

Towards Culture-independent Characterization of Pathogens Recovered from the Urinary Tract

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Urinary tract infections (UTIs) are frequently encountered bacterial infections. The severity of the infection can range from uncomplicated UTIs in young women to life-threatening health care associated sepsis. In hospital treated UTI *Escherichia coli* and *Enterococcus sp.* rank among the three most common bacteria. Currently established microbiological methods require up to three days to identify the bacteria and to provide the full antibiogram. In times of increasing antibiotic resistances faster, culture-independent characterization methods are urgently needed.

In this contribution, we present a Raman spectroscopy based approach to characterize the bacteria directly from the urine of UTI patients. The method includes a short sample preparation step where leukocytes and endothelial cells are removed by filtration. Negative dielectrophoresis is applied to capture the bacteria from the remaining dilute suspension at a selected and well-defined position in space. At this position high quality Raman spectra of the bacteria can be collected. With this combined dielectrophoresis-Raman setup it is possible to distinguish *E. coli* and *E. faecalis* recovered from the urine of UTI patients within less than one hour experimental time.

Further in-vitro experiments are carried out to characterize the antibiotic – bacteria interaction with a special focus on vancomycin. Vancomycin is often used in enterococci infection as a so called “antibiotic of last resort”. However, emerging appearance of vancomycin resistant enterococci (VRE) endanger the successful use of this drug. Raman spectroscopy is utilized to study the interaction of vancomycin with *E. faecalis* and *E. faecium*, both vancomycin sensitive and resistant strains. First changes in the Raman spectra due to the drug action of the drug can already be observed after 30 minutes incubation. Those spectral changes allow an automatic differentiation between vancomycin treated and untreated bacteria using a multivariate classification model.

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