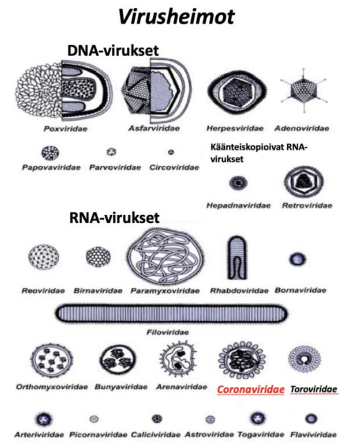
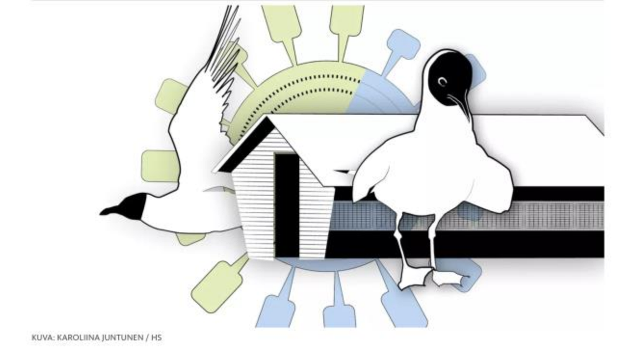
HELSINGIN YLIOPISTO
HELSINGFORS UNIVERSITET
UNIVERSITY OF HELSINKI

Detecting potential new emerging viral threats in clinical and field samples – *early and late alarms*





KUVA: KAROLIINA JUNTUNEN / HS

Olli Vapalahti

MD, Professor of Zoonotic Virology

University of Helsinki
- Department of Virology, Faculty of Medicine
- Microbiology and Epidemiology, Faculty of Veterinary Medicine

Helsinki University Hospital Diagnostic Center - HUSLAB
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Wageningen 24 April 2024

MENU

APERITIF: Some general themes on Emerging Viral Infections

STARTERS: A collection of fresh parapoxviruses, arenaviruses, kolmioviruses and filoviruses detected with genus-specific primers, metagenomics & bioinfo

MAIN COURSE: Emerging flaviviruses (spiced with some other arboviruses) in mosquitoes and ticks detected with genus- and species-specific RT-PCRs or metagenomics and dressed with ARTIC-based sequencing, intra-host variation & phylogenetic analyses

DESSERT: Mink and foxes with highly pathogenic avian influenza

The future of infectious diseases as predicted in the past

- “*The future of infectious diseases will be very dull*”

  Macfarlane Burnet, F. & White, D. O. 1972 *Natural History of Infectious Disease* p263 (Cambridge Univ. Press, 1972).

- “*There would be scant role for infectious disease specialists in the next century, unless they would spend their time culturing one another*”

  Robert Petersdorf, 1986 President of the American Association of Medical Colleges , in *Review of Infectious Diseases* 8, 478-87

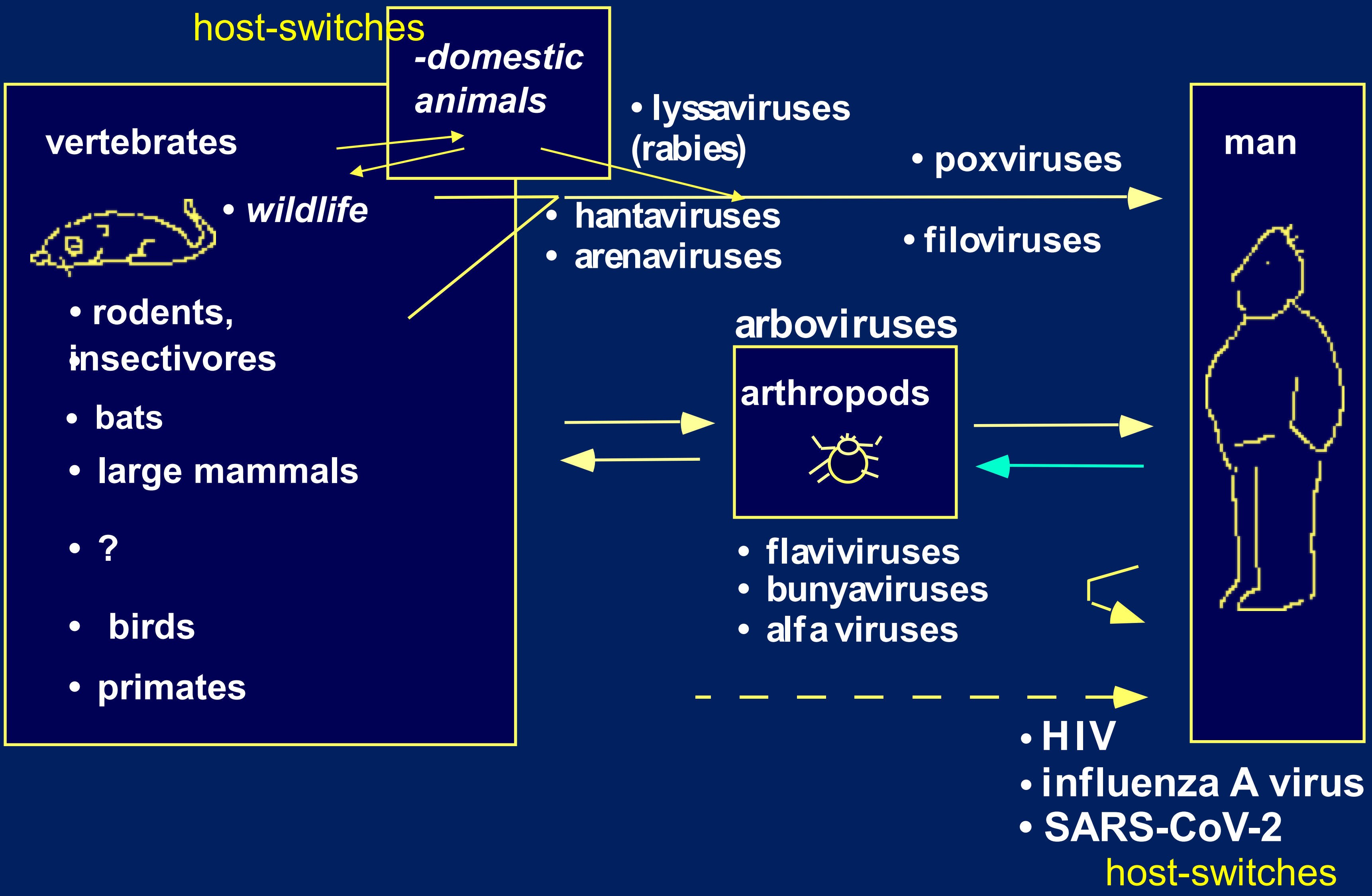
Required for viruses to (re-)‘emerge’

1) Introduction - Pathogen (or its variant)
   - Crossing species or geographical borders

2) Suitable conditions
   - Species distributions, density, contacts; climate, lack of immunity, susceptibility to severe sympotms

3) Lack of control measures
   - Dg, therapy, vaccines, resources, prioritization

EMERGING ZOONOTIC VIRUSES AND HOST-SWITHCES



host-switches

-domestic animals

vertebrates

- *wildlife*
- rodents,
- insectivores
- bats
- large mammals
- ?
- birds
- primates

- lyssaviruses (rabies)
- poxviruses
- hantaviruses
- arenaviruses
- filoviruses

man

arboviruses

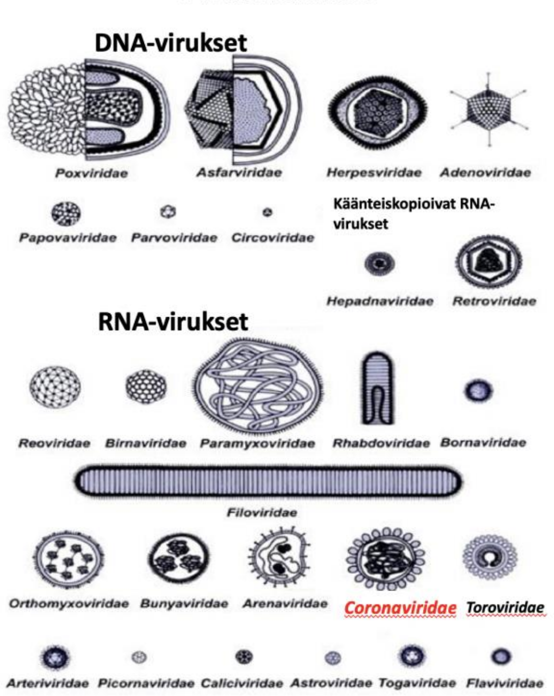
arthropods

- flaviviruses
- bunyaviruses
- alfa viruses

- HIV
- influenza A virus
- SARS-CoV-2

host-switches

Emerging viral infections



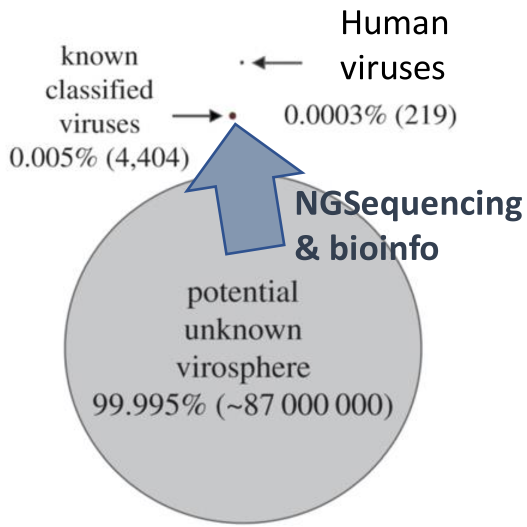
- *global threats/pandemics – regional and local epidemics*

- **megatrends increasing new viral zoonoses, epidemics and pandemics:**

globalisation- tourism - urbanisation –changes in land usage/ environmental (incl. climatic) changes /change in animal husbandry

- Modern diagnostic methods help to identify

- Only a fragment of viruses known – though only some pose threats:



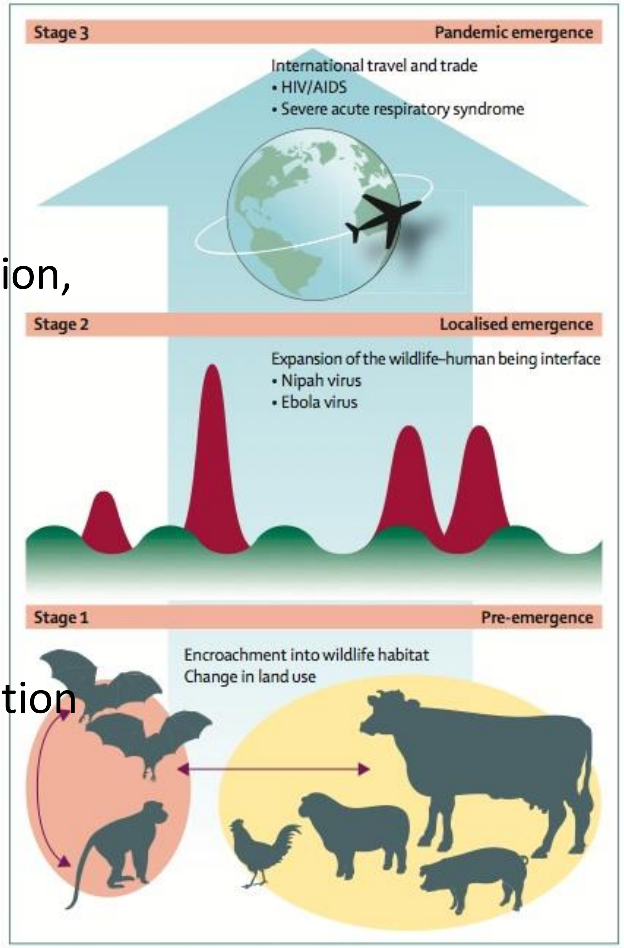
Emerging viruses

- **Diseases** looking for a **virus**
  - Clinical hints, pathology, epi?
  - Association, causation?

- **Virus** looking for a **disease** association
  - Related to pathogens? Pathogenic determinants? Epi?

- Tools for detection

- Pan-genus RT-PCR primers (conserved regions)
- Metagenomics / Bioinfo: Virome. – (‘anything’)
- Serology – reflects structural relatedness (usually more conserved relatedness than with primers)
- Cell culture – (anything that infects your cells)



Mitigation, Control

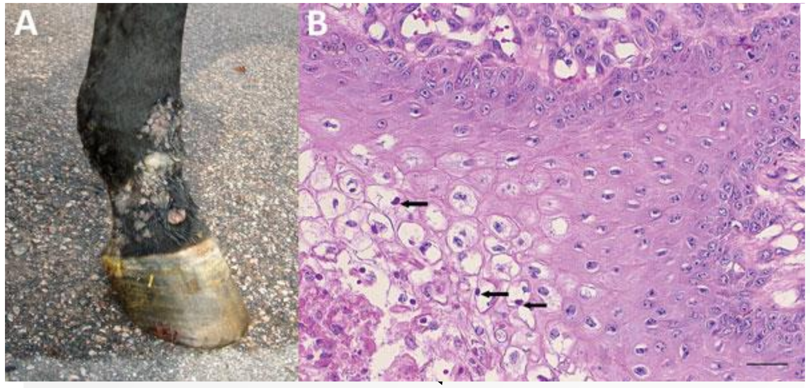
Prevention

Figure 2: Emergence of pandemic zoonotic disease Morse ea, Lancet 2012

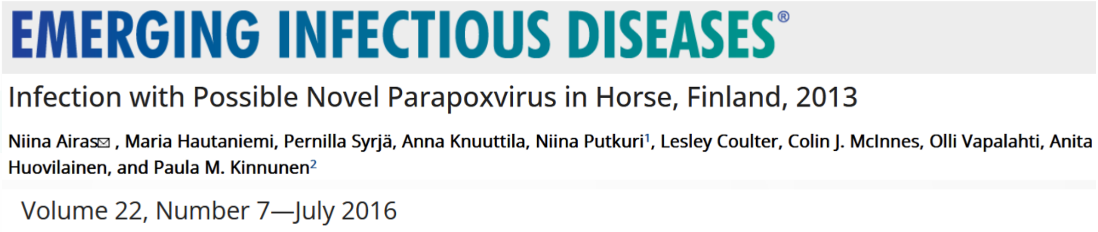
STARTERS

parapoxviruses, arenaviruses, kolmioviruses and filoviruses

from veterinary patient and field samples



New contagious disease in horses 2013, pathology suggests *Poxviridae* → *pan-orthopox - ; pan-parapox+*

