Using Clinical Data to Create a Regional One Health AR Surveillance Database

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ne Health Research

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Meeting Regional Surveillance Needs

Develop integrated antimicrobial resistance (AR) surveillance to encompass:

- Multi-sectorial: human, animal, environmental
- Geographic region-specific

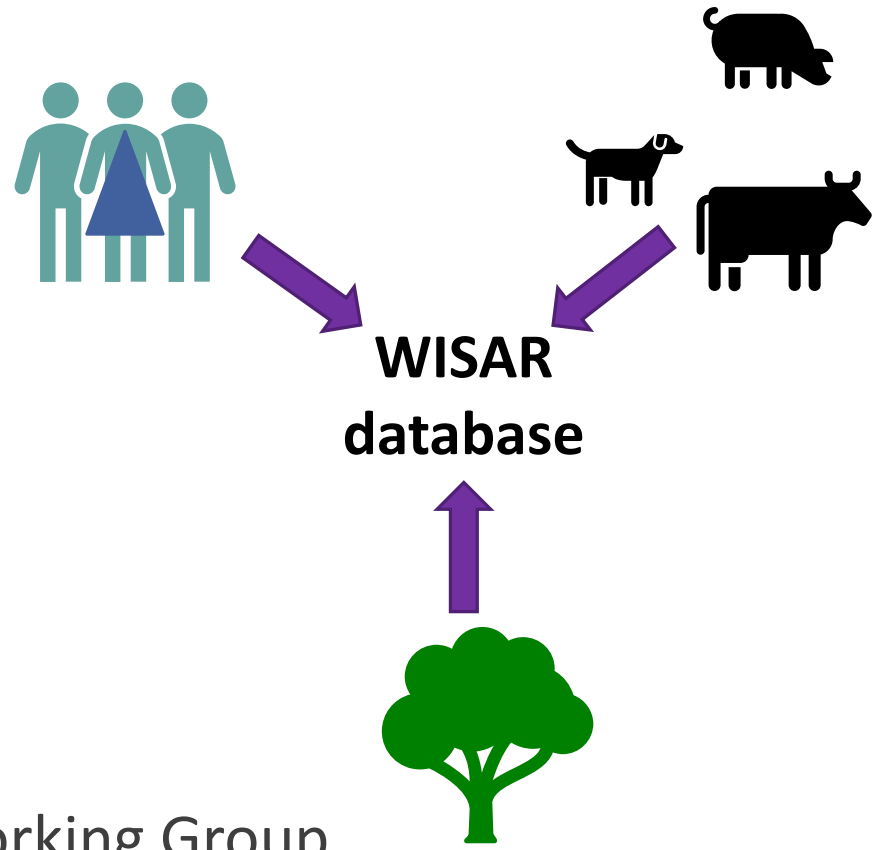
Purpose:

- Detect trends of emerging resistance
- Support local clinical stewardship efforts
- Support shared stewardship activities across sectors

While national data on AMR is useful, there is a need for region specific data. Collecting and interpreting these data provides an opportunity for collaboration and shared stewardship efforts between human, animal, and environmental health professionals. While it is important to detect trends of emerging resistance, it is also important to provide useful tools for antimicrobial stewardship across sectors.

