SARS-CoV-2

The zoonosis from a human perspective

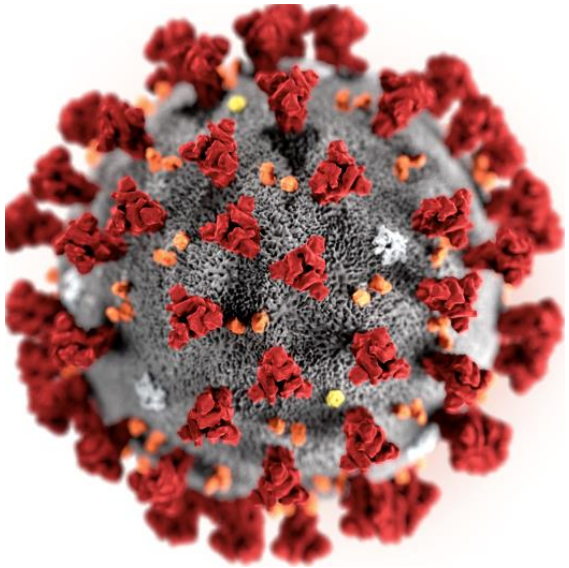


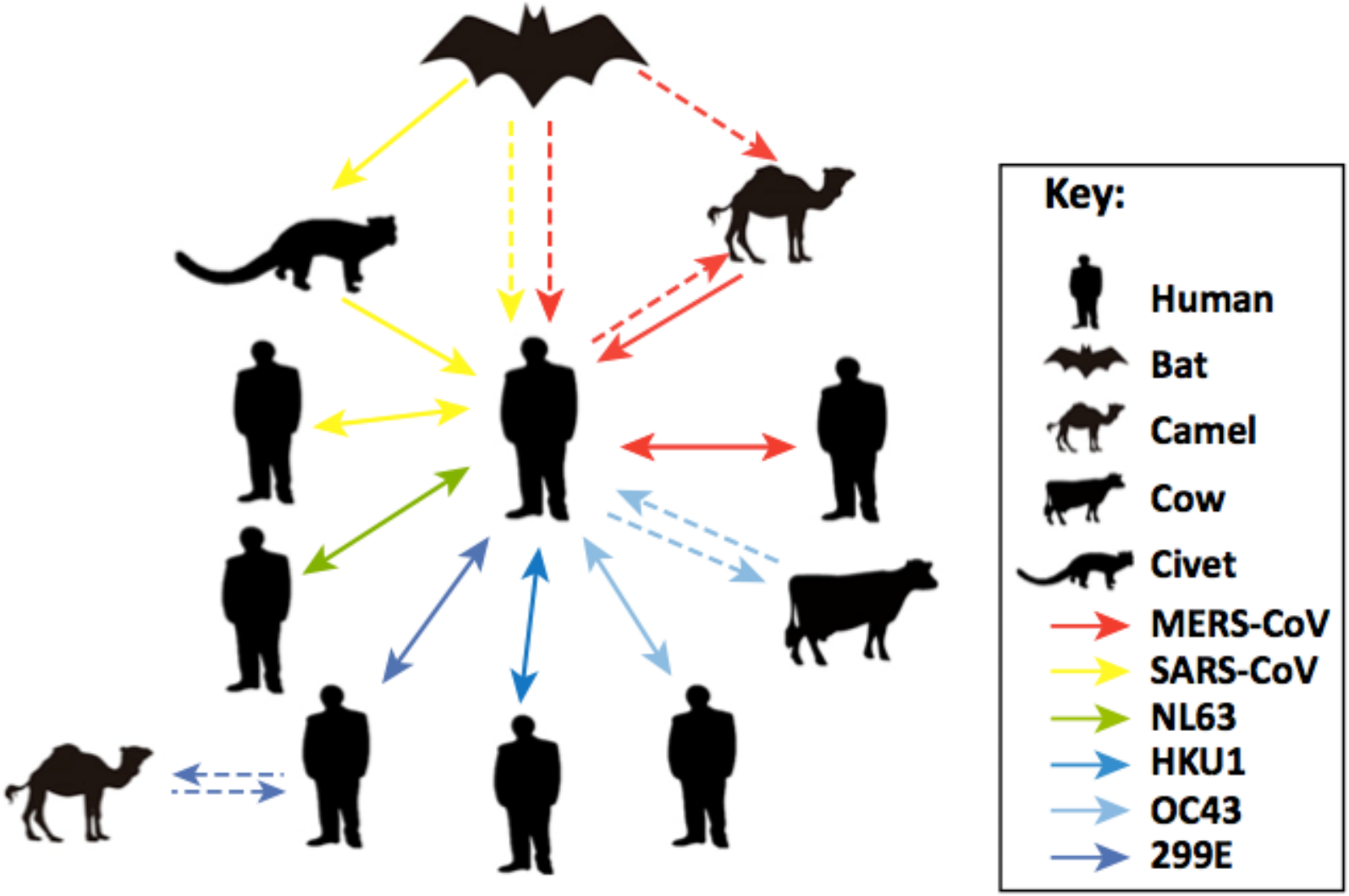
Photo CDC

Eskild Petersen, MD, DMSc, DTM&H

Co-chair
ESCMID Emerging Infections Task Force
(European Societu for Clinical Microbiology and Infectious Diseases)

