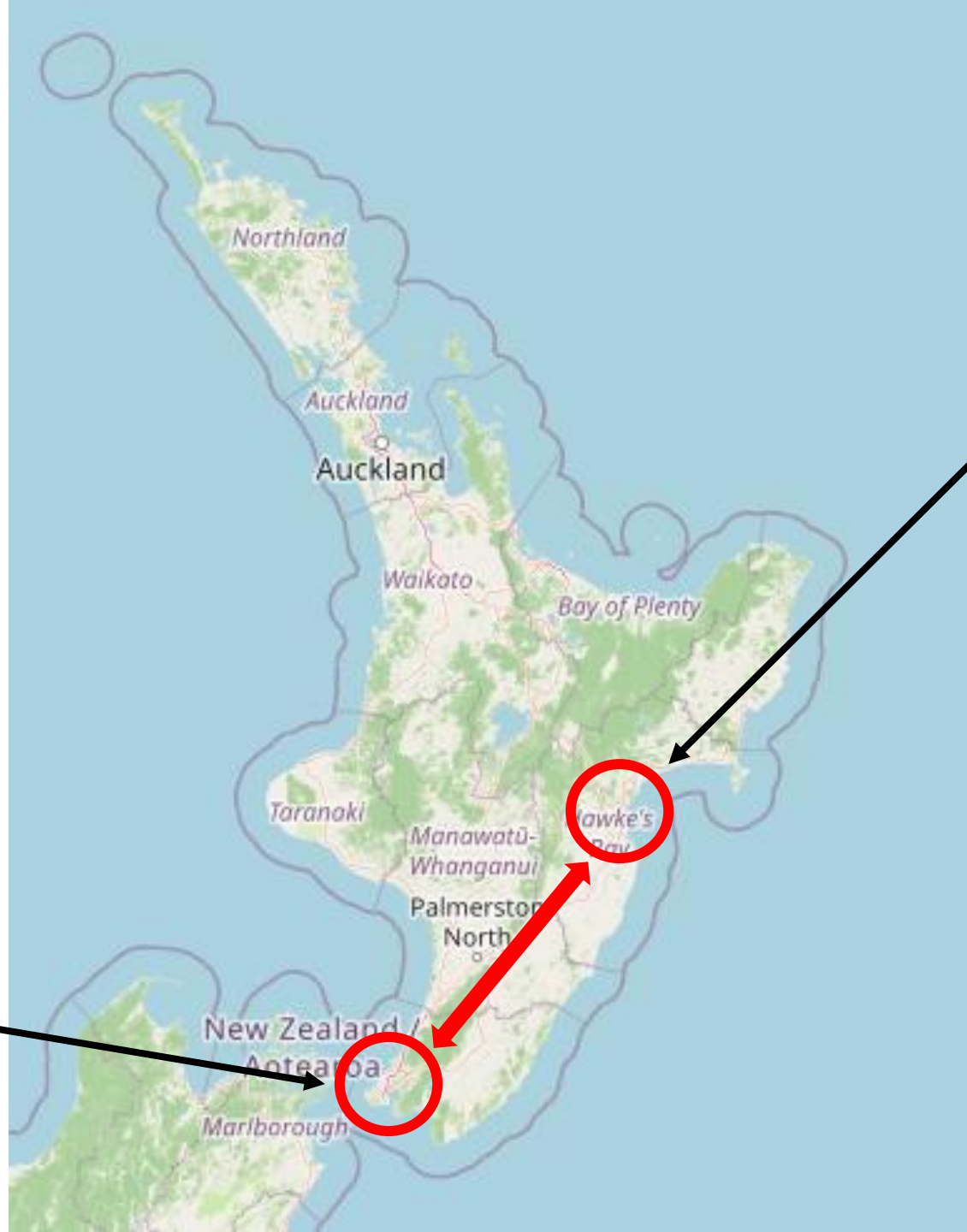
Inter-regional integrated sequencing

- A = Wellington Hospital
- B = Hawke's Bay Hospital
- A is tertiary referral centre for B
- Patients (and their bugs) travel both directions frequently



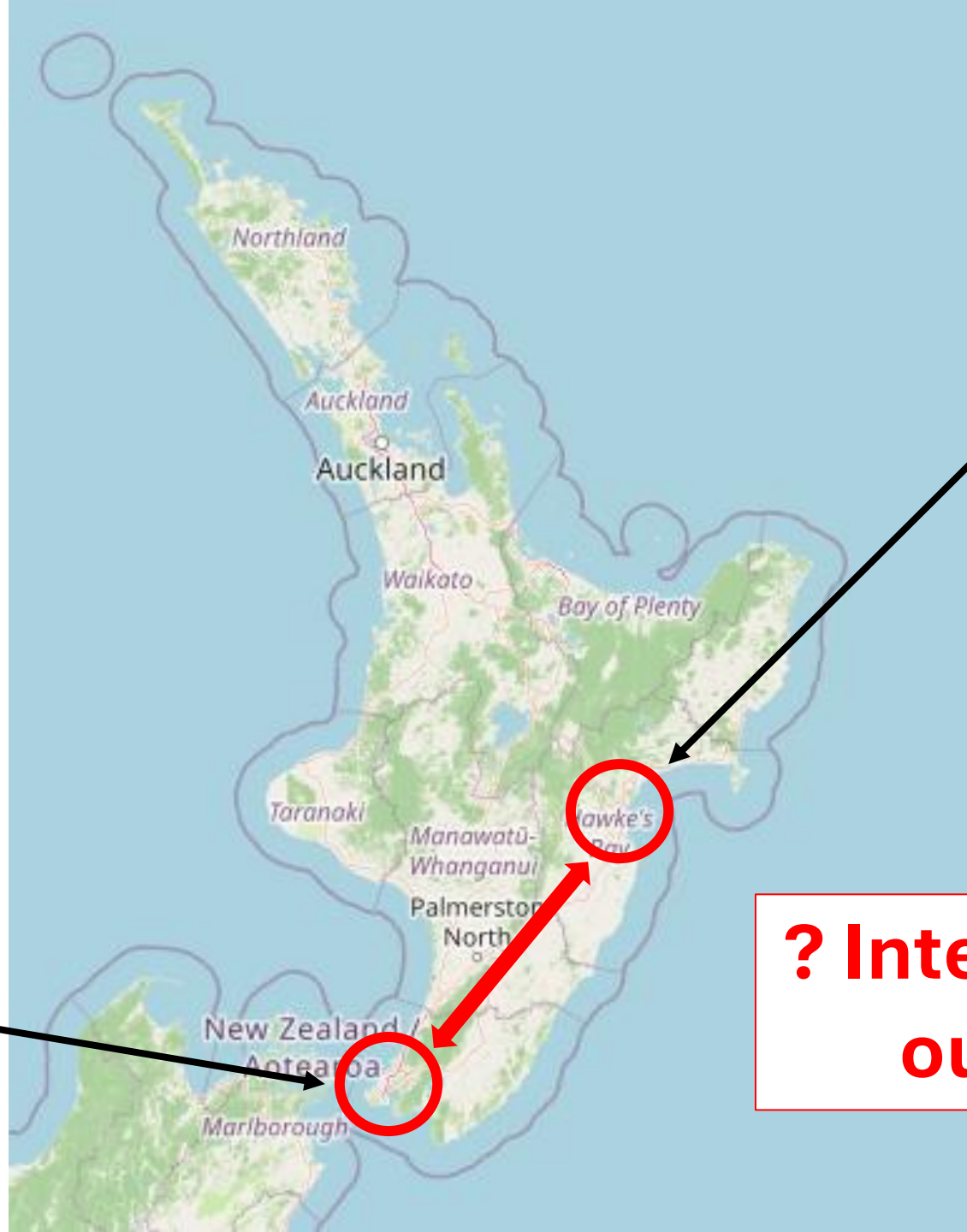


Small outbreak of
Extended-spectrum
beta-lactamase
(ESBL) producing
ST131 *E.coli* in
neonatal unit



