

NBVCG Riga 4-10-2018

Viral infections emerging from wildlife



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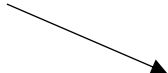
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- Dept of Veterinary Biosciences, Faculty of Veterinary Medicine
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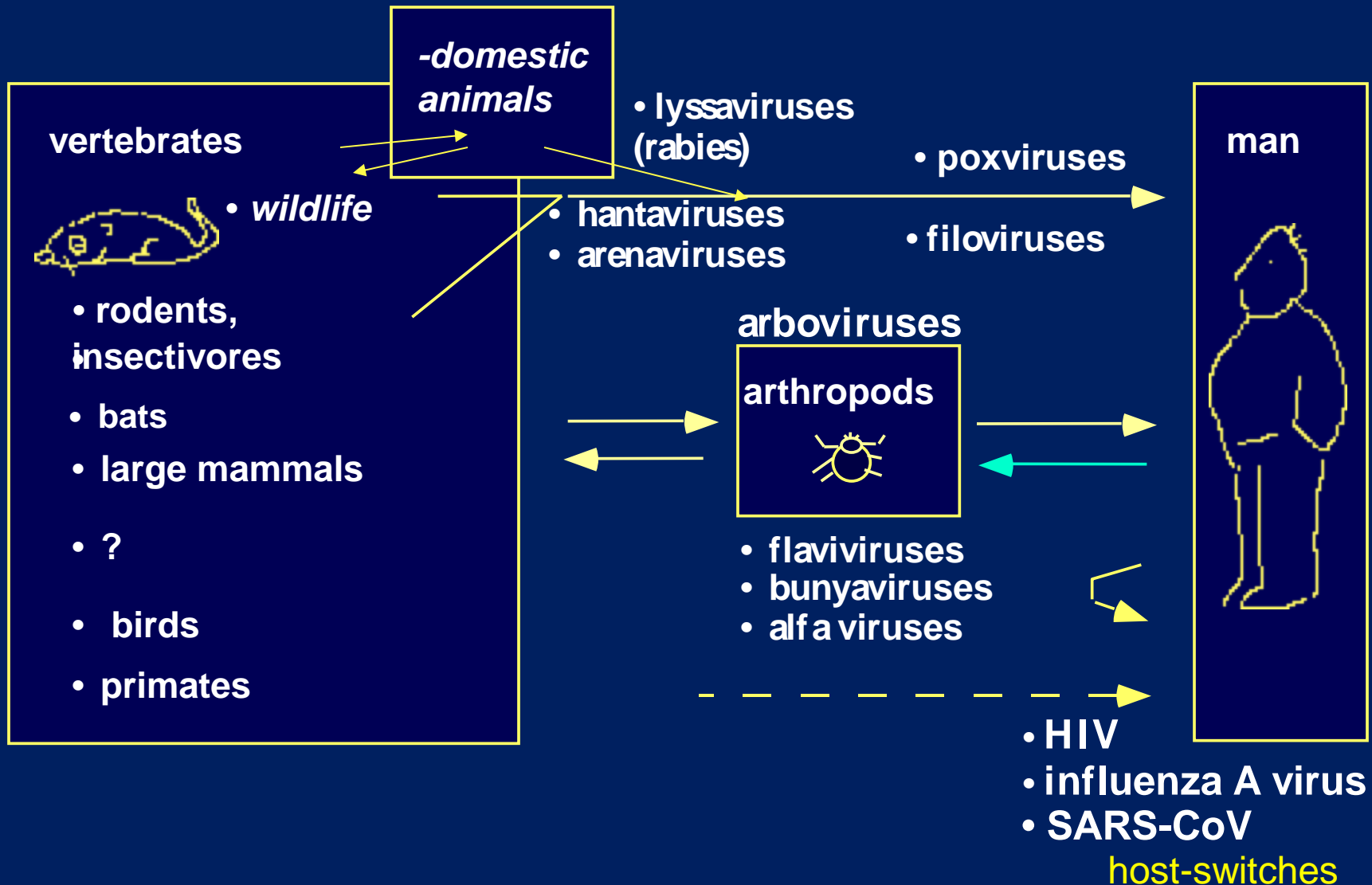
Emerging infections

- **scale:** *global - regional - local*
- **significance:** *human /animal health - food supply - economy*
- **current megatrends favoring emergence:**
globalisation - travel - urbanization - environmental changes - industrial animal husbandry
- but also: modern diagnostic tools

Agenda today

- **general aspects of viral zoonoses emerging from wildlife**
- **viruses/diseases from wildlife (on stage today)**
 - **rodent/insectivore-borne**
 - hantaviruses
 - arenaviruses
 - bornaviruses
 - orthopoxviruses
 - **bird-borne – influenza A virus**  **-arboviruses -TBEV**
 - **bat-borne: lyssaviruses, (filoviruses),**
 - **• Surveillance in Europe, Protective measures, Potential treatments**
 - **metagenomics approaches to study viral diversity, molecular epidemiology, evolution**

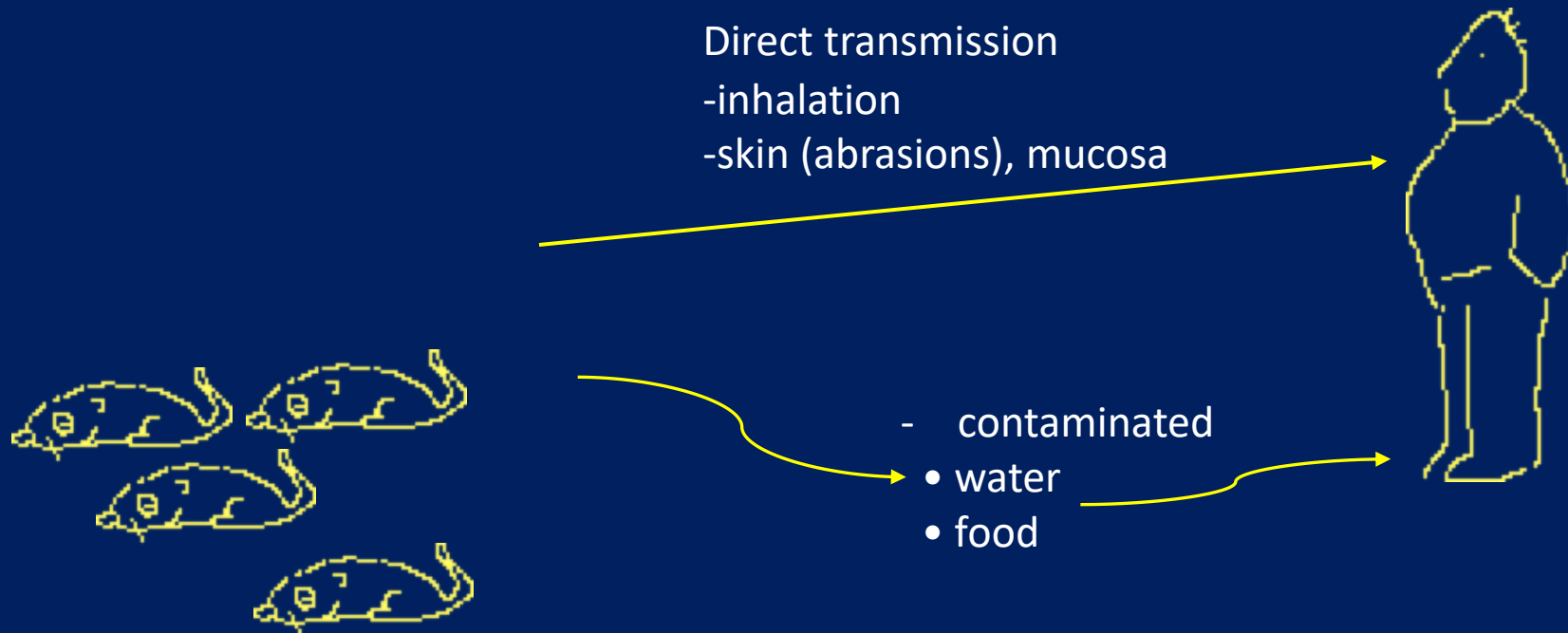
ZOONOTIC VIRUSES AND HOST-SWITCHES



Rodent-borne



Rodent-borne zoonotic infections



Rodent-borne zoonotic infections

Indirect transmission

- via arthropod 

• ticks

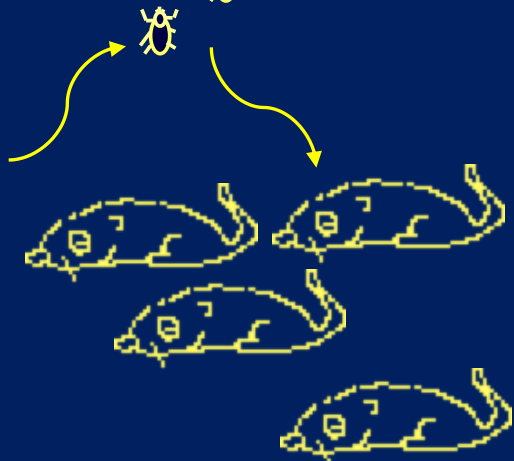
• mosquitoes

• lice

• mites



• as part of complex life cycles



Direct transmission

-inhalation

->skin (abrasions), mucosa

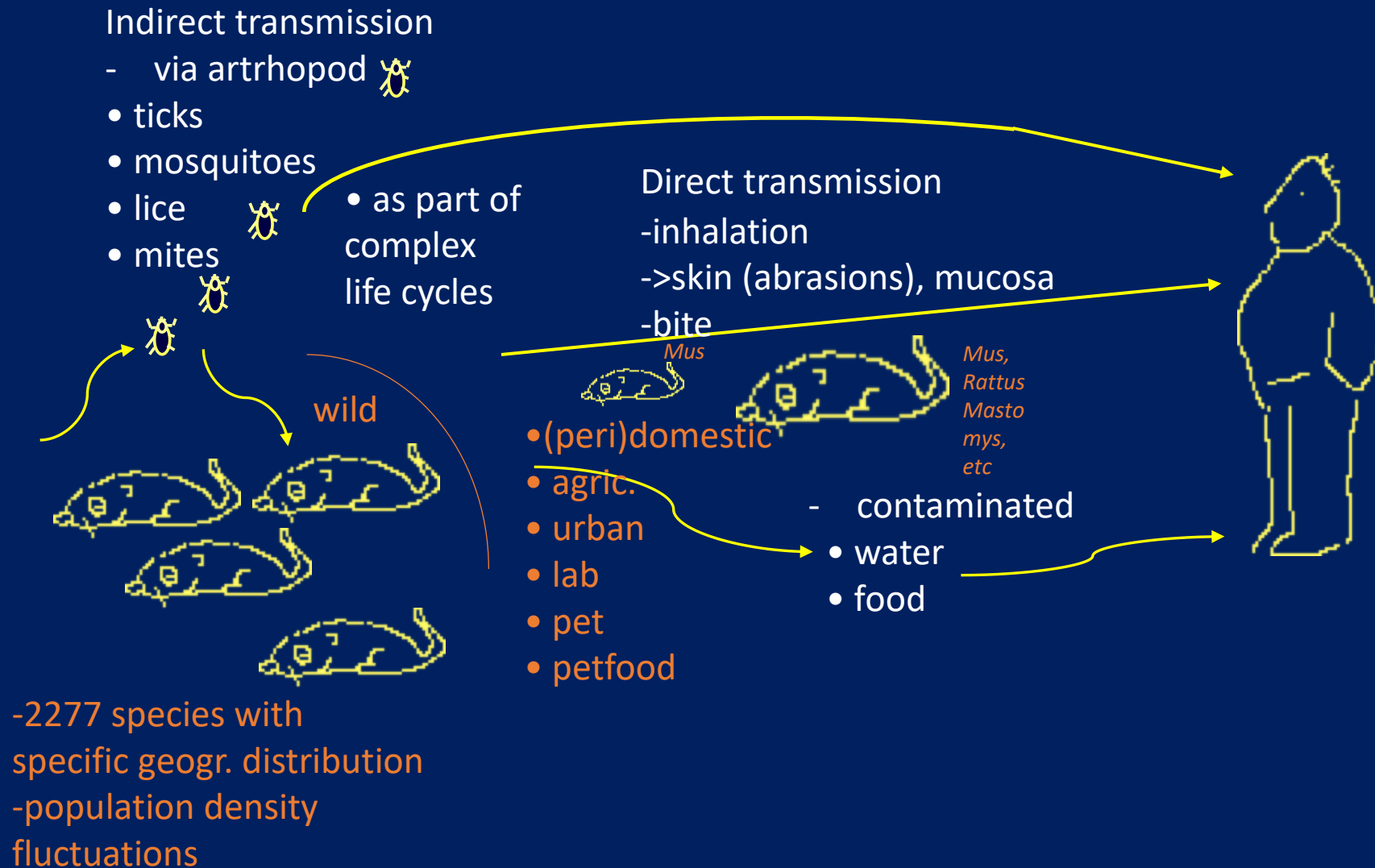
- contaminated

• water

• food





Rodent-borne zoonotic infections



Rodent-borne zoonotic infections

Indirect transmission

- via arthropod 

- ticks
- mosquitoes
- lice 
- mites 

• as part of complex life cycles



Direct transmission

-inhalation
->skin (abrasions), mucosa



• (peri)domestic

- agric.
- urban
- lab
- pet
- petfood

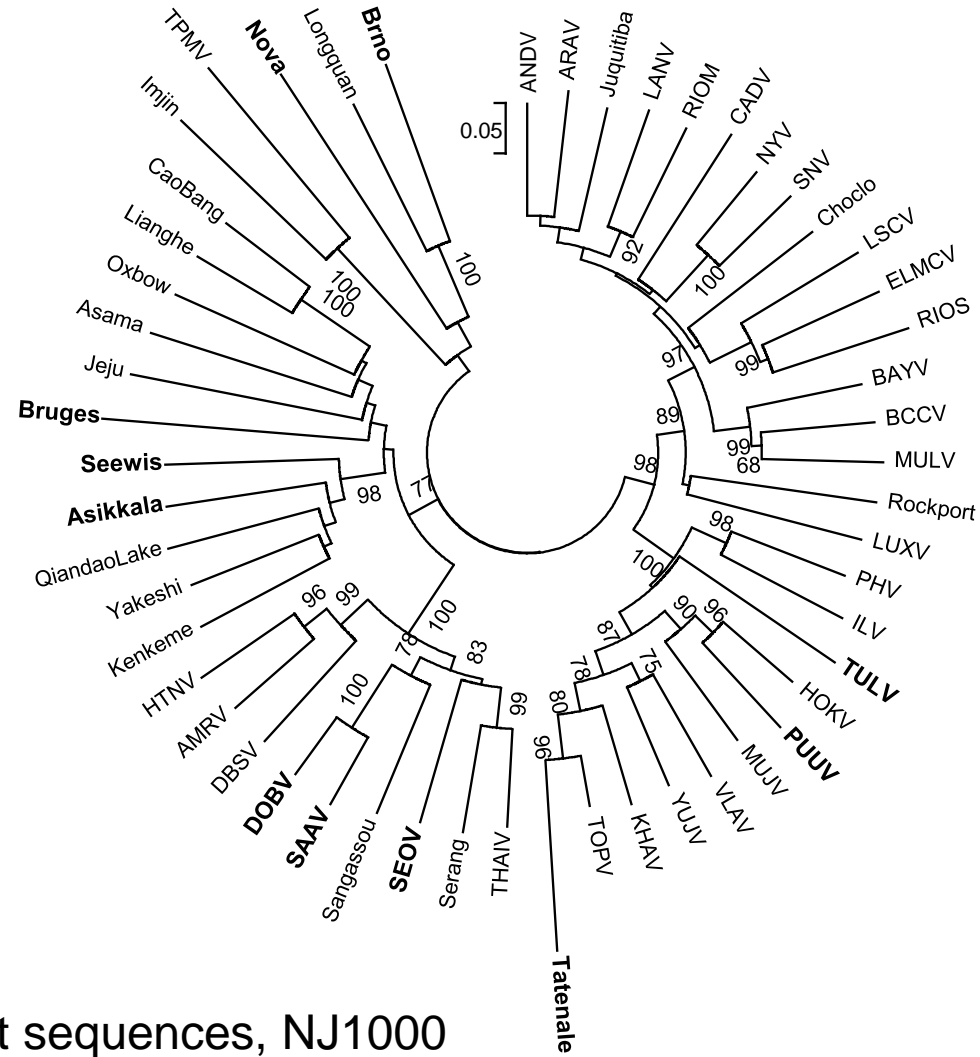
- contaminated

- water
- food



Hantavirus species

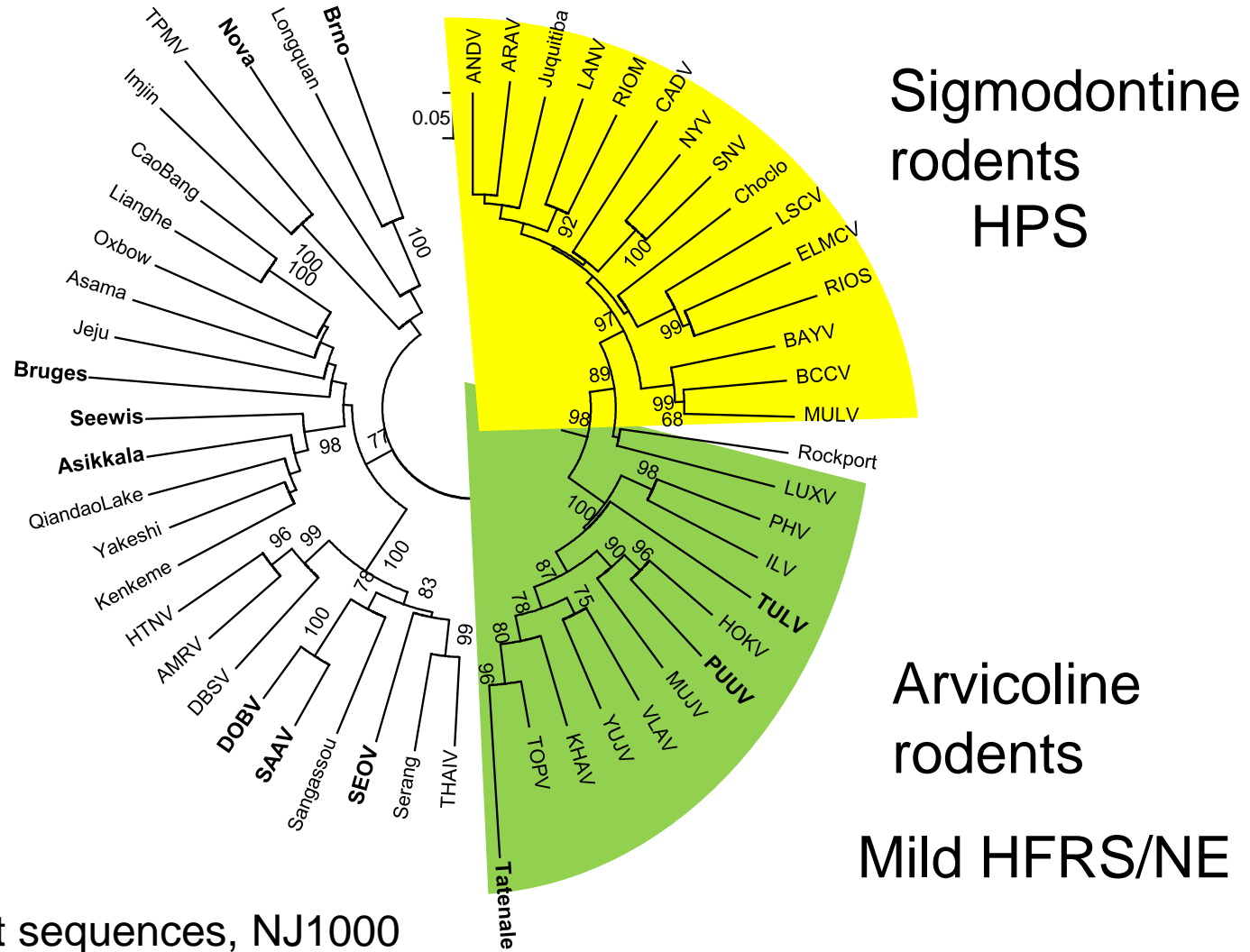
(Europeans in **bold**)



Partial S segment sequences, NJ1000

Hantavirus species

(Europeans in **bold**)



Partial S segment sequences, NJ1000

Hantavirus species

(Europeans in **bold**)