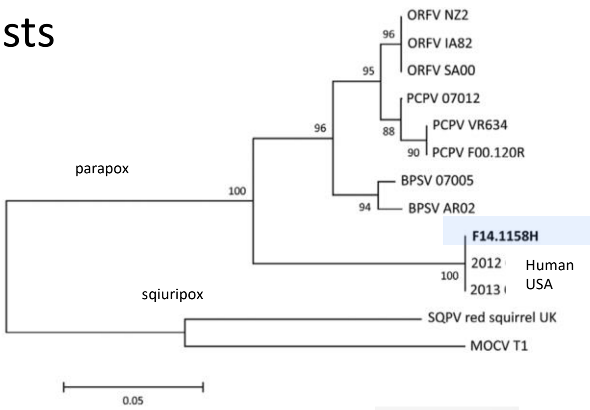


EMERGING INFECTIOUS DISEASES®

Infection with Possible Novel Parapoxvirus in Horse, Finland, 2013

Niina Airas✉, Maria Hautaniemi, Pernilla Syrjä, Anna Knuuttila, Niina Putkuri[1], Lesley Coulter, Colin J. McInnes, Olli Vapalahti, Anita Huovilainen, and Paula M. Kinnunen[2]

Volume 22, Number 7—July 2016

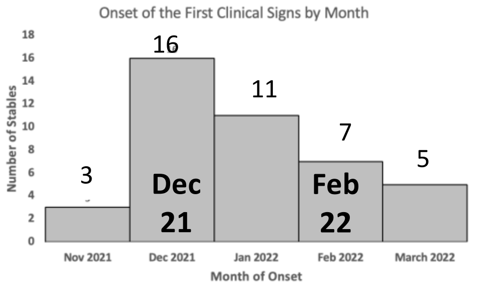


- ’**infectious pastern dermatitis**’ in trotters

– also in winters 2014-15 & -no samples for further research

- 2021-22 hundreds of trotters sick 2-4 d after latest race: Painful pastern dermatitis (severe lameness), out of training 1-2 weeks

No isolate, more sequence of and sensitive RT-PCR for **’Equine parapoxvirus’ EqPPV**



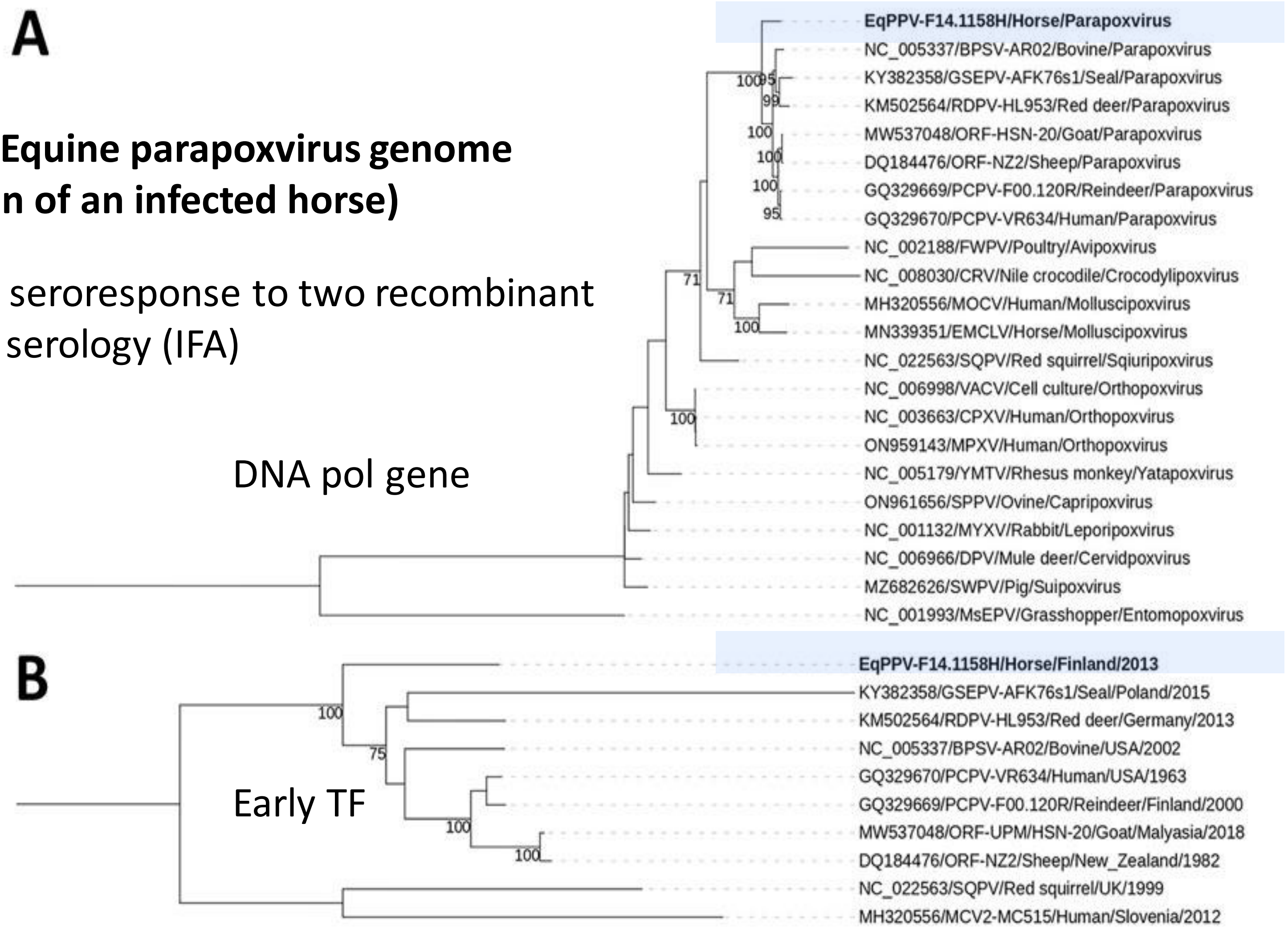
Epidemic curve illustrating the onset of the first clinical signs in the case stables (n=43) by month.

- Risk factor for outbreaks at stables (1/3 of horses affected): having race horses, race events before the disease ($p < .001$)

Virtanen J Gen Virol 2023

121 kb of Equine parapoxvirus genome (skin lesion of an infected horse)

- Strong seroresponse to two recombinant proteins → serology (IFA)



DNA pol gene

Early TF

Osadebe et al
CID 2015

Likely a globally
Occuring
Zoonosis ?


Jenni Virtanen

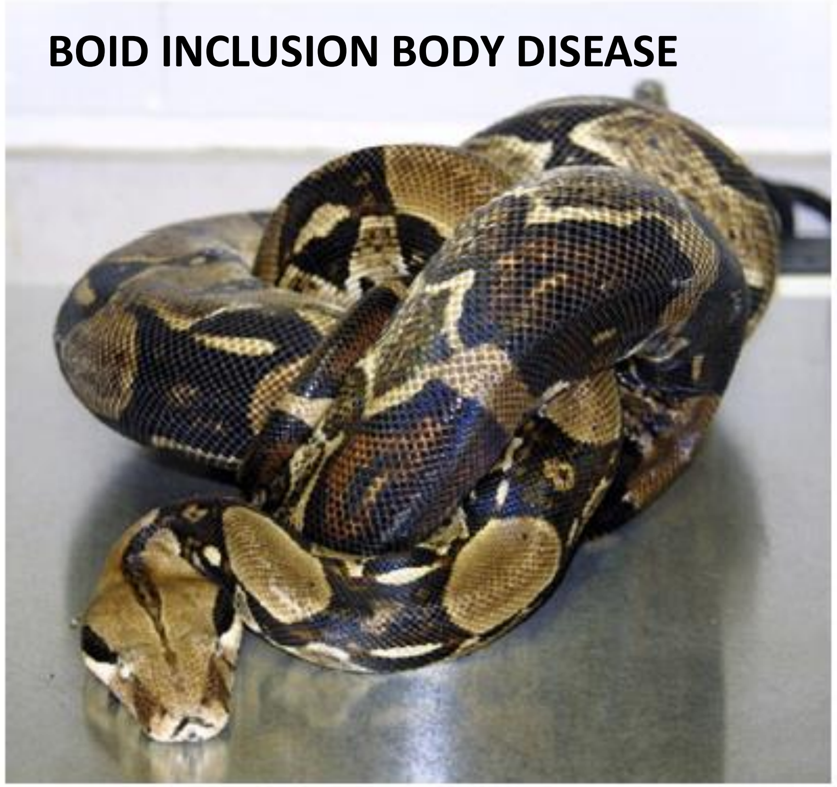

Paula Kinnunen

→ EqPPV represents a novel parapoxvirus

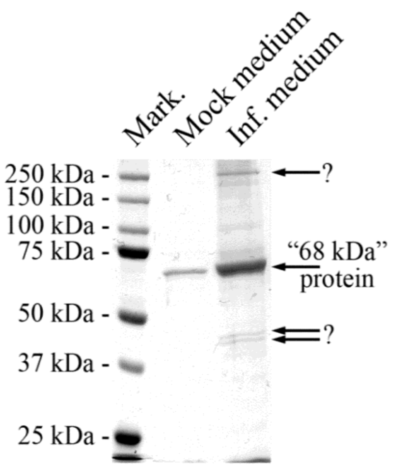
CPXV, cowpox virus; CRV, crocodilepox virus; DPV, deerpox virus; EMCLV, equine molluscum contagiosum-like virus; EqPPV, equine PPV; FWPV, fowlpox virus; MOCV, molluscum contagiosum virus; MPXV, monkeypox virus; MsEPV, melanoplus sanguinipes entomopoxvirus; MYXV, myxoma virus; ORF, open reading frame; PPV, parapoxvirus; SPPV, sheeppox virus; SQPV, squirrelpox virus; SWPV, swinepox virus; VACV, vaccinia virus; YMTV, yaba monkey tumor virus.

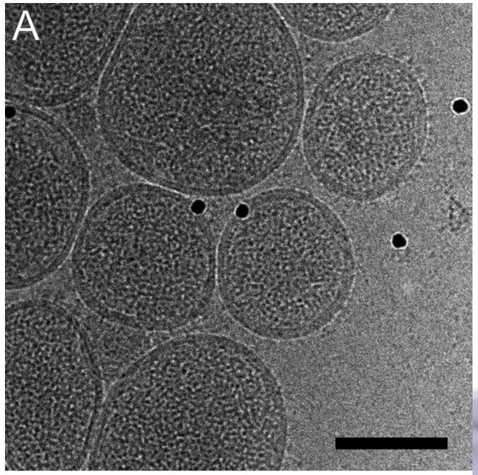
Virtanen J, et al. Emerg Infect Dis. 2023;29

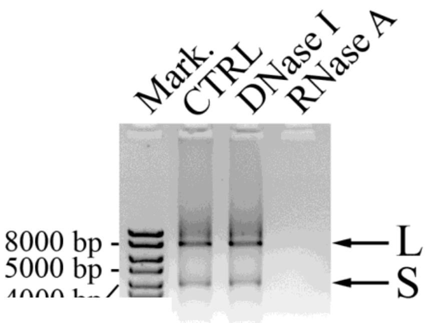
BOID INCLUSION BODY DISEASE



Fatal disease of captive boid snakes

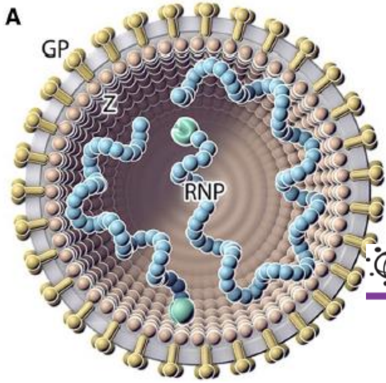


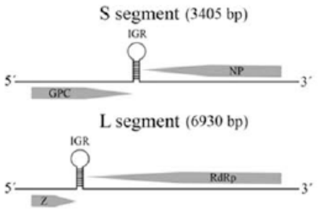


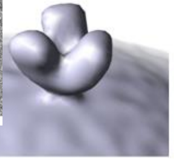


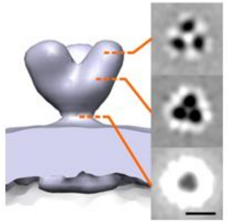

UDO HETZEL


JUSSI HEPOJOKI









Hetzel et al JV 2013
Bodewes JGV 2013
Stenglein mBio 2012

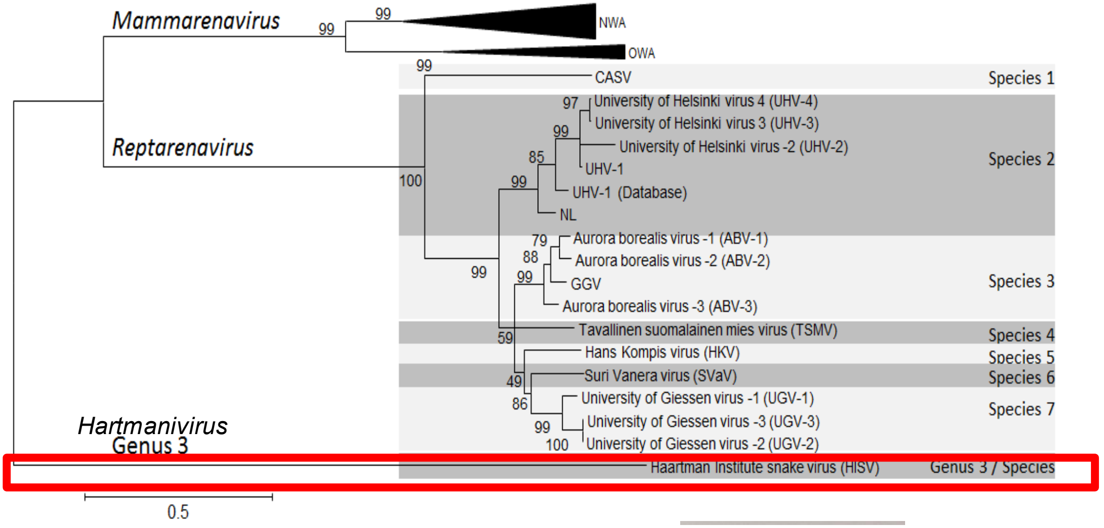
A virus is found and causes the disease !?

