

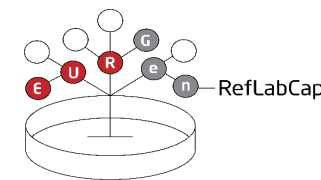
DTU



# Simulated exercise on CPO outbreak – *Pseudomonas aeruginosa*

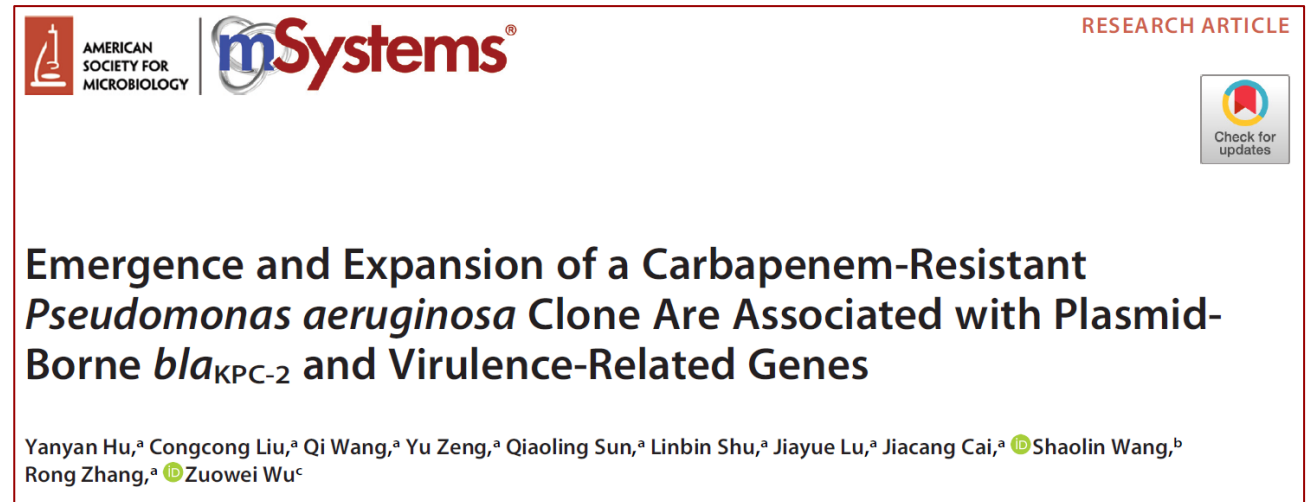
EURGen-RefLabCap  
Virtual multidisciplinary training workshop  
September 2023

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# Scenario- sequence data

- Based on the sequence data from Chinese study 2006-2018
- Dataset is available on NCBI under Project ID PRJNA648026
  - <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA648026>
- The data for non-cluster outbreak are also from the same study.

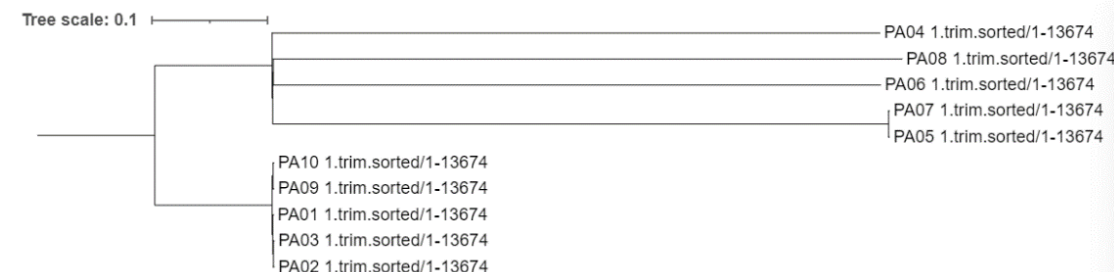


# Scenario- Inject 1.2

- In May 2023, increase detection of CRPa was detected in the ICU
- Archived CRPa samples since Nov 2022 were analysed
- PA04, PA06, and PA08 are not part of any cluster

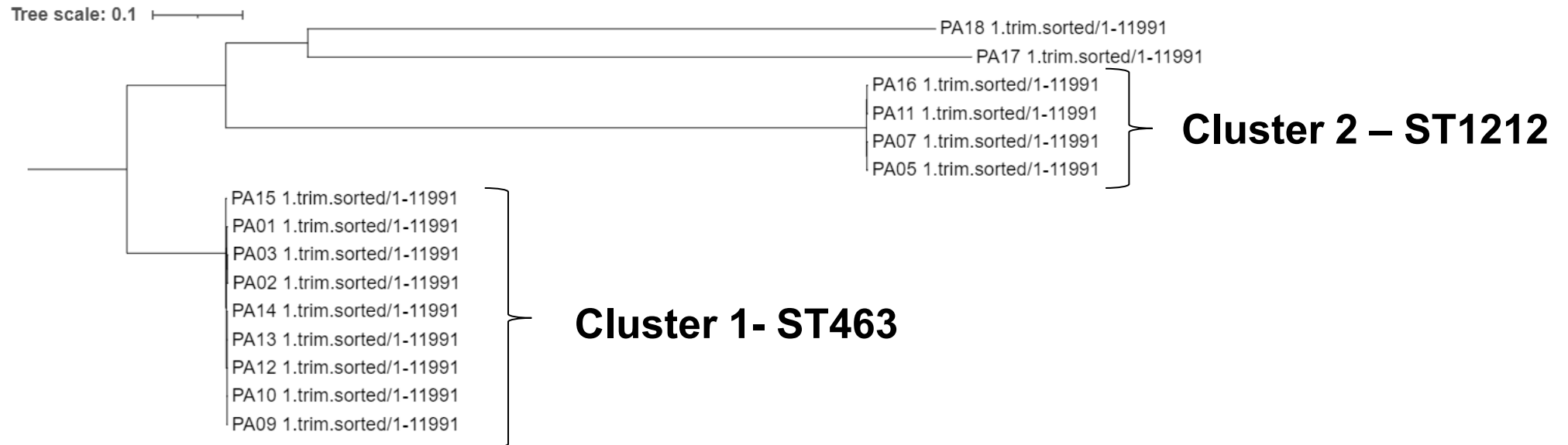
2 Clusters?

| Column1          | PA01_1.tr | PA02_1.tr | PA03_1.tr | PA04_1.tr | PA05_1.tr | PA06_1.tr | PA07_1.tr | PA08_1.tr | PA09_1.tr | PA10_1.tr |
|------------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| PA01_1.tr        | 0         | 4         | 6         | 5171      | 5222      | 5179      | 5224      | 5284      | 15        | 13        |
| PA02_1.tr        | 4         | 0         | 2         | 5169      | 5220      | 5177      | 5222      | 5282      | 13        | 11        |
| PA03_1.tr        | 6         | 2         | 0         | 5171      | 5222      | 5179      | 5224      | 5284      | 15        | 13        |
| PA04_1.tr        | 5171      | 5169      | 5171      | 0         | 6677      | 6593      | 6679      | 6633      | 5180      | 5178      |
| PA05_1.tr        | 5222      | 5220      | 5222      | 6677      | 0         | 6637      | 4         | 6755      | 5231      | 5229      |
| PA06_1.tr        | 5179      | 5177      | 5179      | 6593      | 6637      | 0         | 6639      | 6527      | 5188      | 5186      |
| PA07_1.tr        | 5224      | 5222      | 5224      | 6679      | 4         | 6639      | 0         | 6757      | 5233      | 5231      |
| PA08_1.tr        | 5284      | 5282      | 5284      | 6633      | 6755      | 6527      | 6757      | 0         | 5293      | 5291      |
| PA09_1.tr        | 15        | 13        | 15        | 5180      | 5231      | 5188      | 5233      | 5293      | 0         | 2         |
| PA10_1.tr        | 13        | 11        | 13        | 5178      | 5229      | 5186      | 5231      | 5291      | 2         | 0         |
| min: 2 max: 6757 |           |           |           |           |           |           |           |           |           |           |



