

Obratlovci – zdroj zoonotických virů

Vertebrates as reservoirs of zoonotic viruses



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 (obrtalovec/bezobratlí)- 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 mezi epidemickým 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



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



KE, Puumala

KE, Puumala,
Dobrava, *Bornavirus*



Rousettus aegyptiacus (kaloň egyptský)



Chikungunya, WNV, Marburg (rezervoár)

Epomophorus wahlbergi, E. minimus



Ebola (rezervoár)



Eidolon helvum

Nipah, Hendra

Pteropus spp.



Desmodus rotundus (upír obecný)

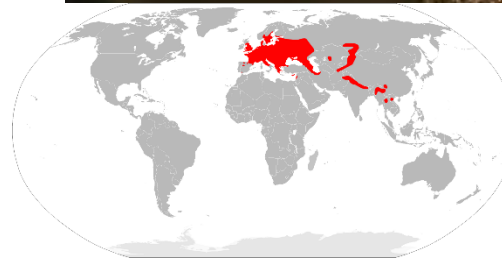
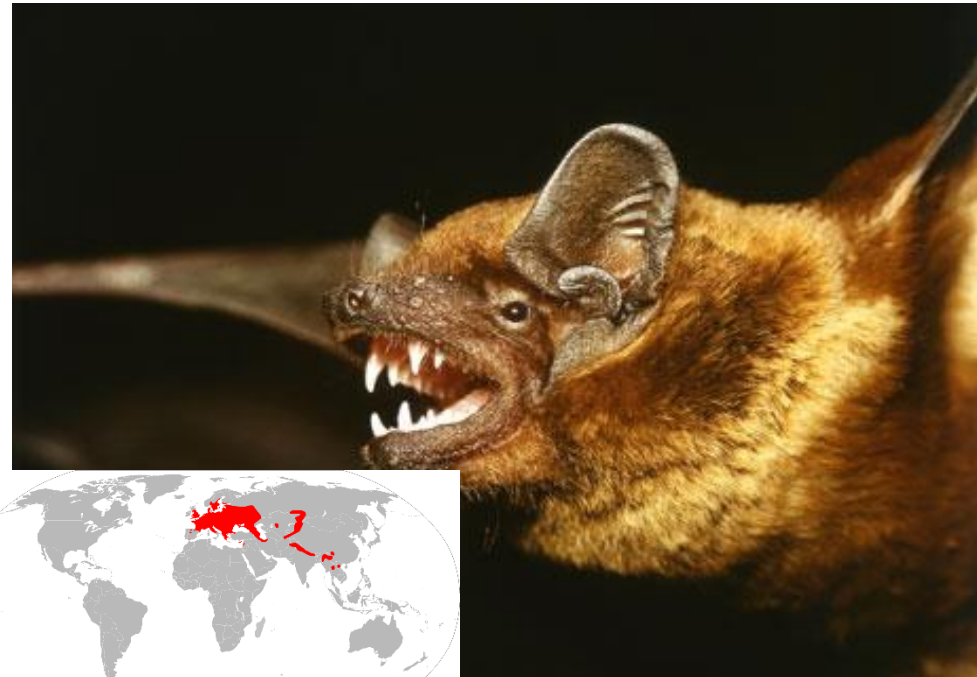
Lyssavirus s.s.



***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



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 Larsen¹, Jannik Fonager¹, Frederikke Kristensen Lomholt¹, Tine Dalby¹, Guido Benedetti¹, Brian Kristensen¹, Tinna Ravnholt Urth¹, Morten Rasmussen¹, Ria Lassaunière¹, Thomas Bruun Rasmussen¹, Bertel Strandbygaard¹, Louise Lohse¹, Manon Chaine¹, Karina Lauenborg Møller¹, Ann-Sofie Nicole Berthelsen¹, Sarah Kristine Nørgaard¹, Ute Wolff Sönksen¹, Anette Ella Boklund², Anne Sofie Hammer², Graham J. Belsham², Tyra Grove Krause¹, Sten Mortensen³, Anette Bøtner^{1,3}, Anders Fomsgaard¹, 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 Oreshkova¹, Robert Jan Molenaar¹, Sandra Vreman¹, Frank Harders¹, Bas B Oude Munnink¹, Renate W Hakze-van der Honing¹, Nora Gerhards¹, Paulien Toltsma¹, Ruth Bouwstra¹, Reina S Sikkema¹, Mirriam GJ Tackx¹, Myrna MT de Rooij¹, Eefke Weesendorp¹, Marc Y Engelsma¹, Christianne JM Brusckhe¹, Lidwien AM Smit¹, Marion Koopmans¹, Wim HM van der Poel¹, Arjan Stegeman¹

