

Antimicrobial Resistance in Canada: What is Keeping Dr. Mulvey Awake at Night?

Michael Mulvey PhD

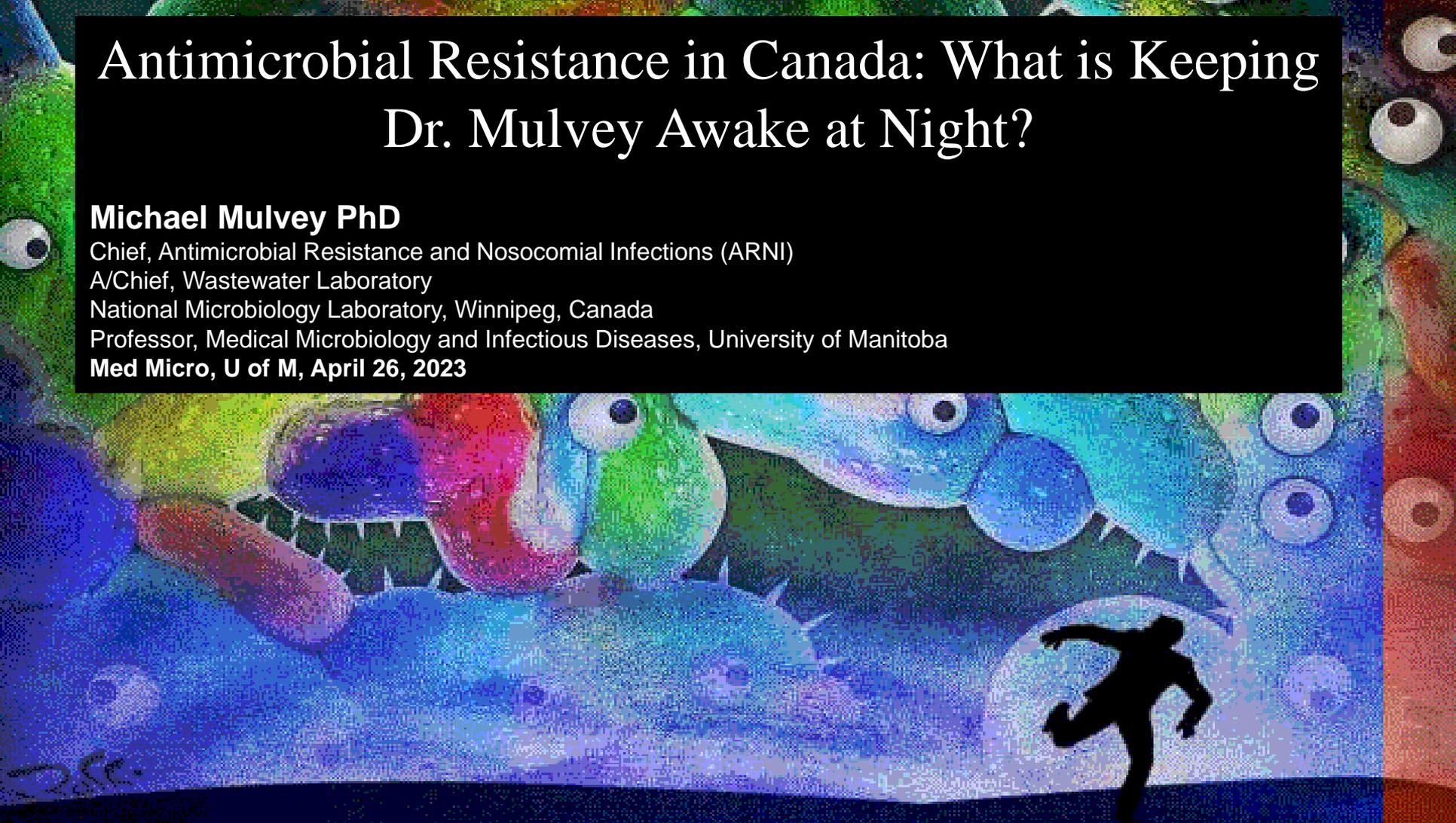
Chief, Antimicrobial Resistance and Nosocomial Infections (ARNI)

A/Chief, Wastewater Laboratory

National Microbiology Laboratory, Winnipeg, Canada

Professor, Medical Microbiology and Infectious Diseases, University of Manitoba

Med Micro, U of M, April 26, 2023



Conflicts of Interest

- None

Overview

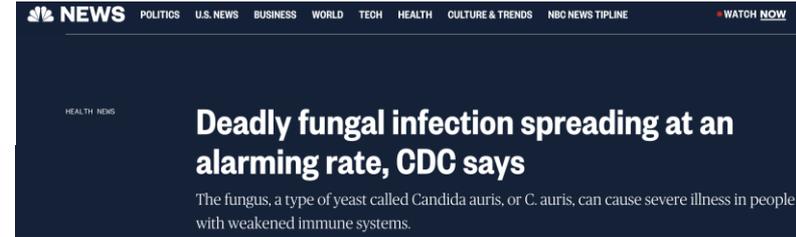
- Emerging/Ongoing AMR Issues in ARNI
- Genomics
- New AMR Surveillance Programs

Candida auris – Dr. Amrita Bharat



Potentially deadly fungus spreading rapidly in US health care facilities

Cases of Candida auris doubled in 2021, according to a new CDC report.



An emerging fungal threat spread at an alarming rate in US health care facilities, study says

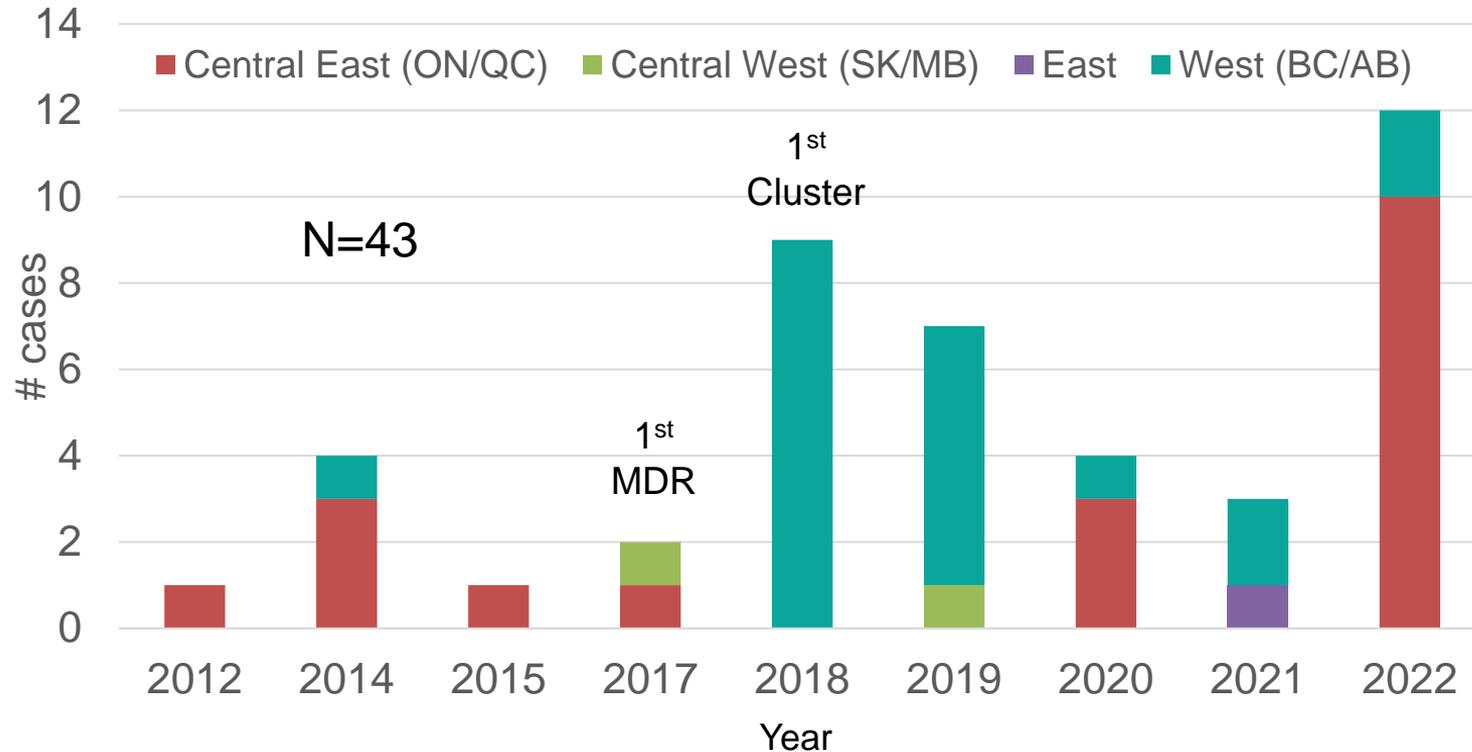
By Janelle Chavez, CNN
Published 5:01 PM EDT, Mon March 20, 2023



CTV News
June 11, 2021 · 🌐

Doctors are warning about the emerging threat of Candida auris, a deadly fungal infection that resists treatment and tends to thrive in hospital settings and long-term care facilities.

Number of *C. auris* cases in Canada, 2012-2022



Schwartz and Hammond. Can Commun Dis Rep. 2017; 43:150–153.