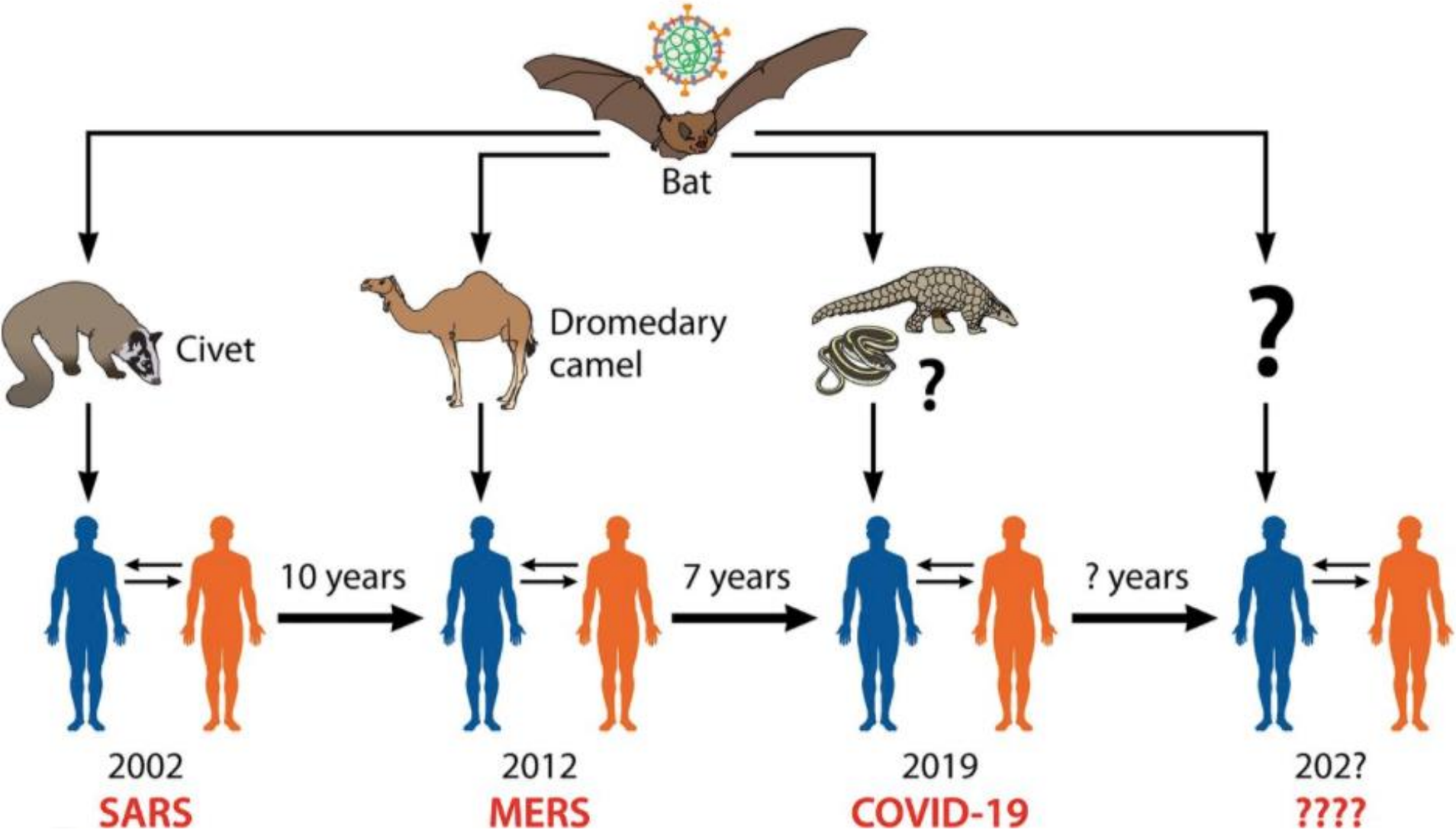
Adjungated Professor
Institute for Clinical Medicine
Aarhus University
Denmark

Intra- and inter species transmission of human Corona virus HCoV



Su S et a. Trends Microbiol 2016;24:490-502

Pathogenic coronavirus



Coronavirus Disease 2019-COVID-19. Dhama K et al. Clin Microbiol Rev. 2020 Jun 24;33(4):e00028-20.

Coronavirus in humans

Until 2020, six CoVs were known to infect humans, including human CoV 229E (HCoV-229E), HCoV-NL63, HCoV-OC43, HCoV-HKU1, SARS-CoV, and MERS-CoV. Although SARS-CoV and MERS-CoV have resulted in outbreaks with high mortality, others remain associated with mild upper-respiratory-tract illnesses

Coronavirus Disease 2019-COVID-19. Dhama K et al. Clin Microbiol Rev. 2020 Jun 24;33(4):e00028-20.

TheScientist
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Where Coronaviruses Come From

EcoHealth Alliance President Peter Daszak speaks with *The Scientist* about how pathogens like 2019-nCoV jump species, and how to head off the next pandemic.

Peter Daszak

There is a very big diversity of these [corona]viruses in the wild. We've been looking at bats ever since the SARS outbreak and bats are the real reservoir for SARS CoV.

And what we found is there's this big diversity: we've found over 50 SARS-related coronaviruses in bats.

Centers for Disease Control and Prevention
MMWR
Morbidity and Mortality Weekly Report
Early Release / Vol. 69
June 8, 2020

First Reported Cases of SARS-CoV-2 Infection in Companion Animals — New York, March–April 2020