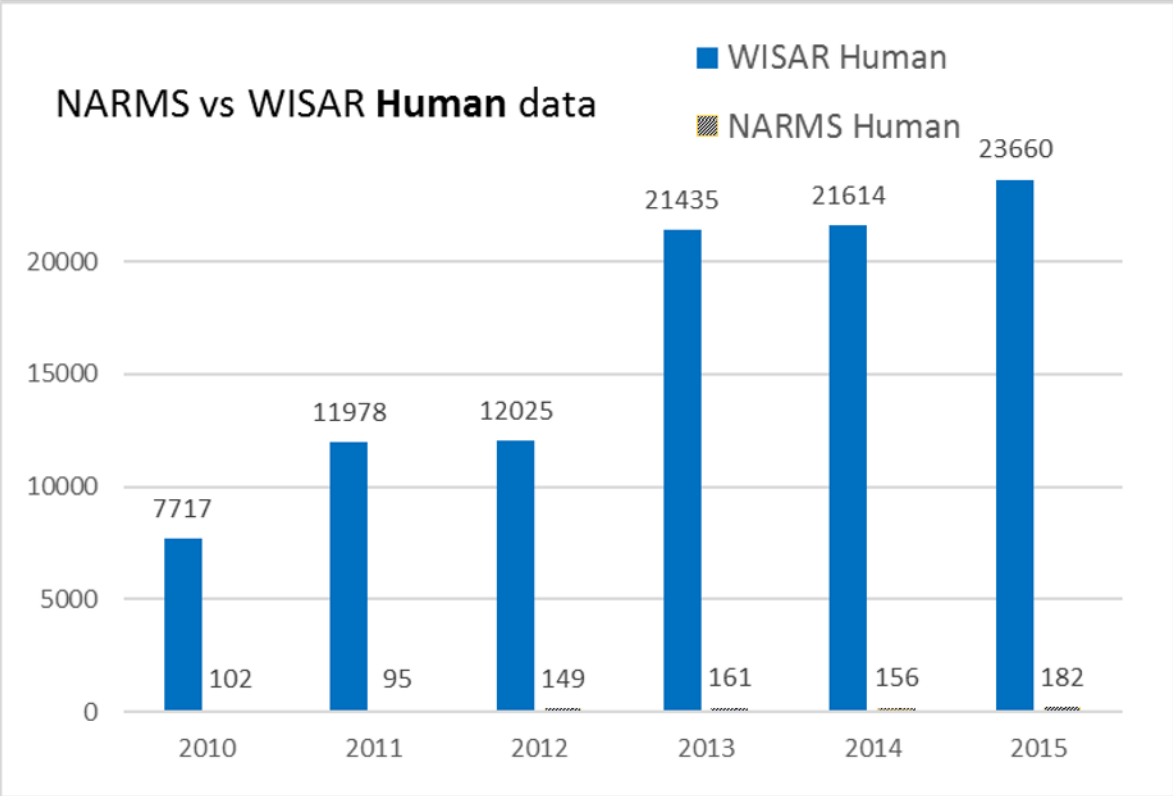
The Washington Integrated Surveillance for AMR (WISAR) Approach

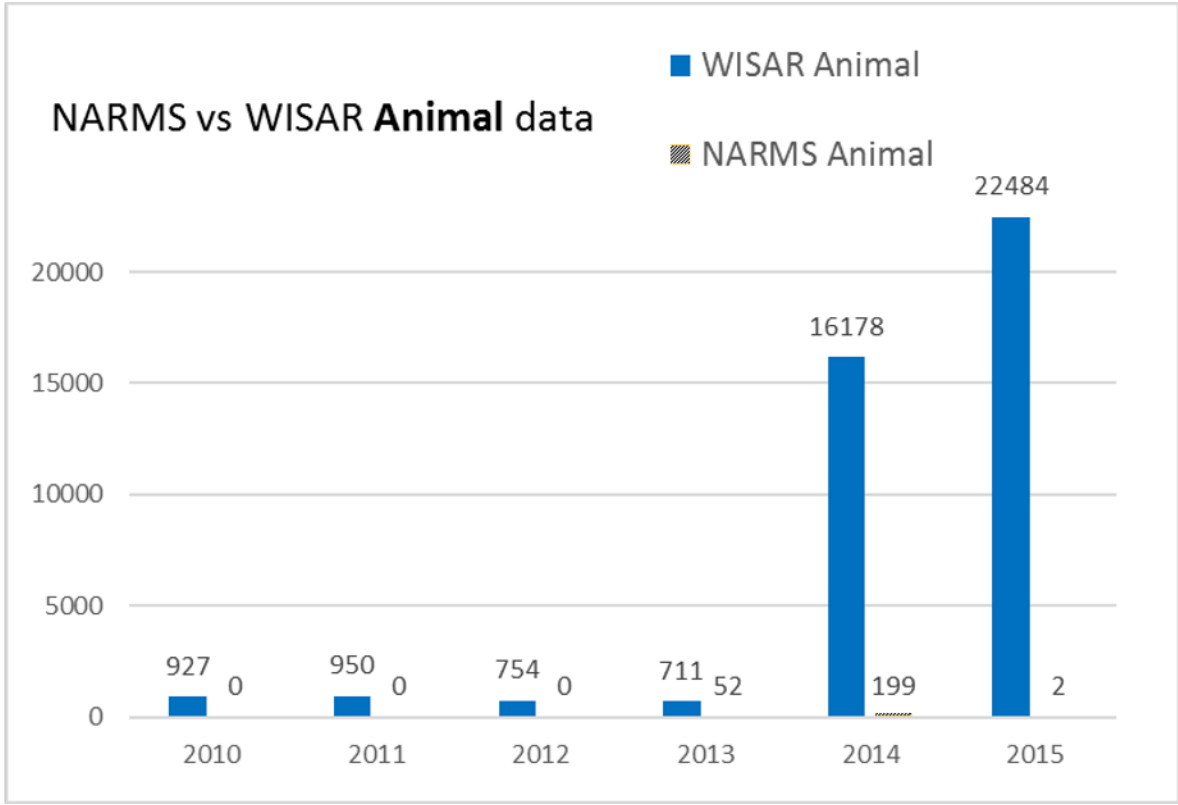
- Existing clinical isolate data from:
  - State NARMS surveillance
  - Hospitals
  - Human and veterinary clinical labs
  - Washington Animal Disease Diagnostic Lab (WADDL)
- Voluntary participation
- De-identification of patient and facility information
- Oversight by statewide One Health AMR Stewardship Working Group



