Antimicrobial Resistance and Nosocomial Pathogens in Canada

May 30th, 2023

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Conflicts of Interest

- None

Overview

- Antimicrobial Resistance and Nosocomial Infections (ARNI)
- AMR Surveillance
- Genomics
- New AMR Surveillance Initiatives

ARNI Reference Services

- Confirmatory testing (phenotypic and genotypic)
  - Identification of rare or novel resistance mechanisms
  - Testing for new antimicrobials
  - Passive surveillance
- Outbreak investigation support
  - WGS for hospital outbreaks
  - Advice to hospital/provincial/federal epidemiologists and microbiologists
  - Support to other countries
- Proficiency Testing and Standards

ARNI Basic and Applied Research

- Characterization of novel resistance mechanisms
- Development of assays to rapidly identify and type pathogens from specimens
- Whole genome sequencing to better understand transmission routes
- Genetic mechanisms of epidemic strains
  - Genomic and proteomic studies

ARNI Surveillance

- Canadian Nosocomial Infection Surveillance Program (CNISP)
- Canadian Integrated Program for Antimicrobial Resistance Surveillance (CIPARS)
- AMRNet
- Carbapenemase-Producing Organisms CPHLN
- CANWARD
- *Neisseria gonorrhoeae*
- *Streptococcus*
- Wastewater

PHAC AMR Priority Organisms 2020

- Methicillin-resistant *Staphylococcus aureus*
- Vancomycin-resistant *Enterococcus*
- Carbapenemase-producing Enterobacterales
- *Clostridioides difficile*
- *Neisseria gonorrhoeae*
- *Mycobacterium tuberculosis* (different NML Lab, Hafid Soulahine)
- *Streptococcus pneumoniae*
- *Streptococcus pyogenes*
- Typhoidal and non-typhoidal *Salmonella enterica*
- *Acinetobacter* species
- *Campylobacter* species
- *Escherichia coli*

https://www.canada.ca/en/public-health/services/publications/drugs-health-products/**canadian-antimicrobial-resistance-surveillance-system-2020-report**.html

Overview

- Life in the Antimicrobial Resistance and Nosocomial Infections Unit (ARNI)
- **AMR Surveillance**
- Genomics
- New AMR Surveillance Initiatives

Canadian Nosocomial Infection Surveillance Program (CNISP)

Overview of CNISP

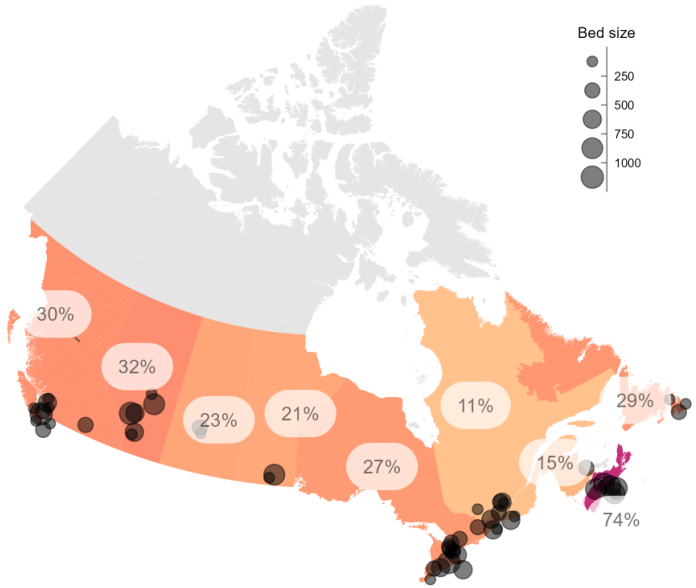
CNISP is a collaboration between the

- 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

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



Current CNISP Surveillance Projects

- ***Clostridioides difficile* infection (CDI)**
- **Methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infection (BSI)**
- Methicillin-susceptibile *Staphylococcus aureus* (MSSA) BSI
- **Vancomycin-resistant enterococci (VRE) BSI**
- Central Line-Associated Bloodstream Infections (CLABSI)
- Hip and knee Surgical Site Infections (SSI)
- Point prevalence surveys
- Cerebrospinal fluid shunt SSI
- Pediatric Cardiac SSI
- ***Candida auris***
- **Carbapenemase-producing organisms (CPO)**
- Antimicrobial Use
- Antibiogram
- Viral Respiratory Infections (VRI) - COVID-19

CNISP surveillance of *Clostridioides difficile* infection (CDI)

https://www.cdc.gov/hai/organisms/cdiff/cdiff_infect.html

- 2004-2005 Pilot study
- HCA-CDI surveillance since 2007
- CA-CDI since 2015

- Stool samples submitted March+April for adult (year round for Peds)

- Primary *C. difficile* isolation
- AST (Etest)
- Toxin PCR
- Ribotyping (replaced PFGE 2018)

- Moving into WGS 2022

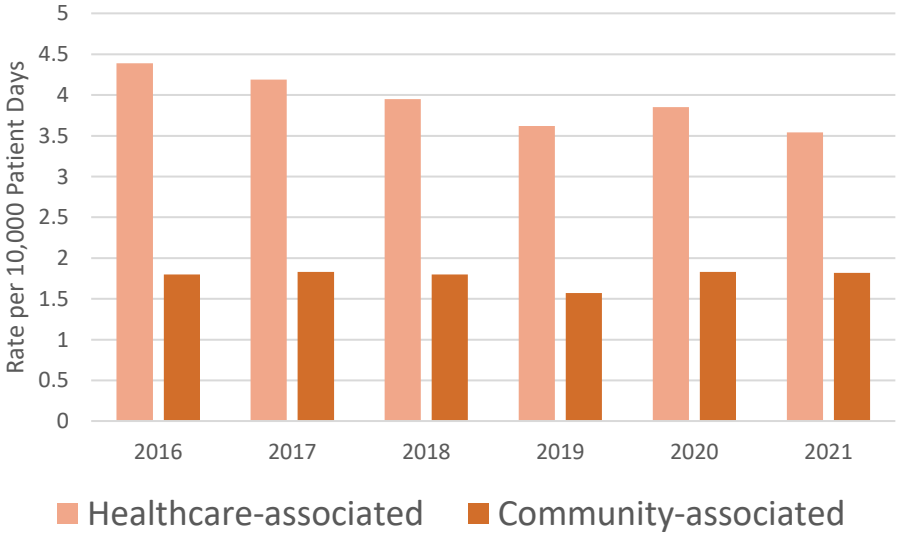
Clostridioides difficile infection (CDI)

Community-associated CDI → **Range: 1.57-1.83 per 10,000 PD**

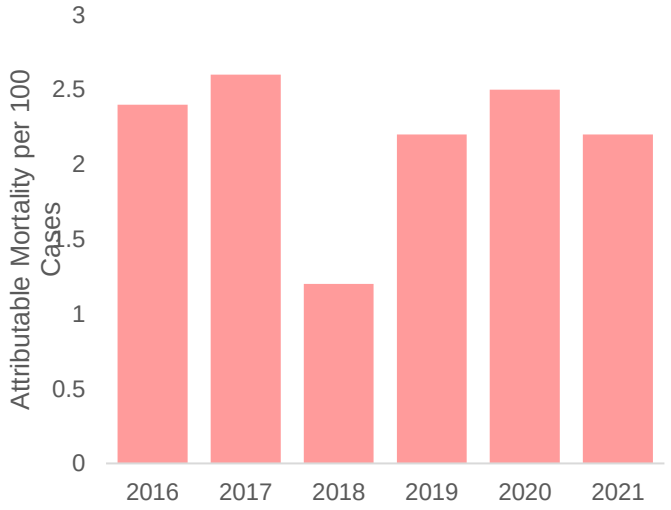
Healthcare-associated CDI ↓ **24%**

CDI attributable mortality → **Range: 1.2%-2.6%**

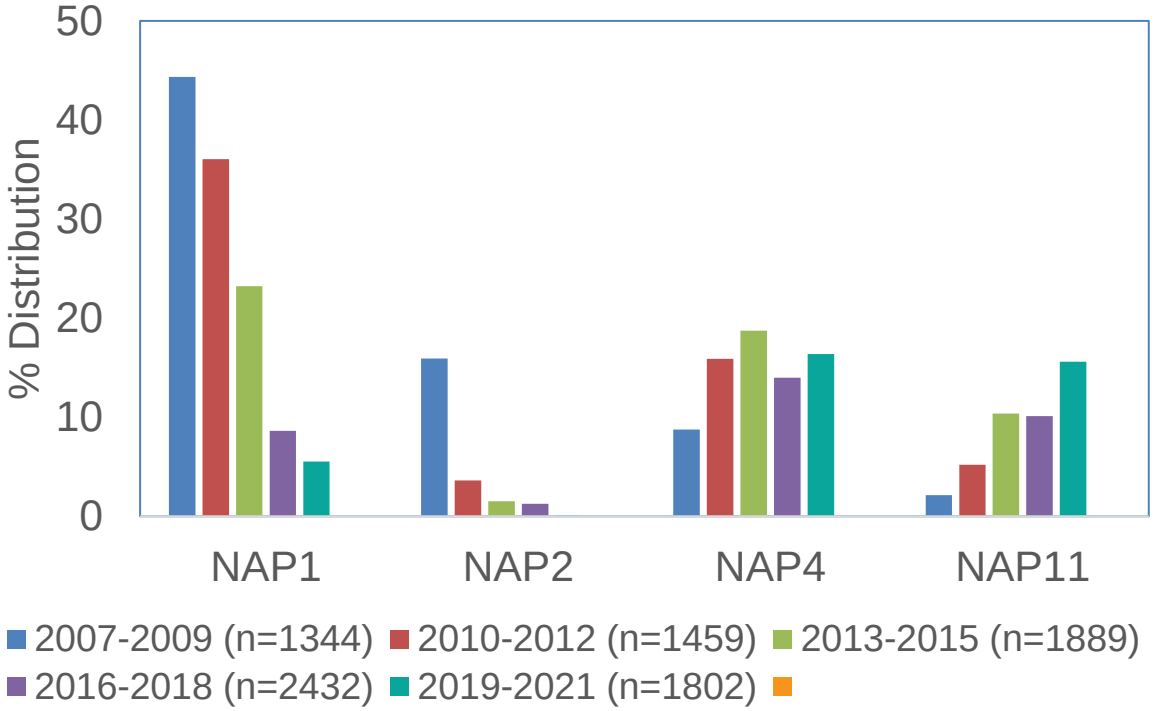
Inpatient healthcare-associated (HA) & community-associated (CA) CDI rates



