Obratlovci - zdroj nákaz, hostitelé, rezervoáry

Osnova přednášky: Obratlovci

1. Obratlovci jako hostitelé a rezervoár původců zoonóz
2. Savci
3. Ptáci
4. Obojživelníci
5. Plazi
6. Ryby

Hostitel – agens v něm bylo detegováno nebo izolováno

Hostitel amplifikátor – vyšší koncentrace patogena a nejméně několik dní v jeho moči, trusu anebo krvi, takže tento hostitel se může stát donorem nákazy (př. JEV)

Rezervoár - zabezpečuje dlouhodobé přežití agens

i v meziepidemickém období

Hostitel nahodilý - nehraje žádnou roli v epizootickém procesu

Hostitel a rezervoár

Role obratlovce	Protilátky	Patogen v krvi, exkretech	Symptomy
Hostitel	+	– nebo +	+ nebo –
Hostitel - amplifikátor	+	++	+ nebo –
Rezervoár*	+	+	**obvykle –**

*** patogen v populaci udržován i v meziepidemickém období**

SAVCI (*Mammalia*)

Řád HMYZOŽRAVCI (*Insectivora*)

Řád LETOUNI (*Chiroptera*)

- Podřád Kaloni (*Megachiroptera*)
- Podřád Netopýři (*Microchiroptera*)

Řád Luskouni (Pholidota)

Řád PRIMÁTI (*Primates*)

Řád ŠELMY (*Carnivora*)

Řád HLODAVCI (*Rodentia*)

Řád ZAJÍCOVITÍ (*Lagomorpha*)

Řád SUDOKOPYTNÍCI (*Artiodactyla*)

Řád LICHOKOPYTNÍCI (*Perissodactyla*)

Řád VAČNATCI (*Marsupialia*)

Erinaceus europaeus (j. západní), *E. concolor* (j. východní)

KE, CCHF, *Leptospira* spp., *Francisella tularensis*,

B. burgdorferi, *Trichophyton* spp.

Sorex araneus (rejsek obecný), Neomys fodiens (rejsek vodní)

KE, Puumala, *Leptospira* spp., *B. burgdorferi*, *F. tularensis*

KE, Puumala, Dobrava, *Bornavirus*, *Leptospira* spp., *B.microti*, *T. gondii*

Rousettus aegyptiacus (kaloň egyptský)

Chikungunya, WNV, Marburg (rezervoár)

Epomophorus wahlbergi, E. minimus

Ebola (rezervoár)

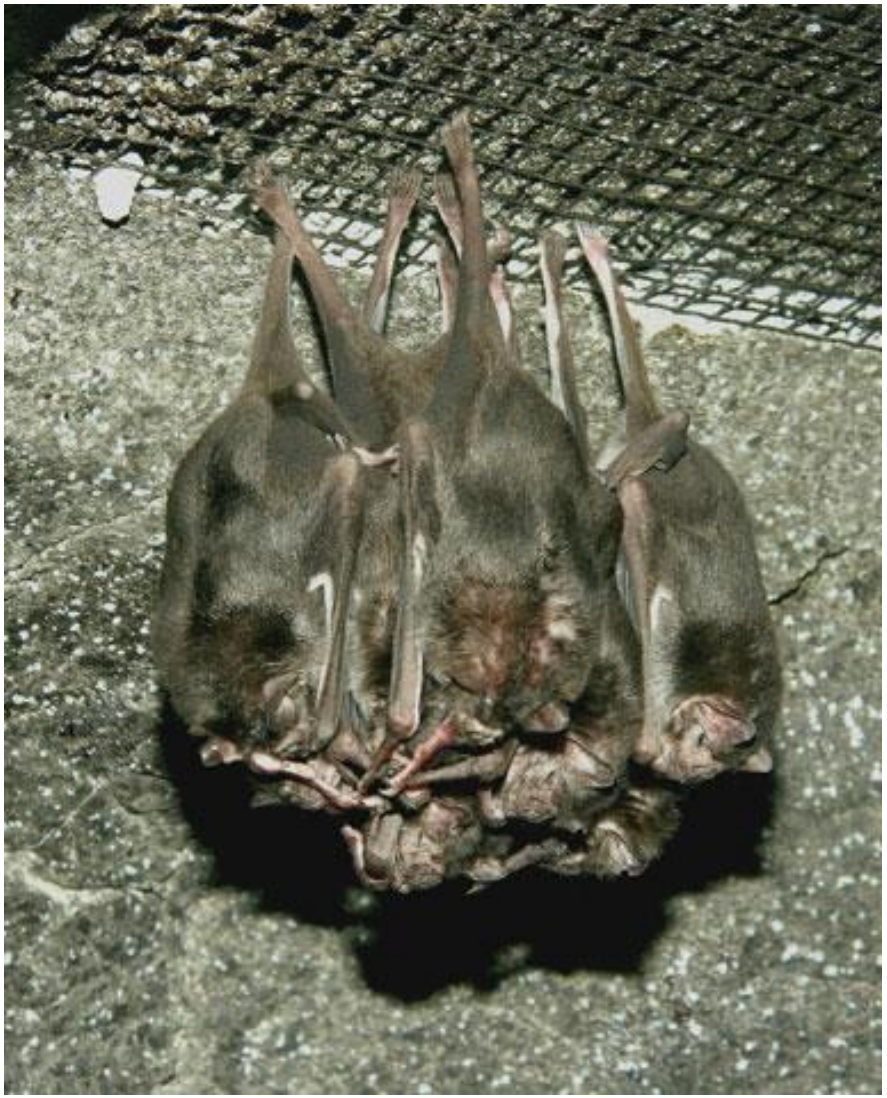
Pteropus spp.

