DESCRIPTION FOR THE GENERAL PUBLIC

The chemical compounds which are present in the environment more and more often have detrimental effects on our health. The most serious ones are tumors and various mutations on the cellular level. Those compounds, from the analytical point of view, can serve as biomarkers, constituting measurable changes in the body's cells and biochemical processes occurring therein. The challenge of the 21st century is therefore searching for effective and reliable methods of identifying biomarkers as well as understanding bodily functions which occur in the living organisms on the molecular level. Bacterial identification is used in a wide variety of applications including microbial forensics, criminal investigations, investigating bio-terrorism threats and environmental studies. Many different methods have been established for fast detection and identification of harmful microorganisms: different staining procedures, specific antibodies, polymerase chain reaction (PCR) or DNA-typing. In general, these methods rely on phenotypic identification of the causative organism using Gram staining, culture and biochemical methods. Unfortunately they have two major disadvantages. First of all, they can only be used for organisms that can be cultivated in vitro, which is highly time-consuming. Clinicians usually make a diagnosis of infection based on an intermittent examination, observing changes in temperature, blood pressure, smell and sight over a period of time. Depending on the severity of the infected wound and infectious agents, this may cause multiple organ dysfunction, failure of body systems and ultimately death. For fast diagnosis, culture of microorganisms or molecular analysis is performed, but these detection methods take up to three days and are unreliable for identification of pathogens in up to 50 % of patients. For this reason rapid, inexpensive and definitive screening tests capable of ruling out an infection or identifying the pathogen with a high degree of accuracy would be beneficial in eliminating empirical treatment. Taking into account the above discussed problem, the **main research problem which we would like to solve is** application of hyphenated separation techniques (CE-LIF-MS/MS, LCxLC-MALDI-TOF-MS, GCxGC-Q-TOF) for the identification and characterization of pathogens in biological samples for medical diagnosis. Finally, the proposed procedures in the long run are supposed to work **as a fast screening identification method for several microbial infections.** This test is supposed to quickly show whether there is an infection growing or not, and if there is some bacteria present, it will give the information whether it is Gram-positive or Gram-negative. Currently this is the fastest way of providing the doctors with such information before they decide to apply a very microbiote-depleting antibiotic therapy.