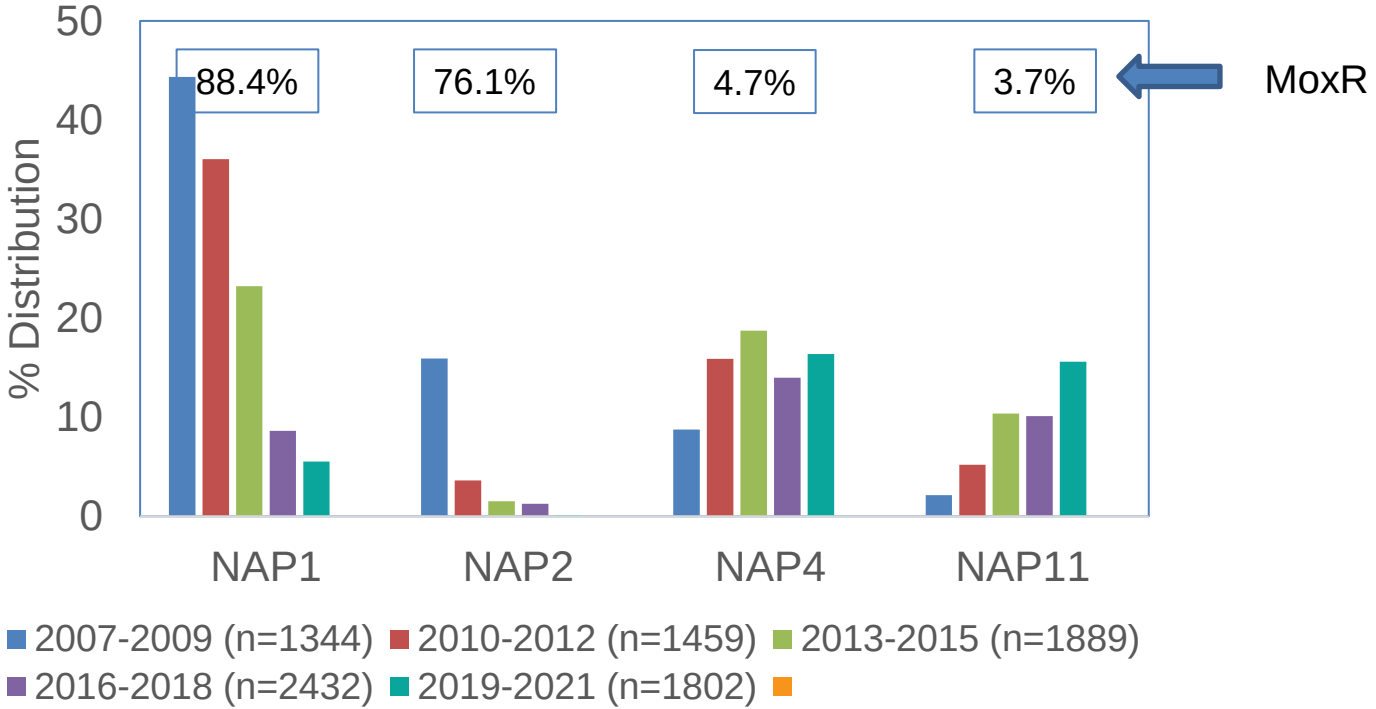
CDI attributable mortality



Changing Molecular Epidemiology of *C .difficile* 2007-2021



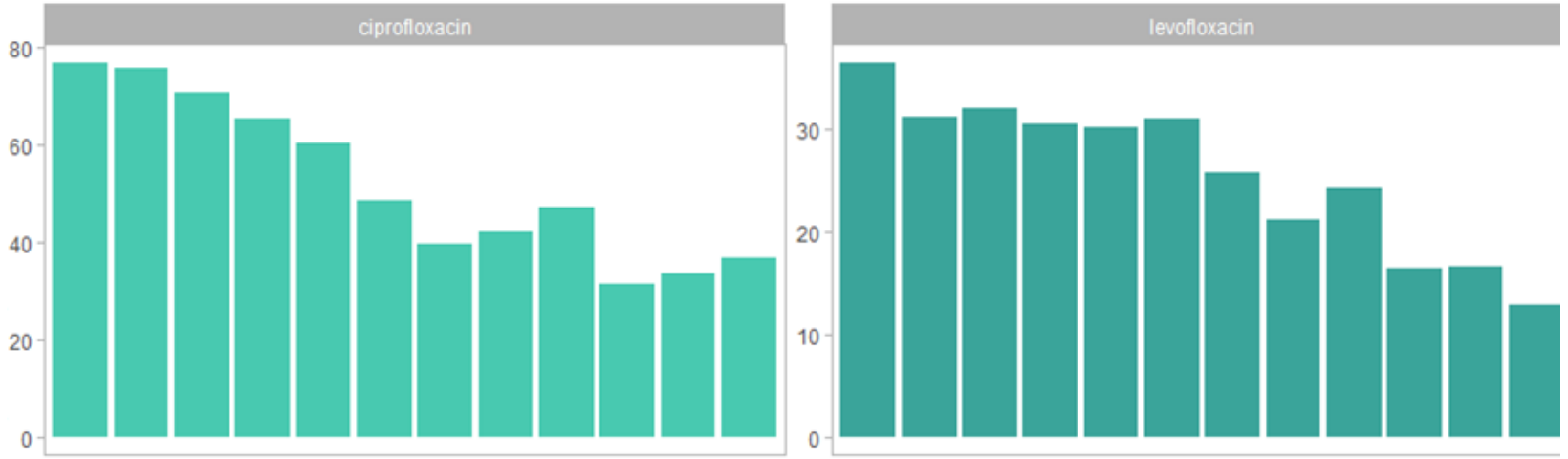
Declining Fluoroquinolone Resistant Strain Types and Emerging Susceptible Types



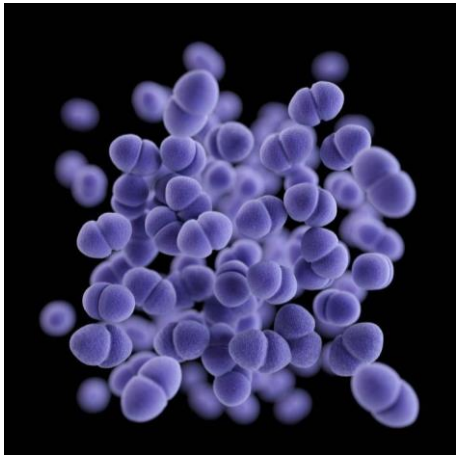
CNISP: Antibiotics with the greatest absolute decreases

- Stewardship highlight for *C. difficile* NAP1

Rate of AMU per 1,000 patient days/
Taux d'AMU pour 1 000 jours-patients



Vancomycin Resistant Enterococci (VRE) bloodstream infection (BSI)



CDC/Dan Higgins - Medical Illustrator, 2013

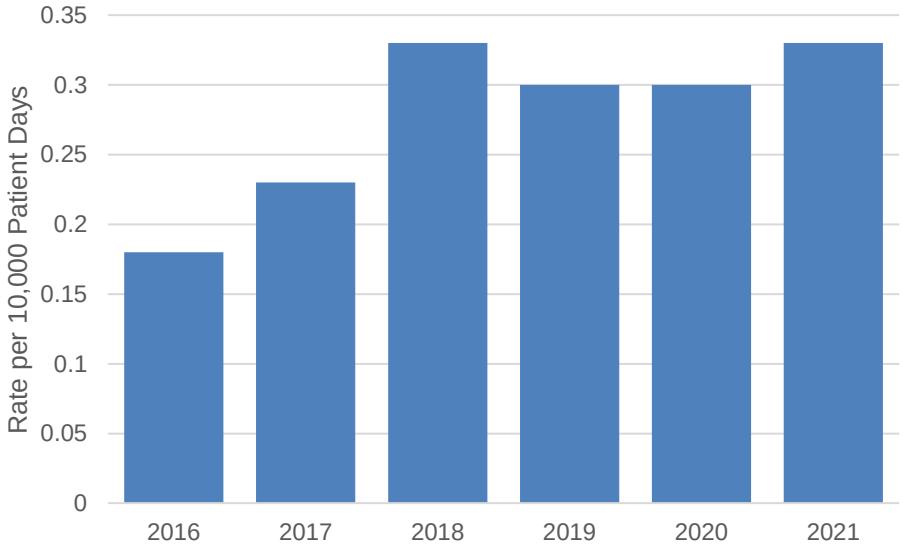
- Surveillance of infections and colonizations since 1999
- Surveillance of only BSI beginning 2018
- AST sensititre
- Van PCR
- WGS (all to be sequenced)

Vancomycin Resistant Enterococci (VRE) bloodstream infection (BSI)

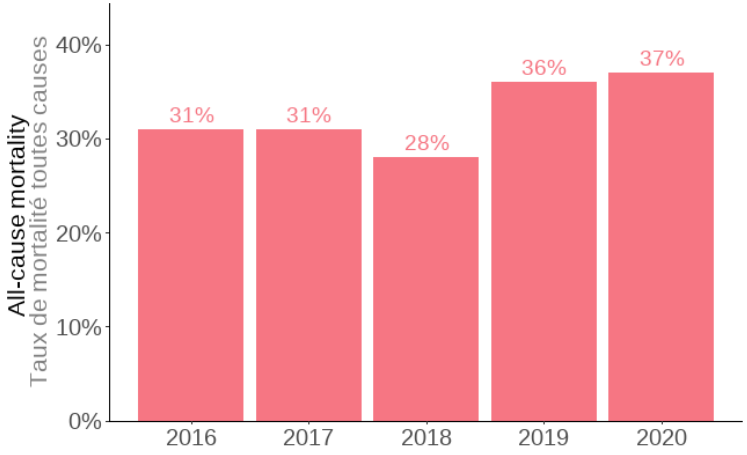
Healthcare-associated VRE 83%

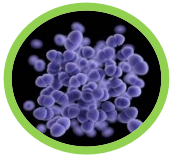
VRE all-cause mortality **Range: 28%-37%**

Inpatient healthcare-associated (HA) VRE rates

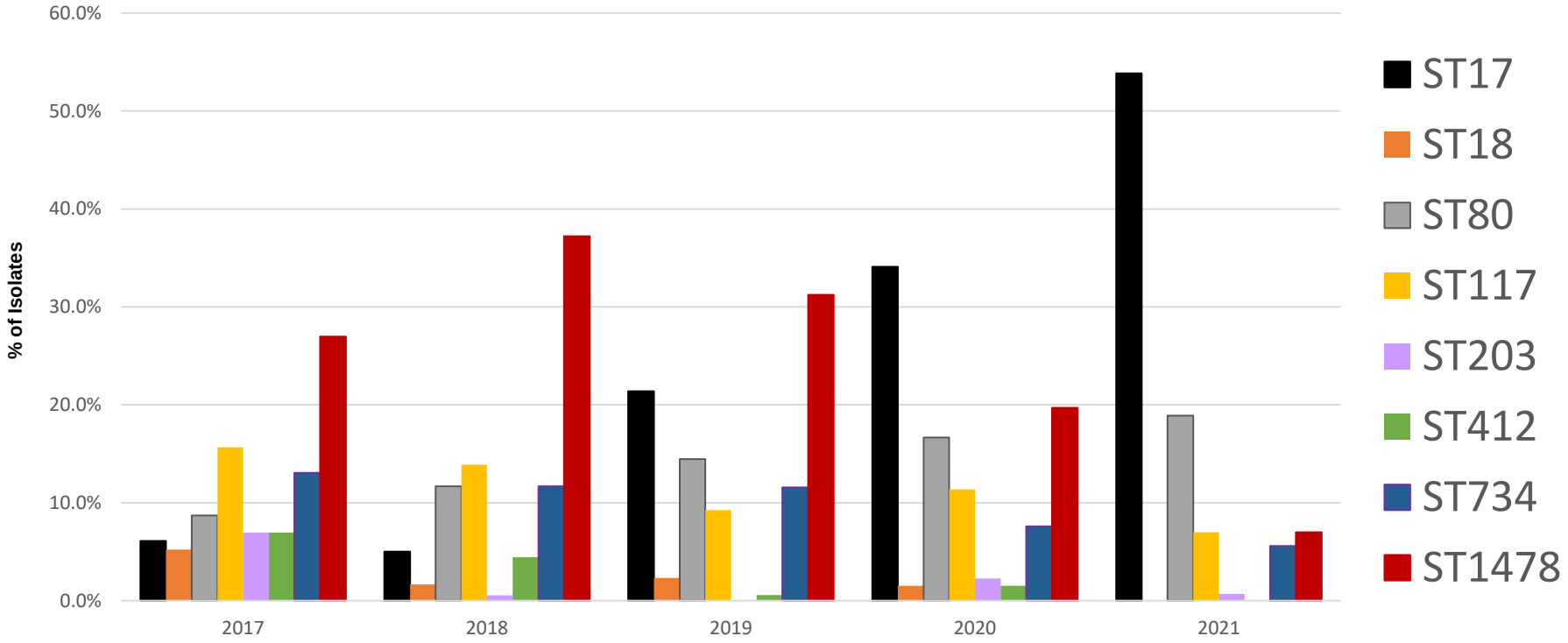


VRE all-cause mortality





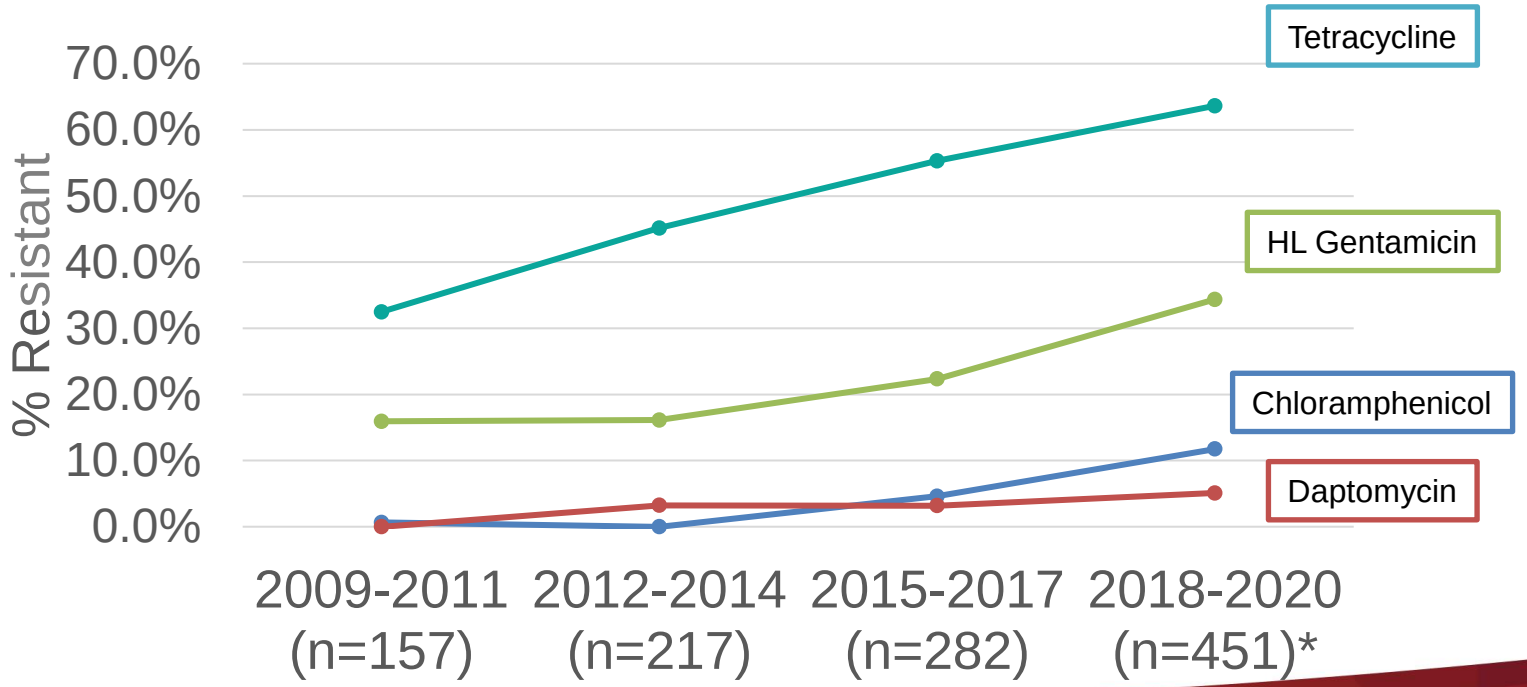
Distribution of VRE Sequence Type by Year, 2017-2021



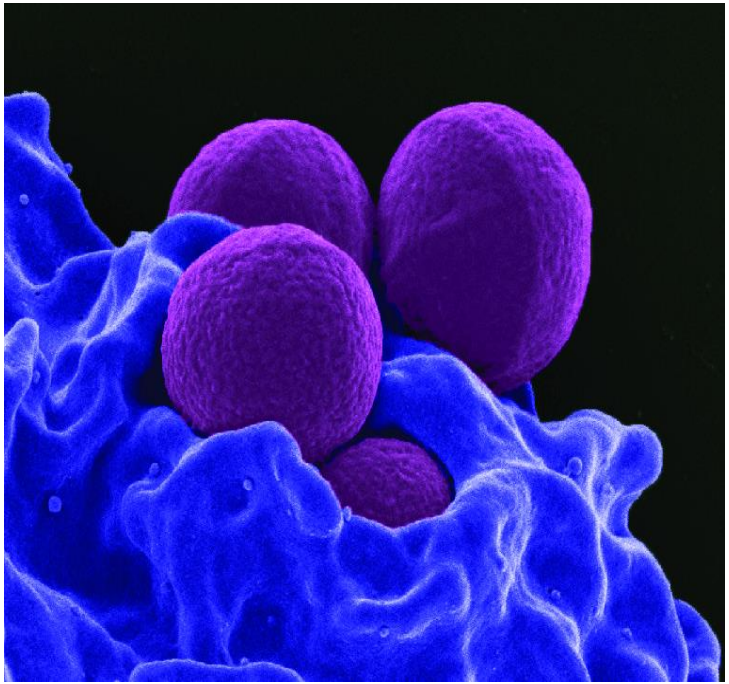
AMMI/CACMID 2023 P033 McCracken et al.