Eidolon helvum

Nipah, Hendra

Desmodus rotundus (upír obecný)

Lyssavirus s.s.



Myotis myotis (netopýr velký), Nyctalus noctula (netopýr rezavý)

Lyssavirus (EBL-2)

Eptesicus serotinus (netopýr večerní), Miniopterus schreibersii (létavec stěhovavý)

Lyssavirus EBL-1
(rezervoár)

Lyssavirus
(Duvenhage, EBL-1)

Rhinolophus affinis, R. malayanus horseshoe bats

SARS-CoV-2 ?

Manis javanica (luskoun ostrovní)

SARS-CoV-2
(mezihostitel?)

Cercopithecus aethiops (kočkodan obecný), Macaca mulatta

Chikungunya,
Marburg,
Ebola

Chikungunya, KFD,
Herpes virus simiae

Papio anubis (pavián anubi)

Trichophyton simii

Neovison vison (norek americký)

SARS-CoV-2

Přenos SARS-CoV-2 z norků na člověka

RAPID COMMUNICATION

Preliminary report of an outbreak of SARS-CoV-2 in mink and mink farmers associated with community spread, Denmark, June to November 2020

Helle Daugaard Larsen[1] , Jannik Fonager[1] , Frederikke Kristensen Lomholt[1] , Tine Dalby[1] , Guido Benedetti[1] , Brian Kristensen[1] , Tinna Ravnholt Urth[1] , Morten Rasmussen[1] , Ria Lassaunière[1] , Thomas Bruun Rasmussen[1] , Bertel Strandbygaard[1] , Louise Lohse[1] , Manon Chaine[1] , Karina Lauenborg Møller[1] , Ann-Sofie Nicole Berthelsen[1] , Sarah Kristine Nørgaard[1] , Ute Wolff Sönksen[1] , Anette Ella Boklund[2] , Anne Sofie Hammer[2] , Graham J. Belsham[2] , Tyra Grove Krause[1] , Sten Mortensen[3] , Anette Bøtner[1,2] , Anders Fomsgaard[1] , Kåre Mølbak[1,2]

1. Statens Serum Institut, Copenhagen, Denmark
2. Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark
3. Department of Animal Health, Danish Veterinary and Food administration, Copenhagen, Denmark

Correspondence: Helle Daugaard Larsen (hdla@ssi.dk)

Citation style for this article:
Larsen Helle Daugaard, Fonager Jannik, Lomholt Frederikke Kristensen, Dalby Tine, Benedetti Guido, Kristensen Brian, Urth Tinna Ravnholt, Rasmussen Morten, Lassaunière Ria, Rasmussen Thomas Bruun, Strandbygaard Bertel, Lohse Louise, Chaine Manon, Møller Karina Lauenborg, Berthelsen Ann-Sofie Nicole, Nørgaard Sarah Kristine, Sönksen Ute Wolff, Boklund Anette Ella, Hammer Anne Sofie, Belsham Graham J., Krause Tyra Grove, Mortensen Sten, Bøtner Anette, Fomsgaard Anders, Mølbak Kåre. Preliminary report of an outbreak of SARS-CoV-2 in mink and mink farmers associated with community spread, Denmark, June to November 2020. Euro Surveill. 2021;26(5):pii=2100009. https://doi.org/10.2807/1560-7917.ES.2021.26.5.210009

Article submitted on 08 Jan 2021 / accepted on 04 Feb 2021 / published on 04 Feb 2021

In June–November 2020, SARS-CoV-2-infected mink were detected in 290 of 1,147 Danish mink farms. In North Denmark Region, 30% (324/1,092) of people found connected to mink farms tested SARS-CoV-2-PCR-positive and approximately 27% (95% confidence interval (CI): 25–30) of SARS-CoV-2-strains from humans in the community were mink-associated. Measures proved insufficient to mitigate spread. On 4 November, the government ordered culling of all Danish mink. Farmed mink constitute a potential virus reservoir challenging pandemic control.

