

Reporting carbapenemase-encoding plasmid transmission to public health labs



Poster No. P1-10

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INTRODUCTION

- Plasmids carry antimicrobial resistance genes (ARGs) and can be infectious agents in hospital as opposed to specific clonal lineages
- Enterobacterales isolates carrying carbapenemase-encoding plasmids are hard to trace with conventional epidemiology
- Reporting plasmid transmission is important for infection prevention and control (IPAC) investigations
- We designed a genome sequencing report template and demonstrate how we report plasmid transmission using cases of NDM carbapenemases from a hospital site

METHODS

- Isolates from a hospital site were sent to the National Microbiology Laboratory for carbapenemase gene confirmation by PCR over 9 months
- 34 isolates were sequenced with Illumina (NextSeq2000, Nextera XT DNA), and a subset (n=26) were also sequenced with Oxford Nanopore Technologies (SQK-RBK110-96, r9.4.1, SUP basecalling)
- Genomes were assembled with Unicycler¹; ARGs and multi-locus sequence type (ST) were detected by StarAMR²
- Clonal transmission events were determined by running SNVPhyl³ on isolates with same ST
- Plasmid transmission events were determined by running clustering analysis via MOB-suite⁴
- ProkSee⁵ and R⁶ for figures and R Markdown report

RESULTS

We generated a **genome sequencing report**:

publique du Canada

GENOME SEQUENCING REPORT NDM carbapenemase analysis for hospital site XX Report generated on 2024-08-07

Read the full report:



- Nine plasmid clusters were identified among 34 isolates (Table 1)
- Plasmid Cluster 1 (NDM-7/IncX3) was the most common cluster (n=19) and is predicted to have spread by both horizontal and clonal transmission
- All isolates in Plasmid Cluster 1 had multiple resistance genes (Figure 1)
- SNV analysis showed all *Enterobacter cloacae* ST1640 isolates (n=8) from Plasmid Cluster 1 are clonally related (Figure 2)
- Plasmid clustering showed Plasmid Cluster 1 has spread to 5 species comprising 9 ST (Figure 3)
- Epidemiology data confirmed 3 groups which agree with plasmid clustering

CONCLUSIONS

- Reporting plasmid transmission is important for hospital sites as results can be used to inform IPAC measures
- Genome sequencing reports made in R Markdown effectively communicates plasmid transmission results to public health labs

Table 1: Summary of plasmid cluster features. Plasmid size is an average of all plasmids in cluster.

Plasmid Cluster	Plasmid type	Plasmid size (kb)	NDM gene	Number of isolates	Number of species	Number of sequence types (ST)	Predicted transmission type
1	IncX3	48	NDM-7	19	5	9	Horizontal & clonal
2	IncFIB/FII	125	NDM-1	3	1	1	Clonal
3	IncHI2/HI2A	285	NDM-1	4	2	2	Horizontal & clonal
4	IncFIA/FIB	138	NDM-5	3	1	1	Clonal
5	IncFIA/FIB/ Col156	126	NDM-5	1	1	1	None
6	IncHI2/HI2A/ Q1	364	NDM-1	1	1	1	None
7	IncHI2A/ rep_cluster_1088	285	NDM-5	1	1	1	None
8	IncC	202	NDM-1	3	3	3	Horizontal
9	IncX3	46	NDM-1	1	1	1	None

Figure 1: **Antimicrobial** resistance genes detected in Plasmid Cluster 1 isolates.

