maturation, a low IgG avidity is indicative of WNV infection within the previous month.

https://doi.org/10.1016/j.ijid.2018.11.287

21.077

Recombinant of PUUV genome S segment isolated from rodents captured in the Republic of Tatarstan, Russia

E. Kabwe [1], Y.N. Davidyuk [1], S.P. Morzunov [2], E.V. Martynova [3], E.E. Garanina [1,*], R.K. Ismagilova [1], S.F. Khaiboullina [4], A.A. Rizvanov [1]

[1] *Kazan (Volga region) Federal University, Openlab "Gene and Cell technologies", Kazan/RU*
[2] *University of Nevada, Reno, Department of Pathology, Nevada, Reno/US*
[3] *Kazan (Volga region) Federal University, Openlab "Gene and Cell technologies", Kazan/US*
[4] *University of Nevada, Reno, Department of Microbiology and Immunology, Nevada, Reno/US*

Purpose: Background: *Puumala* hantavirus (PUUV) is the main cause of hemorrhagic fever with renal syndrome (HRFS) in Russia. Although known to cause HFRS endemic in the Republic of Tatarstan (RT), little is known about the genetic diversity of PUUV in the Republic. Therefore, we sought to characterize variations in PUUV S-segment in bank voles in the RT.

Methods & Materials: Material and methods: Total of 121 bank voles were captured in the north-west regions of RT during the 2014-2015 HFRS outbreak. Total RNA was extracted from lung tissue and used for RT-PCR and sequence analysis.

Results: Results: Comparison analysis of viral S segment sequences (564 bp) revealed 92.9-97.3% nucleotide identity between 29 RT PUUV strains and RUS lineage strains, while the lower similarity of 83.7-87.6% was found in strains from FIN lineage. Interestingly, sequence similarity of four RT PUUV strains and RUS strains was lower 85.8-87.6% than that found in the majority of isolates. Surprisingly, these strains had a higher identity (99.6-99.8%) with strain "Sotkamo" of FIN lineage. Phylogenetic analysis demonstrated that the four strains with low similarity to RUS lineage clustered with the FIN strains cluster. Further analysis of the full coding region of strain "032" S-segment, which had more similarity to FIN lineage, revealed that the partial sequence from 242 to 857 nt was 99.5% identical to "Sotkamo" strain, while the segment from 864 to 1341 nt showed 92.1-93.5% identical to RUS lineage strains.

Conclusion: Conclusion: Therefore, our data suggest that strain "032" could be the progeny of the recombination between RUS and FIN genetic lineages. It remains to be determined if recombinant PUUV strains could cause different clinical presentation of HFRS.

The Russian Government Program of Competitive Growth of Kazan Federal University supported this study. Also, Albert Rizvanov was supported by state assignment 20.5175.2017/6.7 of the Ministry of Education and Science of the Russian Federation.

https://doi.org/10.1016/j.ijid.2018.11.288

21.078

Molecular identification of a presumably novel hantavirus in bronze tube-nosed bat (*Murina aenea*) in Malaysia

B. Zana [1], D. Buzás [1], G. Kemenesi [1,*], T. Görföl [2], G. Csorba [2], M. Madai [3], F. Jakab [1]

[1] *University of Pécs, Institute of Biology, Faculty of Sciences, Pécs/HU*
[2] *Hungarian Natural History Museum, Department of Zoology, Budapest/HU*
[3] *University of Pécs, Szentágothai Research Centre, Virological Research Group, Pécs/HU*

Purpose: Hantaviruses (*Hantaviridae*) cause two types of life-threatening human diseases, hemorrhagic fever with renal syndrome (HFRS) in Eurasia and hantavirus cardiopulmonary syndrome (HCPS) in the Americas. To date, as a consensus, wild rodents were believed as natural hosts of hantaviruses. However, recent studies described several novel hantaviruses in shrews, moles and bats, suggesting the dispersal of hantaviruses in several animal taxa during their evolution. Interestingly, the co-evolutionary analyses of most recent studies have raised the possibility of bats and/or soricomorphs may have served as the primordial mammalian host and harboured the ancestors of rodent-borne hantaviruses.The aim of our study was to investigate the presence of hantaviruses in bat lung tissue homogenates originally collected for taxonomic purposes in Malaysia, 2015.