PLOS | PATHOGENS

RESEARCH ARTICLE

Widespread Recombination, Reassortment, and Transmission of Unbalanced Compound Viral Genotypes in Natural Arenavirus Infections

Mark D. Stenglein[1¤]*, Elliott R. Jacobson[2], Li-Wen Chang[2], Chris Sanders[3], Michelle G. Hawkins[4], David S-M. Guzman[4], Tracy Drazenovich[4], Freeland Dunker[5], Elizabeth K. Kamaka[6], Debbie Fisher[7], Drury R. Reavill[8], Linda F. Meola[9], Gregory Levens[10], Joseph L. DeRisi[1,11]*



AMERICAN SOCIETY FOR MICROBIOLOGY | Microbiology Spectrum

RESEARCH ARTICLE
September/October 2022 Volume 10 Issue 5 e01705-22
https://doi.org/10.1128/spectrum.01705-22

Boid Inclusion Body Disease Is Also a Disease of Wild Boa Constrictors

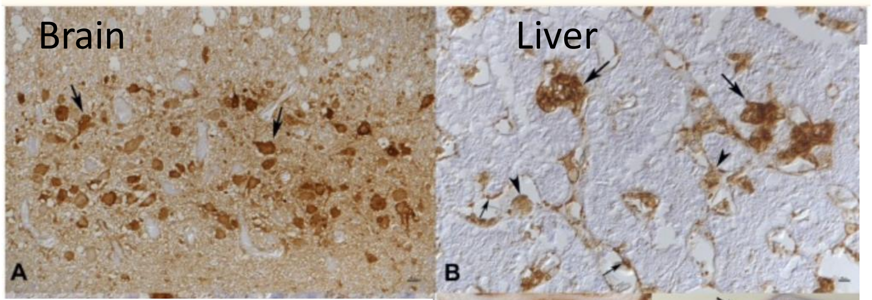
Alejandro Alfaro-Alarcón[a], Udo Hetzel[b,c], Teemu Smura[d], Francesca Baggio[b], Juan Alberto Morales[a], Anja Kipar[b,c], Jussi Hepojoki[b,d]

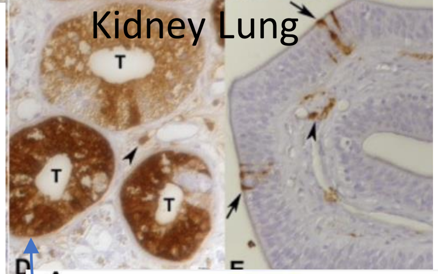
JVI
Journals.ASM.org

Arenavirus Coinfections Are Common in Snakes with Boid Inclusion Body Disease

J. Hepojoki,[a] P. Salmenperä,[b] T. Sironen,[a] U. Hetzel,[c,d] Y. Korzyukov,[a] A. Kipar,[c,d] O. Vapalahti[a,d,e]

Metagenomics: Viromes of boas with CNS signs → HDV-like satellites - *Deltaviruses and other Kolmioviridae*



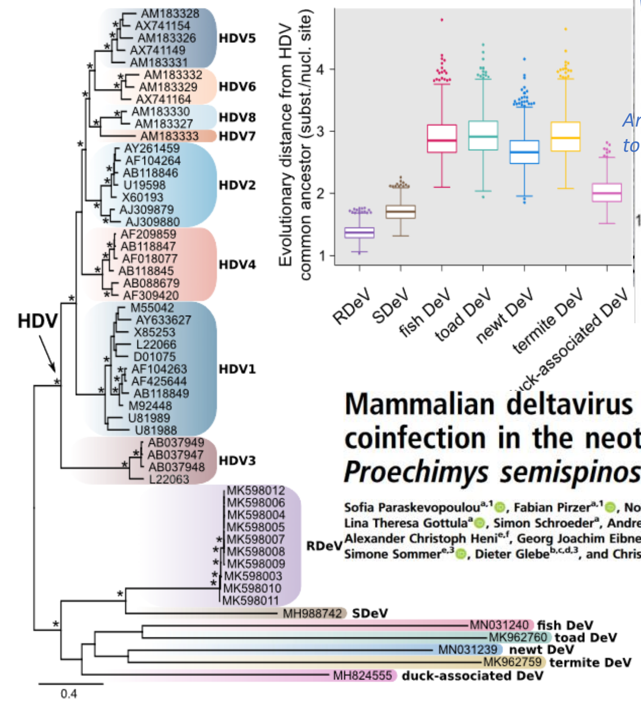


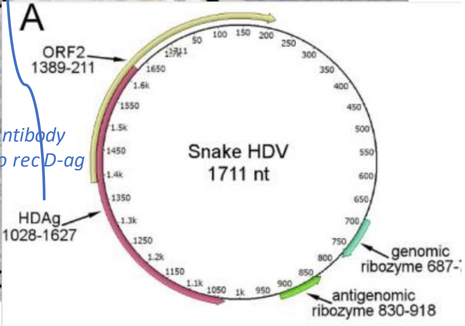
2019

OBSERVATION
Host-Microbe Biology

Identification of a Novel Deltavirus in Boa Constrictors

Udo Hetzel,[a,b] Leonóra Szirovicza,[c] Teemu Smura,[c] Barbara Prähauser,[a] Olli Vapalahti,[b,c,d] Anja Kipar,[a,b] Jussi Hepojoki[a,c*]

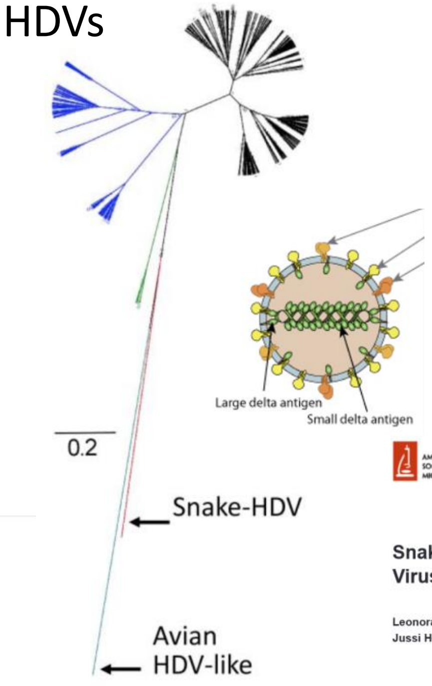




Antibody to rec D-ag

Mammalian deltavirus without hepadnavirus coinfection in the neotropical rodent *Proechimys semispinosus*

Sofia Paraskevopoulou[a,1], Fabian Pirzer[a,1], Nora Goldmann[b,c,d,1], Julian Schmid[e,f], Victor Max Corman[a,g], Lina Theresa Gottula[a], Simon Schroeder[a], Andrea Rasche[a,g], Doreen Muth[a,2], Jan Felix Drexler[a,g,h], Alexander Christoph Heni[e,f], Georg Joachim Eibner[a,e,f], Rachel A. Page[f], Terry C. Jones[a,i], Marcel A. Müller[a,g,h], Simone Sommer[e,3], Dieter Glebe[b,c,d,3], and Christian Drosten[a,g,3]



Wille et al, Viruses 2018

– no hepadna (HBV-like) viruses found!

Hepatitis D virus –like viruses, several new genera in *Kolmioviridae*

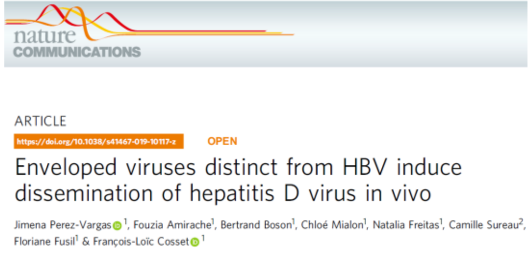
Previously only known to be human & use HBV envelope to spread are actually

- Widespread satellites in animal taxa
- Can use envelope proteins of many helper viruses

RESEARCH ARTICLE
Host-Microbe Biology
March/April 2020 Volume 11 Issue 2 e03250-19
https://doi.org/10.1128/mBio.03250-19

Snake Deltavirus Utilizes Envelope Proteins of Different Viruses To Generate Infectious Particles

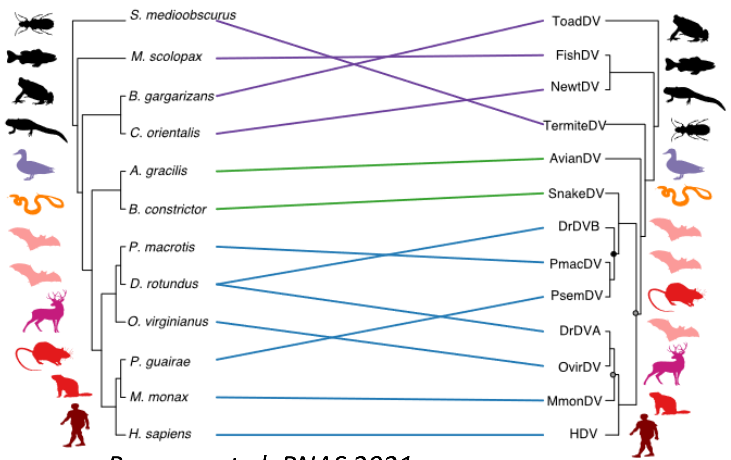
Leonora Szirovicza[a], Udo Hetzel[b,c], Anja Kipar[b,c], Luis Martinez-Sobrido[d], Olli Vapalahti[a,c,e], Jussi Hepojoki[a,b]



ARTICLE
https://doi.org/10.1038/s41467-019-10117-z OPEN

Enveloped viruses distinct from HBV induce dissemination of hepatitis D virus in vivo

Jimena Perez-Vargas[1], Fouzia Amirache[1], Bertrand Boson[1], Chloé Mialon[1], Natalia Freitas[1], Camille Sureau[2], Floriane Fusil[1] & François-Loïc Cosset[1]



Bergner et al, PNAS 2021

Kolmiovirids
-Viruses in search of disease associations?

-> people have searched and found more…

Diversification of mammalian deltaviruses by host shifting

Laura M. Bergner[a,b,1], Richard J. Orton[b], Alice Broos[b], Carlos Tello[c,d], Daniel J. Becker[e], Jorge E. Carrera[f,g]
Arvind H. Patel[b], Roman Biek[a], and Daniel G. Streicker[a,b,1]

PNAS 2021 Vol. 118 No. 3 e2019907118 https://doi.org/10.1073/pnas.2019907118

VIRUS EVOLUTION

doi: 10.1093/ve/veab003
Research Article

Identification of novel avian and mammalian deltaviruses provides new insights into deltavirus evolution

Masashi Iwamoto,[1,2] Yukino Shibata,[3] Junna Kawasaki,[4,5] Shohei Kojima,[4,6] Yung-Tsung Li,[7] Shingo Iwami,[2] Masamichi Muramatsu,[1] Hui-Lin Wu,[7,8] Kazuhiro Wada,[9] Keizo Tomonaga,[4,5,10] Koichi Watashi,[1,11] and Masayuki Horie[4,12,*,†]

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nature

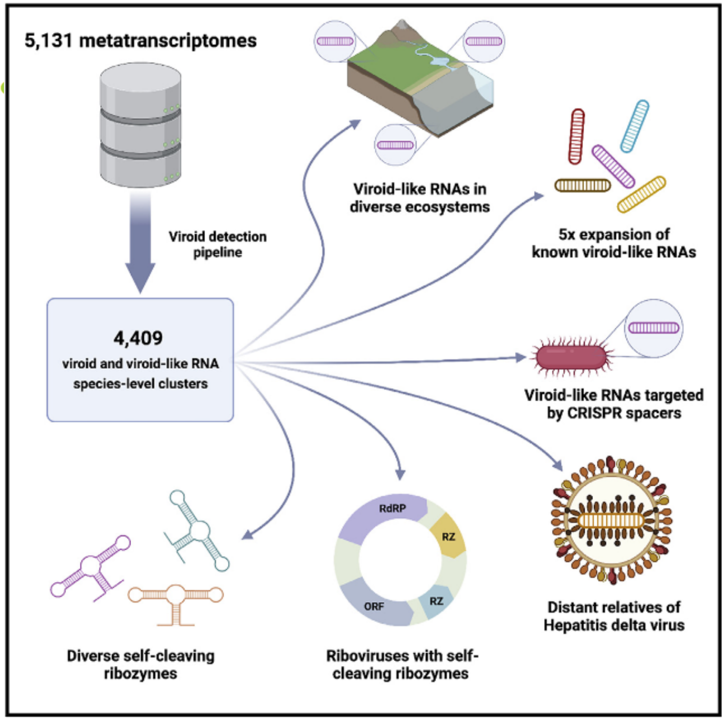
Petabase-scale sequence alignment catalyses viral discovery

https://doi.org/10.1038/s41586-021-04332-2
Received: 10 August 2020
Accepted: 10 December 2021

Robert C. Edgar[1,16], Jeff Taylor[2,16], Victor Lin[3,16], Tomer Altman[4,16], Pierre Barbera[5,16], Dmitry Meleshko[6,7,16], Dan Lohr[8,16], Gherman Novakovsky[9,16], Benjamin Buchfink[10,16], Basem Al-Shayeb[11,16], Jillian F. Banfield[12,16], Marcos de la Peña[13,16], Anton Korobeynikov[6,14,1 Rayan Chikhi[15,16] & Artem Babaian[2,16]✉

Mining metatranscriptomes reveals a vast world of viroid-like circular RNAs

Graphical abstract



Authors

Benjamin D. Lee, Uri Neri, Simon Roux, ..., Uri Gophna, Valerian V. Dolja, Eugene V. Koonin

Correspondence

koonin@ncbi.nlm.nih.gov

In brief

A large-scale survey of covalently closed circular RNA across ecosystems reveals that viroids infect a wide range of host species, extending beyond plants, and identifies additional types of ribozyme activity as well as functional features in these molecules.

