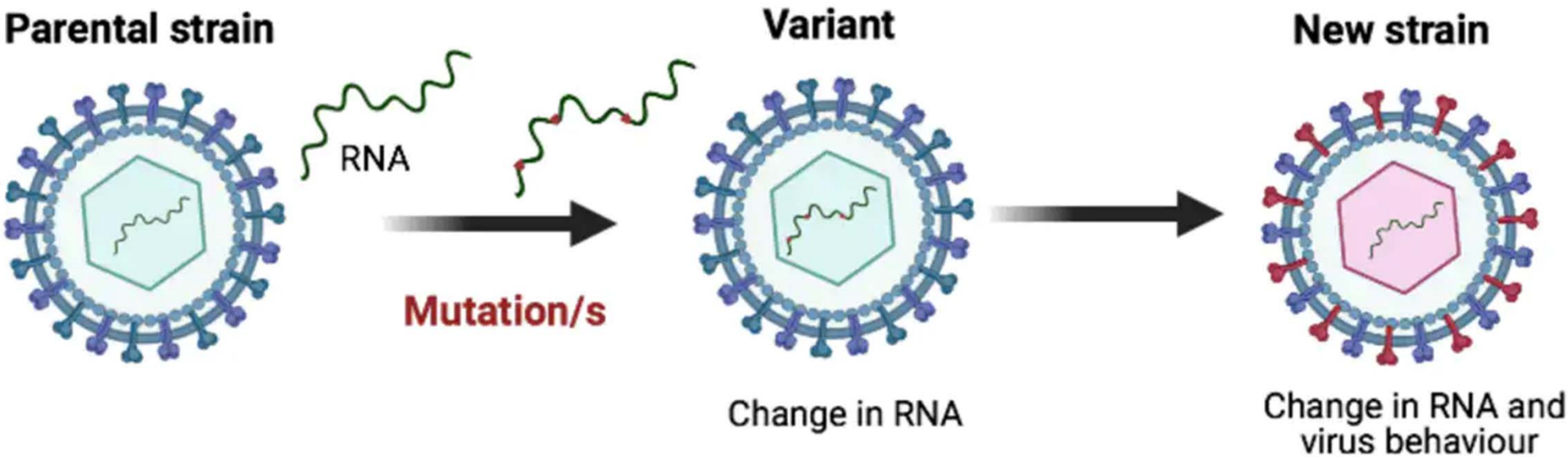
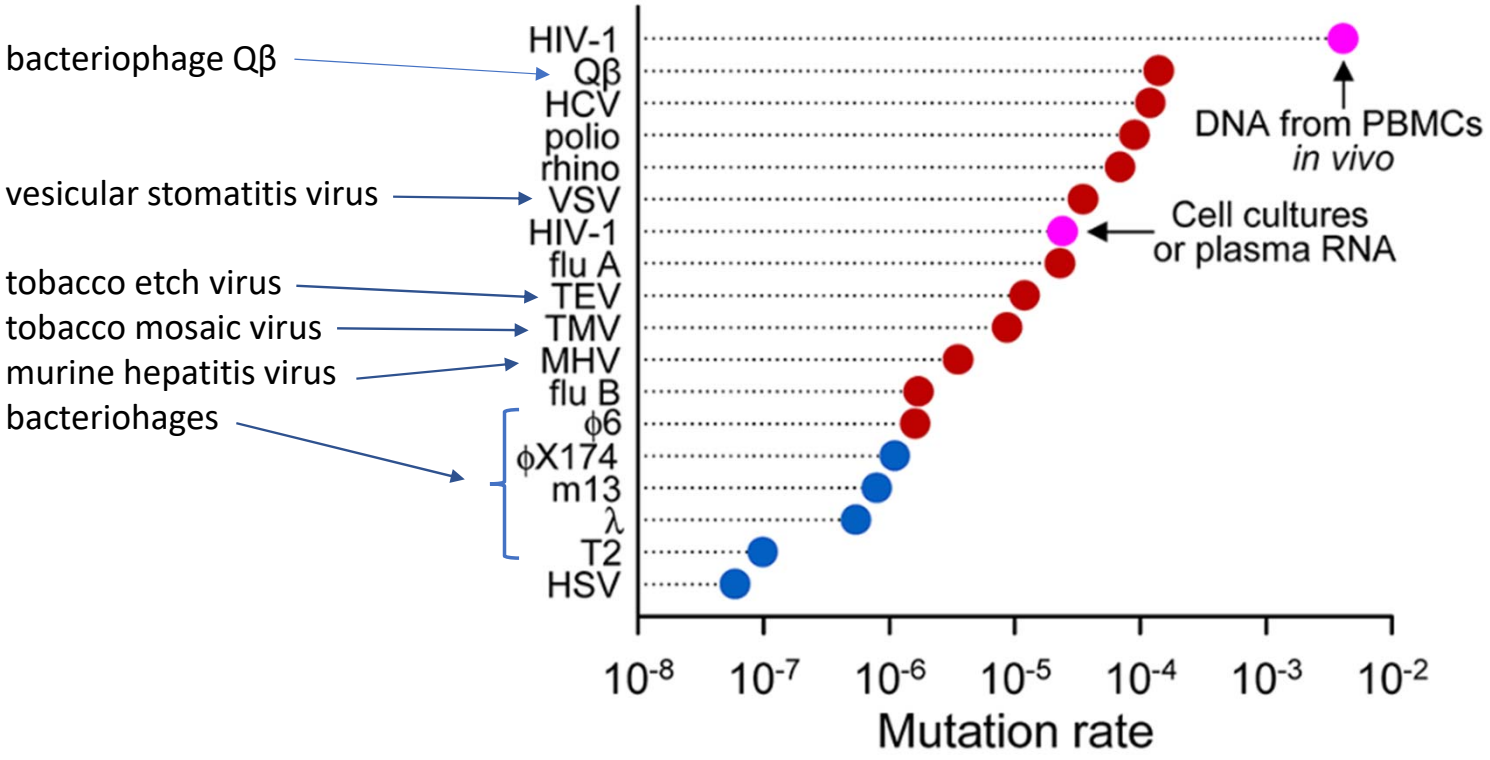