Until recently, Denmark was a leading producer of mink pelts. In June 2020, severe acute respiratory coronavirus 2 (SARS-CoV-2) began to spread among mink farms [1] and, along with infections in mink, infections in people connected to mink farms were detected. Whole genome sequencing (WGS) confirmed community spread of mink-associated SARS-CoV-2 strains (mink variant). We briefly describe the human outbreaks related to mink and the public health response.

(SSI). Case reports were linked to an address register and a database of mink farm owners, provided by the Danish Veterinary and Food Administration (DVFA), thereby identifying human cases residing on mink farms. This group was encouraged to take a weekly PCR-test, in order to prevent spread of infection to the mink. (ii) Contact tracing of human cases, carried out by the Danish Patient Safety Authority, enabled identification of case patients with any connection to mink production. (iii) A surveillance programme established by DVFA, based on submission of samples from dead mink from all mink farms to SSI. (iv) Reporting of clinical signs in mink by veterinarians. Infection in mink on farms was confirmed after sampling by DVFA and submission of samples to SSI for SARS-CoV-2-testing by PCR and antibody test.

Estimates of the cumulative regional incidence rates per 100,000 population of human mink variant strain infections in the community were calculated. This was done by adding the weekly estimates (the number of all SARS-CoV-2-positive samples multiplied by the fre-

RAPID COMMUNICATION

SARS-CoV-2 infection in farmed minks, the Netherlands, April and May 2020

Nadia Oreshkova[1], Robert Jan Molenaar[2] , Sandra Vreman[1] , Frank Harders[1] , Bas B Oude Munnink[3] , Renate W Hakze-van der Honing[4] , Nora Gerhards[5] , Paulien Tolsma[4] , Ruth Bouwstra[2] , Reina S Sikkema[3] , Mirriam GJ Tacken[1] , Myrna MT de Rooij[3] , Eefke Weesendorp[2] , Marc Y Engelsma[4] , Christianne JM Bruschke[6] , Lidwien AM Smit[1] , Marion Koopmans[3] , Wim HM van der Poel[1] , Arjan Stegeman[7]

1. Wageningen Bioveterinary Research, Wageningen University and Research, Lelystad, the Netherlands
2. GD Animal Health, Deventer, the Netherlands
3. Department of Viroscience, Erasmus University Medical Center, Rotterdam, the Netherlands
4. Regional Public Health Service Brabant-Zuid-Oost, Eindhoven, the Netherlands
5. Institute for Risk Assessment Sciences (IRAS), Utrecht University, Utrecht, the Netherlands
6. Ministry of Agriculture, Nature and Food Quality, The Hague, the Netherlands
7. Department of Farm Animal Health, Faculty of Veterinary Medicine, Utrecht University, the Netherlands

Correspondence: Wim H.M. van der Poel (wim.vanderpoel@wur.nl)

Citation style for this article:
Oreshkova Nadia , Molenaar Robert Jan , Vreman Sandra , Harders Frank , Oude Munnink Bas B , Hakze-van der Honing Renate W , Gerhards Nora , Tolsma Paulien , Bouwstra Ruth , Sikkema Reina S , Tacken Mirriam GJ , de Rooij Myrna MT , Weesendorp Eefke , Engelsma Marc Y , Bruschke Christianne JM , Smit Lidwien AM , Koopmans Marion , van der Poel Wim HM , Stegeman Arjan . SARS-CoV-2 infection in farmed minks, the Netherlands, April and May 2020. Euro Surveill. 2020;25(23):pii=2001005. https://doi.org/10.2807/1560-7917.ES.2020.25.23.2001005

Article submitted on 24 May 2020 / accepted on 04 Jun 2020 / published on 11 Jun 2020

Respiratory disease and increased mortality occurred in minks on two farms in the Netherlands, with interstitial pneumonia and SARS-CoV-2 RNA in organ and swab samples. On both farms, at least one worker had coronavirus disease-associated symptoms before the outbreak. Variations in mink-derived viral genomes showed between-mink transmission and no infection link between the farms. Inhalable dust contained viral RNA, indicating possible exposure of workers. One worker is assumed to have attracted the virus from mink.

Currently, humanity is facing a pandemic of a new coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The virus is spreading efficiently

Here, we report SARS-CoV-2 infection of minks on two farms in the Netherlands and describe the associated clinical signs, pathological and virological findings. Sequence analysis of mink-derived viruses pointed at humans as the probable source of the initial infection and demonstrated transmission between minks. Furthermore, the presence of viral RNA in inhalable dust collected from the farms indicated a possible exposure of workers to virus excreted by minks.