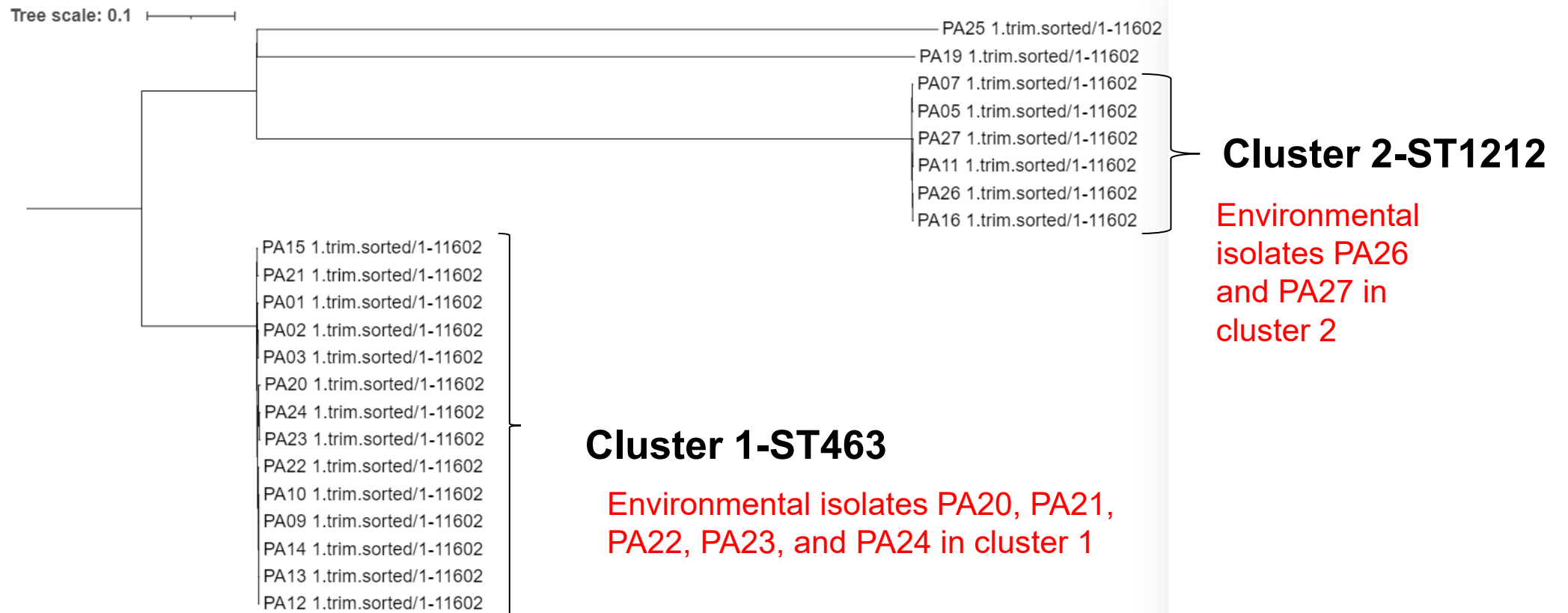
## Inject 2 – Patients from the ICU

- Which isolates are excluded from the cluster?
  - PA17 and PA18 are excluded
  - >5000 SNP difference



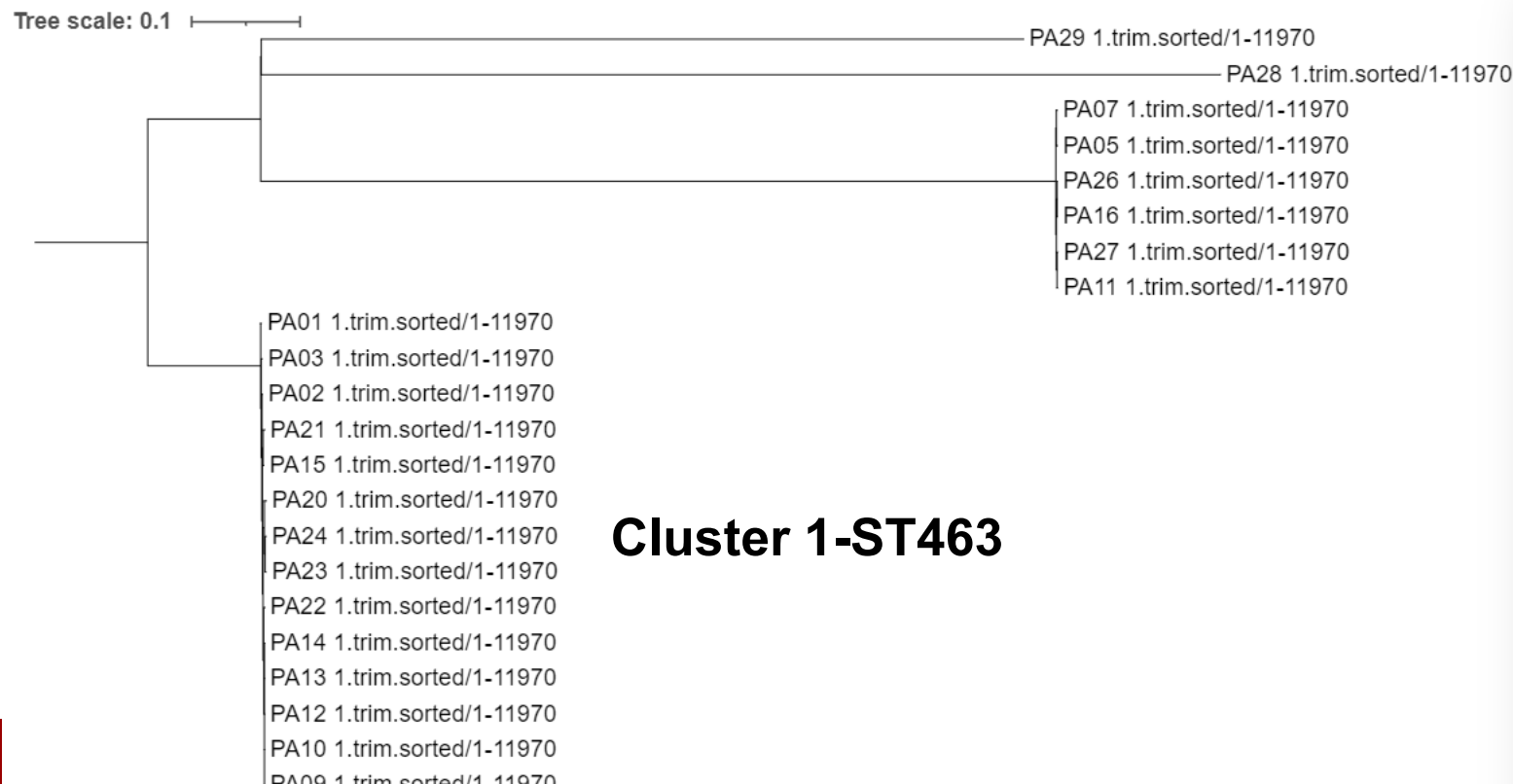
# Inject 3.1 – Environmental samples from ICU

- PA19 and PA25 are excluded
- Environmental reservoir of KPC-2 carrying *P. aeruginosa*



