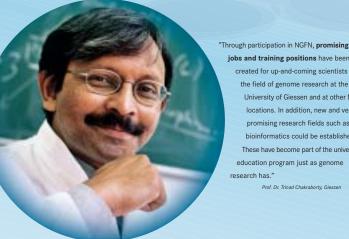
Genome Network Infection and Inflammation

Network and Research

The responses of our organism to infections with different pathogens are the focus of the work in this genome network. At 17 research sites scientists are investigating these processes with the aid of functional genomics, i.e. by studying the functions of our genes and their products. At the research sites chronic inflammatory diseases, autoimmune phenomena, sepsis, tuberculosis, hepatitis, HIV, malaria and other issues involving infectious diseases in the fields of bacteriology, virology and parasitology are studied.



Shortly after her birth, our daughter had sepsis. We thought she was going to die. She was ten weeks premature and quite weak. It's pretty crazy when you think what havoc a tiny pathogen can wreak. That's why I think it's good that genome research is combating infectious diseases. Thus, hopefully many families will be spared what we vent through."



jobs and training positions have been created for up-and-coming scientists in the field of genome research at the University of Giessen and at other NGFN locations. In addition, new and very promising research fields such as bioinformatics could be established. These have become part of the university education program just as genome research has." Prof. Dr. Trinad Chakraborty, Giess

>> Example Blood Poisoning

The causes of blood poisoning (sepsis) are many and diverse: open wounds, pneumonias, infections of the urinary tract or abdominal organs. When the body is not able to isolate the infection or limit it at its source, pathogens gain entrance into the bloodstream. There their poisons set off a catastrophic chain reaction: within a few hours all vital organs are affected and are threatening to fail. Often the sepsis is diagnosed too late and the patient dies, because the first symptoms of sepsis, such as a high fever and low blood pressure, can be und in many other diseases as well. In the industrial nations around 300,000 people die of septic shock every year 🥥

SPONSORED BY THE



Whether or not sepsis actually develops and how severe the course of the disease will be depends on the pathogen and the patient (the condition of the patient's immune system, underlying diseases). Genetic characteristics are crucial, as are the interactions between the patient and the pathogen. Meanwhile, it has become possible to manufacture biochips that show which genes are activated in the pathogen and in the patient during the course of the

disea

>> Solving the Enigma of Sepsis

Within the framework of studies, gene expression profiles of patients with pneumonia and inflammation of the pancreas are being made, as well as of severely injured victims of accidents and of premature babies who have an exceptionally high sepsis risk. The objective is to identify genes which allow a prognosis on the course of a sepsis. Furthermore, scientists are trying to identify genes that increase the risk for sepsis 🎱

)) First Successes

In the meantime, samples from all patient groups could be examined. First results indicate that apparently there are human genes that are generally activated in a bacterial infection. Depending on the kind of disease pathogen, there are also typical activity patterns in the patient on the basis of which scientists can develop characteristic gene expres profiles for the particular pathogen. If profiles were available for all germs, the diagnosis of a sepsis would be considerably easier.

On the basis of a blood sample, the respective cause of the disease could then be identified without having to expend the time and effort to isolate it. The consequence: it would be ea to predict the course of an infection, and targeted drug therapies could be initiated faster and more effectively

Coordination Prof. Dr. Trinad Chakraborty University of Giessen trinad.chakraborty@mikr o.med.uni-gies

NGFN