Rapid Response to MDR *C. auris* in Canada

CANWARD Mycology Surveillance
Drs. Jeff Fuller and George Zhanel
Ended 2016



2017 Canadian Nosocomial Infection Surveillance Program (CNISP) *C. auris* Interest Group

Co-led by Allison McGeer, Amrita Bharat, Robyn Mitchell

- ~45 participating hospitals



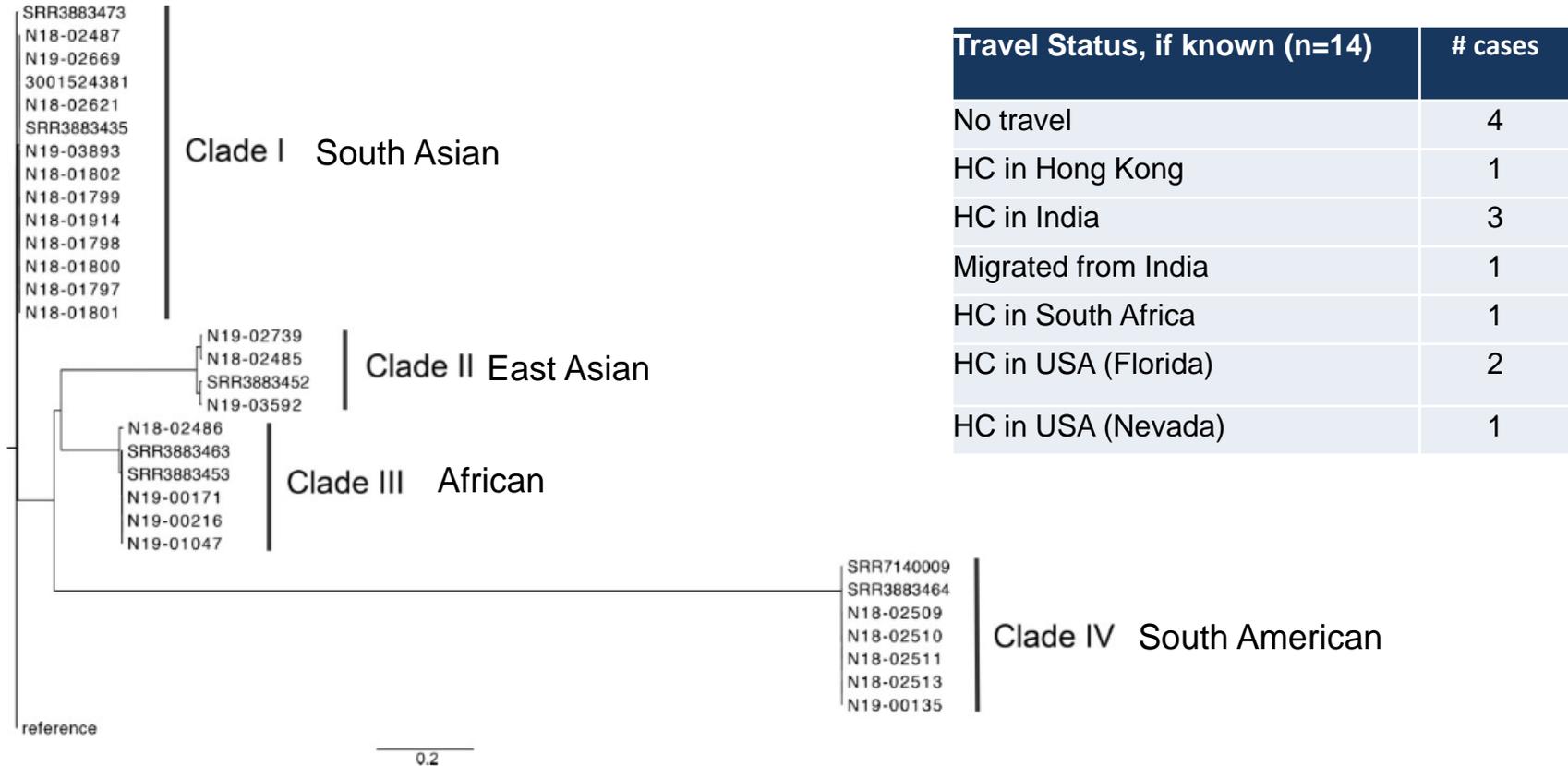
2017 Canadian Public Health Laboratory Network (CPHLN) Mycology Working Group

Co-led by Philippe Dufresne and Amrita Bharat

Linda Hoang, BC Centres for Disease Control, BC
Tanis Dingle, Alberta Health Services, AB
Kathy Malejczyk, Saskatchewan Shared Health, SK
David Alexander, Cadham Provincial Laboratory, MB
Julianne Kus, Public Health Ontario, ON

Caroline Sheitoyan-Pesant, Centre Hospitalier
Universitaire Dr Georges-L.-Dumont, NB
David Haldane, QEII Health Science Centre, NS
Lei Jiao, Eastern Health, NL
Greg German, Health PEI, PEI

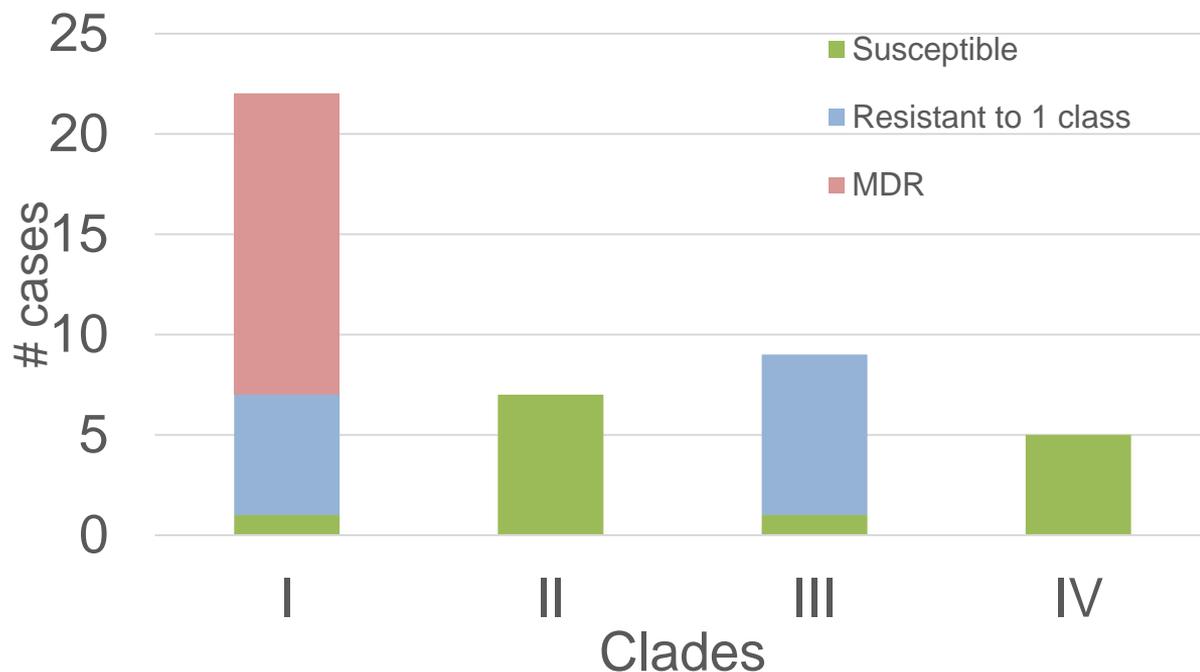
Genomic Clades of *C. auris*



D. DeLuca et al. 2022. Medical Mycology. 60:myab079. doi: 10.1093/mmy/myab079

Antifungal resistance was associated with clades I and III

C. auris in Canada, 2012-2022 (n=43)

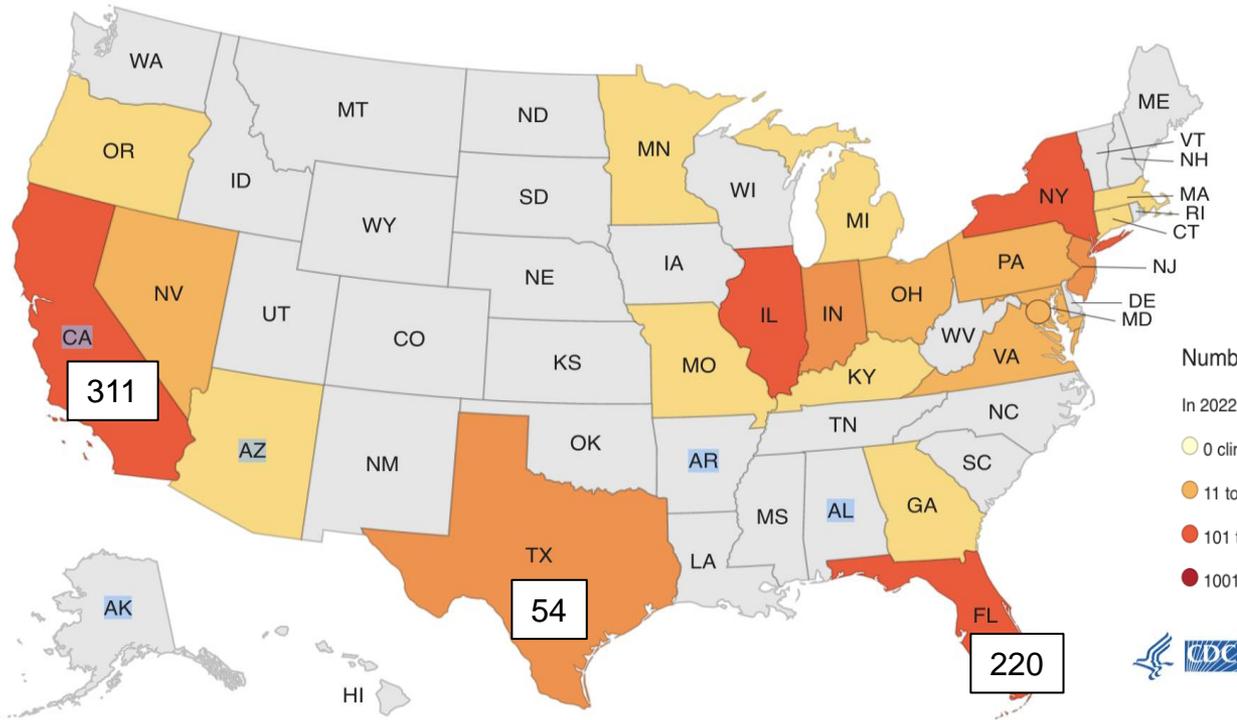


~ one-third of isolates each were resistant to

- 0 classes (susceptible)
- 1 class (azoles)
- 2 classes (azoles and Amphotericin B) MDR

- All MDR isolates were in clade I

USA *C. auris* cases in 2022



Number of *C. auris* clinical cases through December 31, 2022

In 2022, there were 2,377 clinical cases and 5,754 screening cases.