# Inject 3.2 –Final phylogenetic tree

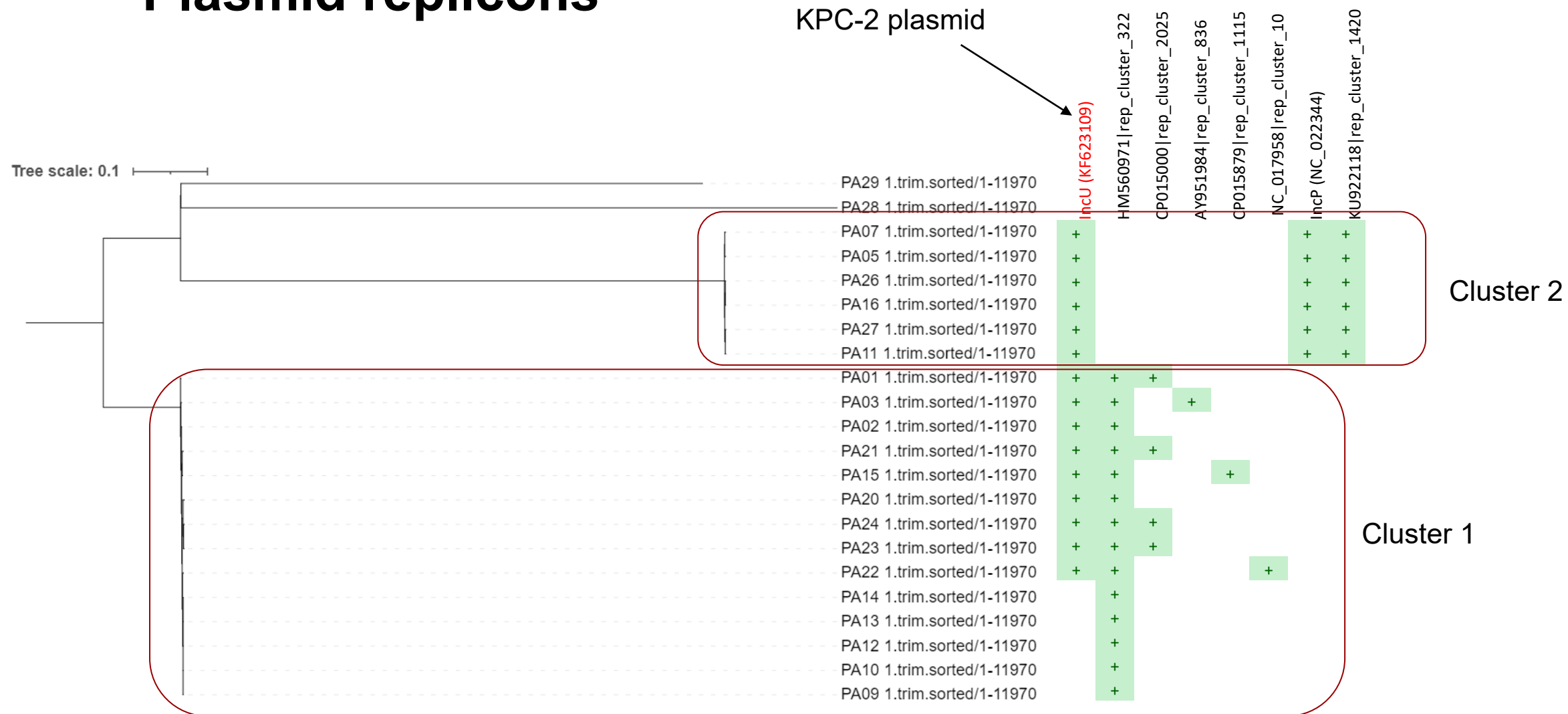
- Outbreak only in the ICU- all non-ICU acquired are not part of any cluster
- Environmental isolates cluster with clinical isolates-
- Possible source is water reservoir?
  - Pseudomonas can persist for longer periods on surfaces due to biofilm formation



**Cluster 2 – ST1212**

**Cluster 1-ST463**

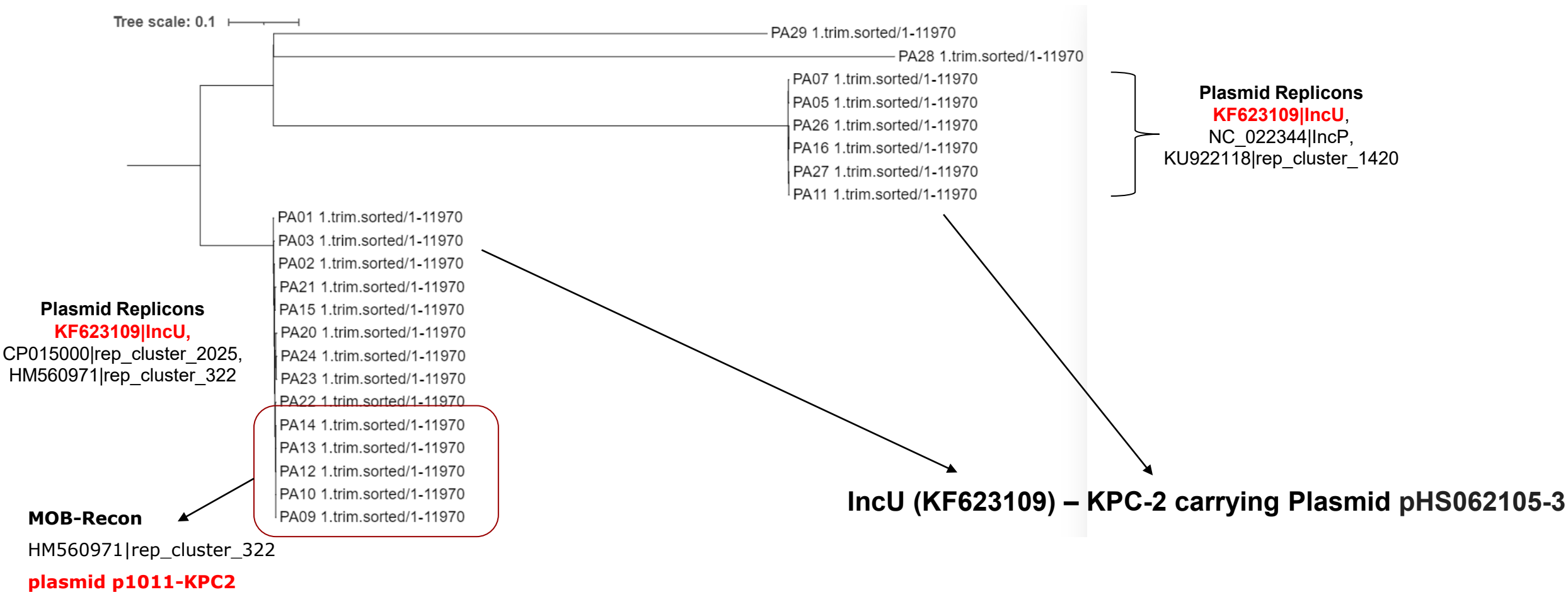
# Plasmid replicons





# Plasmids

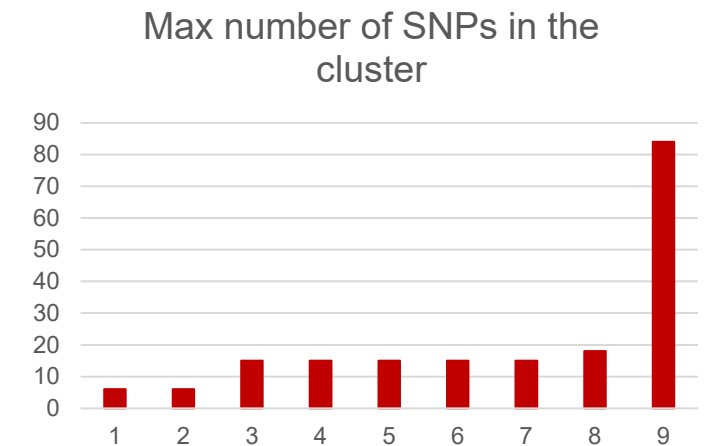
- Cluster 1 and 2 isolates share the same plasmid - IncU (KF623109) – KPC-2 carrying Plasmid pHS062105-3



