Upscaling bacterial overland transport – a multi-parametric approach

Julia Derx[1,8], Rita Linke[2,8], Regina Sommer[3,8], Peter Strauss[4], Alba Hykollari[5], Alexander Faltejsek[6], Jack Schijven[9], Alfred Paul Blaschke[1,8], Alexander Kirschner[3,7,8], and Andreas Farnleitner[2,7,8]

[1]TU Wien, Institute of Hydraulic Engineering and Water Resources Management, Vienna, Austria

[2]TU Wien, Institute of Chemical, Environmental and Bioscience Engineering, Vienna, Austria

[3]Medical University of Vienna, Institute for Hygiene and Applied Immunology, Vienna, Austria

[4]Institute of Land and Water Management Research, Federal Agency for Water Management, Petzenkirchen, Austria

[5]University of Veterinary Medicine, Research Institute for Wildlife Ecology, Vienna, Austria

[6]Vienna Municipal Department 49, Forest administration Lobau, Austria

[7]Karl Landsteiner University of Health Sciences, Division Water Quality and Health, Department of Pharmacology, Physiology, and Microbiology, Krems an der Donau, Austria

[8]Interuniversity Cooperation Centre Water & Health (http://www.waterandhealth.at/)

[9]Utrecht University, Faculty of Geosciences, Department of Earth Sciences, Utrecht, the Netherlands

Water contaminated with human and animal enteric pathogens puts public health at serious risk. All countries and regions of the world require highly robust and effective water management and treatment systems to guarantee safe water and protect public health. To this end, we need accurate predictions of the origin of pathogens , how they move through the environment and where they end up.

This study is part of a four-year project and aims to develop new bacterial overland transport - BOT models to provide answers to the above questions. The project takes a holistic, quantitative approach to transfer BOT model parameters onto large scales. Small-scale precipitation experiments are conducted in the laboratory and larger-scale experiments are conducted using a rainfall simulation under real environmental conditions. The state-of-the-art combination of quantitative, microbiological, and molecular methods and parameters will provide the scientific basis for more accurate predictions of BOT, which eventually may be extended to viruses and protozoa in the future.