

## Zoonoses

358

## Discovery of rodent coronaviruses related to major human and animal pathogens

J. F. Drexler<sup>1</sup>, V. M. Corman<sup>1</sup>, J. Schmidt-Chanasit<sup>2</sup>, Ma. Schlegel<sup>3</sup>, R. Kallies<sup>1</sup>, E. M. Leroy<sup>4</sup>  
A. A. Setién<sup>5</sup>, S. Matthee<sup>6</sup>, C. Reusken<sup>7</sup>, R. G. Ulrich<sup>3</sup>, C. Drosten<sup>1</sup>

<sup>1</sup>University of Bonn Medical Centre, Institute of Virology, Bonn, Germany

<sup>2</sup>Bernhard Nocht Institute for Tropical Medicine, Department of Virology, Hamburg, Germany

<sup>3</sup>Friedrich-Loeffler-Institut, Institute for Novel and Emerging Infectious Diseases, Greifswald-Insel Riems, Germany

<sup>4</sup>Centre International de Recherches Médicales de Franceville, Franceville, Gabon

<sup>5</sup>Hospital de Pediatría, Unidad de Investigación Médica en Inmunología, México DF, Mexico

<sup>6</sup>Stellenbosch University, Department of Conservation Ecology and Entomology, Centre for Invasion Biology, Stellenbosch, South Africa

<sup>7</sup>Netherlands Center for Infectious Disease Control, Bilthoven, Netherlands

Coronaviruses (CoVs) are classified into four genera termed *Alpha*-, *Beta*-, *Gamma*- and *Delta*-coronavirus. In the aftermath of the SARS-CoV pandemic, numerous novel bat CoVs were described, suggesting an origin of mammalian alpha- and betacoronaviruses in bats. The *Betacoronavirus* 2a clade contains major animal and human CoVs (hCoV), including hCoV-OC43, hCoV-HKU1, bovine CoV (BCoV) and Mouse hepatitis virus (MHV). No bat ancestors have ever been detected for this CoV clade. We screened 4,820 rodent sera from Mexico, Germany, the Netherlands, Gabon, South Africa and Thailand by nested RT-PCR for CoVs. CoV RNA could be detected in 56 specimens (1.2%) from all sampling sites. Partial *RNA-dependent RNA polymerase* sequences indicated these viruses corresponded to at least 8 novel CoVs that phylogenetically clustered across the entire 2a CoV clade. Some viruses were closely related to hCoV-OC43, BCoV and MHV. Taxonomic classification was confirmed by full genome sequencing of two representative rodent viruses directly from clinical material. These data suggested an origin of the entire 2a CoV clade in rodents.

Corresponding author:

**Jan Felix Drexler**

drexler@virology-bonn.de