Methods & Materials: Hantavirus specific nested PCR screening of 116 samples targeting the L segment of the virus have revealed the positivity of two lung tissue homogenates originating from *Murina aenea* bat species.

Results: The obtained results indicate the first molecular evidence for hantavirus in *Murina eanae* bat species.

Conclusion: Preliminary sequence analysis of the PCR amplicon suggest the identified virus may represents a novel species within Orthohantavirus genus. Furthermore, our results provide additional genomic data to help extend our knowledge about the evolution of these viruses and we present the first hantavirus sequence from *Murina* bat genus.

https://doi.org/10.1016/j.ijid.2018.11.289

21.079

Canine leishmaniosis and first report of *Leishmania infantum* in the blood of equids in Kabylia (Algeria)

H. Medkour [1], Y. Laidoudi [1], I. Lafri [2], I. Bitam [3], O. Mediannikov [1], B. Davoust [1,*]

[1] *IHU Méditerranée Infection, MEPHI, Marseilles/FR*
[2] *University of Blida 1, Institute of Veterinary Sciences, Blida/DZ*
[3] *Superior School of Sciences and Food Industries, Algiers/DZ*

Purpose: Canine leishmaniosis is a severe zoonotic disease that affects millions of dogs. Algeria is the most affected country in the Mediterranean basin. Both diseased and sub-clinically infected dogs are infectious to sand fly vectors, allowing transmission of the parasite to other dogs, animals or humans. That is why prompt diagnosis of infected dogs is essential. The occurrence *Leishmania infantum* was assessed in domestic dogs from Kabylia (Algeria), by means of PCR and serological analyses.

Methods & Materials: 214 dogs, a donkey and a horse were sampled, in June 2018, from three locations in the Kabylia region: Bouira, Tizi-Ouzou and Sétif. Sera were analyzed using rapid immunomigration test (Witness® Leishmania, Zoetis, France) followed by immunofluorescence test (IFAT) with 1/50 as positivity threshold. Blood samples were analyzed by a real-time PCR pan-*Leishmania* designed system, targeting 28S rRNA gene followed by qPCR targeting *L. infantum* kDNA. All dogs were examined and classed into one of the clinical scores (CS), from CS0 to CS4, per the frequency of their clinical signs.

Results: The total prevalence is of 34.5% (74/214) when at least one of the tests is positive. IFAT was more sensible and the prevalence collected scored a 31.8% (68/214), followed by Witness® Leishmania (29.9%, 64/214) and PCR (4.7%, 10/214). All positive samples on *Leishmania* spp. PCR 28S rRNA were positives for kDNA *L. infantum* specific PCR. The donkey and the horse were, also, positives by the two PCR systems. The equids lived near *Leishmania* infected dogs. Each infected dog where diagnosed in different stages of the disease: 74.3% (55/74) had at least one clinical sign and 25.7% (19/74) were asymptomatics; 43.2% (32/74) had CS1, 21.6% (16/74) had CS2, 5.4% (4/74) had CS3 and 4% had CS4.

Conclusion: Kabylia remains an active focus for CanL with a high prevalence; this epidemiological situation requires the implementation of a national program against this protozoosis. This study highlights, for the first time, *L. infantum* in equids from Algeria which suggests the possible involvement of these animals in the epidemiological chain of *L. infantum* in high-transmission areas. This preliminary study deserves further investigation due to the lack of equids.

https://doi.org/10.1016/j.ijid.2018.11.290

21.080

Phase 2 clinical results: Chikungunya vaccine based on measles vector (MV-CHIK) induces humoral and cellular responses in the presence of pre-existing anti measles immunity

K. Ramsauer[1,*], E. Reisinger[2], C. Firbas[3], U. Wiedermann-Schmidt[4], E. Beubler[5], A. Pfeiffer[1], M. Müllner[6], J. Aberle[7], E. Tauber[1]

[1] *Themis, Vienna/AT*
[2] *Medical University Rostock, Rostock/DE*
[3] *Medical University of Vienna, Clinical Pharmacology, Vienna/AT*
[4] *Medical University of Vienna, Institute of Specific Prophylaxis and Tropical Medicine, Vienna/AT*
[5] *Medical University Graz, Graz/AT*
[6] *Themis, Vienna/MK*
[7] *Medical University of Vienna, Department of Virology, Vienna/AT*

