

**ACRONYM: HECTOR****Title:** The impact of Host restriction of *Escherichia coli* on Transmission dynamics and spread of antimicrobial Resistance**Keywords:** *Escherichia coli*, host restriction, transmission dynamics, One Health, antimicrobial resistance determinants, whole genome sequencing, experimental and mathematical models**Consortium composition:**

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**Abstract:**

The prevalence of antimicrobial resistance (AMR) is increasing rapidly worldwide, including in bacteria colonizing healthy human and animal populations. The recent reports of plasmid mediated colistin resistance, potentially associated with colistin usage in agriculture, further raise fears of infections that have become untreatable due to AMR. The commensal flora of humans and animals is a reservoir of AMR encoding genes and *Escherichia coli* in particular can carry multiple AMR determinants.

Antimicrobial resistance transmission within *E. coli* appears dominated by certain lineages. To what extent these are restricted to certain host species is unknown. Such host restriction may be an important determinant of the likelihood of transmission of resistant *E. coli* between different reservoirs, such as between animal and human hosts. The identification of determinants that allow disentanglement of the different modes of resistance transmission (i.e. bacteria vs mobile genetic elements such as plasmids) is crucial for a more targeted design of interventions to prevent and reduce transmission of resistance.

The proposed research aims to identify determinants of host restriction of *E. coli* and their potential association with antimicrobial resistance transmission and prevalence. We propose a One Health approach using mixed methods, including whole genome sequencing of a large collection of *E. coli* isolates from human, animal and environmental sources in different geographic areas across Europe and in Vietnam, experimental models to study the role of host restriction determinants in transmission and bacterial fitness, and mathematical modelling.

The research should result in a risk-assessment, estimating the contribution of different transmission routes and predicting the effect of interventions on a single route on the overall prevalence in the different compartments. The consortium is uniquely placed to perform this research as it consists of experts in the field of antimicrobial resistance, who work in human and animal health domains, and represent highly complementary disciplines.