Navigating the maze: genetic resistance and data sharing

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Why do we need to genetically “predict” antimicrobial resistance in animal health?
Bacterial sequencing in vet diagnostics

- Performed on cultures (costs ~$50-200)
- Nationally harmonized lab procedures (with FDA/CDC/state health)
- Confirms species, subspecies, isolate relatedness
- Large databases mined to predict features (functional genomics):
  - Serotype
  - Virulence factors
  - Antibiotic resistance gene (ARG) profile

National CARB veterinary surveillance projects

- FDA Veterinary Laboratory Investigation and Response Network
  - 25 vet diagnostic source labs
  - ~2,000 isolates collected in 2017
    - *Salmonella* (all hosts)
    - *E. coli* (dogs)
    - *S. pseudintermedius* (dogs)
    - “Other” (2018)
  - Including whole genome sequencing on a subset (done by 5 additional vet labs) uploaded to NCBI in near real-time
  - NARMS integration
Metadata protections

Data included

- Host species
- Sample type (e.g. feces, respiratory, wound swab)
- Collection date
- State of origin
- Case type
- Lab methods

Not included

- VDL accession number
- Referring DVM
- Animal owner
- Animal name
### Working towards animal health representation in the NCBI database

<table>
<thead>
<tr>
<th>Organism</th>
<th>Total isolates (10/18/18)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Salmonella</td>
<td>155,509</td>
</tr>
<tr>
<td><em>E. Coli</em></td>
<td>55,400</td>
</tr>
<tr>
<td><em>Campylobacter jejuni</em></td>
<td>22,167</td>
</tr>
<tr>
<td><em>Listeria monocytogenes</em></td>
<td>21,016</td>
</tr>
<tr>
<td><em>Klebsiella pneumoniae</em></td>
<td>7,774</td>
</tr>
<tr>
<td><em>Staphylococcus pseudintermedius</em></td>
<td>272</td>
</tr>
</tbody>
</table>
Rethinking the antibiogram: The ARG heat map

Class
- β-Lactam
- Aminoglycoside
- Sulfonamide
- Tetracycline
- Phenicol
- Trimethoprim
- Fosfomycin
- Fluoroquinolone
- Antiseptic

Veterinary Salmonella

FDA Vet-LIRN, data available at ncbi.nlm.nih.gov/pathogens/
Distribution of ARGs in veterinary *Salmonella* by Distance to Human Cases

FDA Vet-LIRN, data available at ncbi.nlm.nih.gov/pathogens/
Most extreme cases highlight role of companion animals in AMR

Canine lung (2017)
- aac(3)-Iid (gentamicin)
- aadA1 (streptomycin)
- aph(3")-Ib (streptomycin)
- aph(3')-Ia (kanamycin)
- aph(6)-Id (streptomycin)
- blaCMY-2 (penicillins, amoxi-clav, cephalosporins)
- blaTEM-1 (penicillins)
- catA1 (phenicols)
- dfrA14 (trimethoprim)
- mph(A) (macrolides)
- qacL (disinfectants)
- sul2, sul 3 (sulfonamides)
- tet(B) (tetracycline)
- gyrA mutations (fluoroquinolones)

Canine lung (2018)
- aac(3)-Iid (gentamicin)
- aadA1, A2, A5 (streptomycin)
- aph(3")-Ib (streptomycin)
- aph(3')-Ia (kanamycin)
- aph(6)-Id (streptomycin)
- blaEC (cephalosporins)
- blaTEM-1 (penicillins)
- catA1, cmlA1, floR (phenicols)
- dfrA12, 17 (trimethoprim)
- Inu(F) (lincomamide)
- mph(A) (macrolides)
- qacL, qacEdelta1 (disinfectants)
- sul1, sul2, sul 3 (sulfonamides)
- tet(B, M) (tetracycline)
One Health AMR Data Sharing

- Meeting sponsored by NY Integrated Food Safety Center of Excellence held May 2018 with stakeholders vet diagnostics and public health
- NARMS and NCBI emerged as “best practice” common databases for AST, WGS, and metadata
- Importance of data integrity, security, and confidentiality
- Reducing granularity of location would allow enhanced metadata to be provided
- A tiered system with a 3rd party protector of identifiable information proposed as safeguard for confidentiality
One Health Data Sharing: next steps

- State-level pilot project
- Identify 3rd parties for tiered confidentiality
- Incorporate animal health data in NARMS from both public/academic and corporate labs
Take-home points

1. People and animals share pathogens and pathogens share genes

2. By monitoring ARGs in animal populations, we can better protect both animal and human health
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