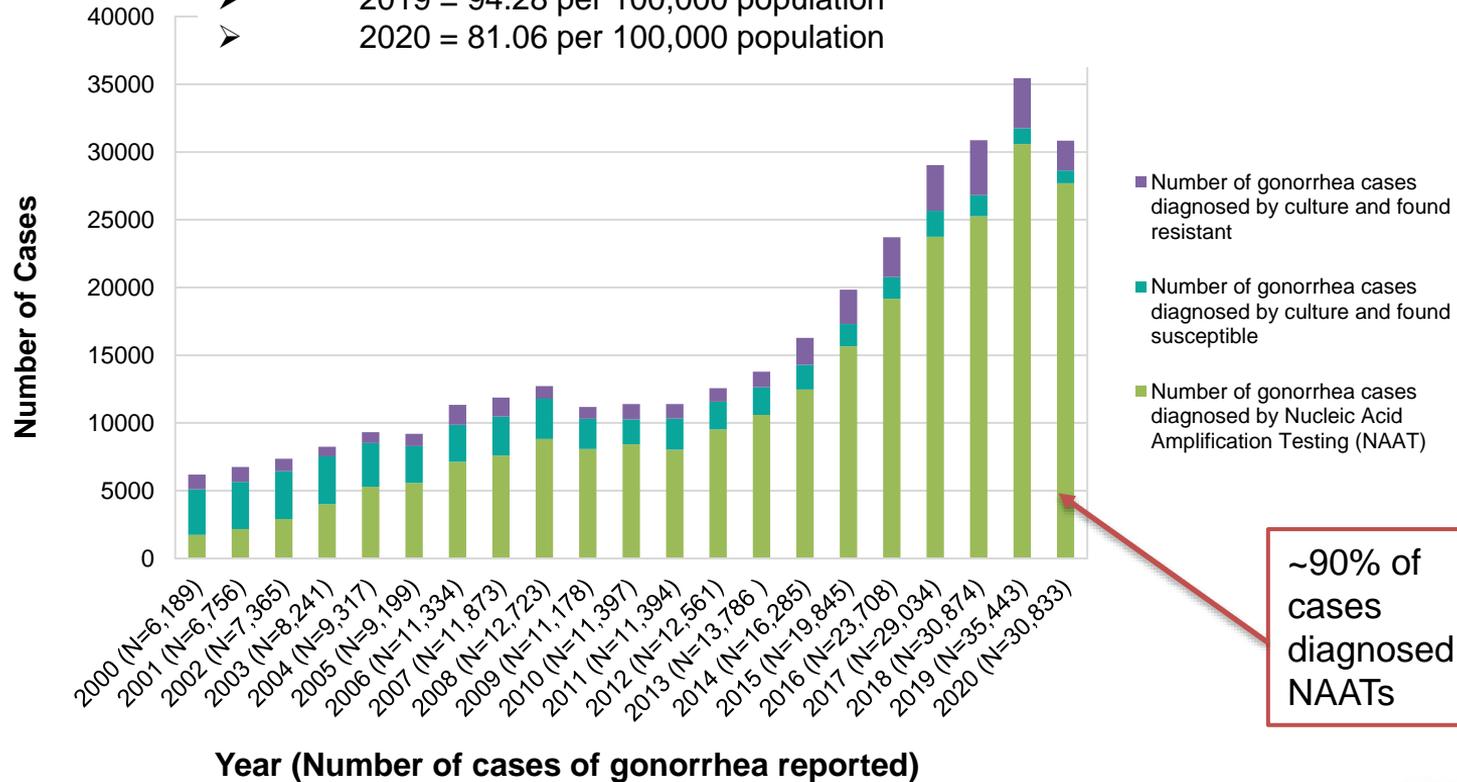
- 0 clinical cases and at least 1 screening case
- 1 to 10
- 11 to 50
- 51 to 100
- 101 to 500
- 501 to 1000
- 1001 or more



N. gonorrhoeae Cases in Canada, 2000 to 2020: Irene Martin

Rates of gonorrhea doubled between 2014 and 2019:

- 2014 = 45.89 per 100,000 population
- 2019 = 94.28 per 100,000 population
- 2020 = 81.06 per 100,000 population



~90% of cases diagnosed by NAATs

Multiplex real-time PCR assays for the prediction of cephalosporin, ciprofloxacin and azithromycin antimicrobial susceptibility of positive *Neisseria gonorrhoeae* nucleic acid amplification test samples

S. W. Peterson^{1*}, I. Martin¹, W. Demczuk¹, N. Barairo¹, P. Naidu², B. Lefebvre³, V. Allen⁴, L. Hoang⁵, T. F. Hatchette⁶, D. Alexander⁷, K. Tomas⁸, M. Trubnikov⁹, T. Wong⁹ and M. R. Mulvey¹

DISPATCHES Emerg Infect Dis. 2021;27(6):1718-1722

Molecular Characterization and Antimicrobial Resistance in *Neisseria gonorrhoeae*, Nunavut Region of Inuit Nunangat, Canada, 2018–2019

Ameeta E. Singh, Jasmine Pawa, Kethika Kulleperuma, Errol Prasad, Sonia Marchand, K. Dionne, Maxim Trubnikov, Tom Wong, Michael R. Mulvey, Irene Martin

A Comparison of Real-Time Polymerase Chain Reaction Assays for the Detection of Antimicrobial Resistance Markers and Sequence Typing From Clinical Nucleic Acid Amplification Test Samples and Matched *Neisseria gonorrhoeae* Culture

Shelley W. Peterson, MSc,* Irene Martin, BSc,* Walter Demczuk, BSc,* Linda Hoang, MD,† John Wylie, PhD,‡ Brigitte Lefebvre, PhD,§ Annie-Claude Labbé, MD,¶ Prenilla Naidu, MD,|| David Haldane, MD,** and Michael R. Mulvey, PhD*

ORIGINAL STUDY

Molecular Surveillance and Prediction of Antimicrobial Resistance of *Neisseria gonorrhoeae* in Northern Alberta, Canada, 2015 to 2018

Daralynn Pilkie, MPH,* Jennifer Gratrix, MSc,† Pam Sawatzky, BSc,‡ Irene Martin, BSc,‡ Ameeta Singh, BMBS, MSc,§ Errol Prasad, DChM,¶ Prenilla Naidu, MD,|| Michael Mulvey, PhD,‡ Tom Wong, MD, MPH,** and Petra Andrea Smyczek, MD, PhD†§

Ceftriaxone-resistant gonorrhea

- Five high-level ceftriaxone resistant gonorrhea cases have been identified in Canada
 - First was identified in 2017

History of reported ceftriaxone-resistant GC internationally:

- **H041** strain: Japan 2009 (*Ohnishi et al. Emerg Infect Dis 2011*)
- **F89** strain: France 2010 & Spain 2011 (*Unemo et al. AAC 2012 & Camara et al. JAC 2012*)
- **A8806** strain: Australia 2013 (*Lahra et al. NEJM 2014*)
- **FC428** strain: Japan 2015 (*Nakayama et al. Emerg Infect Dis 2016*)

Jan 19 2023 – First isolate in USA identified that demonstrated resistance or reduced susceptibility to all drugs recommended for treatment



Rare but seeing related to FC428 reported around the world, including the 5 Canadian cases

 health

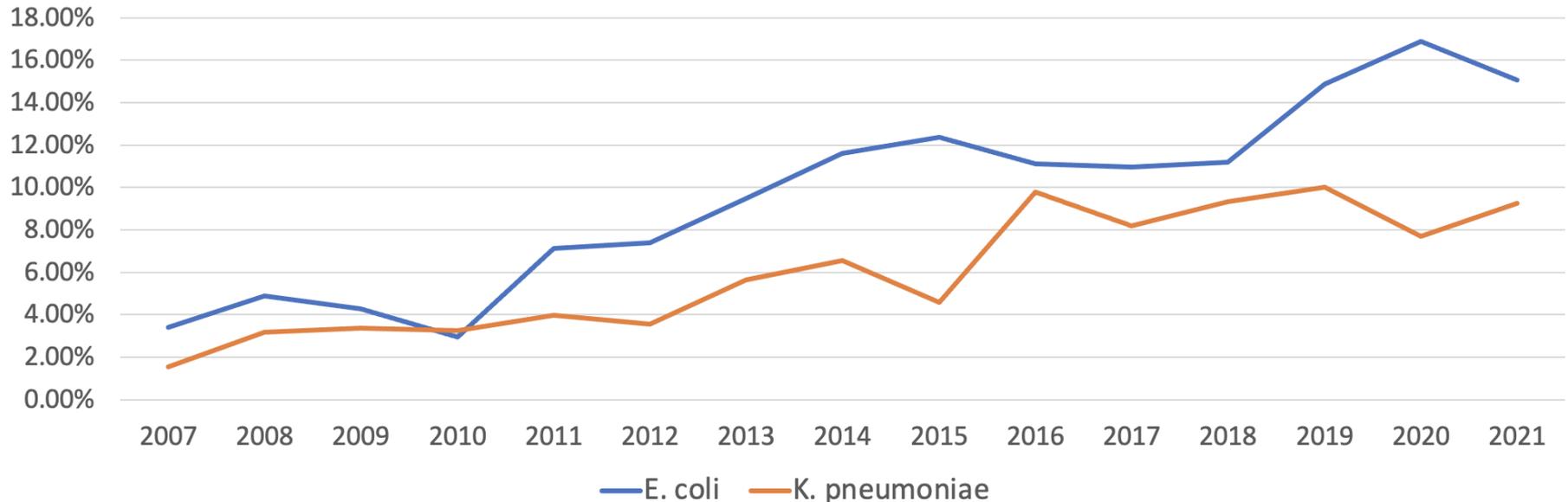
First cases of gonorrhea resistant to several classes of antibiotics identified in the U.S.

by Brenda Goodman, CNN
Published 6:27 PM EST, Thu January 19, 2023

CANWARD ESBLs in Canadian Hospitals

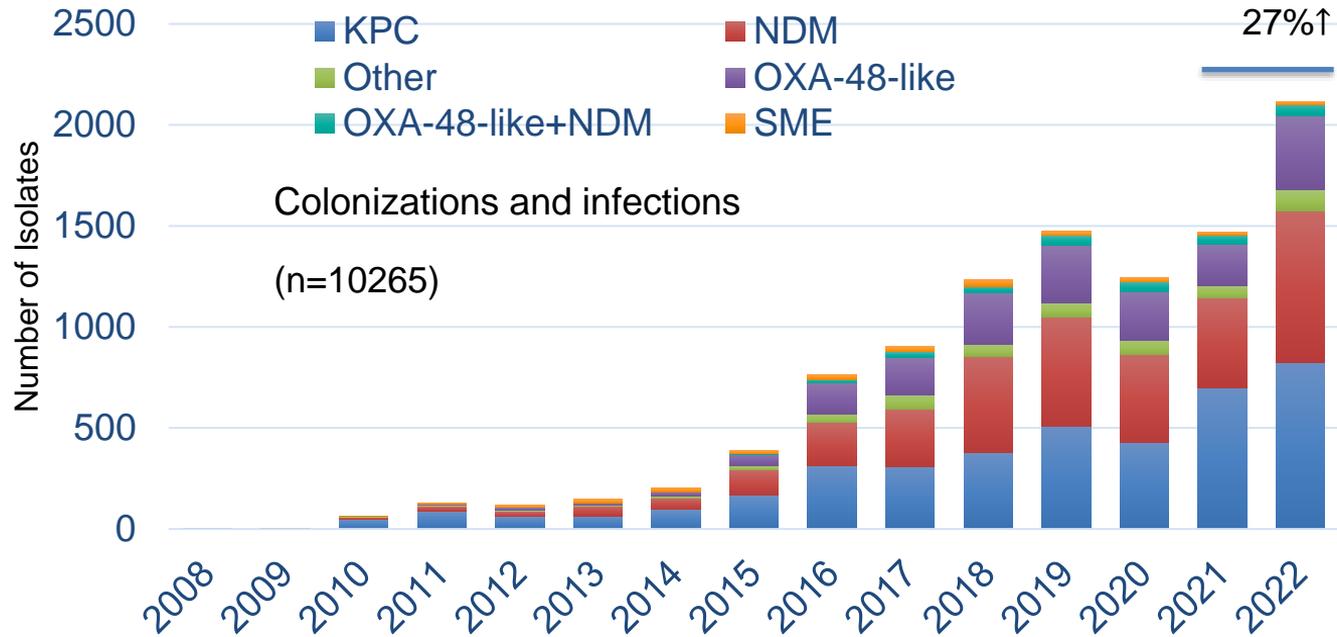
ESBL *E. coli* increased 3.4% (2007) to 15.1% (2021) $P < 0.0001$

ESBL *K. pneumoniae* increased from 1.5% (2007) to 9.3% (2021) $P < 0.0001$



Lagacé-Wiens. ASM Microbe, Accepted 2023.