Mink farming background

Minks are farmed for their fur. In the Netherlands, there are around 125 mink farms, with an average of 5,000 female breeding animals. In 2019, 4 million minks were produced. The sector has around 1,200 full-time and

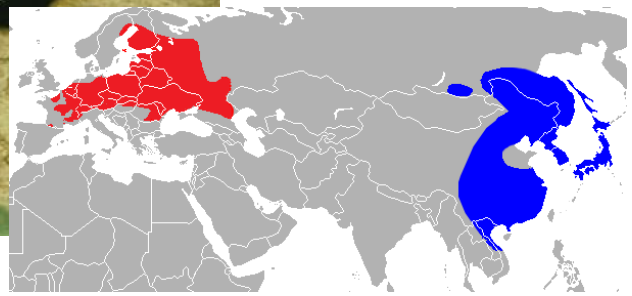
Vulpes vulpes (liška obecná)

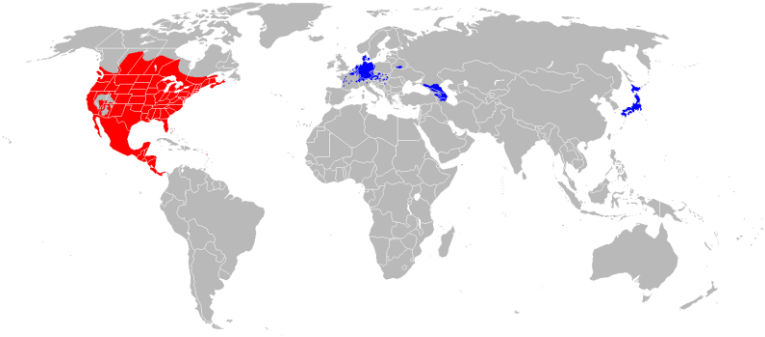
Lyssavirus s.s., KE

Procyon lotor (mýval severní), Nyctereutes procyonoides (psík mývalovitý), Mephitis mephitis (skunk pruhovaný)

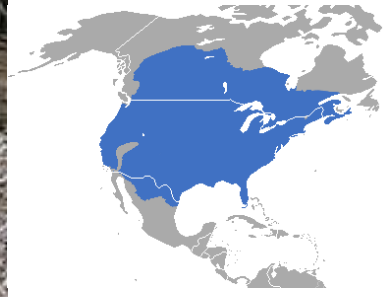
Lyssavirus s.s. (rezervoár)

Lyssavirus s.s.





CTF



Meles meles (jezevec obecný)

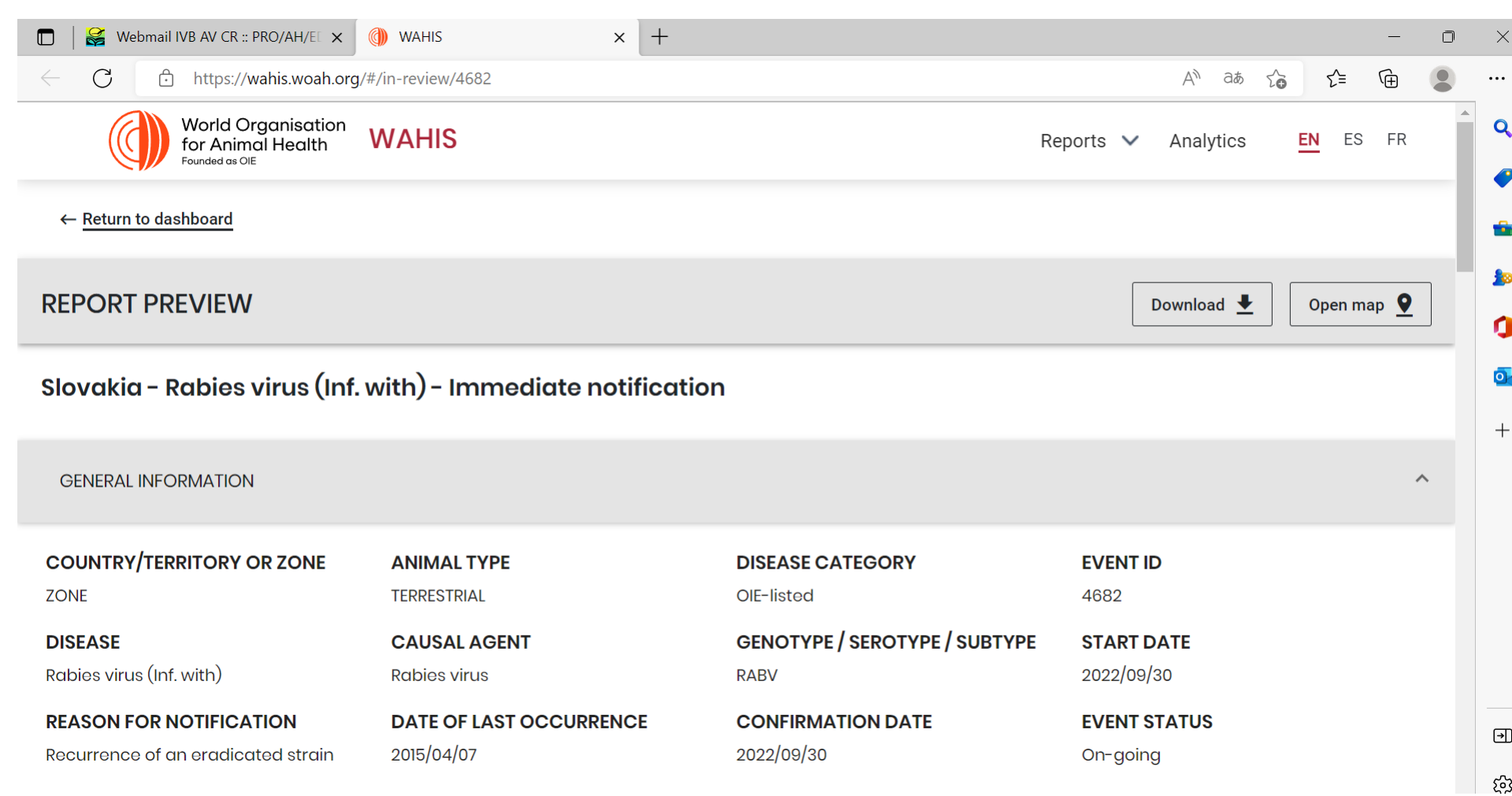
Lyssavirus s.s.