CellPress
OPEN ACCESS

Cell

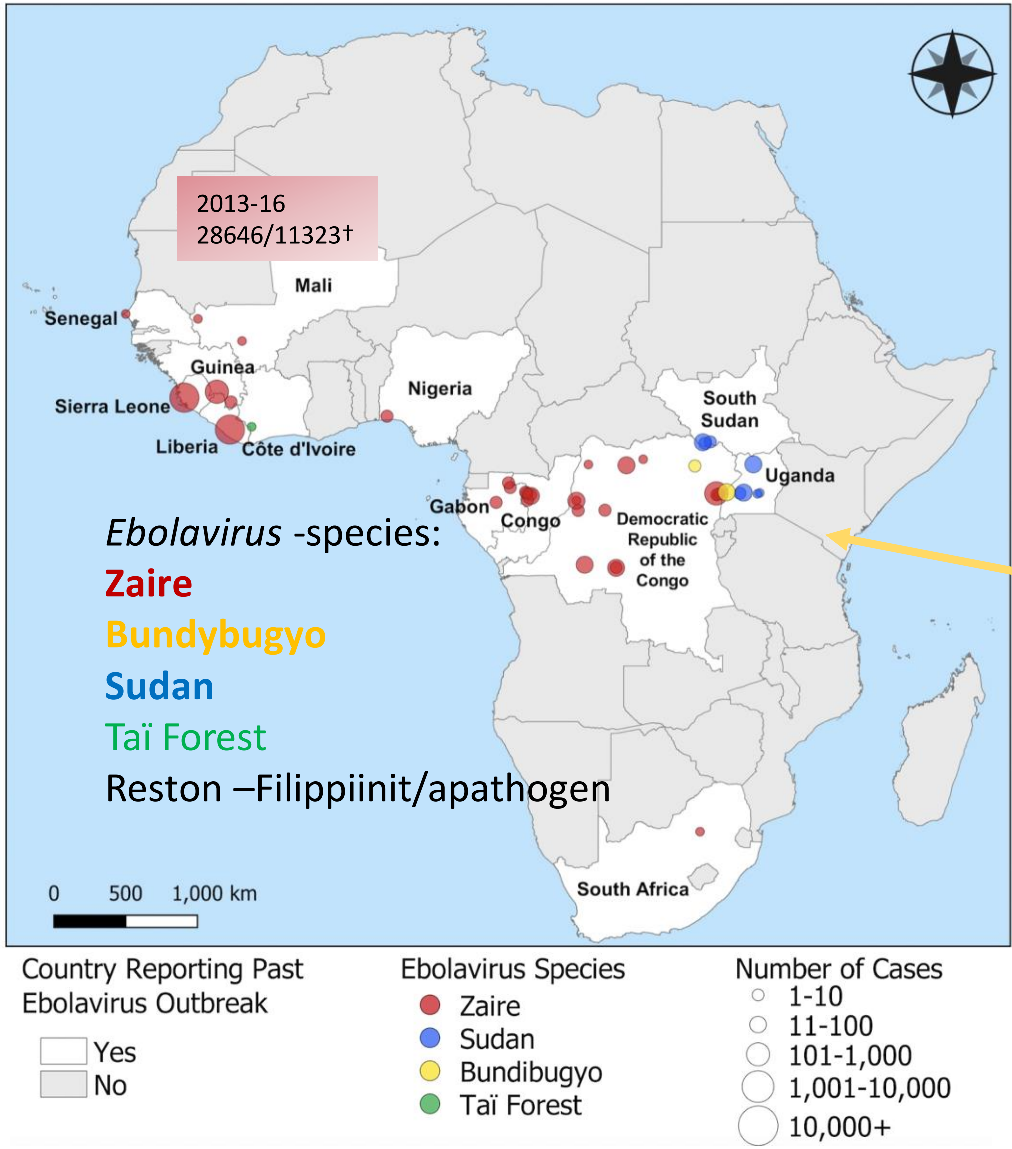
Resource

Mining metatranscriptomes reveals a vast world of viroid-like circular RNAs

Benjamin D. Lee,[1,2] Uri Neri,[3] Simon Roux,[4] Yuri I. Wolf,[1] Antonio Pedro Camargo,[4] Mart Krupovic,[5] RNA Virus Discovery Consortium, Peter Simmonds,[2] Nikos Kyrpides,[4] Uri Gophna,[3] Valerian V. Dolja,[6] and Eugene V. Koonin[1,7,*]

Kolmiovirids
-Viruses in search of disease associations?

Ebolavirus-epidemics/cases since 1976 / CDC Reservoir in (fruit) bats?



2013-16
28646/11323†

Ebolavirus -species:

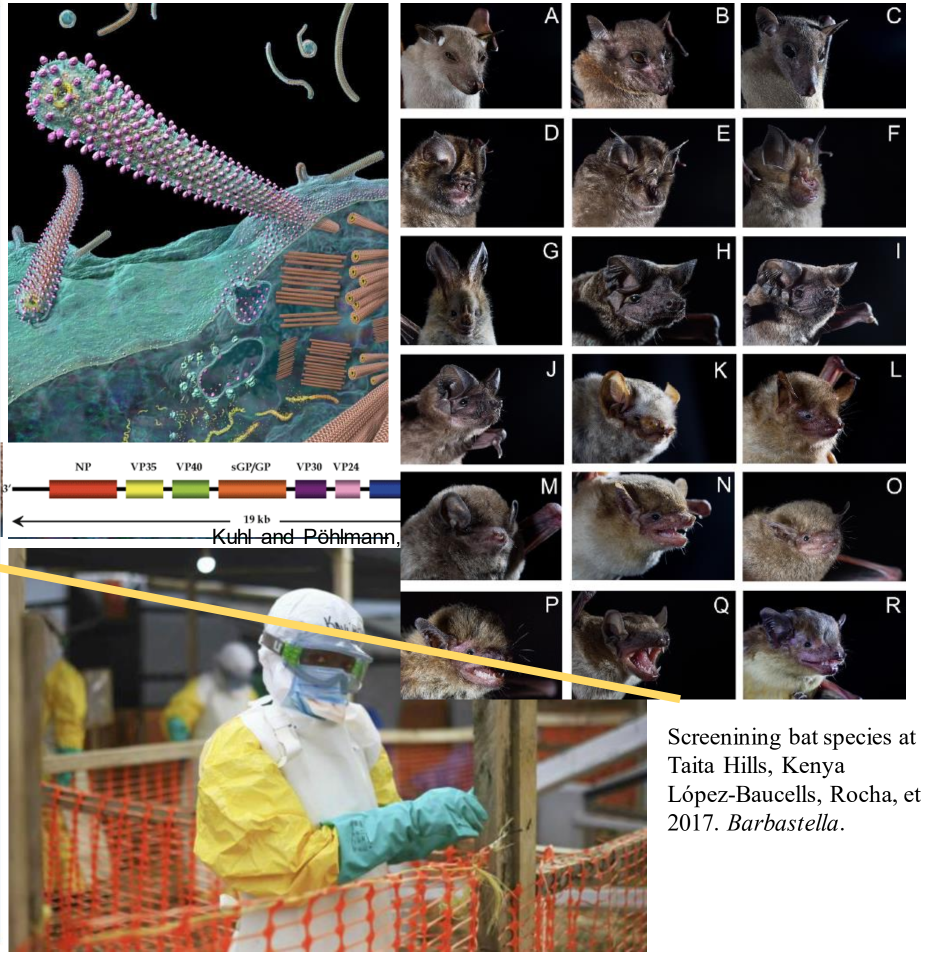
Zaire

Bundybugyo

Sudan

Taï Forest

Reston –Filippiinit/apathogen



Screenining bat species at
Taita Hills, Kenya
López-Baucells, Rocha, et al
2017. *Barbastella*.

Bat filoviruses: new candidate pathogens (?)

SEARCHING FOR NEW VIRUSES FROM BATS

Mops condulyrus
insectivore bat lung sample
→ Screen –molecular tools[a]
→ Sequencing
→ Bioinformatics[b]
full genome of **new Bombali-ebolavirus**

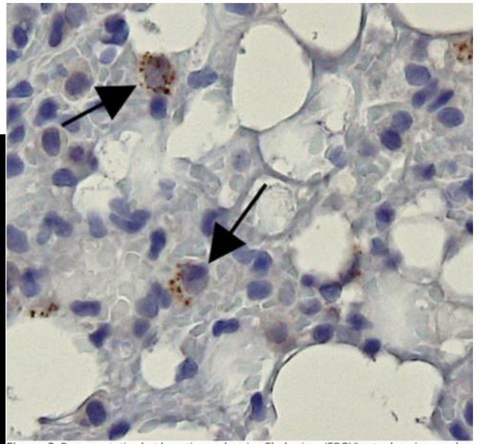
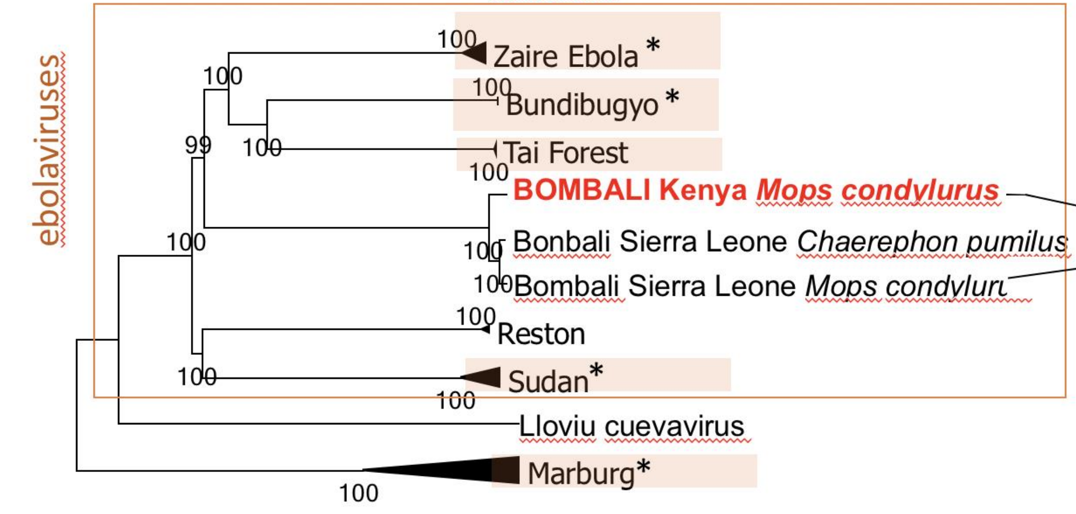


Figure 2. Representative bat lung tissue showing Ebola virus (EBOV) cytoplasmic granules

Kareinen EID 2023

Filovirus phylogenetic tree

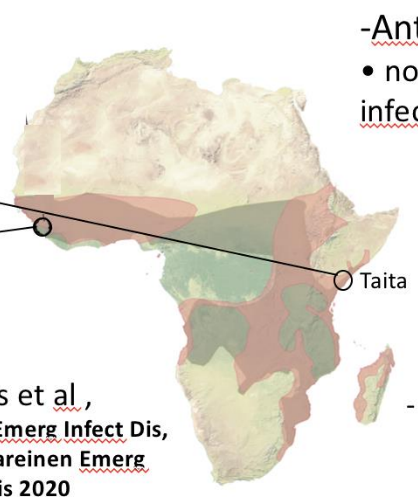
▨ =filoviruses known to be pathogenic to humans



Distribution of bats:

🟩 Angolan free-tailed bat (*Mops condylurus*)

🟥 Little Free-tailed Bat (*Chaerephon pumilus*)



-Antibody tests-humans:

- no evidence of ebolavirus infections in local population

Forbes et al ,
Forbes Emerg Infect Dis, 2019, Kareinen Emerg Infect Dis 2020

- Same species carries Bombali ebolavirus also in West Africa

Kris Forbes

Lauri Kareinen

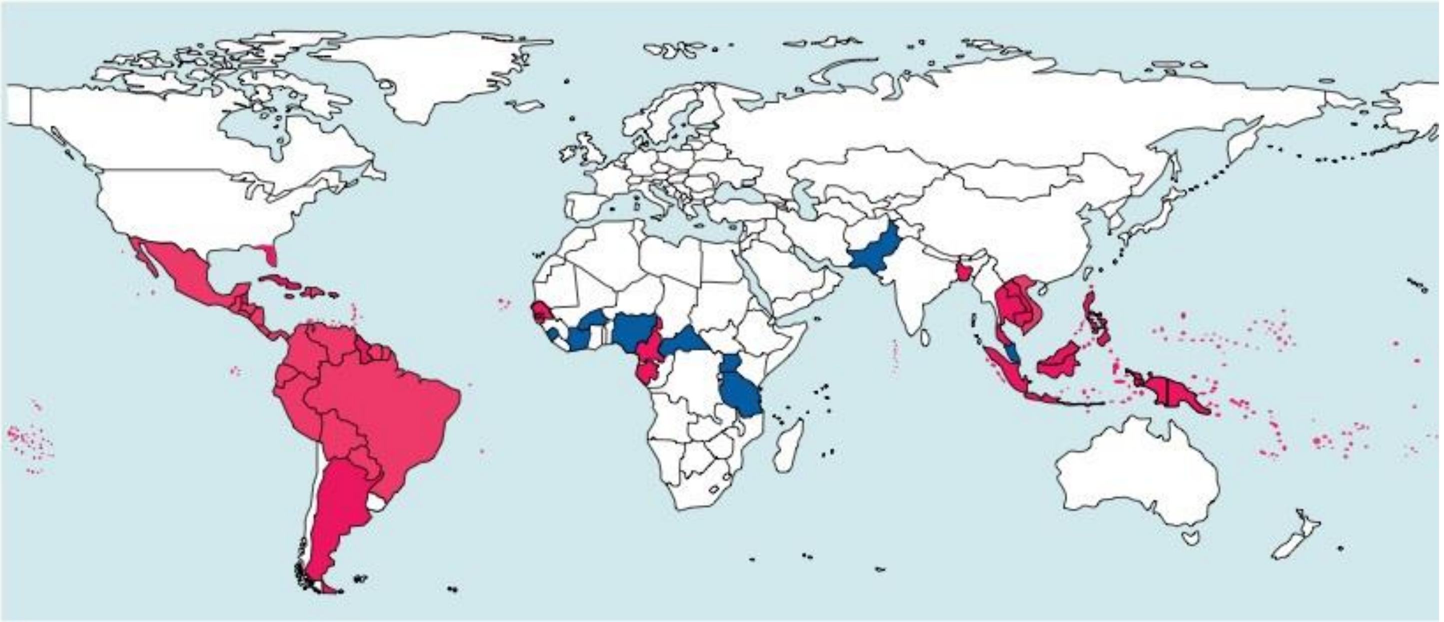
*Large outbreaks; a)Genus-specific pan-filo RT-qPCR (Jääskeläinen JCV 2019) + Illumina NGS + b) Lazypipe (Plyusnin Virus Evol 2020)

MAIN COURSE

Emerging flaviviruses and some other arboviruses in patients samples, mosquitoes and ticks