Vancomycin Resistant Enterococci (VRE) bloodstream infection (BSI)

Increasing Antimicrobial Resistance Trends in VRE



CNISP Surveillance of MRSA bloodstream infection (BSI)



NIAID https://doi.org/10.1371/journal.pbio.2003775.g002

- Surveillance since 1995
  - Previously included colonization and other infections
  - Currently just BSI (2018 on)

- Surveillance year round

- AST (Sensititre)
- rtPCR (mec, nuc, PVL)
- Spa typing (2008+)
- PFGE

- Moving into WGS 2022

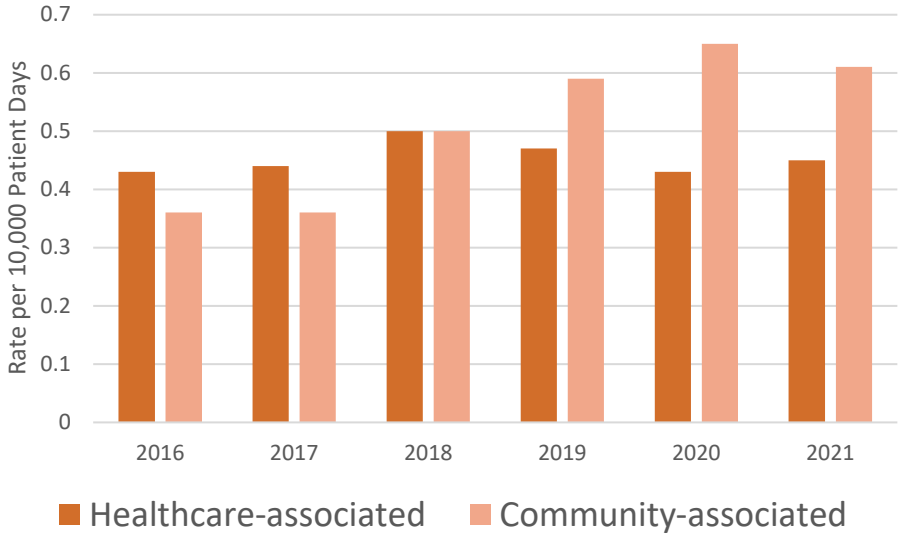
Methicillin-resistant *Staphylococcus aureus* (MRSA) bloodstream infection (BSI)

Community-associated MRSA ↑ **69.4%**

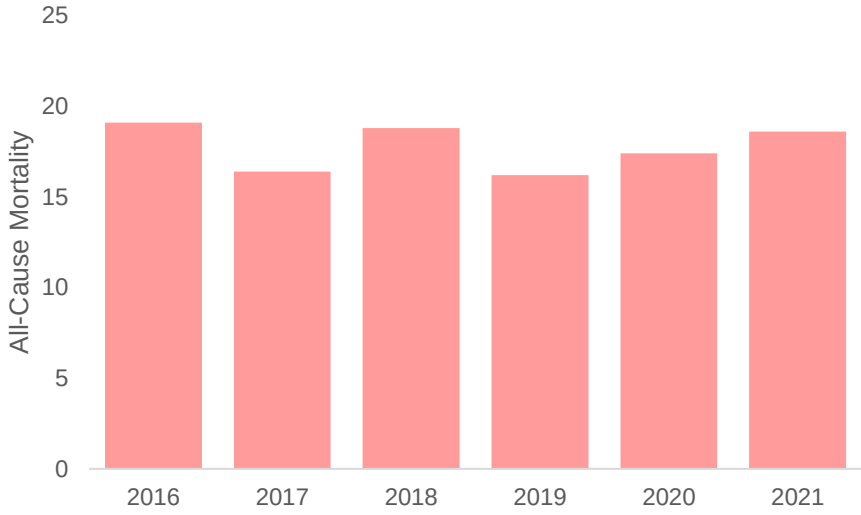
Healthcare-associated MRSA → **Range: 0.43-0.50 per 10,000 PD**

MRSA all-cause mortality → **Range: 16.2%-18.8%**

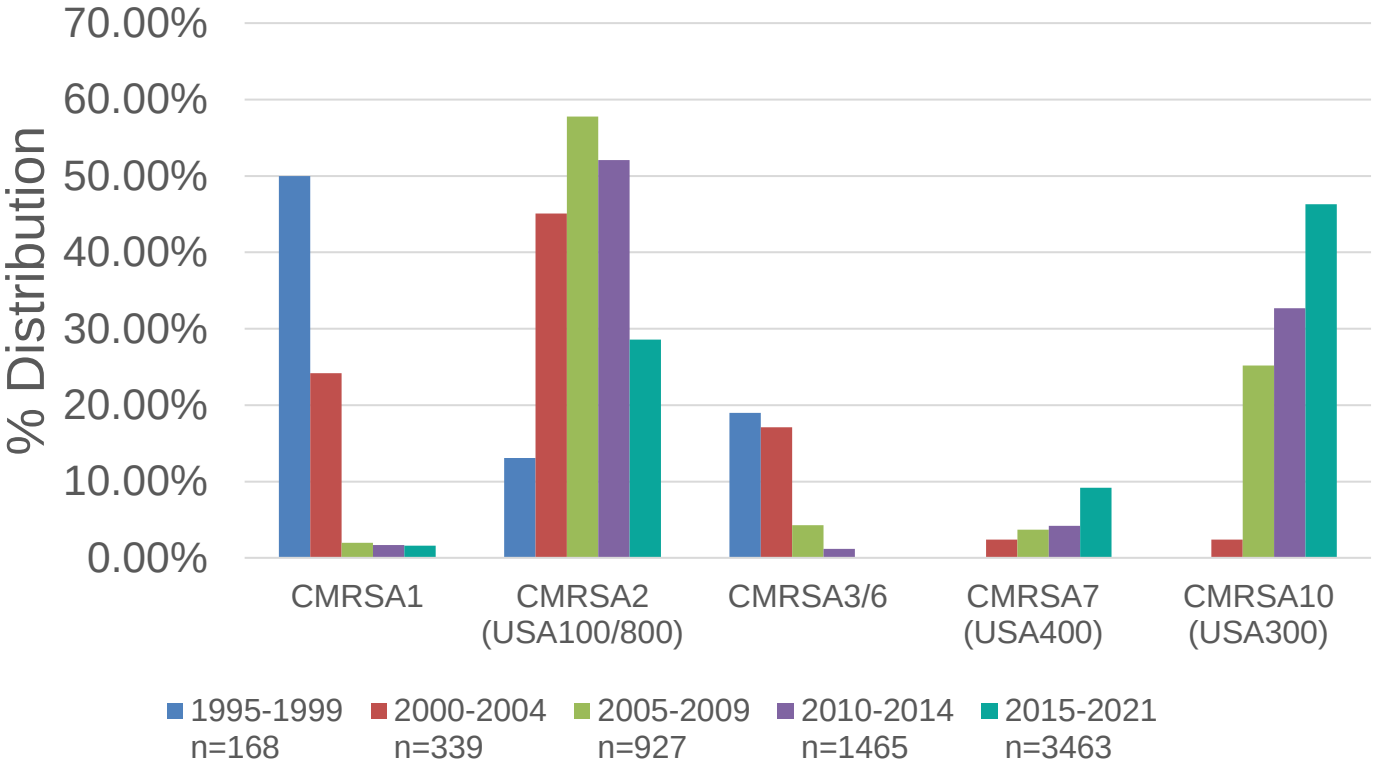
Inpatient healthcare-associated (HA) & community-associated (CA) MRSA rates

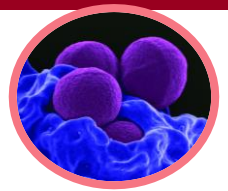


MRSA all-cause mortality

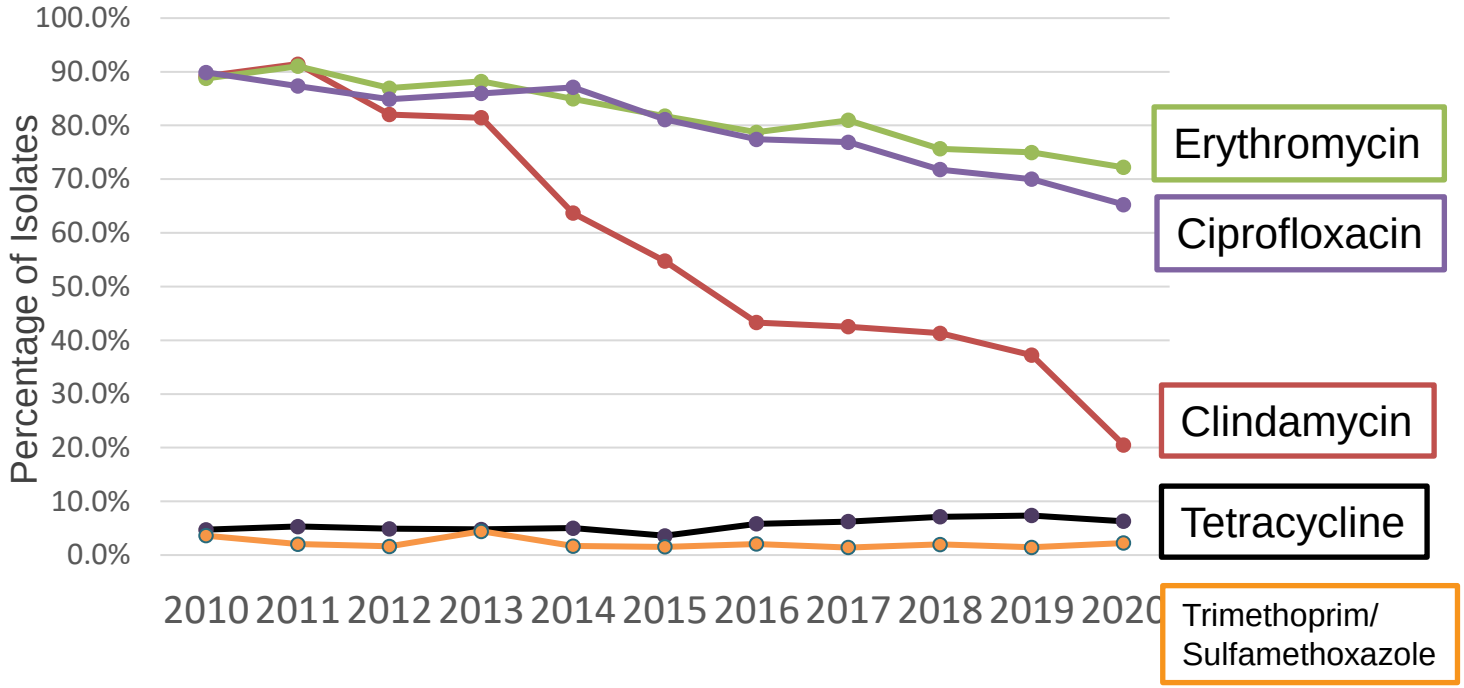


National Distribution of Select Canadian MRSA Epidemic Strains from Bacteremia Cases (CNISP, 1995-2021)





