



B virus, e.g. by generation of HepB-epBHvaccines with broader antigenicity.

Zoonoses and Emerging Viruses

Presentation

Abstract-ID: 578

Cowpox Virus Mature Virion Proteome: Composition, Ubiquitination and Attachment

Joerg Doellinger¹, Andreas Nitsche¹

¹Robert Koch-Institute; Centre for Biological Threats and Special Pathogens; Zbs 1: Highly Pathogenic Viruses

The continuous occurrence of zoonotic cowpox virus (CPXV) infections in Europe shows that poxviruses remain a considerable health threat which emphasizes the relevance of deepening the understanding of virus–host interactions. While there have been reports on the proteome composition of the human pathogenic Vaccinia Virus and Monkeypox Virus, the proteome of the CPXV mature virion is still unknown.

In this study the mature virion (MV) proteome composition of three genetically diverse CPXV (two isolates from rats and one reference strain), showing different pathogenicity in an animal model, was analysed in a label-free quantitative proteomics approach using nanoflow reversed phase liquid chromatography and tandem mass spectrometry (nLC-MS/MS). The conserved virion proteome of CPXV could be described qualitatively and quantitatively and was compared to the literature data of the VACV virion. In addition to earlier proteome studies of poxviruses, ubiquitination of viral proteins as well as protein complex formation during virus attachment to the cell membrane were analysed.

The results indicate that the heterogeneity of the CPXV virions proteome configuration is mainly related to proteins of unknown function or proteins associated to virus–host interaction. Among these identified proteins are host range factors and proteins relevant for immunoevasion. The data further provides first insights into the ubiquitination of the CPXV particle proteome and its interaction with the cell surface on proteomic level.

Zoonoses and Emerging Viruses

Presentation

Abstract-ID: 594

Nova virus as the first mole-borne hantavirus detected in Germany

Lukas Radosa¹, Mathias Schlegel², Sandra Essbauer³, Dirk Höper⁴, Bernd Walther⁵, Detlev H. Krüger⁶, Boris Klempa⁷, Rainer G. Ulrich²

¹Institute of Virology, Charité Medical School, Berlin; ²Institute for Novel and Emerging Infectious Diseases, Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany; ³Bundeswehr Institute of Microbiology, Department Virology & Rickettsiology, München, Germany; ⁴Institute for Virus Diagnostics, Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany; ⁵Erminea GmbH, Münster, Germany; ⁶Institute of Virology, Charité Medical School, Berlin, Germany; ⁷Institute of Virology, Charité Medical School, Berlin, Germany; Institute of Virology, Slovak Academy of Sciences, Bratislava, Slovakia

Our view on hantavirus ecology and host range was fundamentally extended over the last decade; the dogmatic concept of hantaviruses as rodent-borne viruses was changed when Tanganya virus, carried by *Theromys* shrew, was discovered in Africa in 2007. Since then, more than 20 new hantaviruses associated with insectivores were described worldwide. In previous years, our comprehensive screening and subsequent sequence analyses revealed presence of two shrew-borne hantaviruses in Central Europe, Seewis virus (associated with Eurasian common shrew, *Sorex araneus*) and Asikkala virus (associated with Eurasian pygmy shrew, *Sorex minutus*), and showed their broad geographical distribution, high genetic divergence, and strong geographic clustering. Here we report detection and genetic characterization of the mole-borne Nova virus (NVAV), associated with European common mole (*Talpa europaea*) from Germany.

Two samples obtained in the Schwarzwald area out of altogether 21 samples from moles collected in various parts of Germany were found positive in the genus-reactive screening RT-PCR assay. Subsequently, numerous efforts were made to obtain additional genomic data through next-generation sequencing approach as well as sequencing of overlapping PCR fragments. Sequence comparisons of the obtained large (L) and small (S) segment nucleotide sequences with NVAV strains from France and Hungary showed high amount of silent mutations leading to high degree of sequence diversity on nucleotide level (86.6-87.3% sequence identity) but nearly identical amino acid sequences (98.4-98.9% sequence identity). Phylogenetic analyses confirmed that the German strains form a separate clade within the monophyletic group of all available NVAV sequences.

Altogether, our studies showed the presence and revealed first genomic sequence data for the shrew-borne Seewis and Assikala viruses and the mole-borne NVAV in Central Europe. The outcome of our studies will serve as a basis for further steps in evaluation of the public health relevance of these new insectivore-borne viruses.