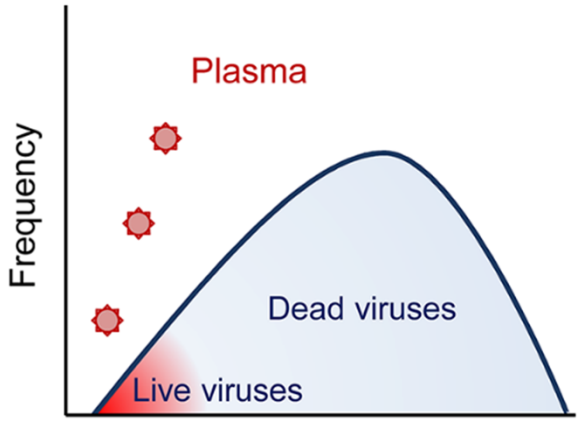
Viruses with mutations become variants. If the variant displays different physical properties to the original virus, we call it a new strain.

Extremely High Mutation Rate of HIV-1 In Vivo

PLOS Biology

José M. Cuevas, et al. PLOS Biology | DOI:10.1371/journal.pbio.1002251 September 16, 2015





This discrepancy occurs because most sequences are **lethally mutated** and are thus unable to reach the plasma

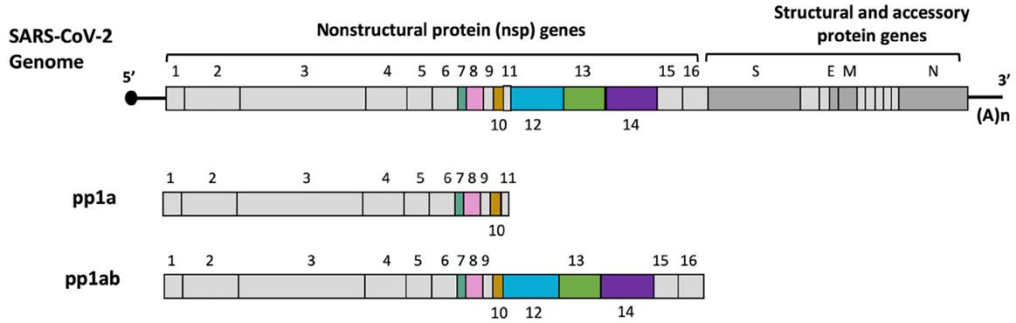
Coronavirus RNA Proofreading: Molecular Basis and Therapeutic Targeting

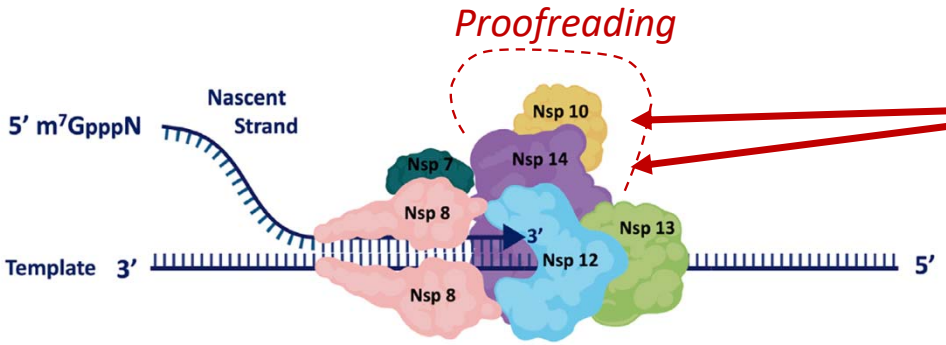
Molecular Cell

Fran Robson, et al. Molecular Cell 2020; 79: 710 – 727.