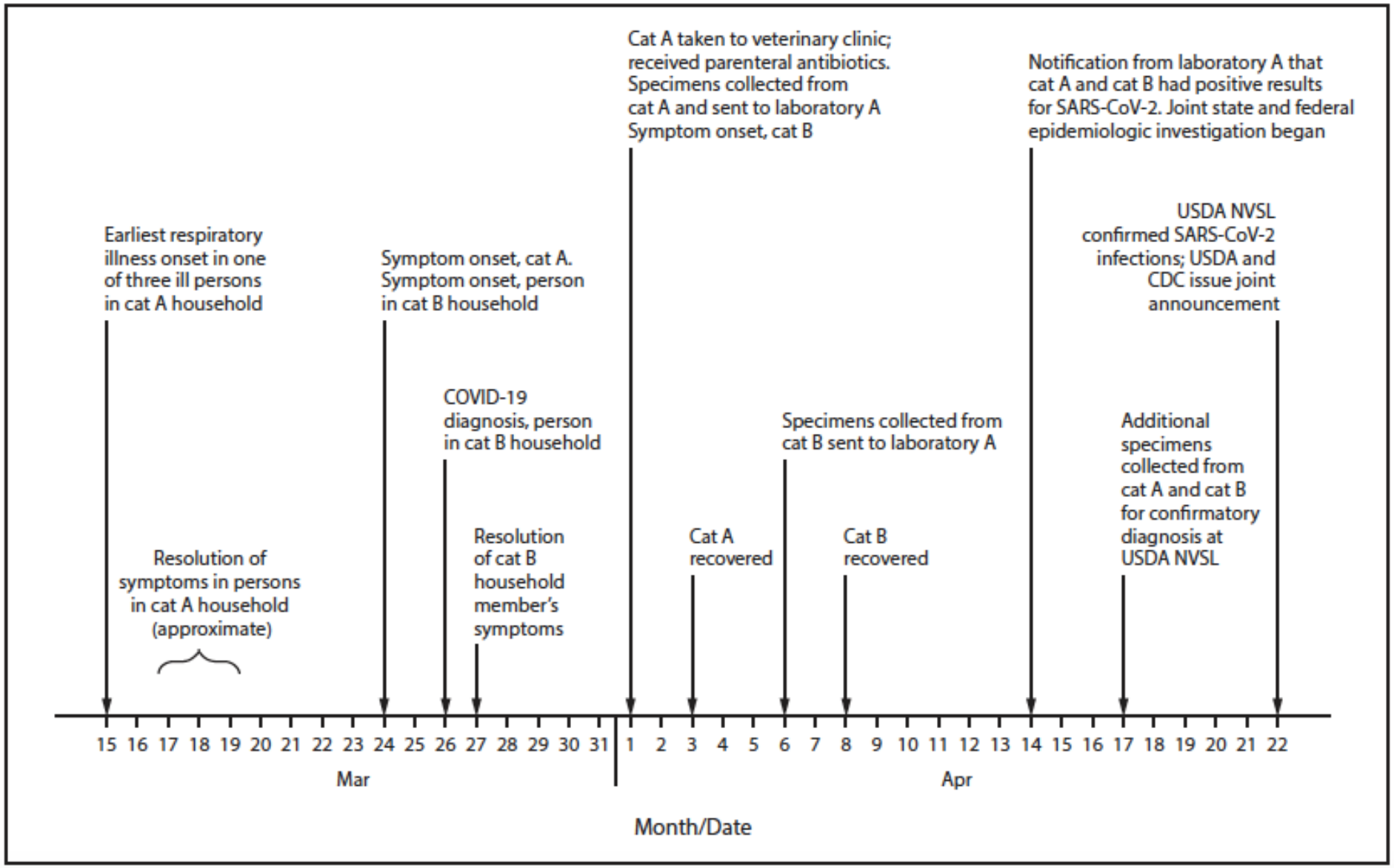
Alexandra Newman DVM[1]; David Smith, DVM[2]; Ria R. Ghai, PhD[3,4]; Ryan M. Wallace, DVM[3,4]; Mia Kim Torchetti, DVM, PhD[5]; Christina Loiacono, DVM, PhD[5]; Laura S. Murrell, MA[3,4]; Ann Carpenter, DVM[3,4]; Scott Moroff, VMD[6]; Jane A. Rooney DVM[7]; Casey Barton Behravesh, DVM, DrPH[3,4]

Two cats infected with SARS-CoV-2

While ACE2 receptor amino acid sequences in different animals show phylogenetic distance with respect to the human ACE2 receptor, the **pangolin**, **cat**, **felines**, and **dog** ACE2 receptor sequences cluster closely, and it predicts that the S protein of SARS-CoV-2 may bind to ACE2 in **domestic cats** and **dogs**, as well as a range of other species, including **pigs, cows, pangolins**, and **Chinese hamsters**.

Hernández M et al. Are Animals a Neglected Transmission Route of SARS-CoV-2? Pathogens. 2020 Jun 18;9(6):E480. doi: 10.3390/pathogens9060480.

FIGURE. Timeline of events related to SARS-CoV-2 infections in two domestic cats (cats A and B) kept as pets in two different households — New York, March 15–April 22, 2020



CORONAVIRUS DISEASE 2019 UPDATE (301): DENMARK (NORTH JUTLAND) NETHERLANDS (NORTH BRABANT) FARMED MINK, SPREAD, CONTROL

A ProMED-mail post
http://www.promedmail.org
ProMED-mail is a program of the
International Society for Infectious Diseases
http://www.isid.org

In this update:
[1] Denmark: 3rd mink farm infected by COVID-19
[2] Netherlands: 18th mink farm infected by COVID-19
[3] Denmark: precautionary measures on mink farms

3 July 2020

ProMED
INTERNATIONAL SOCIETY
FOR INFECTIOUS DISEASES

Mink populations burgeon in the spring, when pups are born, raising concerns about new SARS-CoV-2 outbreaks.
RUSLAN SHAMUKOV/TASS VIA GETTY IMAGES

Coronavirus rips through Dutch mink farms, triggering culls to prevent human infections