Purpose: We have developed a live recombinant measles vector-based vaccine to prevent Chikungunya disease (MV-CHIK). Previously, the safety and immunogenicity was demonstrated in a Phase 1 clinical trial (EudraCT: 2013-001084-23). Here, we will present the final data of a Phase 2 clinical trial in 263 healthy, volunteer adults (NCT02861586). Chikungunya is a rapidly spreading viral disease affecting significant parts of the Americas, India and South East Asia. In the majority of patients, the febrile acute disease turns into a chronic disease causing severe, debilitating arthritis that can last years post-infection. So far, no vaccine or treatment has been licensed.

Methods & Materials: The clinical trial was double blinded, randomized, active - and placebo-controlled, with the objective to evaluate the optimal dose of MV-CHIK vaccine in regard to immunogenicity, safety and tolerability in healthy adult volunteers. Immune responses were determined by induction of neutralizing antibodies by plaque reduction neutralization titer (PRNT).

Results: The vaccine presents with a safety profile in humans that is comparable to the approved control vaccine in the trial. Overall frequency of solicited and unsolicited adverse events (AEs) was low (not more than 30%) and all events were transient. No vaccine related Serious AEs (SAE) were observed. The vaccine induced neutralizing antibodies after a single immunization in up to 93% in the high dose group. A boost substantially increased the neutralizing antibody titers and seroconversion rate. In addition, CHIKV specific T-cell responses were induced following vaccination. Interestingly, the vaccine induced a functional immune response even in the presence of pre-existing anti-measles immunity as demonstrated in a subset of subjects who received a measles prime immunization prior to the Chikungunya vaccine.

Conclusion: The data show that the live recombinant MV-CHIK vaccine is a safe and tolerable vaccine that induces a robust immune response. The data clearly path the way for the preparation of a late stage clinical development program.

https://doi.org/10.1016/j.ijid.2018.11.291

21.082

Emerging human alveolar echinococcosis in Hungary. Early experiences in clinical management in a single center study from 2005-2018

B. Dezsényi[1,*], S. Tóth[1], A. Horváth[1], J. Szlávik[1], Z. Makrai[2], T. Strausz[3], T. Nagy[4], Z. Dubóczki[5], T. Mersich[5], J. Csomor[6], Á. Somorácz[7], L. Nehéz[8], A. Patonai[9], A. Doros[9], J. Danka[10], I. Kucsera[10], H. Auer[11], G. Rezza[12], T.F. Barth[13], A. Casulli[12]

[1] *Dél Pesti Centrum Kórház Országos Hematológiai és Infektológiai Intézet, Infectology, Budapest/HU*
[2] *National Institute of Oncology, Anestesiology and Intensive Therapy, Budapest/HU*
[3] *National Institute of Oncology, Surgical and Molecular Tumour Pathology Center, Budapest/HU*
[4] *National Institute of Oncology, Department of Oncological Internal Medicine and Clinical Pharmacology "B", Budapest/HU*
[5] *National Institute of Oncology, Tumour Surgery Center, Budapest/HU*
[6] *Dél Pesti Centrum Kórház Országos Hematológiai és Infektológiai Intézet, Pathology, Budapest/HU*
[7] *Semmelweis University, 2nd Department of Pathology, Budapest/HU*
[8] *Semmelweis University, 1st Department of Surgery, Budapest/HU*
[9] *Semmelweis University, Department of Transplantation and Surgery, Budapest/HU*
[10] *National Center for Epidemiology, Department of Parasitology, Budapest/HU*
[11] *Meduni Wien, Parasitology, Vienna/AT*
[12] *Instituto Superiore di Sanita, Department of Infectious, Parasitic and Immunomediated Diseases, Rome/IT*
[13] *Ulm University, Institute of Pathology, Ulm/DE*

Purpose: Cystic echinococcosis is the most prevalent reportable helminthosis and also a neglected zoonotic disease in Hungary. Still nowadays the majority of cases are cystic echinococcosis (CE)