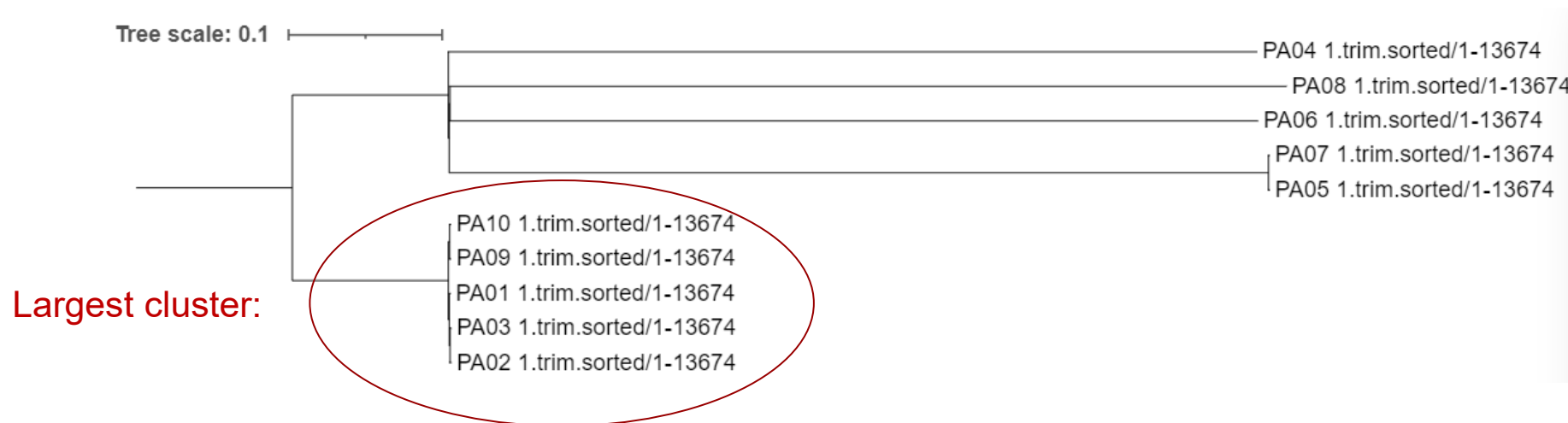
# Survey questions – Results Survey 1

- Inject 1.2 – there were 11 respondents
- Q1: With this preliminary cluster analysis, how many apparent clusters would you investigate further? (Options: 1/2/>2)
- Q2: What is the maximum number of SNPs (variants) in the (largest) cluster?
  - Answers: 6, 15, 18, 84, 5293, 6757

| Answer | Responses (%) |
|--------|---------------|
| 1      | 0             |
| 2      | 9 (82 %)      |
| >2     | 2 (18 %)      |



## Q2: What is the maximum number of SNPs (variants) in the (largest) cluster?



Is it 1 or 2 clusters?

-2 to 6 SNPs vs up to 15?

Too little data to know yet, but based on these SNP data it looks like 1

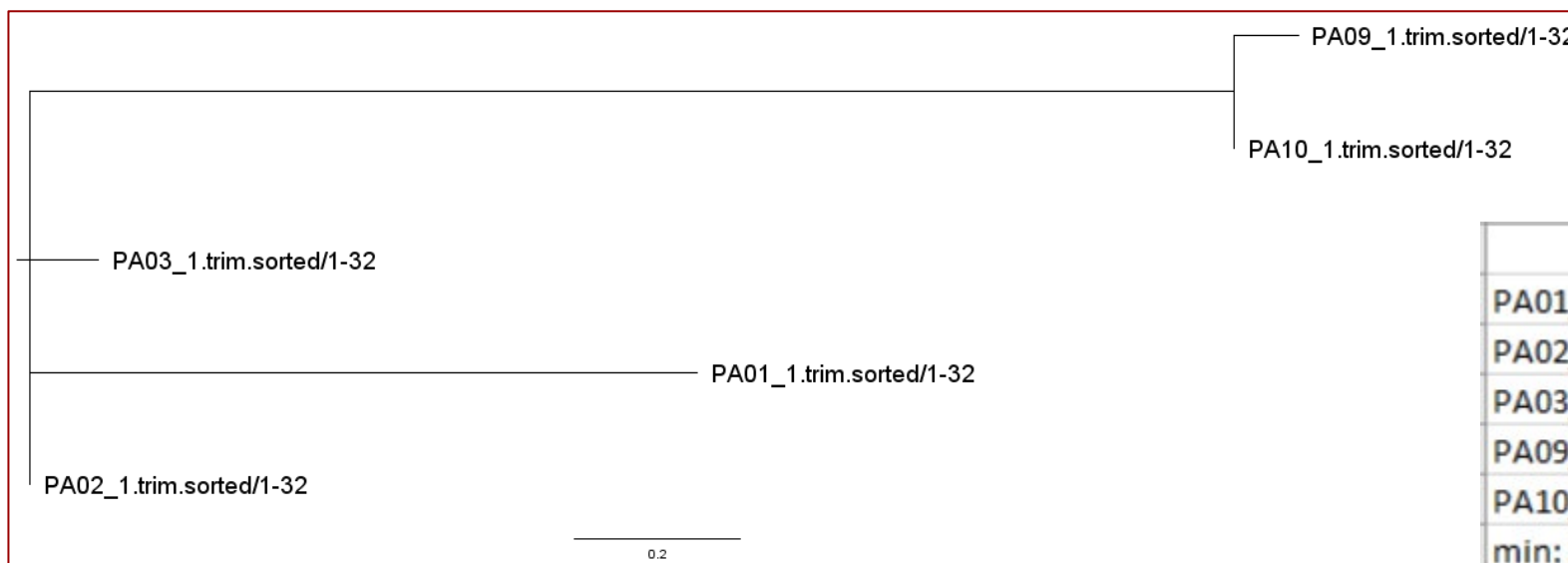
What if we exclude all but the 5 isolates in question?

| Column           | PA01_1.tri | PA02_1.tri | PA03_1.tri | PA04_1.tri | PA05_1.tri | PA06_1.tri | PA07_1.tri | PA08_1.tri | PA09_1.tri | PA10_1.tri |
|------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| PA01_1.          | 0          | 4          | 6          | 5171       | 5222       | 5179       | 5224       | 5284       | 15         | 13         |
| PA02_1.          | 4          | 0          | 2          | 5169       | 5220       | 5177       | 5222       | 5282       | 13         | 11         |
| PA03_1.          | 6          | 2          | 0          | 5171       | 5222       | 5179       | 5224       | 5284       | 15         | 13         |
| PA04_1.          | 5171       | 5169       | 5171       | 0          | 6677       | 6593       | 6679       | 6633       | 5180       | 5178       |
| PA05_1.          | 5222       | 5220       | 5222       | 6677       | 0          | 6637       | 4          | 6755       | 5231       | 5229       |
| PA06_1.          | 5179       | 5177       | 5179       | 6593       | 6637       | 0          | 6639       | 6527       | 5188       | 5186       |
| PA07_1.          | 5224       | 5222       | 5224       | 6679       | 4          | 6639       | 0          | 6757       | 5233       | 5231       |
| PA08_1.          | 5284       | 5282       | 5284       | 6633       | 6755       | 6527       | 6757       | 0          | 5293       | 5291       |
| PA09_1.          | 15         | 13         | 15         | 5180       | 5231       | 5188       | 5233       | 5293       | 0          | 2          |
| PA10_1.          | 13         | 11         | 13         | 5178       | 5229       | 5186       | 5231       | 5291       | 2          | 0          |
| min: 2 max: 6757 |            |            |            |            |            |            |            |            |            |            |

# Q2: What is the maximum number of SNPs (variants) in the (largest) cluster?

Percentage of reference genome covered by all isolates: 96.9940276142812  
 6772091 positions was found in all analyzed genomes.  
 Size of reference genome: 6981967

**Less variation between the isolates**  
 > more bases covered in analysis  
 > higher resolution  
 > more SNPs



|                | PA01_1.tr | PA02_1.tr | PA03_1.tr | PA09_1.tr | PA10_1.trim |
|----------------|-----------|-----------|-----------|-----------|-------------|
| PA01_          | 0         | 13        | 15        | 29        | 27          |
| PA02_          | 13        | 0         | 2         | 18        | 16          |
| PA03_          | 15        | 2         | 0         | 20        | 18          |
| PA09_          | 29        | 18        | 20        | 0         | 2           |
| PA10_          | 27        | 16        | 18        | 2         | 0           |
| min: 2 max: 29 |           |           |           |           |             |

## Further analysis - subtyping

- To strengthen the case definition, we would like you to analyse at least **one representative isolate** from each presumptive outbreak cluster for the questions Q3 – Q8.
- Q3: Do all presumptive outbreak clusters have the same MLST number?  
– Yes: 4 No: 7
- Q4: MLST ST463 (isolate 1,2,3), ST463 (isolate 9, 10), ST 1212 (isolate 5, 7)
- Q5: Do all presumptive outbreak cluster(s) have KPC-genes? Yes (100 %)
- Q6: KPC-variant: blaKPC-2 (100 %)