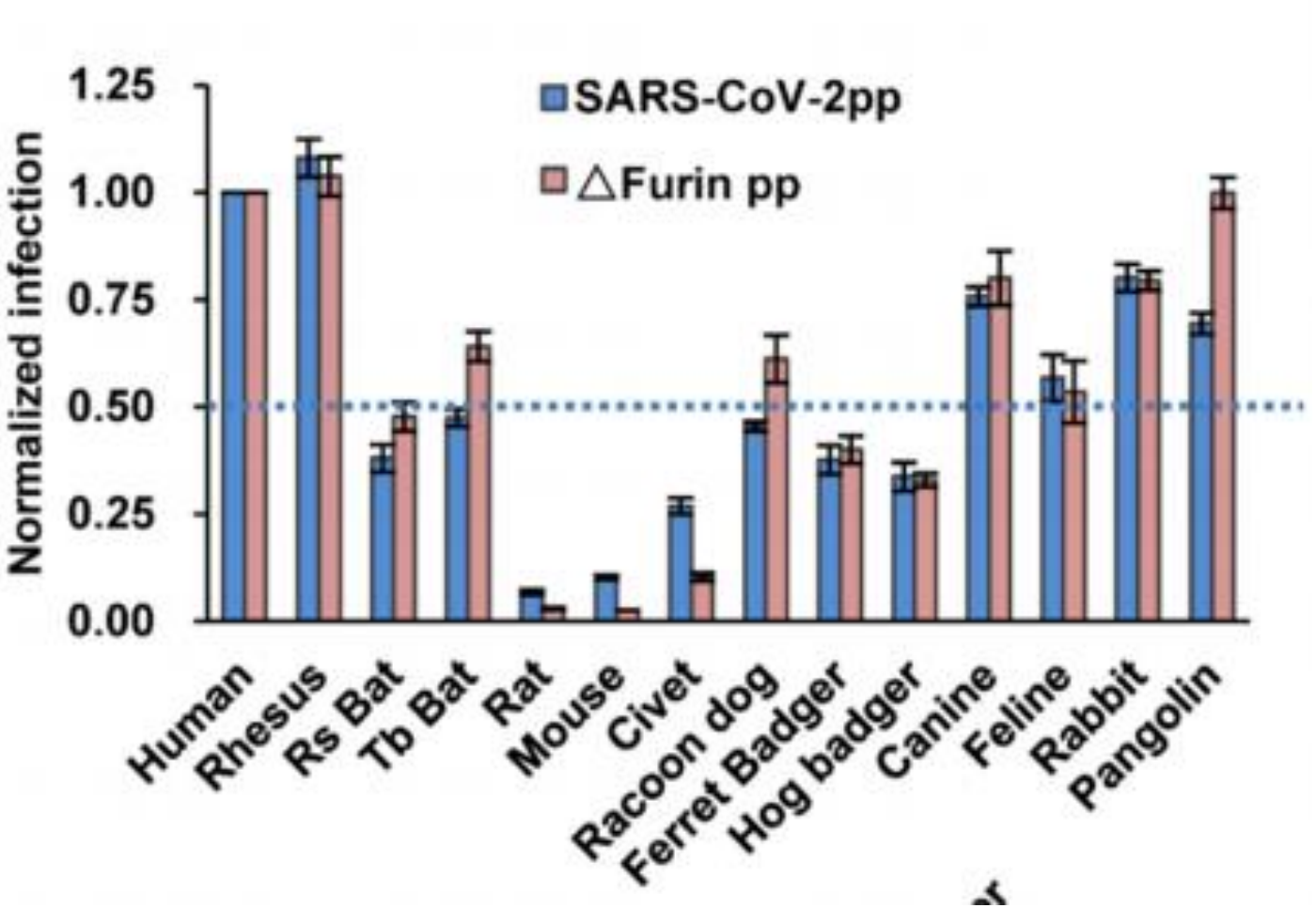
By Martin Enserink | Jun. 9, 2020 , 3:30 PM

The mink most probably were infected

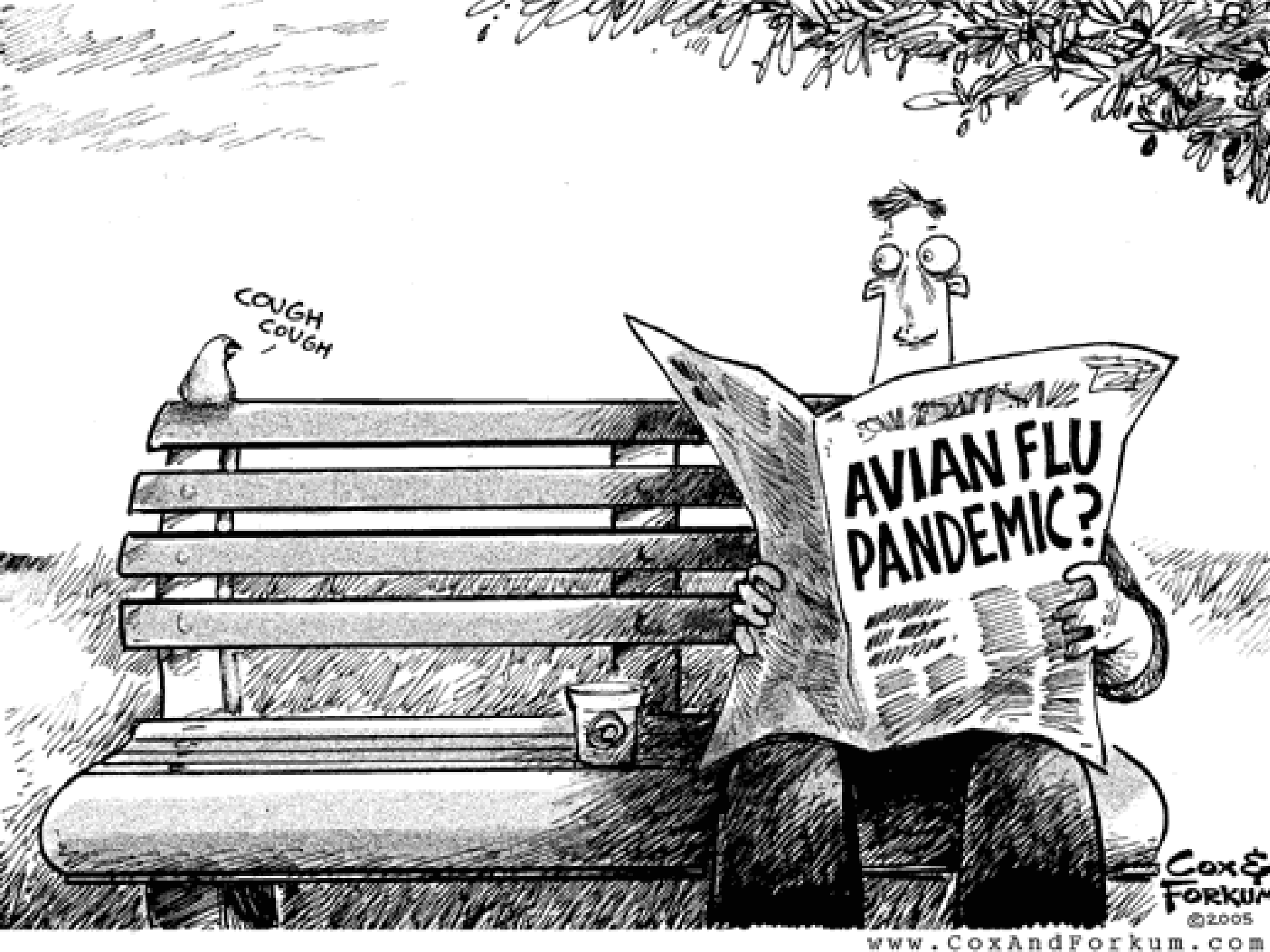
by humans infected with SARS-CoV-2

sciencemag.org/news/2020/06/coronavirus-rips-through-dutch-mink-farms-triggering-culls-prevent-human-infections

All mammals have ACE2 receptors



Broad and differential animal ACE2 receptor usage by SARS-CoV-2 Xuesen Zhao et al. medRxiv 19 April 2020. https://www.biorxiv.org/content/10.1101/2020.04.19.048710v1.full.pdf


COUGH
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2019-nCoV, SARS, MERS and pandemic H1N1

Table 1. Pathogenicity and Transmissibility Characteristics of Recently Emerged Viruses in Relation to Outbreak Containment.