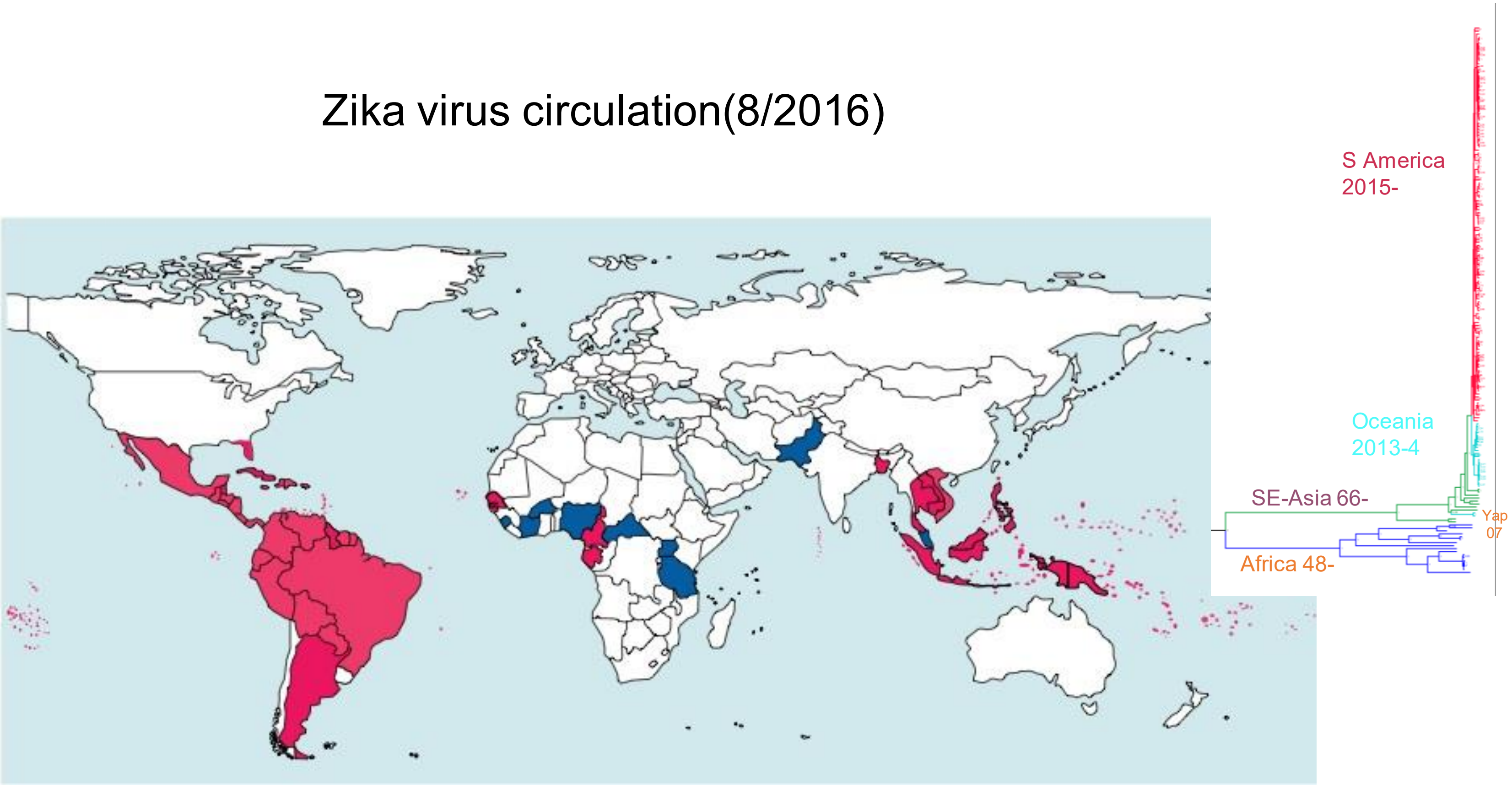
Travelers as sentinels of global emergence (Zika)

Zika virus circulation (8/2016)



-2007 2007 --

Zika virus circulation(8/2016)



-2007 2007 --

ZIKV 2015 infections in Finnish travelers

Severe fetal brain damage

- ZIKV isolated from fetal brain
- ZIKV in maternal blood

ZIKV → Micro-cephaly

Rasmussen NEJM 2016

Dilation of ventricles
Agenesis of corpus callosum
Diffuse atrophy in frontal/parietal cerebral cortex

ZIKV in pregnant female?
pan-flavi-RT-PCR* +
→ ZIKV
Driggers NEJM 2016

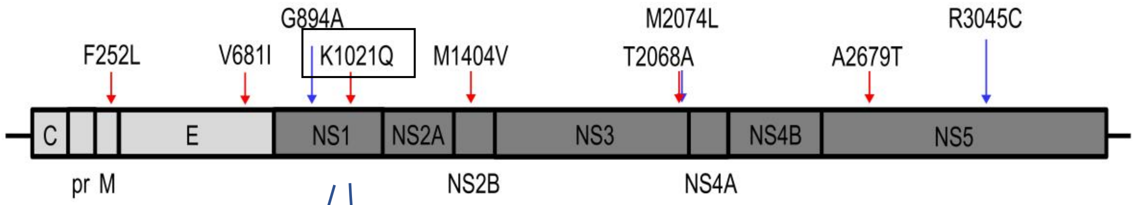
DENV-suspicion:
pan-flavi-RT-PCR +*
urine + (serum -)
→ ZIKV Korhonen Eurosurv 2016

-2007 2007 --

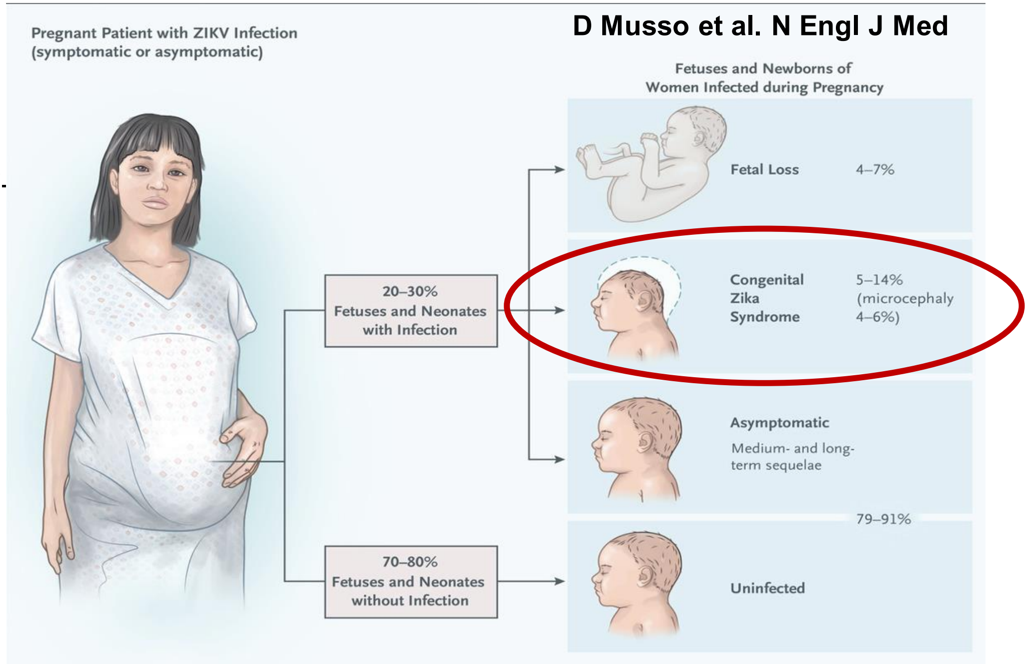
*) Moureau VBZD 2007

ZIKV intrahost variation in the mother →

Aa differences to other Guatemalan ZIKV-



Driggers R et al NEJM 2016

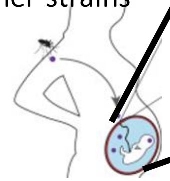

D Musso et al. N Engl J Med

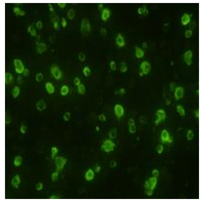
Aa 1021 : K → M → Q

- Maternal blood
- All other strains

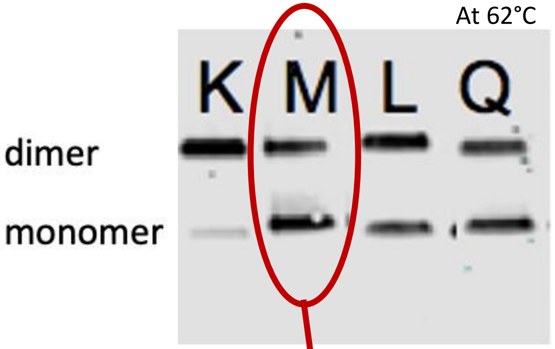
- Fetal brain
- Placenta

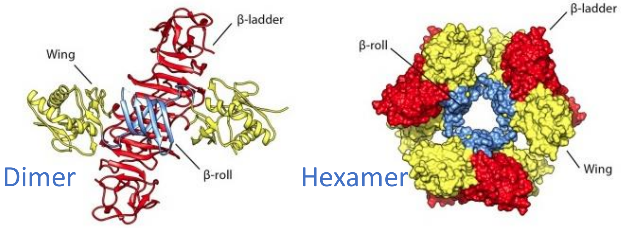
- Cell culture





Smura et al, unpublished





Watterson

Antiviral Res 2016

infectious clone

- Another, convergent mutation from microcephalic brain (Mlakar NEJM 2016) reported to have similar NS1 phenotype (Wang et al Sci Rep 2017)

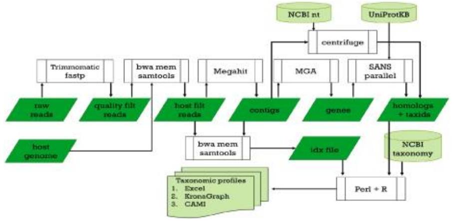
→ Hindbrain organoid infection

→ Transciptomics: Similar cytokine induction as in pregnant mothers with ZIKV and fetal damage (vs ZIKV only)

Single patient sample isolates/tissue distribution/intrahost sequence variation → Information on causality and pathogenesis

Plyusnin I, et al, 2020

Novel NGS pipeline for virus discovery from a wide spectrum of hosts and sample types

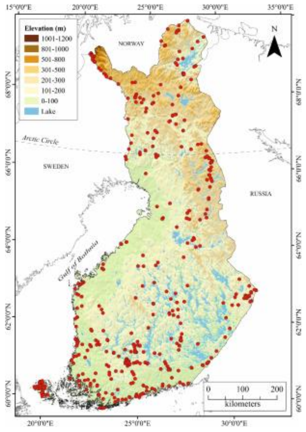


https://www.helsinki.fi/en/projects/lazypipe

Medical and Veterinary Entomology

Culverwell et al, 2020

The mosquitoes of Finland: updated distributions and bionomics



52466 specimens
1031 collections
-> 43 mosq. species

viruses

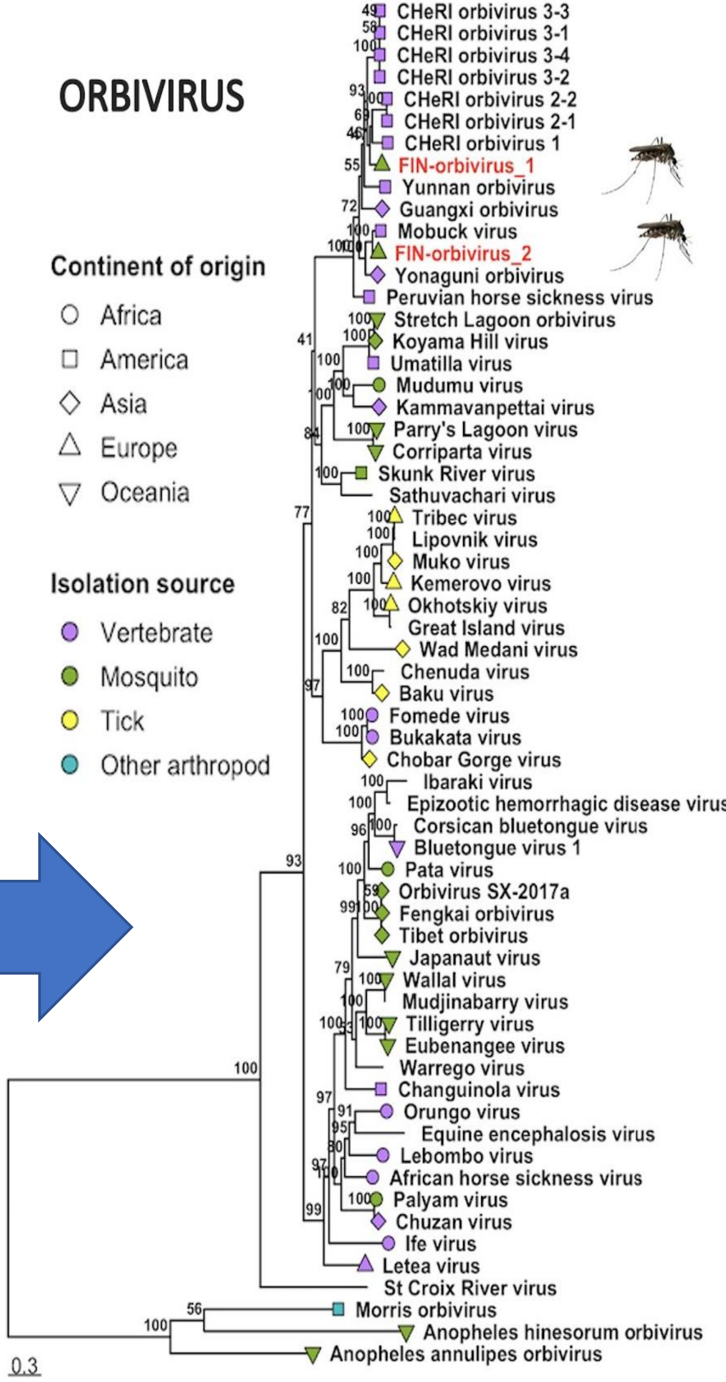
RNA Virome of 9 *Ochlerotatus* Species in Finland

[Truong Nguyen PT et al, 2022](#)

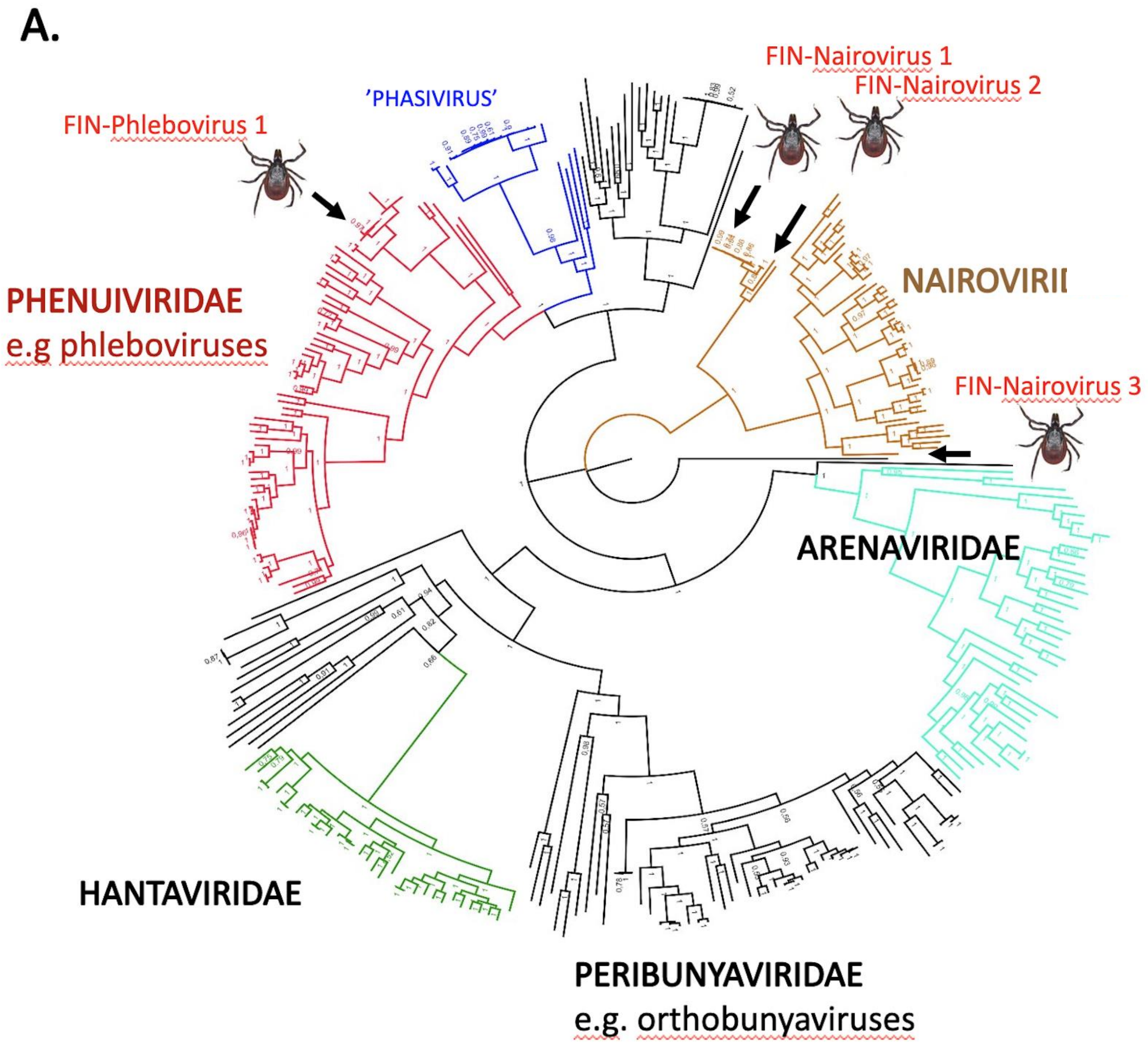
159 virus species in 25 families, 147 tentatively new species

