Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.
Evidence of interspecies transmission of rotavirus G4P[6] strain in Manado, Indonesia

A.F.C. Kalesaran a, A. Thongprachum b, D.H.C. Pangemanan c, S. Takanashi d, S. Okitsu e, J. Tuda e, M. Mizuguchi f, S.M. Warouw g, H. Ushijima h

a Faculty of Public Health, Sam Ratulangi University, Epidemiology, Manado/ID
b Nihon University School of Medicine, Department of Pathology and Microbiology, Tokyo/JP
c Faculty of Medicine, Sam Ratulangi University, Department of Physiology, Manado/ID
d The University of Tokyo, Department of Developmental Medical Sciences, Tokyo/JP
e Faculty of Medicine, Sam Ratulangi University, Department of Parasitology, Manado/ID
f The University of Tokyo, Department of Developmental Medical Sciences, Tokyo/JP
g Faculty of Medicine, Sam Ratulangi University, Department of Pediatrics, Manado/ID
h Oita University, Department of Pediatrics, Oita/JP

Purpose: To investigate the sequence analysis of Manadonese G4P[6] rotavirus strain associated with diarrhea.

Methods & Materials: From April 2013 to July 2014, 441 fecal samples were collected from pediatric inpatients in RSUD Dr. R. D. Kandou Hospital, Manado. The samples were screened for group A rotavirus and 10 other target viruses by multiplex PCR. Positive samples for rotavirus were further analyzed for genotyping and sequence analysis. Phylogenetic trees were constructed by neighbour-joining method.

Results: Group A rotavirus was found as the predominant viral agent (49.9%), with G1P[8] being the most common (69.5%) strain. One case of G4P[6] was found among the positive samples and sequence analysis of VP7 gene showed a close relation with porcine rotavirus strains, while VP4 genes showed a closer relation with human rotavirus strains.

Conclusion: The case of G4P[6] rotavirus strain in this study suggested an evidence of human-animal reassortment and showed a possibility of interspecies transmission between porcine and human.

http://dx.doi.org/10.1016/j.ijid.2016.11.314

Absence of MERS-CoV in domestic camels, Republic of Korea, 2015

H.-J. Kim a, b, J.-S. Choi b, H.-M. Nam a, H.-E. Kang a

a Animal and Plant Quarantine Agency, Kimcheon/KR
b Animal and Plant Quarantine Agency, Kimcheon/KR

Purpose: In the Republic of Korea (ROK), the first human case of Middle East Respiratory Syndrome coronavirus (MERS-CoV) infection was reported on 20 May 2015. It occurred by a traveler who has been traveled to Middle East, since then outbreaks associated with health care facilities were rapidly spreading. Unlike previously reported MERS-CoV occurred countries, explosive outbreaks of MERS-CoV caused public health threat and socio-economic loss in ROK. In these circumstances, increased concern about the camels known as an animal reservoir of MERS-CoV triggered the necessity of MERS-CoV surveillance in domestic camels. Thus, we investigated MERS-CoV infection in all domestic camels in June, 2015 in ROK.

Methods & Materials: We collected nasal swab specimens from 46 camels both dromedaries (Camels dromedarius) and Bactrian (Camels bactrianus) in 10 provinces in ROK. Real-time reverse transcription PCR (RT-PCR) was performed as recommended by the World Health Organization (WHO).

Results: All samples were confirmed as negative for MERS-CoV.

Conclusion: The MERS-CoV outbreaks in ROK are characterized by super-spreading events involving several healthcare facilities, poor infection control and so on. This situation caused panic and strike excessive fear into people thus we took a preventive action against camels. Therefore, we investigated MERS-CoV in domestic camels. Our results indicate the absence of MERS-CoV among domestic camels in ROK. In addition, it suggests that there is no epidemiological relation between camels and outbreak of MERS in ROK.

http://dx.doi.org/10.1016/j.ijid.2016.11.315

Serological survey of hantavirus infection among rodents in Hungary

M. Madai a, *, V. Németh b, M. Oldal a, G. Horváth b, R. Herczeg b, R. Pintér b, A. Kutas a, B. Dallos a, K. Bánya i, F. Jakab a

a University of Pécs, Institute of Biology, Virological Research Group, Pécs, BARANYA/HU
b University of Pécs, Pécs/HU

Purpose: Hantaviruses are found worldwide and are known to cause serious human diseases. Natural hosts are rodents, soricormorphs and bats. Three types of hantaviruses are circulating in Hungary, Dobrava, Puumala and Tula which are carried by mice and voles. Dobrava and Puumala viruses cause human disease. In Hungarian forests the dominant species of rodents are yellow necked mouse (Apodemus flavicollis) striped field mouse (Apodemus agrarius) wood mouse (Apodemus sylvaticus) and bank vole (Myodes glareolus) which are natural reservoirs. The aim of the study was to survey the prevalence of hantaviruses among rodent populations and examine the potential correlation between population densities and seroprevalence.

Methods & Materials: The rodents were trapped at 13 sampling plots on a 149 ha area in the Mecsek Mountains, Hungary from March to Oktober between 2011 and 2014 using a capture- mark-recapture method. Rodent sera were tested for antibodies against the two most significant hantavirus species in Europe, Dobrava-Belgrade (DOBV) and Puumala (PUUV) viruses by ELISA.

Results: Among the 3720 tested sera samples 350 were positive for hantaviruses (DOBV, PUUV). In 2011 the seroprevalence was 14.5% (178/1229), but in 2012 despite of the higher number of rodents it was just 7.4% (122/1638), in 2013 and in 2014 it was about 6%. The seroprevalence was the highest for the Apodemus species in the first two year, then in 2013 and 2014 for the Myodes glareolus. In every year among the hantavirus positive rodents the number of males were higher.

Conclusion: Since the seroprevalence in 2012 decreased to half despite of the higher sample size, it may indicate that the number of infected individuals and community size are not directly proportional. Since in the subsequent years we registered great decrease in population size, but the infection rate stagnated throughout, it may indicate a time delay between community size changing and infection rate alteration. In four years the number of Apodemus species which were originally abundant in the area decreased and the population density of Myodes glareolus became higher. Therefore at the last year of the survey of 2014, the Puumala hantavirus seroprevalence was much higher compared to Dobrava seroprevalence.

http://dx.doi.org/10.1016/j.ijid.2016.11.316