The Washington Integrated Surveillance for AMR (WISAR) database project is a regional and ongoing voluntary effort to access and utilize existing clinical data, with oversight by a multidisciplinary statewide One Health stewardship working group.

Volume of Clinical AMR Data Exceeds NARMS





The WISAR database includes data from 2002-2017. These figures show differences between isolate counts between WISAR and NARMS across a subset of years: 2010-2015. In Washington State, the volume of clinical AR susceptibility testing data in both humans and animals is much greater than that from the NARMS surveillance system.

Challenges: Integrating Human and Animal Data

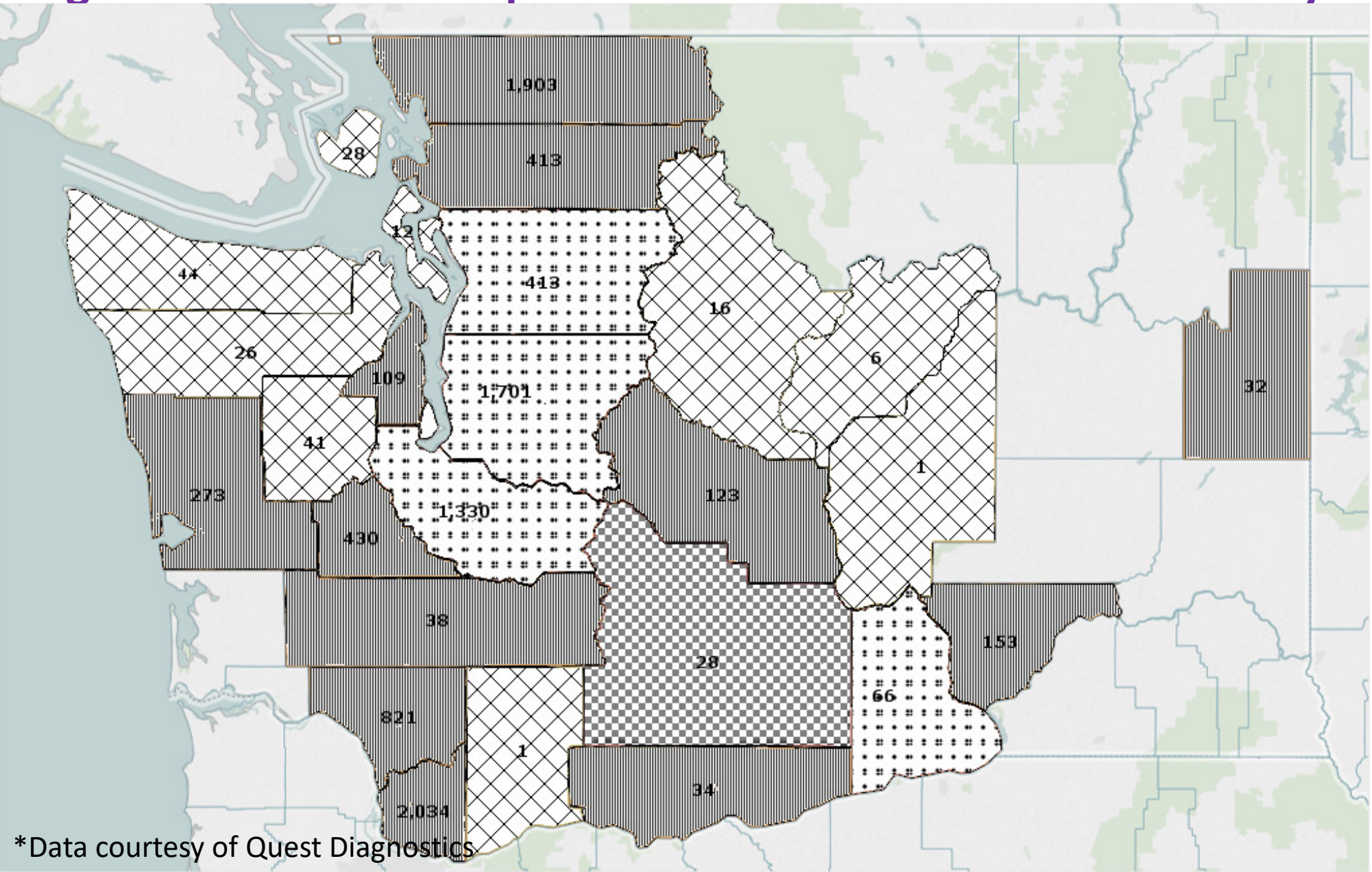
- Different antibiotics used in humans and animals
  - Ceftriaxone vs. ceftiofur
  - Ciprofloxacin vs. enrofloxacin
- Difficulty harmonizing antibiotic susceptibility breakpoints
  - Breakpoint variability across time and species
  - Qualitative vs. quantitative results
- Confidentiality and IRB concerns
- Data integration:
  - How to compare, analyze, display and interpret findings?

Class representatives vary between species and may have different in vitro characteristics on susceptibility testing

Breakpoints have been revised over time and as a results, older data may not be comparable to newer data.

While it is important to look at actual clinical data, there is an ongoing need for caution in interpretation of results.

