Population Dynamics Virtual Seminar

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Phylogeography of pathogenic *E. coli* across Belgium cattle farms

The selection and dissemination of antibiotic resistance is a multifactorial and multi-environment phenomenon. It involves the selection and dissemination of bacteria and resistance genes. *Escherichia coli*, a major cause of infections in humans and animals, but primarily a commensal of a large number of mammalian species is a model species for the analysis and modelling of these processes. Many studies based on surveillance and/or genomic data have investigated these phenomena. The questions addressed include the factors and mechanisms of transmission and the zoonotic component of the transmission of drug-resistant *E. coli* to humans. However, samplings are frequently limited compared to the diversity of the species.

In collaboration with Belgian veterinarians, we have analysed the population of ß-lactam resistant *E. coli* isolated from diarrheic calves in Wallonia and the impact of reducing the use of 3GC and 4GC. This study is based on a collection of 3478 ß-lactam resistant isolates from 829 farms spread over Wallonia, the south part of Belgium, with an area of 16,901 km^2. These strains were systematically isolated during three calving seasons (2017 – 2020). From this unique collection, we have selected, based on clinical and phenotypic data, 769 isolates from 447 farms for genome sequencing. Virtually all the isolates were MDR (resistant to at least three antibiotic classes), likely as a result of antibiotic consumption on dairy farms. Genomic and phylogenetic analysis were contextualized by including the large number of *E. coli* genome sequences available in Enterobase. We have characterized the spatial and temporal dynamics of pathogenic ß-lactam resistant *E. coli* and defined quantitative features of their dissemination.