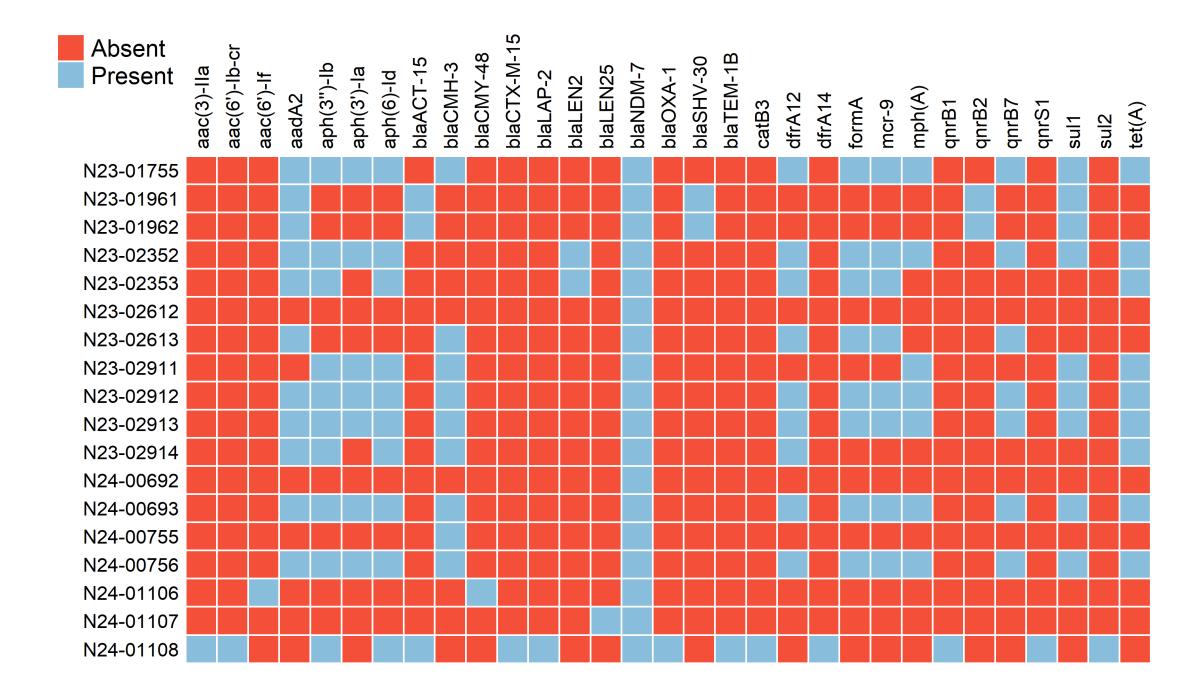


Figure 2: Maximumlikelihood tree based on SNVs for *E. cloacae* ST1690 isolates from plasmid