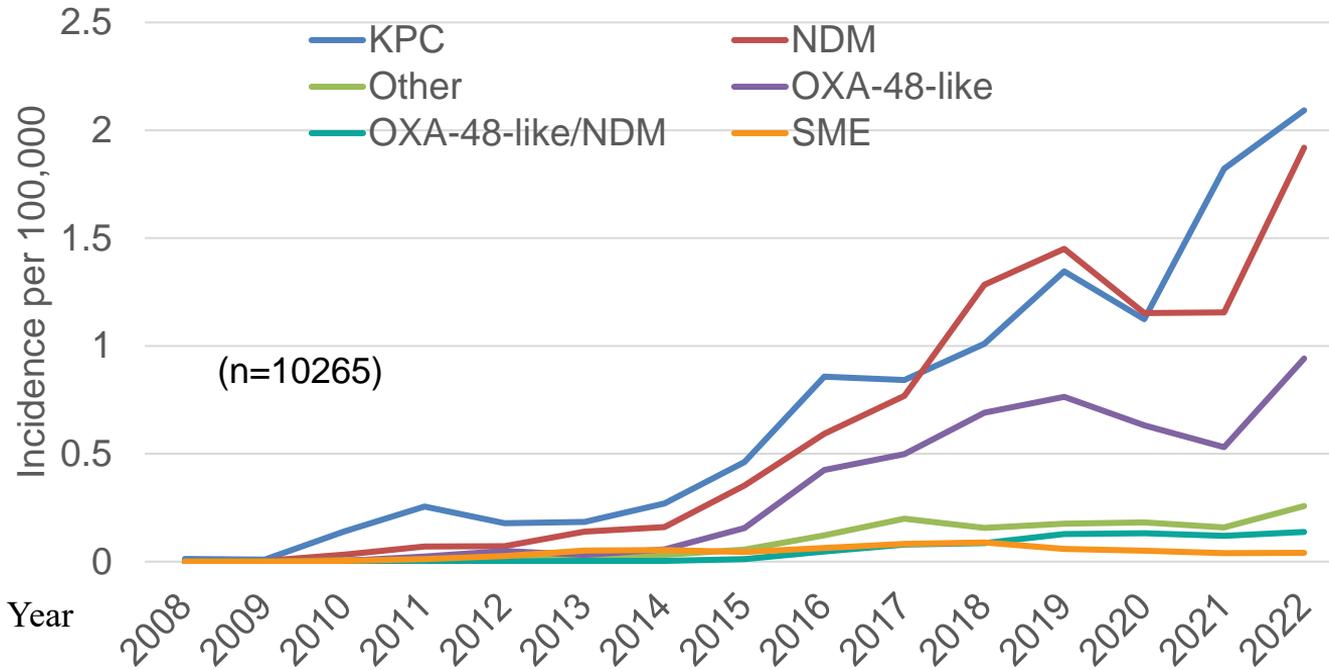
CPE in Canada: CPHLN Data. L. Mataseje



Total number	4	4	63	128	117	148	204	389	764	906	1234	1474	1243	1470	2117
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Year

CPE Rates in Canada

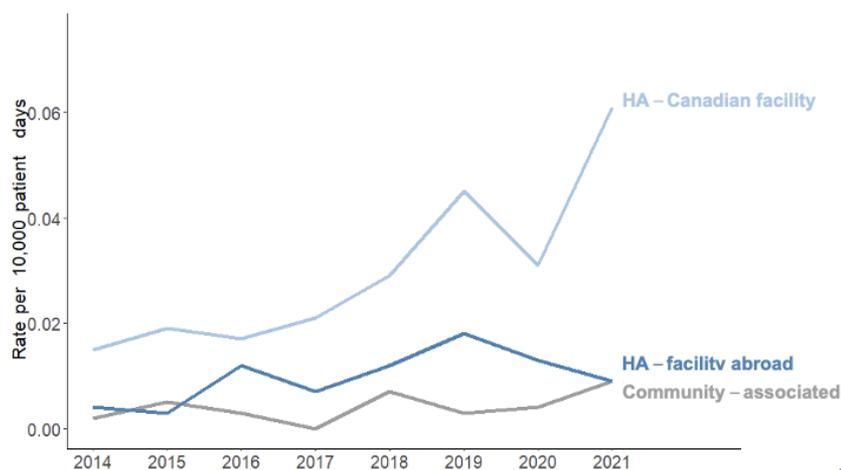


Total number	4	4	63	128	117	148	204	389	764	906	1234	1474	1243	1470	2117
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CNISP CPE and CPA Surveillance

AMMI/CACMID 2023
P036 R. Mitchell et al.
P042 L. Matasje et al.

Figure 4 CPE infection rates by acquisition, CNISP, 2014-2021



32% (96/300) reported international **travel** in the 12 months prior to positive culture



27% (80/294) received **healthcare while abroad**, most commonly in South Asia (46%, 33/71)



24% of inpatients (67/285) were in an **intensive care unit** at the time of positive culture or were admitted following positive culture

17%

30-day all-cause mortality

CIPARS: Carbapenemase Surveillance

Drs. Amrita Bharat and Audrey Charlebois

- Only Canadian human case *S. London* OXA-48, NB, travel history to Morocco (2018)
- Only Canadian animal case *S. London* IMP-64 clinical pig isolates MB (2016)

Imported Seafood 2,584 samples screened 10 CPE identified (2011-15)

Gene Description	Speciation	n	Origin of sample (n)	Sample Types
<i>bla</i> _{NMC}	<i>Enterobacter cloacae</i>	2	Vietnam (2);	CIPARS retail shrimp n=832
	<i>Enterobacter aerogenes</i>	1	Bangladesh (1)	
<i>bla</i> _{VCC}	<i>Vibrio cholerae</i>	2	India (2)	
				Niche market seafood
<i>bla</i> _{NDM} , <i>bla</i> _{TEM} , <i>bla</i> _{OXA-1}	<i>Enterobacter cloacae</i>	2	Vietnam (2)	Clams n=101
<i>bla</i> _{NMC}	<i>Enterobacter cloacae</i>	3	Vietnam (3)	

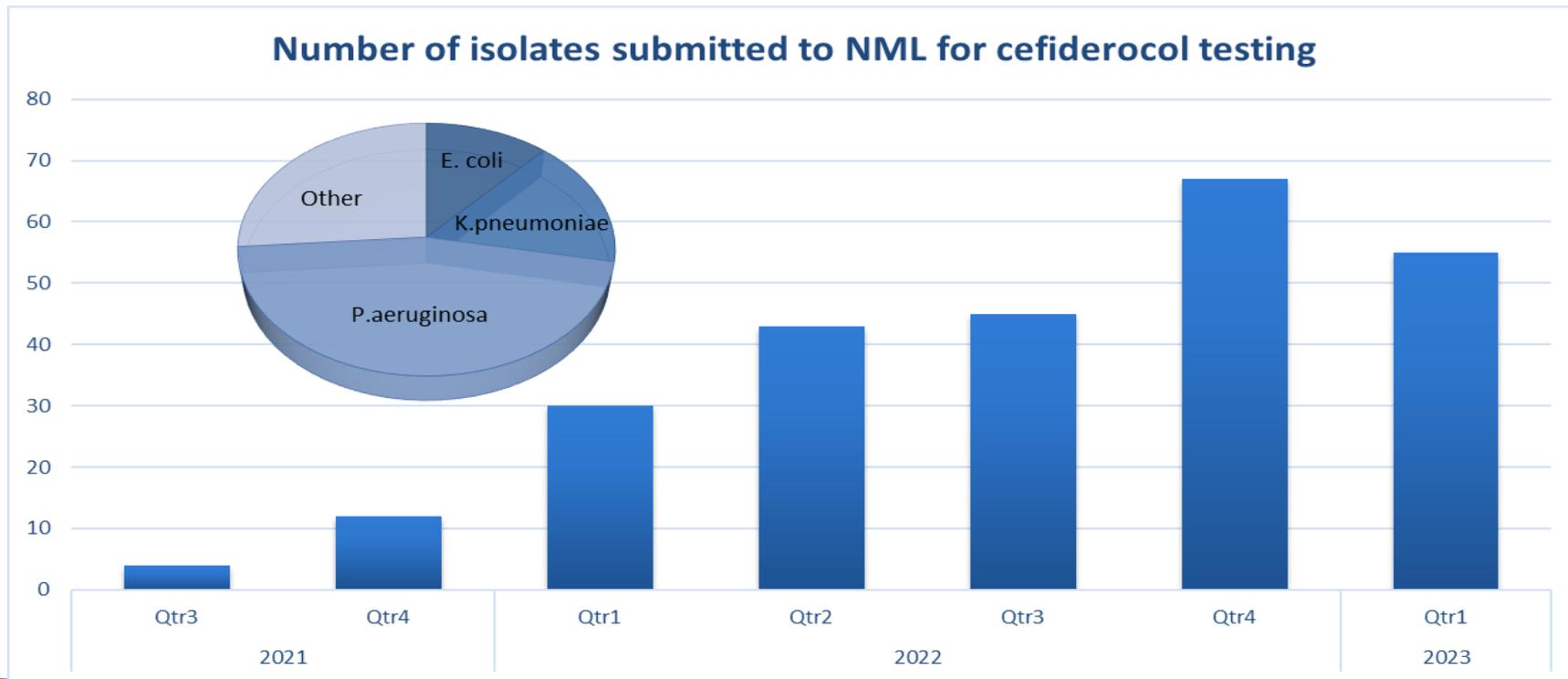
Janecko et al., 2016 Emerg Infect Dis 22:1675-77

Mangat et al., 2016 AAC 60:1819-25

Increased Cefiderocol Reference Testing Requests: Laura Mataseje

- Cefiderocol is an injectable siderophore 4th gen cephalosporin active against many Gram-neg producing β -lactamases including both serine-type (KPC, OXA) and Ambler class B metallo- β -lactamases (VIM, IMP, NDM).

Zhanel et al. 2019 Feb;79:271-289.



