

Diversity of *Helicobacter pylori* in human populations of Central Asia

Initiative: Zwischen Europa und Orient - Mittelasien/Kaukasus im Fokus der Wissenschaft

Bewilligung: 13.10.2005

Laufzeit: 2 Jahre

Helicobacter pylori is a bacterium that colonizes the gastric mucosa of over one half of the global human population. It has been shown that human populations are infected by these bacteria that are specific for each continent and that the genetic diversity of *H.pylori* is a useful tool for distinguishing human populations and identifying traces of ancient and recent human migrations. Human Genetic analyses indicate that the human gene pool in Central Asian and Caucasian populations is highly diverse and is intermediate between Europe and Asia, with components from both sources. An analysis of the diversity of *H.pylori* from Central Asians and Caucasians could test different hypotheses regarding the evolution of these populations and hopefully reveal additional details on the history of human migrations to and from these regions.

Projektbeteiligte

Prof. Dr. Sebastian Suerbaum

Medizinische Hochschule Hannover
Institut für Medizinische Mikrobiologie
und Klinische Epidemiologie
Hannover

Dr. Tamara Aripova

Uzbek Academy of Sciences
Institute of Immunology
Taschkent
Usbekistan

Dr. Tatyana Hegay

Uzbek Academy of Sciences
Institute of Immunology
Taschkent
Usbekistan

Dr. Daniel Falush

University of Oxford
Department of Statistics
Peter Medawar Building
for Pathogen Research
Oxford
Grossbritannien