Regional Variation of Ciprofloxacin Resistance: Human Urinary *E. coli* 2016



Quest Diagnostics™

% Resistance to CIP
- 0%
- 1-5%
- 5-10%
- 15-20%

n= numbers of isolates tested per county

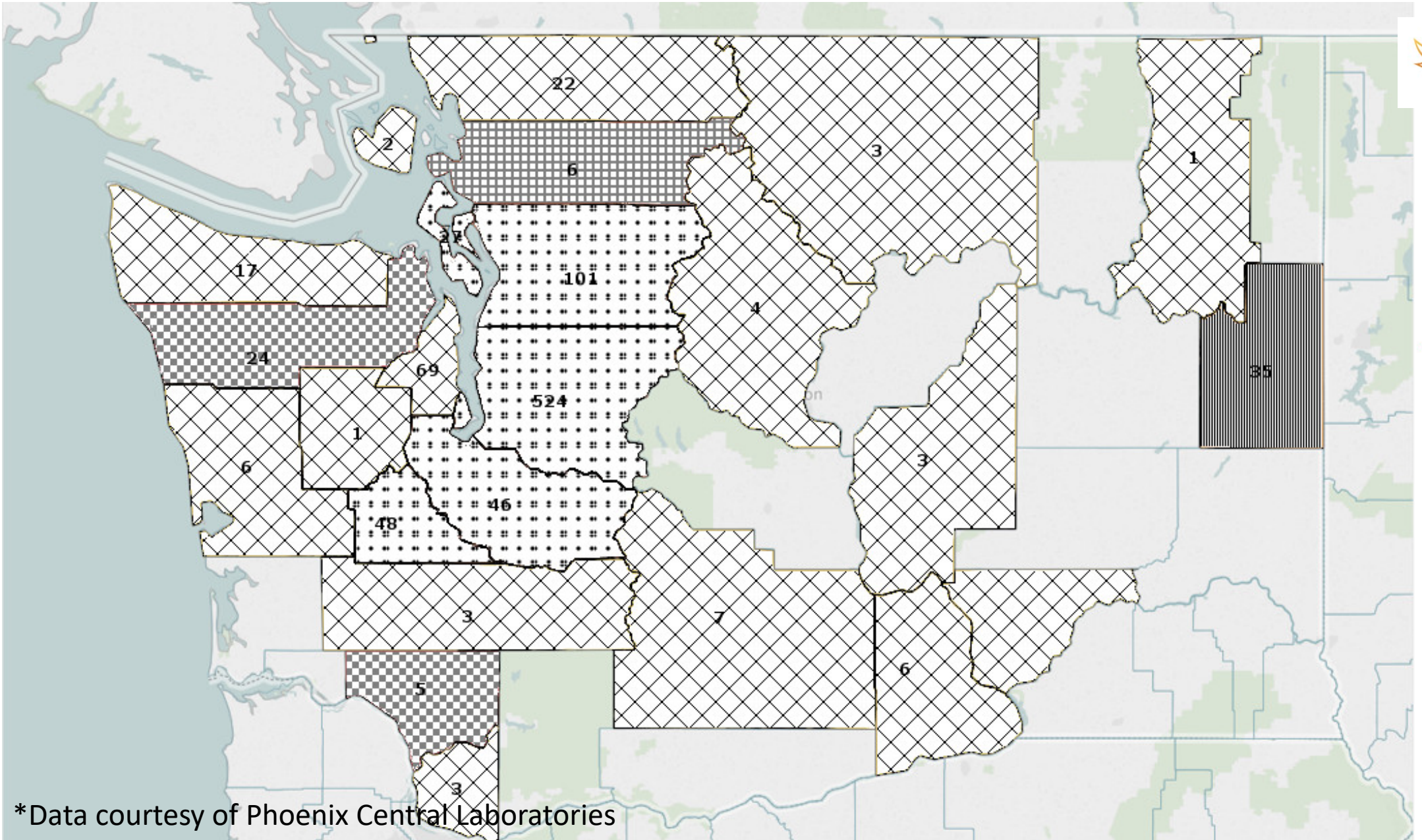
*Data courtesy of Quest Diagnostics

Washington State map of ciprofloxacin AST results: E. coli

Data source: Quest Laboratories

This is an example of how outpatient clinical laboratory data can be used to create “community antibiograms” to guide antimicrobial stewardship.