Canadian Nosocomial Infection Surveillance Program (CNISP)

Dr. George Golding (CNISP Co-chair)

CNISP is a collaboration between the

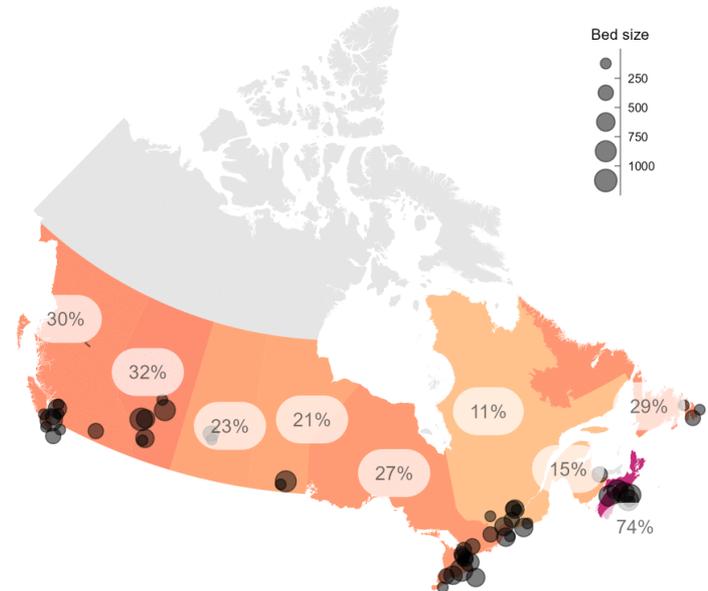
- ❑ Public Health Agency of Canada ([PHAC](#)) including the National Microbiology lab ([NML](#))
- ❑ Association of Medical Microbiology and Infectious Disease ([AMMI](#)) Canada
- ❑ [Sentinel hospitals](#) across Canada

In 2022, CNISP has expanded to include **88 hospitals in 10 provinces and 1 territory** including rural, community and northern hospitals

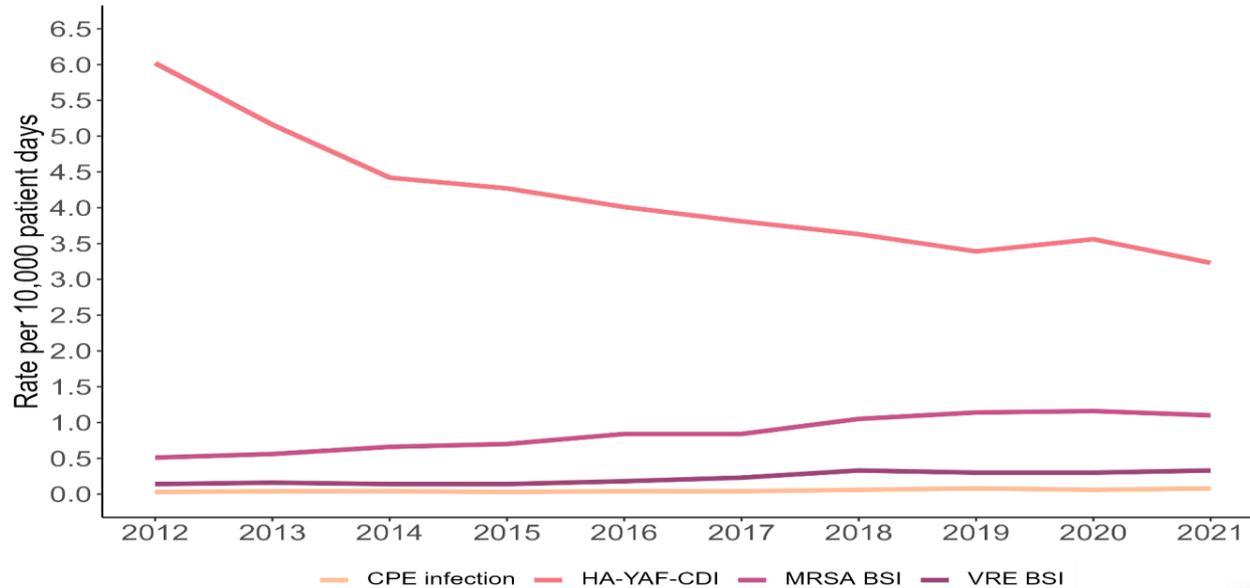
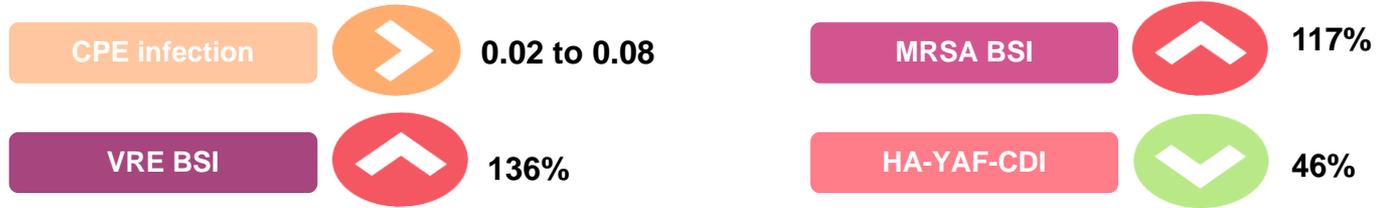
In 2023, potential expansion to 110 hospitals

Overview of CNISP

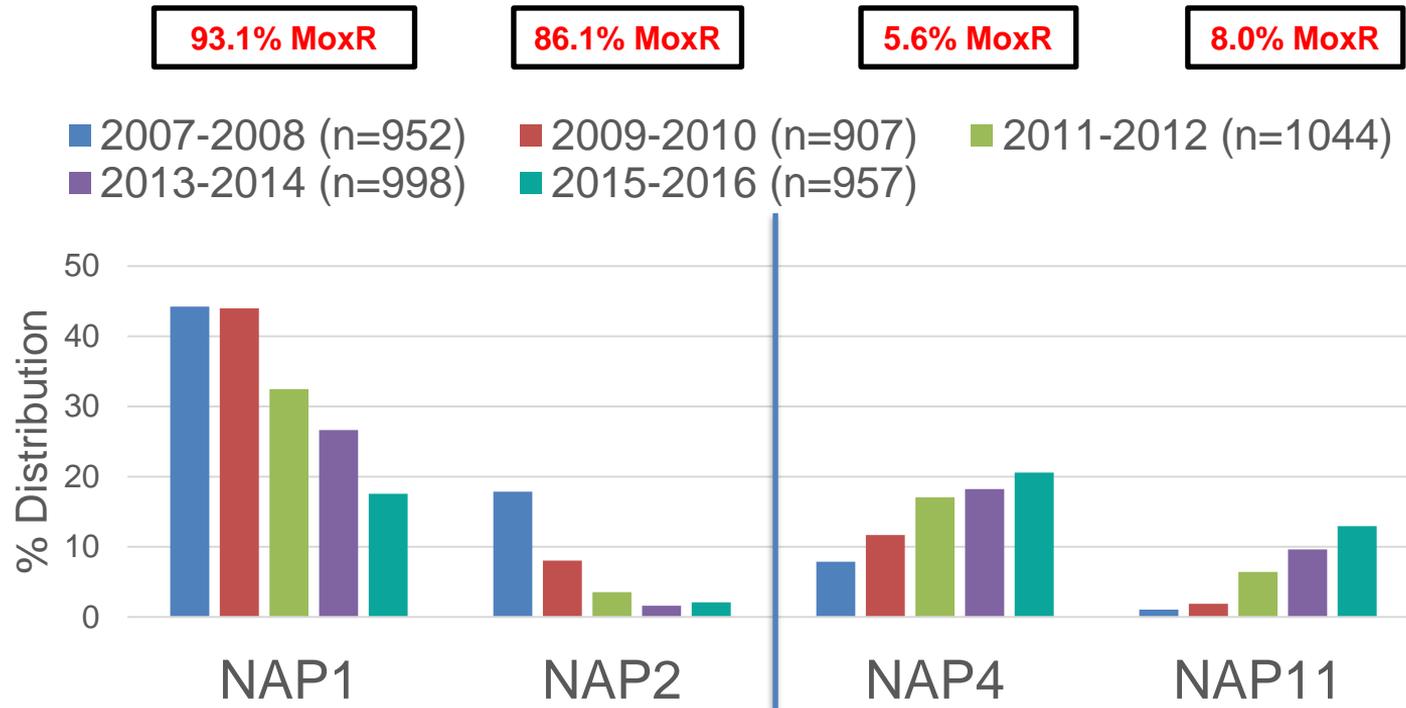
Participating CNISP sites in 2009
Proportion of acute care beds (27%)