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Infant from Hawke's
Bay in our neonatal
unit found to be
colonised with an
ESBL-producing
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ST131 *E.coli*

**? Inter-hospital
outbreak**

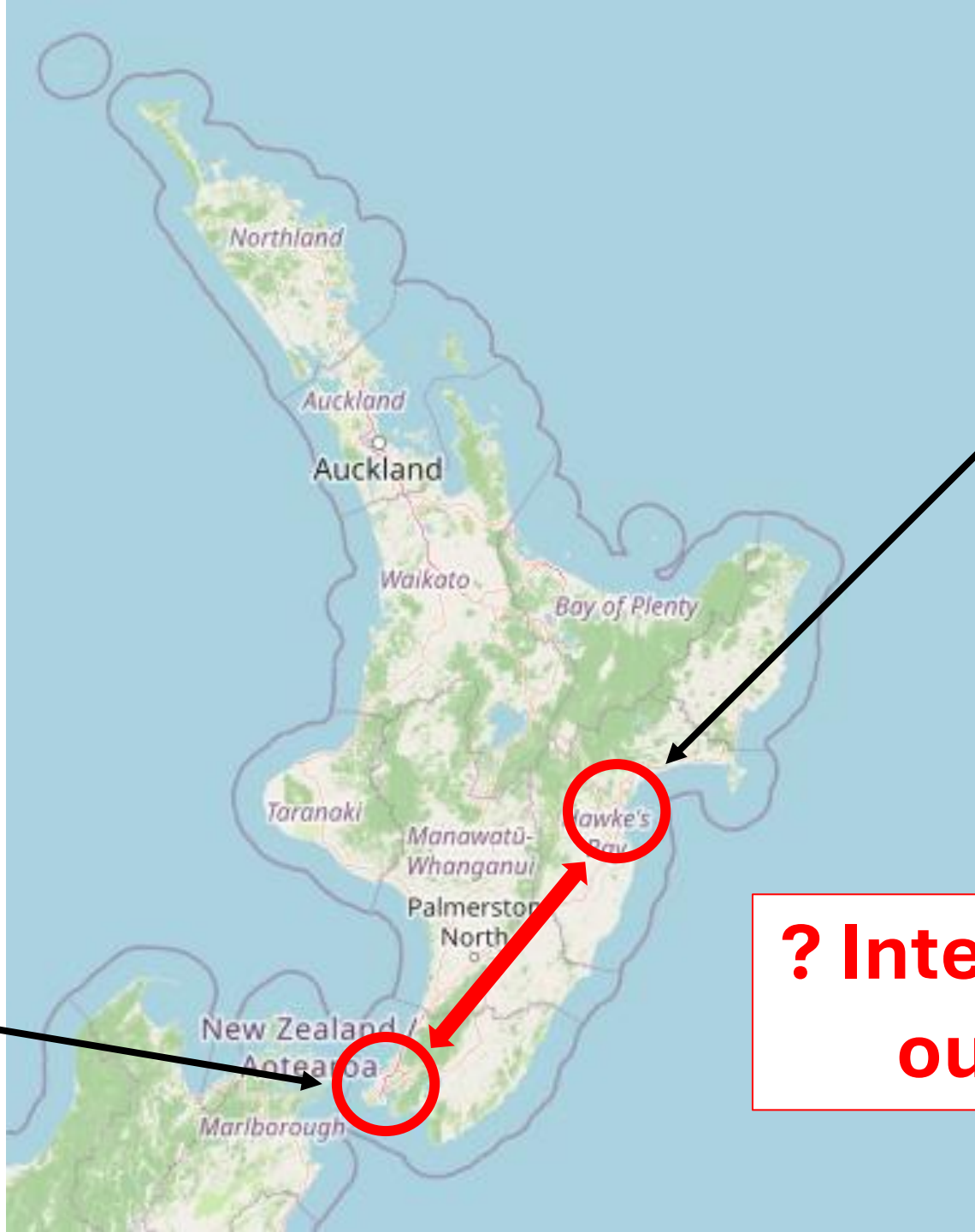


Sequenced in-house

Infant from Hawke's Bay in our neonatal unit found to be colonised with an ESBL-producing ST131 *E.coli*

Small outbreak of Extended-spectrum beta-lactamase (ESBL) producing ST131 *E.coli* in neonatal unit

Sequenced at reference laboratory



? Inter-hospital outbreak

Tuesday 3 June 12:08 pm

From: Maxim Bloomfield [CCDHB] <Maxim.Bloomfield@ccdhb.org.nz>

Sent: Tuesday, 3 June 2025 12:08 pm

To: Alexandra Eustace <Alexandra.Eustace@esr.cri.nz>; Kristin Dyet <Kristin.Dyet@esr.cri.nz>; Sarah Bakker <Sarah.Bakker@esr.cri.nz>

Cc: Rhys White <Rhys.White@esr.cri.nz>

Subject: RE: Final Report issued today for four ESBL- producing E.coli isolates received at ESR 20 May 2025

Thanks Alex

Is there any chance we could have these isolates uploaded to Solu? We've got an ESBL E.coli ST131 in our NICU with a connection to HB, so would be nice to compare.

Cheers

Max

Tuesday 3 June 12:33 pm (25 minutes later)

From: Sarah Bakker <Sarah.Bakker@esr.cri.nz>

Sent: Tuesday, 3 June 2025 12:33 PM

To: Maxim Bloomfield [CCDHB] <Maxim.Bloomfield@ccdhb.org.nz>; Alexandra Eustace <Alexandra.Eustace@esr.cri.nz>; Kristin Dyet <Kristin.Dyet@esr.cri.nz>

Cc: Rhys White <Rhys.White@esr.cri.nz>

Subject: RE: Final Report issued today for four ESBL- producing E.coli isolates received at ESR 20 May 2025

External email - take care with links and attachments

Data is uploading as I'm writing this message – hope it all OK.