Virus	Case Fatality Rate (%)	Pandemic	Contained	Remarks
2019-nCoV	Unknown*	Unknown	No, efforts ongoing	
pH1N1	0.02–0.4	Yes	No, postpandemic circulation and establishment in human population	Est. 200,000 deaths
H7N9	39	No	No, eradication efforts in poultry reservoir ongoing	No human to human transmission
NL63	Unknown	Unknown	No, endemic in human population	
SARS-CoV	9.5	Yes	Yes, eradicated from intermediate animal reservoir	58% of cases result from nosocomial transmission
MERS-CoV	34.4	No	No, continuous circulation in animal reservoir and zoonotic spillover	70% of cases result from nosocomial transmission
Ebola virus (West Africa)	63	No	Yes	

* Number will most likely continue to change until all infected persons recover.

A Novel Coronavirus Emerging in China - Key Questions for Impact Assessment
Munster VJ et al. N Engl J Med 2020 Jan 24

Comparing SARS-CoV-2 with SARS-CoV and influenza pandemics

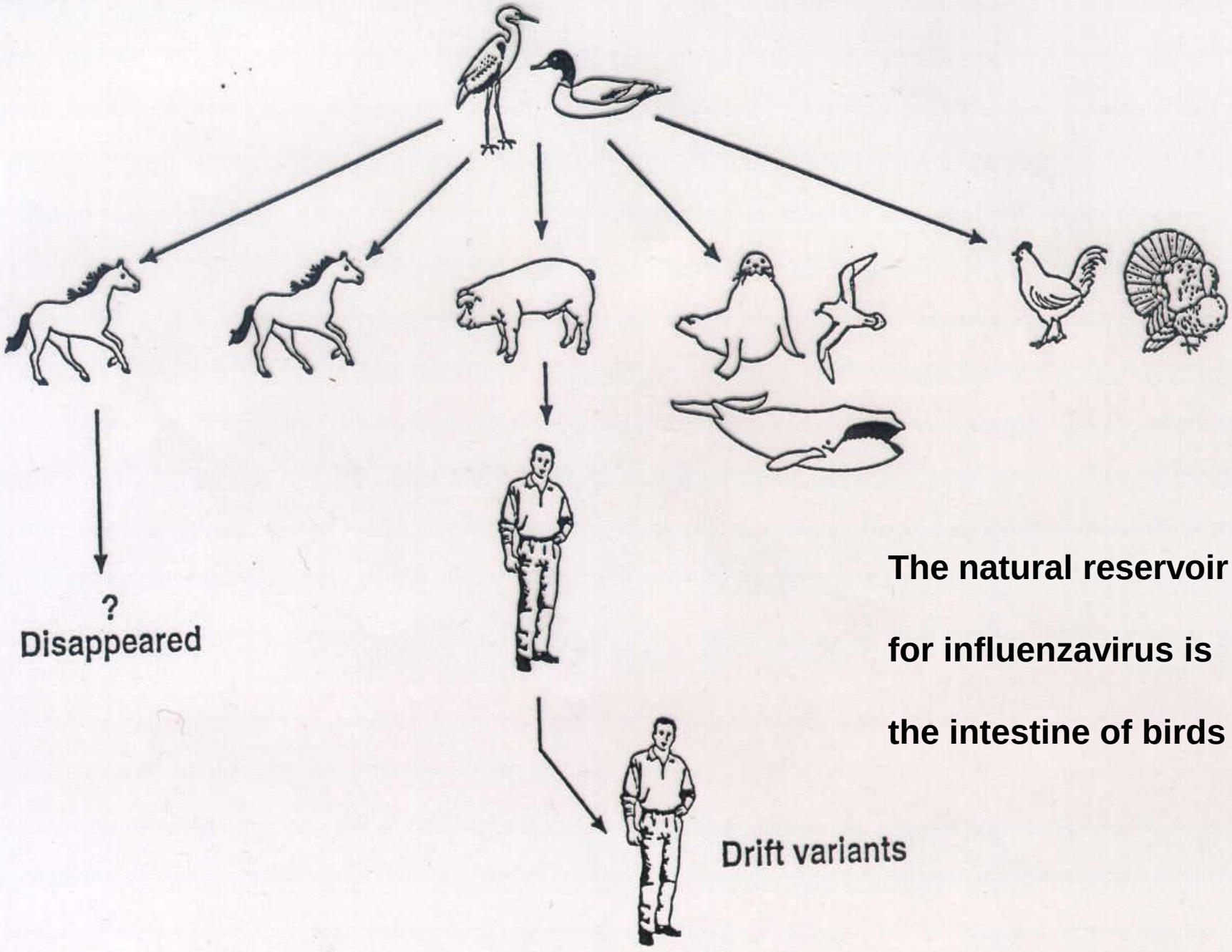
Lancet Infect Dis 2020
Published Online
July 3, 2020
https://doi.org/10.1016/S1473-3099(20)30484-9

Eskild Petersen, Marion Koopmans, Unyeong Go, Davidson H Hamer, Nicola Petrosillo, Francesco Castelli, Merete Storgaard, Sulien Al Khalili, Lone Simonsen

	Number of deaths (adjusted to year 2000 population)	Mean age at death (years)	Years of life lost (adjusted to year 2000 population)
2009 influenza pandemic	7500–44 100*; 8500–17 600†	37·4	334 000–1 973 000; 328 900–680 300
1968 influenza pandemic	86 000‡	62·2	1 693 000
1957 influenza pandemic	150 600‡	64·6	2 698 000
1918 influenza pandemic	1 272 300‡	27·2	63 718 000
1979–2001 average influenza A H3N2 season	47 800	75·7	594 000
2003 SARS-CoV	774	Unknown	Unknown
2012 MERS-CoV	858	>65·0	Unknown
2019 SARS-CoV-2	302 059§	Unknown	Unknown