CNISP rates per 10,000 patient days, 2012 to 2021

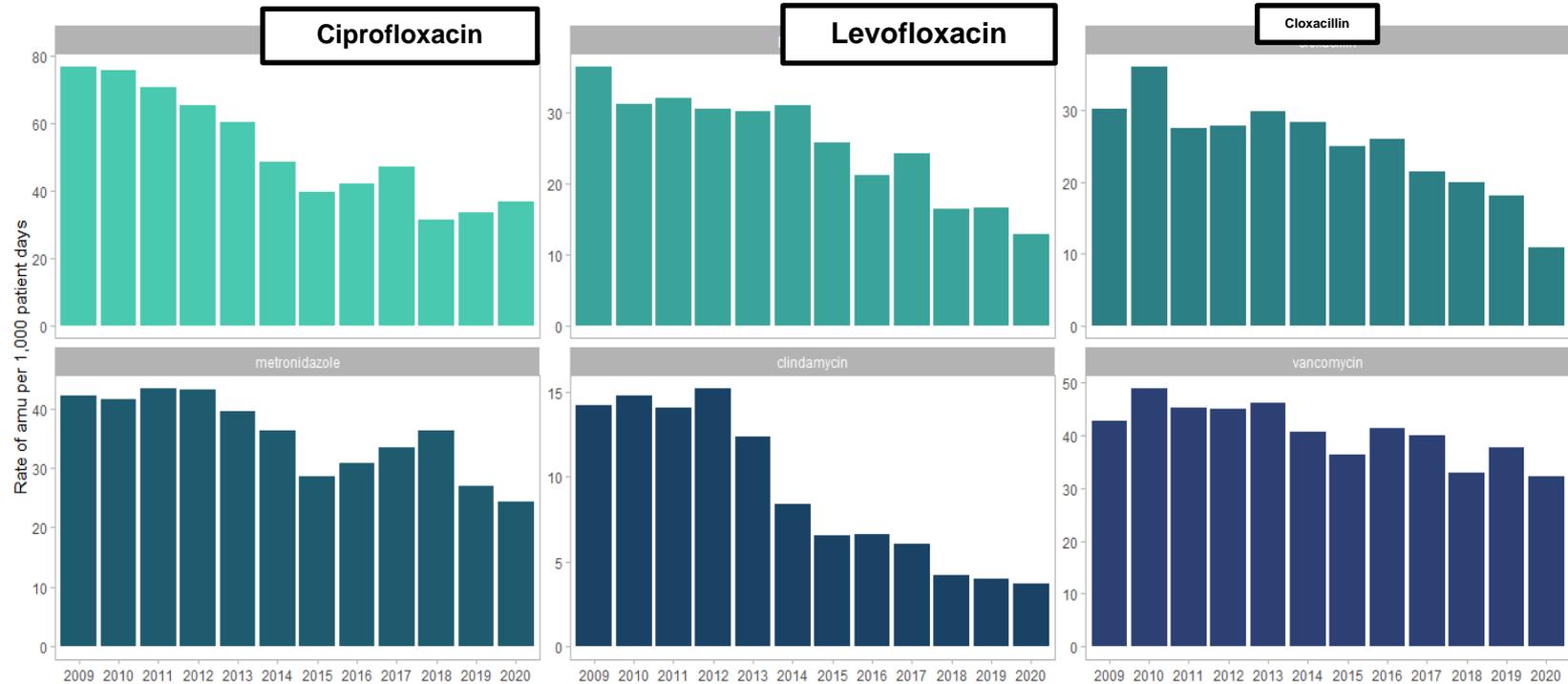


Declining Fluoroquinolone Resistant Strain Types and Emerging Susceptible Types



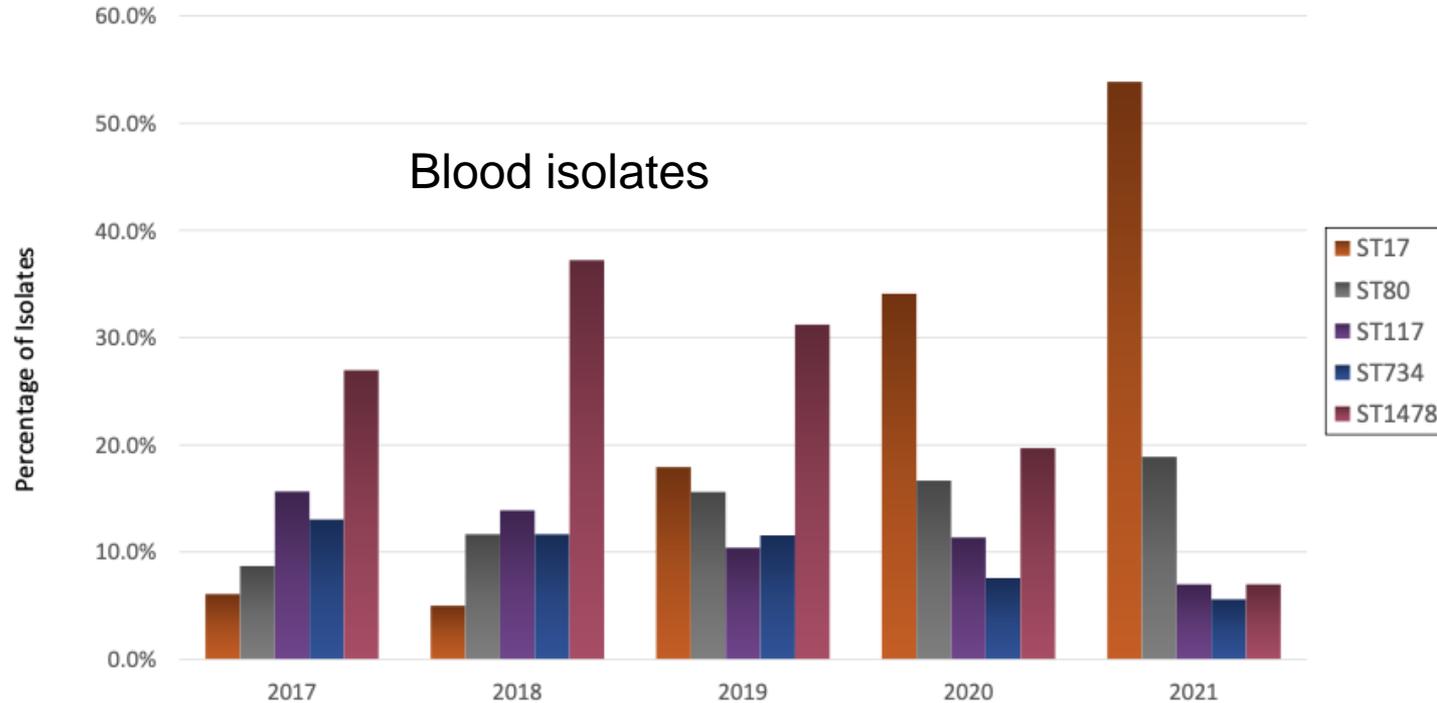
CNISP: Antibiotics with the greatest absolute decreases

- Stewardship highlight for *C. difficile* NAP1



CNISP VRE

Figure 3. Distribution of the top five sequence types by year, 2017-2021.



AMMI/CACMID 2023 P033 McCracken et al.

ARNI Genomics

- Isolates being sequenced and/or analysed at ARNI for surveillance:
 - All human *Salmonella* isolates sequenced by PulseNet Canada and Enteric Disease Program
 - Most *Salmonella* food and animal isolates
 - All CNISP VRE (1999-present) and MRSA (2018-present) blood isolates, *C. difficile* (on-going), and all CNISP CPE and CPA (2010 onward)
 - All *N. gonorrhoeae* being sequenced (Nov 2022 onward)
 - All *S. pneumoniae* and Group A Strep (Nov 2022 onward)
 - All *C. auris* sequenced
- Also sequencing all outbreak isolates submitted to ARNI
- Vision is to sequence all isolates submitted to ARNI Lab
- Incorporating machine learning into our bioinformatics tools (AMR prediction and surveillance/outbreak analysis)

Genomics AMR Prediction

- Predicting AMR for surveillance:
 - Salmonella harmonized with NARMS USA Program
 - *S. pneumoniae*
 - *N. gonorrhoeae*
 - Build safeguards to detect new resistance mechanisms

- Studies for predicting AMR
 - *Escherichia coli* (SIR validation)
 - *Campylobacter* (SIR validation)
 - *Pseudomonas aeruginosa*
 - *Enterococcus* spp.

Journal of Antimicrobial Chemotherapy

J Antimicrob Chemother
doi:10.1093/jac/dkx067

WGS to predict antibiotic MICs for *Neisseria gonorrhoeae*

David W. Eyre^{1-3*}, Dilrini De Silva¹⁻³, Kevin Cole^{4,5}, Joanna Peters^{4,5}, Michelle J. Cole⁶, Yanatan H. Grad^{7,8}, Walter Demczuk⁹, Irene Martin⁹, Michael R. Mulvey⁹, Derrick W. Crook^{1-3,5}, A. Sarah Walker¹⁻³, Tim E. A. Peto¹⁻³ and John Paul^{2,4,5}

MECHANISMS OF RESISTANCE



Equations To Predict Antimicrobial MICs in *Neisseria gonorrhoeae* Using Molecular Antimicrobial Resistance Determinants

Walter Demczuk,^a Irene Martin,^a Pam Sawatzky,^a Vanessa Allen,^b Brigitte Lefebvre,^c Linda Hoang,^d Prenilla Naidu,^e Jessica Minion,^f Paul VanCaeseele,^g David Haldane,^h David W. Eyre,^{h,i} Michael R. Mulvey^a

MECHANISMS OF RESISTANCE



Linear Regression Equations To Predict β -Lactam, Macrolide, Lincosamide, and Fluoroquinolone MICs from Molecular Antimicrobial Resistance Determinants in *Streptococcus pneumoniae*

 Walter Demczuk,^a Irene Martin,^a Averil Griffith,^a Brigitte Lefebvre,^b Allison McGeer,^c Gregory J. Tyrrell,^d  George G. Zhanel,^e  Julianne V. Kus,^g  Linda Hoang,^h Jessica Minion,ⁱ Paul Van Caeseele,^j Rita Raafat Gad,^k David Haldane,^l George Zahariadis,^m Kristen Mead,ⁿ Laura Steven,^o Lori Strudwick,^p Michael R. Mulvey^a

Genomics Clinical Diagnostics



Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

Genomics

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



Identification of bacterial and fungal pathogens directly from clinical blood cultures using whole genome sequencing

S.W. Peterson ^a, W. Demczuk ^a, I. Martin ^a, H. Adam ^b, A. Bharat ^{a,*}, M.R. Mulvey ^{a,1}

^a National Microbiology Laboratory, Public Health Agency of Canada, Winnipeg, Manitoba, Canada
^b Diagnostic Services, Shared Health Manitoba, Health Sciences Centre, Winnipeg, Manitoba, Canada

ARNI Nosocomial Outbreak Reports

GENOME SEQUENCING REPORT

KPC outbreak analysis for the Montreal General Hospital

Report generated on 2023-02-07

SUMMARY

- 13/13 isolates harbour a plasmid containing *bla_{KPC}* within the Tn4401 transposon (Table 1). Among these isolates, four distinct plasmid clusters were identified. See Figure 6 for the predicted transmission schematic.
- The first plasmid cluster encodes *bla_{KPC-3}* on a 75 kb plasmid with a unknown replication type (Figure 4). There is evidence of clonal transmission between *Enterobacter cloacae* isolates (2-5 SNVs) with a novel ST and evidence of plasmid transmission between multiple *E. cloacae* STs and *Citrobacter freundii* ST100.
- The second plasmid cluster encodes *bla_{KPC-3}* on an IncN plasmid (Figure 5). There is evidence of clonal transmission among *E. cloacae* ST97 (1 SNV). Although the plasmids are similar, the Tn4401 transposon variants are not the same between *E. cloacae* ST97, *E. cloacae* ST177, and *K. oxytoca* ST108. Further epidemiological data is recommended to confirm the link between *E. cloacae* ST97, ST100, and *K. oxytoca*.
- The third plasmid cluster encodes two copies of *bla_{KPC-2}* on an IncP plasmid which is found in two *C. freundii* ST22 isolates (7 SNVs), indicating likely clonal transmission.
- The fourth plasmid cluster is an IncN plasmid in *C. freundii* ST22, which differs by 430-433 SNVs from the other *C. freundii* ST22. This IncN plasmid is unrelated to the IncN plasmids in cluster002.
- All plasmids group within known Canadian plasmid clusters.

SAMPLE DETAILS

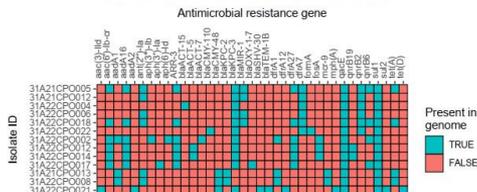
Table 1: Line list of queried isolates

NRHP	Organism	Date of positive culture	Sequence type	QPO gene	ST401 variant	Plasmid type	Size (kb)	Plasmid cluster
31A21CP0007	Enterobacteriaceae	17-Jun-2021	novel	KPC-3	31A2103-3	unknown/ST	74.2	001
31A21CP0017	Enterobacteriaceae	27-Jun-2021	novel	KPC-3	31A2103-3	unknown/ST	74.2	001
31A21CP0004	Enterobacteriaceae	14-Jun-2021	novel	KPC-3	31A2103-3	unknown/ST	74.2	001
31A22CP0006	Enterobacteriaceae	9-Sep-2022	novel	KPC-3	31A2103-3	unknown/ST	74.2	001
31A22CP0007	Enterobacteriaceae	14-Sep-2022	novel	KPC-3	31A2103-3	unknown/ST	74.2	001
31A22CP0007	Citrobacter freundii	7-Jun-2022	300	KPC-3	31A2103-3	unknown/ST	74.8	001
31A22CP0007	Enterobacteriaceae	12-Feb-2022	ST97	KPC-3	31A2103-3	IncN	67.9	002
31A22CP0017	Enterobacteriaceae	27-Jun-2022	97	KPC-3	31A2103-3	IncN	67.9	002
31A22CP0021	Enterobacteriaceae	18-Jun-2022	ST22	KPC-3	31A2103-3	IncN	72.1	002
31A22CP0021	Enterobacteriaceae	18-Jun-2022	ST22	KPC-3	31A2103-3	IncN	72.1	002

GENOME SEQUENCING REPORT

ANTIMICROBIAL RESISTANCE GENES

Figure 1: Resistance genes detected in genome sequencing data

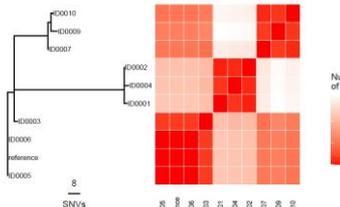


GENOME SEQUENCING REPORT

PHYLOGENETIC CLUSTERING ANALYSIS

The overall tree was constructed using reference genome ID0006. Three clusters were identified and all environmental isolates clustered together. The closest clinical cluster to the environmental cluster was ID0003 at a distance of 19 SNVs, however cluster was 20 SNVs.

