

## **Understanding the prevalence of Antimicrobial Resistance in livestock and risk of zoonotic transmission – a comparative study between the United Kingdom, Thailand and Argentina**

### **Supervisory team:**

**Main supervisor:** Prof Matthew Avison (University of Bristol)

**Second supervisor:** Dr Kristen Reyher (University of Bristol)

**Host institution:** University of Bristol

### **Project description:**

Antimicrobial resistance (AMR) is an increasing threat to public health and food security worldwide. AMR itself is a natural phenomenon, however the increasing use of antibiotics places selective pressure on resistant bacteria. Evidence of AMR emergence in livestock and subsequent transmission to humans has placed antimicrobial use and biosecurity in the agricultural sector under increasing scrutiny. Resistant infections in animals also have an increasing impact on global food security. However, the true scale of AMR transmission within and between farms, and between humans and farms, is unclear.

This project takes a global One Health approach to understanding AMR, building on existing consortium projects in the UK, Argentina and Thailand. The project aims to extend earlier studies by comparing *Escherichia coli* resistant to critically important antibiotics from humans with those collected in parallel from farm animals in the same geographical region.

Specifically, it will add value to three existing consortium projects:

- One Health Selection and Transmission of Antimicrobial Resistance (OH-STAR; NERC/BBSRC/MRC funded).
- Future-proofing Antibacterial resistance Risk Management Surveillance and Stewardship in the Argentinian Farming Environment (FARMS-SAFE; BBSRC Funded).
- One Health Drivers of AMR in Thailand (OH-DART; MRC funded).

The PhD project will include analysis of *E. coli* isolates from livestock and people within the same geographical range. Isolates will undergo phenotypic and whole genome sequence based assessment of AMR. Bioinformatics approaches will be used to determine sequence types, resistance genes and plasmid replicon types. Phylogenetic analysis will be performed to assess farm-to-farm and farm-to-human transmission. Data from the UK, Argentina and Thailand will be compared to understand transmission of AMR in a global context.

We aim to communicate research findings to farmers, veterinary practices and healthcare systems, with the intention of supporting sustainable livestock production.

This PhD studentship would suit an applicant with cross-disciplinary interests and experience in molecular microbiology, genomics and veterinary science.