Regional Variation of Enrofloxacin Resistance: Canine Urinary *E. coli* 2016



PHOENIX LAB Excellence in Veterinary Science & Service

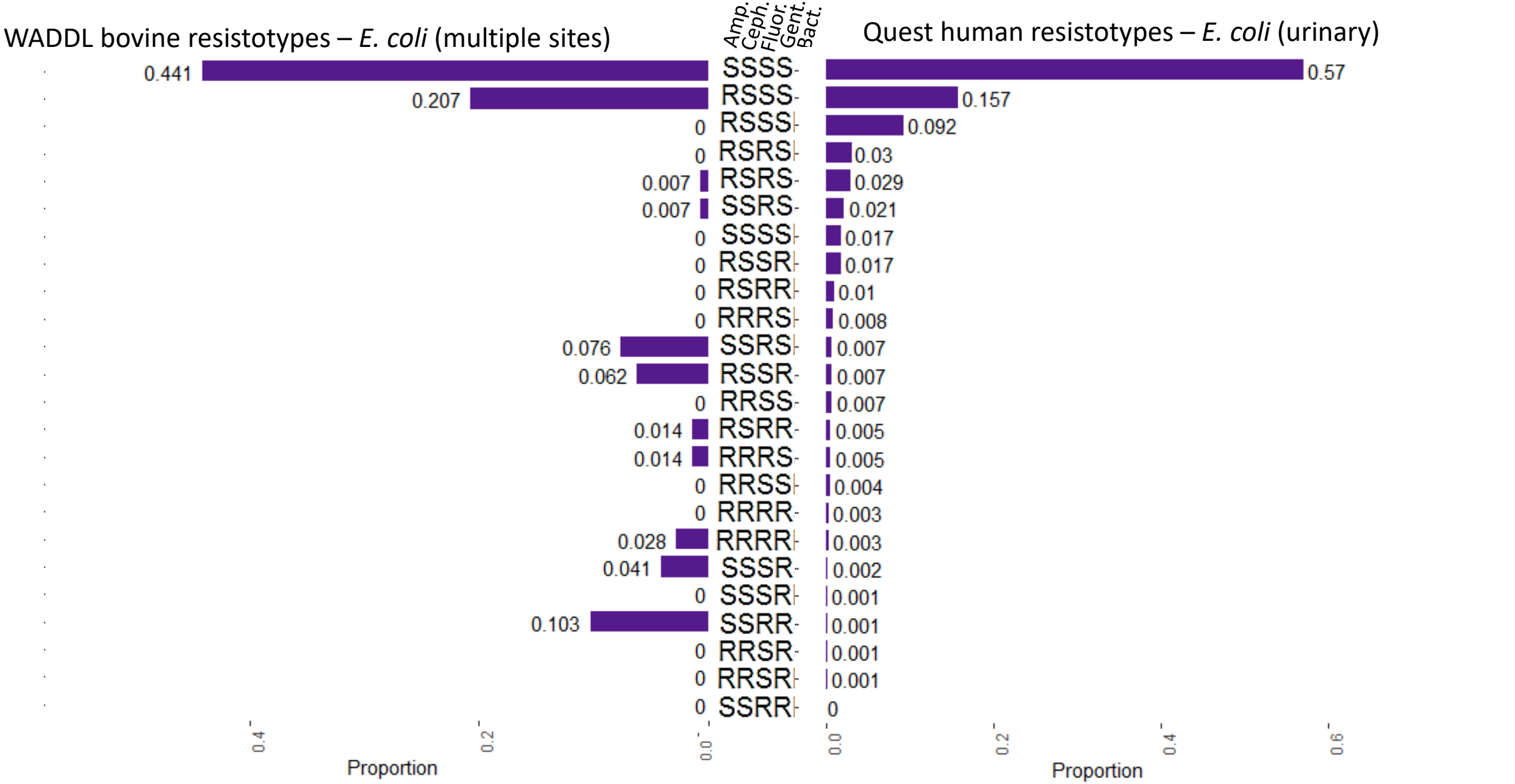
% Resistance to ENR
- 0%
- 1-5%
- 5-10%
- 15-30%
- >30%

n= numbers of isolates tested per county

*Data courtesy of Phoenix Central Laboratories

This is an example of how veterinary clinical laboratory data from animals can be used to create “community antibiograms” to guide veterinary antimicrobial stewardship.