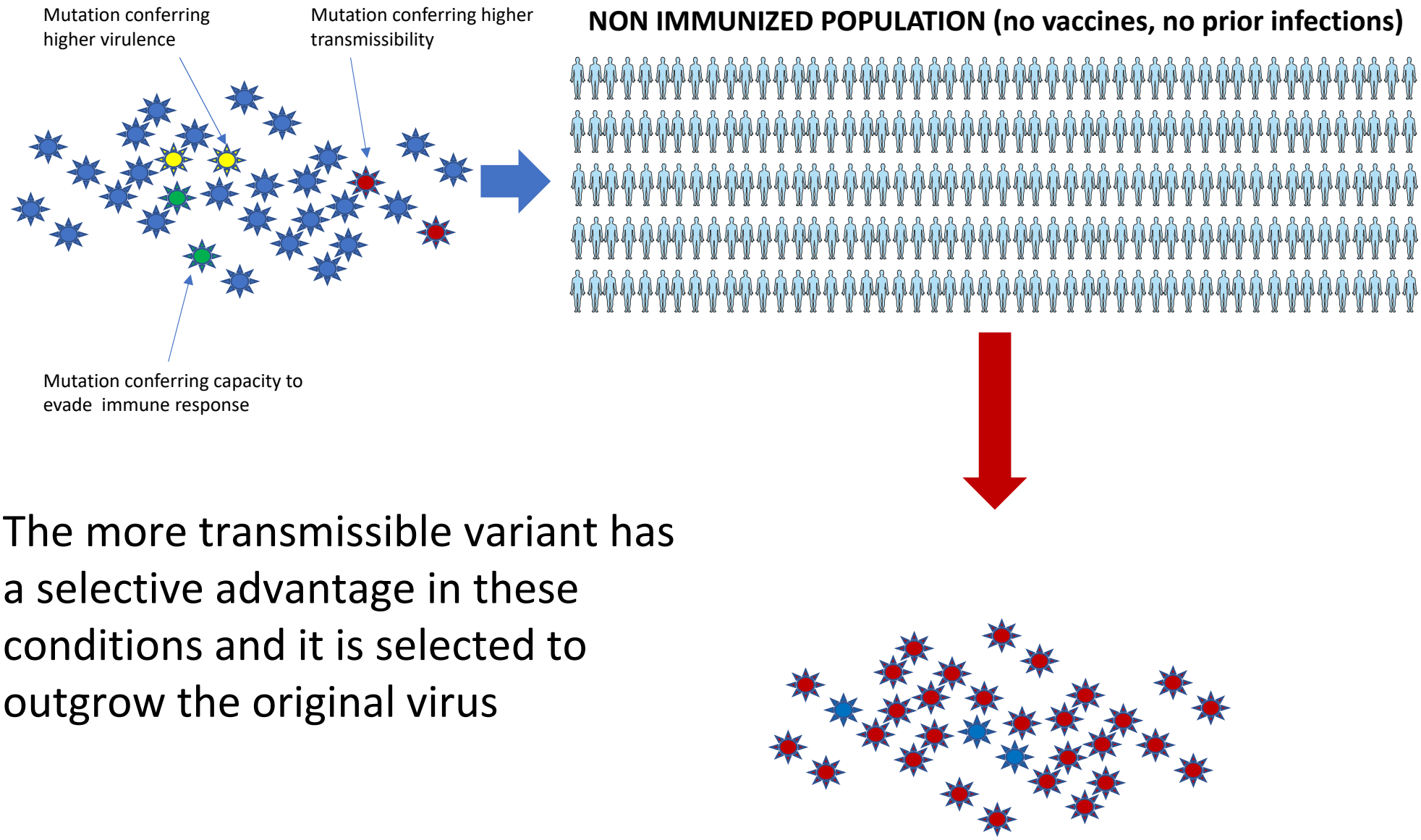
RNA virus replication typically has a high error rate (or low viral fidelity) that results in the virus existing as diverse populations of genome mutants or ‘‘quasispecies’’.

While low replicative fidelity allows the RNA viruses to adapt to different replicative environments and selective pressures, it is also associated with an increased chance of error catastrophe leading to viral extinction. This suggests the need for a finely tuned balance between quasispecies diversity and replicative fitness for viral virulence and evolution.

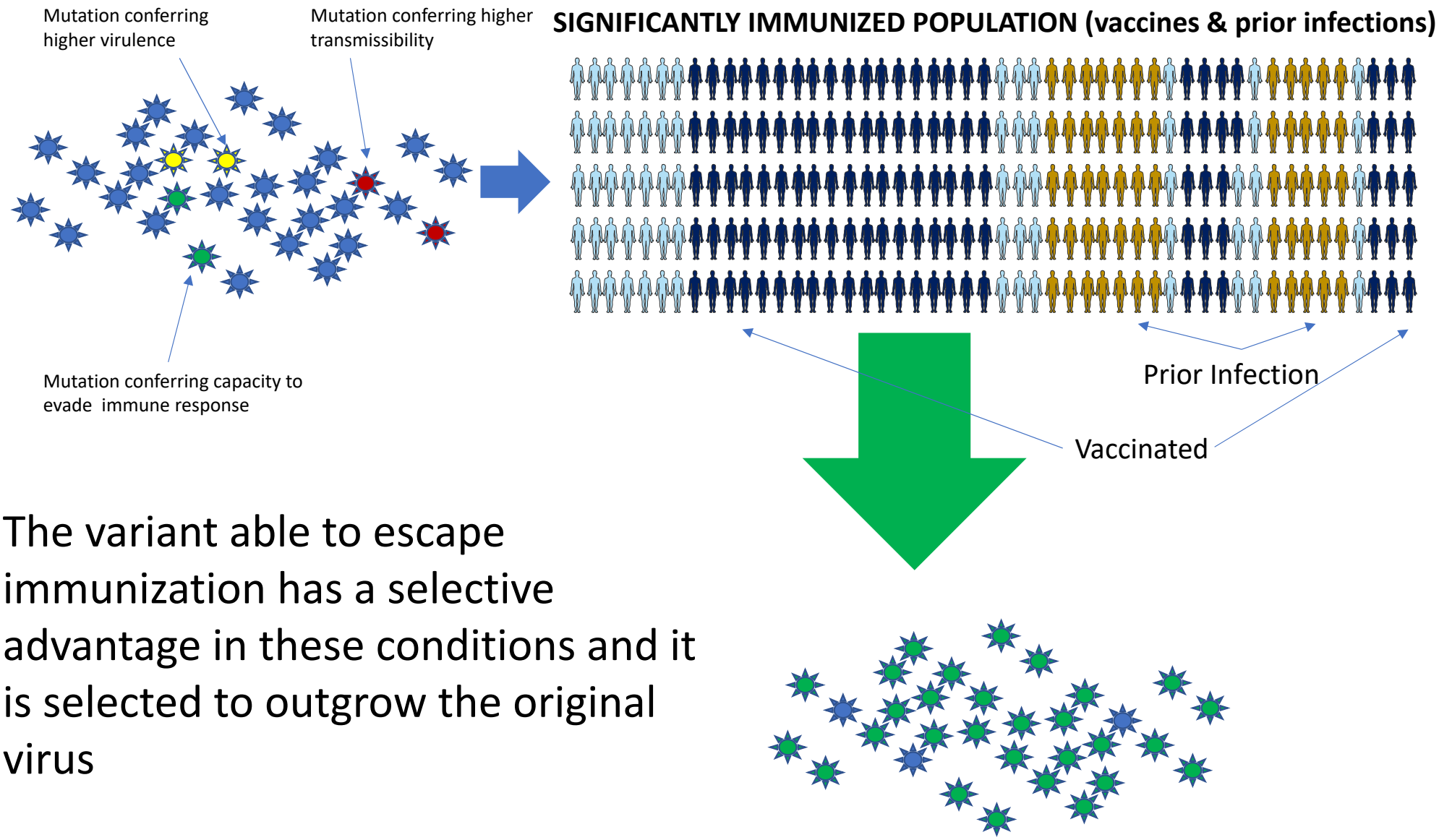




Nsp12-RdRp replicates and transcribes the genome and sgmRNAs. Nsp7/nsp8 proteins confer processivity to the polymerase. Nsp13 unwinds dsRNA ahead of the polymerase. **Nsp14-ExoN** complexed with its co-factor **nsp10** proofreads the nascent RNA strand and excises misincorporated nucleotides.



