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 Soulhine)
- *Streptococcus pneumoniae*
- *Streptococcus pyogenes*
- Typhoidal and non-typhoidal *Salmonella enterica*
- *Acinetobacter* species
- *Campylobacter* species
- *Escherichia coli*

Overview

• Life in the Antimicrobial Resistance and Nosocomial Infections Unit (ARNI)

• AMR Surveillance
  • Genomics
  • New AMR Surveillance Initiatives
Canadian Nosocomial Infection Surveillance Program (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
Current CNISP Surveillance Projects

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

- 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

https://www.cdc.gov/hai/organisms/cdiff/cdiff_infect.html
*Clostridioides difficile* infection (CDI)

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

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

- **Healthcare-associated CDI**
  - 24%

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

**Rate per 10,000 Patient Days**

- Healthcare-associated
- Community-associated

**Attributable Mortality per 100 Cases**

- 2016: 2.5
- 2017: 2.5
- 2018: 1.0
- 2019: 2.5
- 2020: 2.5
- 2021: 2.5
Changing Molecular Epidemiology of *C. difficile* 2007-2021

![Bar chart showing the distribution of NAP1, NAP2, NAP4, and NAP11 from 2007 to 2021.](image)

Declining Fluoroquinolone Resistant Strain Types and Emerging Susceptible Types

- **NAP1**: 88.4%
- **NAP2**: 76.1%
- **NAP4**: 4.7%
- **NAP11**: 3.7%

**MoxR**

Data distribution by year:
- 2007-2009 (n=1344)
- 2010-2012 (n=1459)
- 2013-2015 (n=1889)
- 2016-2018 (n=2432)
- 2019-2021 (n=1802)
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)

- 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

Rate per 10,000 Patient Days

<table>
<thead>
<tr>
<th>Year</th>
<th>Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>2016</td>
<td>0.15</td>
</tr>
<tr>
<td>2017</td>
<td>0.2</td>
</tr>
<tr>
<td>2018</td>
<td>0.3</td>
</tr>
<tr>
<td>2019</td>
<td>0.3</td>
</tr>
<tr>
<td>2020</td>
<td>0.3</td>
</tr>
<tr>
<td>2021</td>
<td>0.35</td>
</tr>
</tbody>
</table>

VRE all-cause mortality

<table>
<thead>
<tr>
<th>Year</th>
<th>Mortality</th>
</tr>
</thead>
<tbody>
<tr>
<td>2016</td>
<td>31%</td>
</tr>
<tr>
<td>2017</td>
<td>31%</td>
</tr>
<tr>
<td>2018</td>
<td>28%</td>
</tr>
<tr>
<td>2019</td>
<td>36%</td>
</tr>
<tr>
<td>2020</td>
<td>37%</td>
</tr>
</tbody>
</table>
Vancomycin Resistant Enterococci (VRE) bloodstream infection (BSI)

Increasing Antimicrobial Resistance Trends in VRE

% Resistant

<table>
<thead>
<tr>
<th>Year</th>
<th>Tetracycline</th>
<th>HL Gentamicin</th>
<th>Chloramphenicol</th>
<th>Daptomycin</th>
</tr>
</thead>
<tbody>
<tr>
<td>2009-2011</td>
<td>0.0%</td>
<td>0%</td>
<td>10.0%</td>
<td>0.0%</td>
</tr>
<tr>
<td>2012-2014</td>
<td>10.0%</td>
<td>20.0%</td>
<td>30.0%</td>
<td>5.0%</td>
</tr>
<tr>
<td>2015-2017</td>
<td>20.0%</td>
<td>40.0%</td>
<td>50.0%</td>
<td>10.0%</td>
</tr>
<tr>
<td>2018-2020</td>
<td>30.0%</td>
<td>50.0%</td>
<td>60.0%</td>
<td>15.0%</td>
</tr>
</tbody>
</table>

(n=157) (n=217) (n=282) (n=451)*
CNISP Surveillance of MRSA bloodstream infection (BSI)

- 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

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

<table>
<thead>
<tr>
<th>Year</th>
<th>Healthcare-associated</th>
<th>Community-associated</th>
</tr>
</thead>
<tbody>
<tr>
<td>2016</td>
<td>0.43</td>
<td>0.15</td>
</tr>
<tr>
<td>2017</td>
<td>0.45</td>
<td>0.16</td>
</tr>
<tr>
<td>2018</td>
<td>0.47</td>
<td>0.18</td>
</tr>
<tr>
<td>2019</td>
<td>0.49</td>
<td>0.20</td>
</tr>
<tr>
<td>2020</td>
<td>0.51</td>
<td>0.22</td>
</tr>
<tr>
<td>2021</td>
<td>0.53</td>
<td>0.24</td>
</tr>
</tbody>
</table>