# Are all KPC-genes found on a contig, which also contain a plasmid replicon? And which?

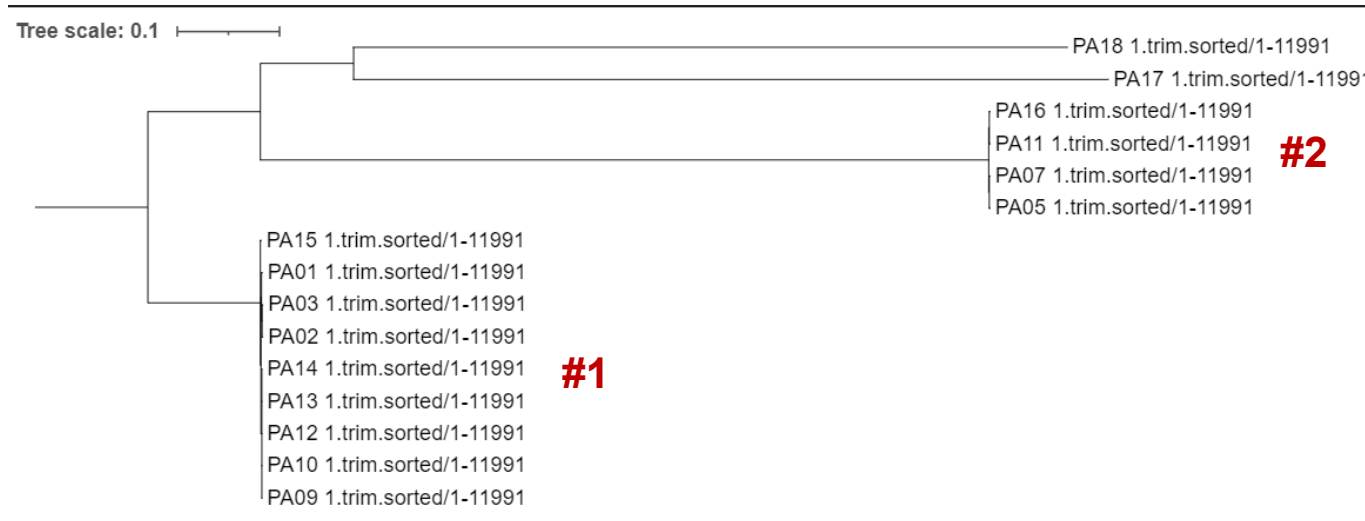
- IncU (KF623109)
- rep\_cluster\_322;rep\_cluster\_836;rep\_cluster\_10;rep\_cluster\_2238;rep\_cluster\_1115
- rep\_cluster\_322 and rep\_cluster\_1420
- IncU; rep\_cluster\_322

**Remember that plasmid analysis is somewhat limited with Illumina reads!**

- blaKPC-2 (AY034847) and IncU was detected on contig18 in PA01.
- blaKPC-2 (AY034847) and IncU was detected on contig 29 in PA05.
- blaKPC-2(AY034847) was detected on contig46, but no replicons was detected on the same contig in PA09.
- So there might be 3 outbreaks, as the biggest one might be two outbreaks.

## Survey 2 - question to Inject 2

- Based on the analysis results from Inject 1.2, at least two distinct clusters have been identified, as several isolates have been typed to either ST463 (Cluster#1) and ST1212 (Cluster#2). Non-clustering isolates from Inject 1.2 have been excluded, and eight new isolates (Inject 2) have been included in a new SNP-based cluster analysis.
- Q1/Q2: How many of the eight Inject 2 isolates seem to be part of Cluster#1/2, based on the SNP analysis alone?



### Cluster#1 (ST463)

4 new: PA12, 13, 14, 15 –if all in one cluster

### Cluster#2 (ST1212)

2 new: PA11 + PA16

Everyone agreed – except one that included the inject 3 isolates

# Survey 2 – outbreak transmission

- Q3: Based on the sample and patient metadata from Injects 1 and 2, would you consider the outbreak to be ICU related only?

| Isolate name | sex | age | Date of Isolation | Final outcome | colonization                 | comorbidities                            | Acquisition site |
|--------------|-----|-----|-------------------|---------------|------------------------------|------------------------------------------|------------------|
| PA01         | M   | 60  | 20-11-2022        | Discharge     | Urinary tract                | Chronic Kidney disease                   | ICU              |
| PA02         | F   | 57  | 15-12-2022        | Discharge     | Urinary tract                | Renal Transplant, hematologic malignancy | ICU              |
| PA03         | M   | 65  | 07-01-2023        | Discharge     | Intestinal                   | Severe aplastic anemia                   | ICU              |
| PA04         | F   | 64  | 10-01-2023        | Discharge     | Wound                        | Asthma, rheumatoid arthritis             | non-ICU          |
| PA05         | M   | 40  | 15-01-2023        | Discharge     | Respiratory and Intestinal   | Tetraparesis                             | ICU              |
| PA06         | M   | 34  | 10-02-2023        | Death         | Blood. Septic shock          | Renal Transplant, hematologic malignancy | non-ICU          |
| PA07         | M   | 68  | 12-02-2023        | Discharge     | Urinary tract and intestinal | HIV, Lymphoma B                          | ICU              |
| PA08         | M   | 65  | 16-03-2023        | Discharge     | Urinary tract                | Renal transplant                         | non-ICU          |
| PA09         | F   | 60  | 28-04-2023        | Discharge     | Urinary tract and intestinal | Chronic heart disease                    | ICU              |
| PA10         | M   | 52  | 28-04-2023        | Discharge     | Peritonitis and Intestinal   | Renal transplant                         | ICU              |
| PA11         | M   | 70  | 03-05-2023        | Death         | Intestinal                   | Liver Transplant                         | ICU              |
| PA12         | F   | 62  | 15-05-2023        | Discharge     | blood                        | Renal transplant                         | ICU              |
| PA13         | M   | 18  | 15-05-2023        | Discharge     | Urinary tract                | Renal and Liver transplant               | ICU              |
| PA14         | F   | 45  | 20-05-2023        | Discharge     | Urinary tract                | Denutrition                              | ICU              |
| PA15         | F   | 69  | 22-05-2023        | Discharge     | Intestinal                   | Chronic heart disease                    | ICU              |
| PA16         | M   | 53  | 22-05-2023        | Discharge     | intestinal                   | Stem cell transplant                     | ICU              |
| PA17         | M   | 51  | 05-06-2023        | Discharge     | Urinary tract                | Renal transplant                         | non-ICU          |

In case definition: The case is defined as non-ICU acquired if the positive sample was collected before the patient's admission to the ICU or within 48h of admission to the ICU

10/11 answer YES

There should also be an option **"based on metadata unlikely, but keep investigating"**: PA06 and PA08 appear to have plasmid encoded KPC gene; both have comorbidities which would increase the likelihood of ICU contact (direct or indirect).



## Survey 2 – outbreak transmission - comments

- All the patients (both cluster 1 and 2 ) are from the ICU.
- The isolates of the 2 clusters were acquired in the ICU in 2 different periods; cluster 1 from 20/11/2022 to 22/5/2023 and cluster 2 from 15/1/2023 to 22/5/2023 whereas even in August environmental isolates from both clusters were recovered.
- Of note, from January to May, the 2 different STs (463 and 1212) co-circulated in the same ICU. Furthermore the 2 CRPA isolates from the urology department were not part of the clusters.