Oviječ maskovaný (*Paguma larvata*)

SARS-CoV

jezevec šedý (Melogale moschata)

SARS-CoV



EPIDEMIOLOGICAL COMMENTS

The badger was observed with behavioral changes, on which it was euthanized and the body sent to laboratory for testing, samples confirmed rabies, all necessary measures ordered, zones established, emergency vaccination of susceptible animals done; for being only one single case reported after genotyping results - very high percentage of homology with rabies viruses circulating in Poland, Ukraine, and Hungary, case close to Ukraine and Poland border.

Cynomys ludovicianus (psoun prériový), Citellus citellus (sysel obecný), Spermophilus richardsoni (sysel Richardsonův)

Y. pestis

Tamias minimus (čipmank malý), T. sibiricus (burunduk páskovaný)

CTF, KE, Y. pestis

https://www.nejm.org/doi/full/10.1056/NEJMoa1415627

Improved Protocols for Ventilator Liberation

What's the diagnosis?

Monkeypox

Safety and Efficacy of a Monoclonal Antibody against Malaria in Mali

ORIGINAL ARTICLE BRIEF REPORT

A Variegated Squirrel Bornavirus Associated with Fatal Human Encephalitis

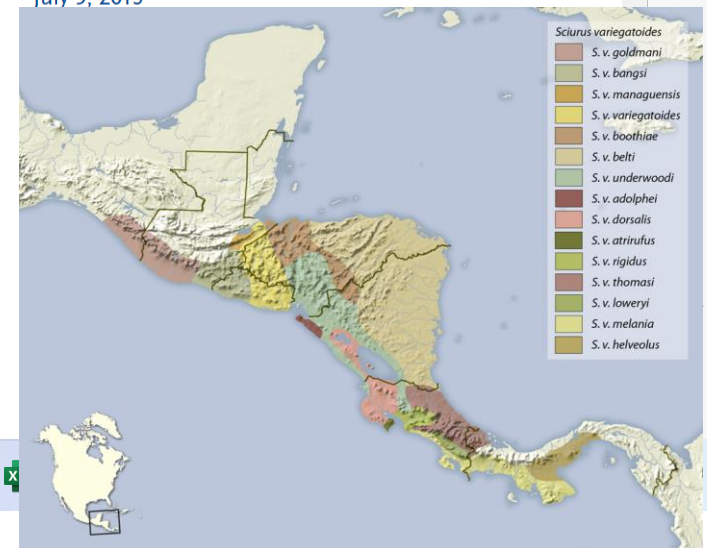
Bernd Hoffmann, D.V.M., Dennis Tappe, M.D., Dirk Höper, M.Sc., Christiane Herden, D.V.M., Annemarie Boldt, M.D., Christian Mawrin, M.D., Olaf Niederstraßer, M.D., Tobias Müller, M.D., Maria Jenckel, M.Sc., Elisabeth van der Grinten, D.V.M., Christian Lutter, D.V.M., Björn Abendroth, M.Sc., Jens P. Teifke, D.V.M., Daniel Cadar, D.V.M., Ph.D., Jonas Schmidt-Chanasit, M.D., Rainer G. Ulrich, Ph.D., and Martin Beer, D.V.M.