Insectivores
-Shrews, -Moles

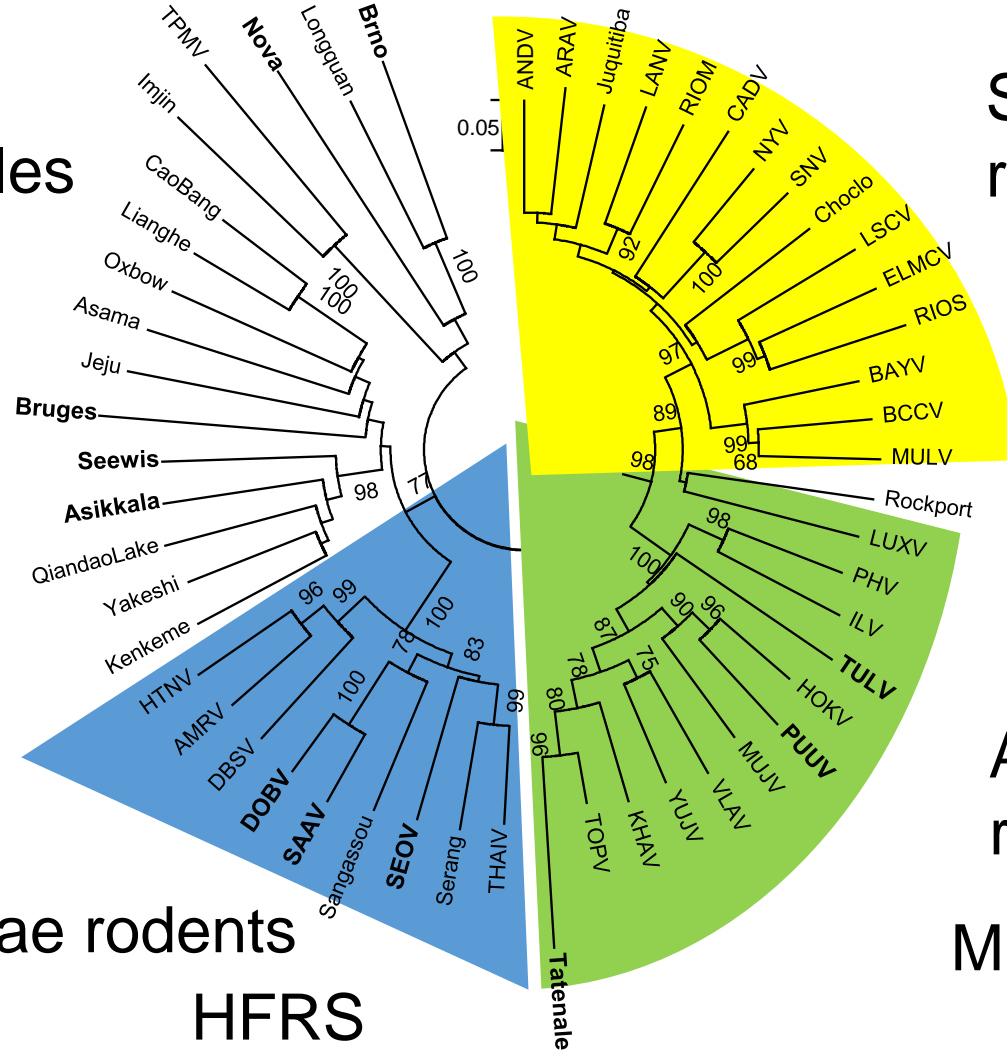
Bats

Sigmodontine
rodents
HPS

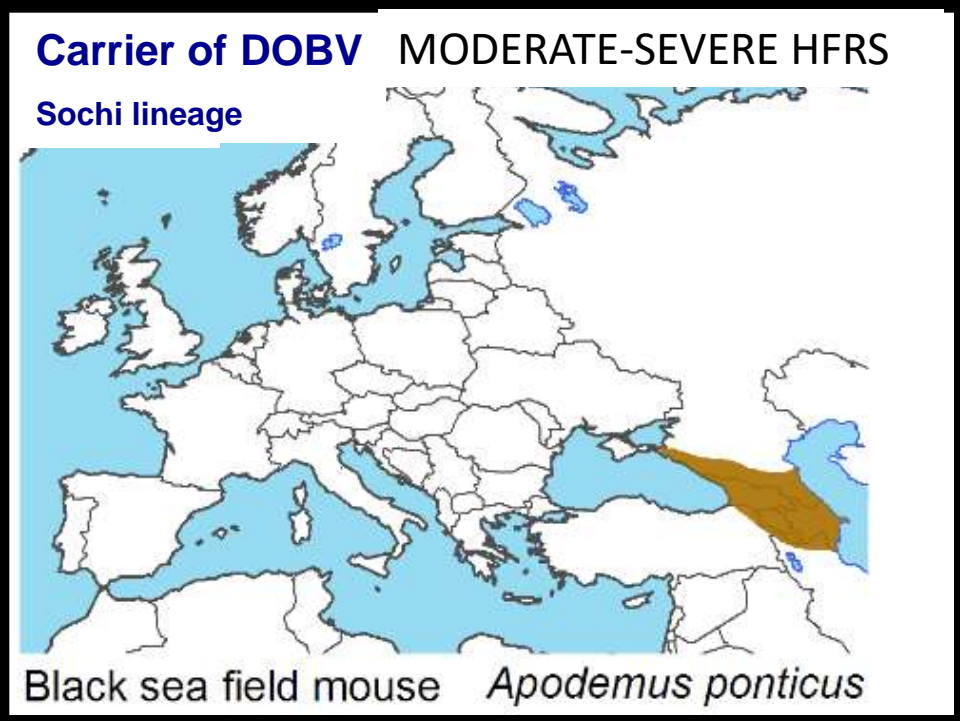
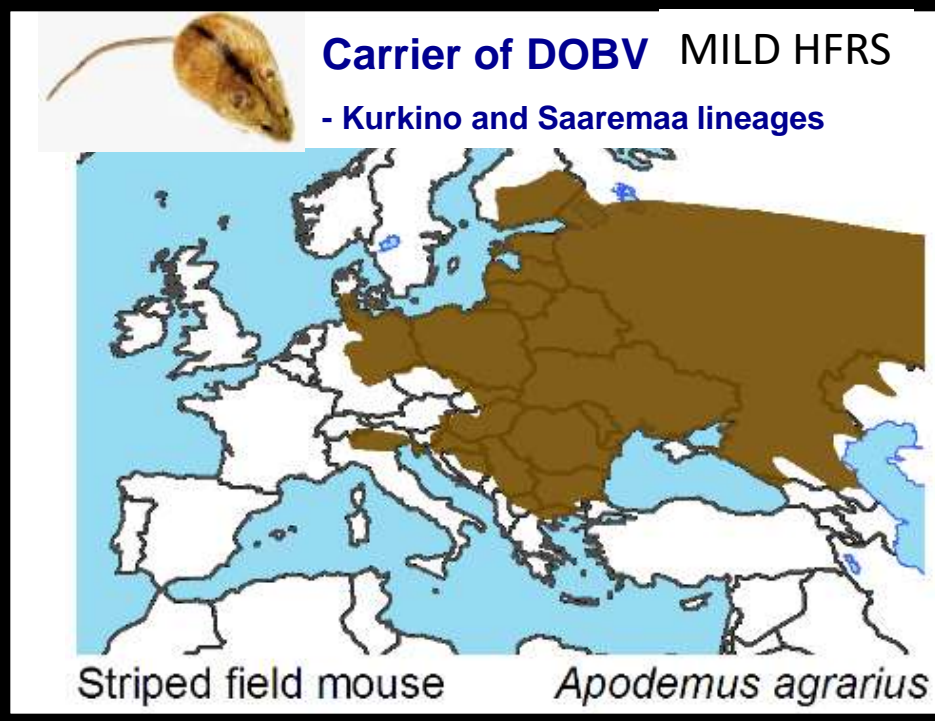
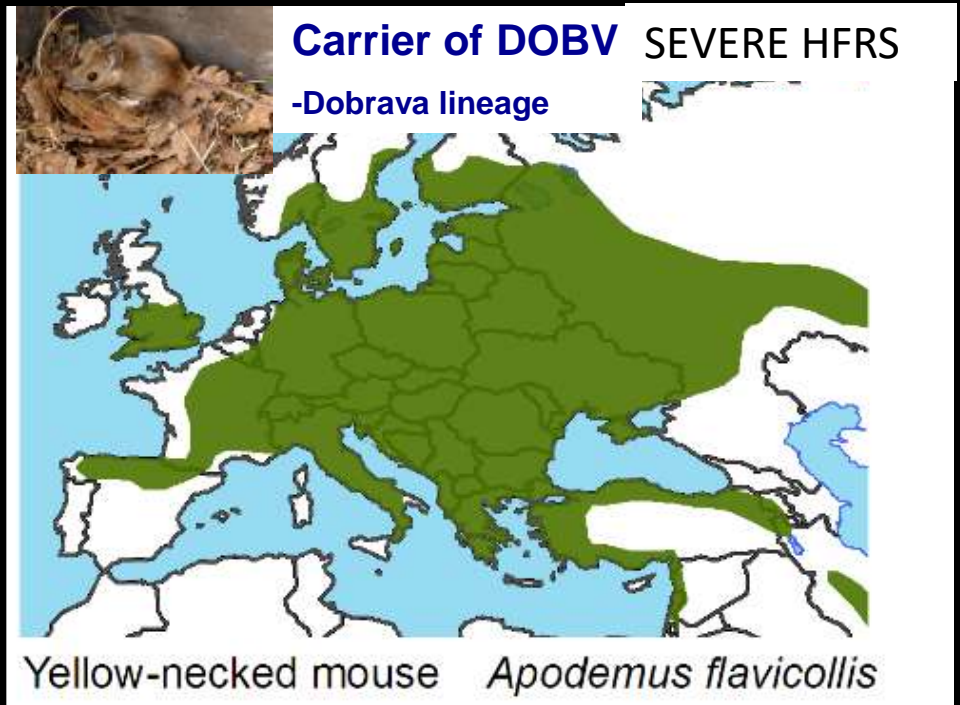
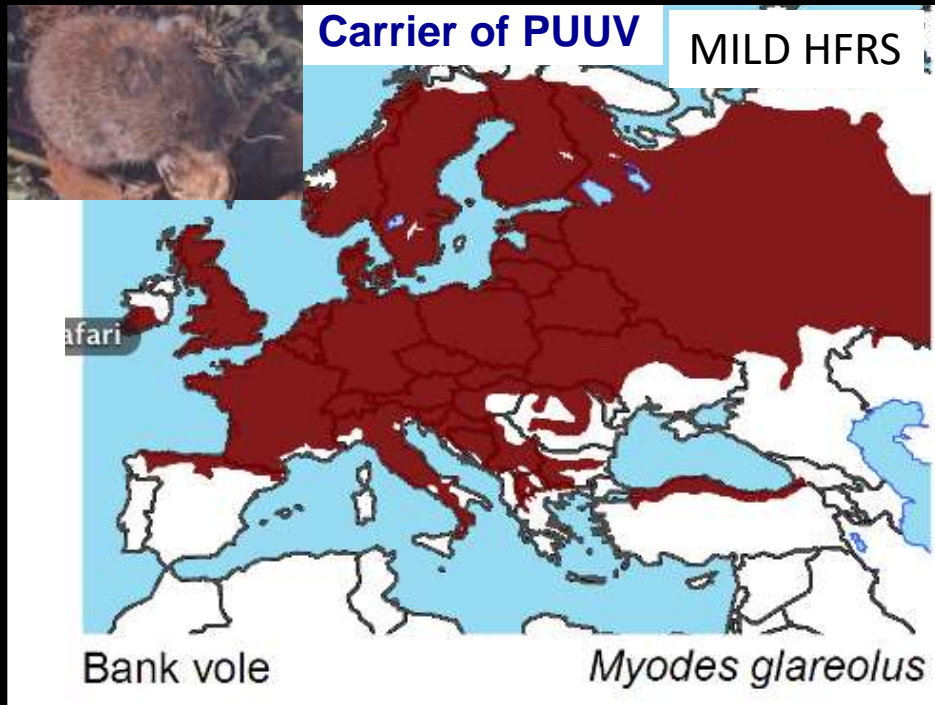
Muridae rodents
HFRS

Arvicoline
rodents

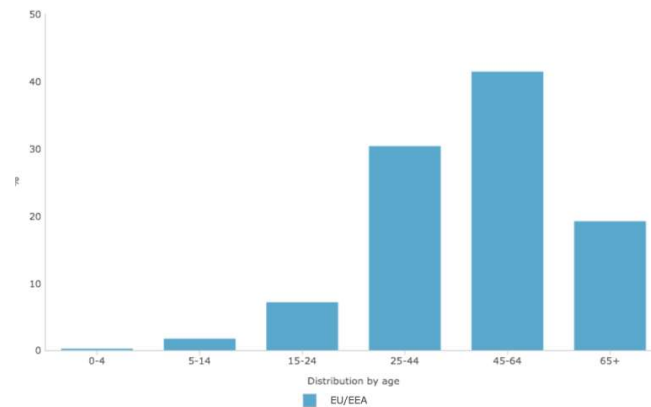
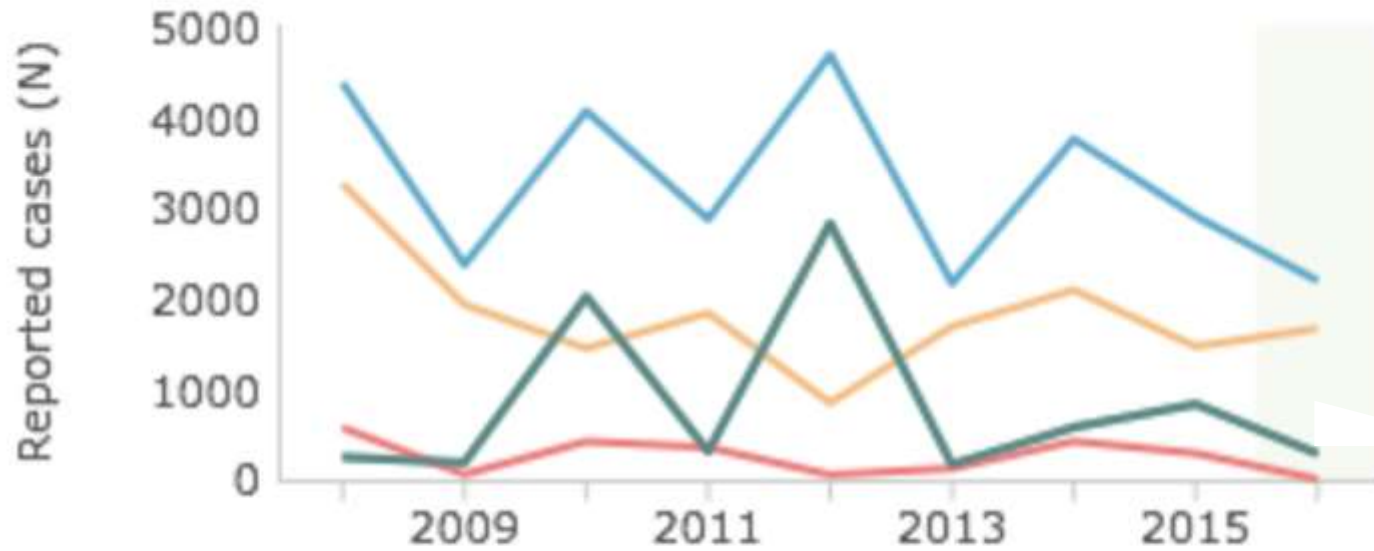
Mild HFRS/NE



Partial S segment sequences, NJ1000



Hantavirus infections in Europe (EU/EEA) 2008-16 and Germany, Finland and Sweden



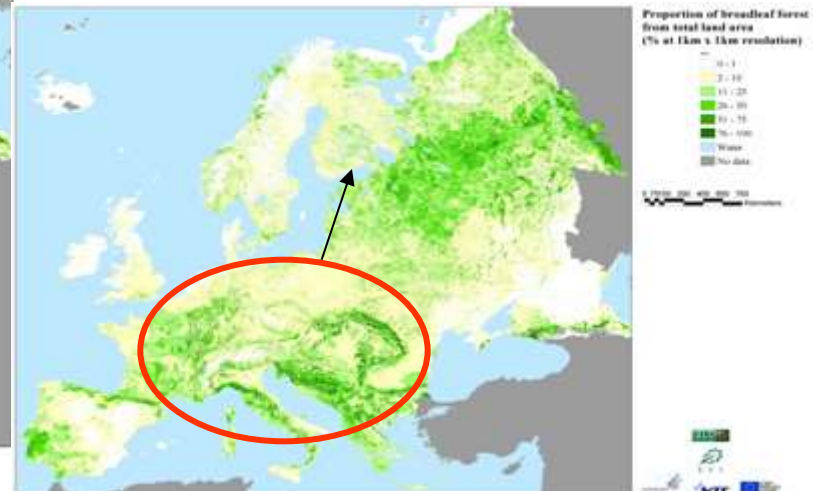
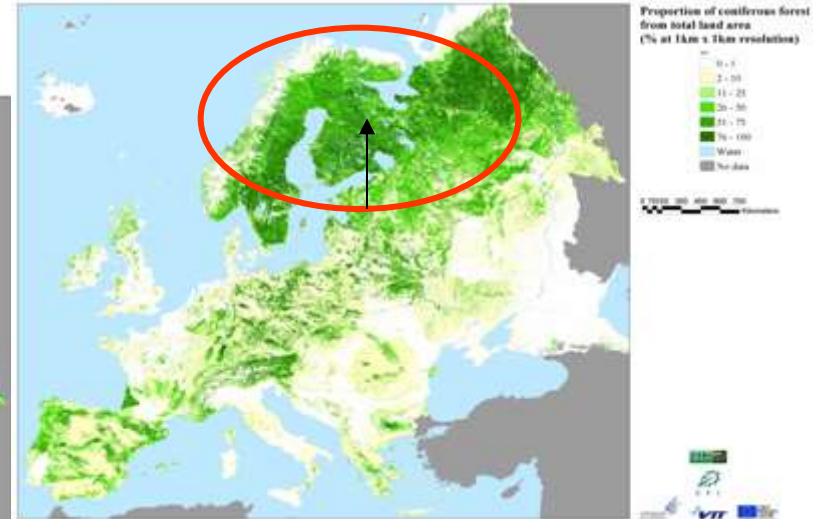
Forest coverage in Europe (by EFI) and rodent patterns

Total



Forest landscape
homo/ heterogeneity

conif., cyclic snowy world



decid., mast driven dynamics

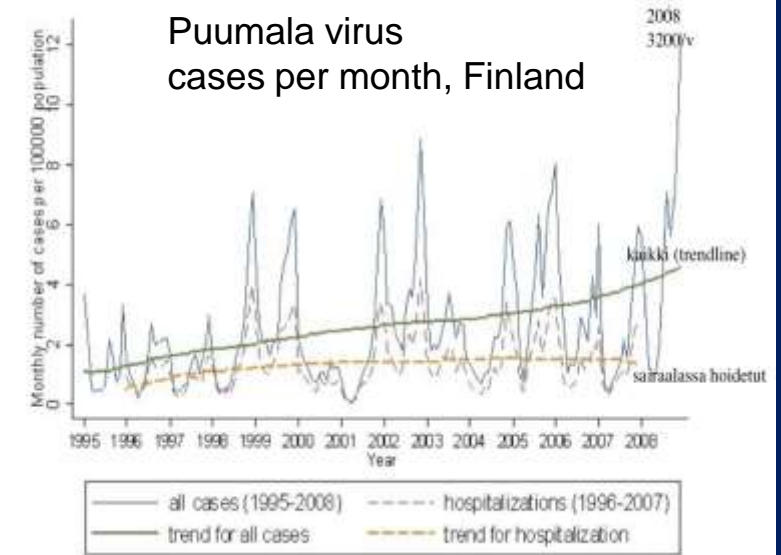
Bank vole (*Myodes glareolus*)



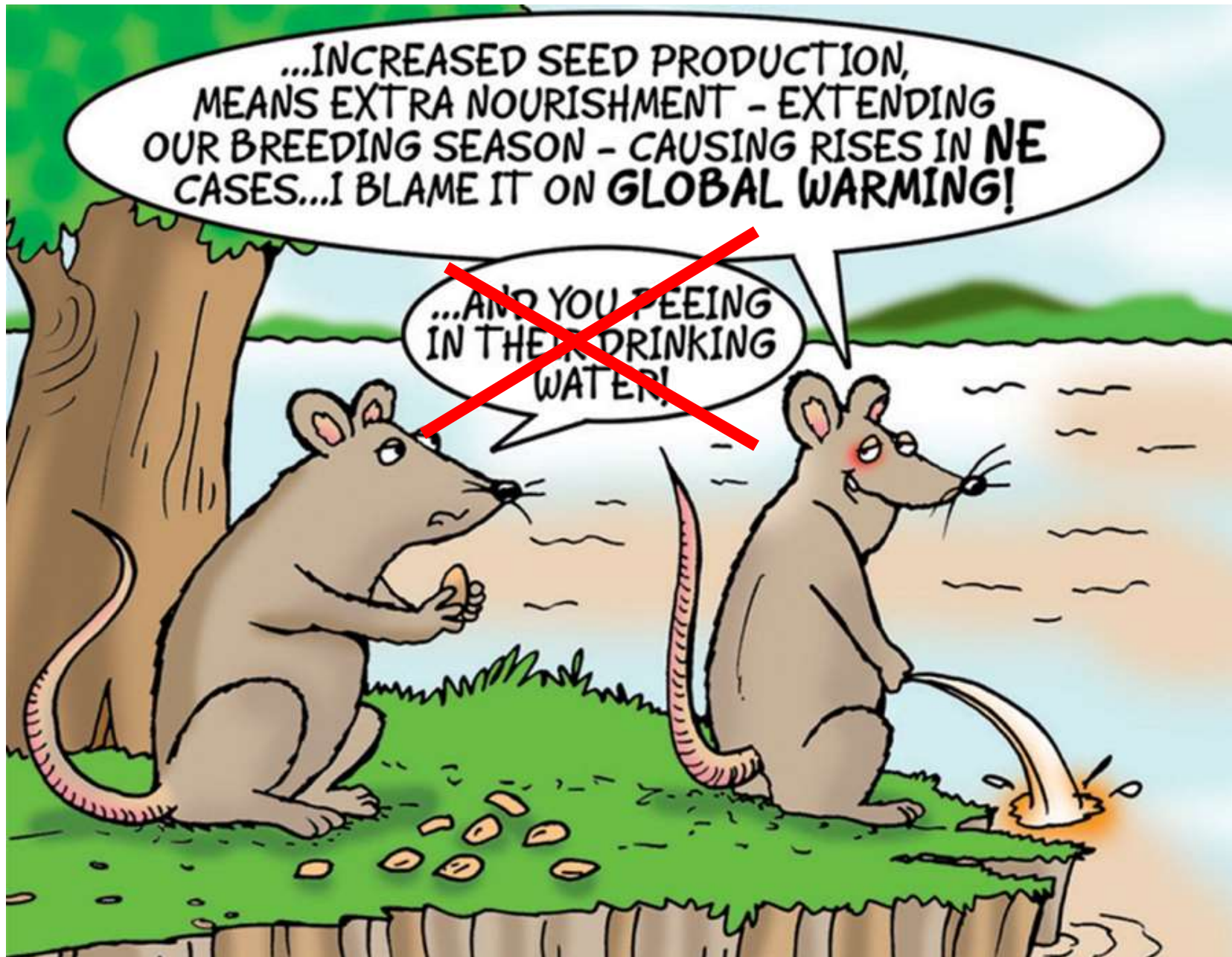
Spring Autumn Spring Autumn Spring Autumn

1996-2008

Puumala virus
cases per month, Finland



Excreta are infectious 2
weeks in RT, Kaliio J Gen Virol 06



Dixon, Lancet Infectious Diseases, March 2009

Main risk factors for Puumala virus:

- smoking
- house has openings allowing rodents to enter

→ transmission indoors
inhalation



Rattus norvegicus



Seoul virus:

increasing threat

- Pet rats
- Wild/urban population
- Rats raised for "reptile food"
- Experimental animals

- **United Kingdom:** Jameson L et al: Pet rats as a source of hantavirus in England and Wales, 2013. [Euro Surveill.](#) 2013
- **Sweden:** Lundkvist Å, et al: Pet rat harbouring Seoul hantavirus in Sweden, [Euro Surveill.](#) 2013
- **France:** • Reynes J, et al. Seoul Virus Infection in Humans, France, 2014–2016. [Emerg Infect Dis.](#) 2017 (3 cases, construction worker, pet rat owner, person raising rats as a food source for snakes)
- **Belgium:** Plyusnina A, Genetic characterization of seoul hantavirus originated from norway rats (Rattus norvegicus) captured in Belgium. [J Med Virol](#), 2012.
- **The Netherlands:** Verner-Carlsson J, First evidence of Seoul hantavirus in the wild rat population in the Netherlands. [Infect Ecol Epidemiol.](#) 2015

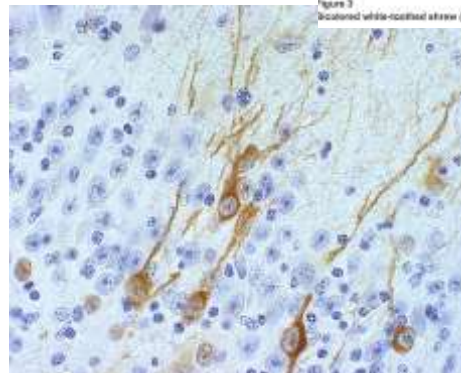
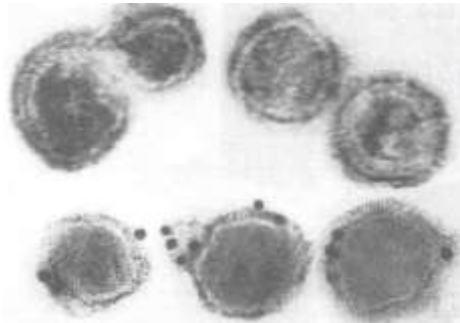
Most common pet rodent species (Finland)

Family	Genus	Species	English name	Natural distribution
Caviidae	Cavia	porcellus	guinea pig, cavy	S America
Chinchillidae	Chinchilla	lanigera	chinchilla	S America (Andes)
Cricetidae	Cricetulus	barabensis (griseus)	Chinese hamster	China, Mongolia
	Mesocricetus	auratus	Golden/ Syrian hamster	SE Europe Middle East
	Phodopus	campbelli	Campbell's Dwarf hamster	Mongolia, China, C Asia
		roborovskii	Roborovski hamster	Mongolia, N China
		sungorus	Djungarian / Winter-white Russian hamster	Kazakstan, Mongolia, Siberia
Muridae	Acomys	cahirinus	Cairo Spiny mouse	N Africa, Middle East
	Lemniscomys	barbarus	Barbary striped grass mouse	N, C Africa
	Mastomys	natalensis	Natal multimammate mouse	Africa
	Meriones	unguiculatus	Mongolian gerbil	Mongolia
	Mus	musculus	Mouse, Fancy mouse	Global
	Rattus	norvegicus	Fancy rat	Global
Octodontidae	Octodon	degus	degu, brush-tailed rat	S America (Andes)
Sciuridae	Cynomys	ludovicianus	Prairie dog	N America
	Tamias	sibiricus	Siberian chipmunk	Siberia

Borna disease virus (BDV)



- *Mononegavirales*:
- genome 8.9 kb RNA; replikaatio ja transcription in the nucleus
- neurotropic
- infect many vertebrates, also human, lethal CNS disease found in horse, sheep, cat(?)
- reservoir: shrew (*Crocidura leucodon*)
- BoDV gene sequences integrated to mammalian genomes

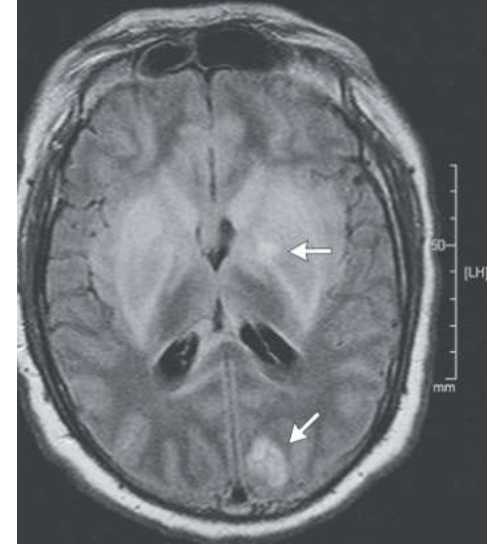


stutz, Tübingen

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.



