Session: Microbial ecology of antimicrobial resistance.

Title: Genome resolved metagenomics revealed the impact of AMR strain colonization and antibiotic treatment in complex microbiota *in vitro*.

Authors: Alessia Pennacchia1, Anna Greppi1, Benoit Pugin1, Roger Stephan2, Christophe Lacroix1, Florentin Constancias1

1 Laboratory of Food Biotechnology, Institute of Food, Nutrition and Health, ETH Zurich, 8092 Zürich, Switzerland

2 Institute for Food Safety and Hygiene, Section of Veterinary Bacteriology, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland

Key words: AMR, genome-resolved metagenomics, mobilome, strain dynamic, evolution, resistome.

Microbiota of human and animal gastrointestinal tracts represent complex ecosystems and important reservoirs of AMR genes – i.e., resistome - contributing to the emergence and spread of multi-resistant pathogenic bacteria.

While the composition of the microbiota and resistome in human and animal gastrointestinal tract (GIT) has been documented, the drivers influencing the resistome have been poorly investigated. The potential of exogenous strains carrying AMR genes and different antimicrobial (AM) pressure in shaping GIT resistome structure and bacterial population dynamics remains unclear.

To address those questions, we designed in vitro PolyFermS continuous fermentations enabling controlled and replicated experiments. Chicken and human microbiota were inoculated with AMR strains isolated from chicken meat (i.e., ESBL E. coli and VRE E. faecium) and submitted to antibiotic treatment (i.e., cefotaxime and vancomycin). We characterized the dynamic of taxonomic and metabolic activity of bacterial communities and in silico-mobilome classification, genome resolved metagenomics approaches were used to describe resistome structure, bacterial populations dynamics, AMR genes evolution and potential transfer among bacterial taxa.

Our results revealed that inoculated strains were not able to colonize microbiota models without AM selective pressure. While the abundance of Enterobacteriaceae appeared to drive the resistome in the chicken model, a dose-dependent increase of AMR gene abundance was observed in human microbiota indicating a potential co-selection of multidrug-resistant strains. Altogether, this study provides insights in strain-level dynamics, changes in the resistome structure, evolution of resistance genes and factors associated with variations of dissemination potential.

Main author: Alessia Pennachhia

Presenting author: Alessia Pennachhia