Trends in MRSA AMR



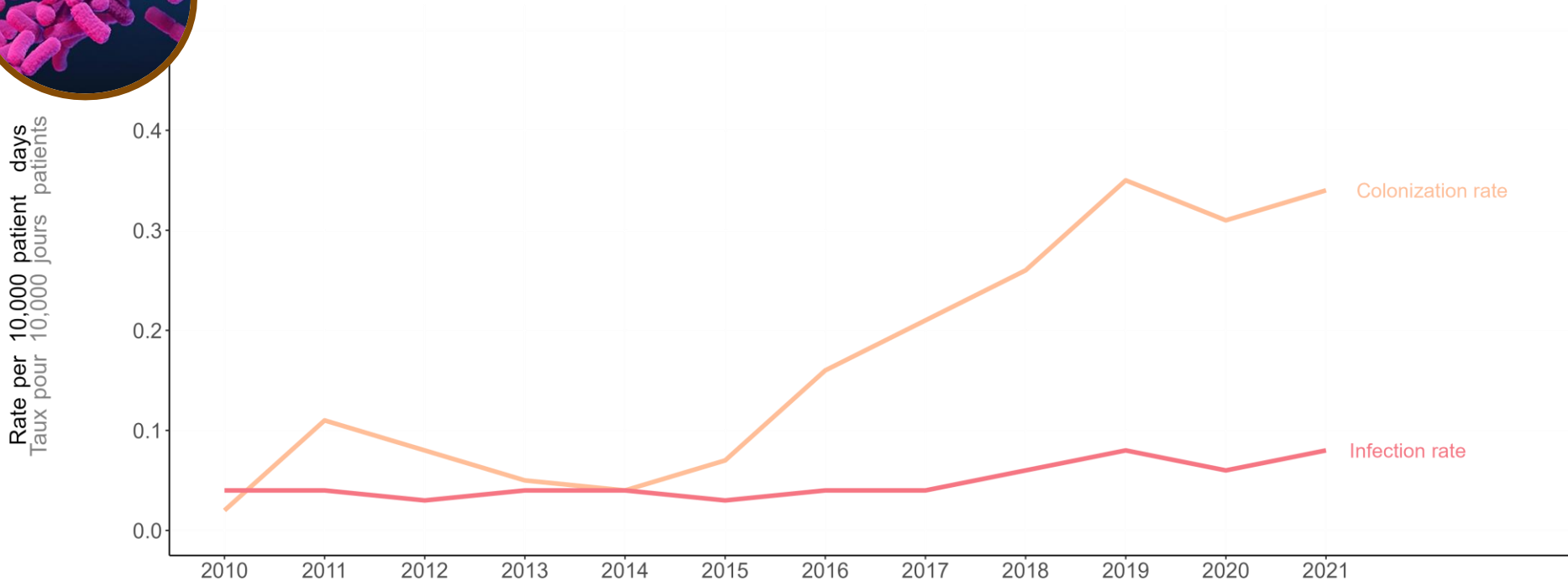
MRSA CLD Resistance and Usage

CNISP surveillance of Carbapenemase-producing *Enterobacterales* (CPE)

Stephanie Rossow, Centers for Disease Control and Prevention/Antibiotic Resistance Coordination & Strategy Unit

- Surveillance of CPE infections and colonizations since 2010
- Select Environmental
- WGS
- AST Sensititre

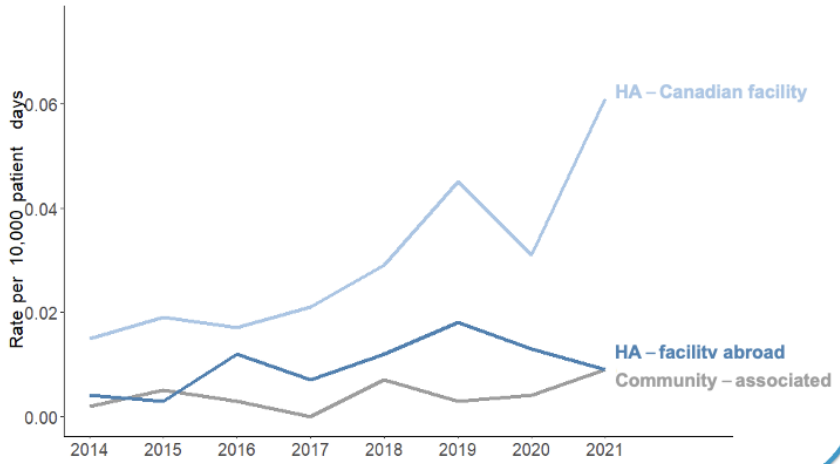
CPE infection and colonization rates, 2010-2021



	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021
No. infections	11	14	12	19	22	17	20	21	36	50	36	53
No. colonizations	6	37	27	24	24	37	89	119	148	223	193	222

CNISP CPE Surveillance

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)

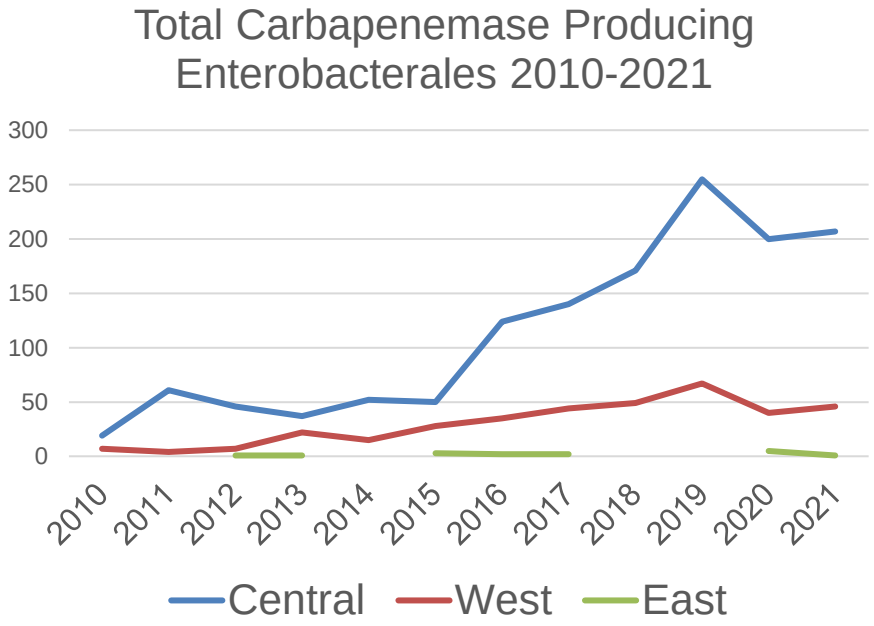
24% of inpatients (67/285) were in an **intensive care unit** at the time of positive culture or were admitted following positive culture

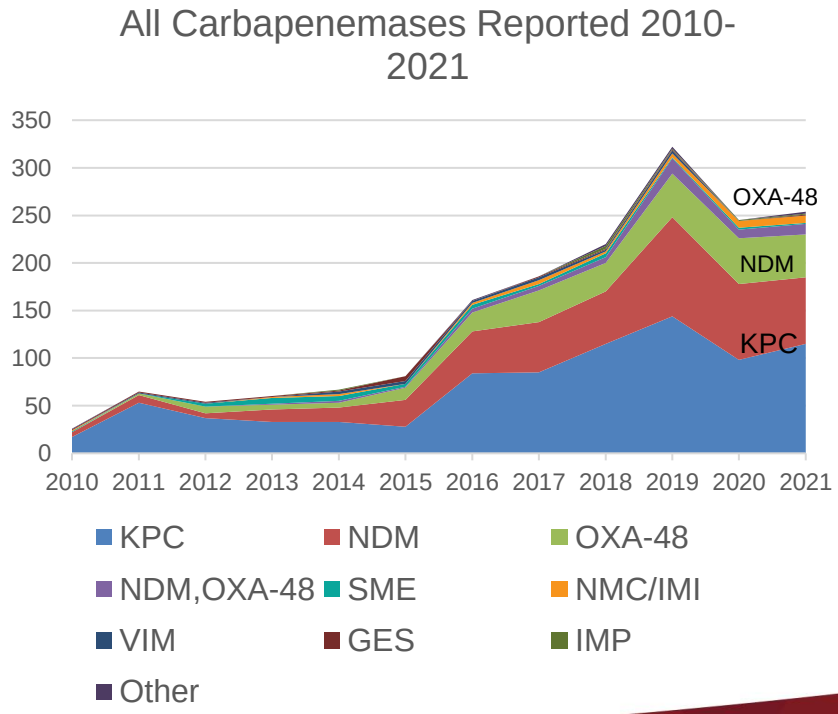
17%

30-day all-cause mortality

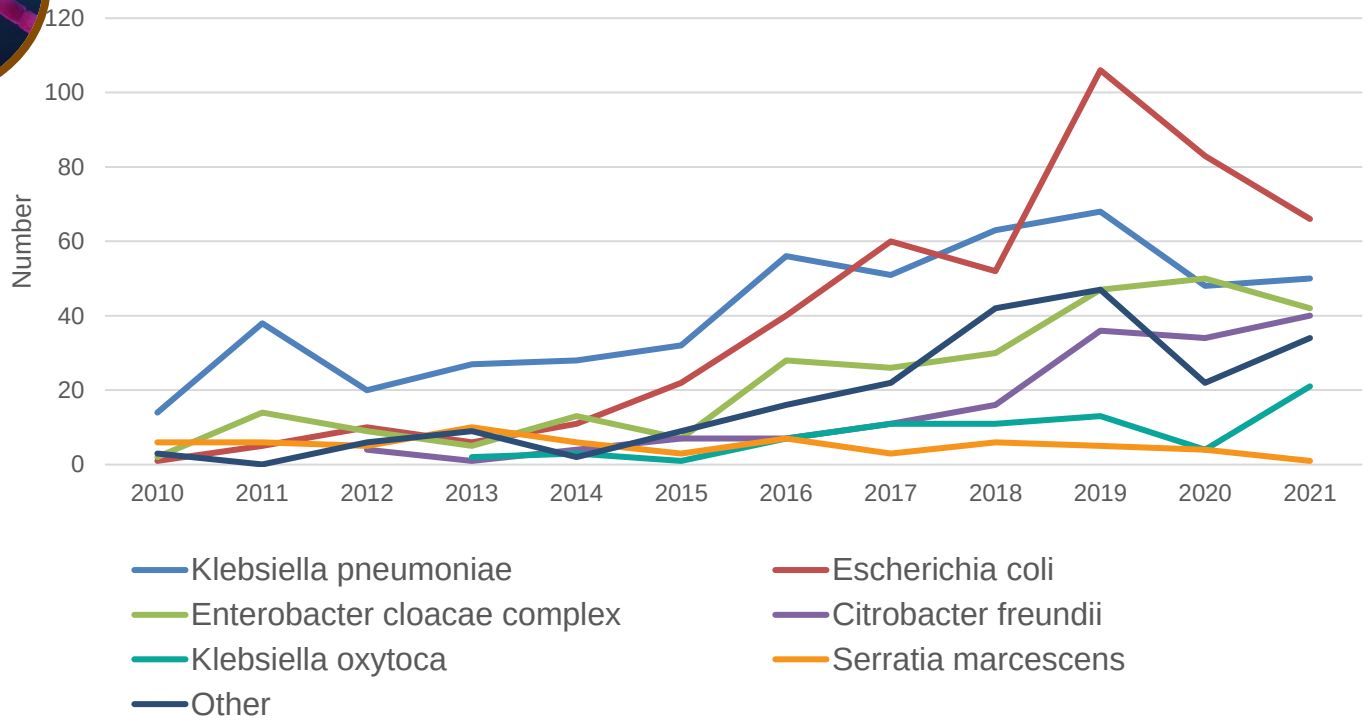
AMMI/CACMID 2023, P036 R. Mitchell et al.; P042 L. Matasje et al.

CPE


Total Carbapenemase Producing Enterobacterales 2010-2021
300
250
200
150
100
50
0
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
Central
West
East


All Carbapenemases Reported 2010-2021
350
300
250
200
150
100
50
0
2010
2011
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
OXA-48
NDM
KPC
KPC
NDM
OXA-48
NDM,OXA-48
SME
NMC/IMI
VIM
GES
IMP
Other