N24-00756

N24-00755

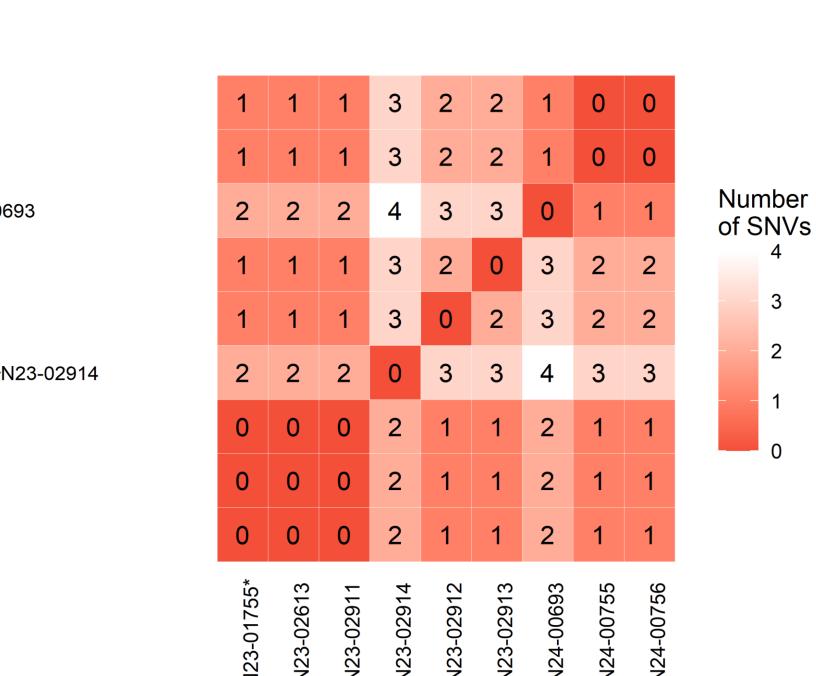
-N23-02912

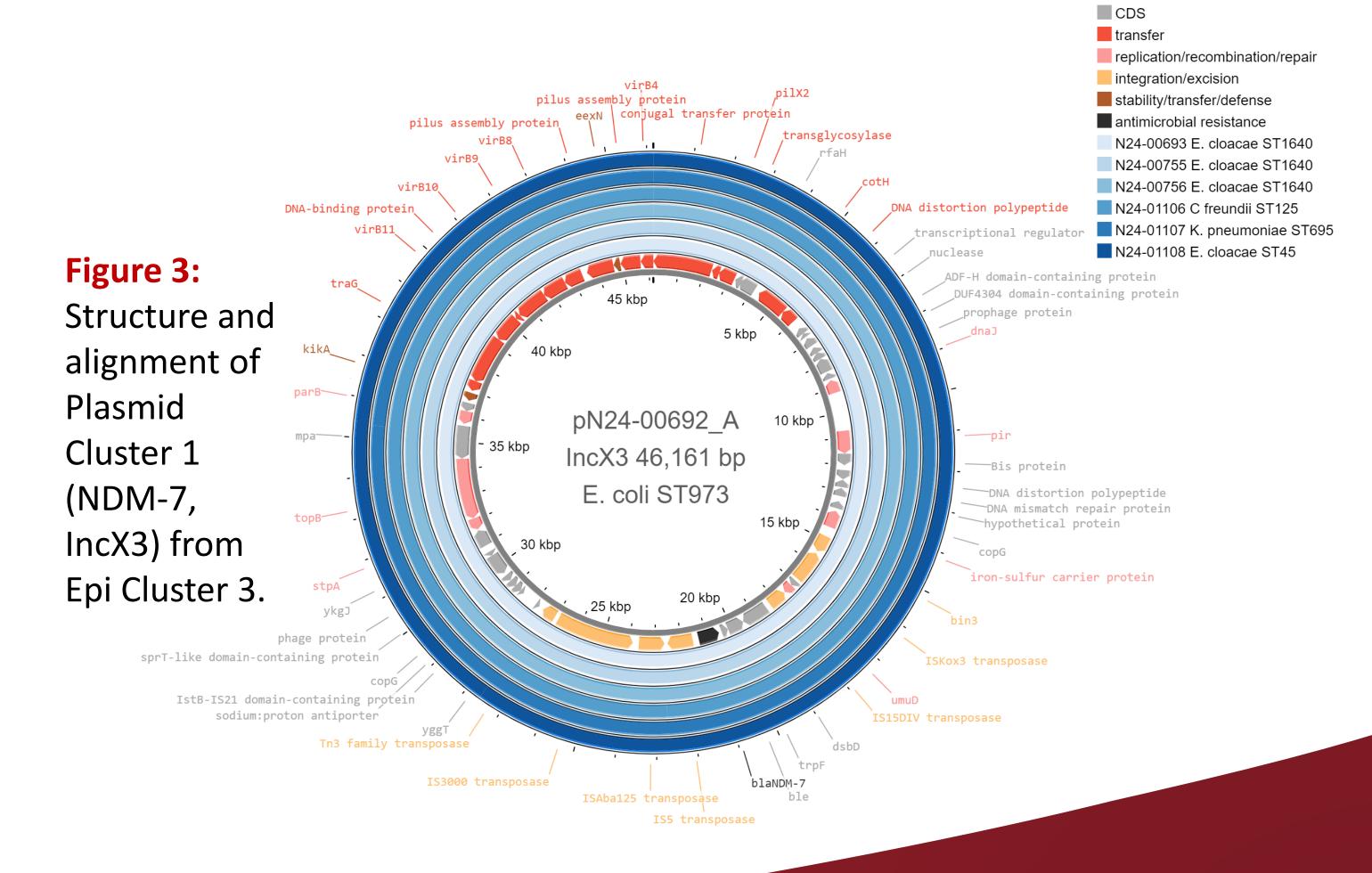
N23-02911

N23-02613

N23-01755*

cluster 1. Asterisks (*) indicate the reference.





References: ¹DOI:10.1371/journal.pcbi.1005595; ²DOI:10.3390/microorganisms10020292; ³DOI:10.1099/mgen.0.000116; ⁴DOI:10.1099/mgen.0.000206; ⁵DOI:10.1093/nar/gkad326; ⁶www.R-project.org. This template was inspired by the British Columbia Centre for Disease Control (BCCDC).