Prevalence Of Antimicrobial Resistance Genes In Nepal Using A One Health Approach

Cristin Young, Dibesh Khamcharya, Manisha Bista, Ajay Sharma, Tracey Goldstein, Simon Anthony, Duncan Temple-Lang, Jonna Mazet, Woutrina Smith, and Christine Kreuder Johnson
Transmission Routes of Antimicrobial Resistance

Transmission Routes of Antimicrobial Resistance

PREDICT Project

- USAID Emerging Pandemic Threats program
- One health surveillance strategy for emerging zoonotic viruses in 30 countries in Asia and Africa

Concurrent sampling of wildlife, livestock, and people

Identify cross-species transmission and spillover
Antimicrobial use in the livestock sector

Why Nepal?

- Widespread use in humans and animals
- Inappropriate and frequent prescribing
- High prevalence of resistance

(Van Boeckel et al., 2015)
Objectives:

- Characterize resistome of community
- Examine highest concentrations of genes
STUDY DESIGN

35 households

humans
- 2 oral swabs
- 2 fecal swabs

animals
- 2 oral swabs
- 2 fecal swabs

water
- 1 filter
- 50 ml filtered water

rodents
- 2 fecal swabs

+ risk factor survey: animal contact, antibiotic use, medical history, access to healthcare

Total humans
n=67

Total animals
n=77

Total water
n=17
Laboratory Analysis

QIAGEN microbial DNA qPCR array for 87 resistance genes

- Aminoglycoside, β-lactam, erythromycin, fluoroquinolone, macrolide-lincosamide-streptogramin B, tetracycline, vancomycin, and multidrug resistance classification groups
- Ct < 34 : positive
- Ct 34-37 : inconclusive
- Ct > 37 : negative
  - For analysis, coded inconclusive as negative

Number of antimicrobial resistance genes positive per specimen by sample type
Proportion of samples positive by source sampled and antibiotic resistance classification group

\[
\text{Proportion positive} = \frac{\text{sum}(\# \text{ specimens positive for all genes in group})}{\# \text{ specimens potentially positive} \times \text{number of genes in group}}
\]
Proportion of samples positive by source sampled and antibiotic resistance genes

Proportion positive = \( \frac{\text{sum}(\# \text{ specimens positive for all genes in group})}{\# \text{ specimens potentially positive}} \)
Proportion of samples positive (>0.50) by source sampled and antibiotic resistance genes

Proportion positive = sum(# specimens positive for all genes in group) / (# specimens potentially positive)
Antimicrobial resistance gene bipartite network analysis

Legend
- human
- gene
- chicken
- duck
- water
- shrew
- swine
- rodent

Note: color based on sources sampled and size based on network degree
Conclusions

- *ermB, mefA, tetA, tetB* most commonly detected genes
  - Antibiotics associated with these genes widely used in Nepal (azithromycin, doxycycline)
- Prevalence patterns:
  - Gene prevalence varied markedly by species and sample type
  - Detection of same gene among different species was widespread
- Next steps:
  - Culture-based methods + metagenomics to characterize bacterial reservoirs
  - Increased wildlife and environmental sampling
Many thanks to:

• Center for Molecular Dynamics, Nepal lab and field teams

• One Health Institute lab team

• PREDICT project