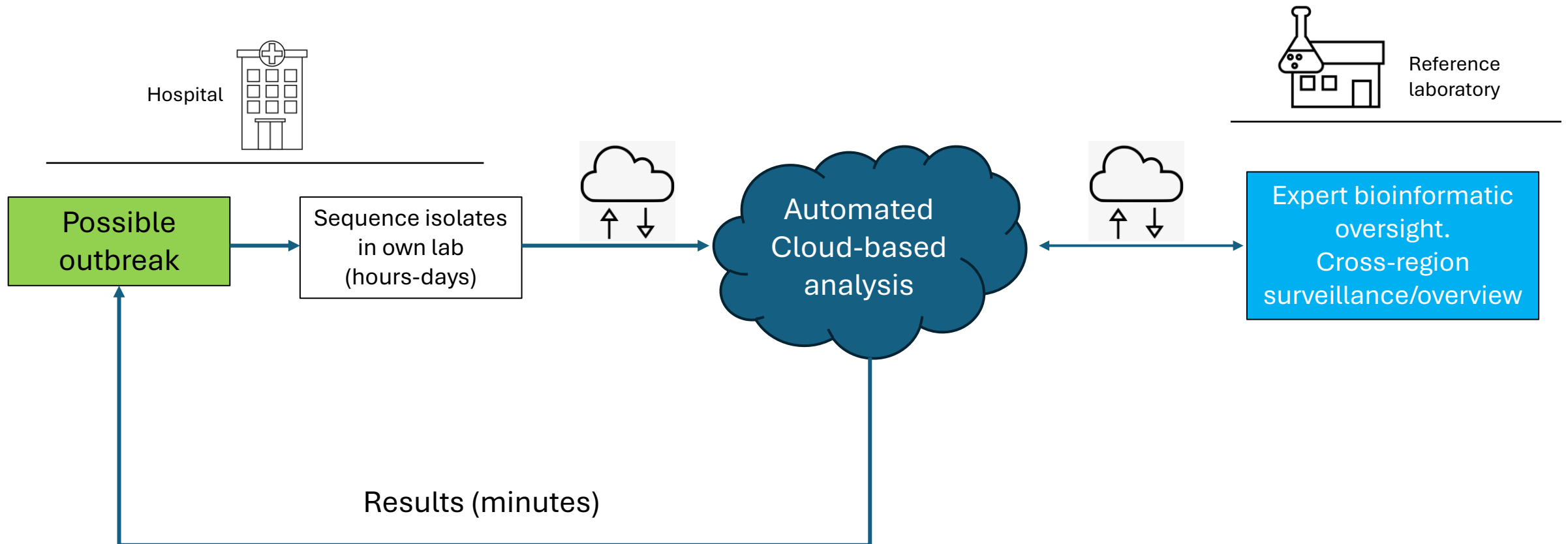
Cheers

Sarah

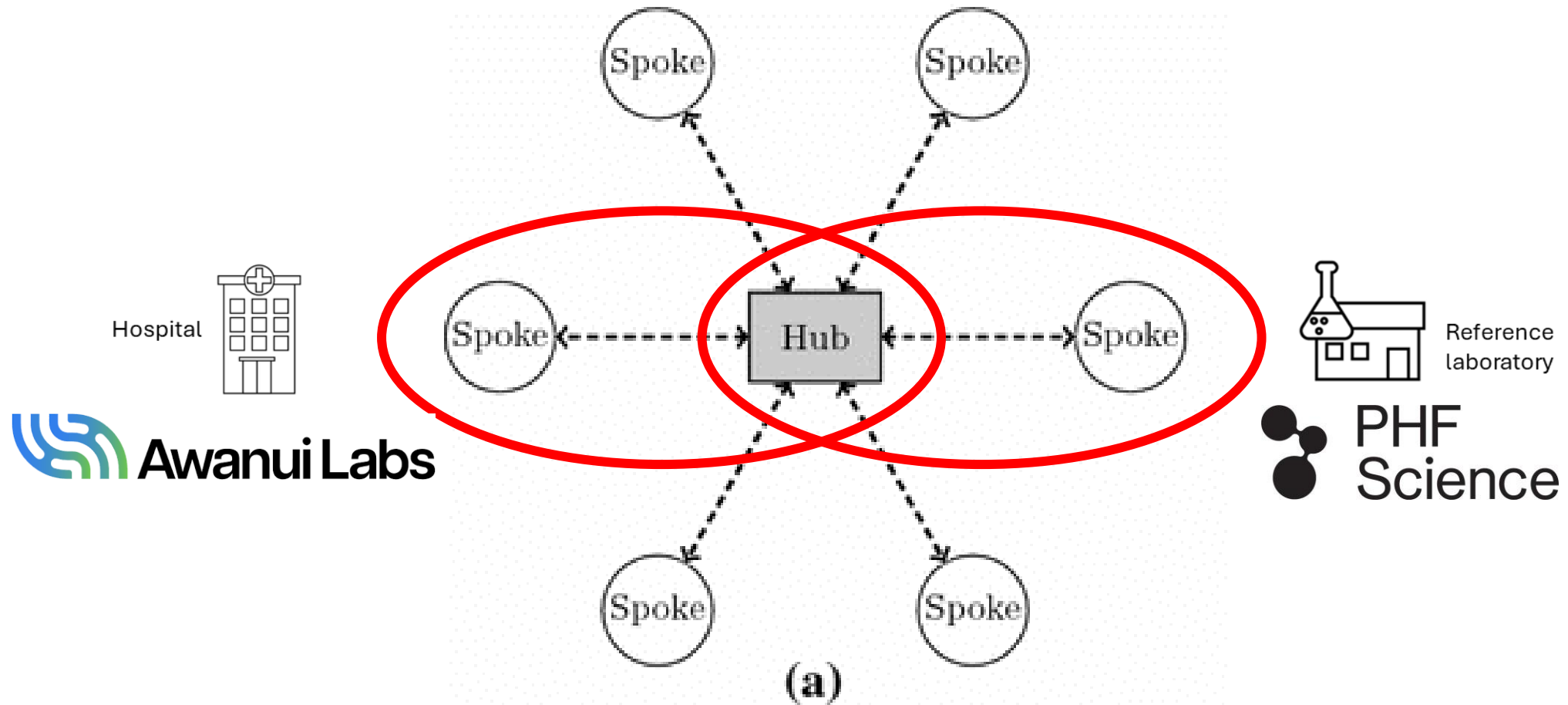
Tuesday 3 June 1:03 pm (30 minutes later)



