



Universität
Basel

Research Project

Development of a Swiss surveillance database for molecular epidemiology of multi-drug resistant pathogens

Third-party funded project

Project title Development of a Swiss surveillance database for molecular epidemiology of multi-drug resistant pathogens

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Organisation / Research unit

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Project start 01.01.2018

Probable end 31.12.2020

Status Completed

Background:

Multi-drug resistant (MDR) bacterial pathogens clearly pose an important challenge to our society at multiple levels: in humans, MDR pathogens are increasingly detected and associated with significant morbidity, mortality and health care costs. Similarly, in veterinary medicine, MDR bacteria lead to a high economic burden and constitute a reservoir for dangerous zoonoses representing a serious public health concern. The spread of many bacterial pathogens is complex, and understanding the most important routes of transmission is a precondition for effective countermeasures. A better understanding of transmission events and dynamics between compartments (animals and humans) would be a critical guide to containment. We anticipate that a shared surveillance database between human and veterinary medicine coupled to state-of-the-art automated phylogenetic analysis will enable a more complete and detailed surveillance of MDR pathogens and actionable results for public health policy.

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Objective of the project:

The main goal is to connect human and veterinary microbiology laboratories through a shared framework for near real-time molecular epidemiology of MDR bacterial pathogens, which will allow to perform transmission and outbreak surveillance between different species and the environment.

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Specific aims include:

- Implementation of an active surveillance system using MRSA as a proof-of-concept, which can be expanded to many other one-health related MDR pathogens.
- Continuous development of a highly flexible surveillance tool, which allows to incorporate molecular epidemiological data from whole genome sequencing (WGS) and important metadata information.
- Development of a semi-automated modelling tool to assess transmission rates between geographic locations, hospitals, communities, and species over time and space.
- Preparation for expansion with different other species including carbapenemase-producing Enterobacteriaceae

- Connection to international databases for global surveillance

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Keywords Multi-drug resistant pathogens, antibiotic resistance, whole genome sequencing, transmission, molecular epidemiology, pathogen modelling

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Add publication

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Specify cooperation partners