Cell culture

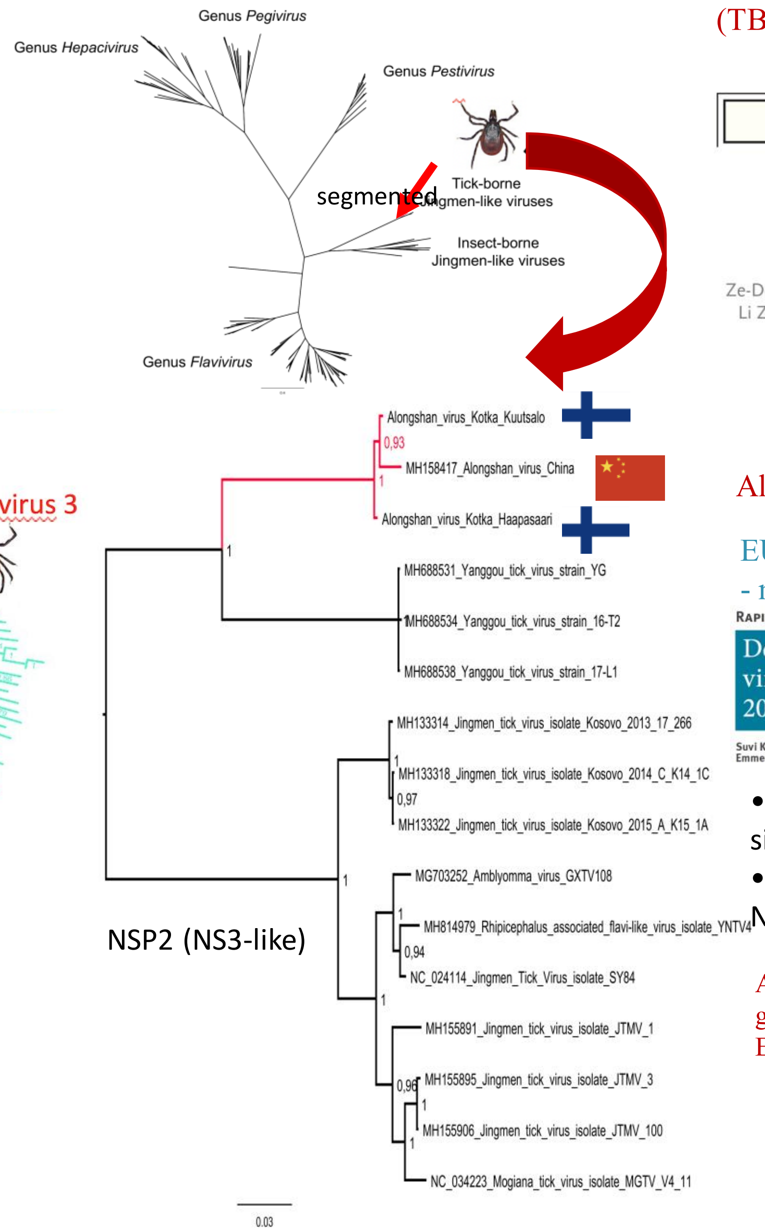
Eili Huhtamo



I. ricinus and *persulcatus* virome shows presence of a new pathogen to Europe



FLAVIVIRIDAE



CHINA: ALONGSHAN is human PATHOGEN (TBE-like disease)


The NEW ENGLAND JOURNAL of MEDICINE

ORIGINAL ARTICLE

A New Segmented Virus Associated with Human Febrile Illness in China

Ze-Dong Wang, Ph.D., Bo Wang, M.D., Feng Wei, Ph.D., Shu-Zheng Han, M.S., Li Zhang, B.Sc., Zheng-Tao Yang, Ph.D., Yan Yan, Ph.D., Xiao-Long Lv, M.S., Liang Li, Ph.D., Shu-Chao Wang, Ph.D., Ming-Xin Song, Ph.D., Hao-Ji Zhang, Ph.D., Shu-Jian Huang, Ph.D., Jidang Chen, Ph.D., Fu-Qiang Huang, Ph.D., Shuang Li, B.Sc., Huan-Huan Liu, B.Sc., Jian Hong, Ph.D., Yu-Lan Jin, Ph.D., Wei Wang, M.S., Ji-Yong Zhou, Ph.D., and Quan Liu, Ph.D.

2019

Also in cattle, sheep

EUROPE: ALONGSHAN PRESENT IN TICKS,
- no evidence in HUMANS

Eurosurveillance 2019


RAPID COMMUNICATION

Detection of novel tick-borne pathogen, Alongshan virus, in *Ixodes ricinus* ticks, south-eastern Finland, 2019

Suvi Kuivanen[1,8], Lev Levanov[1,8], Lauri Kareinen[1], Tarja Sironen[1,2], Anne J. Jääskeläinen[7], Ilya Plyusnin[2], Fathiah Zakham[1], Petra Emmerich[3,4], Jonas Schmidt-Chanasit[3,5], Jussi Hepojoki[1,6], Teemu Smura[1,7,8], Olli Vapalahti[1,2,7,8]

- Alongshan-virus also in Europe, very similar to Chinese strains
- TBE suspects –> no Alongshan RNA/Abs N= 900, Finland

Also in Germany (Lower Saxony, antibodies in game and domestic animals, 1 RNA + deer), Ebert et al *Microorganisms* 23

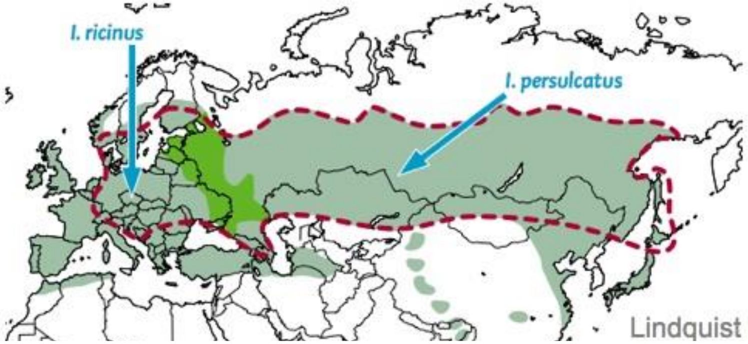
Tick-borne encephalitis virus

Genus Orthoflavivirus, *Family Flaviviridae*

- **TBEV VECTORS**

Ixodes ricinus - sheep tick → (TBEV European subtype)
Ixodes persulcatus - taiga tick → (TBEV - Siberian and Far Eastern subtypes)

1-2 % †



Lindquist & Vapalahti, Lancet 2008

-Virus occurs typically in foci, suitable climate enhances transmission via co-feeding

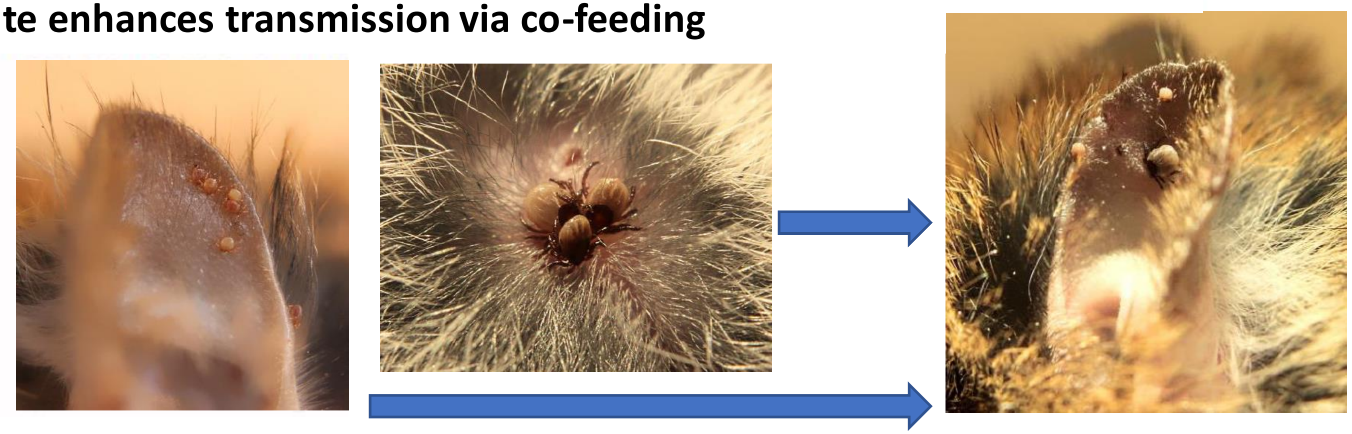


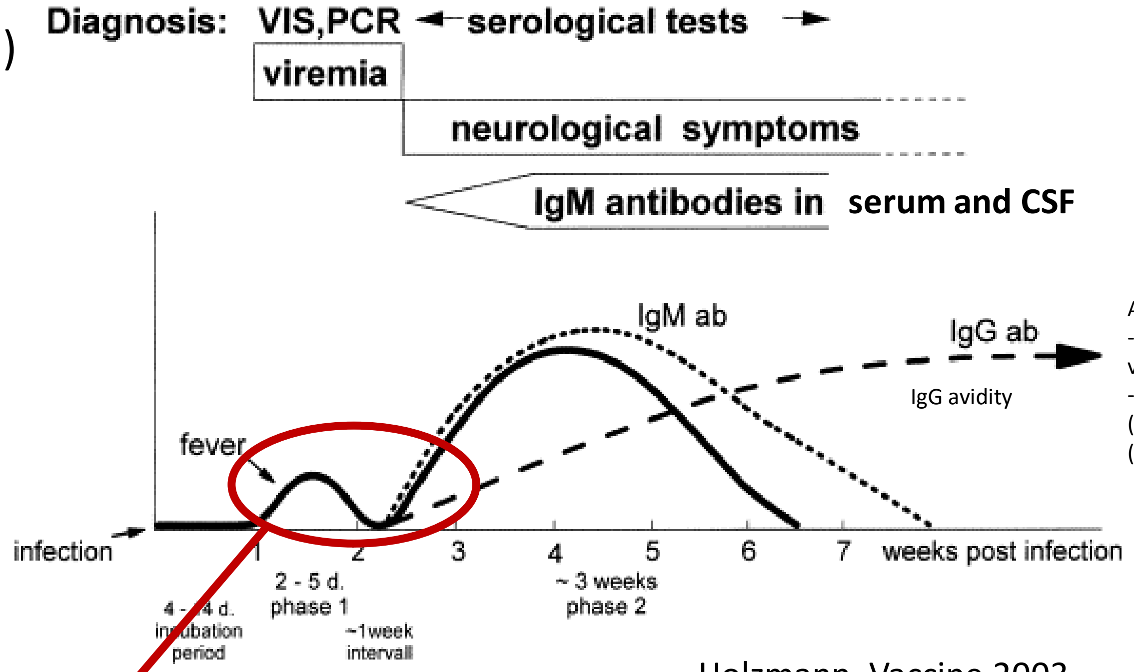
Foto:
Heikki Henttonen

Tick-borne encephalitis, TBEV

Transmission: tick bite (1-2% TBEV+ in risk areas) or unpasteurized milk

- often biphasic
  - 1st phase: 1(-3) weeks after bite, "flu-like", mild – patients viremic

  ~ 1 week
  - 2nd phase: CNS infection
- Case-fatality in Europe < 2%
- Diagnosis: antibodies in serum or CSF



Antibodies to :
-Viral envelope protein: vaccine and infection
-NS1 :
(only) infection
(Albinsson 2018, 2024)

Holzmann, Vaccine 2003

TBEV RNA found in - 1st phase sera/blood, in brain in lethal cases, occasionally in CSF/2nd phase

For more ->'One Health' samples:
Ticks (e.g.0,2-2%), Animals: (e.g. rodent brain)