Variagated squirrel

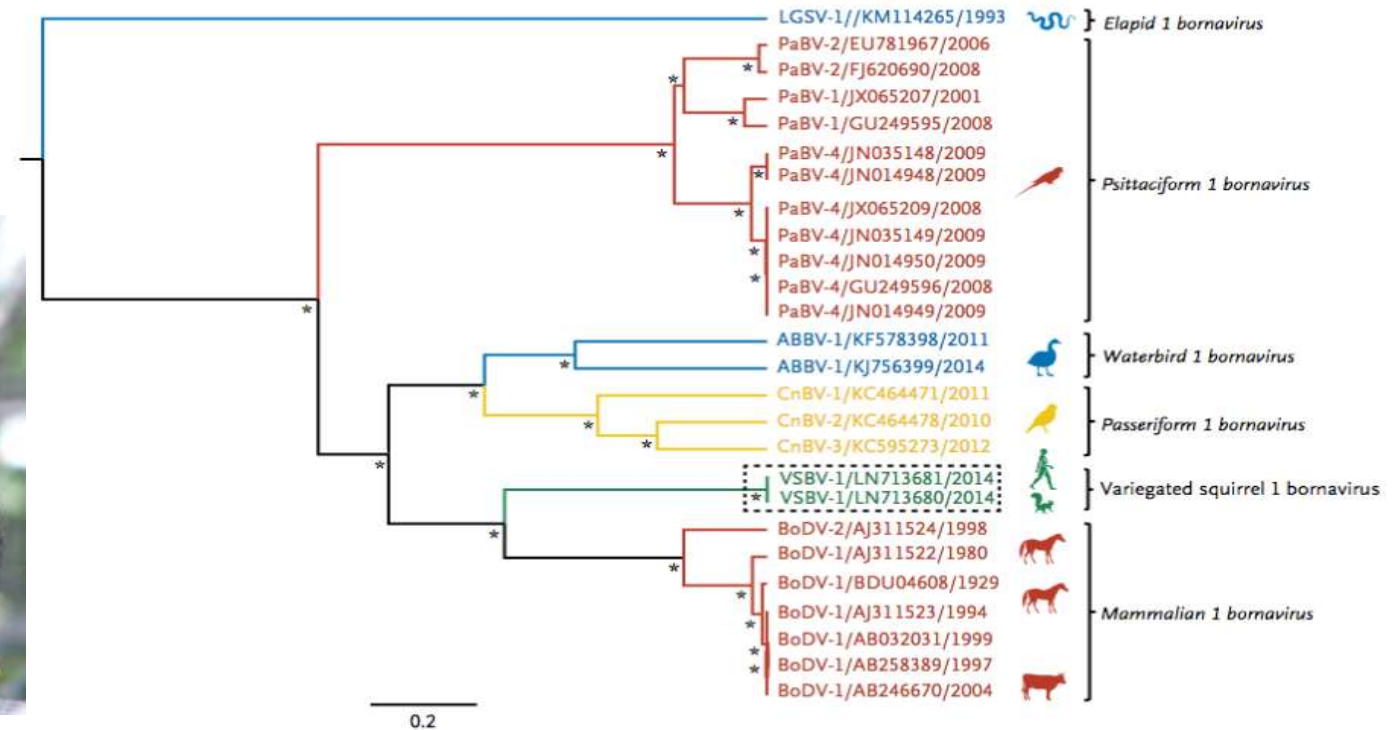


Figure 2. Phylogenetic Analysis of the Members of the Bornavirus Genus, Including the Putative Variagated Squirrel 1 Bornavirus (VSBV-1)

Lethal encephalitis of "classical" BoDV, via transplantation, Germany (RKI/FLI reported 3/2018)

- cluster of 3 solid organ recipients from a single donor from southern Germany, 2 died.
- Organ donor died of unrelated reasons/ not of neurological disease.
- 100 d after receiving transplants (2 kidney, 1 liver transplant) → severe encephalitis/encephalopathy while being on standard immunosuppression therapy. Both kidney recipients fell into a coma and died. Liverrecipient survived with residual degenerative optic nerve atrophy.
- Diagnostics/ FLI:
 - BoDV-1 genome in both kidney transplant recipients by RT-qPCR and NGS
 - BoDV-1-specific seroconversion in all patients.
 - IHC, ISH : presence of BoDV-1 antigens and RNA.
- additional lethal case of encephalitis due to BoDV-1 found in southern Germany during the investigation of this transmission cluster with no epidemiological link, another patient with encephalitis is currently under investigation; these patients have not received any organ transplantation .

Poxviridae

Genus/species reservoir geographic distr other hosts infected

Orthopoxvirus			
Variola virus	Humans (labs?)	Worldwide (extinct)	None
Vaccinia virus	?	Worldwide	Humans, cows, buffaloes, rodents
Cowpox virus	Rodents	Europe, W Asia	Cats, humans, cows, zoo animals
Ectromelia virus	(Lab) rodents	Europe, Japan, China	Fox, mink
Monkeypox virus	Squirrels	W and Central Africa	Monkeys, humans, prairie dogs
Camelpox virus	Camels	Africa, Asia	None
Raccoon poxvirus	Raccoons	E USA	None
Parapoxvirus			
Pseudocowpox virus	Cattle	Worldwide	Humans
Orf virus	Sheep	Worldwide	Reindeer, Humans

Cowpox in humans – more after cessation of smallpox vaccinations



Tarvainen et al 2001



Pelkonen & al. 2003



Becker & al. 2009



Heilbronner & al. 2004



Paula Kinnunen 2009



Cowpox in animals

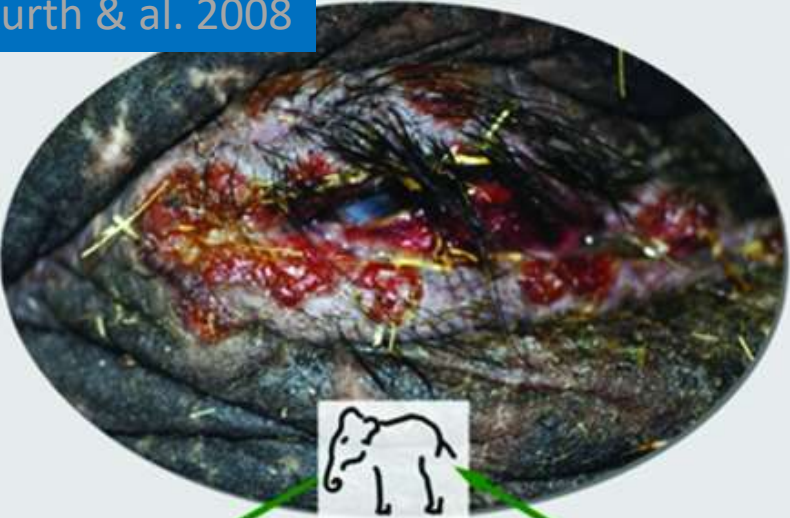


Courtesy of Aiden Foster



Courtesy of Malcolm Bennett

Kurth & al. 2008

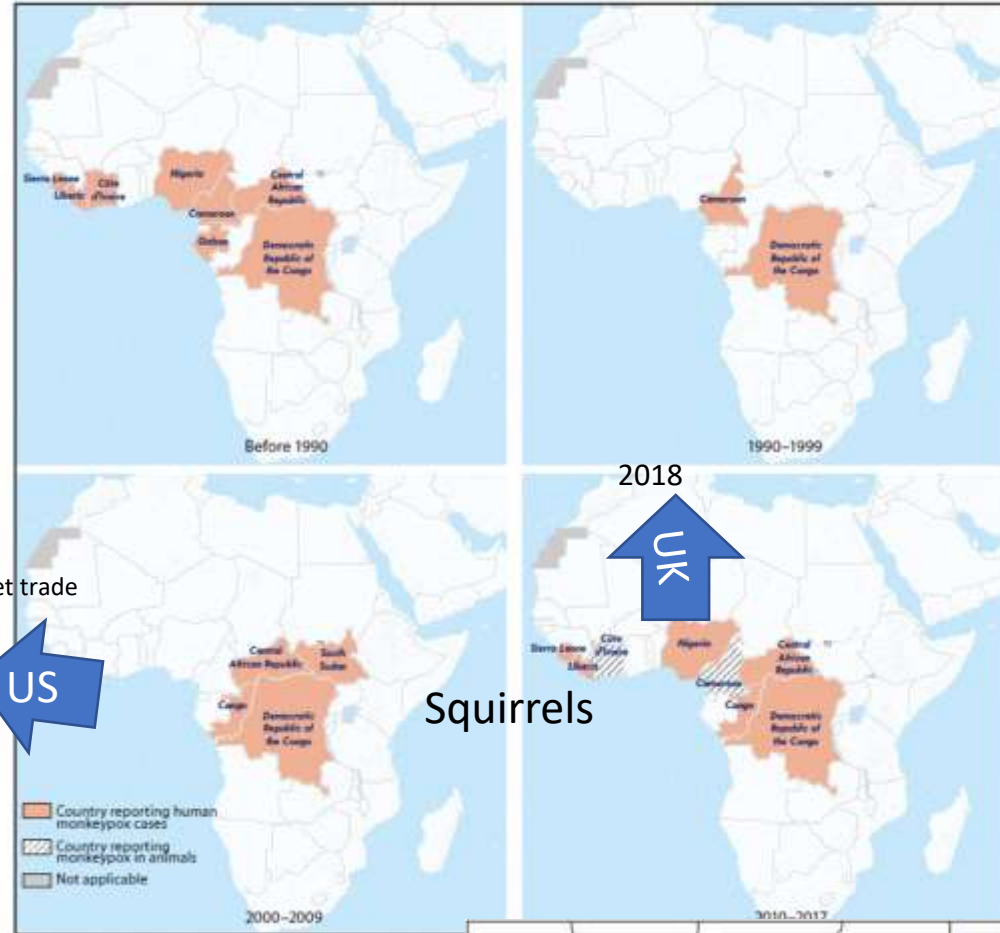


Circulation in wild rodent populations of Eurasia



FIGURE. Countries reporting monkeypox cases in humans and animals – West and Central Africa, 1970-2017*

Monkeypox



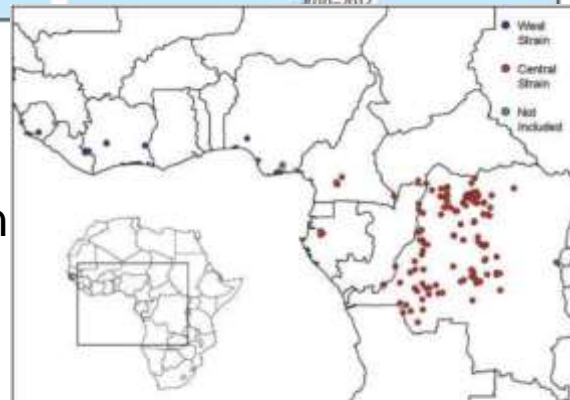
* Current as of February 25, 2018.



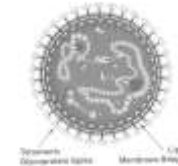
Prairie dogs
et al,
2003



African Rodent Importation Ban

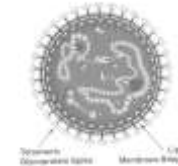


LCMV (lymphocytic coriomeningitis) infections - arenavirus



- ✓ Asymptomatic infection (most common)
- ✓ Influenza-like disease (common)
- ✓ Aseptic meningitis (most common complication)
- ✓ Meningoencefalomyelitis (rare)
- ✓ Severe infection of immunosuppressed (transplantation)
- ✓ Congenital-infections can be manifested by:
 - ✓ Hydrocephalus, mikrocephalus
 - ✓ Chorioretinitis
 - ✓ Mental or psychomotor retardation

Dg: RT-PCR, serology (IFA; EIA, WB), isolation
from: wild mice, pet mice and hamsters



LCMV-IF: Mammalogists and Veterinarians

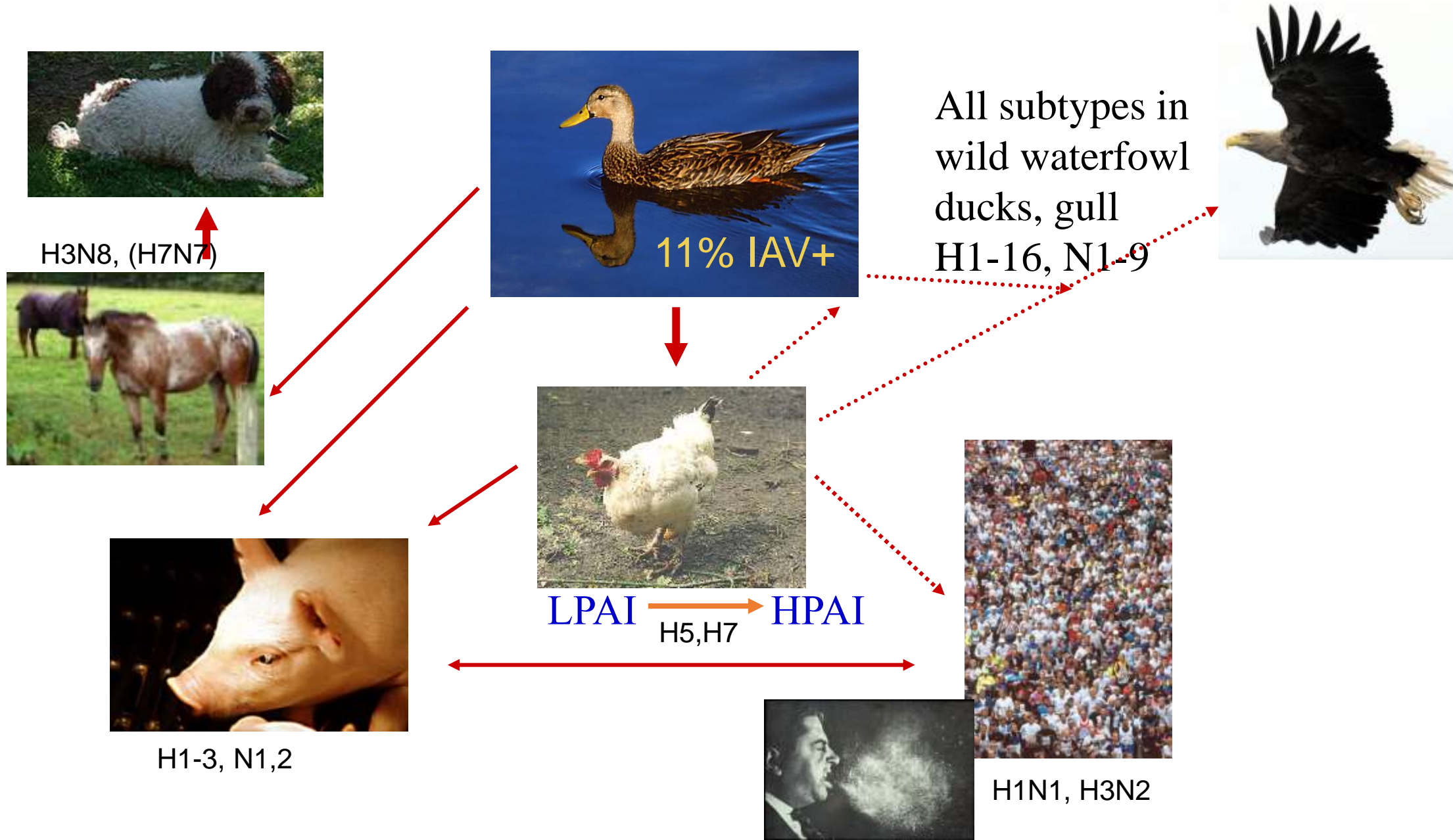
Mammalogists				
Place	Year	NO TOT	NO POS	% POS
Southampton	1995	155	6	3,9
Jyväskylä	1999	152	10	6,6
Praha	2003	69	2	2,9
	TOT	376	18	4,8

Veterinarians				
	Year	NO TOT	NO POS	% POS
	2001	150	15	10

BIRD-BORNE



Influenza A virus hosts



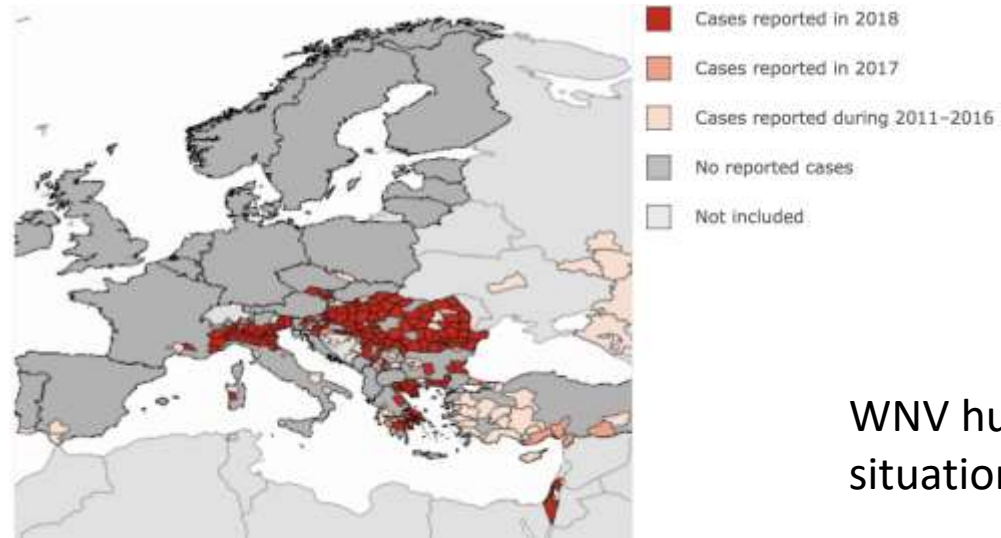


wet market chicks

MIGRATORY BIRDS AS (ArBo)VIRUS DISTRIBUTORS

mosquito-borne:

- West Nile virus
- Usutu virus
- Sindbis-virus
- Tick-borne encephalitis virus



WNV human infections
situation 28 Sept 2018

Tick-borne encephalitis virus

Genus *Flavivirus*, Family *Flaviviridae*

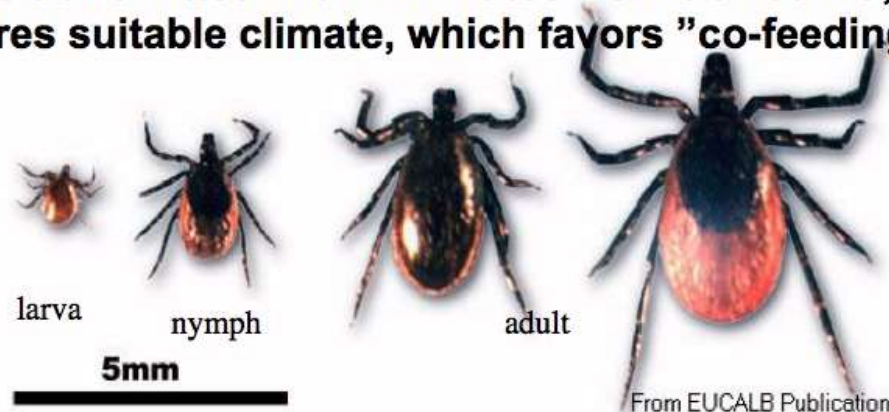
• TBEV VECTORS

Ixodes ricinus - sheep tick (TBEV European subtype)

Ixodes persulcatus - taiga tick (TBEV - Siberian and Far Eastern subtypes)



- virus transmitted within minutes from tick saliva, cycle in nature requires suitable climate, which favors "co-feeding"



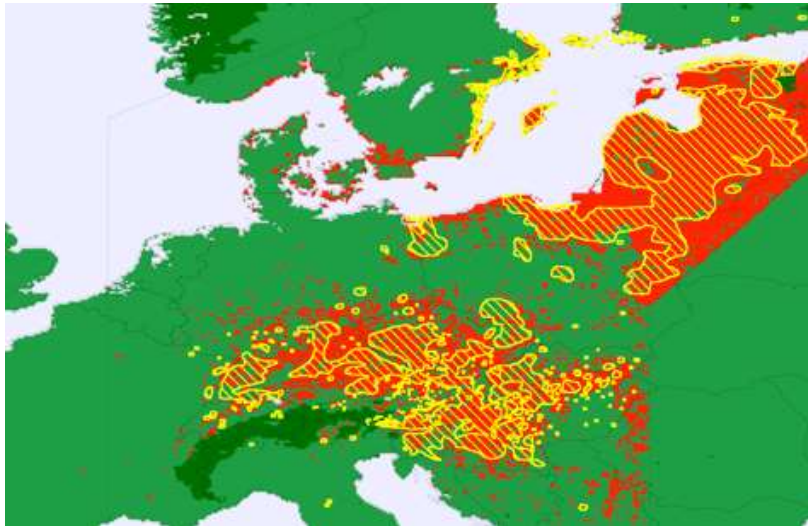
(also milk transmission)