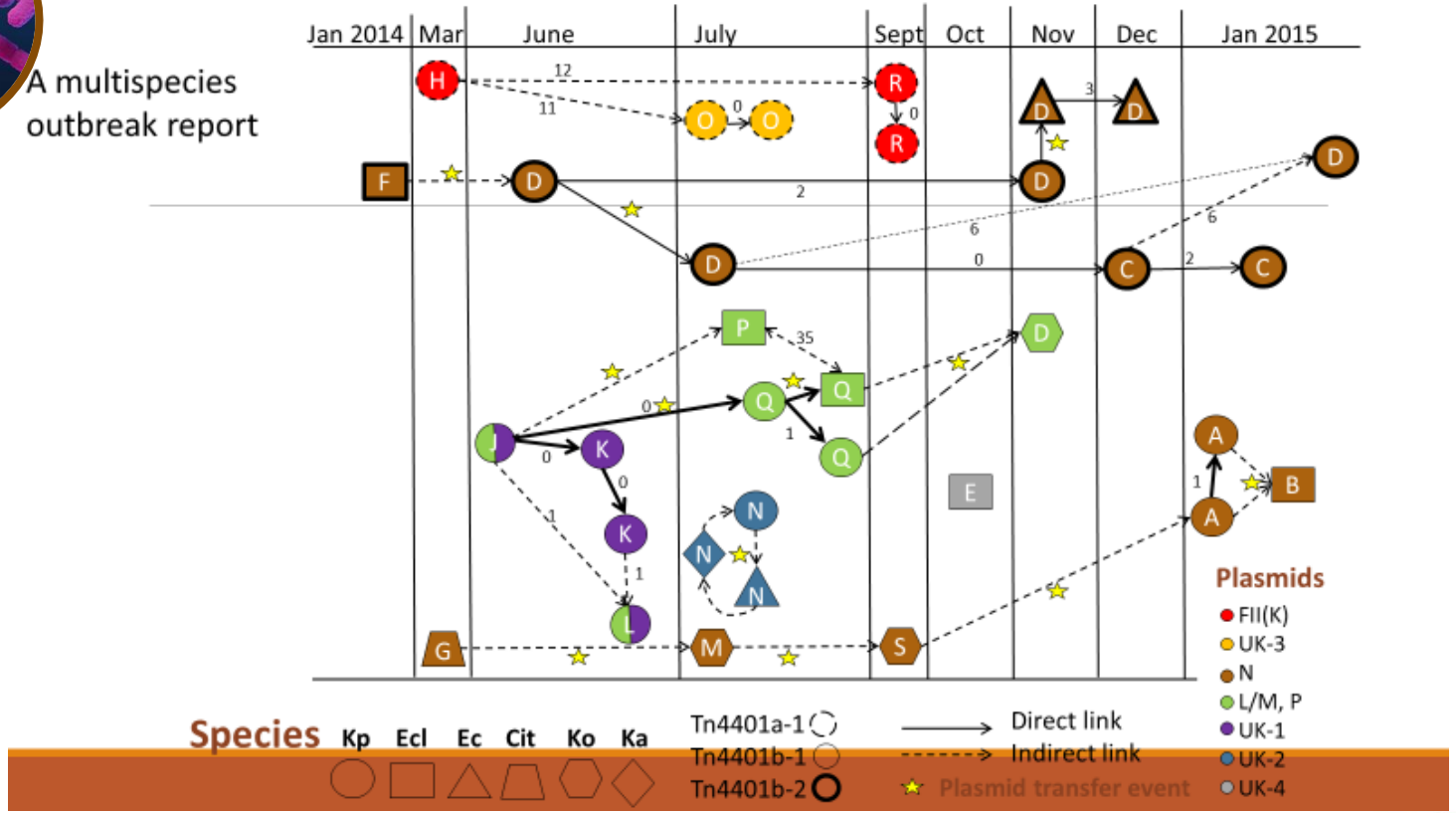
Distribution of Organisms 2010-2021



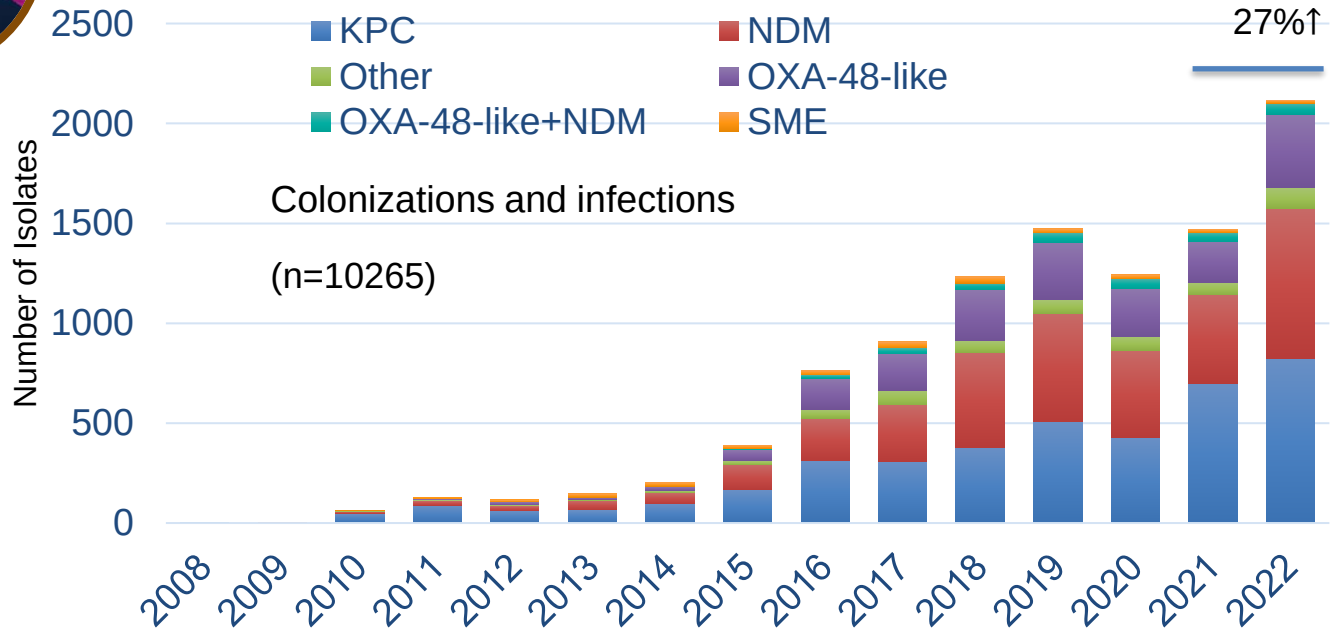
- Similar to some Provincial reports there is a decline in *E.coli*

The Major Challenge IPC of CPOs

A multispecies outbreak report



CPE in Canada: CPHLN Data. L. Mataseje



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

Year

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
bla_{NMC}	***Enterobacter cloaceae***	2	Vietnam (2); Bangladesh (1)	CIPARS retail shrimp n=832
	Enterobacter aerogenes	1		
bla_{VCC}	***Vibrio cholerae***	2	India (2)	
				Niche market seafood
bla_{NDM}, bla_{TEM}, bla_{OXA-1}	***Enterobacter cloaceae***	2	Vietnam (2)	Clams n=101
bla_{NMC}	***Enterobacter cloaceae***	3	Vietnam (3)	

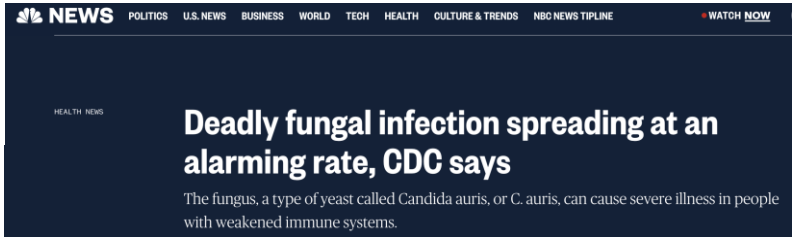
Janecko et al., 2016 Emerg Infect Dis 22:1675-77
Mangat et al., 2016 AAC 60:1819-25

Candida auris – Dr. Amrita Bharat

abc NEWS

Potentially deadly fungus spreading rapidly in US health care facilities

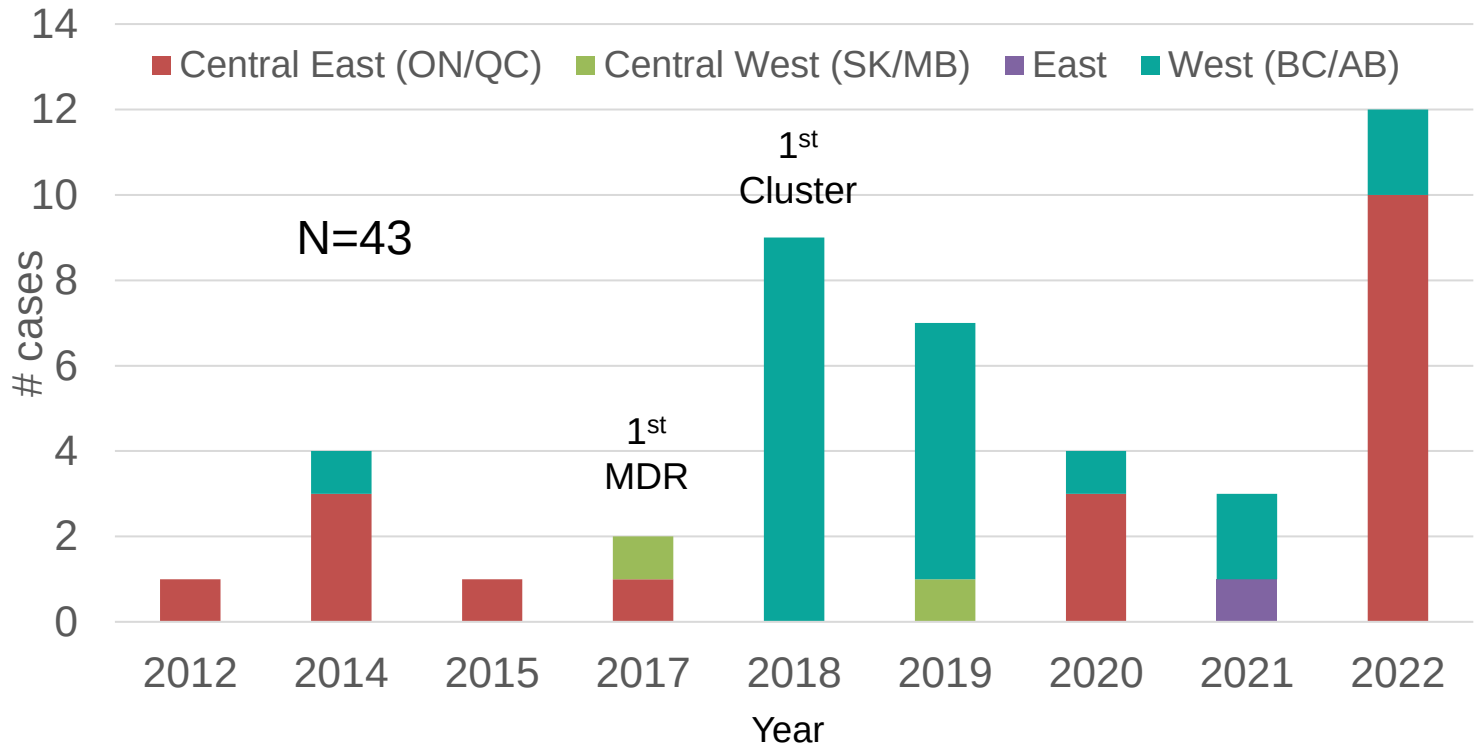
Cases of Candida auris doubled in 2021, according to a new CDC report.