The more transmissible variant has a selective advantage in these conditions and it is selected to outgrow the original virus



The variant able to escape immunization has a selective advantage in these conditions and it is selected to outgrow the original virus

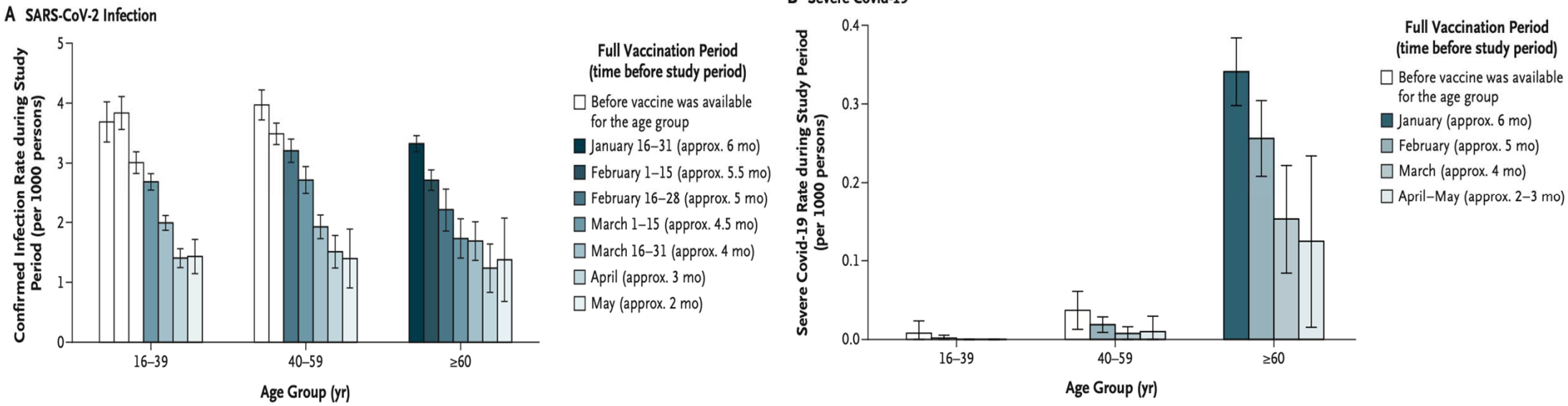
Waning Immunity after the BNT162b2 Vaccine in Israel

Yair Goldberg, et al. NEJM 2021; Oct 27,
DOI: 10.1056/NEJMoa2114228

The NEW ENGLAND JOURNAL of MEDICINE

Infections that had been documented in the period from July 11 through 31, 2021

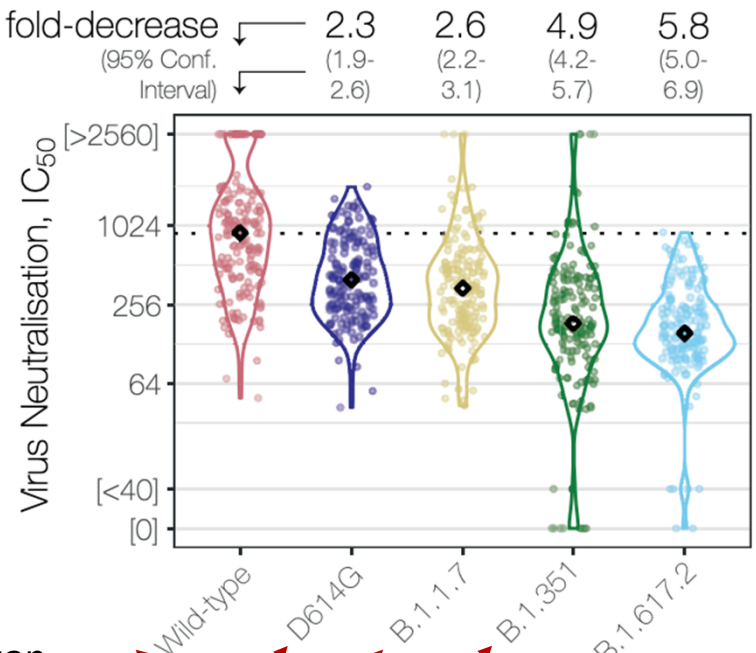
The start date was selected as a time when the virus **had already spread throughout the entire country** and across population sectors. The **end date** was just after Israel had initiated a campaign regarding the use of a **booster vaccine (third dose).**



Neutralising antibody activity against SARS-CoV-2 VOCs B.1.617.2 and B.1.351 by BNT162b2 vaccination

Emma C Wall, et al. www.thelancet.com **Published online June 3, 2021**
https://doi.org/10.1016/S0140-6736(21)01290-3

Neutralising antibody titres (NAbTs) against five SARS-CoV-2 strains from 159 study participants who had received 2 doses of BNT162b2.