July 9, 2015

27 References 163 Citing Articles Letters

Summary

Between 2011 and 2013, three breeders of variegated squirrels (*Sciurus variegatoides*) had encephalitis with similar clinical signs and died 2 to 4 months after onset of the clinical symptoms. With the use of a metagenomic approach that incorporated next-generation sequencing and real-time reverse-transcriptase quantitative polymerase



Sciurus variagatoides

Kostarika

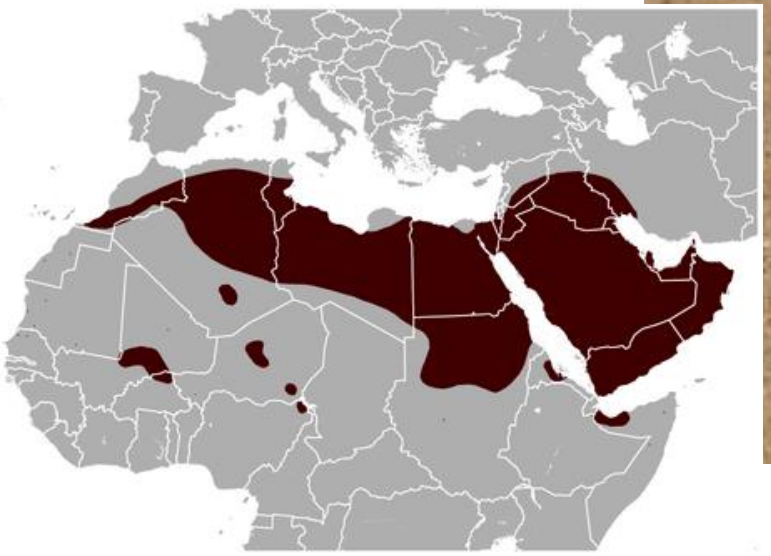
Sciurus vulgaris (veverka obecná), S. carolinensis (veverka popelavá)

KE, TAH, Puumala,
Lyssavirus s.s.,
B.burgdorferi

Castor canadensis (bobr kanadský)

F. tularensis

Jaculus jaculus (tarbík egyptský)



Y. pestis, Y. pseudotuberculosis

Cricetus cricetus (křeček polní), Mesocricetus auratus (křeček zlatý)

Hantavirus, *Lyssavirus* s.s., LCM, *Leptospira* spp., *Y. pestis*

Peromyscus leucopus (křeček bělonohý)

EEE, *B.burgdorferi*,

A. phagocytophilum

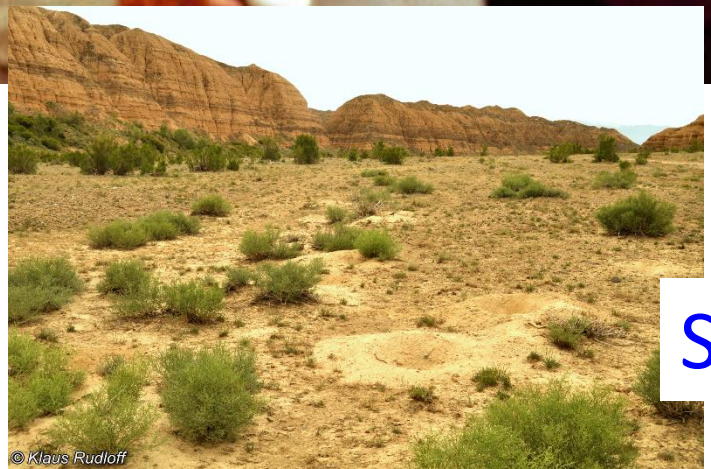
P. maniculatus (křeček dlouhoocasý)

Powassan, Sin Nombre, CTF, *Y. pestis*

Rhombomys opimus (pískomil velký), Psammomys obesus (pískomil tlustý)

Y. pestis, B. duttoni,

B. persica, Leishmania spp.



Střední Asie

Myodes glareolus (norník rudý), Microtus (hraboš polní) arvalis, M. agrestis (hraboš mokřadní)

CEE, Puumala (rezervoár), Tula, LCM, *B. burgdorferi*, *Leptospira* spp.,

B. microti

Arvicola terrestris (hryzec vodní),
Ondatra zibethicus (ondatra pižmová)

Puumala, Lyssavirus s.s., *Leptospira* spp.

OHF

Myocastor coypus (nutrie říční)