## Q4: does any of the Cluster#1 isolates carry the same KPC-plasmid as Cluster#2 isolates?

**Bonus question!**

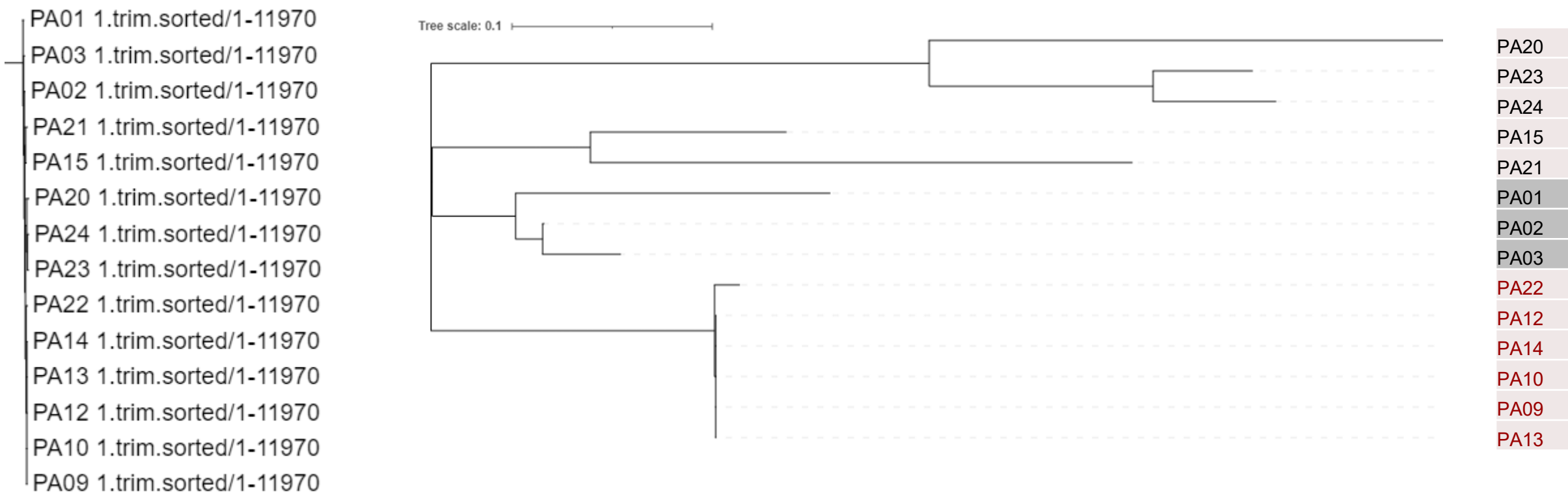


- **Yes**, for example, isolates PA01, PA02 and PA3 of cluster 1 carried an IncU KPC-plasmid like the isolates PA05 and PA07 of cluster 2.
- Is it possible to talk not only for clonal transmission of 2 STs but also for a plasmid-mediated outbreak of KPC-producing *P. aeruginosa* between 2 different clones?
- Further experiments (eg conjugation experiments and plasmid study with long reads wgs) would be necessary to study this hypothesis



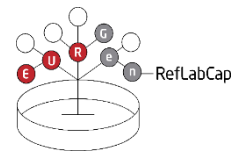
- **Maybe** - while there is significant similarity cluster#1 plasmid has 60 kb, Cluster#2 plasmid has 52 kb plasmid, so the plasmids are not completely the same (possible deletion/insertion?)
- **No**, all the Cluster #2 isolates have the same replicon type and plasmid size, which is different than the Cluster #1 isolates.

# Q5: Using all injects, determine how many isolates are clustering with the PA01 isolate?

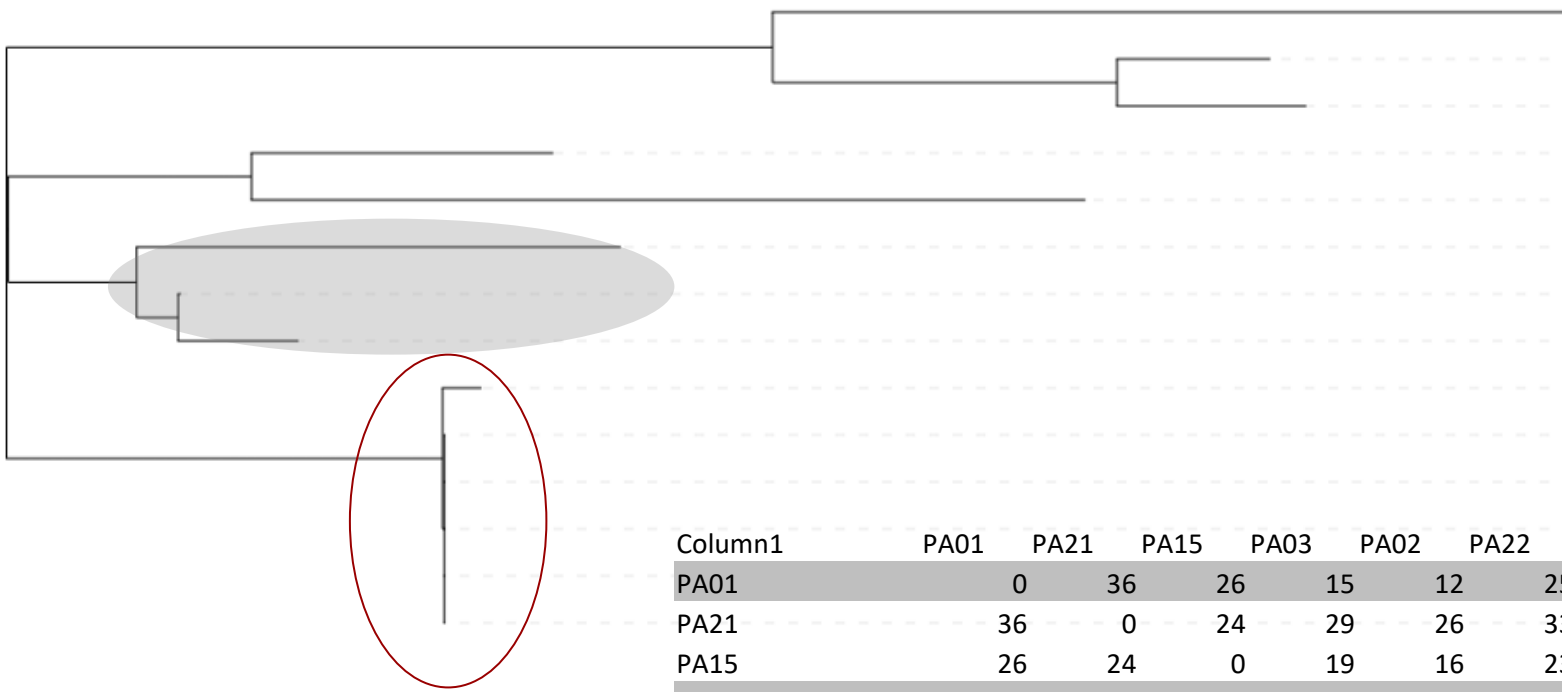


**Full cluster ST463**

Tree scale: 0.1



# Full cluster ST463



| Column1 | PA01 | PA21 | PA15 | PA03 | PA02 | PA22 | PA12 | PA13 | PA09 | PA20 | PA10 | PA14 | PA24 | PA23 |
|---------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| PA01    | 0    | 36   | 26   | 15   | 12   | 25   | 24   | 24   | 24   | 44   | 24   | 24   | 42   | 41   |
| PA21    | 36   | 0    | 24   | 29   | 26   | 33   | 32   | 32   | 32   | 52   | 32   | 32   | 50   | 49   |
| PA15    | 26   | 24   | 0    | 19   | 16   | 23   | 22   | 22   | 22   | 42   | 22   | 22   | 40   | 39   |
| PA03    | 15   | 29   | 19   | 0    | 3    | 18   | 17   | 17   | 17   | 37   | 17   | 17   | 35   | 34   |
| PA02    | 12   | 26   | 16   | 3    | 0    | 15   | 14   | 14   | 14   | 34   | 14   | 14   | 32   | 31   |
| PA22    | 25   | 33   | 23   | 18   | 15   | 0    | 1    | 1    | 1    | 39   | 1    | 1    | 37   | 36   |
| PA12    | 24   | 32   | 22   | 17   | 14   | 1    | 0    | 0    | 0    | 38   | 0    | 0    | 36   | 35   |
| PA13    | 24   | 32   | 22   | 17   | 14   | 1    | 0    | 0    | 0    | 38   | 0    | 0    | 36   | 35   |
| PA09    | 24   | 32   | 22   | 17   | 14   | 1    | 0    | 0    | 0    | 38   | 0    | 0    | 36   | 35   |
| PA20    | 44   | 52   | 42   | 37   | 34   | 39   | 38   | 38   | 38   | 0    | 38   | 38   | 30   | 29   |
| PA10    | 24   | 32   | 22   | 17   | 14   | 1    | 0    | 0    | 0    | 38   | 0    | 0    | 36   | 35   |
| PA14    | 24   | 32   | 22   | 17   | 14   | 1    | 0    | 0    | 0    | 38   | 0    | 0    | 36   | 35   |
| PA24    | 42   | 50   | 40   | 35   | 32   | 37   | 36   | 36   | 36   | 30   | 36   | 36   | 0    | 9    |
| PA23    | 41   | 49   | 39   | 34   | 31   | 36   | 35   | 35   | 35   | 29   | 35   | 35   | 9    | 0    |