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, Toltsma Paulien, Bouwstra Ruth, Sikkema Reina S, Tackx Mirriam GJ, de Rooij Myrna MT, Weesendorp Eefke, Engelsma Marc Y, Brusckhe 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(3):pii=2001005. <https://doi.org/10.2807/1560-7917.ES.2020.25.3.2001005>

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

Dánsko,
Nizozemí

Vulpes vulpes (liška obecná)

Lyssavirus s.s., KE



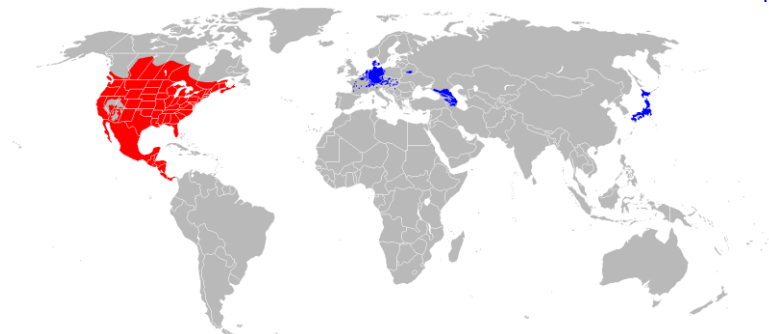
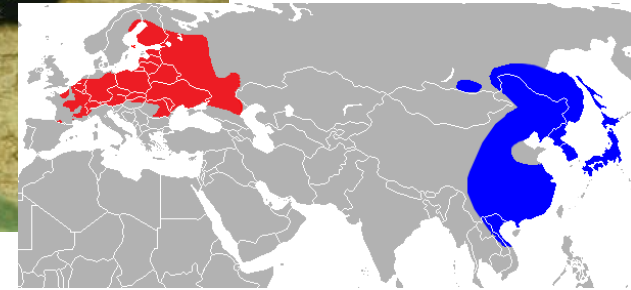
Procyon lotor (mýval severní), *Nyctereutes procyonoides* (psík mývalovitý), *Mephitis mephitis* (skunk pruhovaný)



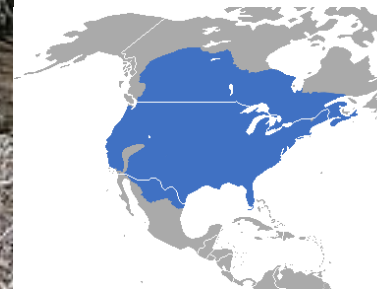
Lyssavirus s.s.
(rezervoár)



Lyssavirus s.s.



CTF



Meles meles (jezevec obecný)



Lyssavirus s.s.

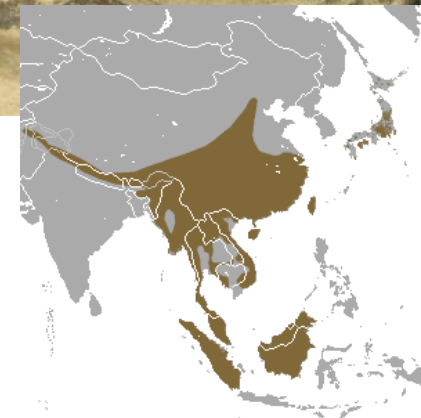
Ovíječ maskovaný (*Paguma larvata*)

SARS-CoV



jezevec šedý (*Melogale moschata*)

SARS-CoV



World Organisation for Animal Health
Founded as OIE

WAHIS

Reports Analytics EN ES FR

← [Return to dashboard](#)

REPORT PREVIEW

Download Open map

Slovakia - Rabies virus (Inf. with) - Immediate notification

GENERAL INFORMATION

COUNTRY/TERRITORY OR ZONE	ANIMAL TYPE	DISEASE CATEGORY	EVENT ID
ZONE	TERRESTRIAL	OIE-listed	4682
DISEASE	CAUSAL AGENT	GENOTYPE / SEROTYPE / SUBTYPE	START DATE
Rabies virus (Inf. with)	Rabies virus	RABV	2022/09/30
REASON FOR NOTIFICATION	DATE OF LAST OCCURRENCE	CONFIRMATION DATE	EVENT STATUS
Recurrence of an eradicated strain	2015/04/07	2022/09/30	On-going