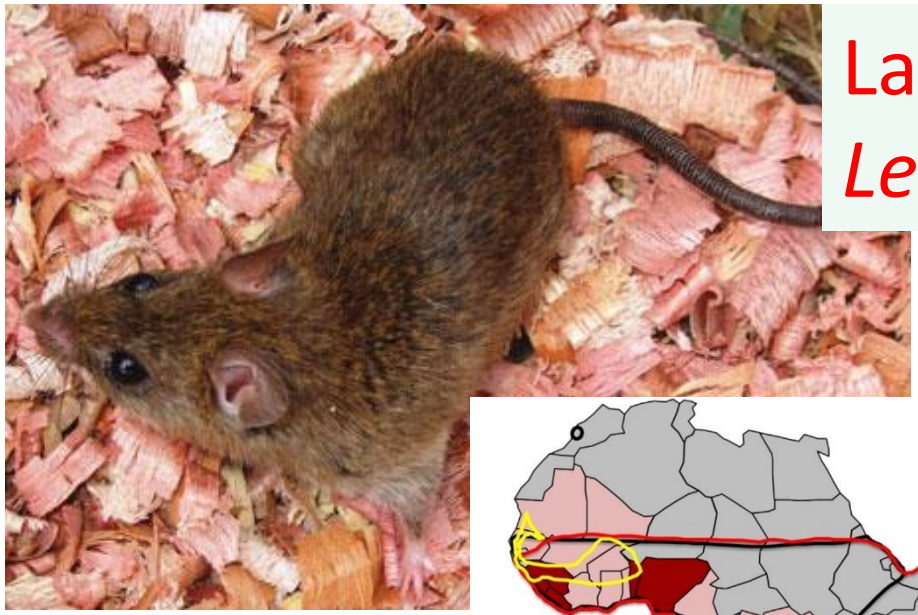
Lyssavirus s.s.

Leptospira spp.

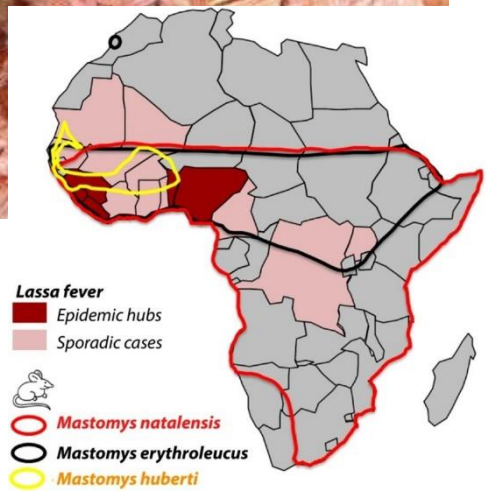
Apodemus flavicollis (myšice lesní), A. agrarius (m. temnopásá)

KE, hantaviry (Dobrava), *B.burgdorferi*, *A.phagocytophilum*, *Leptospira* spp.

Mastomys natalensis (krysa mnohobradavková), Arvicanthis niloticus (myš nilská)



Lassa, *Y. pestis*, *Leishmania* spp.



WNV, *Y. pestis*, *Leishmania* spp.

Mus musculus (myš obecná)

Puumala, Seoul, Sin Nombre, Junin, LCM, *Cardiovirus* EMC, R. akari, *Leptospira* spp., *Y. pestis*, *Trichophyton* spp., *Microsporum* spp., *P. carinii*, *T. gondii*

Rattus rattus (krysa obecná),
R. norvegicus (potkan obecný)

Hantaviry (Seoul), *Lyssavirus* s.s., LCM, virus hepatitidy E

O. tsutsugamushi, *R. akari*, *Leptospira* spp., *Spirillum minus*, *Streptobacillus moniliformis*, *Y. pseudotuberculosis*, *Histoplasma capsulatum*, *Pneumocystis* carinii, *Leishmania* spp. *T. gondii*

Lepus europaeus (zajíc polní),
Oryctolagus cuniculus (králík divoký)

F. tularensis,
mikrosporidie

WNV, TAH, CEE,
CCHF, *Leptospira* spp.

Sus scrofa (prase divoké), Phacochoerus aethiopicus (prase bradavičnaté)

T. brucei rhodesiense

JE, HEV, ASF

Leptospira pomona

Capreolus capreolus (srnec obecný),
Cervus elaphus (jelen evropský)

Lyssavirus s.s.,

A. phagocytophilum

Bison bison (bizon americký), B. bonasus (zubr evropský)

B. abortus, M. bovis

Tradiční rekonstrukce areálu uváděná ve starší literatuře (viz např. Pucek et al. 2004)
Rekonstrukce areálu na základě paleoklimatických a paleovegetačních modelů (Kuemmerle et al. 2012)
Pravděpodobný výskyt v pohoří Elborz (Heptner et al. 1988)
Doložené rozšíření v posledních 8 000 let (střední a pozdní holocén, upraveno podle Kuemmerle et al. 2012)
Nížinná linie - volně žijící populace a stáda ≥10 kusů
Nížinně-kavkazská linie - volně žijící populace a stáda ≥10 kusů

Odocoileus virginianus (jelenec běloocasý)
White-tailed deer

Multiple spillovers and onward transmission of SARS-Cov-2 in free-living and captive White-tailed deer (*Odocoileus virginianus*)

Authors: Suresh V. Kuchipudi,[1#] Meera Surendran-Nair[1], Rachel M. Ruden[2,3], Michelle Yon[4], Ruth H. Nissly[1], Rahul K. Nelli[3], Lingling Li[4], Bhushan M. Jayarao[4], Kurt J. Vandegrift[5], Costas D. Maranas[6], Nicole Levine[7], Katriina Willgert[8], Andrew J. K. Conlan[8], Randall J. Olsen[9,10], James J. Davis[11], James M. Musser[9,10], Peter J. Hudson[5], and Vivek Kapur[7#]

SARS-CoV-2?