min: 0 max: 52

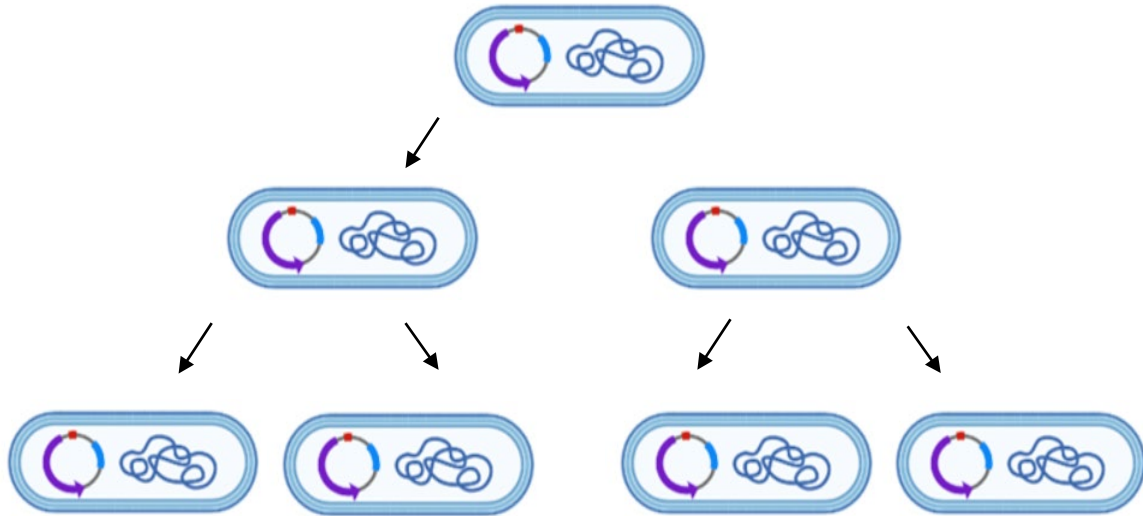
## Q6 Can the SNP analysis reveal the likely source of the ST463 outbreak in the ICU

- 10/11 answers YES!
- Comment from last:
  - Sinks drains 1 and 4, sink elbows 1 and 4 and sink pipe 3 clustered in ST463 cluster
  - Sink drain 3 and sink elbow 3 with ST1212 cluster.
  - Furthermore, the isolation even of the same strain from a sink does not prove that the sink is the source of the outbreak, since it could be the result of the outbreak.
  - Anyway, the added value of the environmental matching with the clinical isolates is the evidence of the persistent survival of carbapenem resistant Pa isolates in the ICU environment and thus of not proper cleaning procedures
- Additional comment:
  - There is a link with an isolate from a sink, but since the isolation data is later than the index patient, it is hard to say if the sink is the source

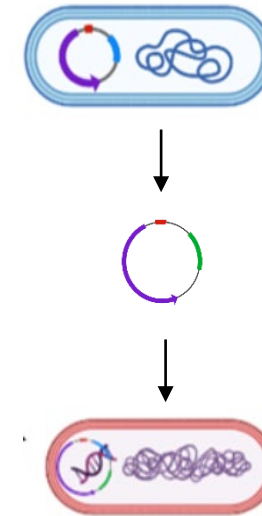
## Q7 Can the SNP analysis reveal the likely source of the ST1212 outbreak in the ICU

- 11/11 answers YES!
- Comment:
  - The isolation even of the same strain from a sink does not prove that the sink is the source of the outbreak, since it could be the result of the outbreak.
- Additional comment:
  - There is a link with an isolate from a sink, but since the isolation data is later than the index patient, it is hard to say if the sink is the source

# Dissemination of resistance



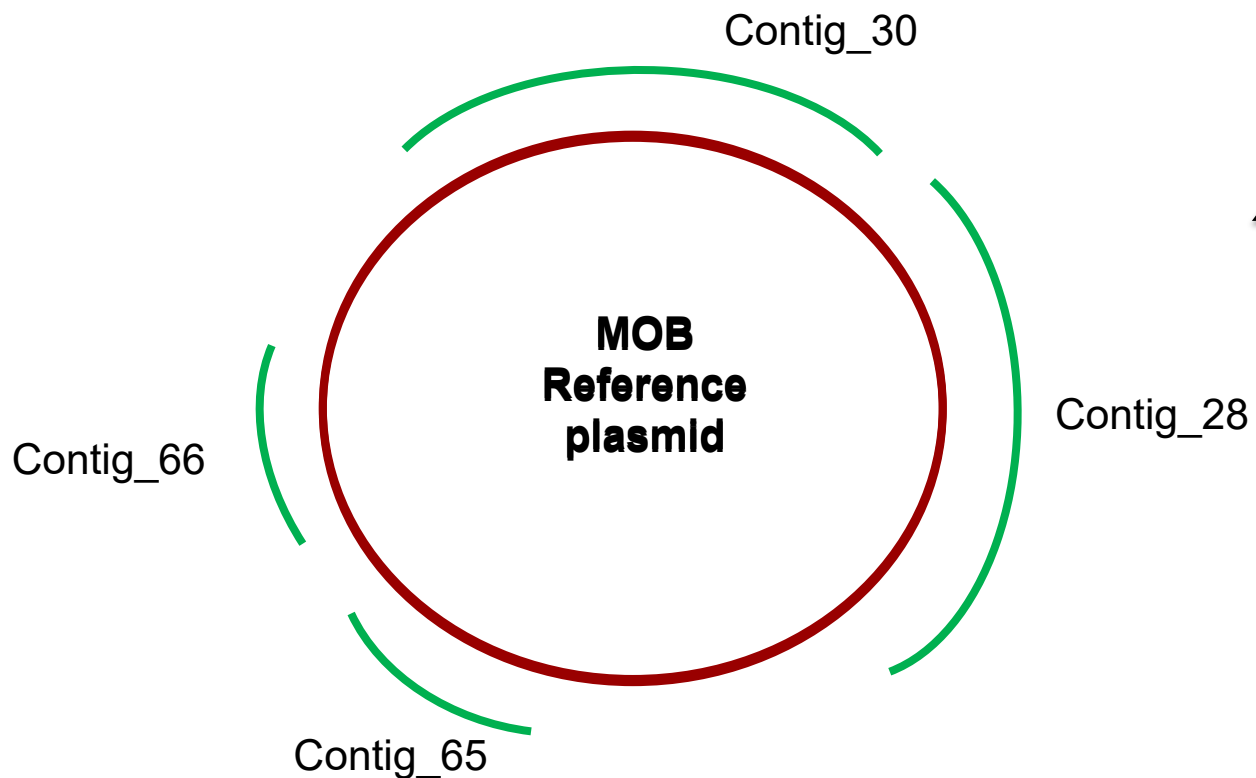
**Vertical spread of resistance  
(clonal spread)**



**Horizontal spread of resistance  
(plasmid/MGE transfer )**

# MOB- Recon

- Plasmid Reconstruction from bacterial draft assemblies
- Outputs contigs belonging to a particular plasmid



Contig\_1  
Contig\_2  
Contig\_3  
Contig\_4

..  
.....  
.....