TBE - sensitive to climate

- Fragile ecological cycle, cofeeding

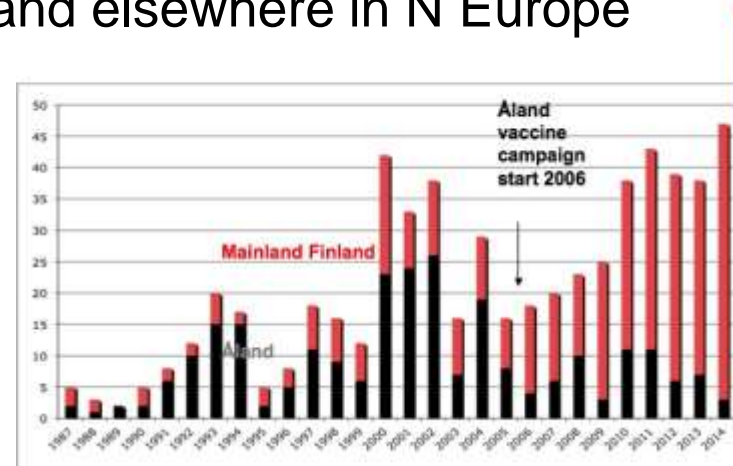


- “Focal” occurrence -climate influences

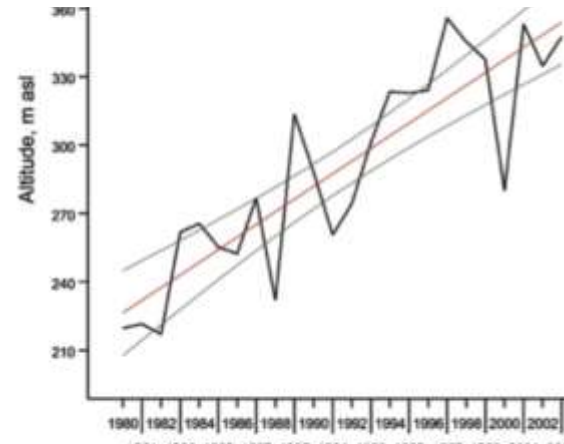


Randolph SE (2000), *Advances in Parasitology* 47, 217-243

- Case numbers rising in Finland and elsewhere in N Europe



- TBE risk areas are rising on the mountains in C Europe

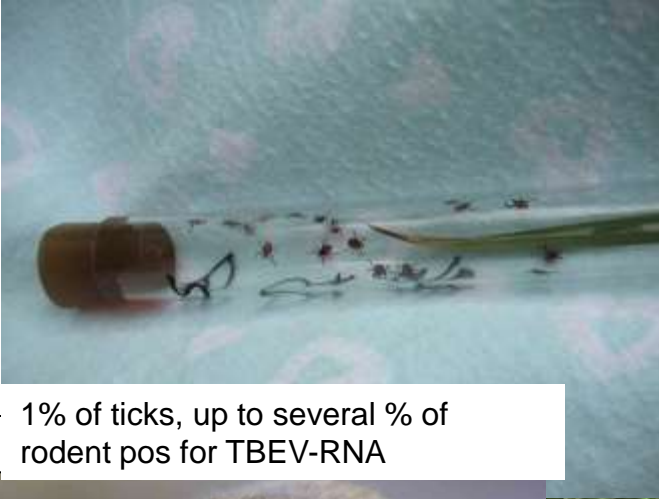


CLIMATE WARMING and TICK-BORNE ENCEPHALITIS, SLOVAKIA

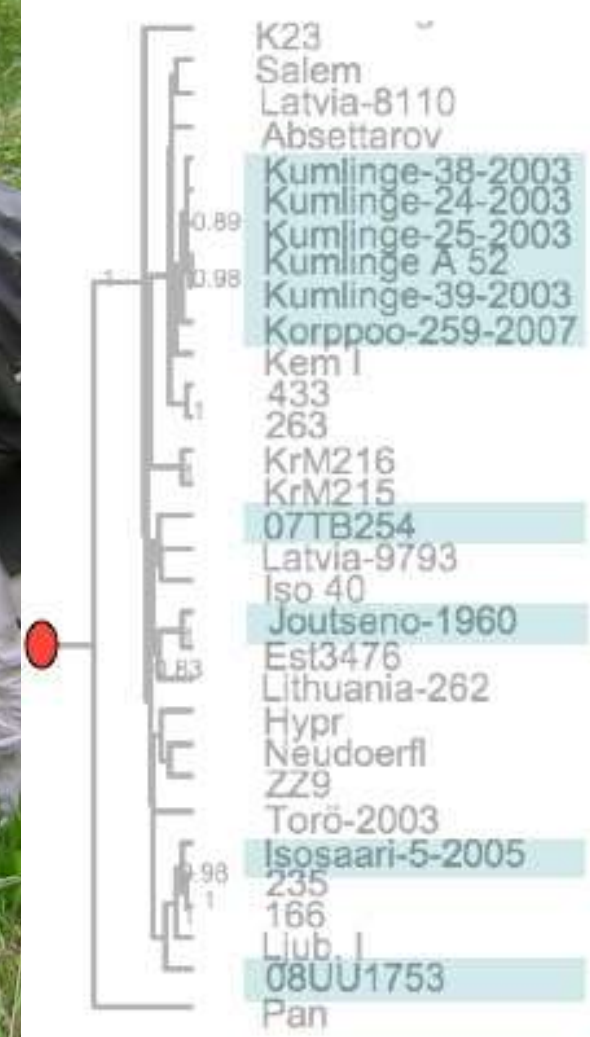
Lukan et al, *Emerg Infect Dis*, 2010

TBE focus investigations

(--> molecular epidemiology)



1% of ticks, up to several % of rodent pos for TBEV-RNA

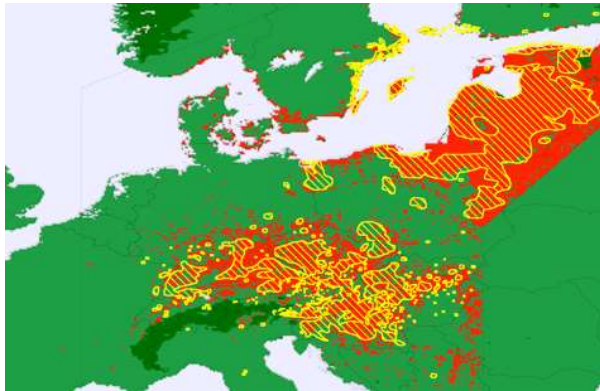
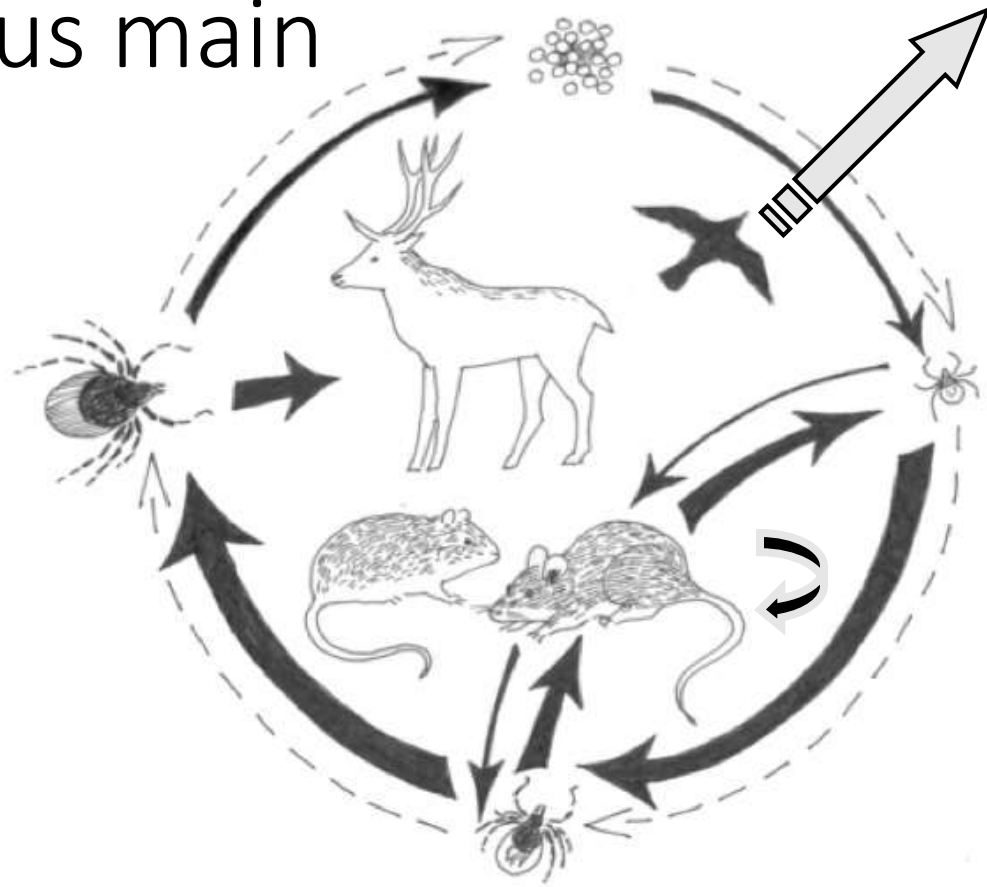


Suomalais
kannat

photo: Ola Nordsteien. Jomfruland bird observatory Sept 2003
Greenfinch, *Carduelis chloris*,



TBE focus main players

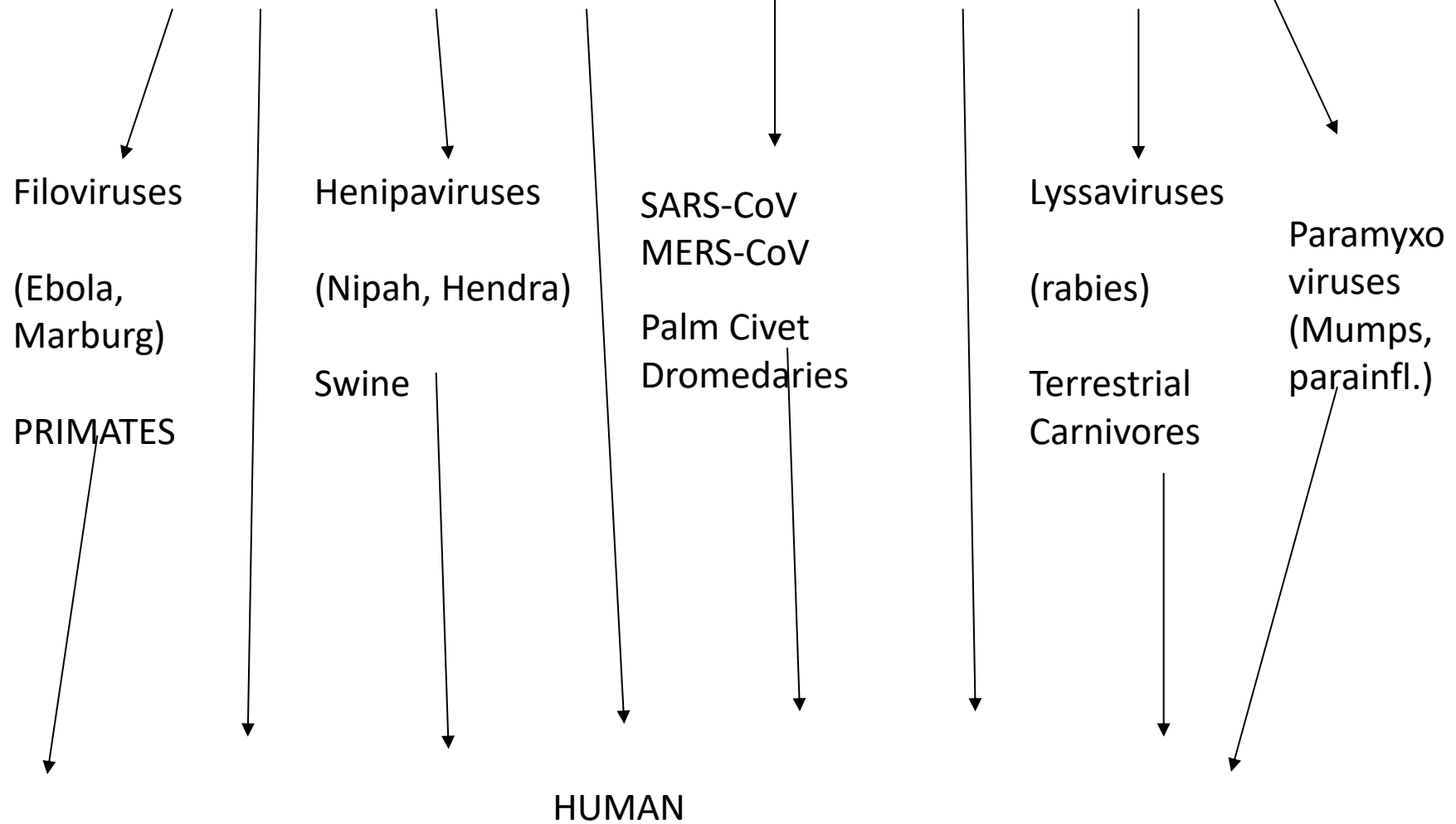


BAT-BORNE



© Pat Morris / www.ardea.com

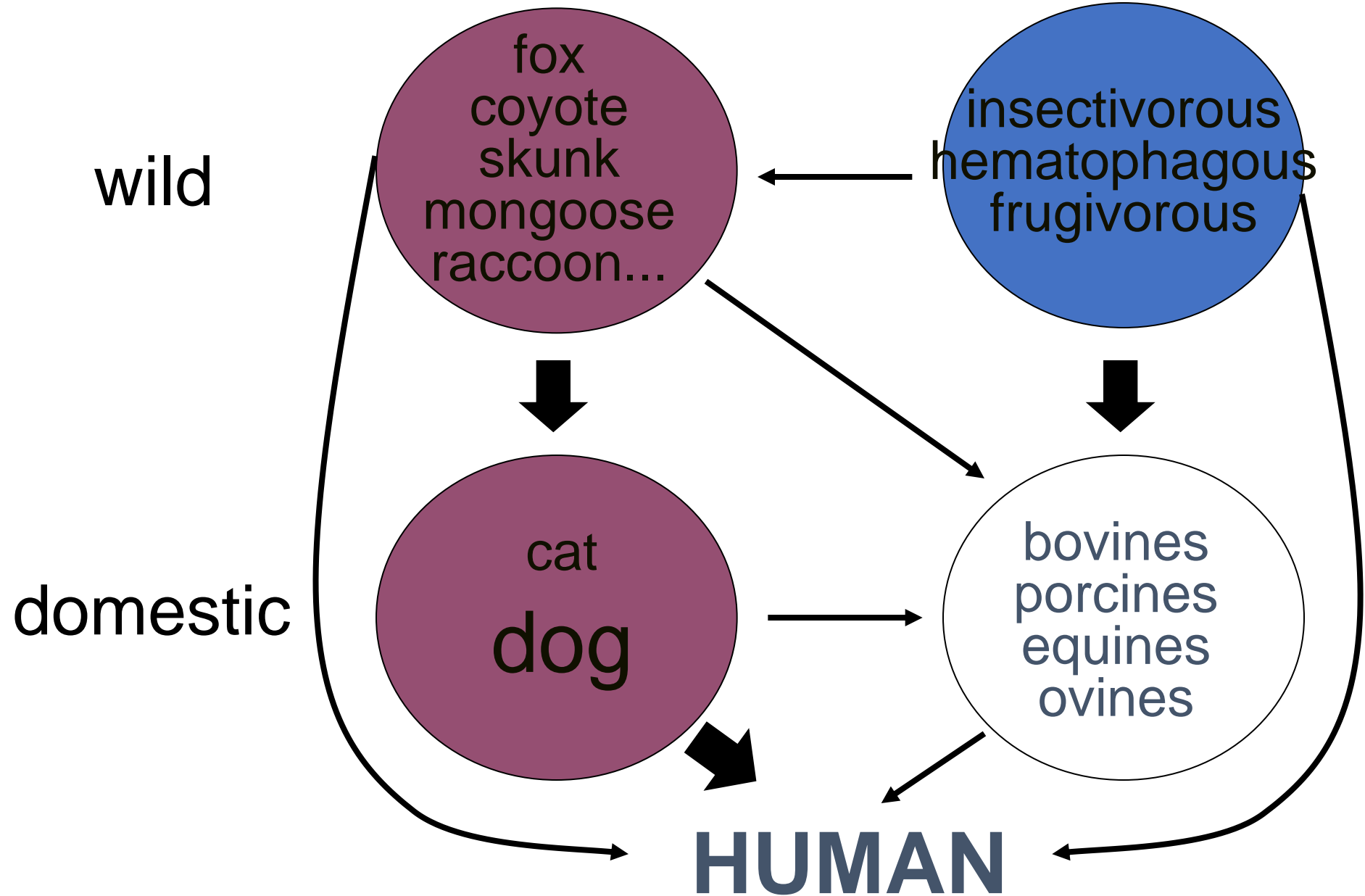
BATS, FRUIT BATS (specific host species)



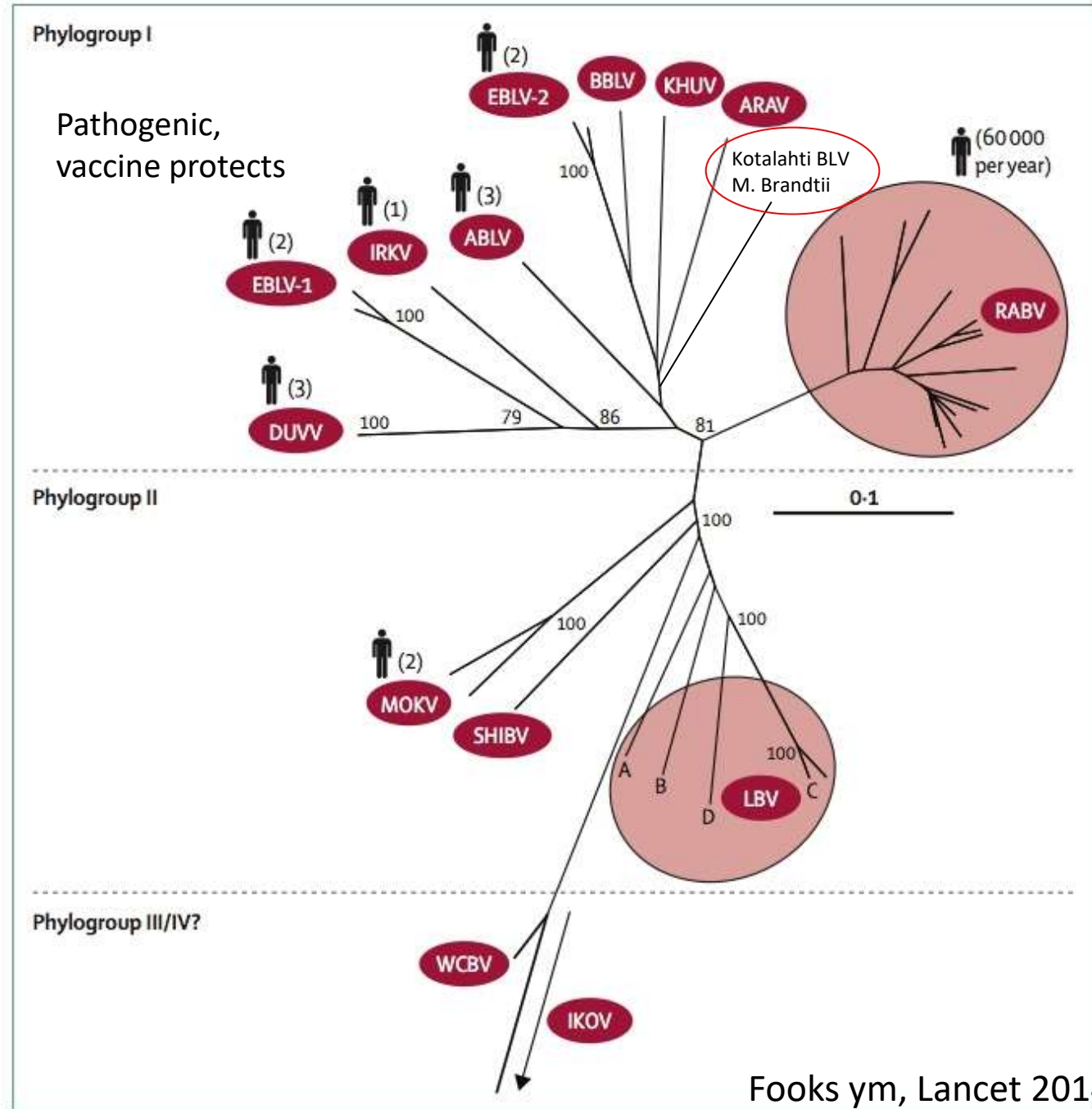
vectors

carnivora

chiroptera



Lyssavirus Phylogenetic tree

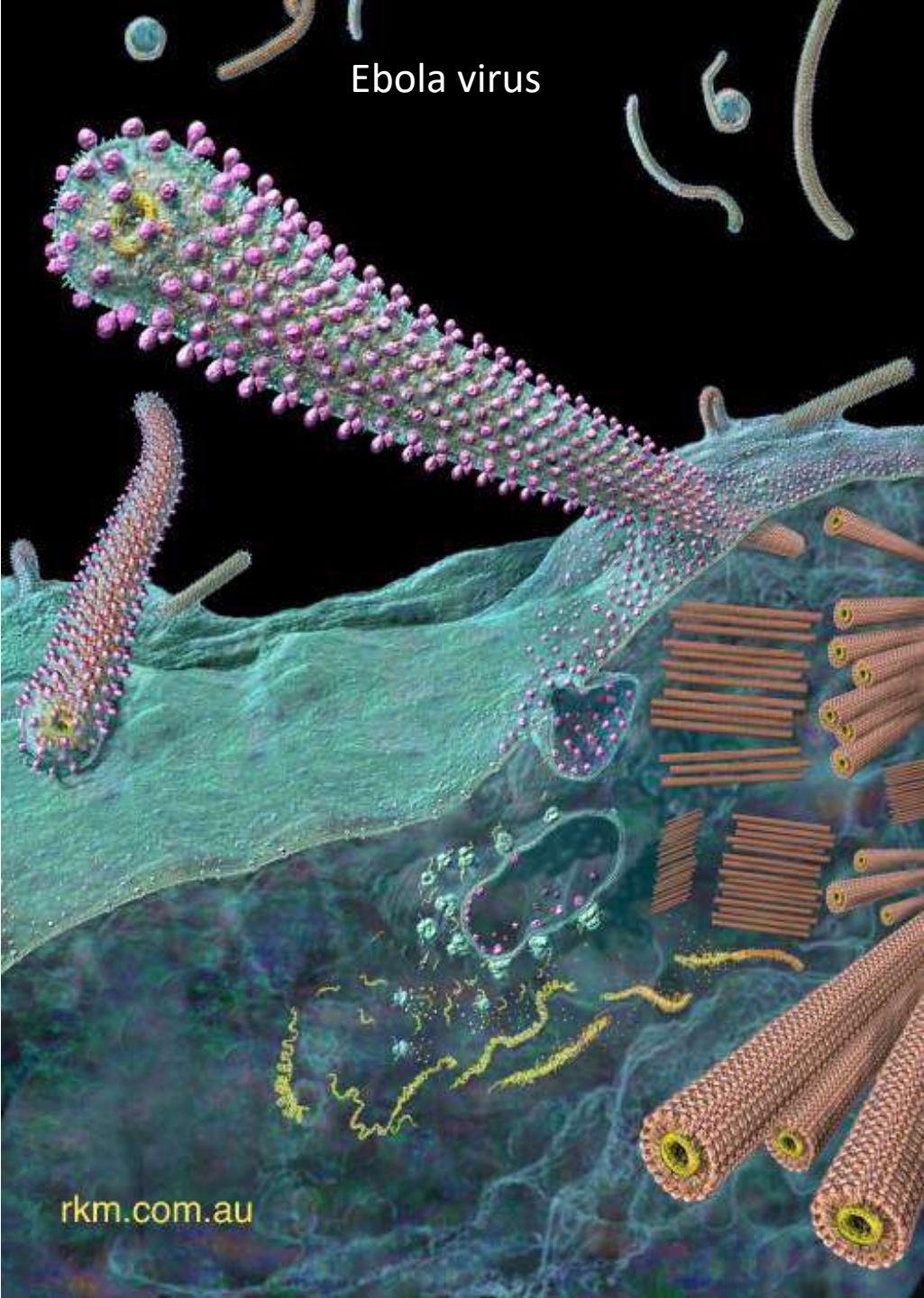


Fooks ym, Lancet 2014

BLV=bat lyssavirus

Figure 2: Phylogenetic tree of the lyssavirus phylogroups and their respective species