MERS-CoV=Middle East respiratory syndrome coronavirus. SARS-CoV=severe acute respiratory syndrome coronavirus. SARS-CoV-2=severe acute respiratory syndrome coronavirus 2. *Range based on estimates of excess pneumonia and influenza deaths (lower range number) and all-cause deaths (upper range number); estimated from projections of mortality surveillance from 122 cities. †Probabilistic estimates from the Centers for Disease Control and Prevention using 2009 pandemic survey data.[36] ‡Estimates based on the excess mortality approach applied to final national vital statistics and adjusted to year 2000 population-age structure. §As per the May 17, 2020, WHO situation report.[4]

Table 3: **Mortality from influenza and coronaviruses**[30,31]



The natural reservoir for influenzavirus is the intestine of birds

Available online at www.sciencedirect.com
SCIENCE DIRECT®
Virus Research 109 (2005) 181–190
Virus Research
www.elsevier.com/locate/virusres

New avian influenza A virus subtype combination H5N7 identified in Danish mallard ducks

K. Bragstad[a], P.H. Jørgensen[b], K.J. Handberg[b], S. Mellergaard[c], S. Corbet[a], A. Fomsgaard[a,*]

[a] *Department of Virology, Statens Serum Institut, 5 Artillerivej, DK-2300 Copenhagen S, Denmark*
[b] *Avian Virology, Danish Institute for Food and Veterinary Research, Department of Poultry, Fish and Fur Animals, Ministry of Food, Agriculture and Fisheries, Aarhus, Denmark*
[c] *Danish Veterinary and Food Administration, Søborg, Denmark*

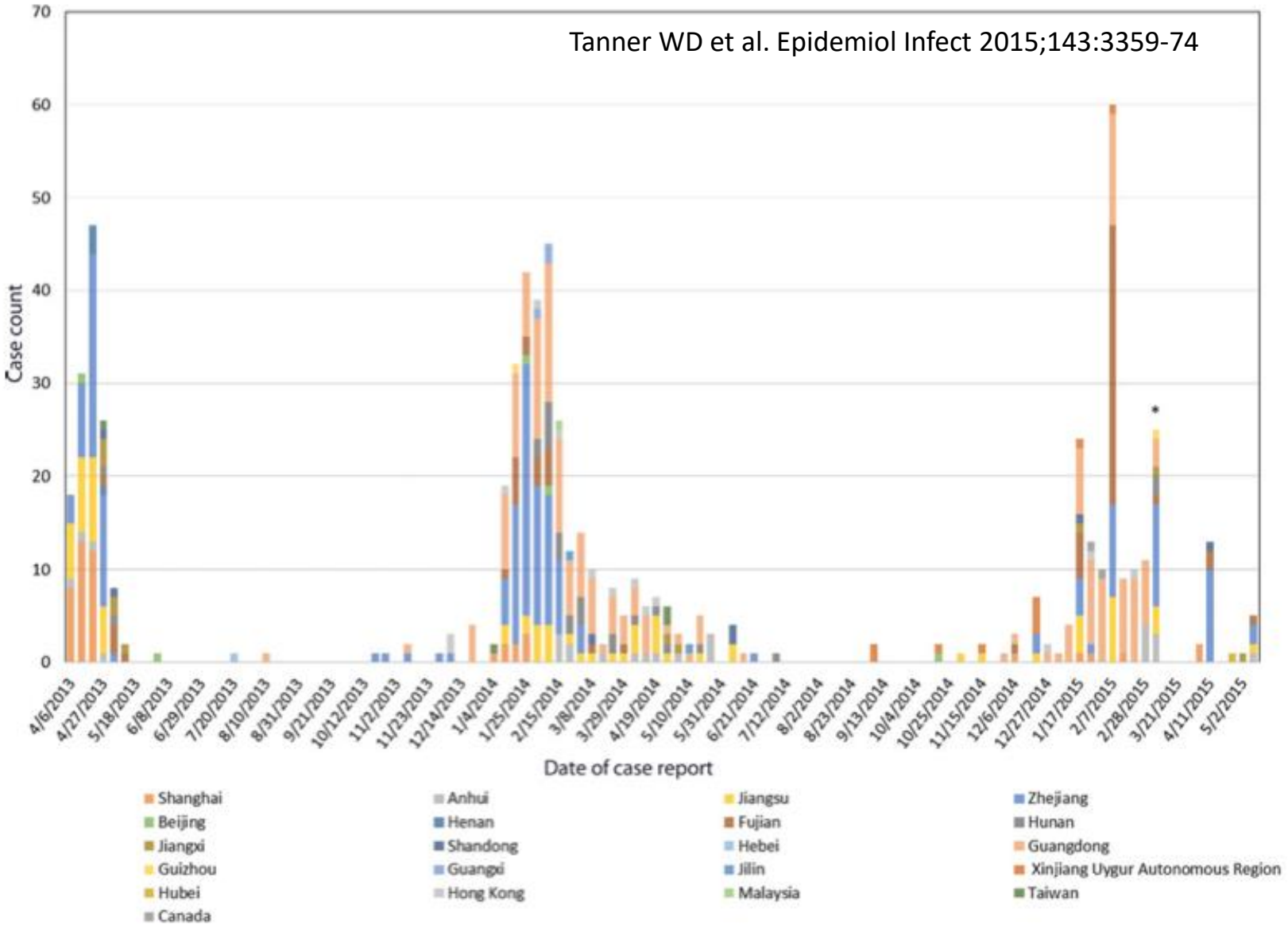
Received 3 September 2004; received in revised form 13 December 2004; accepted 13 December 2004
Available online 30 January 2005