Decentralised sequencing model



Decentralised hub and spoke model



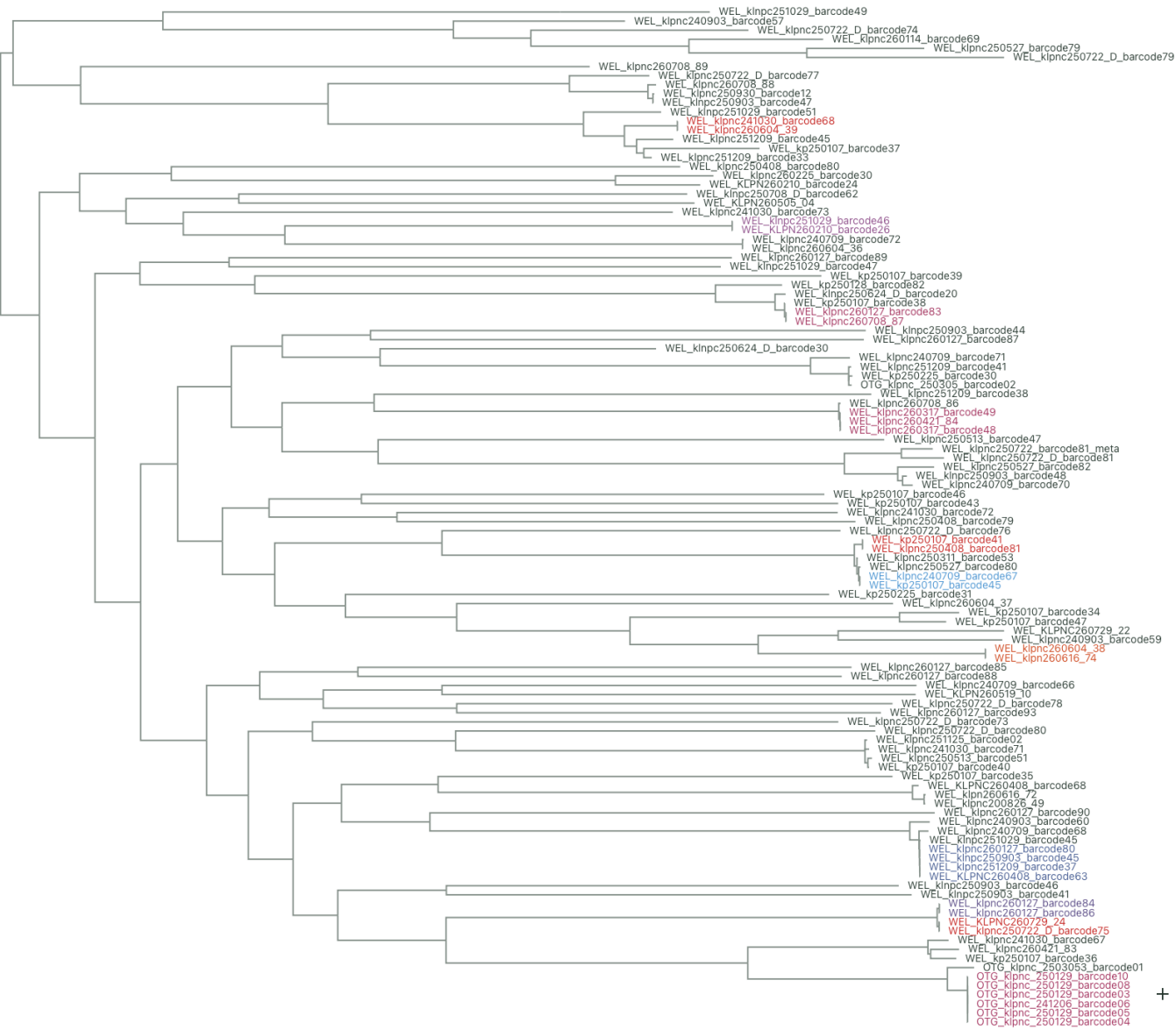
Understanding local organism behaviour

Klebsiella pneumoniae



Clusters

- Kp1
- Kp2
- Kp3
- Kp4
- Kp5
- Kp6
- Kp7 Monitoring
- Kp8 No action needed
- Kp9 No action needed
- Kp10 No action needed
- Kp11 Monitoring