Nokireki et al 2018



Ebola virus

rkm.com.au

Family **Filoviridae**

Genus: *Marburgvirus*

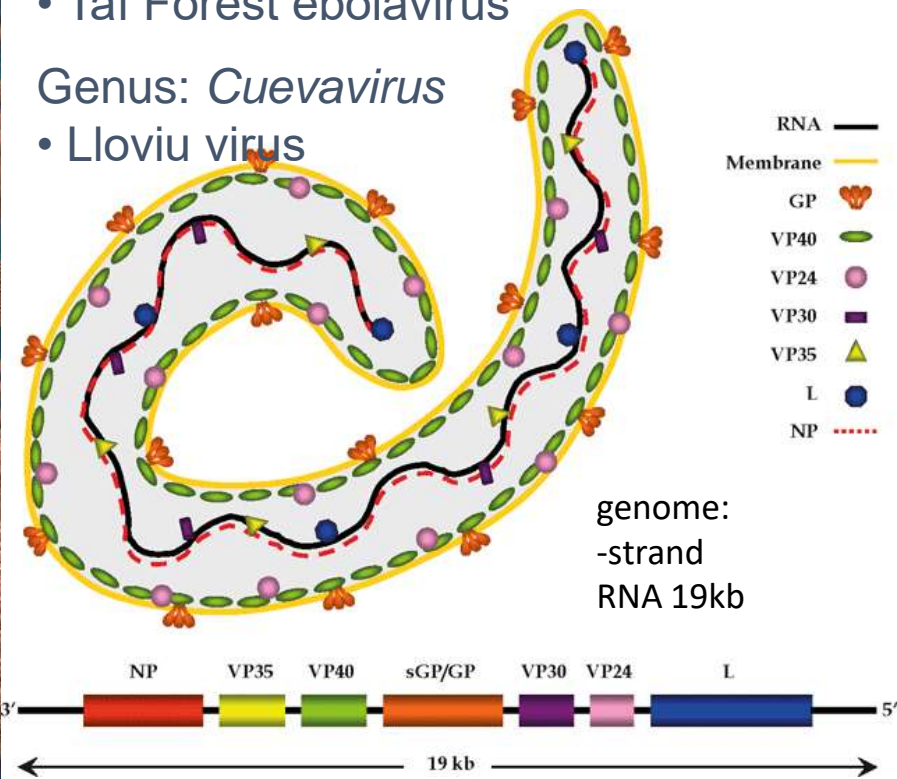
- Marburgvirus

Genus: *Ebolavirus*

- **Zaire ebolavirus**
- **Sudan ebolavirus**
- Bombali ebolavirus
- Reston ebolavirus
- **Bundibugyo ebolavirus**
- Taï Forest ebolavirus

Genus: *Cuevavirus*

- Lloviu virus



- RNA ———
- Membrane ———
- GP 🍊
- VP40 🟢
- VP24 🟡
- VP30 🟣
- VP35 🟩
- L 🔵
- NP - - - -

rodent/shrew/bat-borne
disease agents.

(Zoonotic viral
agents from wildlife)

hanta arena ortho- borna lyssa TBEV
(LCMV) pox

• Surveillance in Europe

notifiable reported to ECDC none none-alert and RRA on Monkeypox none-alert and RRA on emergence animal and human cases reported notifiable reported to ECDC

• Protective measures

avoid inhaling rodent-contaminated. dust (use masks, gloves, rodent control) gloves smallpox vaccine inactivation by 30 min 56°C or detergents avoid exotic squirrels pre-exposure vaccination PEP pre-exposure vaccination - avoid tick bites and unpasteurized goat milk

• Potential treatments

- (antivirals) antivirals - PEP - dialysis (5%)

• Cases in Europe

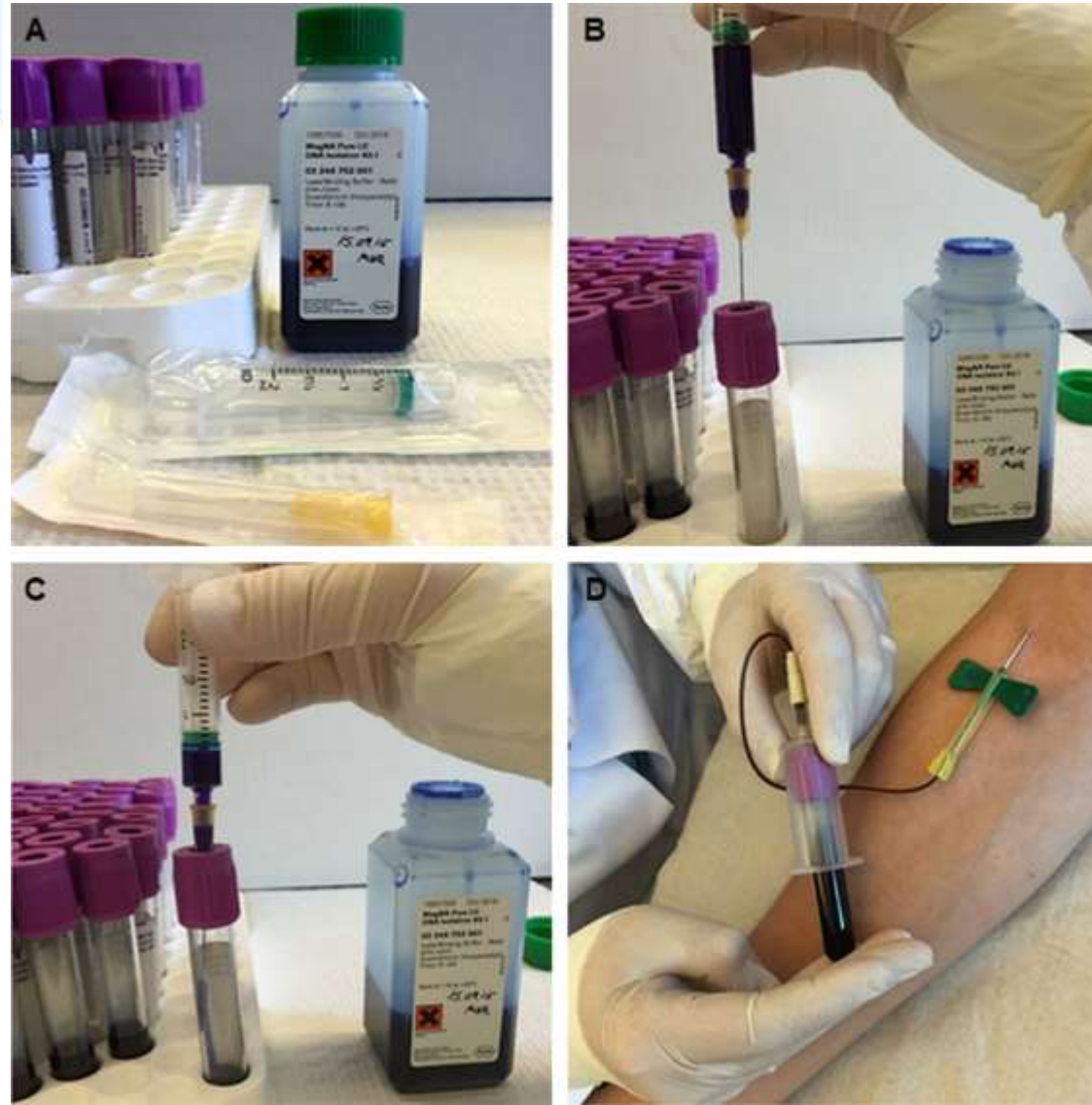
thousands mainly PUUV rare rare rare rare thousands mainly Eur subtype

diagnostic samples

inactivation for transport+ preservation

developed for ebola bed-side inactivation Rosenstierne MW JCM 2016

→ applicabel also for veterinary samples



How to screen for new/emerging (wildlife) viruses ?

PCR



NGS



known classified viruses → • 0.005% (4,404)
← • human viruses 0.0003% (219)

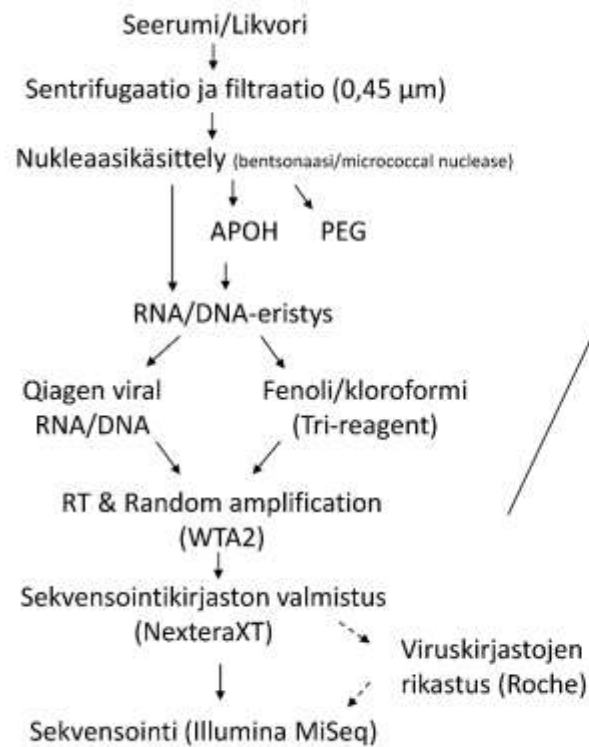


Antibodies

- Less biased / 'Hypothesis-free'
 - for wildlife particularly suitable
- Less sensitive to genetic variation
- Emerging infections
- Co-infections

Wet lab:

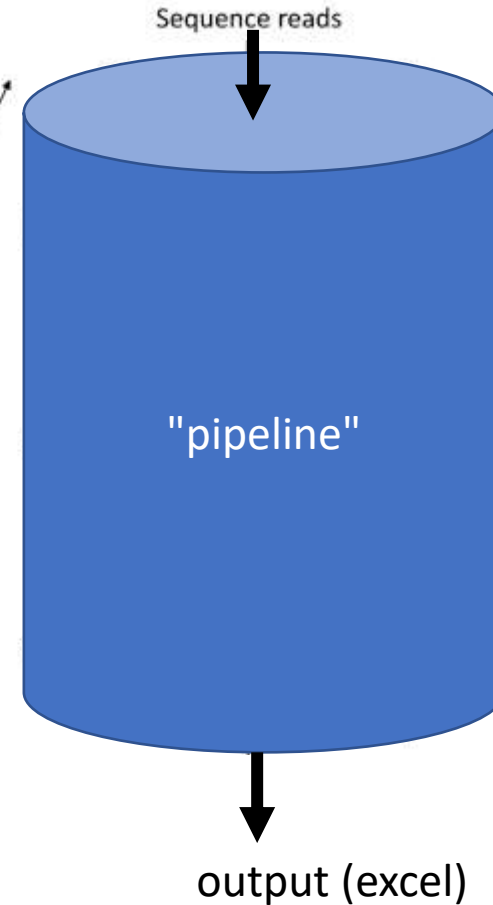
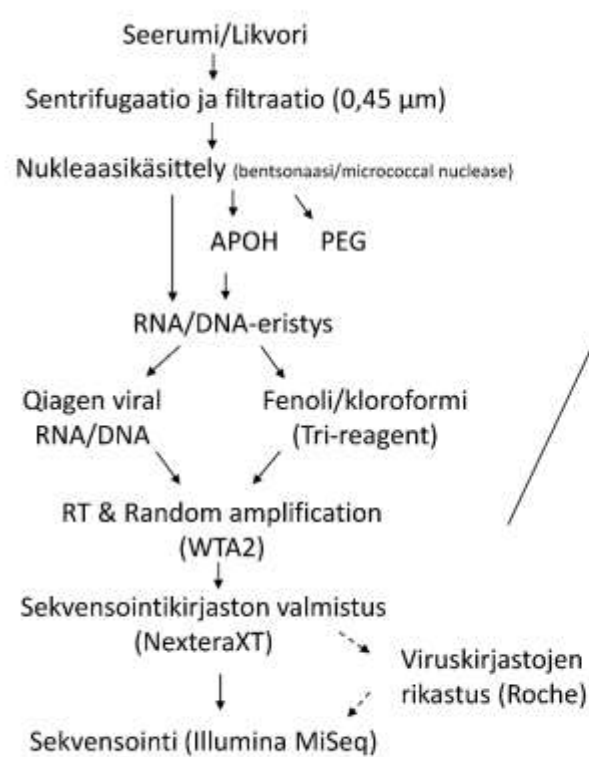
Bioinformatics:



Smura T, Plyusnin I, et al, "Lazypipe"

Wet lab:

Bioinformatics:



"Lazypipe"

Detection of any virus up to 30 % identity with previously characterized viruses
e.g. new virus genera



Smura T, Plyusnin I, et al, "Lazypipe"

origins

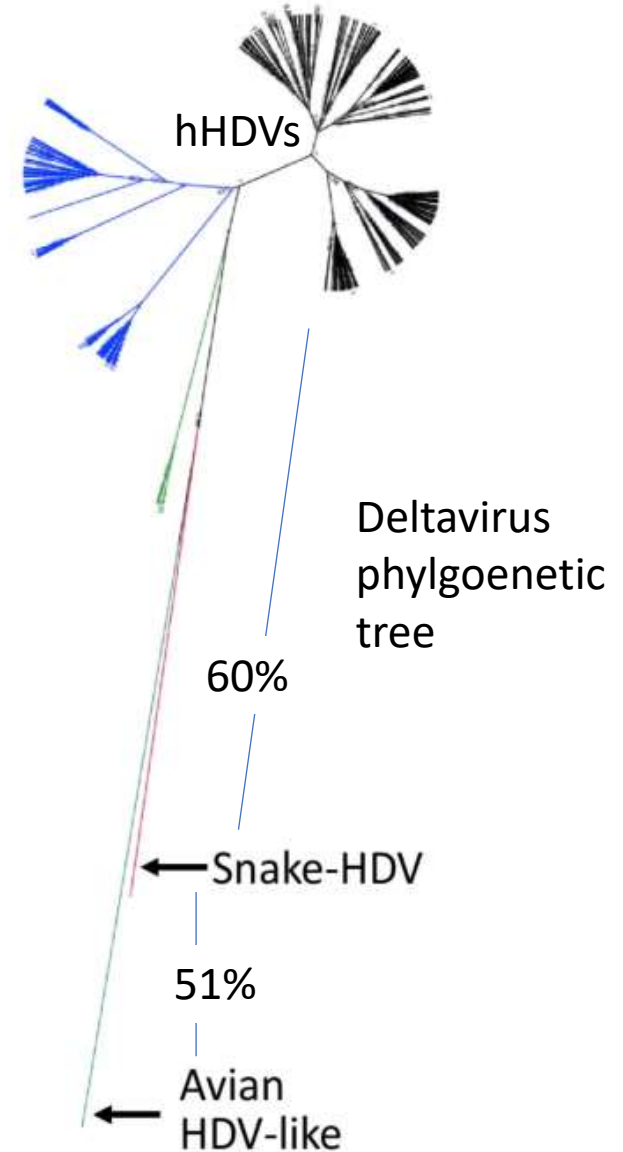
- Hep A rodents?
- Hep B bats?
- Hep C rodents?
- Hep D ?? none
- Hep E rodents, deer..



Discovery (with NGS) of new snake deltavirus

— replicates in tissues without hepadnavirus helper

	origins
Hep A	rodents?
Hep B	bats?
Hep C	rodents?
Hep D	?? none
Hep E	rodents, deer..



Discovery (with NGS) of new snake deltavirus

— replicates in tissues without hepadnavirus helper

- Snake deltavirus D-ag expression

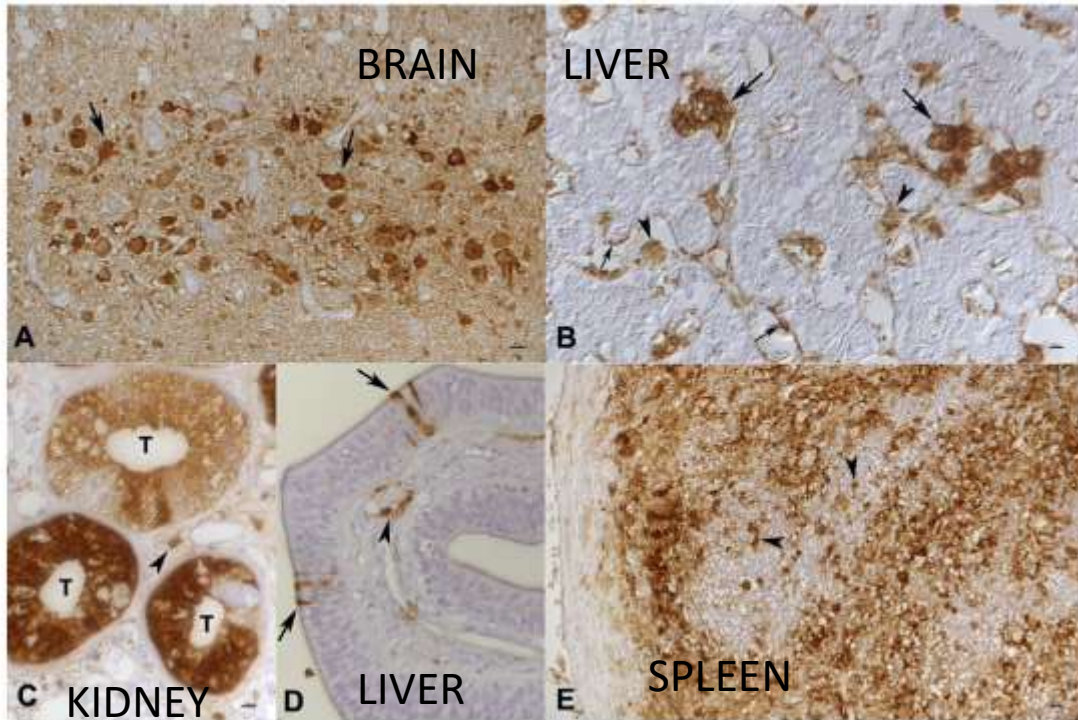
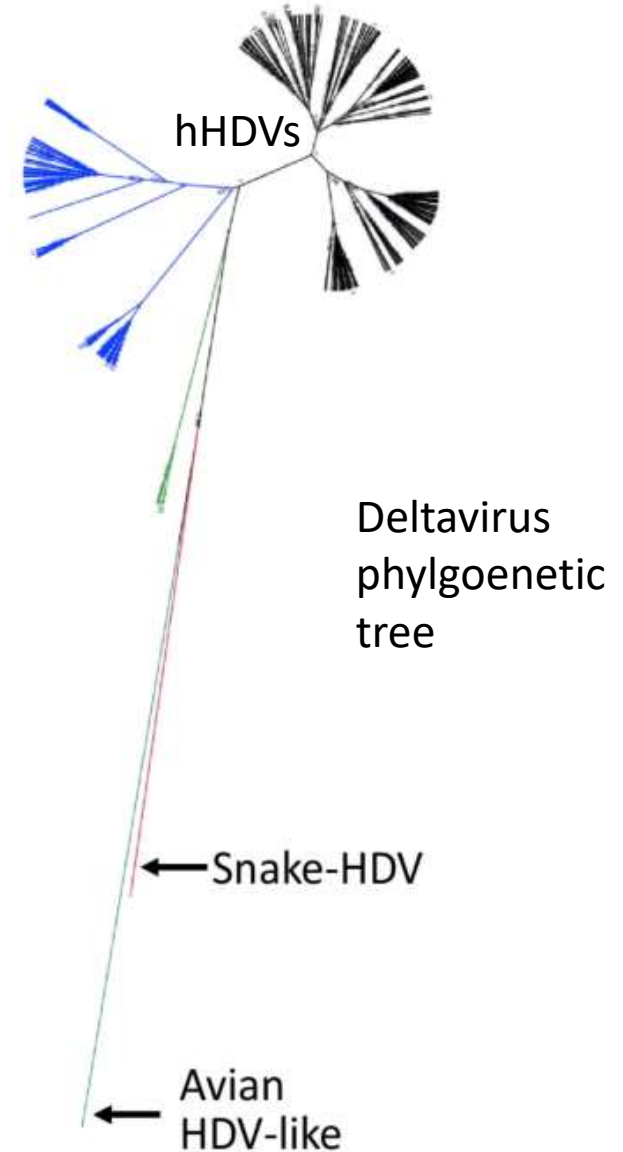


Figure 2.



	origins
Hep A	rodents?
Hep B	bats?
Hep C	rodents?
Hep D	?? none
Hep E	rodents, deer..

University of Helsinki
Taita Research Station, Kenya



JANE JA AATOS
ERKON SÄÄTIÖ

Helsinki University Hospital Funds



9th European Meeting on Viral Zoonoses

September 29 – October 2, 2019
St. Raphaël, France

Organizing committee
Noël Tordo, Åke Lundkvist, Alain Kohl
Alexander Plyusnin, Olli Vapalahti

VENUE

St Raphaël Palais des Congrès
Côte d'Azur, France
(1h from Nice airport)



info

www.euroviralzoon.com

Lazypipe:

a new pipeline for NGS assembly and annotation

Ilja plyusnin: manuscript

- UNIX/perl script
 - Input: Illumina paired-end libraries
1. Quality control: filter short reads, adapter sequences, low quality sequences with Trimmomatic
 2. Filter host genome with BWA MEM
 3. Assemble with Velvet or Megahit
 4. De novo gene detection with MetaGene
 5. Taxonomic annotation of contigs with SANSparallel and custom perl scripts
 6. Realigning reads to assembly with BWA MEM
 7. Generating taxonomic abundance tables, contig annotation tables and binning contigs by taxa
 8. Realigning contigs within taxa with R
 9. Quality control: generating plots for post assembly and post annotation quality control
 10. Collect files for sharing and cleanup

Discovery with NGS of new snake deltavirus

replicates in tissues without hepadnavirus

- origins
- Hep A ?
 - Hep B bats?
 - Hep C rodents?
 - Hep D none
 - Hep E rodent, deer...