– 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

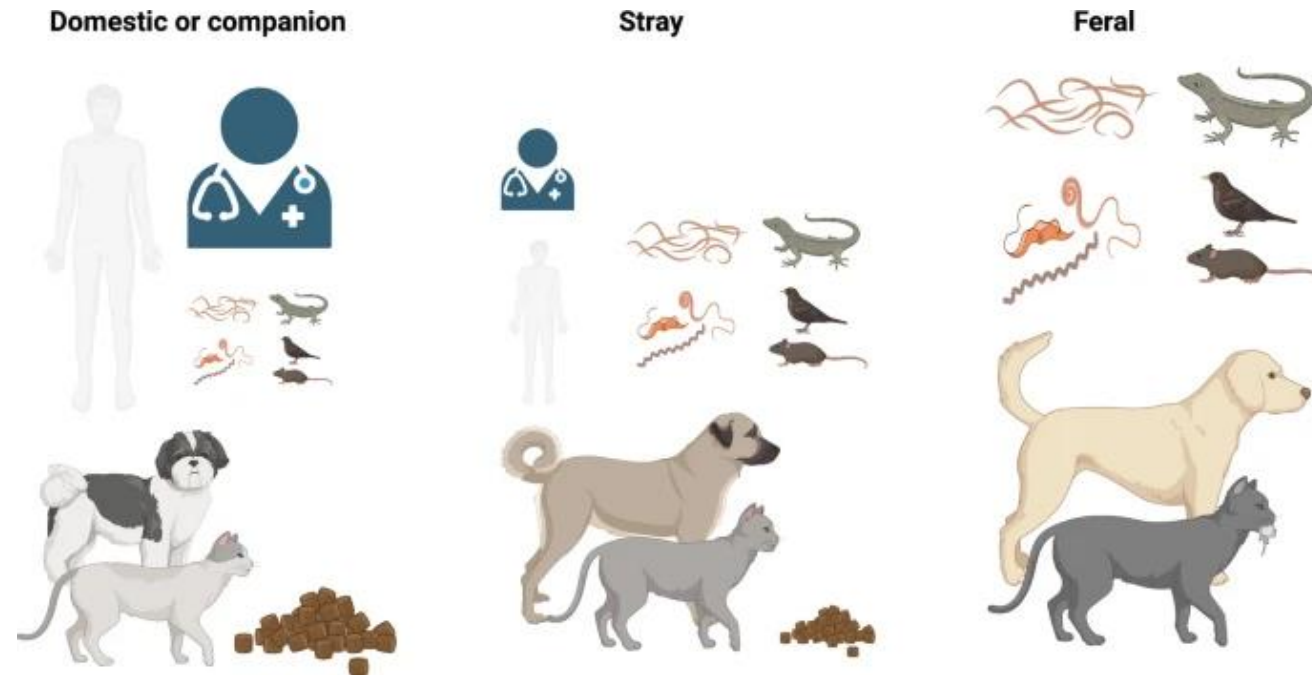
Kočka (*Felis catus*, *Felis silvestris*)



Lyssavirus s.s

Hostitelé klíšťat a blech (riziko přenosu řady dalších agens)

Pes (*Canis familiaris*)



- *Lyssavirus s.s.*
- Hostitelé klíšťat a blech (riziko přenosu řady dalších agens)

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

CTF, KE



■ Extant (resident) ■ Introduced

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.

Article Figures/Media Metrics
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)**



Lyssavirus s.s., KE,
TAH, Puumala



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

Hantavirus, *Lyssavirus* s.s., LCM



Peromyscus leucopus (křeček bělonohý)



EEE



P. maniculatus (křeček dlouhoocasý)

Powassan, Sin Nombre, CTF

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



CEE, Puumala (rezervoár), Tula, LCM



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



Puumala, Lyssavirus s.s.

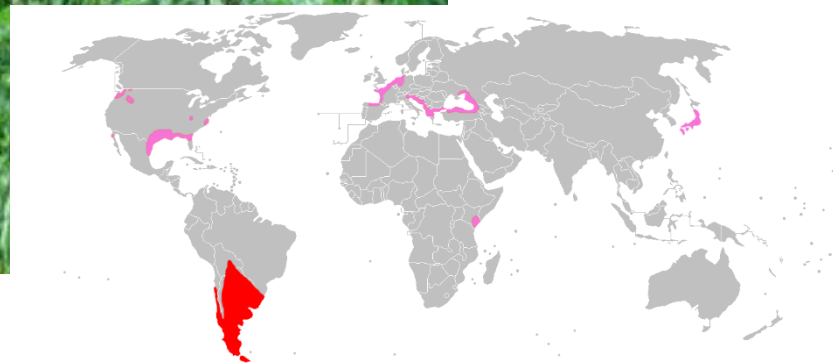
OHF



Myocastor coypus (nutrie říční)



Lyssavirus s.s.



