

**Title** - Decoding polymicrobial interactions in catheter-associated urinary tract infections

**Authors** - Ashim Kumar Dubey<sup>1</sup>, Adrian Egli<sup>2</sup>, Knut Drescher<sup>3</sup>, John McKinney<sup>1</sup>

**Affiliation** - <sup>1</sup> School of Life Sciences, Swiss Federal Institute of Technology, Lausanne (EPFL)

<sup>2</sup> Institute of Medical Microbiology, University of Zurich

<sup>3</sup> Biozentrum, University of Basel

**Abstract** -

Urinary tract infections (UTIs) are one of the leading causes of bacterial morbidity, with millions of cases reported annually. Though uropathogenic *E. coli* (UPEC) is the primary culprit, it frequently coexists with other uropathogens. The association of polymicrobial infections with heightened disease severity is well-documented. However, despite their clinical significance, the impact of the infections' polymicrobial nature on disease outcomes is poorly understood. This is particularly crucial for catheterized patients, as the catheter's presence enhances microbial colonization and biofilm formation. Both pathogen-pathogen and host-pathogen interactions in polymicrobial infections play pivotal roles in shaping treatment outcomes, ranging from subdued host immune responses to increased antibiotic tolerance. Current clinical therapies often treat monomicrobial and polymicrobial infections alike. Thus, there is a pressing need for a comprehensive study to unravel how pathogen partners influence UPEC's infectious potential in catheterized patients, for the development of targeted and efficacious treatment strategies.

To gain insights into the patient cohort and identify relevant microbial combinations for public health, we conducted an extensive analysis of anonymized urine data from previous years at the Institute of Medical Microbiology, Zurich. This dataset included information on age, gender, and antibiotic resistance patterns. Additionally, we collected, characterized, and sequenced clinical isolates of the most commonly found microbes in monomicrobial and bimicrobial infections, constructing a bioinformatic landscape to explore bacterial genetic factors associated with polymicrobial and catheter-related infections. Our future studies aim to decode the impact of these polymicrobial interactions on catheter-associated biofilms and determine whether alterations in the community structure of these biofilms can influence treatment outcomes, such as antibiotic tolerance and resistance to clearance. Subsequent investigations in bladder microtissue models will provide fresh insights into the ecological interactions within the diverse niches of a catheterized human bladder during polymicrobial infections, with the ultimate goal of improving infection outcomes of catheter-associated urinary tract infection (CAUTI) patients.