Snake deltavirus D-ag expression

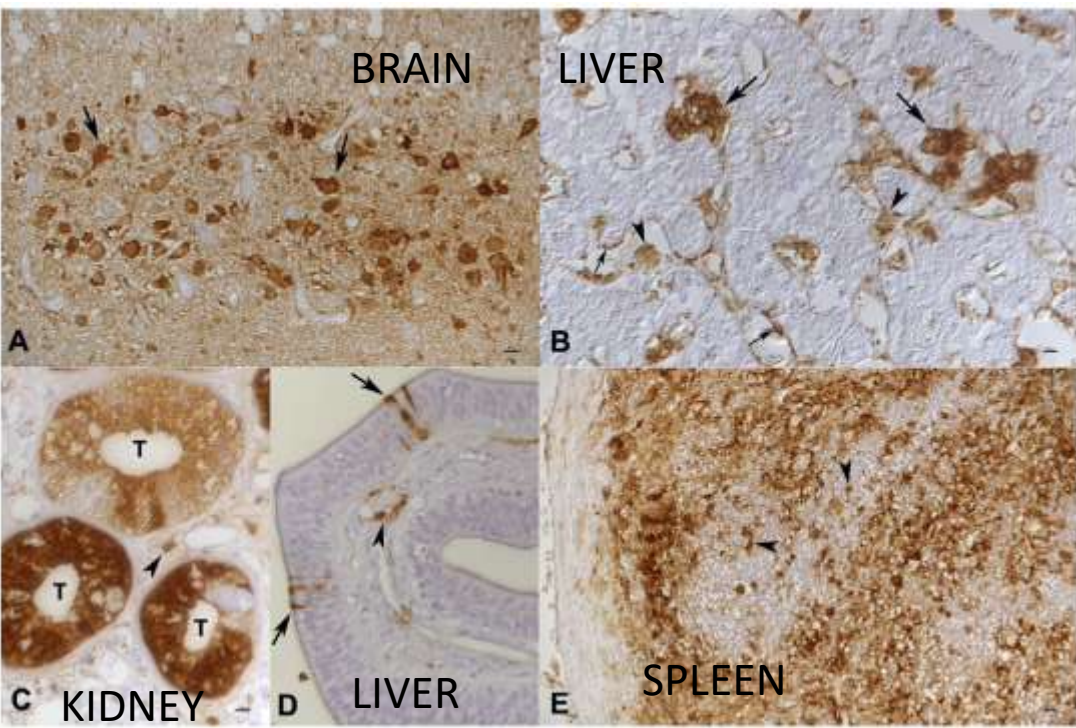
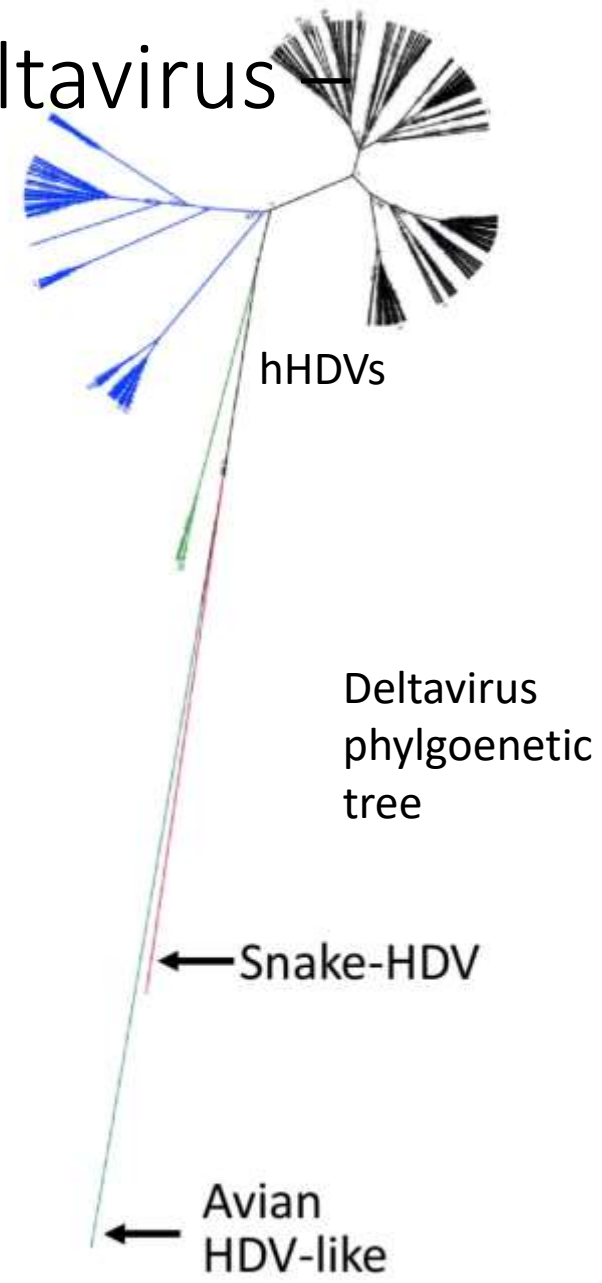
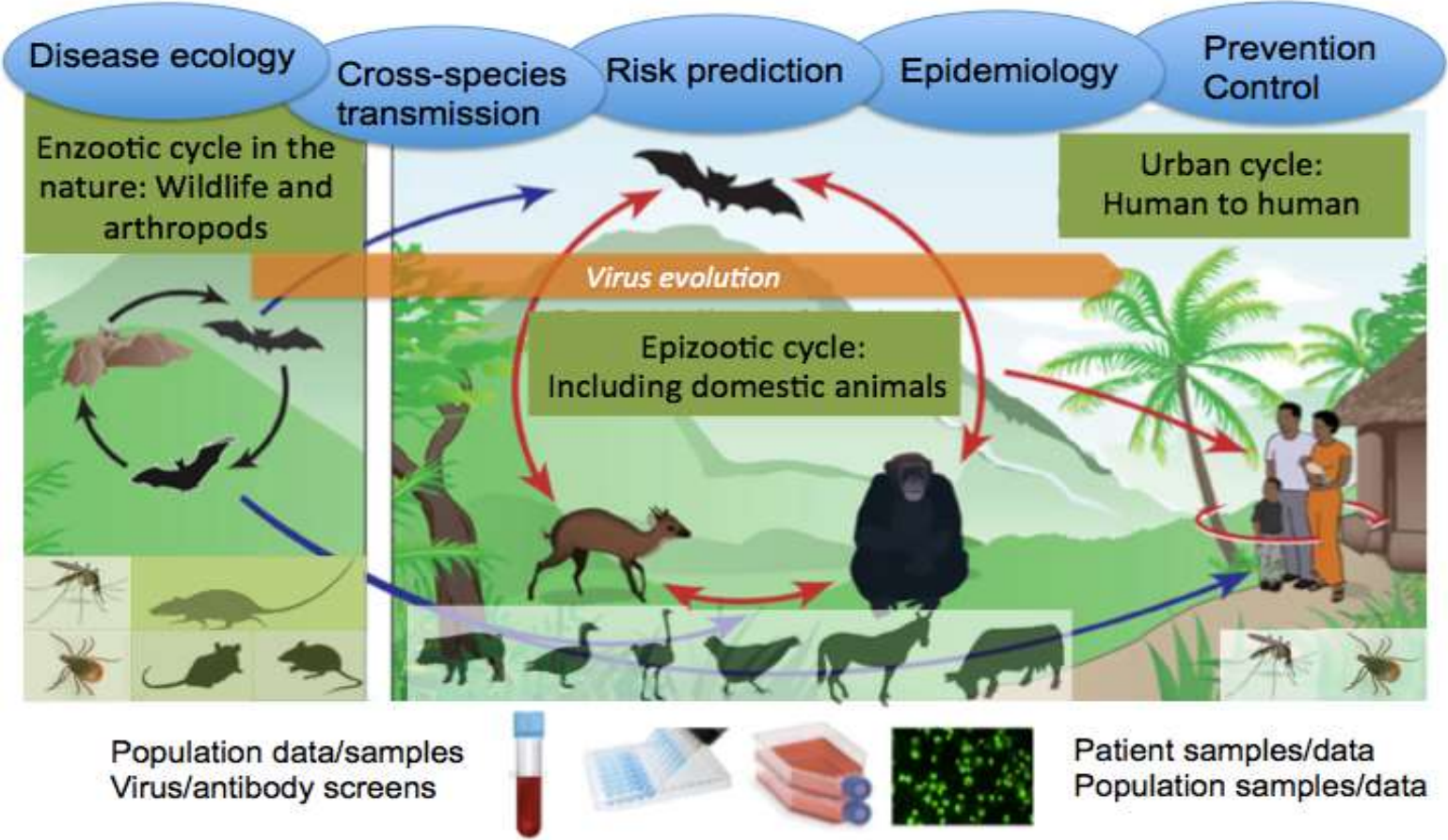


Figure 2.

A) Brain. D-ag expressed in neurons. **B)** Liver. Individual hepatocytes (large arrows), macrophages (arrowheads) and endothelial cells (small arrows) express D-ag. **C)** Kidney. In tubules (T), intense viral antigen expression. **D)** Lung. individual epithelial cells (arrows); some leukocytes express viral antigen (arrowhead). **E)** Spleen with extensive viral antigen expression.



Emerging zoonoses



Modified from <https://www.cdc.gov/vhf/ebola/resources/virus-ecology-fr.html>.

Emerging infections

bird flu



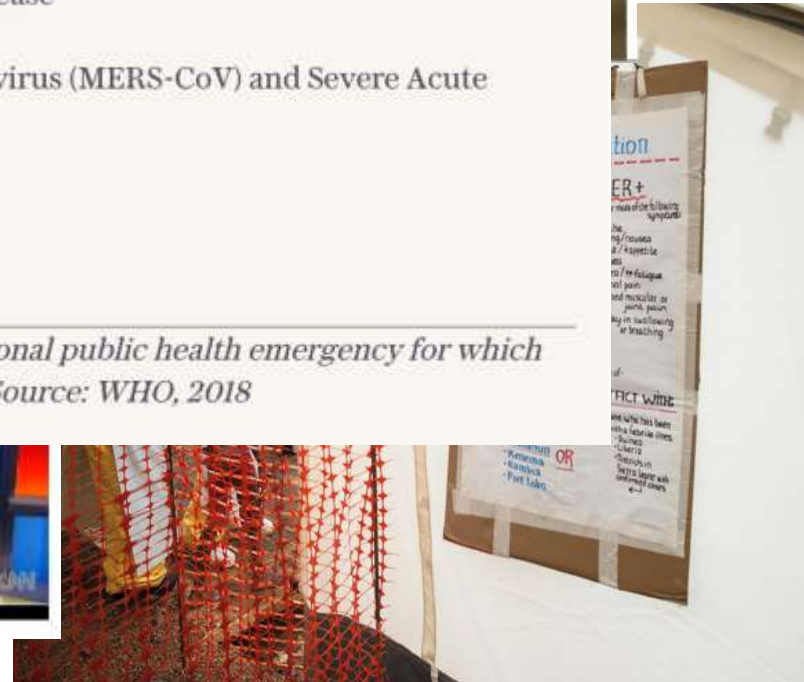
zika



Watchlist | Diseases threatening a public health emergency

- ◆ Crimean-Congo haemorrhagic fever (CCHF)
- ◆ Ebola virus disease and Marburg virus disease
- ◆ Lassa fever
- ◆ Middle East respiratory syndrome coronavirus (MERS-CoV) and Severe Acute Respiratory Syndrome (SARS)
- ◆ Nipah and henipaviral diseases
- ◆ Rift Valley fever (RVF)
- ◆ Zika
- ◆ Disease X

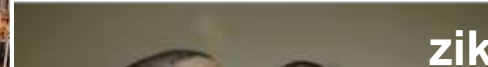
Diseases posing significant risk of an international public health emergency for which there is no, or insufficient, countermeasures. Source: WHO, 2018



Emerging infections



bird flu



zika

Watchlist | Diseases threatening a public health emergency

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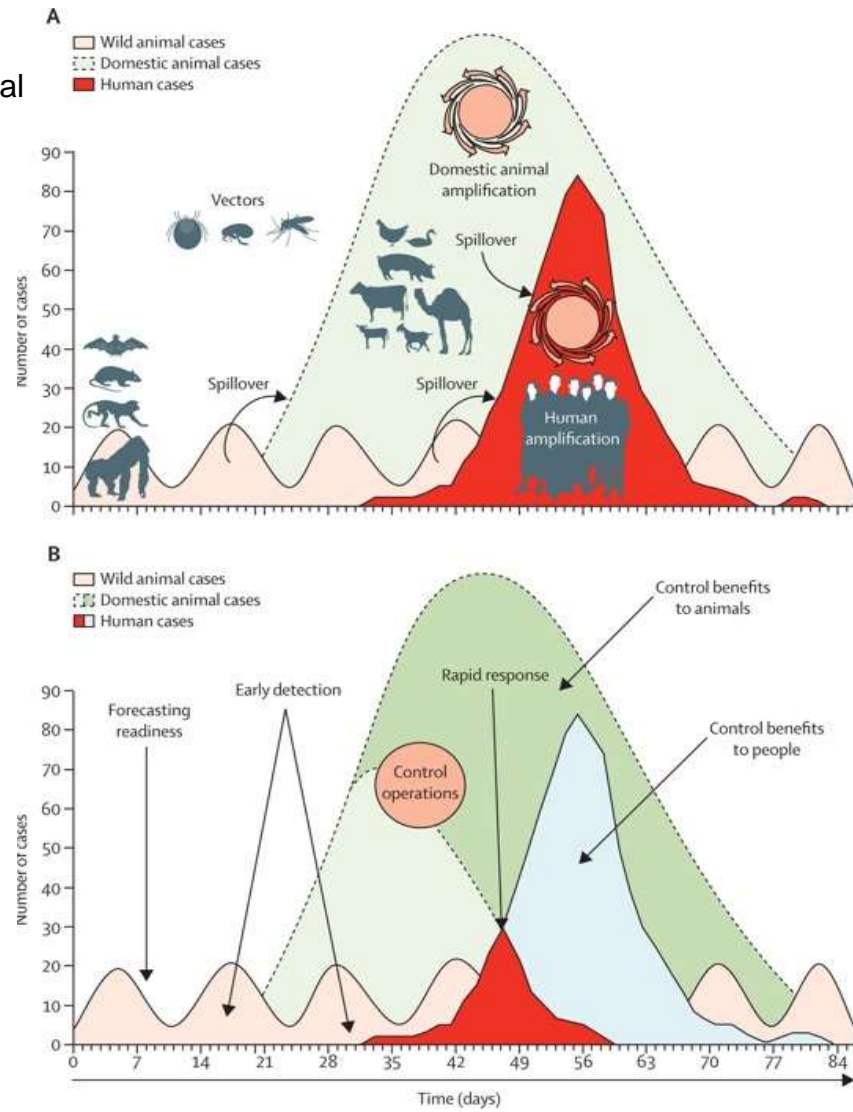
'Disease X' | The mystery killer keeping scientists awake at night

A WHO committee of leading virologists, bacteriologists and infectious disease experts has identified a new global threat. 'Disease X' joins the ranks of Ebola, Zika, and SARS with its potential for epidemics or pandemics.

But what is it? And how could it manifest?



Karesh et al
Lancet
2012



One Health approach



Phylogenetic tree of filoviruses + filovirus-like sequences integrated to mammalian genome

Taylor et al

Evidence that ebolaviruses and cuevaviruses have been diverging from marburgviruses since the Miocene. Peer J 2014

[PeerJ](https://doi.org/10.7554/peerj.2014.2:e556). 2014 Sep 2;2:e556. 2014

→ IN THE GENOME OF MICE AND VOLES CAN BE FOUND INTEGRATED GENES OR PARTS OF GENES OF EBOLAVIRUS /CUEVAVIRUS ANCESTORS
 → FILOVIRUS COMMON ANCESTOR INFECTED MAMMALS MILLIONS OF YEARS AGO

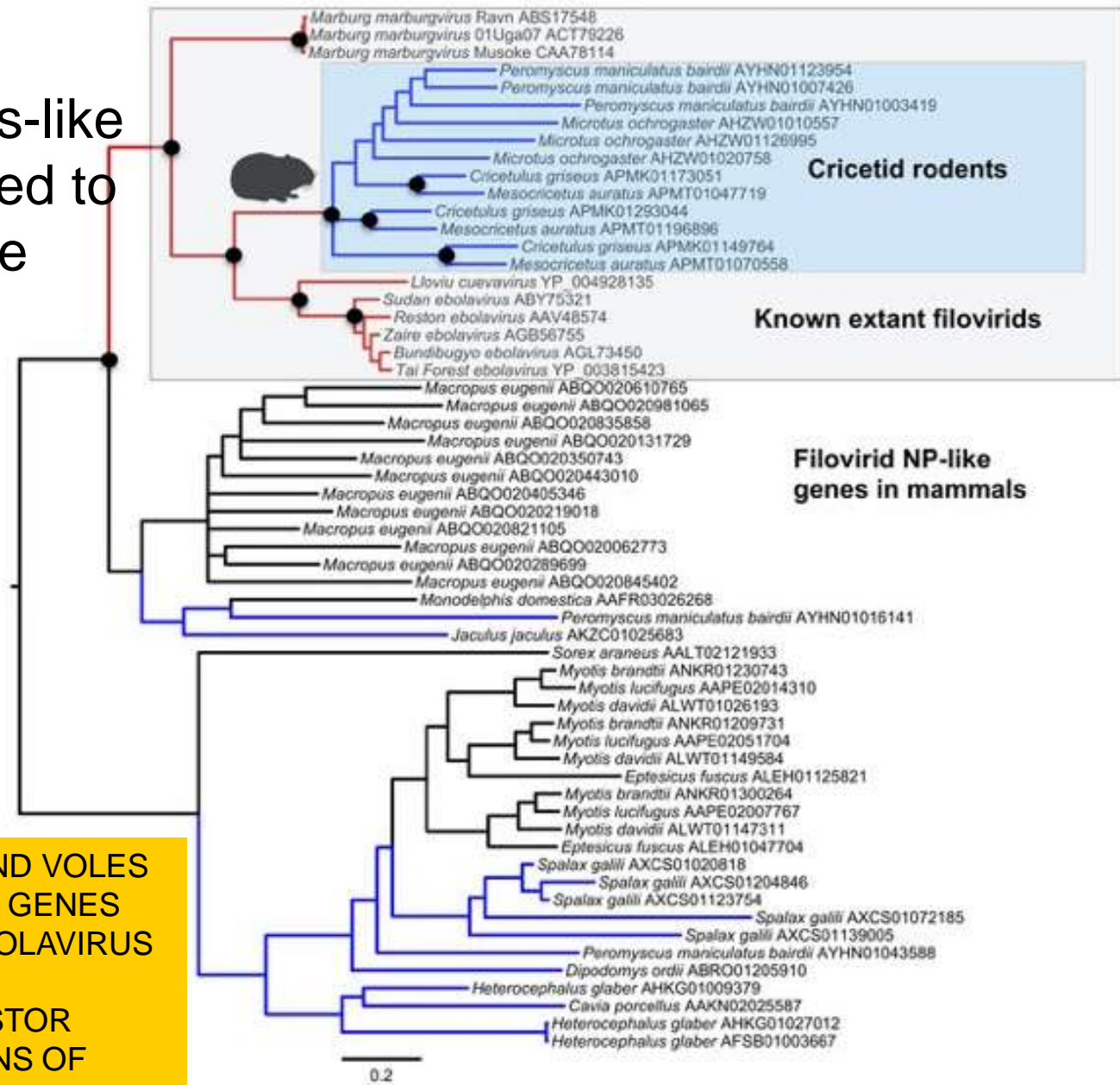


Figure 1: Phylogenetic relationships of filovirid NP-like paleoviruses in mammalian genomes and amino acid sequences from extant filovirids.

Fighting Ebola

diagnostics

real-time-RT-PCRs, POC antigen and RNA tests

Jääskeläinen et al JCV 2015; bed-side inactivation Rosenstierne MW JCM 2016

→ containment

control measures, quarantine

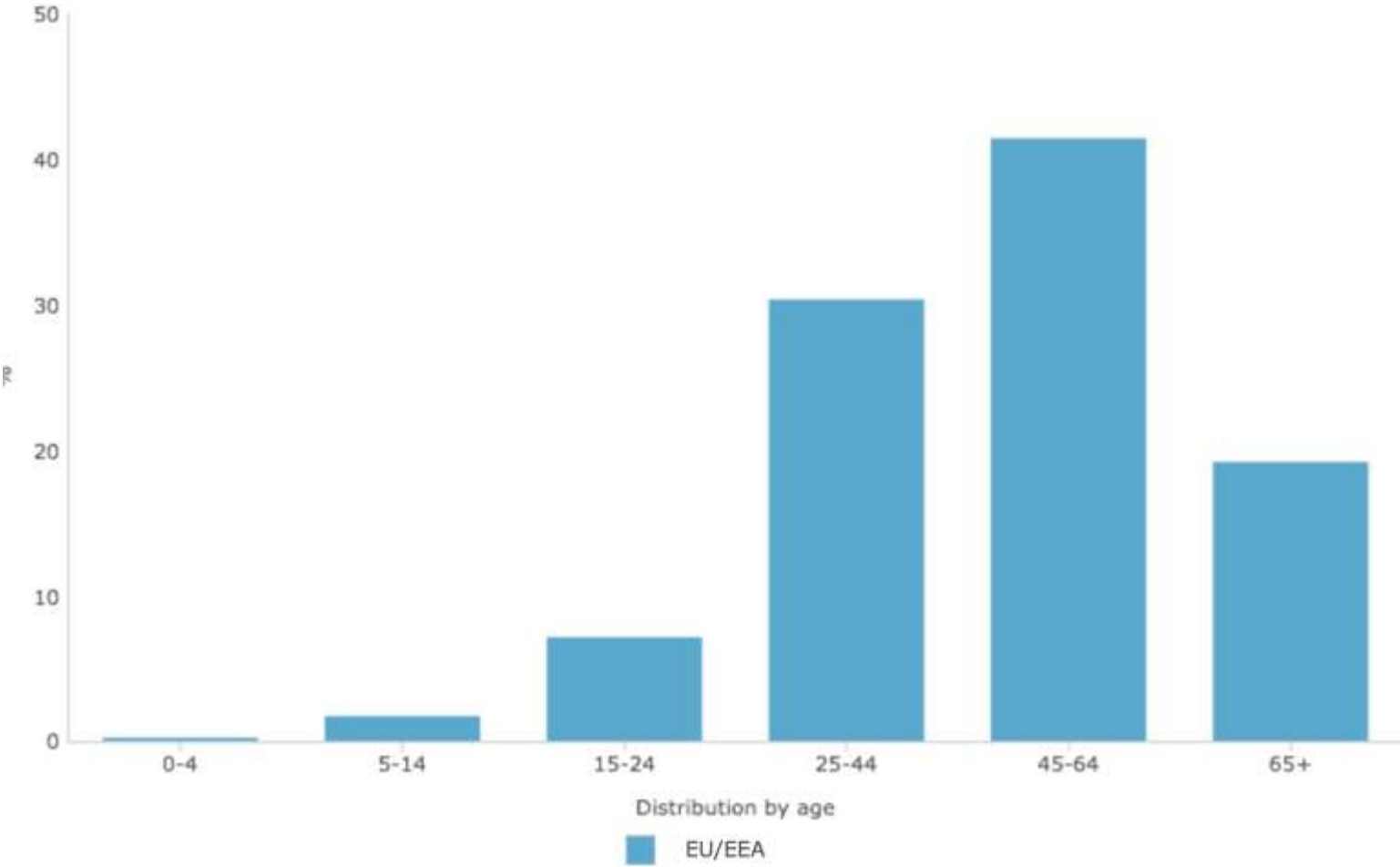


→ vaccines
.. → antivirals

Wolz A.
N Engl J Med 2014

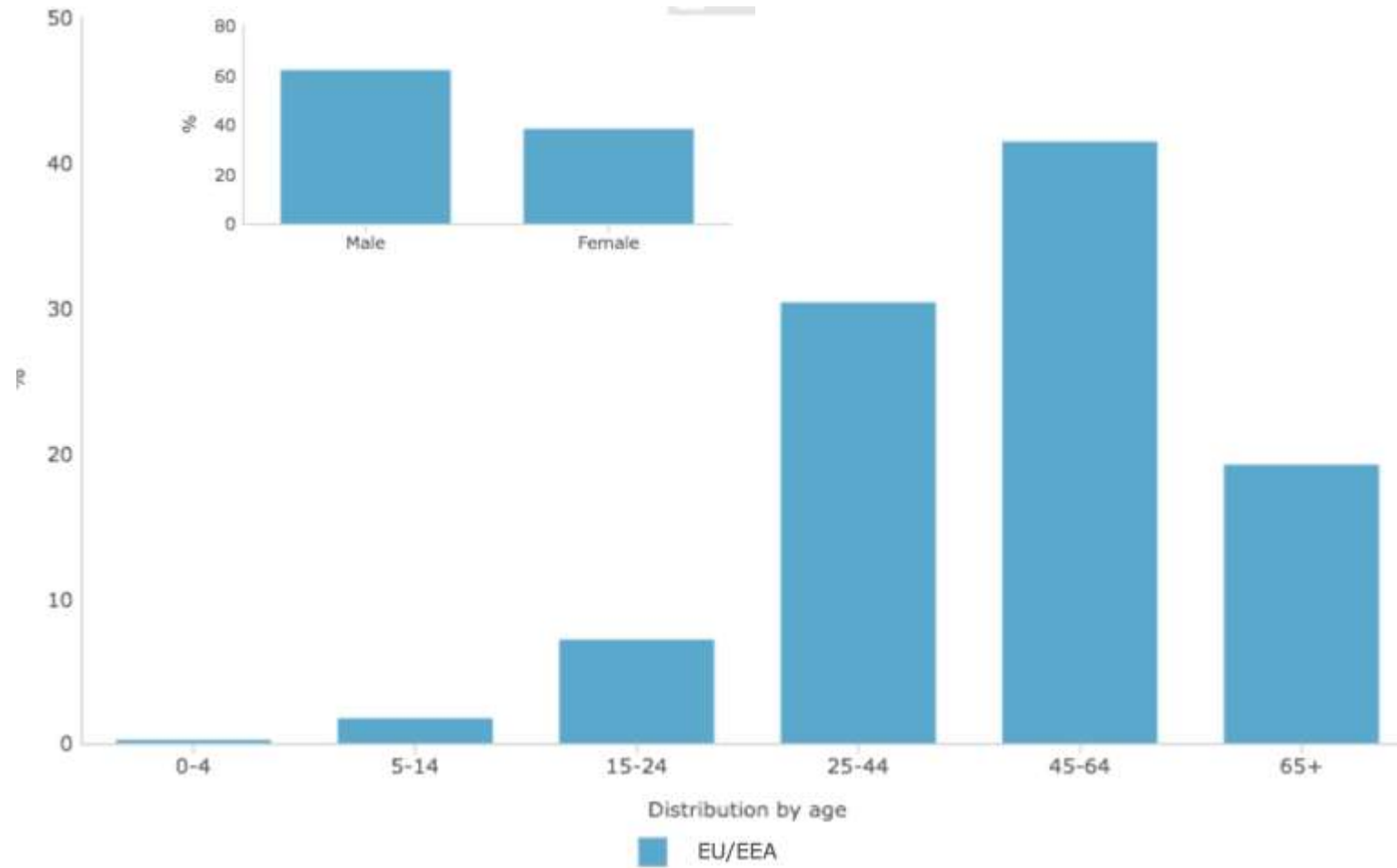
Control through containment: patient isolation, diagnostics, contact tracing, and safe burial practices