Virus Whuan

Virus D614G (March 2020, EU)

UK Variant (“Alpha”)

South African Variant (“Beta”)

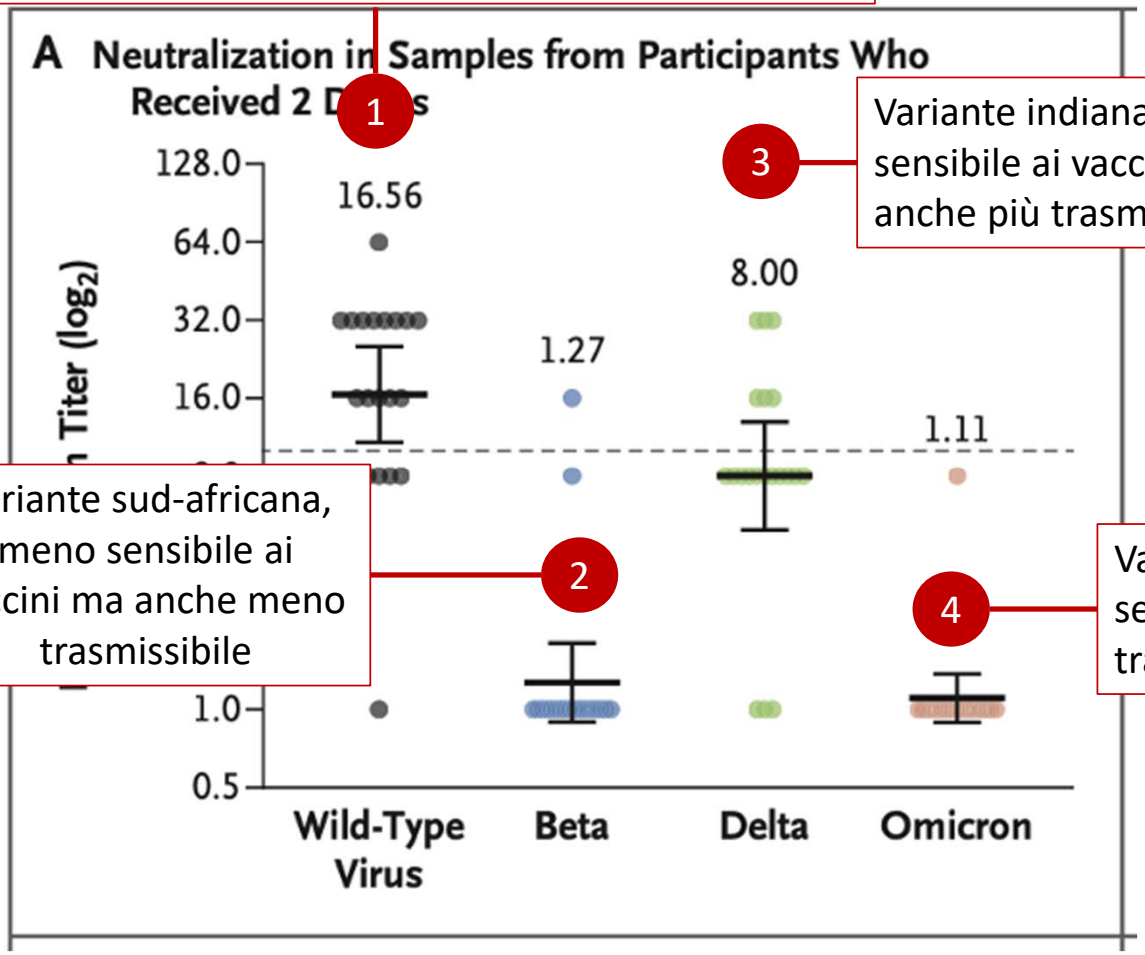
Indian Variant (“Delta”)

Third BNT162b2 Vaccination Neutralization of SARS-CoV-2 Omicron Infection

The NEW ENGLAND JOURNAL of MEDICINE

Ital Nemet, et al. December 29, 2021, at NEJM.org. **DOI: 10.1056/NEJMc2119358**

Virus originale Wuhan, su cui sono “tarati” i vaccini



Variante indiana, sensibile ai vaccini ma anche più trasmissibile

Variante sud-africana, meno sensibile ai vaccini ma anche meno trasmissibile

Variante Omicron, meno sensibile ai vaccini, molto più trasmissibile ma meno virulenta

Neutralization Efficiency against Wild-Type Virus and the Beta, Delta, and Omicron Variants of Concern.

m samples were obtained from 20 health care workers had received two doses of the BNT162b2 vaccine els A and B) and from 20 who had received three doses els C and D). Samples were tested by microneu- tralization against wild-type severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and the B.1.351 (beta), B.1.617.2 (delta), and B.1.1.529 (omicron) variants of concern. Dashed lines in Panels A and C indicate the cutoff titer. Geometric mean titers (horizontal lines) with 95% confidence intervals (I bars) are presented, as well as the geometric mean titer value. Dots indicate individual serum samples. The factor reduction as s shown for samples obtained ved two doses of vaccine m participants who had or these analyses, the mean factor differences between wild-type SARS-CoV-2 and the variants of concern were calculated for each participant; the means of the individual values are shown here. Error bars in Panels B and D indicate the standard error.

*****PRE-PRINT – NOT PEER REVIEWED*****

THE UNIVERSITY of EDINBURGH

Severity of Omicron variant of concern and vaccine effectiveness against symptomatic disease: national cohort with nested test negative design study in Scotland

Professor Aziz Sheikh MD, Usher Institute, University of Edinburgh, Edinburgh, UK

	S Gene Status	N	Person Years	Hospital Admissions	Expected Admissions	Observed/ Expected	LCL	UCL
All cases linking into the EAVE II dataset	S Positive	119100	4375.1	856	856.9	1	0.93	1.07
	S Negative	22205	413.4	15	46.6	→ 0.32	0.19	0.52
	OMICRON							
All cases	S Positive	126464	4643.5	967	903.7	1.07	1	1.14
OMICRON	S Negative	23830	443.1	18	50.1	→ 0.36	0.22	0.56
All cases followed up for at least 7 days	S Positive	102765	4096.2	824	824.9	1	0.93	1.07
	S Negative	4111	140.2	7	21.2	→ 0.33	0.15	0.65
	OMICRON							
All cases aged 20-59	S Positive	68035	2489.4	575	575.6	1	0.92	1.08
	S Negative	17302	322.9	15	34.4	→ 0.44	0.25	0.7
	OMICRON							

