

**ACRONYM: STARCS****Title: Selection and Transmission of Antimicrobial Resistance in Complex Systems****Keywords: Selection and transmission of antibiotic resistance, metagenomics, Extended-Spectrum Beta-Lactamases, human medicine, veterinary medicine, animal models****Consortium composition:**

Type	Name	Institute	Country
C	van Schaik, Willem	University Medical Center Utrecht [UMCU] / Dept. of Medical Microbiology	Netherlands
P	Mevius, Dik J.	Wageningen University and Research / Central Veterinary Institute	Netherlands
P	Andersson, Dan I.	University of Uppsala / Dept. Of Medical Biochemistry and Microbiology	Sweden
P	Coque, Teresa M.	Ramón y Cajal University Hospital / Dept. of Microbiology	Spain
P	Kozsul, Romain	Institut Pasteur / Department of Genomes and Genetics	France
P	Woolhouse, Mark E.J.	University of Edinburgh / Centre for Immunity, Infection & Evolution	United Kingdom
P	Malhotra-Kumar, Surbhi	University of Antwerp / Laboratory of Medical Microbiology, Vaccine & Infectious Disease Institute	Belgium

**Abstract:**

Selection and transmission are key determinants for the dissemination of antimicrobial resistance (AMR) across the planet. These determinants of AMR are frequently studied in laboratory settings while in reality they occur in complex systems, e.g. in microbial communities that colonize human and animal guts or in environmental ecosystems. The central aim of STARCS (Selection and Transmission of Antimicrobial Resistance in Complex Systems) is to characterize and quantify the processes of selection and transmission of AMR genes and drug-resistant bacteria in complex (eco)systems from a 'One Health' perspective and to integrate these elements into predictive mathematical models, which will be used to inform policy development.

To reach this goal, the consortium will (i) develop and implement innovative metagenomics methodologies to map the expression of AMR genes and their linkage to bacterial hosts and mobile genetic elements in human, animal and environmental samples, (ii) use relevant animal models (using mice and ducks) and observational studies (in hospitals and in dogs and their owners) to analyse and quantify the processes of selection and transmission of drug-resistant Enterobacteriaceae (specifically Extended Spectrum Beta-Lactamase producing *Escherichia coli*) and (iii) implement state-of-the-art epidemiological modelling to quantify the spread of ESBL-producing *E. coli* between humans and animals.

STARCS will develop technological breakthroughs to assess selection and transmission dynamics on the level of the resistance gene, the mobile genetic element, the bacterium, the human-animal-environment interface and in clinical settings. This project will deliver important knowledge into selection and transmission of AMR, will provide the scientific community with novel tools to study

selection and transfer of AMR in complex systems and will result in much-needed guidance towards policy decisions by international and national institutions. Ultimately the results from STARCS will form an evidence-based foundation for the development of new regulations, aimed at curbing the spread of AMR.