

**ACRONYM:** PET-Risk

**Title:** Risk of companion animal to human transmission of antimicrobial resistance during different types of animal infection

**Keywords:** Companion animals; Humans; AMR dynamics; Infection Control measures; Colonization

**Consortium composition:**

Type	Name	Institute	Country
C	Pomba, Constança Ferreira	University of Lisbon / Faculty of Veterinary Medicine	Portugal
P	Schwarz, Stefan	Friedrich Loeffler Institute Institute of Farm Animal Genetics	Germany
P	Weese, Scott	University of Guelph/ Ontario Veterinary College, Pathobiology / Animal Health Laboratory	Canada
P	Loeffler, Anette	The Royal Veterinary College, Dept. Clinical Science & Services	UK

**Abstract:**

The close contact of pets with humans provides excellent opportunities for interspecies transmission of resistant bacteria and their resistance genes in either direction. Infections in humans due to antimicrobial resistant bacteria originating from pets are becoming a concern. While any animal-human contact offers a chance of transmission, it is generally accepted that a high bacterial burden and high antimicrobial resistance gene copy numbers are present during an active infection. There is a gap of knowledge on the dynamics of transmission and selection of antimicrobial resistance at the pet-human interface. Animals may exchange antimicrobial-resistant bacteria and resistance genes with humans, but the extent to which this happens is unknown.

PET-Risk will evaluate the transfer of antimicrobial resistance between pets and household members during animal infections and determine which type of infection (skin and soft tissue vs. urinary tract infections) presents a higher risk of transmission to humans. Furthermore, in a longitudinal study we will collect samples of infected animals under antimicrobial treatment, and their household members at several time points, which will allow the assessment of critical control points at which interventions could substantially affect the spread of resistance.

The causality and directionality of pet-human spread of resistance genes will be established by using state-of-the-art techniques in order to design and evaluate preventive and intervening measures for reducing the public health risks of antimicrobial resistance.