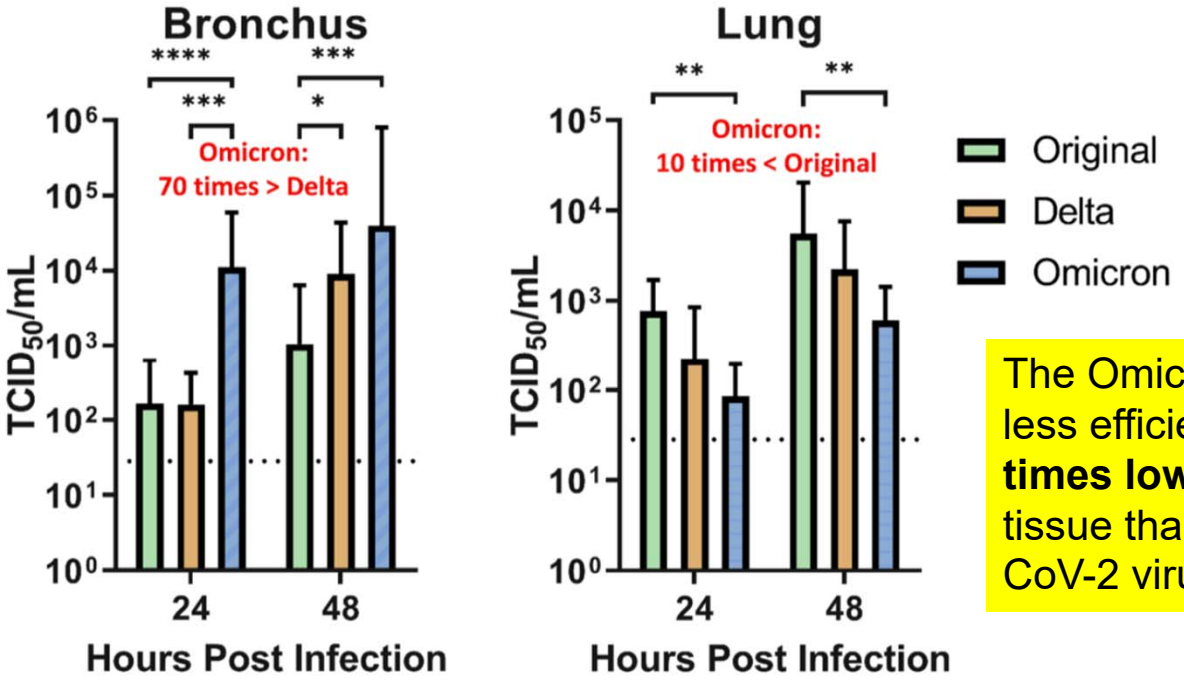
HKU Med LKS Faculty of Medicine The University of Hong Kong 香港大學李嘉誠醫學院

Michael Chan Chi-wai, et al.

News

HKUMed finds Omicron SARS-CoV-2 can infect faster and better than Delta in human bronchus but with less severe infection in lung

At 24 hours after infection, the Omicron variant replicated around **70 times higher** than the Delta variant and the original SARS-CoV-2 virus.



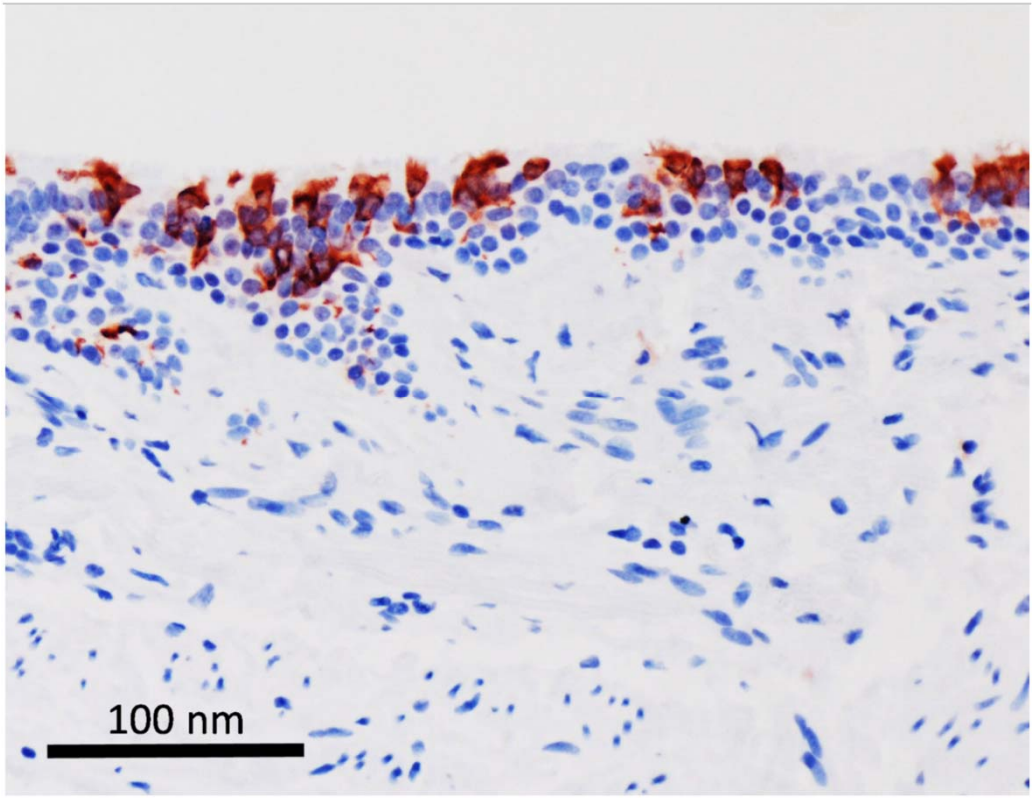
The Omicron variant replicated less efficiently (**more than 10 times lower**) in the human lung tissue than the original SARS-CoV-2 virus

