

ACRONYM: TransComp-ESC-R

Title: Genomic approach to transmission and compartmentalization of extended-spectrum cephalosporin resistance in Enterobacteriaceae from animals and humans

Keywords: Extended-spectrum cephalosporin resistance, Enterobacteriaceae, transmission pathways, compartmentalization, genome sequencing, in vivo transmission, proteome

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Abstract:

Resistance to extended-spectrum cephalosporins (ESC) in Enterobacteriaceae is a major challenge for public health worldwide. Its international presence in almost every ecological niche and biological compartment with still ongoing dynamic expansion makes it an ideal target to study the spread of AMR.

This project intends to use genomic, evolutionary, transcriptomics, proteomics and experimental approaches to assess the similarities between a variety of ecological niches and biological compartments formed by Enterobacteriaceae species, host species/source (humans, dogs, cattle, swine, chicken, meat products) and geography (Europe: Germany and France, and North America: Canada). These similarities will serve as a basis to identify and focus further on clonal lineages and plasmids able to spread across compartments, using whole genome and plasmid sequencing. A combination of phylogenetic and epidemiologic analyses will allow an assessment of the directionality of transmission between compartments. These analyses will be complemented by series of experiments on transmission of ESC resistance plasmids in vivo in two animal models (chicken and cattle) and on effects of ESC resistance plasmids on the bacterial transcriptome and proteome and its association with plasmid maintenance.

These experiments will help to identify major transmission pathways between animals and humans and potential new intervention targets for the control of ESC resistance. The team assembled for this

project consists of experienced researchers with a wide spectrum of expertise ideal for the successful completion of a study of antimicrobial resistance in the context of One Health.