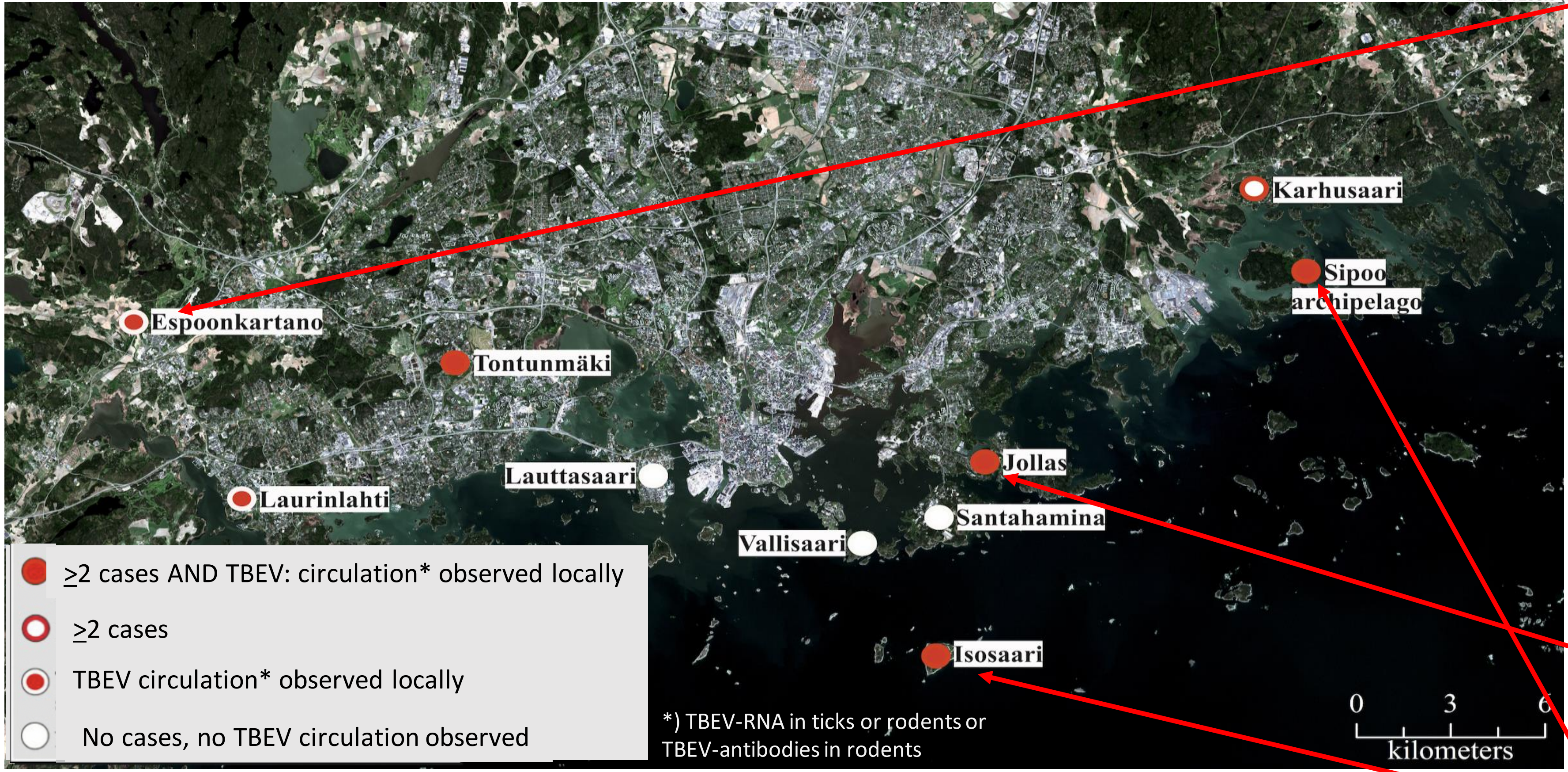
In some *foci* that we have researched

~1/200 of ticks positive

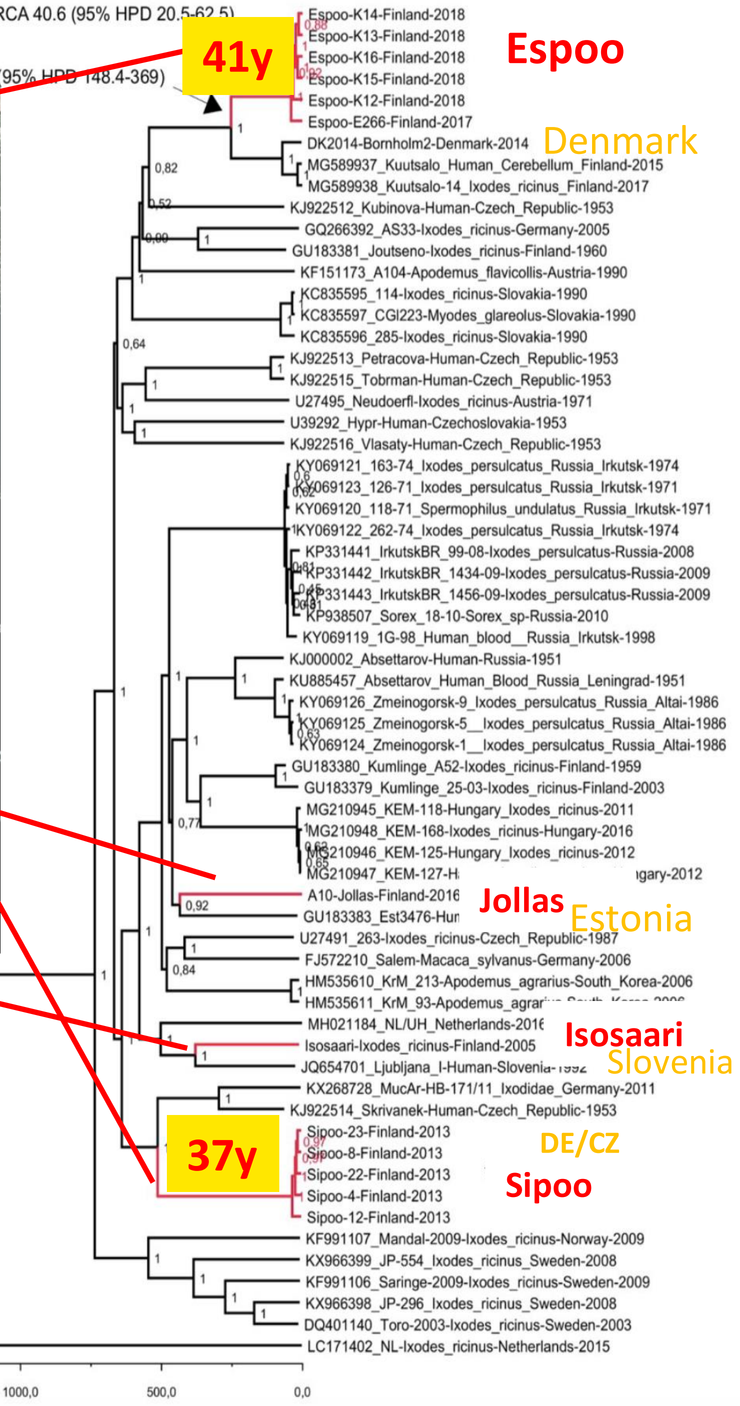
~1/10 of rodent brains
TBEV-RNA positive, also in winter

Pos. samples → RNA -> Illumina NGS sequencing
→ Bioinformatics → Full TBEV genome → Phylogenetic analysis

TBEV arrival and spread in Helsinki



*) TBEV-RNA in ticks or rodents or TBEV-antibodies in rodents



TBEV full genomes,
Phylogeny and molecular clock

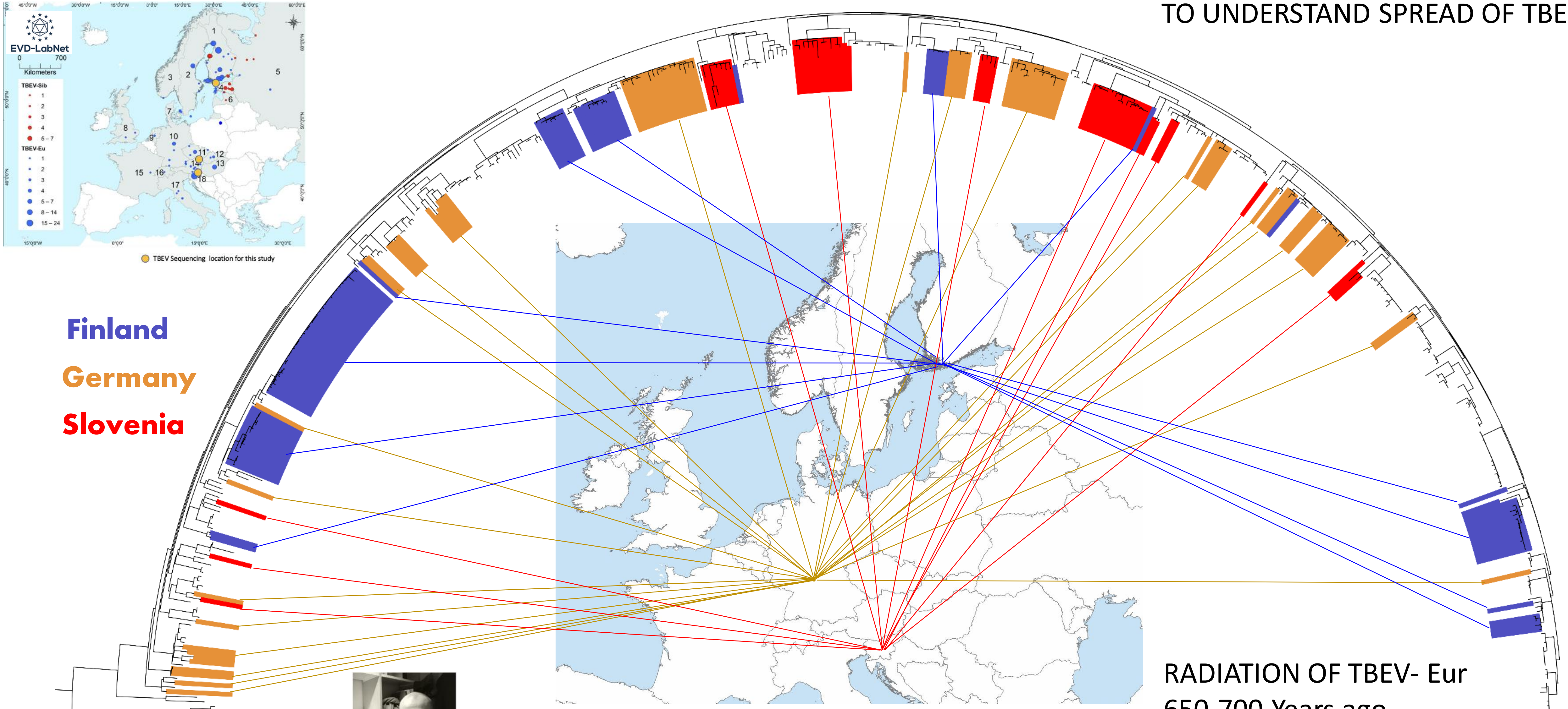
SMURA YM, EMERG MICROB & INFECT 2019, 1: 675-683

- **VERY FOCAL**
- **NO GEOGRAPHIC CONTINUITY**
- **LONG BRANCH LENGTH TO THE CLOSEST RELATIVE**

- Compatible with occasional establishment of airborne foci

Europe: TBEV phylogeny (full-genome + E)
+ “pending” sequences from some countries

1 HEALTH FIELD SAMPLES
COMPLEMENT CLINICAL SAMPLES
TO UNDERSTAND SPREAD OF TBEV



RADIATION OF TBEV- Eur
650-700 Years ago

mutation rate 2.32 x 10^-5
[95%HPD 1.76-2.90 x 10-5]

Smura et al
In preparation
EVD-LabNet collaboratio

‘Everything is everywhere’

Teemu Smura

—

DESSERT

Highly pathogenic avian influenza in mink and foxes

FINLAND/ Fur farms H5N1 HPAI

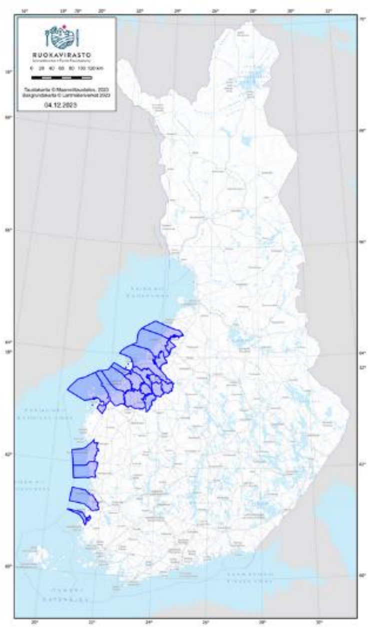
Finnish Food Administration:
H5 HPAI in 2023in

Wild birds

Fur farms

Passive surveillance

Kartta kunnista, joissa todettu lintuinfluenssatapauksia turkistarhoilla vuonna 2023



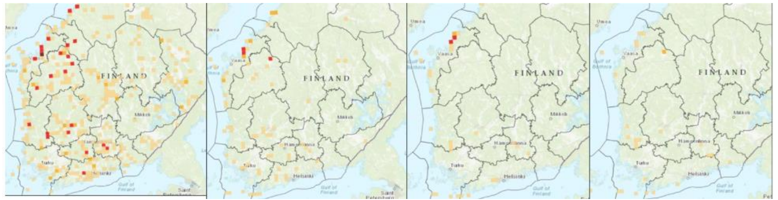
Active surveillance

Passive surveillance (by farmers) initially identified **32** farms H5N1 + by PCR

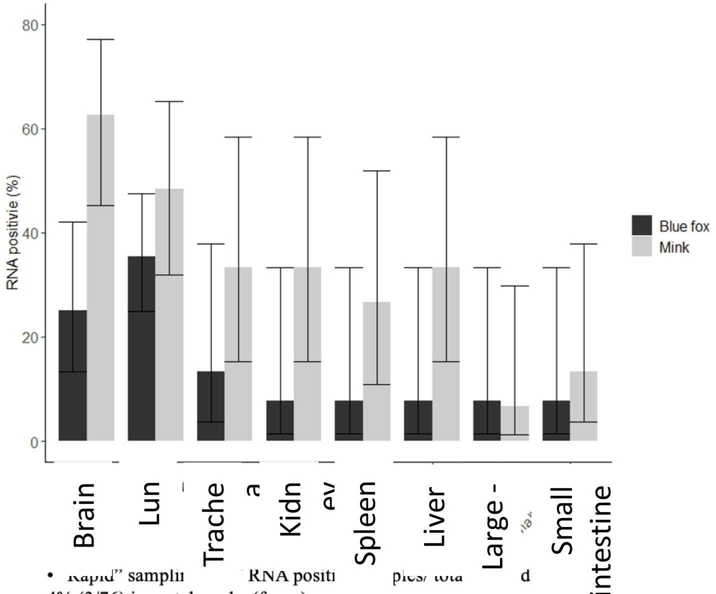
Active surveillance by serology, additional **42/392** farms (3 mink farms) + identified

- Some farms pelted the animals before surveillance samples were collected
- Animals culled also after positive serology

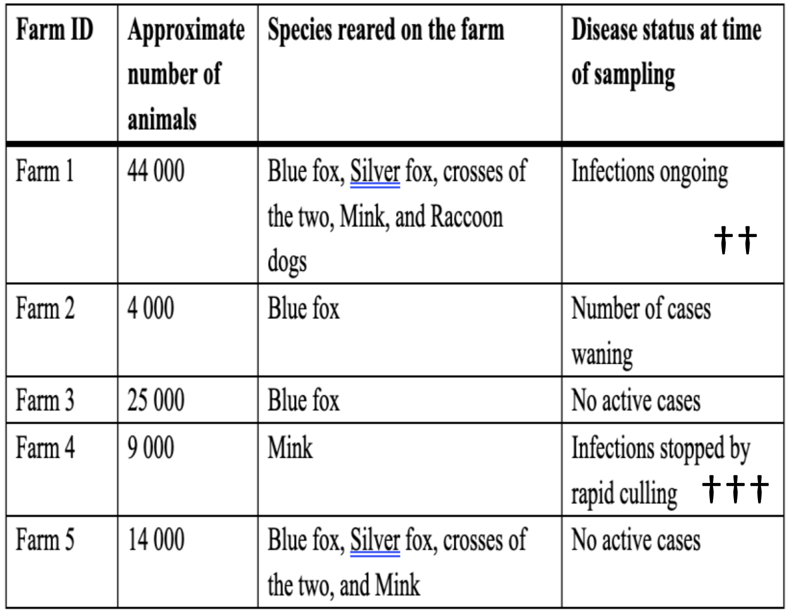
Observed black-headed gulls 2023 FFA/Birdlife Finland