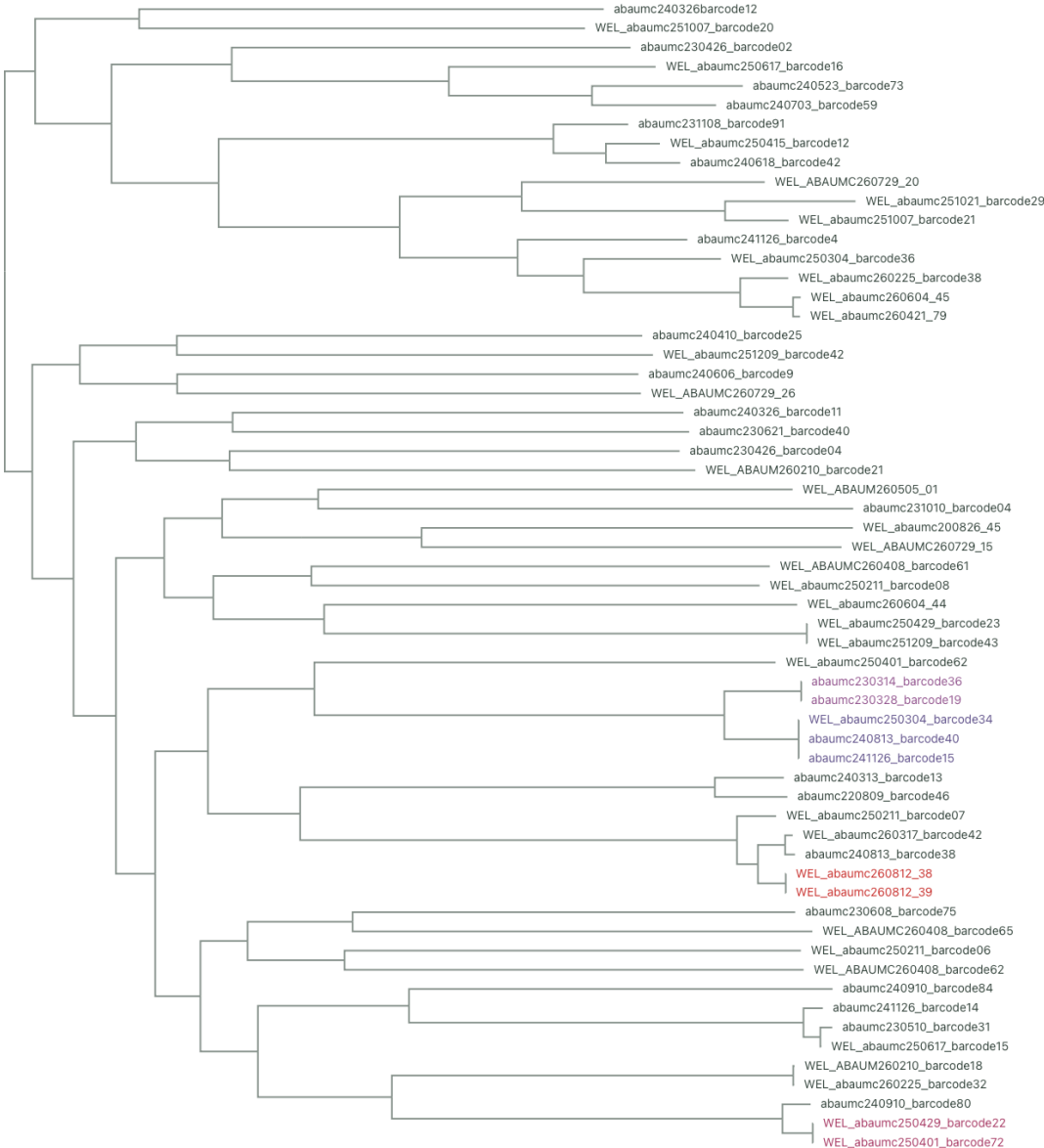


Acinetobacter baumannii



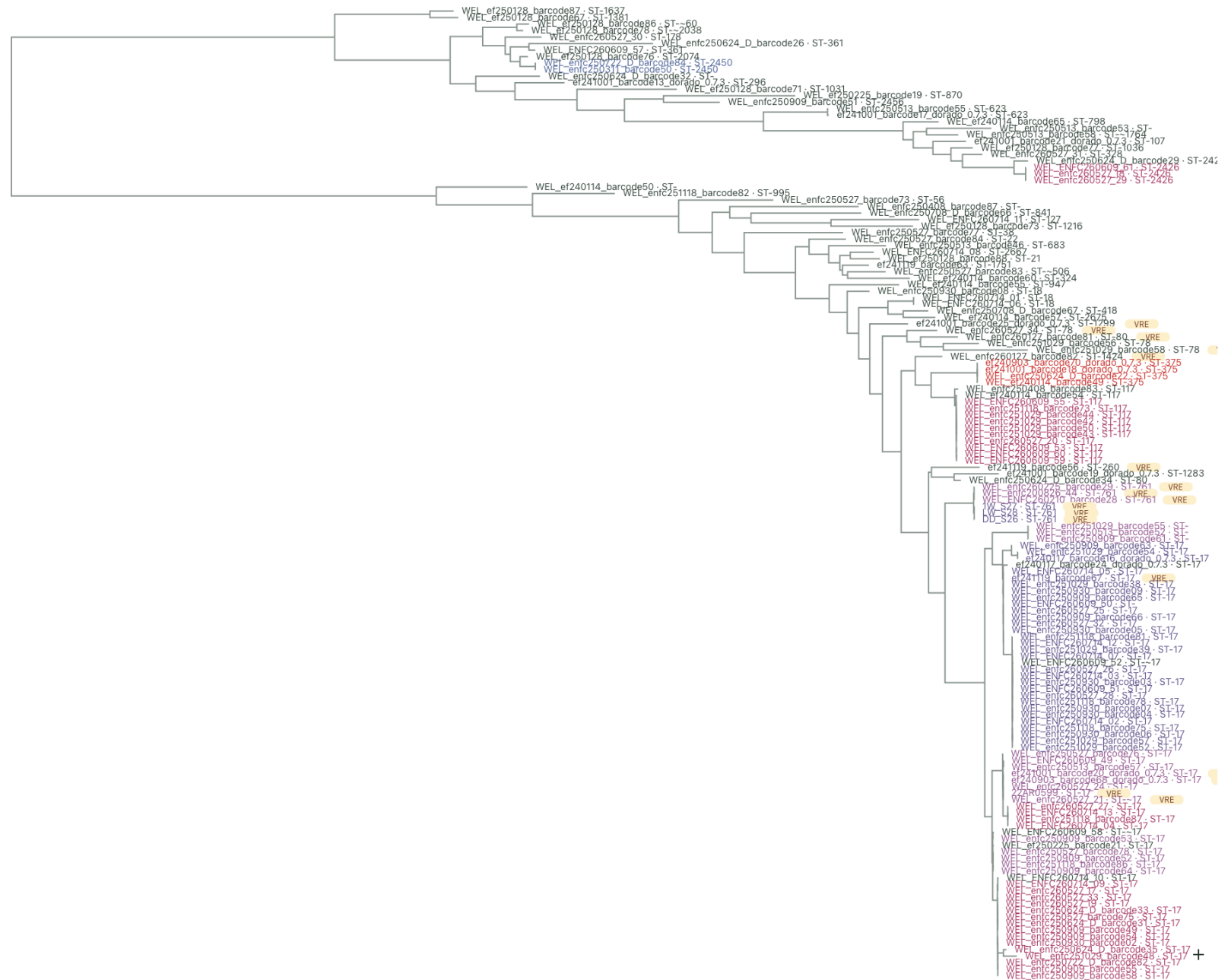
Clusters

- Ab1
- Ab2
- Ab3
- Ab4



Ef1 —
 Ef2 —
 Ef3 —
 Ef4 —
 Ef6 —
 Ef7 —
 Ef8 —
 Ef9 —
 Ef10 —
 Ef11 —
 Ef12 —

Under investigation

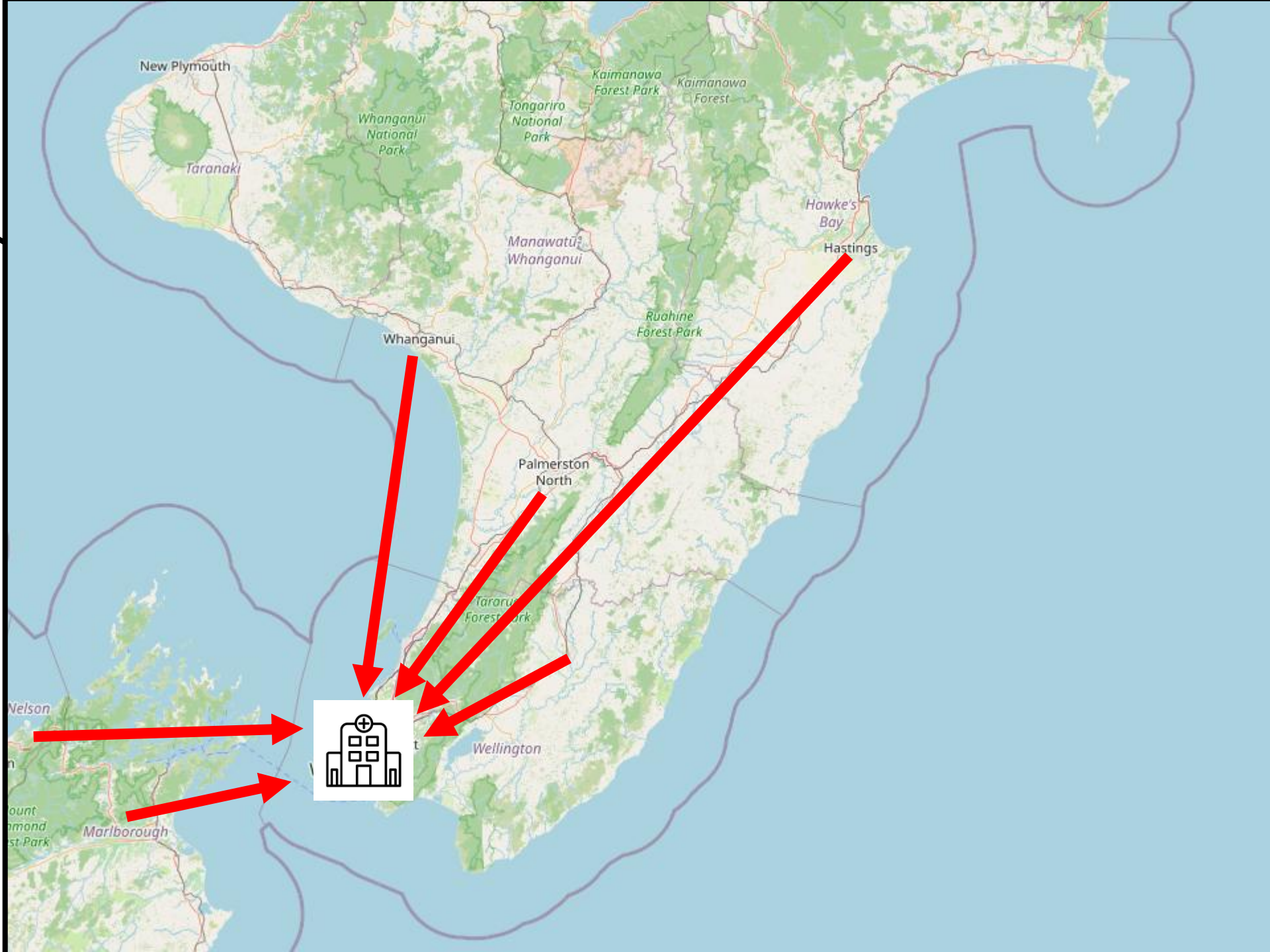


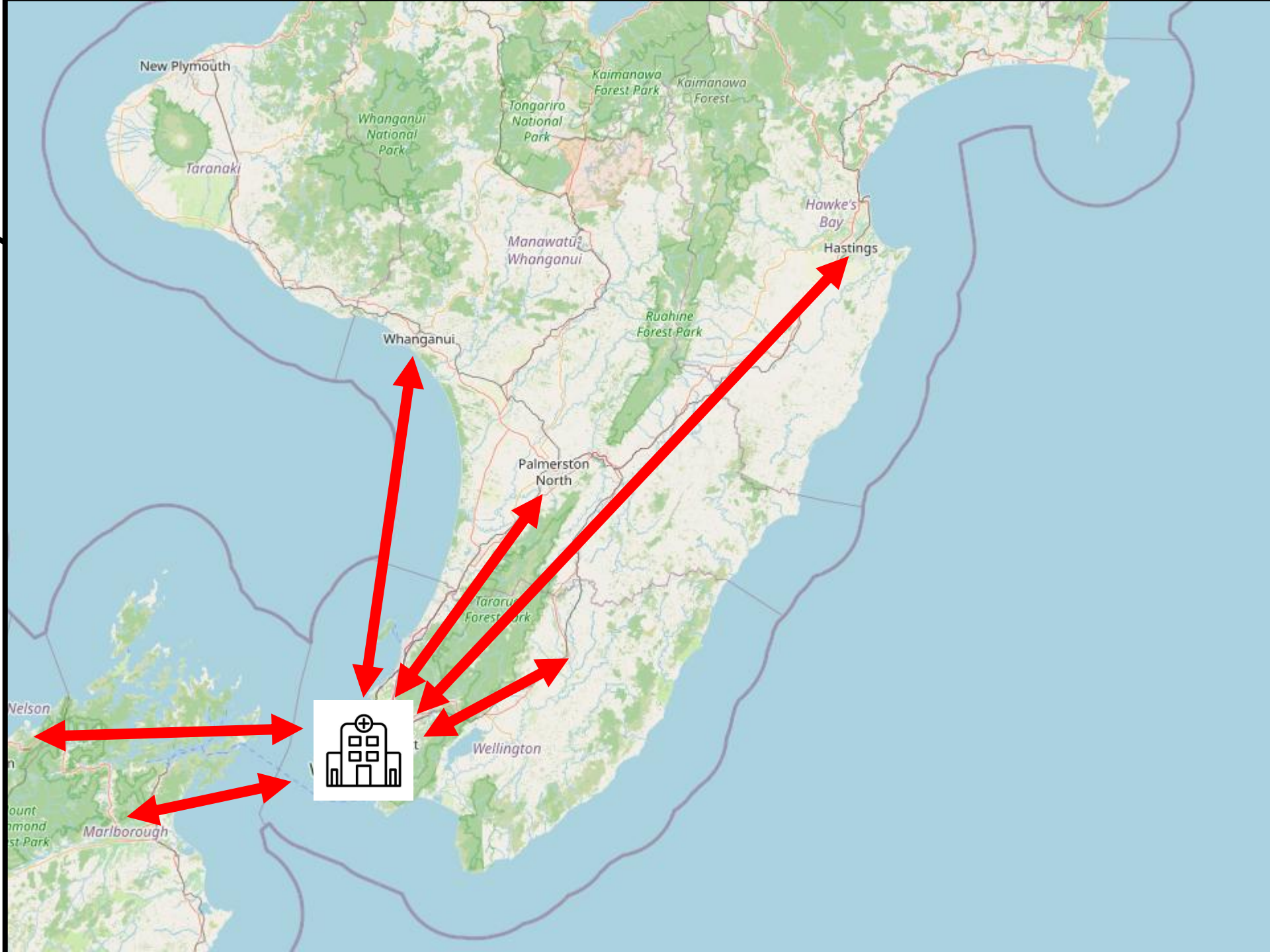
A tale of three organisms

- *Klebsiella pneumoniae* and *Acinetobacter baumannii*
 - Appear to very rarely transmit in our setting
 - We have now stopped isolating ESBL *K. pneumoniae*
 - Free up single rooms, improve patient flow
- *Enterococcus faecium*
 - Appears to readily transmit in our setting
 - Dominated by 2-3 main clones
 - At this point these clones are VSE...