**All-Cause Mortality**

<table>
<thead>
<tr>
<th>Year</th>
<th>Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>2016</td>
<td>20</td>
</tr>
<tr>
<td>2017</td>
<td>18</td>
</tr>
<tr>
<td>2018</td>
<td>18</td>
</tr>
<tr>
<td>2019</td>
<td>18</td>
</tr>
<tr>
<td>2020</td>
<td>18</td>
</tr>
<tr>
<td>2021</td>
<td>18</td>
</tr>
</tbody>
</table>
National Distribution of Select Canadian MRSA Epidemic Strains from Bacteremia Cases (CNISP, 1995-2021)

<table>
<thead>
<tr>
<th>CMRSA1</th>
<th>CMRSA2 (USA100/800)</th>
<th>CMRSA3/6</th>
<th>CMRSA7 (USA400)</th>
<th>CMRSA10 (USA300)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.00%</td>
<td>10.00%</td>
<td>20.00%</td>
<td>30.00%</td>
<td>40.00%</td>
</tr>
</tbody>
</table>

- **CMRSA1**: 0.00% distribution
- **CMRSA2 (USA100/800)**: 10.00% distribution
- **CMRSA3/6**: 20.00% distribution
- **CMRSA7 (USA400)**: 30.00% distribution
- **CMRSA10 (USA300)**: 40.00% distribution

**Yearly Distribution**:
- **1995-1999**: n=168
- **2000-2004**: n=339
- **2005-2009**: n=927
- **2010-2014**: n=1465
- **2015-2021**: n=3463
Trends in MRSA AMR

Percentage of Isolates

Erythromycin
Ciprofloxacin
Clindamycin
Tetracycline
Trimethoprim/ Sulfamethoxazole
MRSA CLD Resistance and Usage

2021 data are preliminary / Les données de 2021 sont préliminaires

% of isolates / % d’isolats

- CMRSA2
- CMRSA10
- CMRSA7
- USA1100

Legend:
- t002 n=497
- t008 n=1275
- t024 n=115
- t574 n=75
- t1508 n=227
- t128 n=57
- t019 n=83

Bar chart showing the percentage of isolates resistant to clindamycin from 2009 to 2020.
CNISP surveillance of Carbapenemase-producing *Enterobacterales* (CPE)

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

Stephanie Rossow, Centers for Disease Control and Prevention/Antibiotic Resistance Coordination & Strategy Unit
CPE infection and colonization rates, 2010-2021

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

Total Carbapenemase Producing Enterobacterales 2010-2021

All Carbapenemases Reported 2010-2021

- KPC
- NDM
- OXA-48
- NDM,OXA-48
- SME
- VIM
- GES
- NMC/IMI
- IMP
- Other
• Similar to some Provincial reports there is a decline in *E.coli*
A multispecies outbreak report

The Major Challenge IPC of CPOs

Species

<table>
<thead>
<tr>
<th>Kp</th>
<th>Ecl</th>
<th>Ec</th>
<th>Cit</th>
<th>Ko</th>
<th>Ka</th>
</tr>
</thead>
<tbody>
<tr>
<td>○</td>
<td>□</td>
<td>△</td>
<td>□</td>
<td>△</td>
<td>○</td>
</tr>
</tbody>
</table>

Plasmids

- FII(K)
- UK-3
- N
- I/M, P
- UK-1
- UK-2
- UK-4

Direct link
Indirect link
Plasmid transfer event

Jan 2014  Mar  | June | July | Sept | Oct | Nov | Dec | Jan 2015

H 12  11  0 0  R  0  0  D  3  3  6  6  C
F  D  D  2  6  0  0  C
D  D  D  D  6  2  1  1  A
G  J  K  K  0  0  0  1  1  1  B
M  N  N  4  35  1  ▲  ▲  ▲
CPE in Canada: CPHLN Data. L. Mataseje

Colonizations and infections

(n=10265)

<table>
<thead>
<tr>
<th>Year</th>
<th>Total number</th>
</tr>
</thead>
<tbody>
<tr>
<td>2008</td>
<td>4</td>
</tr>
<tr>
<td>2009</td>
<td>4</td>
</tr>
<tr>
<td>2010</td>
<td>63</td>
</tr>
<tr>
<td>2011</td>
<td>128</td>
</tr>
<tr>
<td>2012</td>
<td>117</td>
</tr>
<tr>
<td>2013</td>
<td>148</td>
</tr>
<tr>
<td>2014</td>
<td>204</td>
</tr>
<tr>
<td>2015</td>
<td>389</td>
</tr>
<tr>
<td>2016</td>
<td>764</td>
</tr>
<tr>
<td>2017</td>
<td>906</td>
</tr>
<tr>
<td>2018</td>
<td>1234</td>
</tr>
<tr>
<td>2019</td>
<td>1474</td>
</tr>
<tr>
<td>2020</td>
<td>1243</td>
</tr>
<tr>
<td>2021</td>
<td>1470</td>
</tr>
<tr>
<td>2022</td>
<td>2117</td>
</tr>
</tbody>
</table>
CIPARS: Carbapenemase Surveillance
Drs. Amrita Bharat and Audrey Charlebois