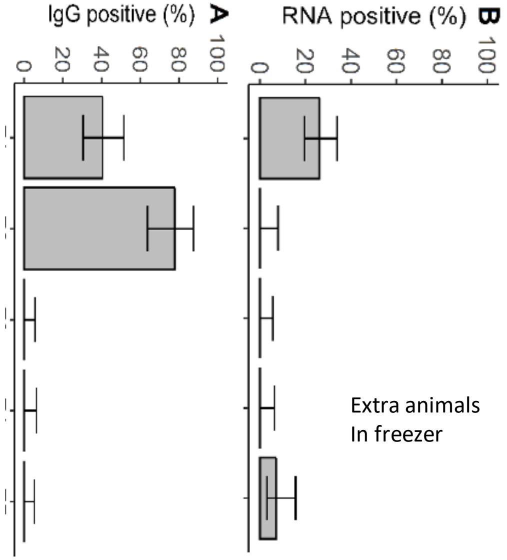
HPAIV RNA +



5 farms studied by UH (animals N=428)



Farm ID	Approximate number of animals	Species reared on the farm	Disease status at time of sampling
Farm 1	44 000	Blue fox, Silver fox, crosses of the two, Mink, and Raccoon dogs	Infections ongoing ††
Farm 2	4 000	Blue fox	Number of cases waning
Farm 3	25 000	Blue fox	No active cases
Farm 4	9 000	Mink	Infections stopped by rapid culling †††
Farm 5	14 000	Blue fox, Silver fox, crosses of the two, and Mink	No active cases



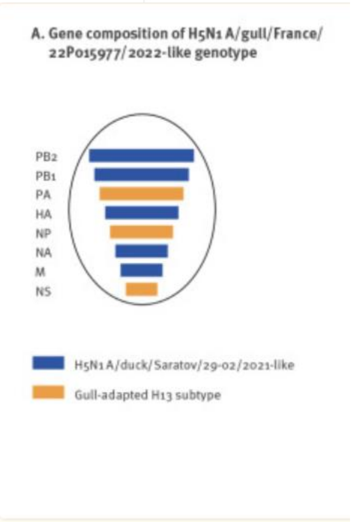
Extra animals
In freezer

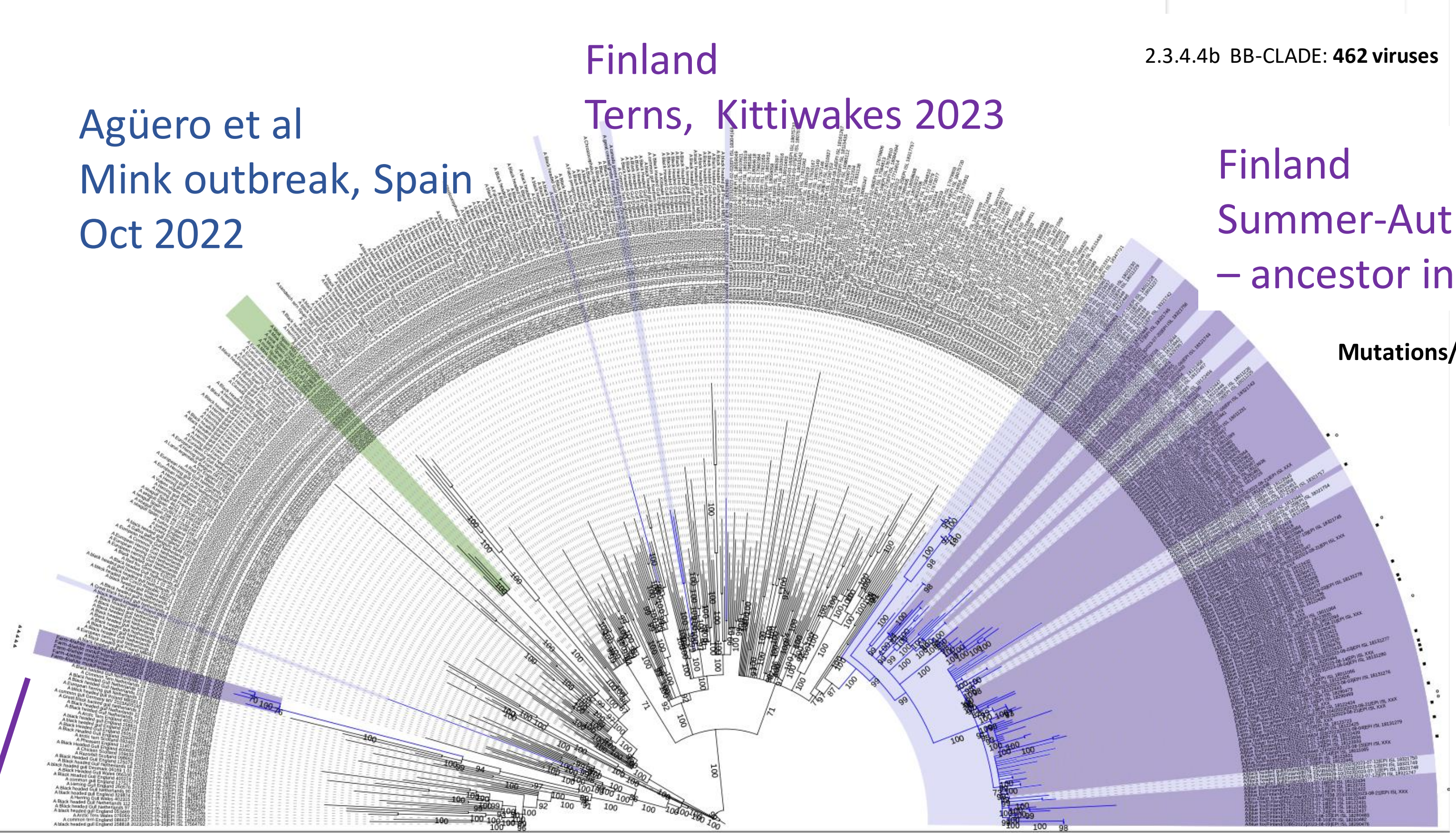
- ”Rapid” sampling: AIV RNA positive samples/ total studied

3.95% (3/76) in rectal swabs (foxes)
10.52% (8/76) in respiratory swabs (1 + for both)
8,4% (19/224) in brain aspirates (6 only in brain, different set of farms).

HPAI H5N1 clade 2.3.4.4b – genotype BB

5/2022
onwards


A. Gene composition of H5N1 A/gull/France/22P015977/2022-like genotype



2.3.4.4b BB-CLADE: **462 viruses**

Agüero et al
Mink outbreak, Spain
Oct 2022

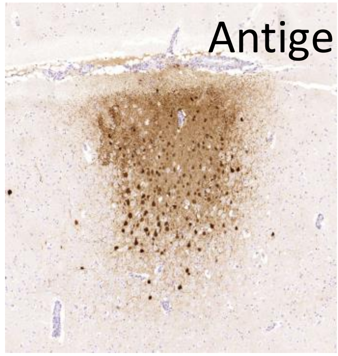
Finland
Terns, Kittiwakes 2023

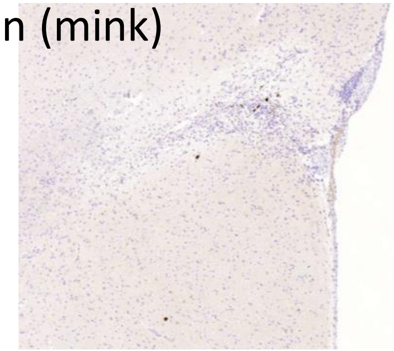
Finland
Summer-Autumn 2023
– ancestor in March

Finland
Oct 2023

Mutations/PB2: **T271A (7 BLUE FOX)**
M535I (3 BLUE FOX)
E627K (15/16 MINK, 2/82 FOX)


Lytic necrosis of liver


Antigen detection in the brain (mink)




HE stain (brain)

TAKE-HOME (doggy-bag)

- **Studies of weird clinical cases and clusters** as collaborations of clinical and research and vet/hum public health laboratories essential (although regulations and funding gaps makes this more challenging) for etiology as well as **active surveillance** for alert and (early) **alarm**

- As **human societies grow in size and complexity, we create an endless variety of opportunities for** genetically unstable **infectious agents** to emerge into the unfilled ecologic niches we continue to create.

- Science will surely bring us many **life-saving drugs, vaccines, and diagnostics;** however, there is no reason to think that these alone can overcome the threat of **ever more frequent and deadly emergences** of infectious diseases.

Perspective

Emerging Pandemic Diseases: How We Got to COVID-19

Cell 2020 David M. Morens[1,*] and Anthony S. Fauci[1]

THANK YOU!

ZIKA:
Mariia Bogacheva, Lev Levanov, Suvi Kuivanen, Teemu Smura, Ilja Weinstein, Jussi Hepojoki, Essi Korhonen, Eili Huhtamo

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Jussi Hepojoki, Annika Lintala
Lenonora Szirovicza, Willem Sander, Yegor Korzykov
Anja Kipar, Udo Hetzel, Francesca Baggio, Eva Dervas,
Eleni Michalopoulou, Saskia Keller, Katharina Windbichler,
Tanja Thiele… Lisbeth Nufer, Barbara Prähauser,
Sabine Wunderlin Giuliani, Theresa Pesch

Universität Zürich

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Jääskeläinen, Ilkka Kivistö, Hussein Alburkat, Ilja
Weinsterin, Dufton Mwaengo, Ali Mirazimi, Omu
Anzala (univ. of Nairobi)

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Maija Suvanto, Victor Olander, Eili Huhtamo, Lev
Levanov, L Kareinen L, Sironen T, Anne
Jääskeläinen, I Weinstein I, Fathiah Zakham, P.
Emmerich, Jonas Schmidt-Chanasit J (BNITM),
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Jenni Virtanen
Nina Suomalainen , Ella Lintunen
Karoliina Hagner , Antti Sukura
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Lea Uotinen Jenni Westerback
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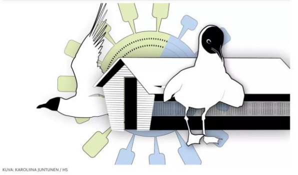
Esa Pohjolainen, Kati Kuipers, Leena Palmunen, Mira Utriainen, Tinja Hyvönen,
Konstantin Saarela
FLI: Martin Beer, Timm Harder, Anne Pohlmann, Ann Kathrin Ahrens et al
THL: Pamela Österlund, Veera Avelin, Eda Altan, Erika Lindh et al
UTU: Laura Kakkola Ilkka Julkunen, Pekka Kolehmainen, Pinja Jalkanen


KUVA: KAROLIINA JUNTUNEN / HS

TBE

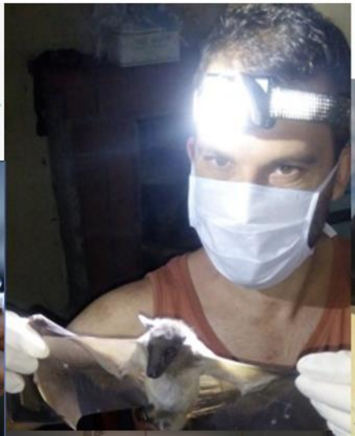
EVD-LabNet

ecdc EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

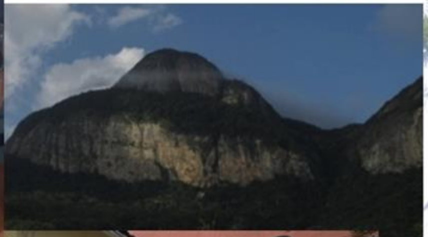

Equine dermatitis outbreak associated with parapoxvirus

Jenni Virtanen[1,2,*], Katja Hautala[1], Mira Utriainen[2], Lara Dutra[2], Katarina Eskola[3,4], Niina Airas[1], Ruut Uusitalo[1,2,5], Ella Ahvenainen[2], Teemu Smura[2], Tarja Sironen[1,2], Olli Vapalahti[1,2], Ravi Kant[1,2], Anna-Maija K. Virtala[1] and Paula M. Kinnunen[1]

1) **Teemu Smura, Viktor Olander, Tarja Sironen, Mert Erdin, Essi Korhonen, Ruut Uusitalo, Olli Vapalahti:** Viral Zoonoses Research Unit, Departments of Virology and Veterinary Biosciences, University of Helsinki & Department of Virology and Immunology, Helsinki University Hospital and University of Helsinki, Helsinki, Finland
2) **Julia Geller,** Department of Virology and Immunology, National Institute for Health Development, Tallinn, Estonia
3) **Samo Zakotnik, Miša Korva, Tatjana Avšič-Županc** University of Ljubljana, Slovenia
4) **John Pettersson,** Folkhälsomyndigheten, Sweden
5) **Maciej Grzybek, Martyna Krupińska** Division of Tropical Parasitology, Institute of Maritime and Tropical Medicine, Medical University of Gdańsk, Poland
6) **Jeremy Camp, Stephan Aberle**, Department of Virology, Medical University of Vienna, Austria
7) **Giulietta Venturi,** National Reference Laboratory for Arboviruses, Department of Infectious Diseases, Istituto Superiore di Sanità, Rome, Italy
8) **Haná Zelena**, University of Ostrava, Czech Republic
9) **Kamelia Stanoeva,** RIVM, The Netherlands
10) **Åke Lundkvist** University of Uppsala, Sweden
11) **Celine Grossner, Tamas Bakonyi,** ECDC, Solna, Sweden



University of Helsinki
Taita Research Station, Kenya



Viral Zoonoses Research Unit

HOH
HELSINKI ONE HEALTH

THANKS FOR ALL COLLEAGUES , COLLABORATORS, FUNDERS AND YOU FOR LISTENING!

ecdc EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

veo

VECLIMIT

Maanpuolustuksen neuvottelukunta MATINE

JUHO VAINION SÄÄTIÖ

SIGRID JUSELIUS STIFTELSE

ACADEMY OF FINLAND

J&AE JANE JA AATOS ERKON SÄÄTIÖ

Helsinki University Hospital Funds

huslab

DURABLE
Research Network against Epidemics

12) Newest phylogeography: **Guy Baele , Philippe Lemey**, KU Leuven, Belgium

Science

$15
9 MARCH 2018
sciencemag.org

AAAS

HOW LIES SPREAD

On social media, false news beats the truth

pp. 1094 & 1146

Vosoughi et al, *Science* 2018
126 000 tweets studied 2006-2017 (3M people > 4.5M retweets)

False news reached more people than the truth;
- the top 1% of false news cascades →1000 -100,000 people,
- truth rarely diffused to more than 1000 people.

- Falsehood also diffused faster than the truth.

The degree of novelty and the emotional reactions may be responsible for the differences observed.