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

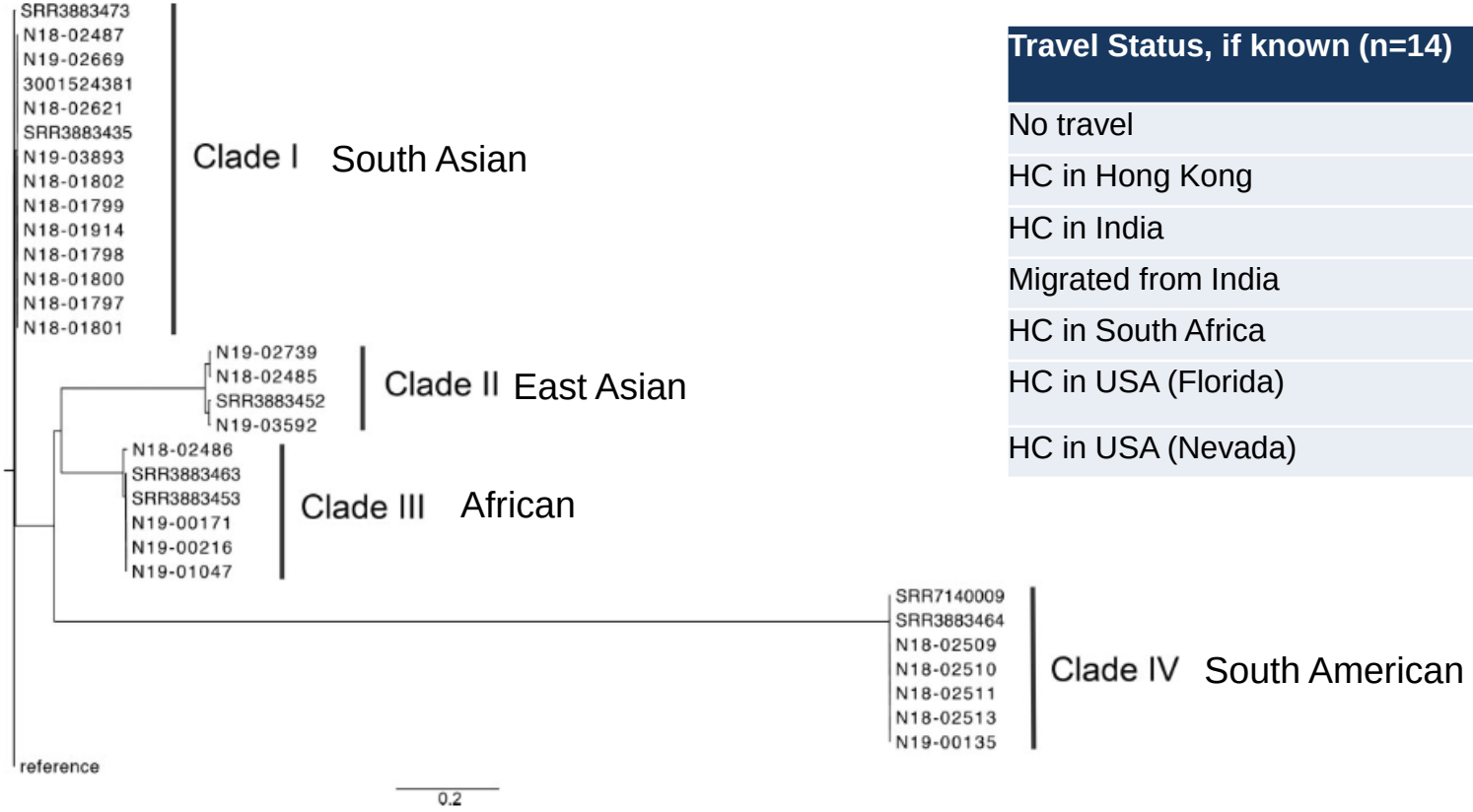
- ~45 participating hospitals

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

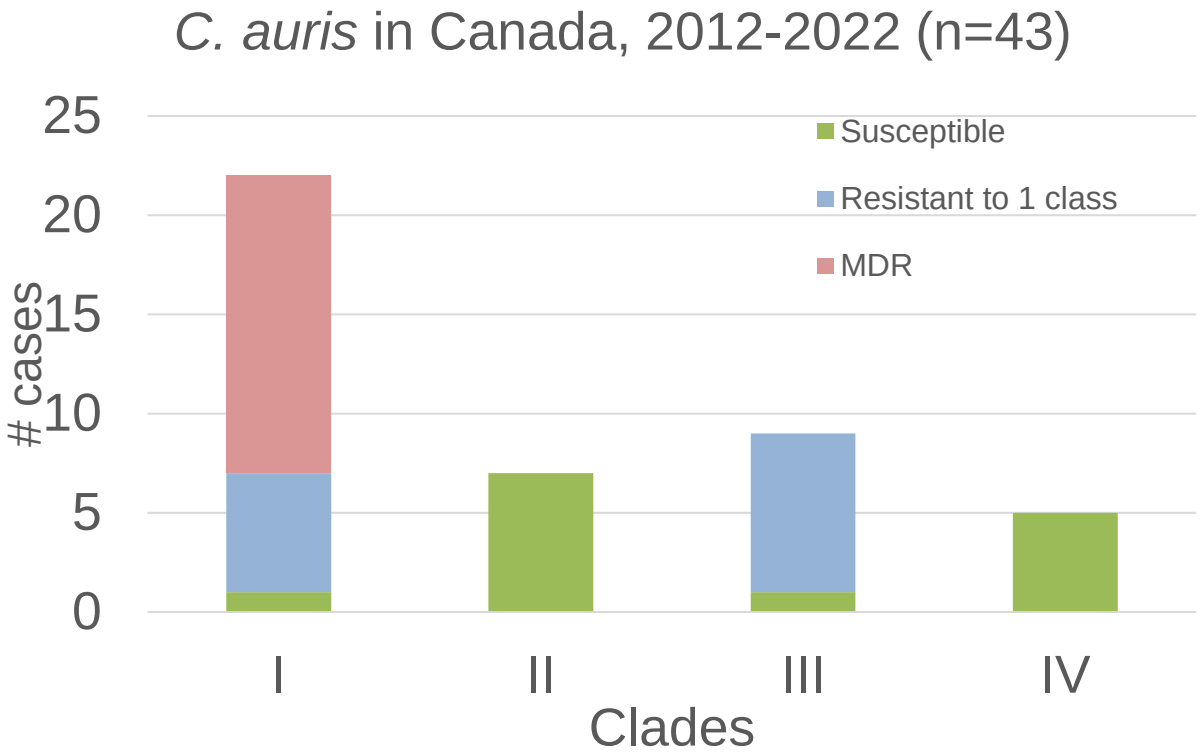
Genomic Clades of *C. auris*



Travel Status, if known (n=14)	# cases
No travel	4
HC in Hong Kong	1
HC in India	3
Migrated from India	1
HC in South Africa	1
HC in USA (Florida)	2
HC in USA (Nevada)	1

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

Antifungal resistance was associated with clades I and III

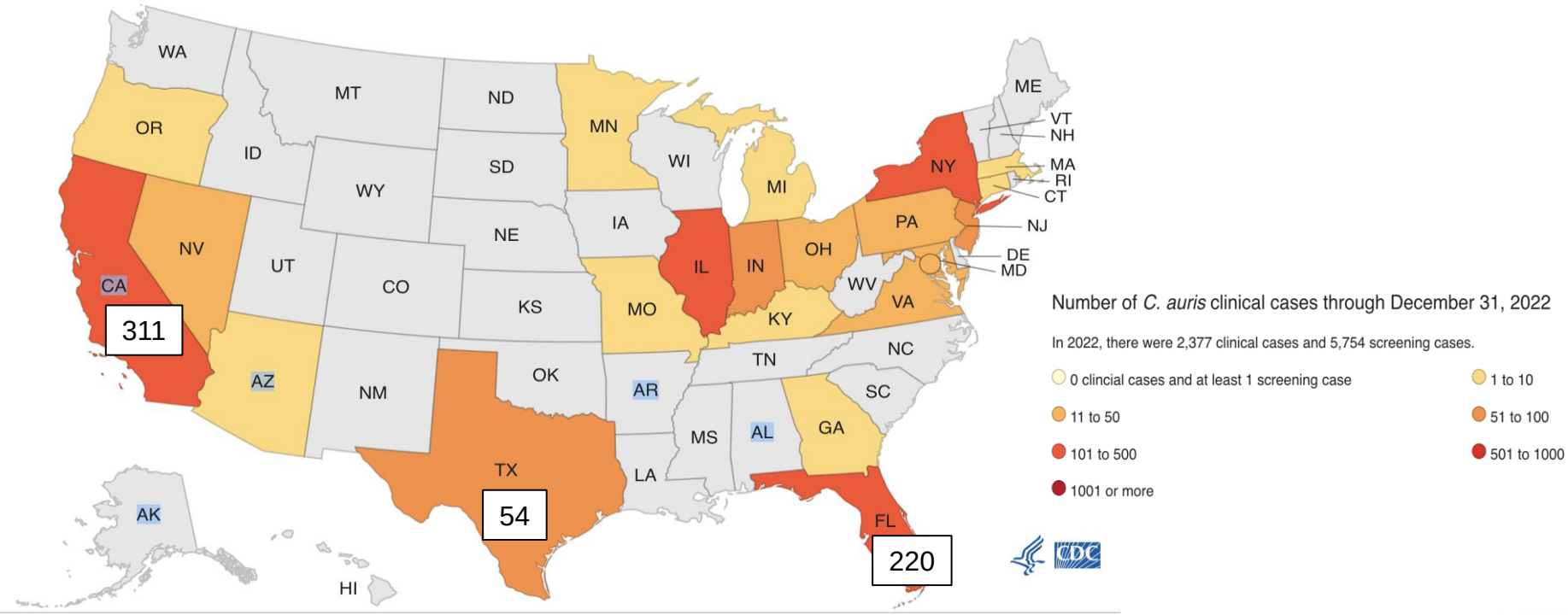


~ one-third of isolates each were resistant to

- 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



Overview

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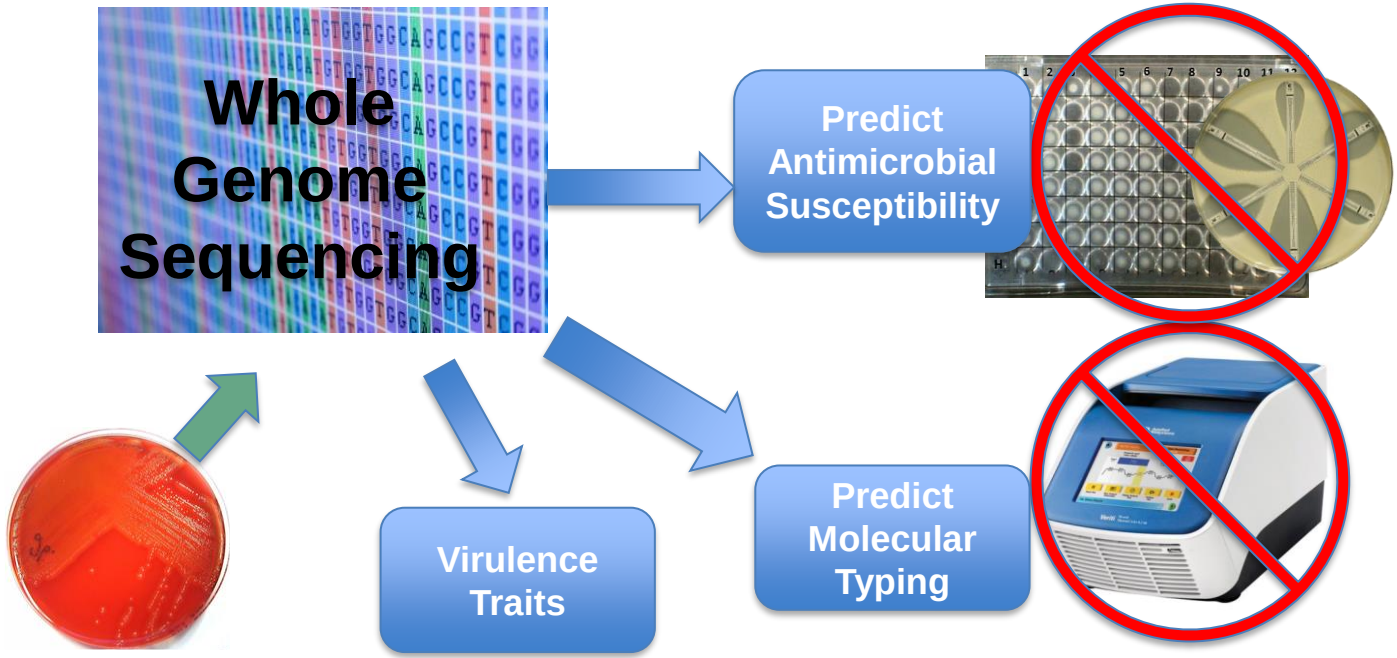
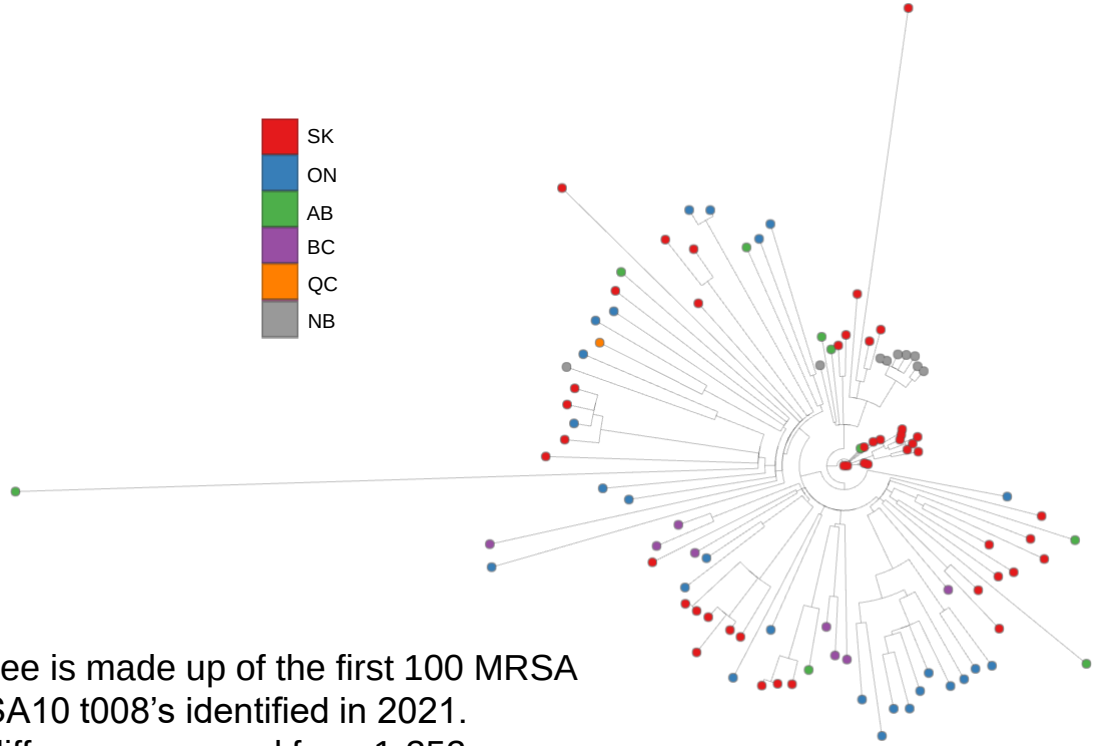
- AMR Surveillance
- Genomics
- New AMR Surveillance Initiatives

The Transition to Whole Genome Sequencing

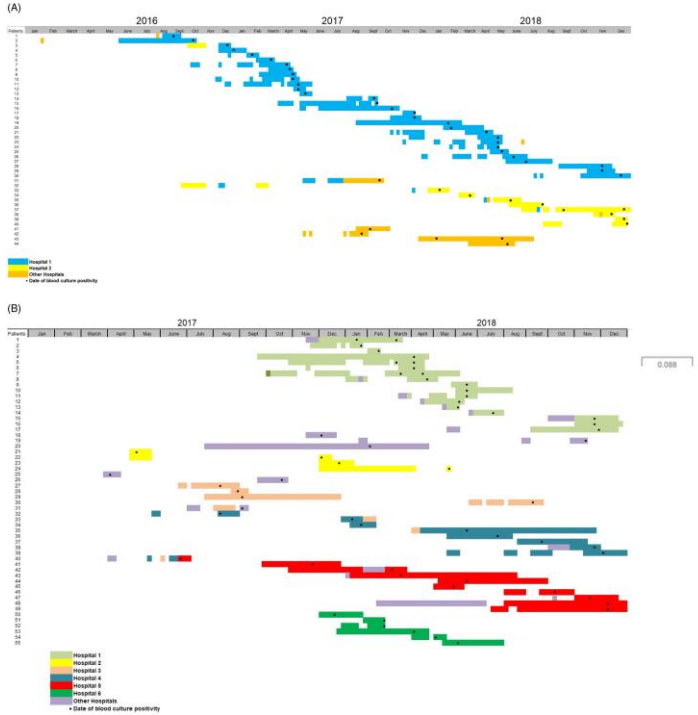


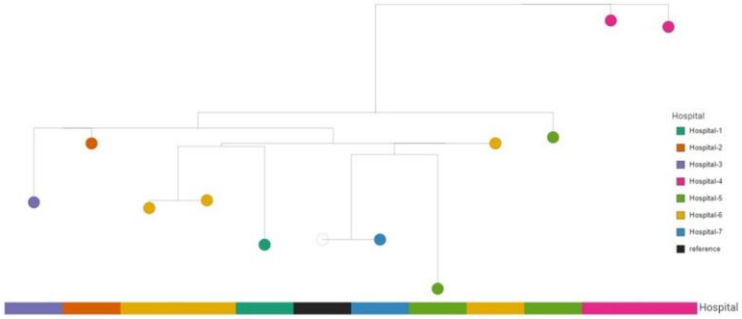
WGS vs traditional spa typing for MRSA



This tree is made up of the first 100 MRSA CMRSA10 t008's identified in 2021.
SNV differences ranged from 1-352.