Figure 2: Maximum Likelihood Tree (PhyML) based on SNVs from a multi-sequence alignment. Isolate ID0006 is the reference genome.



PLASMID PANGENOMES

Plasmid coding sequence content was compared within each plasmid cluster by creating a pangenome plot of all genes found within each plasmid. Core genes are present within each plasmid whereas variable accessory genes present only in select isolates will be indicated by gaps.

The pangenome of the *bla_{KPC-3}*-encoding plasmids in cluster001 are shown in Figure 4. Plasmid CDs are identical except for two IS3 family transposons from 10.7 kb - 12.1 kb in 31A22CP0022.

The pangenome of the *bla_{KPC-3}*-encoding IncN plasmids in cluster002 are shown in Figure 5. Plasmid CDs are identical except for a 10 kb island from 27.5 - 38 kb containing duplicates of *folP*, *emrE*, *pspF*, and *yghA* found in 31A22CP0002 and 31A22CP0017.

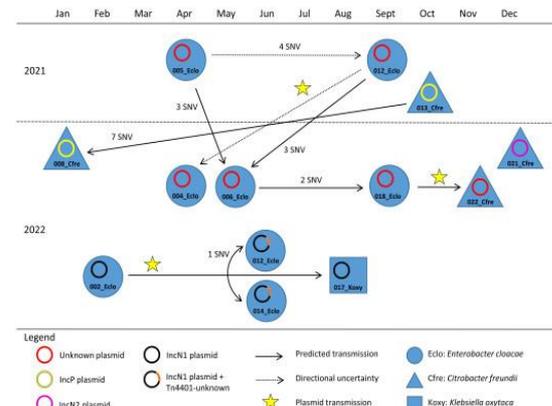
Figure 4: Plasmid pangenome analysis for *bla_{KPC-3}*-encoding 75 kb plasmids with unclassified replication type in cluster001



GENOME SEQUENCING REPORT

PREDICTED TRANSMISSION

Figure 6: Predicted transmission of *bla_{KPC}*-encoding plasmids among isolates from 2021 - 2022. All isolate numbers are represented by the last 3 digits and SNV distances are only shown between isolates with the same sequence type.

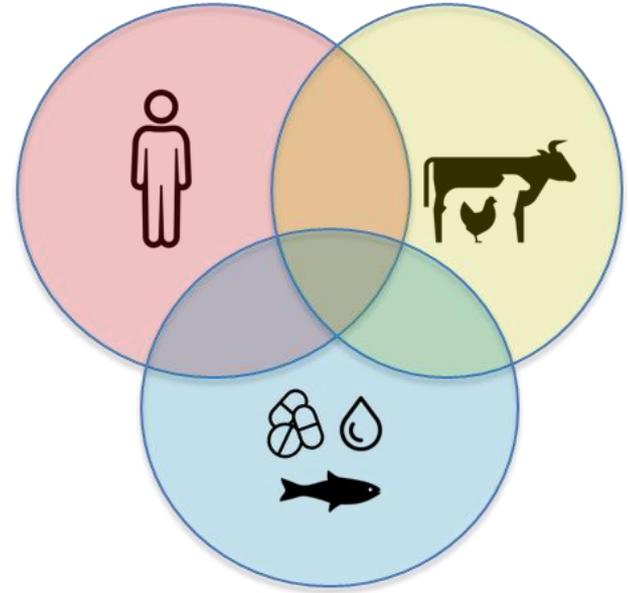


Collaboration with Dr. Hoang BCCDC

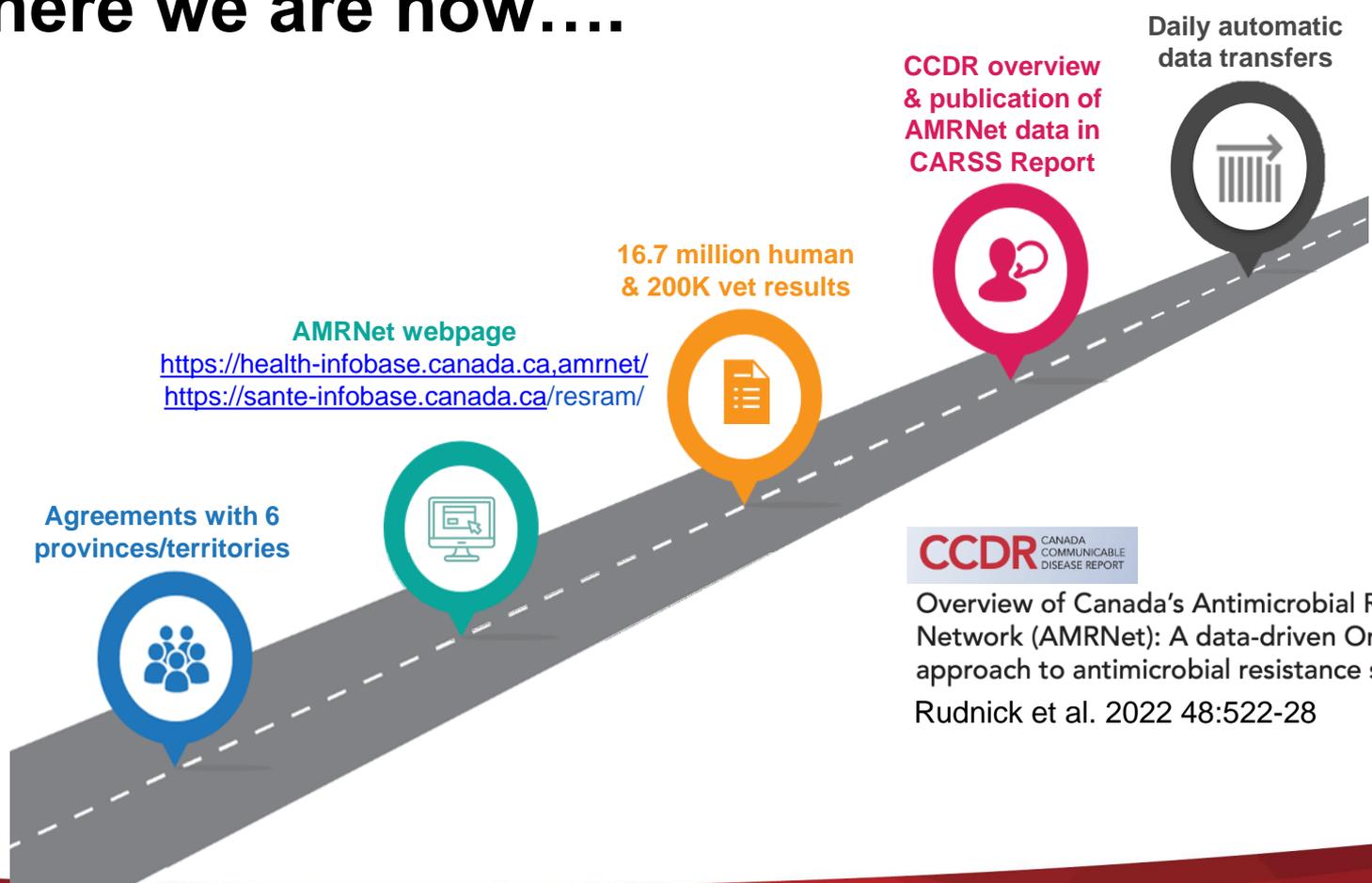
AMR Net

Drs. Wallice Rudnick, Shamir Mukai, and Michael Mulvey

- PHAC-funded lab-based AMR surveillance program under development
- Collaboration between PHAC, provincial/territorial public health, and human/animal labs
- Captures existing information on antimicrobial susceptibility testing from human clinical and veterinary labs
- Includes all bacterial and fungal organisms
- One-health, integrated approach

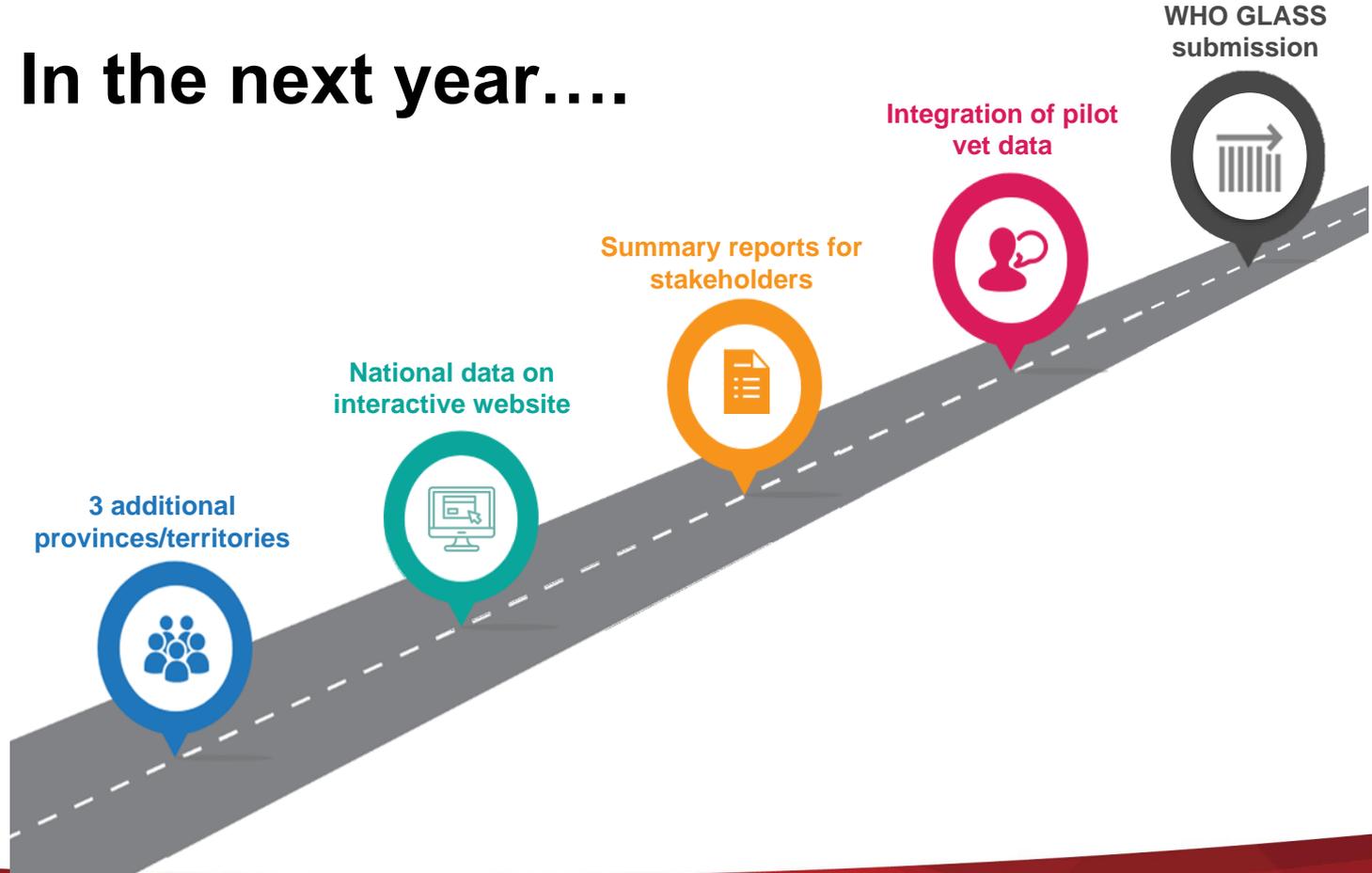


Where we are now....