Phenotypic variation between bovine and human *E.coli* isolates



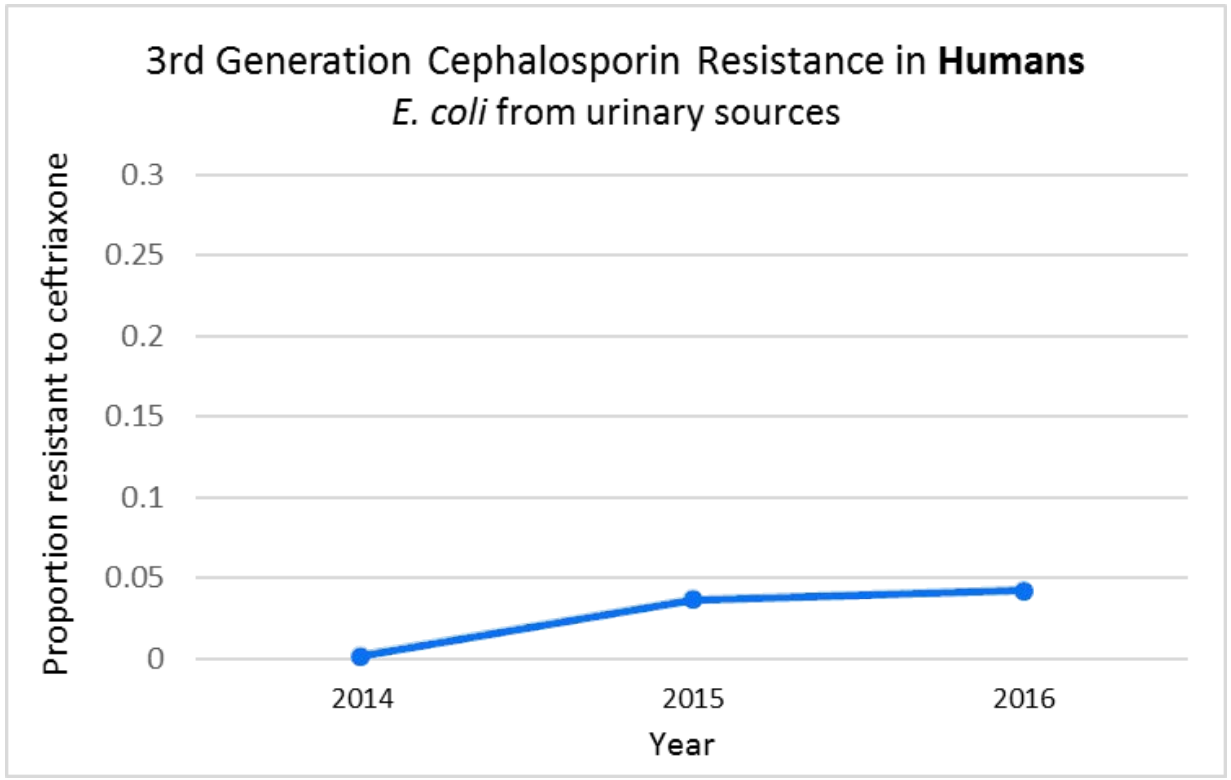
Conventional susceptibility testing allows for comparisons of phenotype patterns between species-with the need for caution about interpretation due to sampling differences etc.

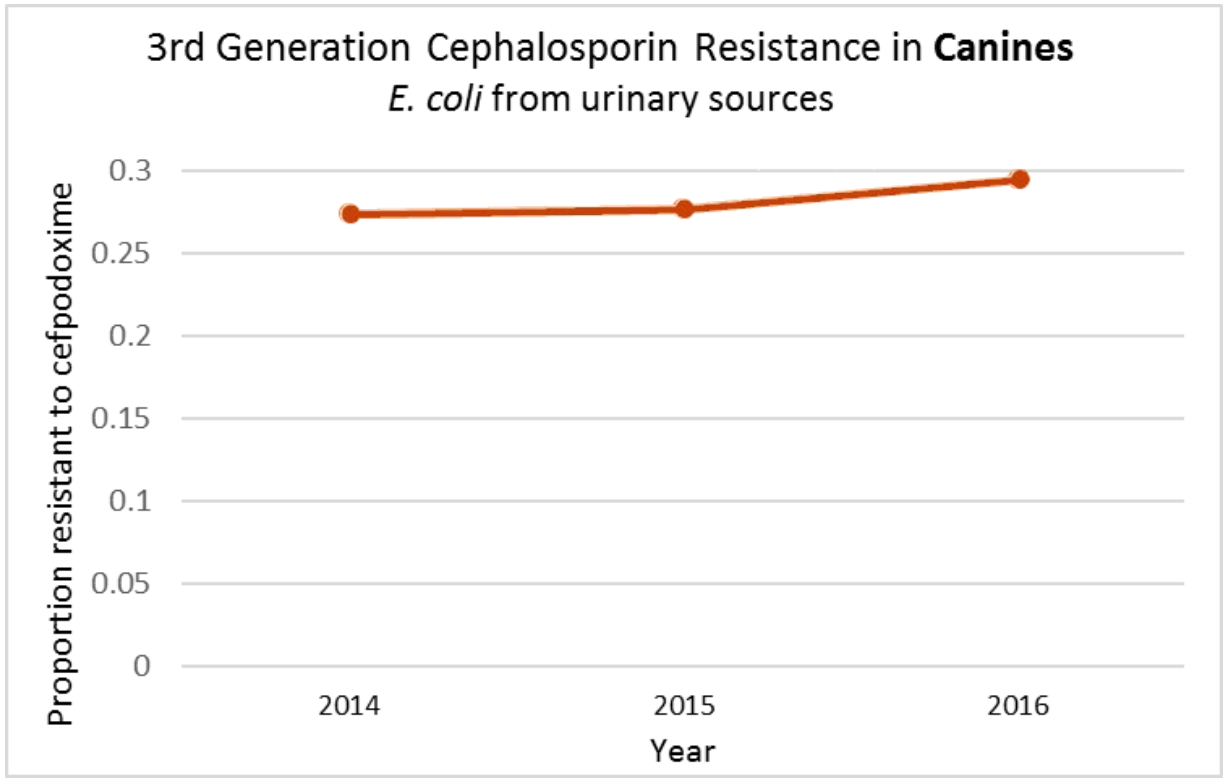
These resistotype plots show phenotypic trends of 5 antibiotic classes of interest (Ampicillins, 3rd generation cephalosporins, fluoroquinolones, aminoglycosides and trimethoprim sulfides) from human and bovine *E. coli*. Human samples are subset to include only urinary *E. coli* and the bovine data are subset to include *E. coli* from multiple sources (Feces, lung aspirate, abscess, blood, milk, intestine, semen). The bovine and human samples include isolates from all ages.