HKU Med LKS Faculty of Medicine The University of Hong Kong 香港大學李嘉誠醫學院

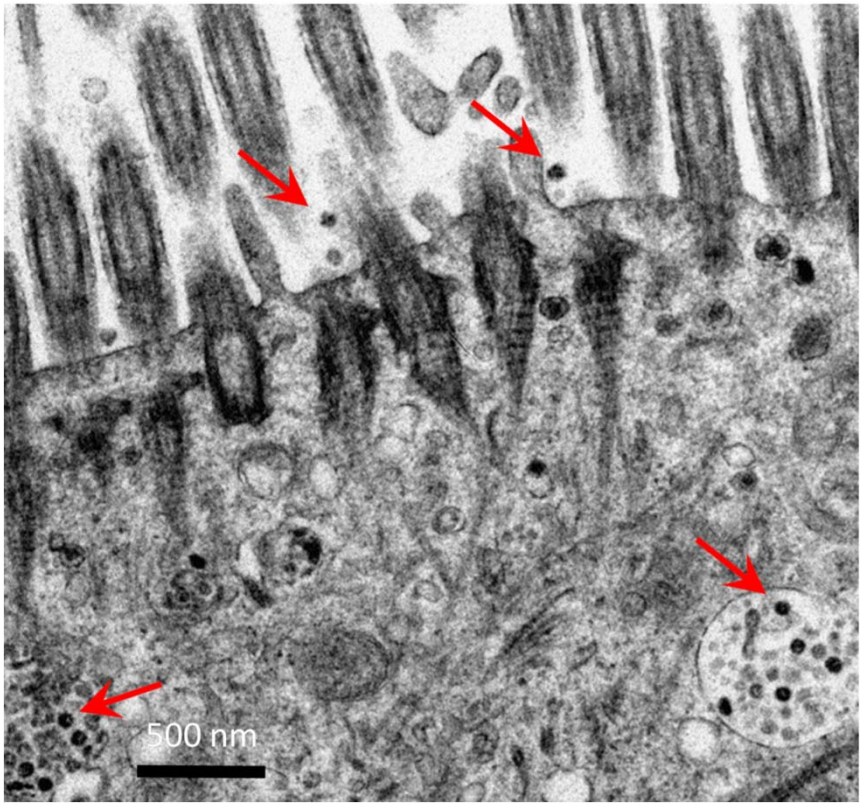
Michael Chan Chi-wai, et al.

News

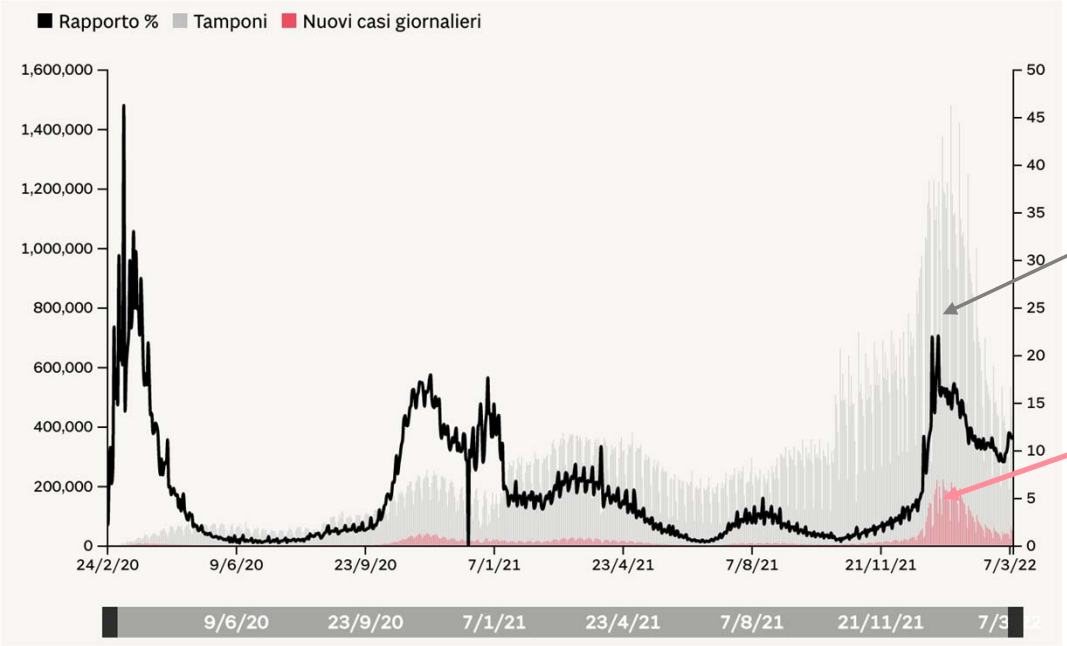
HKUMed finds Omicron SARS-CoV-2 can infect faster and better than Delta in human bronchus but with less severe infection in lung



Omicron variant of SARS-CoV-2 (in red) infected human bronchus tissues.



Electron micrograph of the human bronchus tissues after infection with SARS-CoV-2. Red arrows showing viral particles.