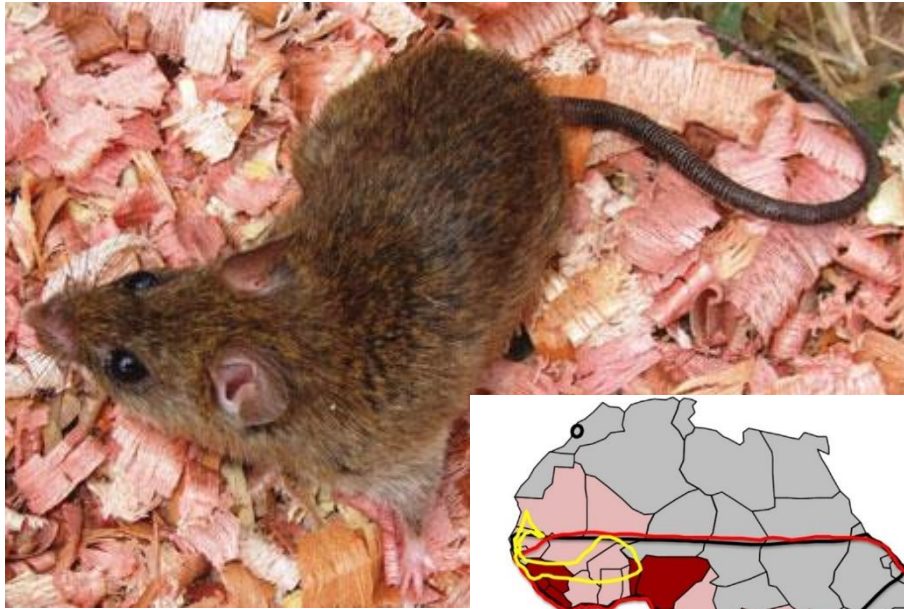
***Apodemus flavicollis* (myšice lesní),
A. agrarius (m. temnopásá)**



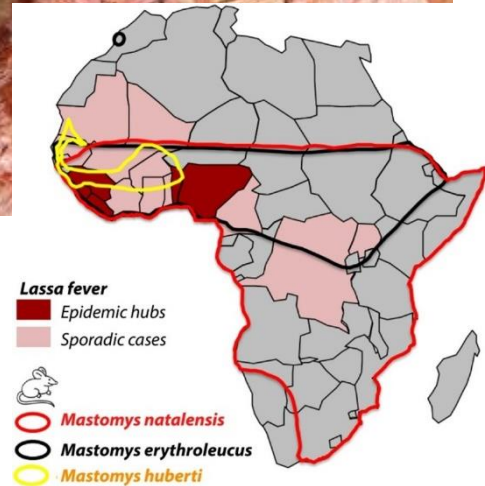
KE, hantaviry (Dobrava)



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



Lassa



WNV



Mus musculus (myš obecná)



Puumala, Seoul, Sin Nombre, Junin, LCMV, *Cardiovirus* EMC

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



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



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



CCHF, WNV, TAH,
CEE, HEV,



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



T. brucei
rhodesiense

JE, HEV, ASF



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



Lyssavirus s.s., HEV



Odocoileus virginianus (jelenec běloocasý) White-tailed deer

bioRxiv preprint doi: <https://doi.org/10.1101/2021.10.31.466677>; this version posted November 1, 2021. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

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-Nair¹, Rachel M. Ruden^{2,3}, Michelle Yon⁴, Ruth H. Nissly¹, Rahul K. Nelli³, Lingling Li⁴, Bhushan M. Jayarao⁴, Kurt J. Vandegrift⁵, Costas D. Maranas⁶, Nicole Levine⁷, Katriina Willgert⁸, Andrew J. K. Conlan⁸, Randall J. Olsen^{9,10}, James J. Davis¹¹, James M. Musser^{9,10}, Peter J. Hudson⁵, and Vivek Kapur^{7#}

SARS-CoV-2?

Deer-to-deer transmission



DALŠÍ SKUPINY OBROTLOVCŮ

Ptáci (Aves)

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.), Usutu virus (kos černý), 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, raci, bahňáci), *Paramyxovirus* NDV.

Anser indicus H5N1



Larus ridibundus



H5N1

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).

Obojživelníci (*Amphibia*)

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