Hantavirus infections – age distribution

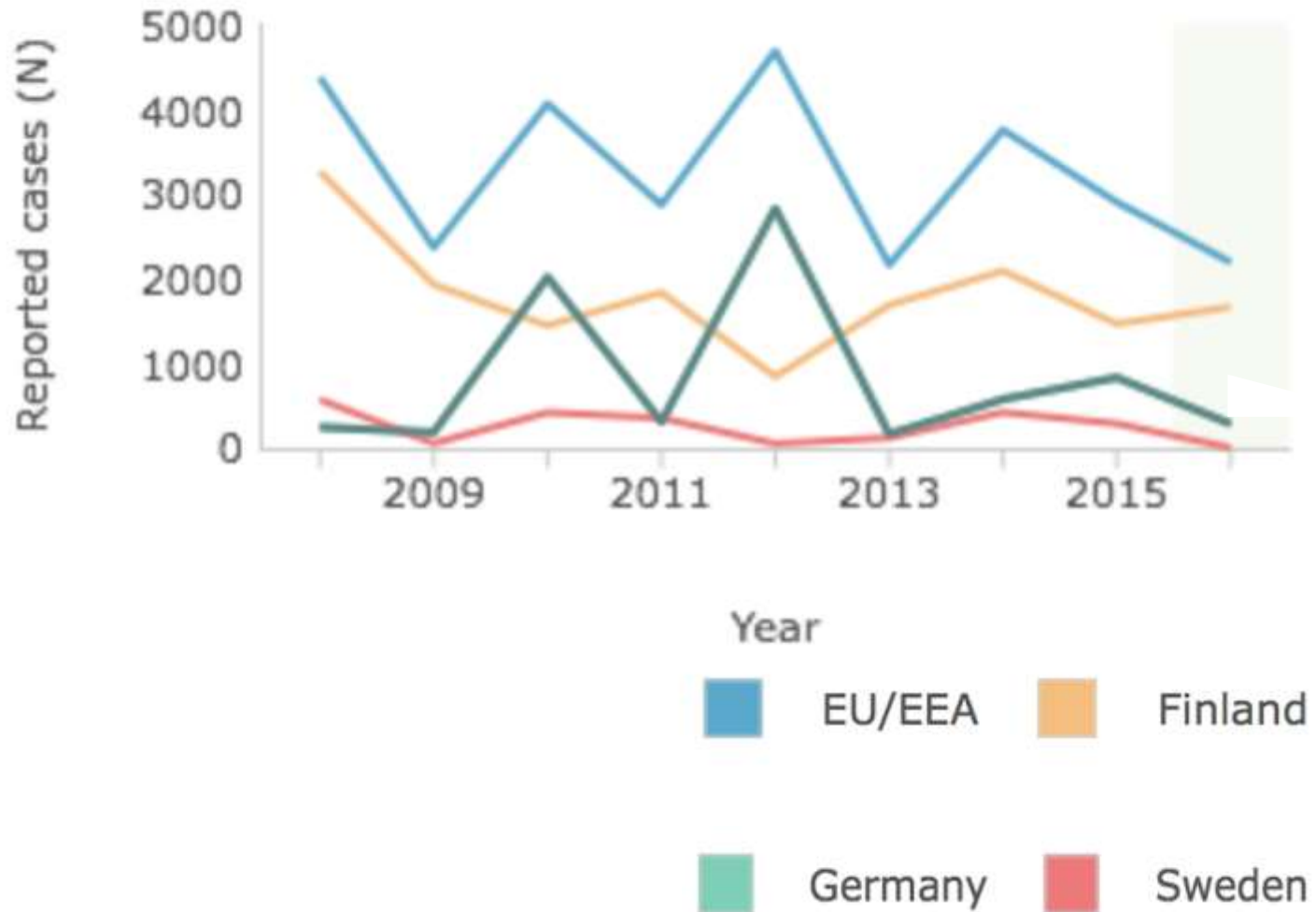


Hantavirus infections – age distribution

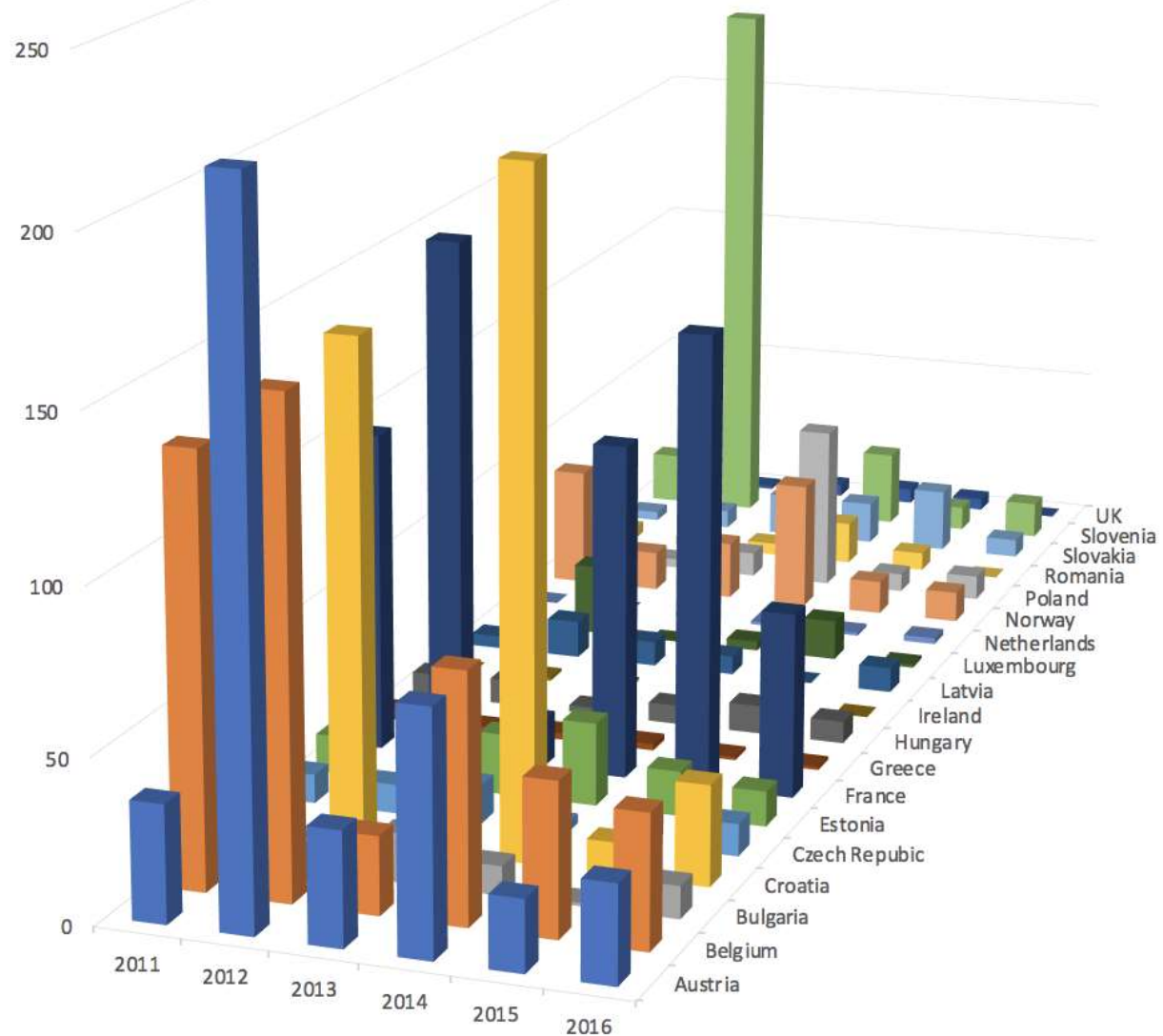
Gender distribution



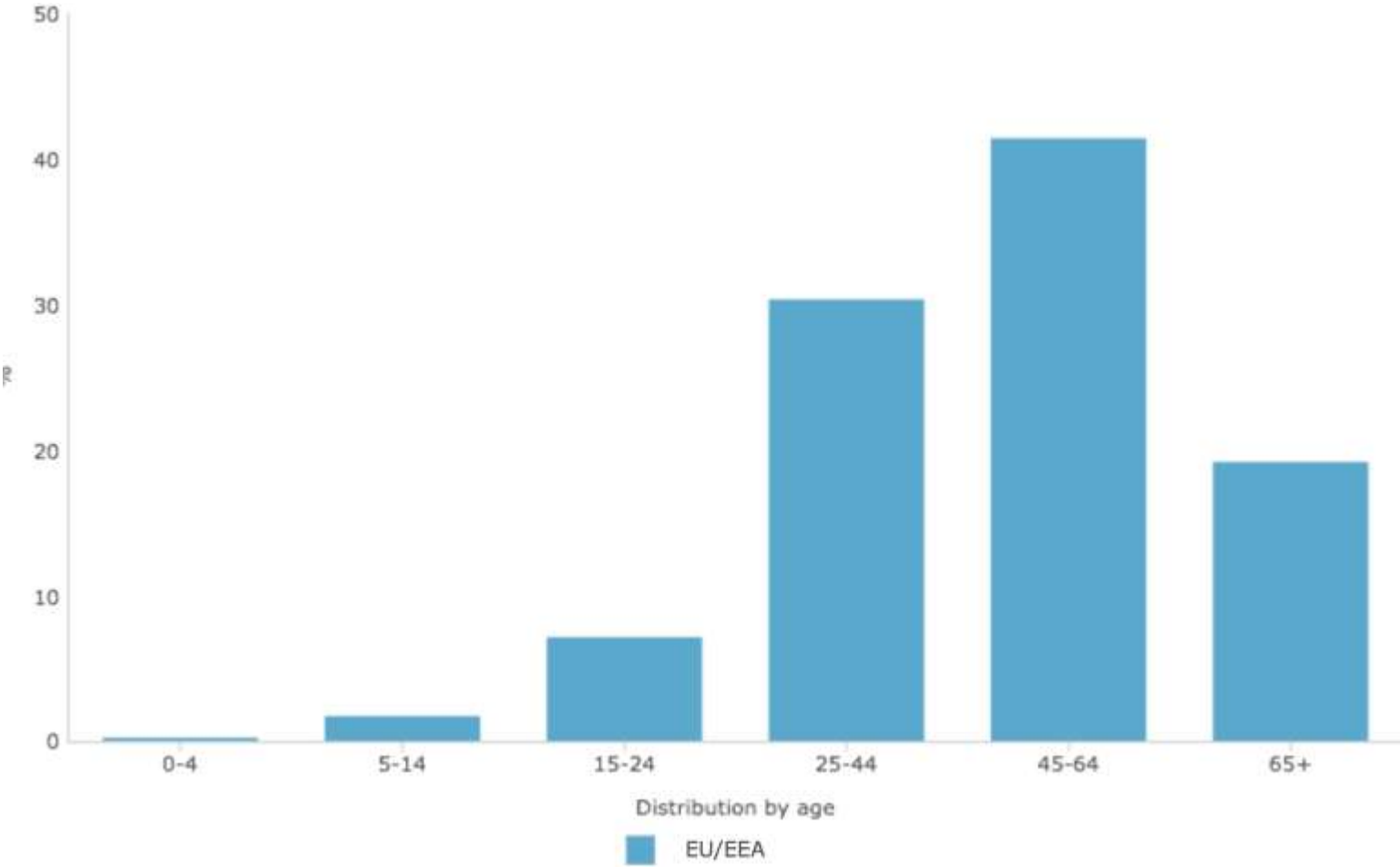
Hantavirus infections in Europe (EU/EEA) 2008-16 and Germany, Finland and Sweden



Hantavirus cases in EU/EEA countries (other than FIN, GER, SWE) 2011-16

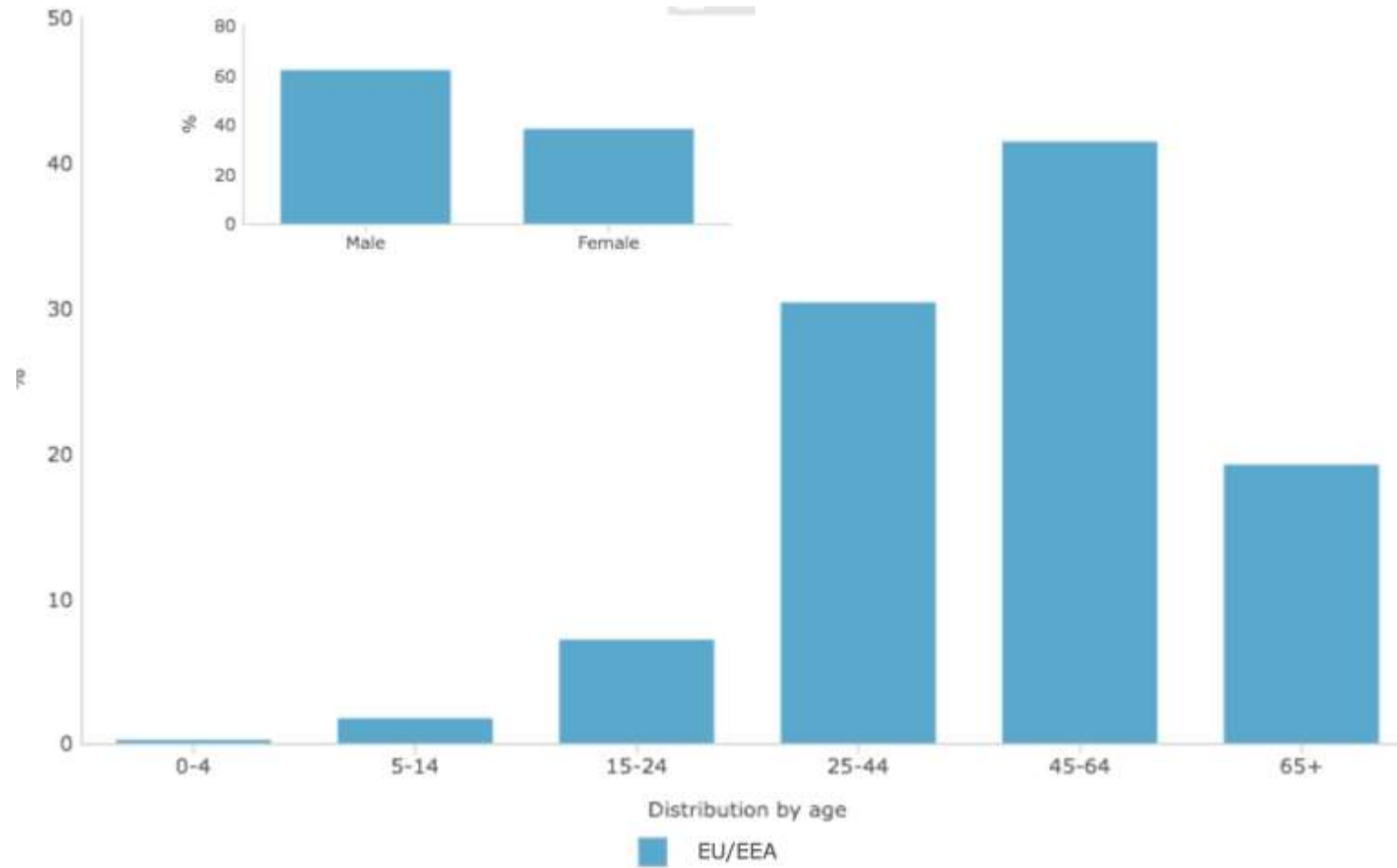


Hantavirus infections – age distribution



Hantavirus infections – age distribution

Gender distribution

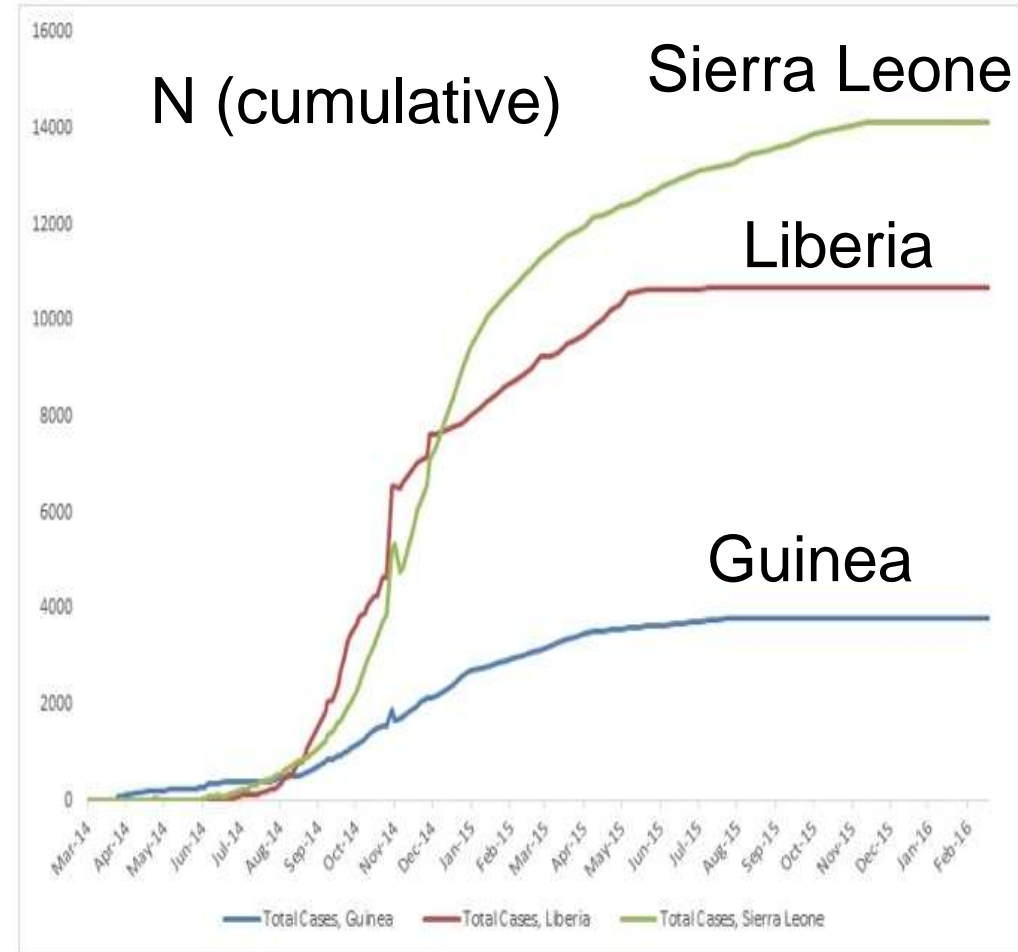


EBOLA - WEST AFRICAN outbreak

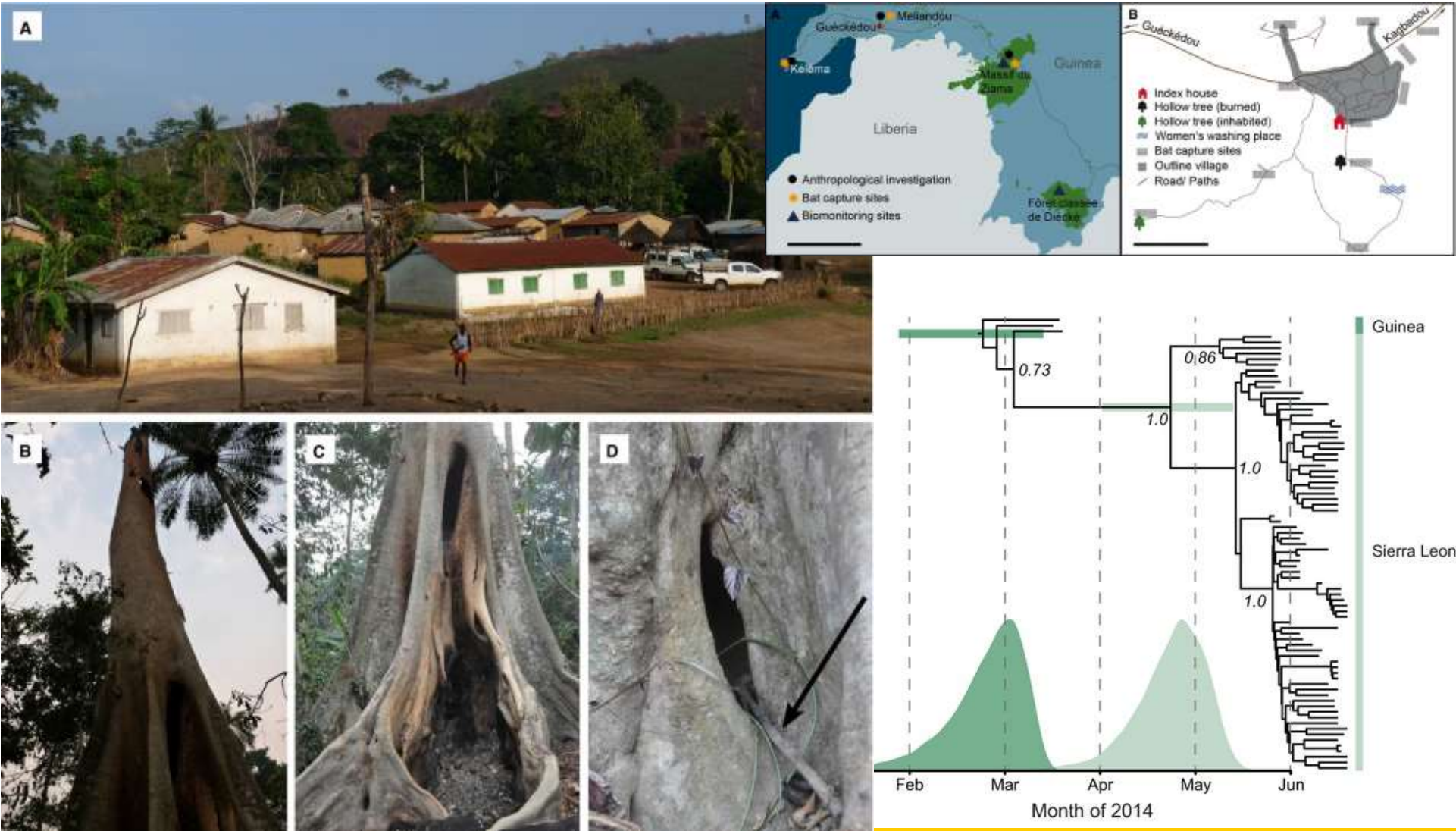


Country	Total Cases (Suspected, Probable, and Confirmed)	Confirmed Cases	Total Deaths
Guinea ²	3811	3355	2543
Sierra Leone ³	14124	8706	3956
Liberia ⁴	10675	3160	4809
Total	28610	15221	11308

Graph 1: Total suspected, probable, and confirmed cases of Ebola virus disease in Guinea, Liberia, and Sierra Leone, March 25, 2014 - February 14, 2016, by date of WHO Situation Report, n=28603



Graph 1 shows the total reported suspected, probable, and confirmed cases in Guinea, Liberia, and Sierra Leone provided in [WHO situation reports](#) beginning on March 25, 2014 through the most recent situation report on February 17, 2016.