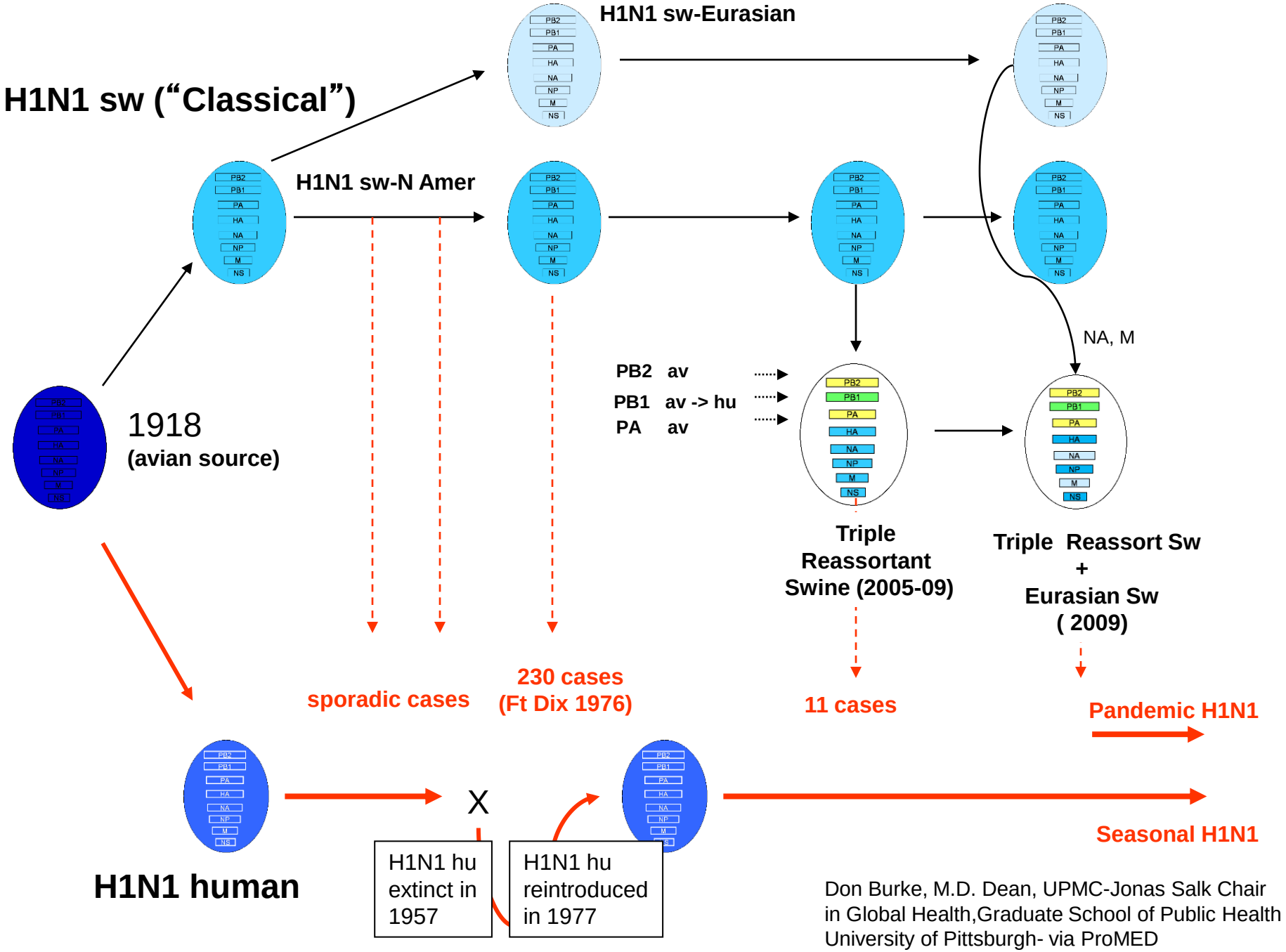
A recombinant avian infleunza from a H7N7 outbreak in Italy in 1998 and a H5N2 from an outbreak in The Netherlands in 2001 surface in Denmark in 2003.

