

ACRONYM: MODERN

Title: Understanding and modelling reservoirs, vehicles and transmission of ESBL-producing Enterobacteriaceae in the community and long term care facilities

Keywords: Extended-spectrum beta-lactamases, transmission, long-term care facilities, food, wastewater, mathematical models, and molecular epidemiology

Consortium composition:

Type	Name	Institute	Country
C	Rodríguez-Baño, Jesús	Hospital Universitario Virgen Macarena, Sevilla/ Enfermedades Infecciosas	Spain
P	Tacconelli, Evelina	University Hospital of Tübingen / Department of Infectious Diseases	Germany
P	Harbarth, Stephan	University of Geneva / Infection Control Program	Switzerland
P	Kluytmans, Jan	University Medical Center Utrecht / Julius Center for Health Sciences and Primary Care.	Netherlands
P	Hocquet, Didier	University Hospital Besançon / Infection Control Unit	France
P	Cooper, Ben	University of Oxford, Nuffield / Department of Clinical Medicine / Centre for Tropical Medicine and Global health, Nuffield	United Kingdom

Abstract:

The continuing spread of extended-spectrum beta-lactamase-producing Enterobacteriaceae (ESBL-PE) is among the most important problems in antimicrobial resistance. It is also a good model to investigate the epidemiological complexity of resistance in Enterobacteriaceae. Available data on the transmission determinants of ESBL-PE in community settings are scarce, methodologically limited and mostly based on single centre studies. A comprehensive investigation using present typing and modelling techniques is warranted to develop a sound quantitative understanding of the interactions involved.

A consortium of investigators with diverse expertise from countries with high and low endemicity of ESBL-EP has been created. Transmission and persistence of ESBL-PE within households and long-term care facilities will be studied. Individual and group-level determinants for transmission and persistence will be quantified, together with other ecological variables including environmental, food and wastewater contamination. Advanced molecular typing techniques and state of the art analytical methods will be used.

Data generated in this project will directly inform a suite of mathematical models which, in addition to encapsulating current understanding of the processes, will be used to explore the potential effectiveness of different interventions to control ESBL-PE spread.

The expected outputs are a comprehensive characterisation of ESBL-PE transmission considering bacterial clones and mobile genetic elements, as well as individual and ecologic-level factors in different settings, to inform public health authorities about interventions that should be prioritised to control transmission of these organisms.