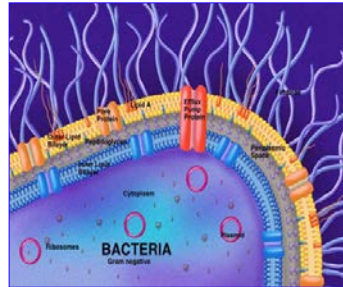
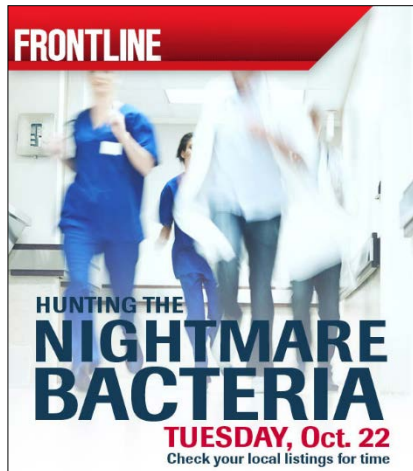
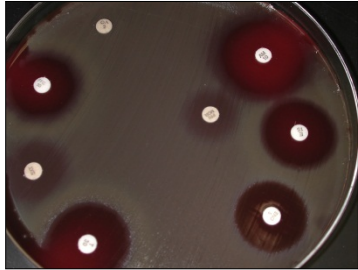


# Can We Build the Perfect One Health AMR Intersection



# 2017 NIAA Antibiotic Symposium

- **What are the Major Gaps in Knowledge or Translation?**
- **How Do We Find the Answers to What We Don't Know?**