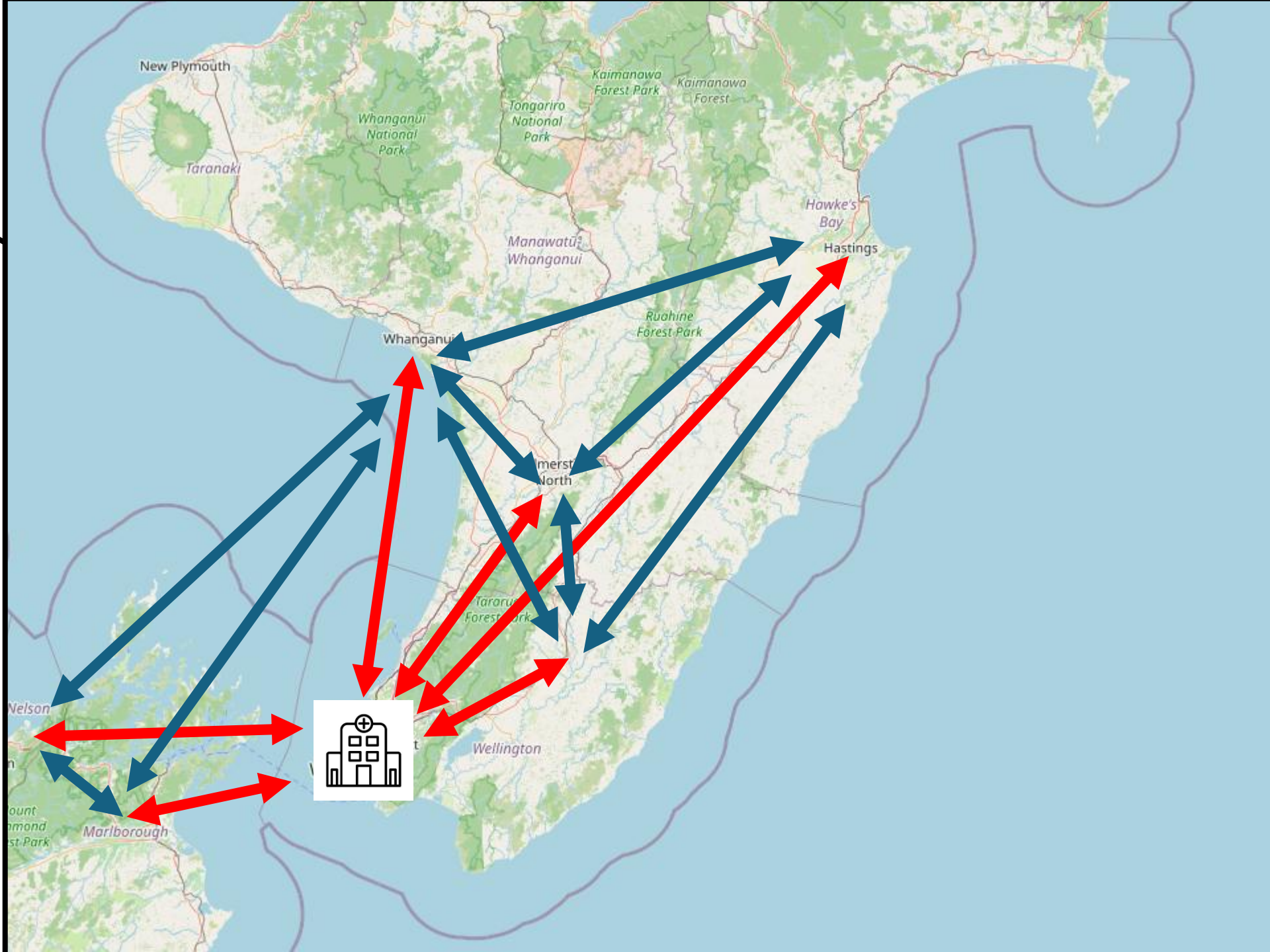
Moving towards a regional model

We have gained an understanding of how bugs behave in our hospital context.
Now we want to understand how they behave within our hospital network.



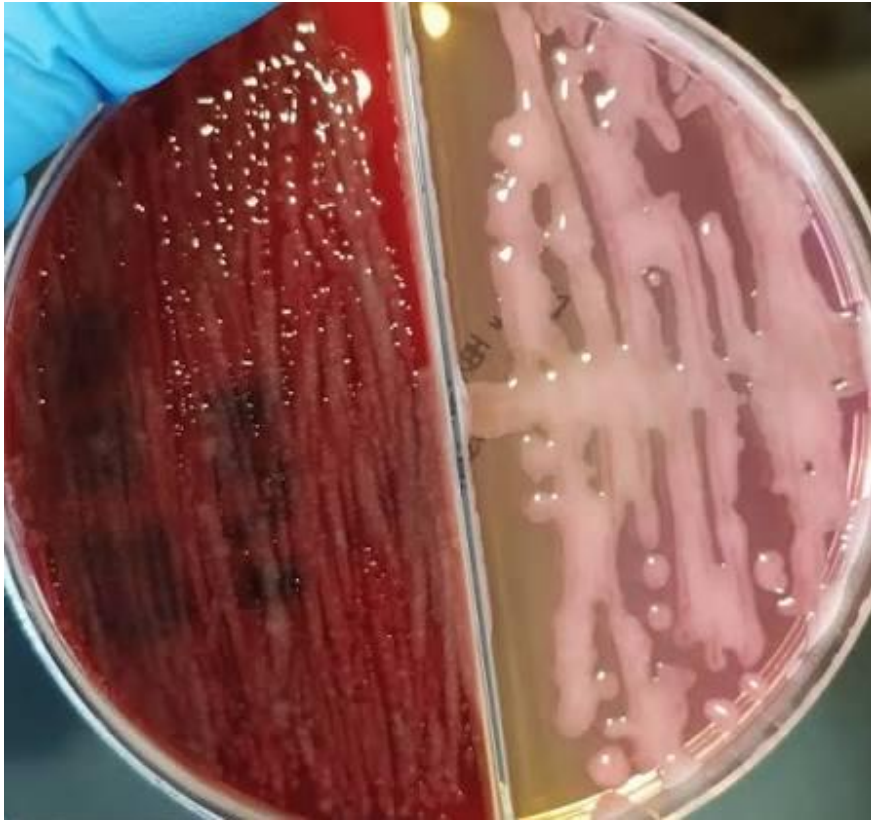


<https://mangomap.com/visionstream/maps/66161/lower-north-island-region#>



Two things that happened last
week

ESBL *Kleb pneumoniae*



ESBL *Kleb pneumoniae*



NDM *E.coli* !!