Emergence of VRE ST1478





Evidence of both intrahospital and regional interhospital spread.

Kleinman DR et al. Infect Control Hosp Epidemiol. 2023 Jan;44(1):17-23.

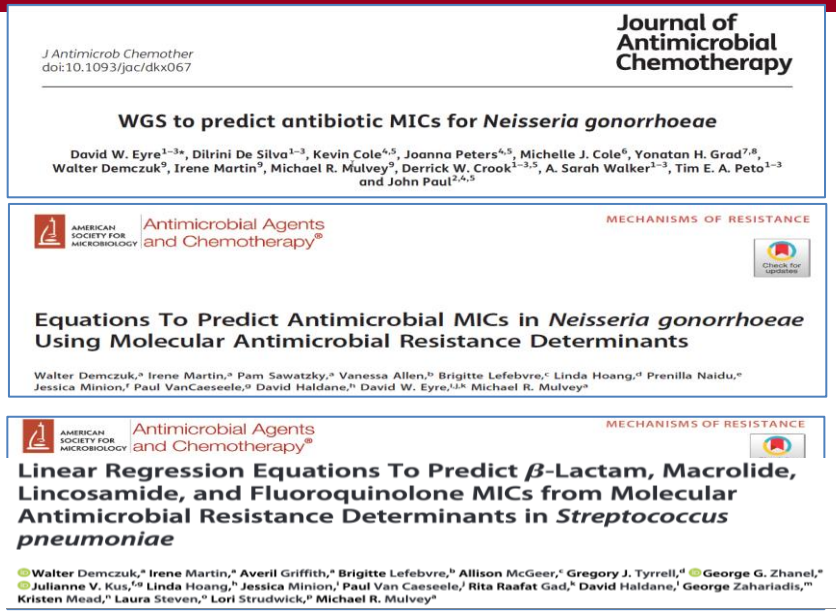
ARNI Genomics

- 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.
  - *MRSA*



J Antimicrob Chemother
doi:10.1093/jac/dkx067

Journal of Antimicrobial Chemotherapy

WGS to predict antibiotic MICs for *Neisseria gonorrhoeae*

David W. Eyre[1–3]*, Dilrini De Silva[1–3], Kevin Cole[4,5], Joanna Peters[4,5], Michelle J. Cole[6], Yonatan H. Grad[7,8], Walter Demczuk[9], Irene Martin[9], Michael R. Mulvey[9], Derrick W. Crook[1–3,5], A. Sarah Walker[1–3], Tim E. A. Peto[1–3] and John Paul[2,4,5]

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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,[i,j,k] Michael R. Mulvey[a]

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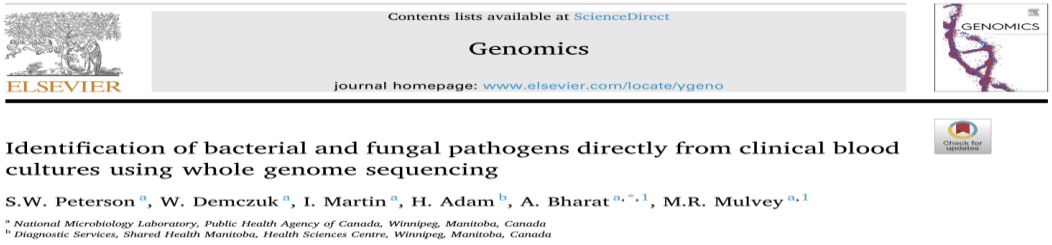
MECHANISMS OF RESISTANCE

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,[f,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

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,*,1], 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

Public Health Agency of Canada | Agence de la santé publique du Canada

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 replicon 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

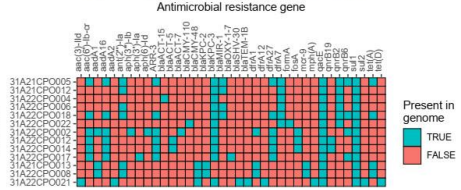
NMLPID	Organism	Date of positive culture	Sequence type	CPO gene	Tn4401 variant	Plasmid type*	Size (kb)	Plasmid cluster
31A21CP0005	Enterobacter cloacae	19-Apr-2021	novel1	KPC-3	Tn4401b-3	unclassified1	74.6	001
31A21CP0012	Enterobacter cloacae	27-Sep-2021	novel1	KPC-3	Tn4401b-3	unclassified1	74.6	001
31A22CP0004	Enterobacter cloacae	4-Apr-2022	740	KPC-3	Tn4401b-3	unclassified1	74.6	001
31A22CP0006	Enterobacter cloacae	9-May-2022	novel1	KPC-3	Tn4401b-3	unclassified1	74.6	001
31A22CP0018	Enterobacter cloacae	5-Sep-2022	novel1	KPC-3	Tn4401b-3	unclassified1	74.6	001
31A22CP0022	Citrobacter freundii	7-Nov-2022	100	KPC-3	Tn4401b-3	unclassified1	75.8	001
31A22CP0002	Enterobacter cloacae	14-Feb-2022	177	KPC-3	Tn4401b-3	IncN	67.9	002
31A22CP0012	Enterobacter cloacae	27-Jun-2022	97	KPC-3	Tn4401b-unknown	IncN	61.0	002
31A22CP0014	Enterobacter cloacae	28-Jun-2022	97	KPC-3	Tn4401b-unknown	IncN	57.1	002

GENOME SEQUENCING REPORT

Public Health Agency of Canada | Agence de la santé publique du Canada

ANTIMICROBIAL RESISTANCE GENES

Figure 1: Resistance genes detected in genome sequencing data



GENOME SEQUENCING REPORT

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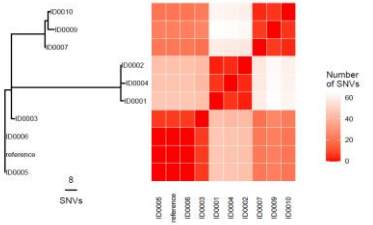
PHYLOGENETIC CLUSTERING ANALYSIS

The overall tree was conducted 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.



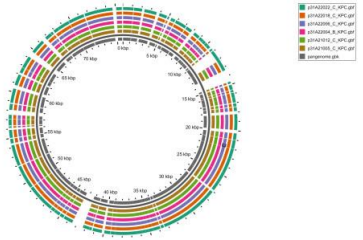
PLASMID PANGENOMES

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 CDSs are identical except for two IS3 family transposases from 10.7 kb - 12.1 kb in 31A22CPO022.

The pangenome of the bla_{KPC-3}-encoding IncN plasmids in cluster002 are shown in Figure 5. Plasmid CDSs are identical except for a 10 kb island from 27.5 - 38 kb containing duplicates of *folP*, *emrE*, *pspF*, and *yghA* found in 31A22CPO002 and 31A22CPO017.

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



GENOME SEQUENCING REPORT

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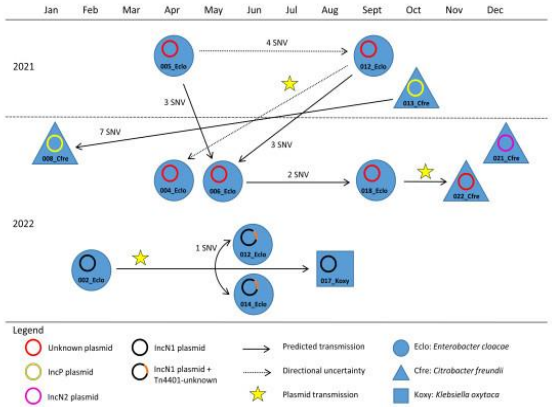
PREDICTED TRANSMISSION

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

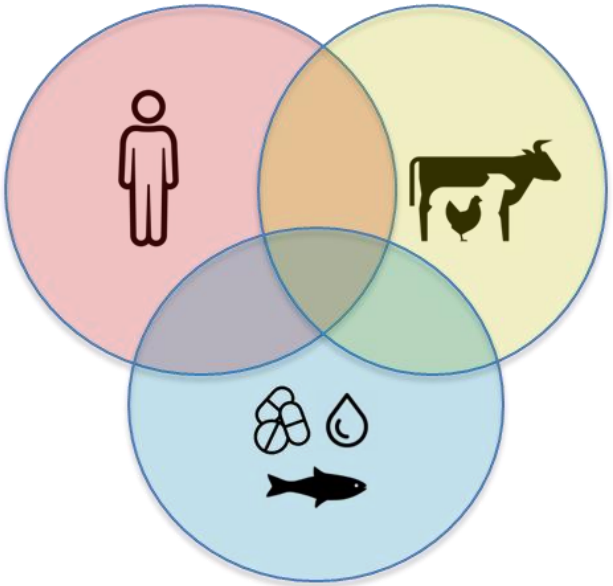
Overview

- Life in the Antimicrobial Resistance and Nosocomial Infections Unit (ARNI)
- AMR Surveillance
- Genomics
- New AMR Surveillance Initiatives

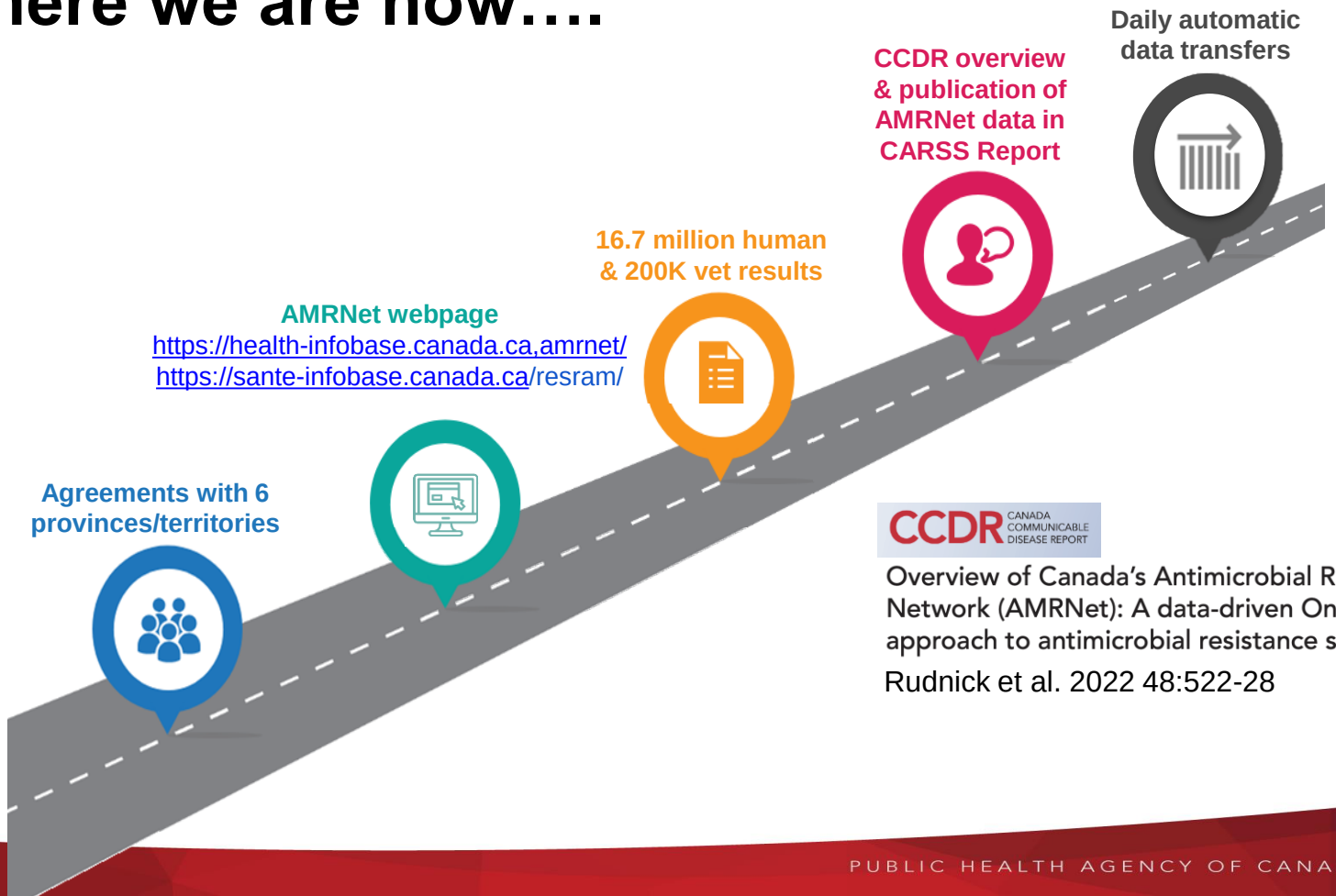
AMR Net

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….