# 2017 NIAA Antibiotic Symposium

- **What are the Major Gaps in Knowledge or Translation?**

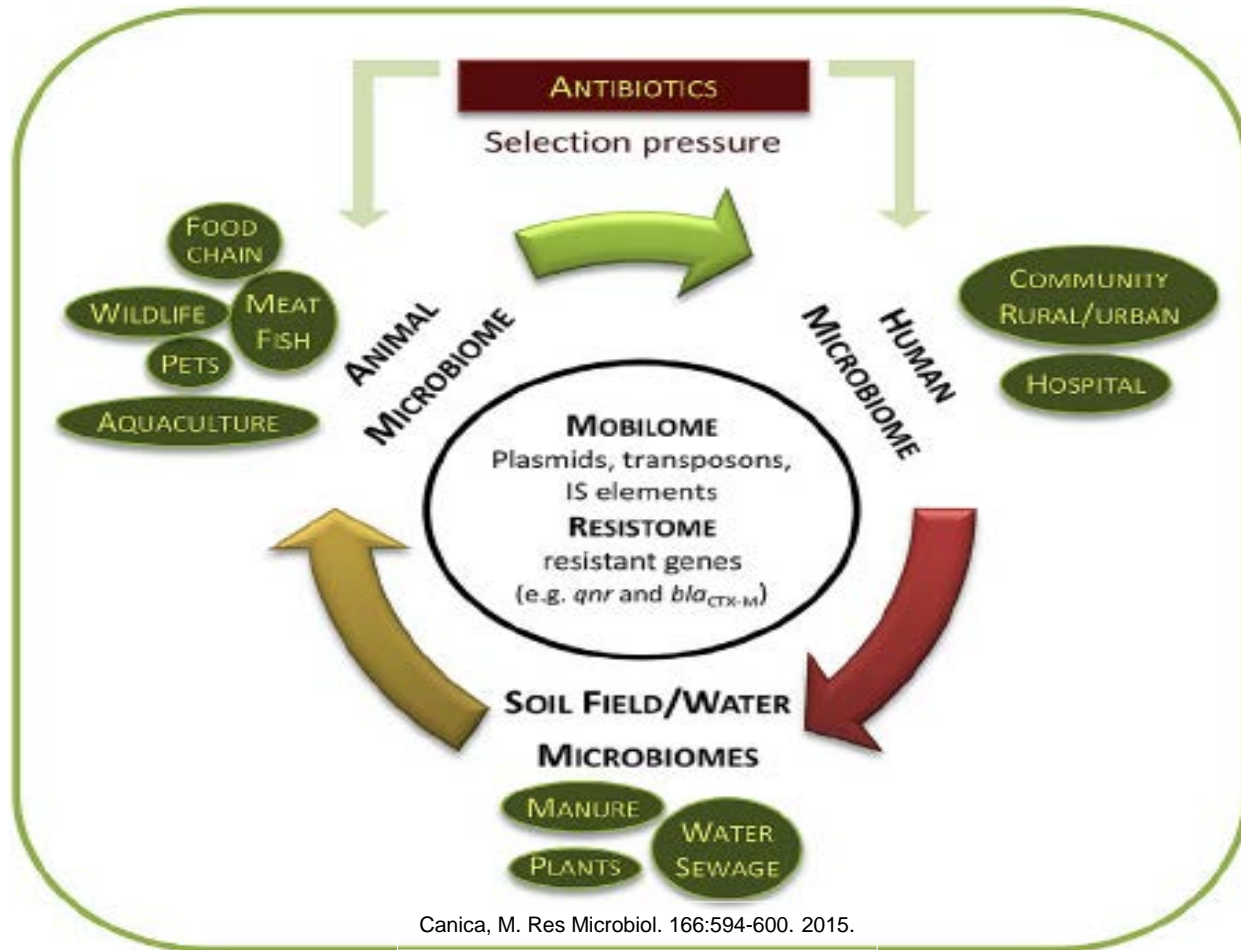
# The Antimicrobial Resistome

The resistome comprises **all** the antimicrobial resistance genes and their precursors in pathogenic and non-pathogenic bacteria (including antibiotic-producing bacteria)

ancient, diverse and widespread

Wright, G. 2007. Nature Reviews Microbiol. 5:175-186.

# Genes Move Laterally Through the Resistome



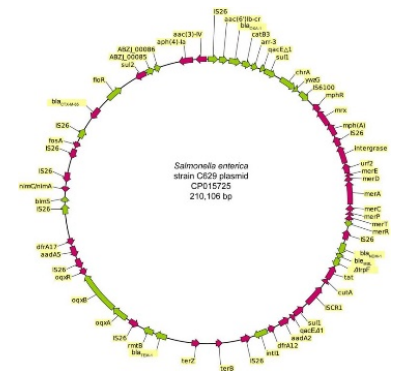
AMR genes do not respect boundaries

Very large gene pool

Canica, M. Res Microbiol. 166:594-600. 2015.

# Major Gaps

- How do resistance mechanisms evolve over time?
  - Origins of resistant genes/organisms
    - Resistome
  - Diverse selection pressures (heavy metals, disinfectants, other)
  - Establishment and sustainability
- How is resistance transferred and how often
  - Mobile elements (plasmids, transposons, integrons)
    - Mobilome
  - Gene linkage (chimeras)



# Major Gaps

- What is the contribution of the normal microbiomes to antimicrobial resistance?
  - Disruption consequences
  - Return of susceptible populations
  - Innocent bystanders
- What factors contribute to the selection and dissemination of resistant microbes
  - Appropriate PK/PD parameters
    - Dose, frequency of dose, route of administration, duration
    - Optimize therapy while minimizing resistance development
  - Organism and host factors

# Major Gaps

- How important is the environmental dimension of antimicrobial resistance?
  - Anthropogenic impacts in soil and water
  - What can be done?
- What are the niches where pathogens and environmental organisms co-exist
  - What drives gene exchange in the environment?
  - Are there bottlenecks or can we create ones to prevent gene transfer
    - CTX-M beta-lactamases in *Kluyvera*
    - qnr genes in waterborne *Vibrio*, *Shewanella* and *Aeromonas*



# 2017 NIAA Antibiotic Symposium

- **How Do We Find the Answers to What We Don't Know?**

# Finding Answers

- **Strengthen the Knowledge base**
  - **Identify and prioritize data gaps**
    - **Research, stewardship, infection prevention and control, diagnostics, product development, alternatives, integrated surveillance, education/outreach, national policy and guidance, risk analysis**
    - **Share and align priorities where possible**
  - **Publish findings to various audiences in a timely manner**
  - **Use data to formulate science based public health policy**
    - **Develop metrics for success**
    - **Reevaluate over time**
  - **Seek international harmonization and coordination where possible**
  - **Coordinate and direct resources collaboratively**

# Finding Answers

- **Create strategic public-private partnership(s) and coordinated road maps**
  - Bridge different sectors and disciplines – gather and integrate information
  - Strengthen partnerships and leverage resources
    - Academia
    - Industry
    - Federal government
    - Professional organizations
    - Consumer advocacy organizations
    - Citizens
  - Global consortiums where appropriate
  - Develop funding mechanisms
  - Action plans – **move knowledge to implementation**

# Building a One Health AMR Prevention Intersectoral



The Future is Round



Real. Life. Solutions.™