Deer-to-deer transmission

B. burgdorferi, A. phagocytophilum

DALŠÍ SKUPINY OBRATLOVCŮ

Ptáci (Aves) (1/3)

VIRY

alfaviry Sindbis (koloniální vodní ptáci a pěvci), EEE, WEE (hlavně pěvci, bažant), Mayaro, Ross River a Barmah Forest, flaviviry JE (volavkovití, pěvci), WNV (vodní ptáci, havranovití, ojediněle další pěvci, hrdlička divoká aj.), SLE (vrabec domácí, holub domácí aj.), Murray Valley encefalitidy (volavkovití), Rocio (pěvci), LI (kur rousný, *Lagopus lagopus scoticus*), CEE (lesní ptáci) a KFD, *Bunyavirus* Oropouche, orbiviry Kemerovo (rehek zahradní) a Tribeč (špaček, pěnkava), *Orthomyxovirus* influenza A (slepice, krůta; přírodním rezervoárem jsou volně žijící vodní ptáci - vrubozobí, racci, bahňáci), *Paramyxovirus* NDV.

PTÁCI (Aves) (2/3)

BAKTÉRIE

Chlamydophila psittaci (rezervoár), *Clostridium difficile* (drůbež), *C. botulinum* (slepice aj.), *Listeria monocytogenes* (drůbež aj.), *Erysipelothrix rhusiopathiae* (krůta, slepice), *Staphylococcus aureus, Borrelia garinii* (lesní a mořští ptáci), *Campylobacter jejuni* (rezervoár, slepice), *C. coli, C. laridis*, *Salmonella typhimurium* (racek, vrabec, holub), *S. enteritidis* (slepice, racek aj.), *S. derby, S. panama* a jiné sérovary, enteropatogenní *Escherichia coli* (drůbež), *Yersinia pseudotuberculosis*,

Y. enterocolitica, *Pasteurella multocida*, *Mycobacterium avium* (rezervoár: havran, bažant, vrabec, holub hřivnáč, drůbež).

Ptáci (3/3)

HOUBY

Microsporum gallinae a *Trichophyton simii* (slepice), *Histoplasma casulatum* (ptáci jsou 'pronájemci' - houba roste v trusu špačků, vlhovců *Agelaius phoeniceus*, *Quiscalus quiscula* a lelků *Steatornis caripensis* na jejich hromadných nocovištích), *Cryptococcus neoformans* (holubi a některé druhy okrasných ptáků jsou 'pronájemci').

PRVOCI

Giardia lamblia, *Toxoplasma gondii, Cryptosporidium meleagridis* (drůbež). MIKROSPORIDIE: *Encephalitozoon hellem* (papoušci, vodní ptáci), *E. intestinalis* (vodní ptáci).

JINÍ EUKARYONTI: *Blastocystis* (slepice).

Columba livia f. domestica

Chlamydophila psittaci, Cryptococcus neoformans

Anser indicus H5N1

Larus ridibundus

Salmonella enterica

Ptačí bazar (alkouni aj.) na útesech Moherských (Irsko)

PLAZI (*Reptilia*)

VIRY: alfaviry WEE (hadi 3 rodů) a Mayaro (varan *Ameiva ameiva*, iguán *Tropidurus torquatus*), *Flavivirus* OHF (ještěrky) a WNV (aligátoři).

BAKTERIE: *Borrelia hermsii* a příbuzné druhy (agamy),

B. lusitaniae (ještěrky), *Listeria monocytogenes*, *Salmonella enterica* (některé sérovary patogenní pro člověka), *Yersinia enterocolitica.*

HOUBY: *Basidiobolus* (krokodýl).

PRVOCI: *Trypanosoma brucei rhodesiense*.

Obojživelníci (*Amphibia*)

VIRY: alfaviry WEE (*Rana pipiens*) a Sindbis (*Rana ridibunda*), *Flavivirus* OHF a WNV (*Rana* sp.).

BAKTERIE: *Yersinia enterocolitica.*

HOUBY: *Basidiobolus ranarum.*

PROTISTA: *Rhinosporidium seeberi.*

RYBY (*Pisces*)

BAKTÉRIE

Neorickettsia sennetsu, *Yersinia enterocolitica*, enterotoxigenní *Escherichia coli, Salmonella* spp., *Vibrio parahaemolyticus*, *V. vulnificus* (mořské ryby), *V. metschnikovii*, *Listeria monocytogenes*, *Erysipelothrix rhusiopathiae*, *Clostridium botulinum* typy E a F, *C. perfringens*, *Mycobacterium marinum*, *M. abscessus (atypické rychle rostoucí mykobaktérie)*

PROTISTA

Rhinosporidium seeberi