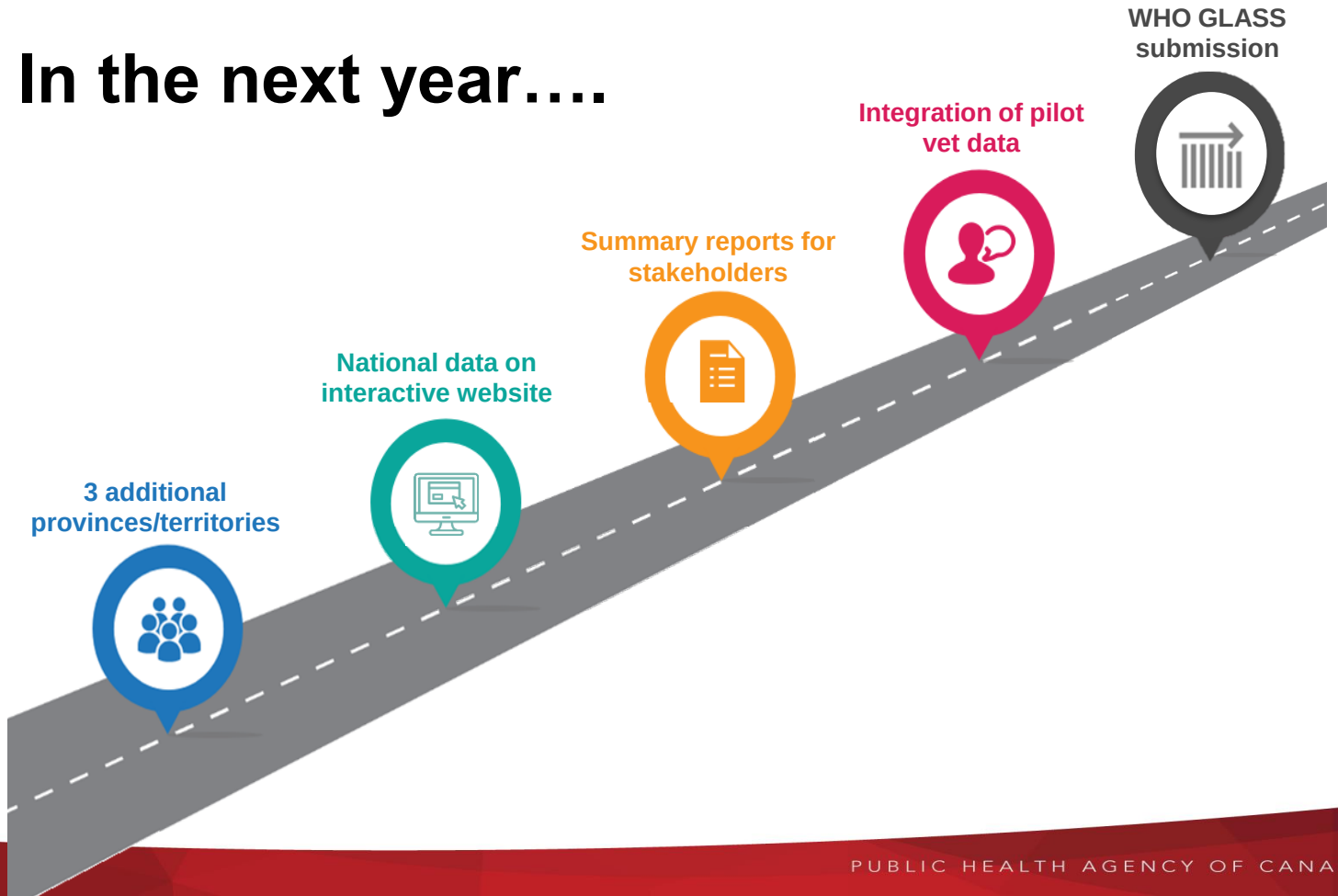


CCDR CANADA COMMUNICABLE DISEASE REPORT

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….



Mock Data

Antimicrobial Susceptibilty Testing Summary

PHAC AMRNet

08 March, 2023

E. coli

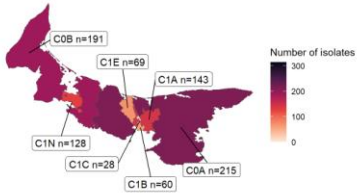
Please note that duplicates have been removed for all analyses presented here. Between 2016 and 2021, data on 10,000 *E. coli* isolates were submitted and included in the analysis below.

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

mmary reports for stakeholders

Integration of pilot vet data

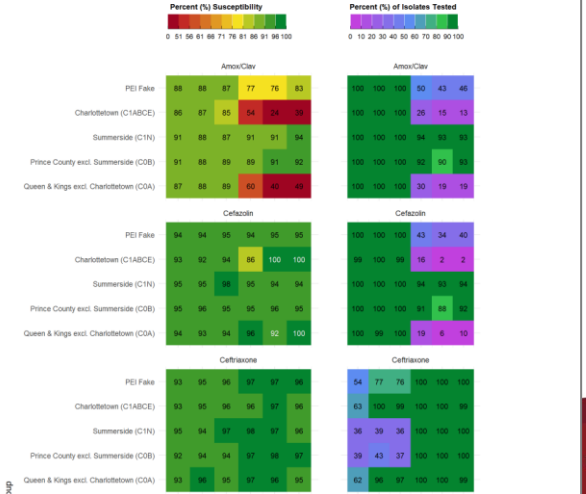
WHO GLASS submission

Mock 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.

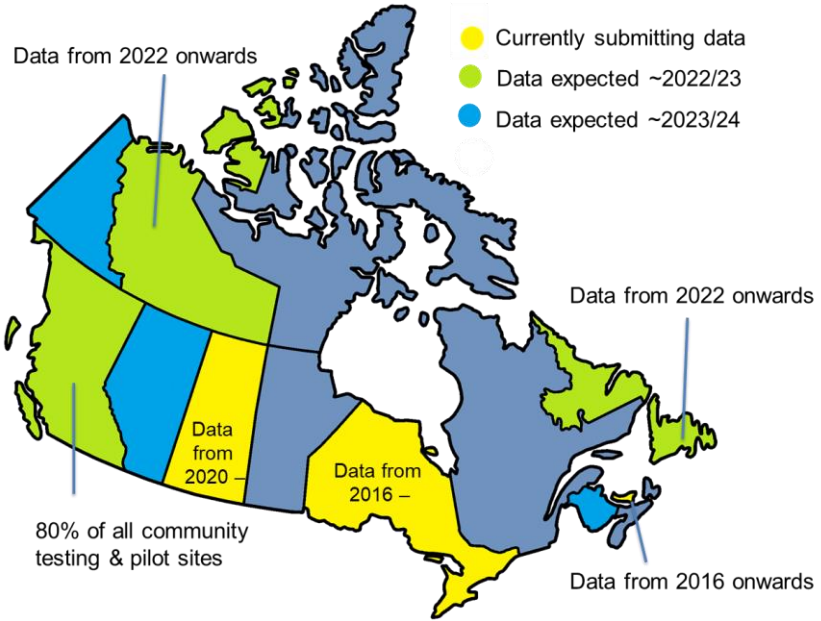
Number of isolates by FSA | Urine (all) | Urine (Inpatient and Outpatient) | Blood | All source

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.



Summary

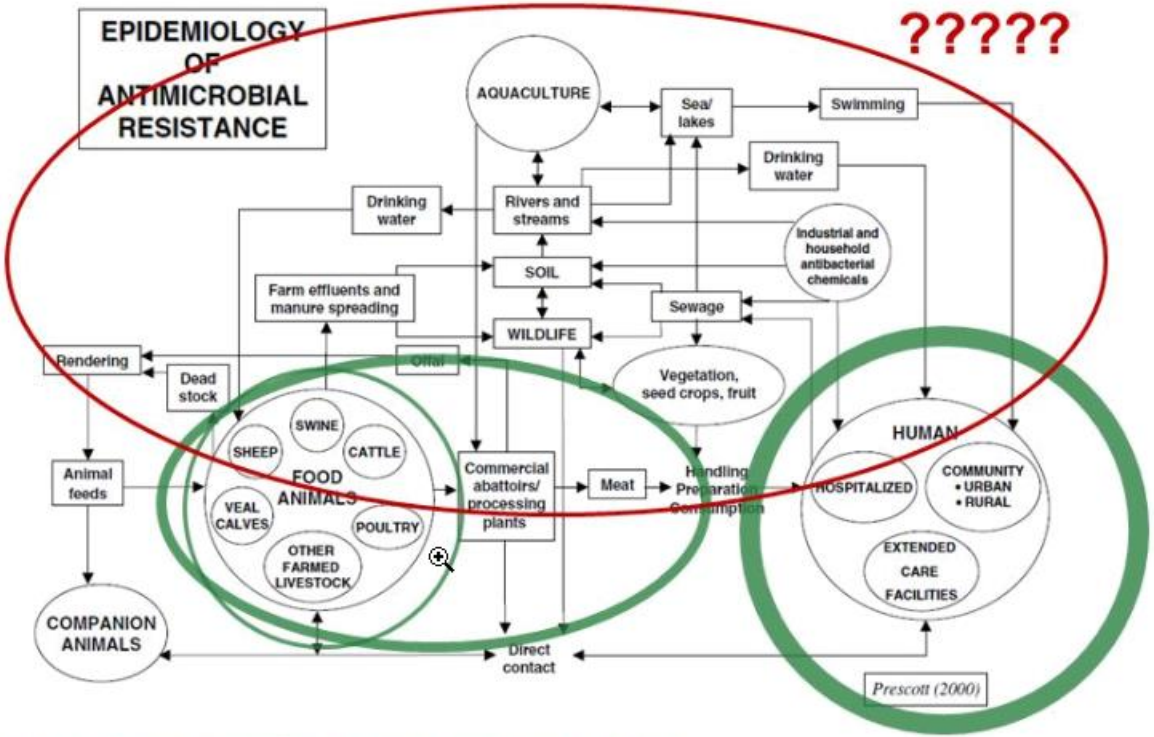
- Early days
- Stable long-term funding
- Very positive responses and early support at FTP level
- Pilot: SES factors collaboration with StatCan and SK
- Data sharing/requests:
  - Human: WHO GLASS, PHAC programs (CARSS, CNISP), Non-profit
  - Vet: CIPARS, industry-affiliated network
- AMRNet Vet pilots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



The “One-Health” AMR Model

http://www.phac-aspc.gc.ca/owoh-umus/index-eng.php

The 'Confusogram'

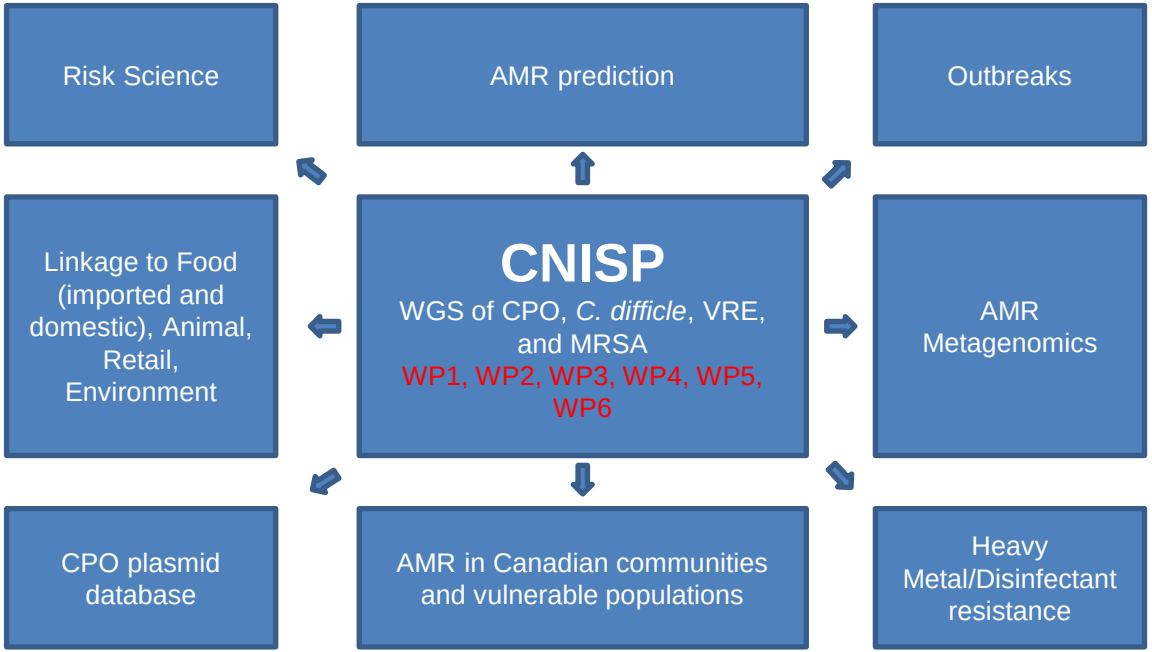


J. F. Prescott *et al.* (2000) Antimicrobial Therapy in Veterinary Medicine

Genomics Research Development Initiative (GRDI)

- 5 year funded interdepartmental shared priority project on AMR
- PHAC, AAFC, CFIA, DFO, ECCC
- 6 work packages to assess the dissemination of priority AMR pathogens affecting human and animal health across the farm to fork to clinic continuum

GRDI AMR2 CNISP Contributions



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, intl1, 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

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