Genome assembly



# Running MOB-Recon in Galaxy

Tools

mob

Upload Data

Show Sections

**MOB-Recon** Type contigs and extract plasmid sequences

**MOB-Typer** Get the plasmid type and mobility given its sequence

**Manipulate loom object** Add layers, or row/column attributes to a loom file

**Calculate presence absence table** calculate presence absence table from observation data

**Ocean biodiversity indicators** from OBIS

WORKFLOWS

**MOB-Recon** Type contigs and extract plasmid sequences  
(Galaxy Version 3.0.3+galaxy0)

Run Tool

**Tool Parameters**

Input \*

47: PA09.fa

FASTA file with contig(s)

**Advanced parameters**

**Additional Options**

**Email notification**

No

Send an email notification when the job completes.

Run Tool

1. Select MOB-Recon

2. Select the fasta file

3. Click "Run Tool"

# Running MOB-Recon in Galaxy

Accession numbers

| Column 15             |
|-----------------------|
| mash_nearest_neighbor |
| MH734334              |
| CP030914              |

| Column 1   | Column 2    | Column 3 | Column 4          | Column 5                         |
|------------|-------------|----------|-------------------|----------------------------------|
| sample_id  | num_contigs | size     | gc                | md5                              |
| PA09:AE788 | 4           | 58870    | 8.49838627484287  | b2a428305be86dbe3e470d3203df366f |
| PA09:AF876 | 11          | 107167   | 60.49250235613575 | e003859c40da9a5f5e9c904e8dc14d1b |

Two plasmids  
reconstructed

1. Open the report file

**National Library of Medicine**  
 National Center for Biotechnology Information

Nucleotide

GenBank

**Pseudomonas aeruginosa strain 1011 plasmid p1011-KPC2, c**

GenBank: MH734334.1

[FASTA](#) [Graphics](#)

History

Assembly
 14.1 MB
 5
 47
 2

51: MOB-Recon on PA09.fa: Ch  
romosomal sequences

50: MOB-Recon on PA09.fa: A  
ggregate MOB-typer report for  
all contigs

49: MOB-Recon on PA09.fa: Ov  
erall contig MOB-recon report

48: MOB-Recon on PA09.fa: Pl  
asmids

a list with 2 datasets

# Running MOB-Recon in Galaxy

```
CAIACGCCCCIGGGTGGCAICGGAAACAGGCIGCCGATAGAACAGGICTIGGGAGAAGTCGGTGCCGTCGGCCAGTGGCAATTC
ATCCTGCAGGATCGGTTCTGTCGGCCGGCATAACCAAGTTCGTAGAAGCGACGTAGATCCGCTCGGCCCTGGCCGAGGTGATCCG
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GCGGTAGACGACCATCCGCACGCGCCGCTGTTG
```

```
>NODE_64_length_1605_cov_22.153586
```

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ACATCCTGCTCTGGGAAGAACACGTCGGCCCCATCCCAACCGGCCATTGCGTCTGCTTCAAGGACAACAACAAGCAGAACGTC
GTCATCGACAACCTGGAACCTCATCACCCGGGCCGAACGCATGCGTCGCAACTCCATCCATCGCTATCCACCTGAGCTGAAGAG
CGCAATCCGCGTCATCAGCAAGCTCAAGCGCACCATTCAGGAGGTCGAGCATGAAAAACAAGATTGAGGATCTGCGTAATCAC
CTCTTCGCCACCATCGAAGGCCTGCTGGACGAAGAGAACCCTCTGGATATCGAACGCGCGAAAGCGGTGGCTCATGTGGGTTT
GGTGATCATCGAGTCGCCAAGGTGGAGGTGAAAGCGCTGGAGATCATCGCGCCCCGGGTGGAAGCACGTTTCATGCAGATCG
GCCGGGAGGACTCGAAGTGAGTGTTCTGGAACACGCGCCGCACTCCGTGAGGCGGAGCAAGGGGTACTCGGTGGCCTGA
TGCTGGACAACGCGGCATGGGACATTGTGCGCGATCACCTGCAGAAGGAGGACTTCTCCGGCATGAACATCGGCTGATTTTC
ACCGCCATCAGCGAGTTGGCCGCGAAGGACGCCCGTTTGACGTGTCGACGGTGTGGAAGCGATCGAAGACCTTCAGAAGC
CGGCGGGCTGGCTACCTCGGCCAGCTCGCTGACAACACGCCCTCCGTGGCCAATATCGAGGCTTACGCGCAGATCGTTCGCG
ATCGGGCGCACCTGAGGCTCTTGATGTCTCTCGGGCACCACTGCACCAGAACCAGGCTCGAACCACAGGCGAATCCCTGTGAG
GTTCAGGAGGAGATCGAGCAGAAGCTGTTGCGCCTCGGCCAAGATCAGCACAAGTCCGACTTTGTGATATCAACAAGGCGCT
CGCGAGGATCGTCGACACCATCGATTACCGCTTCAACAACAACGTGACGGTAACGGGGGTCCCAGAGGCTGAAGGATCTCG
ACGAGCTCACCGGCGGACTACAGAAGTCGGATCTCATCATCGTCGGTGCCCGTCCCTCGATGGGCAAAACGTCGTTTGCCTC
AACCTTATCGAGCCGCGCTGCAGAGCGACCAACAGAAGTCTGTCCAAGTTTACAGCATGGAAATGCCGGCAGAGCAGCTGCT
GTTCAGGCTGGCCGCCCTGCTTGCCCATCTGGACCTTGGAAGCTGATGAAAGGCCAACTGCAAGAGGAGGATTGGCCCCGGC
TGCTGTGTCGCGATCAAGCGCATAAACAAGATATGGCAGCCGCTGGTCATCAACGACAGGGCAACCTCTCGCCGACGGAGCTA
CGTGCCAAAGTACGCCGTGCGGCCAGGAAGTACGGCCATCCCGTGTGATCTTGGTCGACTACCTACAACGATGCGCTGCCC
AGGCTTGGAAAACCGAGCCACCGAGATCTCGGAGATATCCCGCTCGCTGAAAGCACTGGCCAAGGAGATGGATTGCCCCGTG
TGGCCTGTCCAGCTCAATCGCAGCTGGAGAACCAGGCCGAACAAGCGACCGAACAACGACGACCTGCGTGAGAGCGGCGCA
ATCGAGCAGGACGCGGACGTGATCATGT
```

```
>NODE_65_length_1552_cov_22.536140
```

```
CCGGGCGCCGCGAAGGAACTACGCATCAGTGGTCTCTCGCTGTTGAGCTGCAGCCAGGTCTCCATCTCTGCCAGGGAGCGG
GGAAGGCTGTGCGTGGCAGCAGCAGTCAGGAGGCGTTTACCAGTTCTGAAAGCAGCGACGATCGTTCTGTGCGCTGCAGGC
CAGGTCTGATGCGCGGAACGACGATGCGGACCTCTGTGCGCAGTTGAGCGAGCTCGTCAGCAACCGGCCGGTAAGCGGTGA
CGTCAGGCATCGCGCGCTACCTCCTTGGGATCTTTGAGGACAGTTCCAGCGACTCTCGATGCGCTTTTGTGGTGCCTGC
```

a list with 2 datasets

History: Assembly

## MOB-Recon on PA09.fa: Plasmids

a list with 2 datasets

Download

1: plasmid\_AE788



2: plasmid\_AF876



11 sequences

format **fasta**, database ?



```
>NODE_29_length_25438_cov_21.469638
```

```
GCCAGGTCCAGCGGCTGCTTGGCTGGGCGTTCTTCTCGGCCAGCT
CGAAGTCCTTGACGGGGAATCGAATCCTTCGGGAACGAAGACCTG
GCCTTGACTTTCGAAACGAAGCGGCGCTGGATCACCGTCGGCGAA
ATGACCTCGCGTTTGGTATTGCGGGTCAGCCCGCCGCAAGGCCGA
```

Download the reconstructed plasmid sequences

Thank you

Questions?

Please remember to answer the evaluation survey