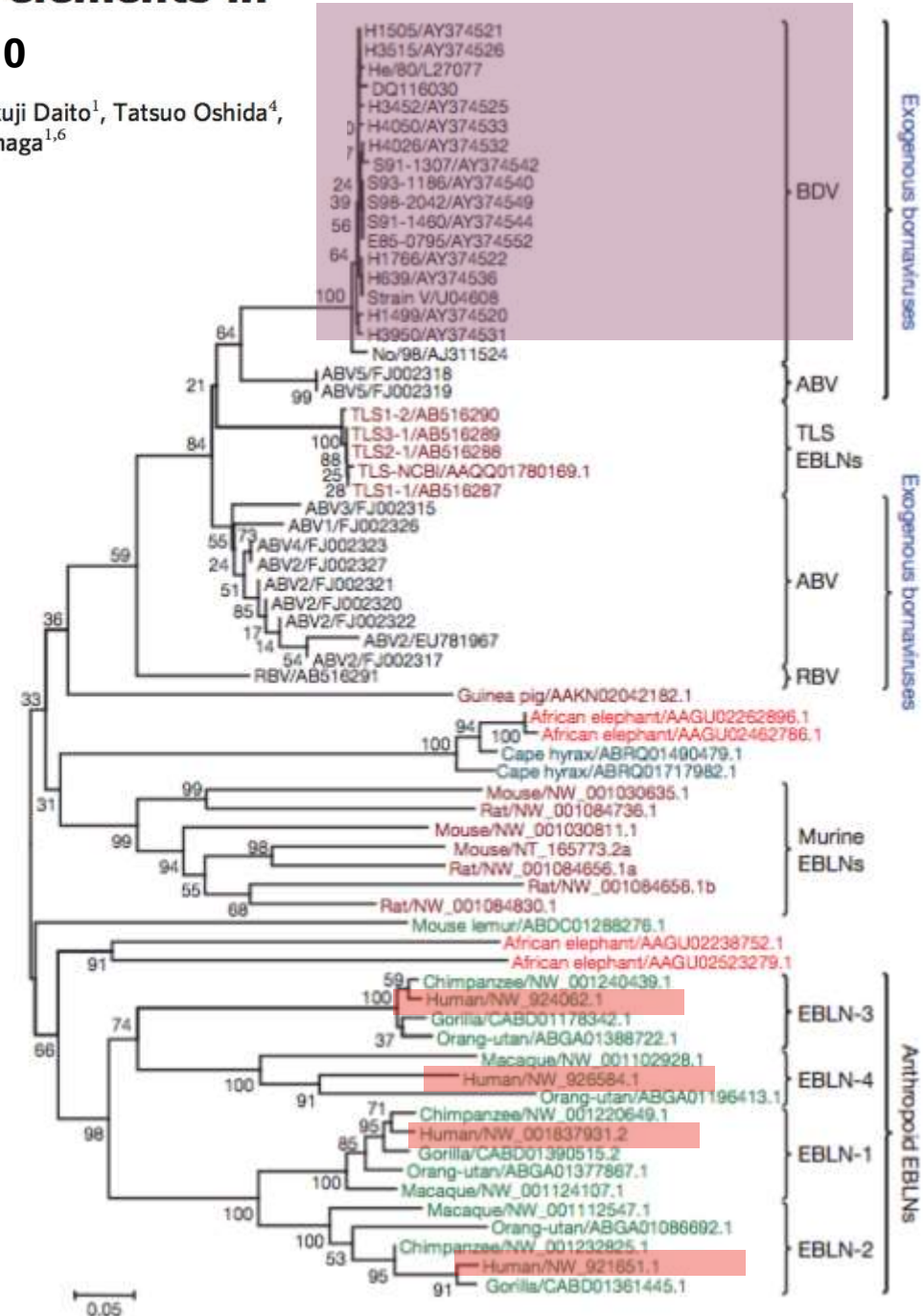


-IN FEBRUARY 2014 Ebola virus spread FROM GUINEA TO SIERRA LEONE
 - THE WHOLE W AFRICA EPIDEMIC MOST PROBABLY ORIGINATES FROM A SINGLE ZONOTIC TRANSMISSION EVENT - involving a 2-year-old boy in Meliandou, Guinea, who might have been infected by hunting or playing with insectivorous free-tailed bats living in a nearby hollow tree

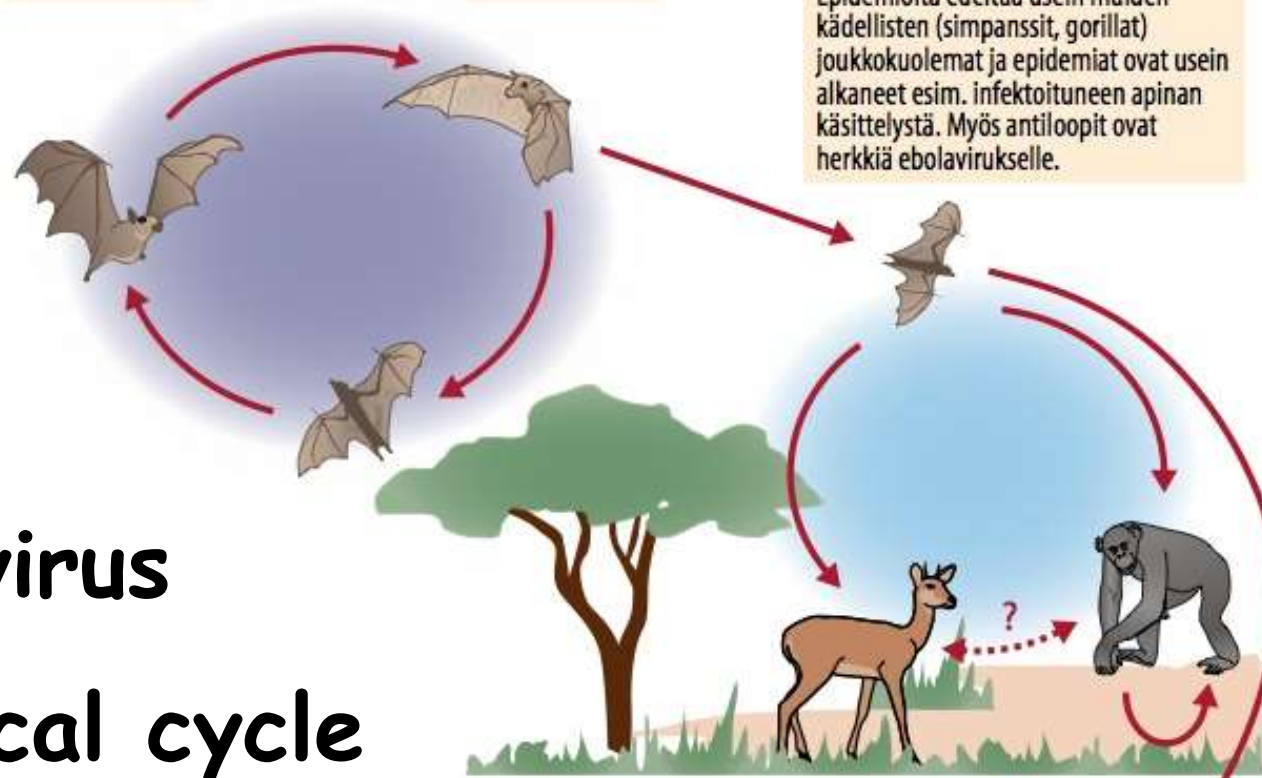
Endogenous non-retroviral RNA virus elements in mammalian genomes

Nature, 2010

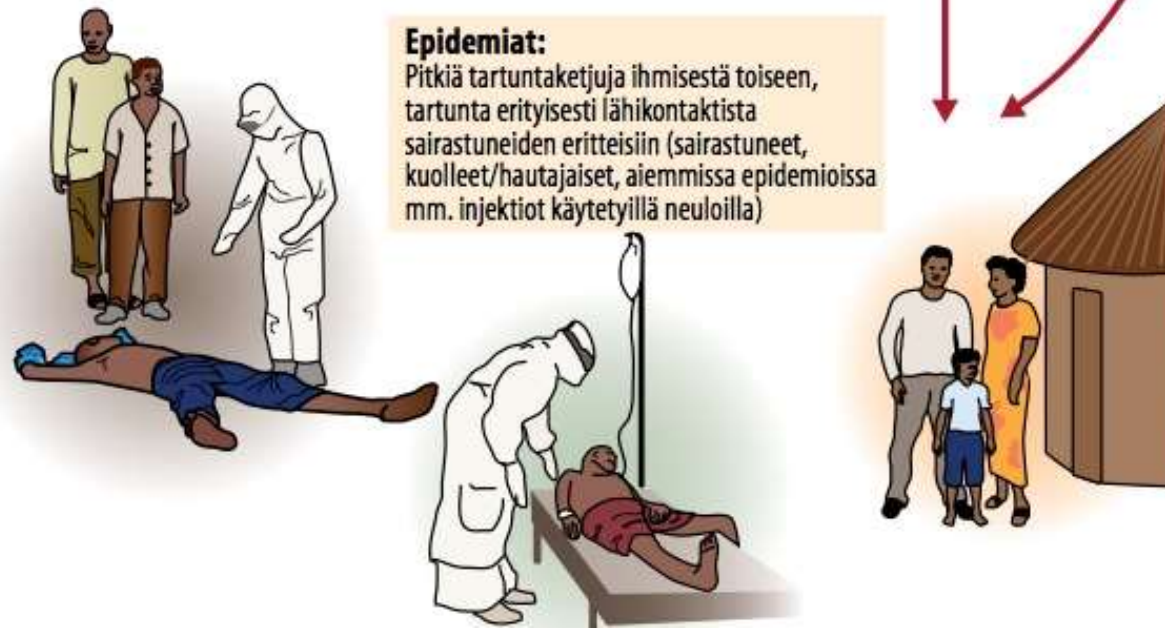
Masayuki Horie^{1*}, Tomoyuki Honda^{1,2*}, Yoshiyuki Suzuki³, Yuki Kobayashi³, Takuji Daito¹, Tatsuo Oshida⁴, Kazuyoshi Ikuta¹, Patric Jern⁵, Takashi Gojobori³, John M. Coffin⁵ & Keizo Tomonaga^{1,6}



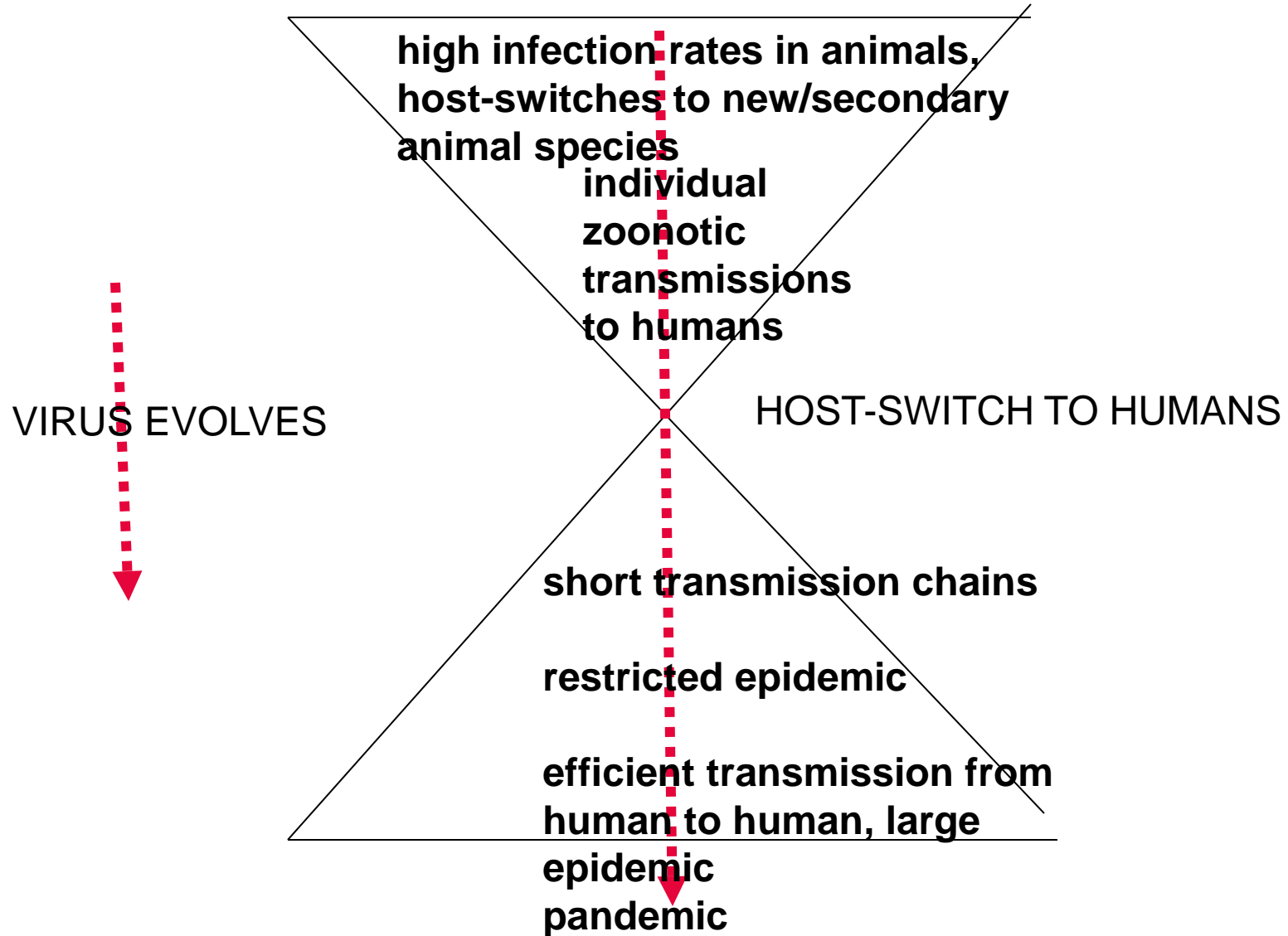
Ebola virus ecological cycle



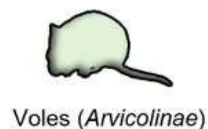
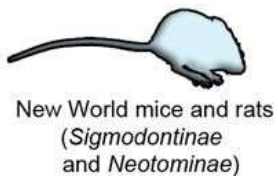
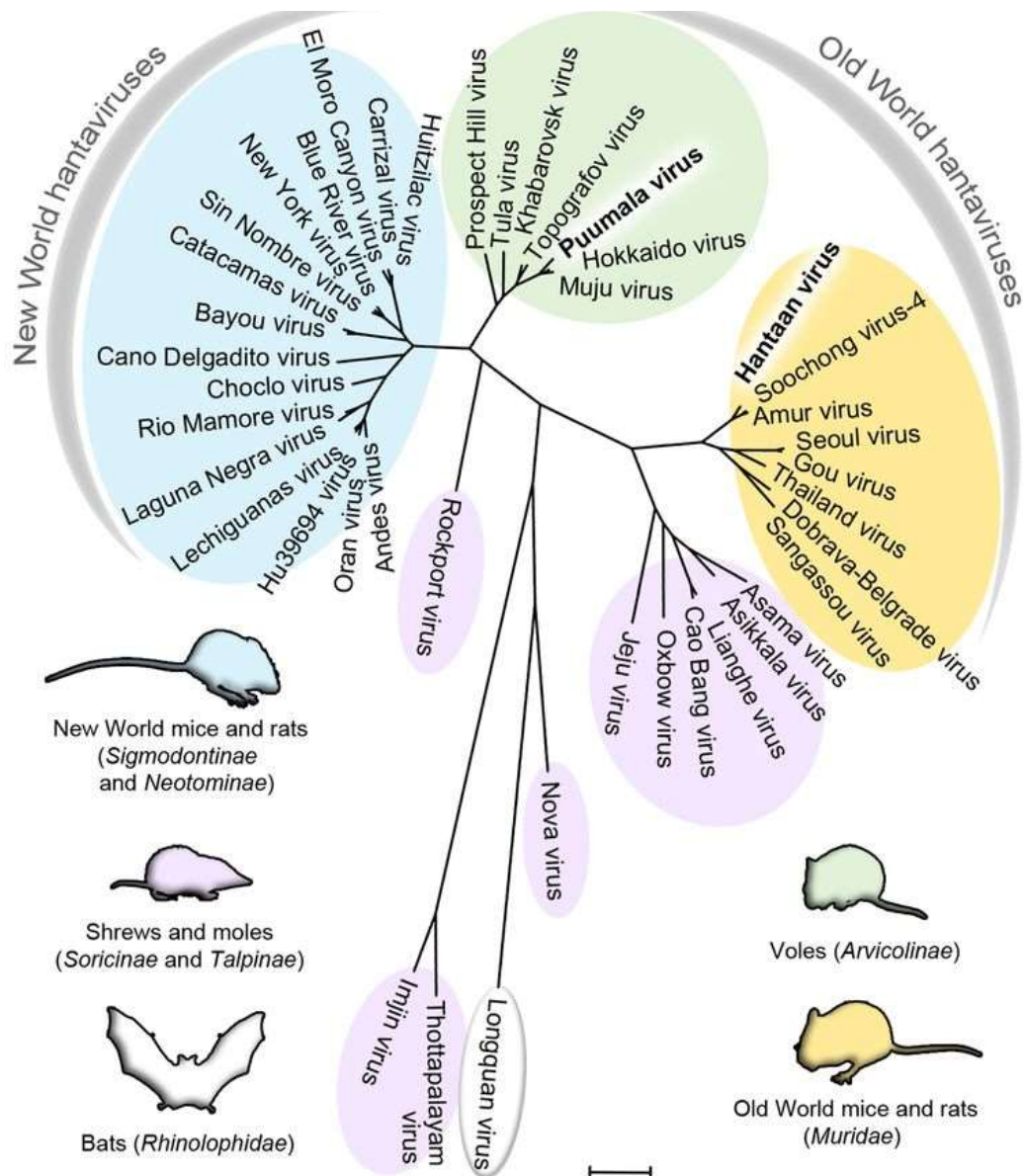
Epidemioita edustaa usein maahan
kädellisten (simpanssit, gorillat)
joukkokuolemat ja epidemiat ovat usein
alkaneet esim. infektoituneen apinan
käsittelystä. Myös antiloopit ovat
herkkiä ebolavirukselle.



Epidemiat:
Pitkiä tartuntaketjuja ihmisestä toiseen,
tartunta erityisesti lähikontaktista
sairastuneiden eritteisiin (sairastuneet,
kuolleet/hautajaiset, aiemmissa epidemioissa
mm. injektioit käytetyillä neuloilla)



Hantaviruses Gn phylogeny



Ilona Rissanen et al. J. Virol. 2017;91:e00378-17

Disease:

- Hemorrhagic fever with renal syndrome (HFRS)

- Puumala -mainly mild, (NE)
- Seoul –moderate
- HTN, DOBV- more often severe.

0.1-0.4 %

- Saaremaa
- Kurkino
- Sochi
- Dobrava

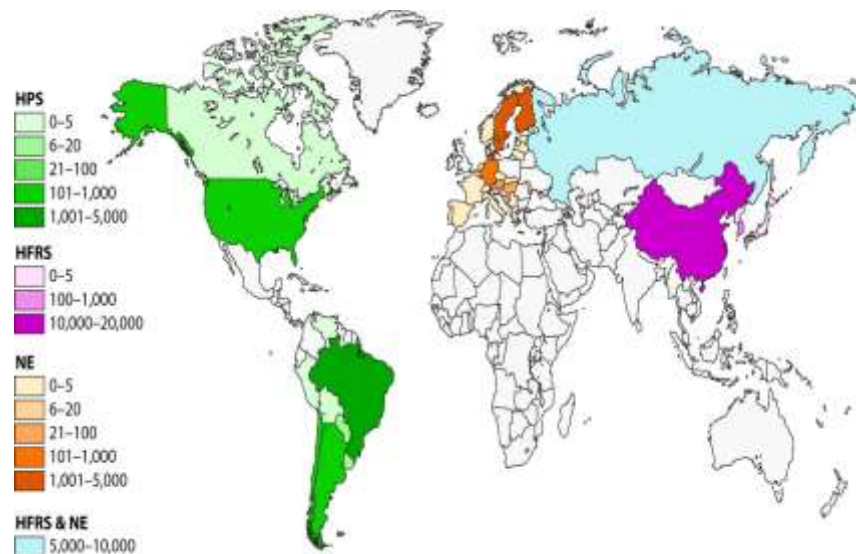
- Hantavirus (cardio)pulmonary syndrome

- Sin Nombre
- Andes
- Araraquara (and others)

40 %



Hantavirus disease burden globally (cases per year)



Jonsson, de Figueiredo, Vapalahti, Clin. Microbiol. Rev. 2010x