This approach can generate hypotheses that can be tested through molecular analyses in the future.

The only veterinary breakpoints for E. coli mastitis in cattle are for ceftiofur and ampicillin. CLSI breakpoints were used for human and bovine isolates keeping in mind the caveat of combinational animal-specific and human-specific break points for making comparisons in antibiotic resistance.

Use Caution in Comparing and Interpreting Findings Across Species





Data: Quest Diagnostic data and Phoenix Central Laboratories data

3rd generation cephalosporines was represented by ceftriaxone in humans and cefpodoxime in canines.

The differences in resistance could be due to a number of factors, so use caution in making comparisons!

- Sampling bias – differential sampling in dogs vs. humans due to insurance, etc.
- Differences between class representatives
- Other

Next Steps

- Incorporating molecular data
- Increase environmental data
- Using antibiograms to support stewardship by human and veterinary medical health care provi

Sample Antibiogram: Urinary isolates for Humans vs. Canine
% Susceptible

Organism	Host species	Total # of isolates tested	Penicillins	3rd Generation Cephalosporins	Fluoriquinoloes	Aminoglycosides	Trimethoprim-sulfa
Escherichia coli	*Human*	*31245*	62	97	87	95	80
	Canine	*3838*	72	84	93	93	92
Proteus spp.	*Human*	*1392*	81	98	89	93	83
	Canine	*878*	92	96	98	93	93
Staphylococcus spp.	*Human*	*1449*	-	-	67	96	23
	Canine	*974*	-	96	92	89	90
Pseudomonas spp.	*Human*	*545*	-	-	77	92	-
	Canine	*94*	-	-	78	92	-

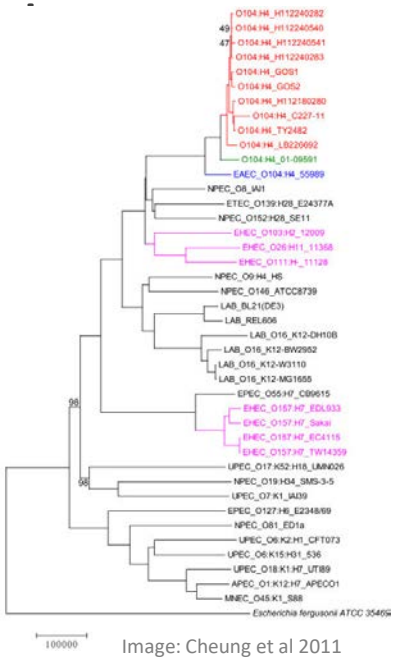


Image: Cheung et al 2011

Antibiogram: Subset to include urinary isolates from humans and canines in Washington state collected from clinical data.

Sample is from year range 2013-2017.

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