LPAI = Low Pathogenic Avian Influenza,

HPAI = High Pathogenic Avian Influenza

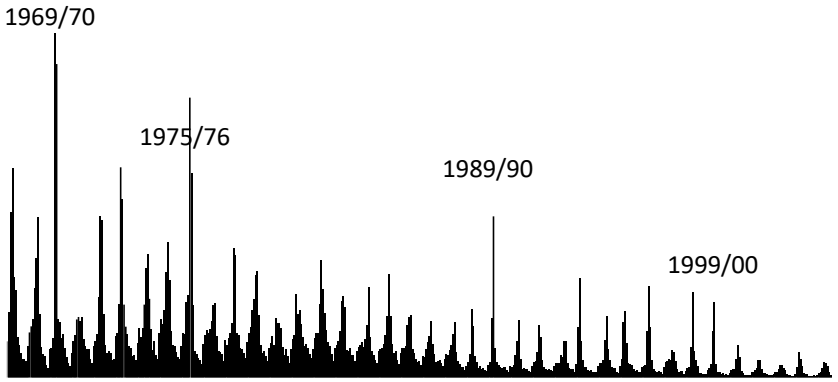
Human H7N9 cases since 2013

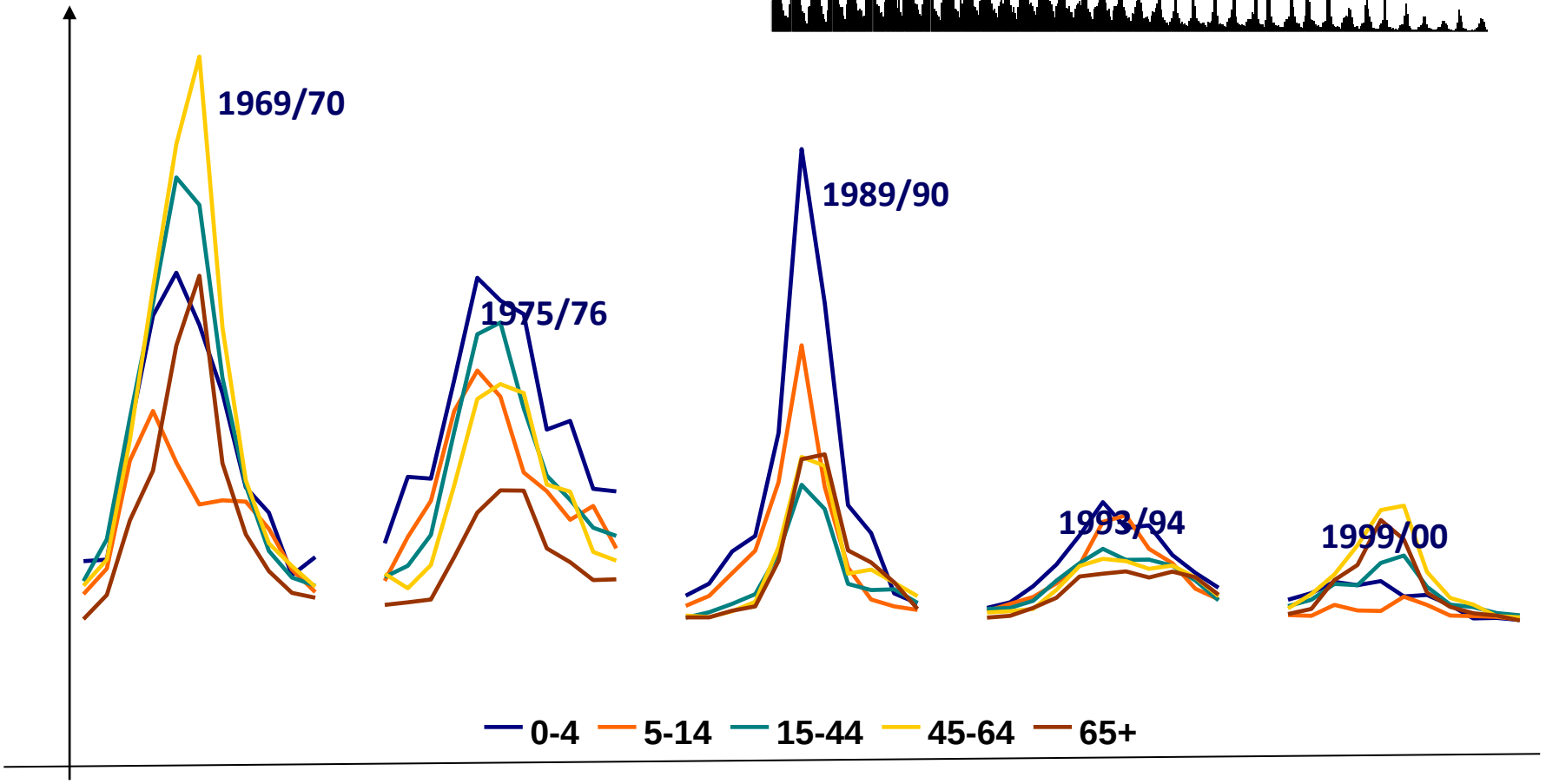




Don Burke, M.D. Dean, UPMC-Jonas Salk Chair in Global Health,Graduate School of Public Health University of Pittsburgh- via ProMED

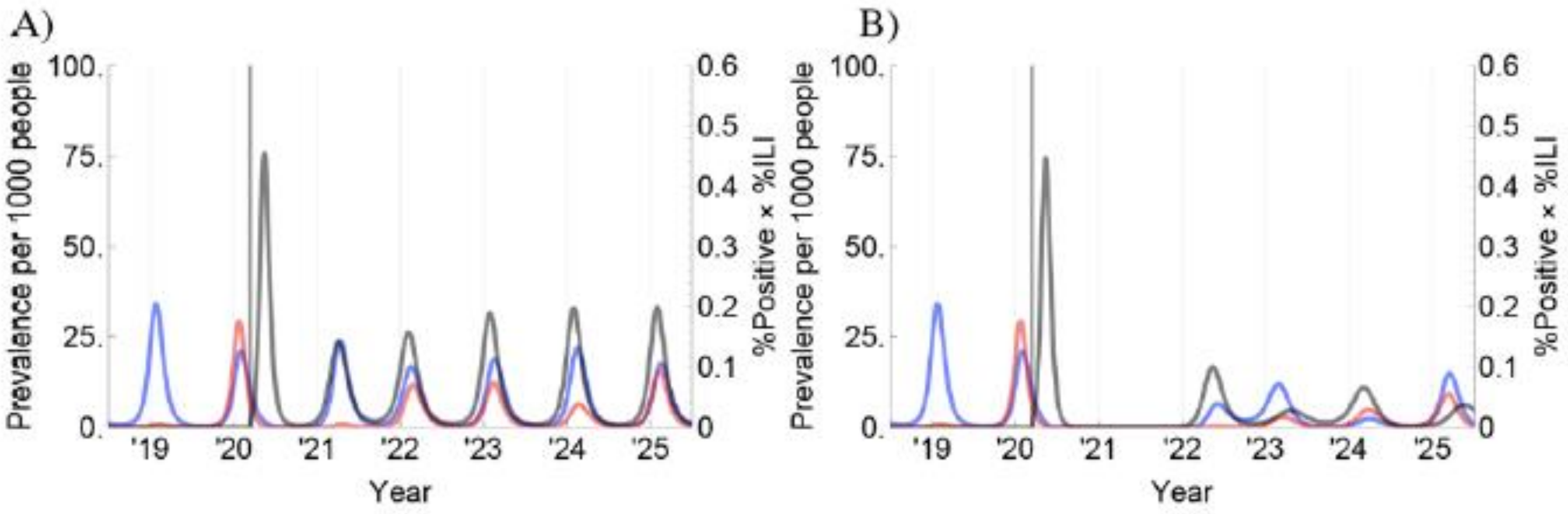
Incidence of ILI by age over selected 11 week epidemic periods in the UK





Fleming DM et al. J Public Health 2008;30:91-8.

SARS-CoV-2 – modeling the future



A short duration (1/σ3 = 40 weeks) of SARS-CoV-2 immunity could yield annual SARS-CoV-2 outbreaks.
(B) Longer-term SARS-CoV-2 immunity (1/σ3 = 104 weeks) could yield biennial outbreaks, possibly with smaller outbreaks in the intervening years.

Projecting the Transmission Dynamics of SARS-CoV-2 Through the Postpandemic Period
Stephen M Kissler et al. Science. 2020 May 22;368(6493):860-868.

In conclusion

SARS-CoV-2 like other CoV's can infect humans and a broad range of mammals but has not been reported in birds.

This is not surprising given that the ACE2 receptor is found in all mammals with little genetic variation.

From a transmission point of view, SARS-CoV-2, has a high affinity for the human host like the human influenza's.

Transmission between humans and mammals have been observed especially for mink and a few cases of dogs, cats and tigers.

The importance for the human epidemiology remain to be determined.