- Only Canadian animal case S. London IMP-64 clinical pig isolates MB (2016)

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

<table>
<thead>
<tr>
<th>Gene Description</th>
<th>Speciation</th>
<th>n</th>
<th>Origin of sample (n)</th>
<th>Sample Types</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\text{bla}_{\text{NMC}}$</td>
<td>$\text{Enterobacter cloaceae}$</td>
<td>2</td>
<td>Vietnam (2); Bangladesh (1)</td>
<td>CIPARS retail shrimp n=832</td>
</tr>
<tr>
<td>$\text{bla}_{\text{VCC}}$</td>
<td>$\text{Enterobacter aerogenes}$</td>
<td>1</td>
<td>Bangladesh (1)</td>
<td></td>
</tr>
<tr>
<td>$\text{bla}<em>{\text{NDC}, \text{bla}</em>{\text{TEM}}, \text{bla}<em>{\text{OXA-1}}, \text{bla}</em>{\text{NMC}}}$</td>
<td>$\text{Vibrio cholerae}$</td>
<td>2</td>
<td>India (2)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>$\text{Enterobacter cloaceae}$</td>
<td>3</td>
<td>Vietnam (3)</td>
<td>Clams n=101</td>
</tr>
</tbody>
</table>

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

CDC warns of "alarming" rise of potentially deadly fungal threat in hospitals

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

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 \textit{C. auris} cases in Canada, 2012-2022

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**

<table>
<thead>
<tr>
<th>Status</th>
<th># cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>No travel</td>
<td>4</td>
</tr>
<tr>
<td>HC in Hong Kong</td>
<td>1</td>
</tr>
<tr>
<td>HC in India</td>
<td>3</td>
</tr>
<tr>
<td>Migrated from India</td>
<td>1</td>
</tr>
<tr>
<td>HC in South Africa</td>
<td>1</td>
</tr>
<tr>
<td>HC in USA (Florida)</td>
<td>2</td>
</tr>
<tr>
<td>HC in USA (Nevada)</td>
<td>1</td>
</tr>
</tbody>
</table>

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

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**
Overview

• Life in the Antimicrobial Resistance and Nosocomial Infections Unit (ARNI)

• AMR Surveillance

• Genomics

• New AMR Surveillance Initiatives
The Transition to Whole Genome Sequencing

Whole Genome Sequencing

Predict Antimicrobial Susceptibility

Predict Molecular Typing

Virulence Traits

PUBLIC HEALTH AGENCY OF CANADA >
This tree is made up of the first 100 MRSA CMRSA10 t008’s identified in 2021. SNV differences ranged from 1-352.
Evidence of both intrahospital and regional interhospital spread.

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

Genomics Clinical Diagnostics

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

S.W. Peterson, W. Demczuk, I. Martin, H. Adam, A. Bharat, M.R. Mulvey
ARNI Nosocomial Outbreak Reports

Collaboration with Dr. Hoang BCCDC
Overview

- Life in the Antimicrobial Resistance and Nosocomial Infections Unit (ARNI)

- AMR Surveillance

- Genomics

- New AMR Surveillance Initiatives
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....

Agreements with 6 provinces/territories

AMRNet webpage
https://health-infobase.canada.ca/amrnet/
https://sante-infobase.canada.ca/resram/

16.7 million human & 200K vet results

CCDR overview & publication of AMRNet data in CARSS Report

Daily automatic data transfers

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....

- National data on interactive website
- Summary reports for stakeholders
- Integration of pilot vet data
- 3 additional provinces/territories
- WHO GLASS submission
National data on interactive website
3 additional provinces/territories

In the next year….

Summary reports for stakeholders
Integration of pilot vet data
WHO GLASS submission

Mock Data

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 10,500 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 PSA

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

Pseudomonas

Please note that duplicates have been removed for all analyses presented here. Between 2016 and 2021, data on 10,500 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 PSA

Mock Data
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

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

- Risk Science
- Linkage to Food (imported and domestic), Animal, Retail, Environment
- CPO plasmid database
- AMR prediction
- Outbreaks
- AMR Metagenomics
- Heavy Metal/Disinfectant resistance

CNISP
- WGS of CPO, *C. difficile*, VRE, and MRSA
- WP1, WP2, WP3, WP4, WP5, WP6

AMR in Canadian communities and vulnerable populations

AMR prediction

Outbreaks
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
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• CANWARD

• The Canadian Public Health Laboratory Network

• Canadian Animal Health Laboratory Network

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