Overview of Canada's Antimicrobial Resistance Network (AMRNet): A data-driven One Health approach to antimicrobial resistance surveillance
Rudnick et al. 2022 48:522-28

In the next year....



Antimicrobial Susceptibility Testing Summary

PHAC AMRNet
08 March, 2023

E. coli

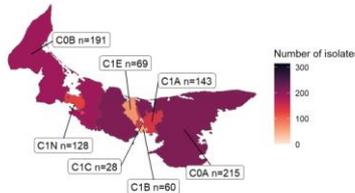
Please note that duplicates have been removed for all analyses presented here. Between 2016 and 2021, data on 10,000 *E. coli* isolates were submitted and included in the analysis below.

De-duplication method: Only the 1st *E. coli* isolate from a given patient in a given calendar year is included.

The percent of isolates tested represents the percent of isolates in a category with any susceptibility testing results that have been tested for the specific antimicrobial or combination. AMRNet does not collect information on isolates that do not undergo susceptibility testing.

Number of isolates by FSA Urine (all) Urine (inpatient and Outpatient) Blood All source

The map below show the number of isolates included in the analyses in 2021 by FSA. Please note that number of submitted isolates change year to year and differ between specimen types and FSAs.



Pseudomonas

Please note that duplicates have been removed for all analyses presented here. Between 2016 and 2021, data on 10,000 *Pseudomonas* isolates were submitted and included.

De-duplication method: Only the 1st *Pseudomonas* isolate from a given patient in a given calendar year is included.

The percent of isolates tested represents the percent of isolates in a category with any susceptibility testing results that have been tested for the specific antimicrobial or combination. AMRNet does not collect information on isolates that do not undergo susceptibility testing.

Number of isolates by FSA Urine Blood Respiratory Wound Non-blood All source



Summary reports for stakeholders



WHO GLASS submission



Integration of pilot vet data



The percent of isolates tested represents the percent of isolates in a category with any susceptibility testing results that have been tested for the specific antimicrobial or combination. AMRNet does not collect information on isolates that do not undergo susceptibility testing.

Number of isolates by FSA Urine (all) Urine (inpatient and Outpatient) Blood All source

The heatmap below includes *E. coli* from urine 2016 to 2021. Isolates from FSAs outside of PEI have been excluded. White text on the heatmap indicates fewer than 30 isolates represented.



	Amoxiclav					Amoxiclav						
PEI Fake	88	88	87	77	76	83	100	100	100	90	43	46
Charlottetown (CIABCE)	88	87	85	54	24	39	100	100	100	26	15	13
Summerside (C1N)	91	88	87	91	91	94	100	100	100	94	93	93
Prince County exci. Summerside (COB)	91	88	89	89	91	92	100	100	100	92	90	93
Queen & Kings exci. Charlottetown (COA)	87	88	89	60	40	49	100	100	100	30	19	19
	Cefazolin					Cefazolin						
PEI Fake	94	94	95	94	95	95	100	100	100	43	34	40
Charlottetown (CIABCE)	93	92	94	86	100	100	99	100	99	16	2	2
Summerside (C1N)	95	95	96	95	94	94	100	100	100	94	93	94
Prince County exci. Summerside (COB)	95	96	95	95	96	95	100	100	100	91	88	92
Queen & Kings exci. Charlottetown (COA)	94	93	94	56	92	100	100	99	100	19	8	10
	Ceftriaxone					Ceftriaxone						
PEI Fake	93	95	96	97	97	96	94	77	76	100	100	100
Charlottetown (CIABCE)	93	95	96	96	97	96	83	100	99	100	100	99
Summerside (C1N)	95	94	97	96	97	96	96	39	36	100	100	100
Prince County exci. Summerside (COB)	92	94	94	97	96	97	39	43	37	100	100	100
Queen & Kings exci. Charlottetown (COA)	93	96	95	97	96	95	62	95	101	100	100	93

Data requested by WHO in 2022

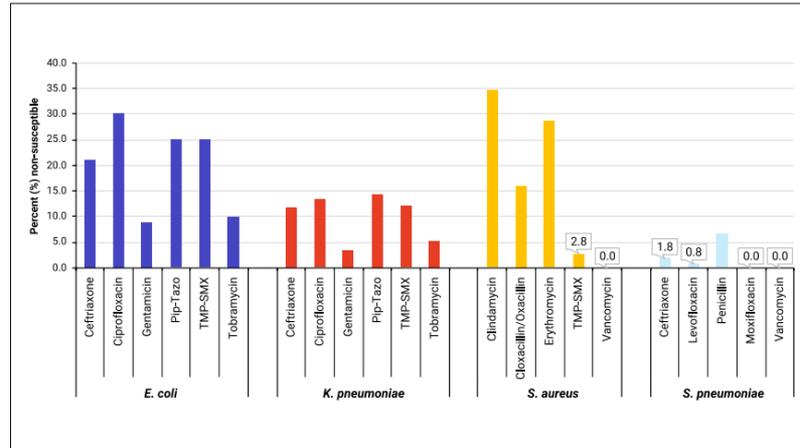


Specimen-Pathogen combinations to be included

Specimen	Pathogen:							
	STAAUR	STRPNE	KLEPNE	ESCCOL	ACISPP	SALSPP	SHISPP	NEIGON
BLOOD	●	●	●	●	●	●		
URINE			●	●				
STOOL						●	●	
GENITAL								●

● = combinations submitted by AMRNet (267k isolates)

Figure 19. Antimicrobial susceptibility results from blood isolates, AMRNet, 2020



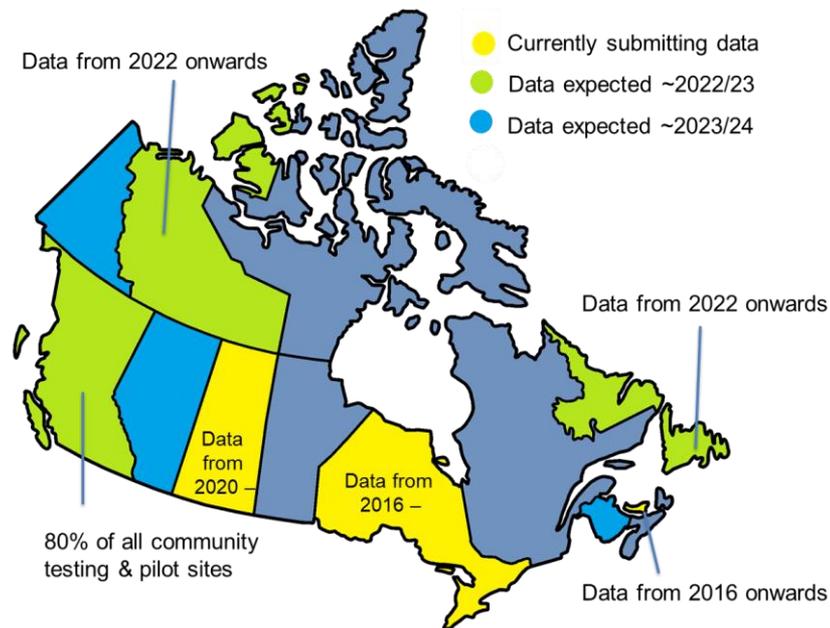
AMRNet data visualized in 2022 CARSS report

WHO GLASS submission



Summary

- Early days
- Stable long-term funding
- Very positive responses and early support at FTP level
- Pilot: SES factors collaboration with StatCan and SK
- Data sharing/requests:
 - Human: WHO GLASS, PHAC programs (CARSS, CNISP), Non-profit
 - Vet: CIPARS, industry-affiliated network
- AMRNet Vet pilots with ON, SK & PEI
- Federal data: *C. difficile* (CNISP), *N. gonorrhoeae* (ESAG), *Salmonella* (CIPARS) data transfer approved



Wastewater AMR: Dr. Chand Mangat

- New surveillance program for AMR in wastewater
 - Community-based surveillance is a gap in our current complement of tests
 - Near-term technical goals
 - Develop a robust/stable method for tracking AMR genes, pathogens and plasmids (2 year)
 - qPCR panel to begin and transitioning to omics
- Development plan
- qPCR -> metagenomics -> quantitative metagenomics - > long-read
- 20 sites to be tested for weekly
 - Technically aligned with developing US-CDC program
 - US-CDC qPCR panel is below, will choose 8 indicators
 - mcr-1, vanA, NDM, KPC, VIM, CTX-M (group 1), CMY-2, TEM, SHV, int11, tetW, IMP

Establishment of a Phage Biobank at NML

- Alternatives to antimicrobial therapy
- Funding requested to establish a new lab to identify phage active against highly drug resistant AMR pathogens
- Phage therapy recently being approved for treatment of difficult to treat infections (compassionate use)
 - USA first case 2018
 - Canada first case 2022
 - Other countries ahead of Canada and USA
 - Clinical trials underway
- Why NML? Perfect location.
 - AMR pathogen collection for over 30 years
 - Wastewater collections and manure samples for isolation of phage
- Working with AMMI Canada Phage WG
- More info to come

Summary

- The Antimicrobial Resistance and Nosocomial Infections Laboratory (ARNI) is here to support your laboratories

What is Keeping Dr. Mulvey Awake at Night?



Acknowledgements

- The ARNI Team
- Canadian Nosocomial Infection Surveillance Program
- Canadian Integrated Program for Antimicrobial Resistance Surveillance
- CANWARD
- The Canadian Public Health Laboratory Network
- Canadian Animal Health Laboratory Network
- All of the many clinical laboratories interested in working with ARNI