Clusters

Ec1 —

Ec2 —

Ec3 —

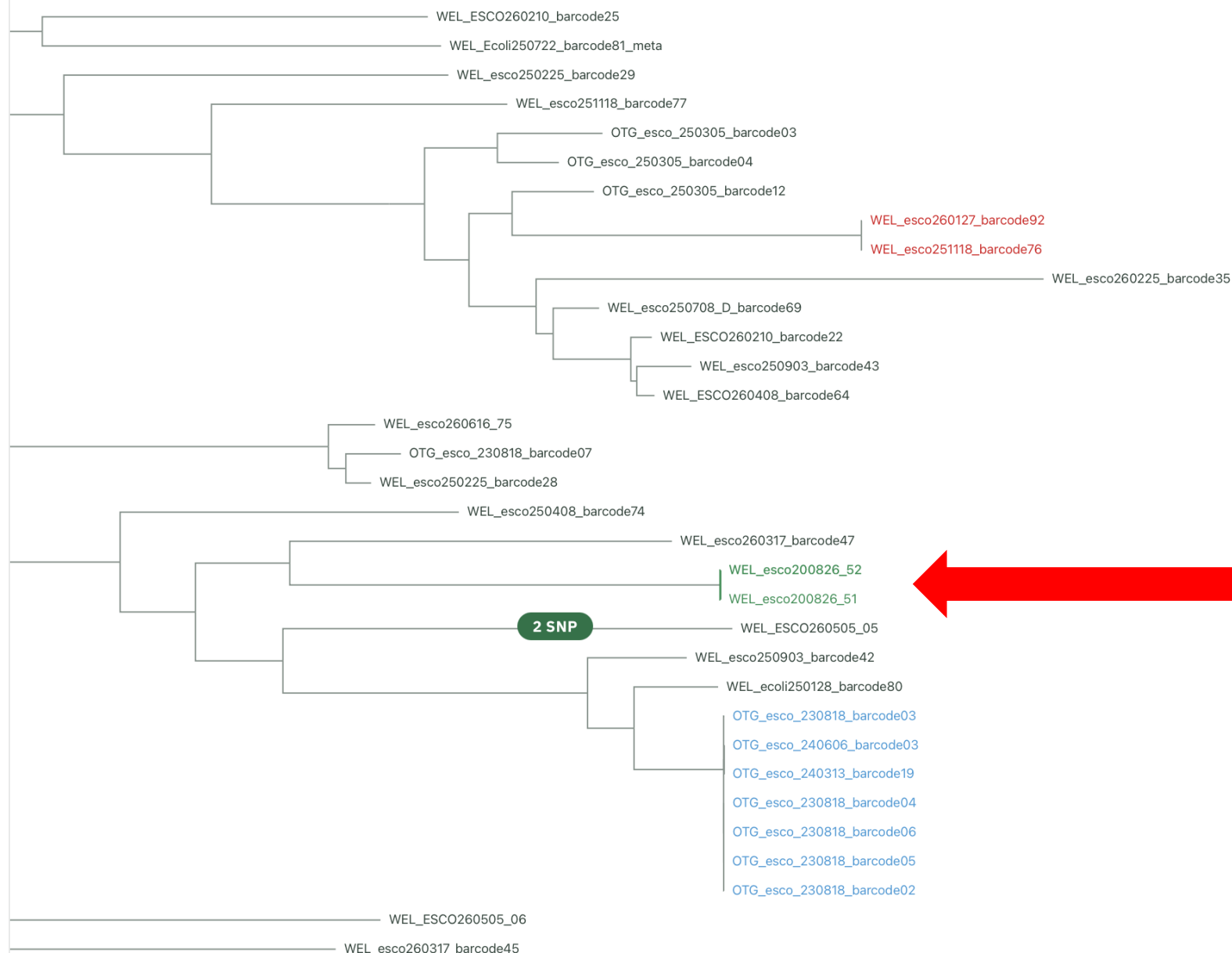
Ec4 —

Ec5 —

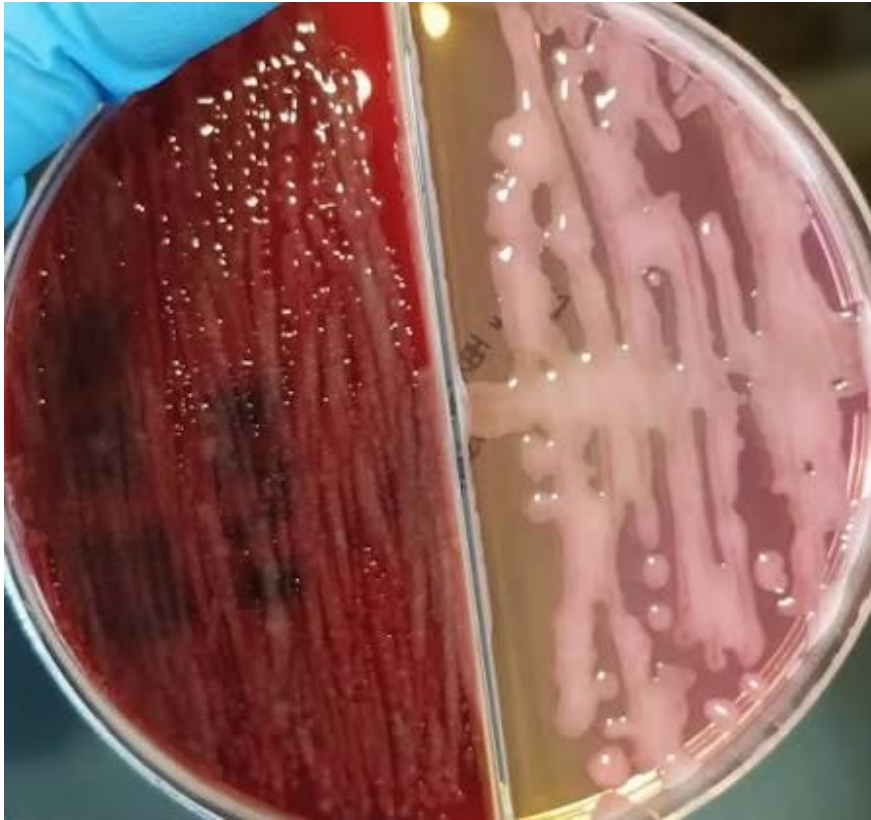
Ec6 —

Ec7 —

Ec8 Resolved ▾



ESBL *Kleb pneumoniae*



ESBL *Kleb pneumoniae*



NDM *E.coli* !!

 Reply  Reply All  Forward



Sun 16/08/2026 5:33 PM

Maxim Bloomfield [CCDHB]

VRE in medical ward long stayer

To **Infection_Control** [HVDHB]

Cc Matthew Kelly [HVDHB]; Andrea Peat [3DHB]; Melissa Tan [HVDHB]; James Chancellor [3DHB]; Michelle Balm [CCDHB]



[REDACTED]

I let the DNM know and requested enhanced contact. We will try to get this one sequenced soonish to see if related to any others we know of.

Cheers

Max

4 days later...

Ef11 (*E. faecium*)

Under investigation

Automatically detected cluster with 3 samples.

Notes 1

+ Add note

MB

Two cases from Jan-Feb 2026 were presumed transmission in Hutt Hospital. 200826_44 is a patient who has spent a long time on medical ward also in Hutt. Investigating for possible epi links/overlaps.

Max Bloomfield · 21 Aug, 2026, 09:03

Cluster samples

☐	Sample	↕	QC	Species	↕	MLST	↕	AMR genes	↕	Plasmids	↕	Cluster	Created by	↓
☐	WEL_enfc200826_44		▾	<i>Enterococcus faecium</i>		761	▾	19 VRE	▾	3	▾	Ef11	▾	MB 21/8/2026
☐	WEL_enfc260225_ba...		▾	<i>Enterococcus faecium</i>		761	▾	23 VRE	▾	3	▾	Ef11	▾	MB 26/2/2026
☐	WEL_ENFC260210_ba...		▾	<i>Enterococcus faecium</i>		761	▾	19 VRE	▾	3	▾	Ef11	▾	MB 11/2/2026

Context

Phylogenetic tree

Clusters

Ef11



Genomics and IPC

- Brings a much higher level of precision to IPC decision making
- Allows decisions to be based what we know has happened, rather than what we guess may have happened
- The faster you can get results the higher the potential positive impact
- Eventually we will regionalize and then nationalize real-time decentralized IPC genomics!



Acknowledgements



Samantha Hutton

Megan Burton

Brandon Su

Jamaal Jeram

Claire Tarring

Amruta Unka

Charles Velasco

Arleen Donaldson

Koen van der Werff



Rhys White

David Winter

Donia Macartney-Coxson

Formerly of PHF Science:

Joep de Ligt

Matt Storey

Miles Benton

Te Whatu Ora
Health New Zealand

Capital, Coast and Hutt Valley

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