Tamponi

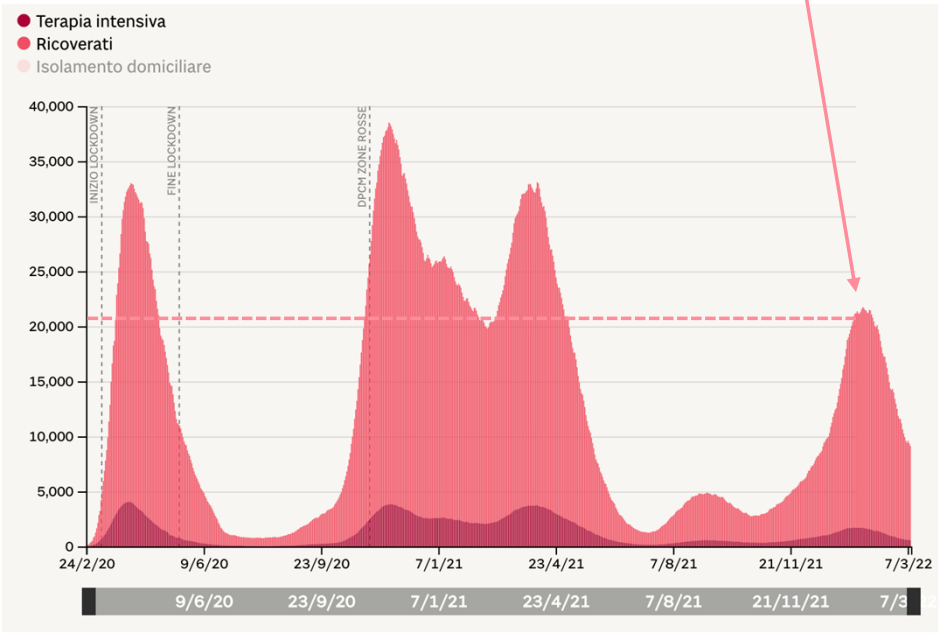
Nuove infezioni / die

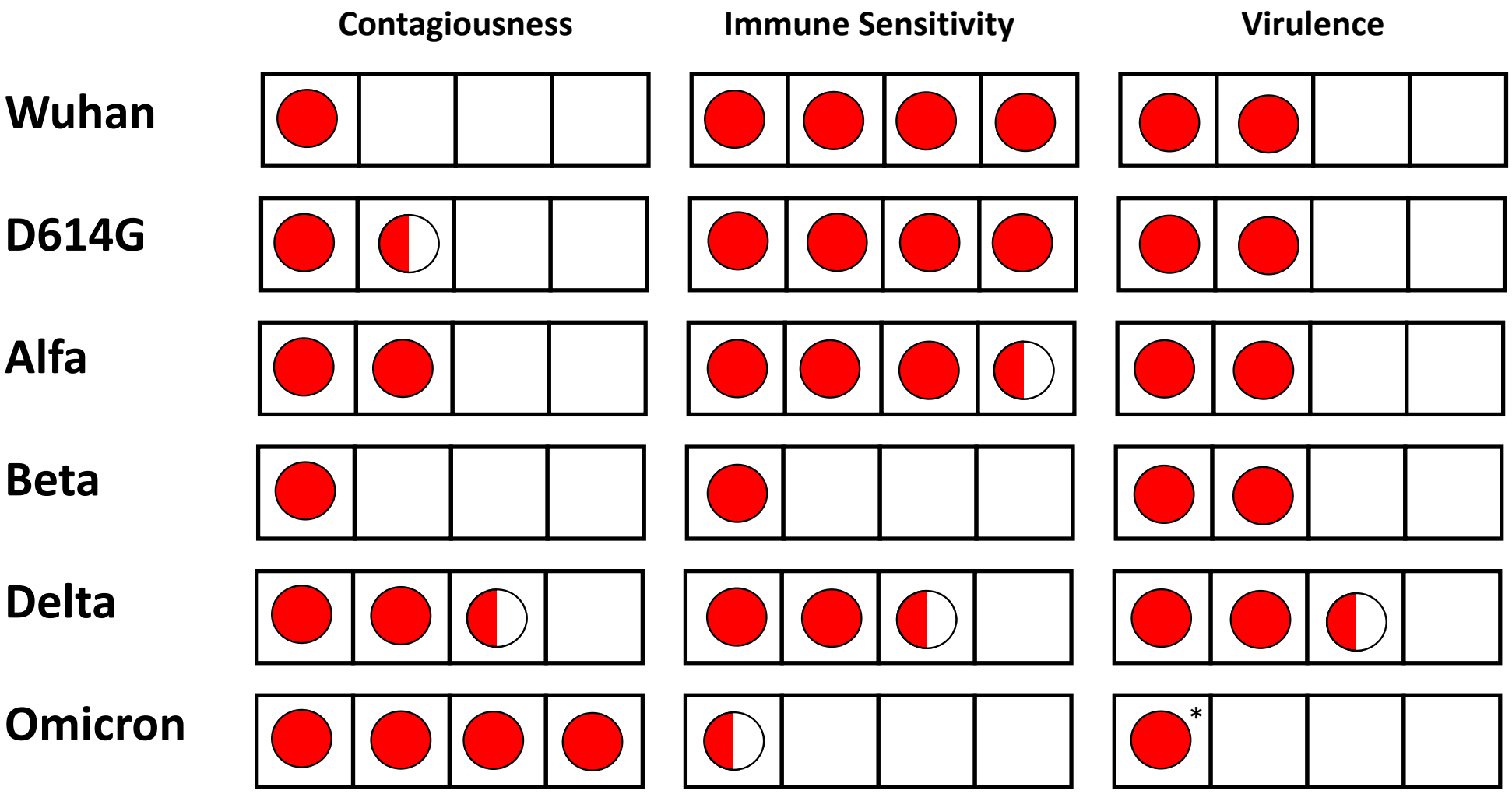
Ricoveri

Population Immunity

+

Reduced Virulence




Contagiousness
Immune Sensitivity
Virulence
Wuhan
D614G
Alfa
Beta
Delta
Omicron
*
* Effect of Vaccination to be considered

Prediction and prevention of the next pandemic zoonosis

Lancet 2012; 380: 1956–65

Stephen S Morse, Jonna A K Mazet, Mark Woolhouse, Colin R Parrish, Dennis Carroll, William B Karesh, Carlos Zambrana-Torrelio, W Ian Lipkin, Peter Daszak

Most pandemics—eg, HIV/AIDS, severe acute respiratory syndrome, pandemic influenza—originate in animals, are caused by viruses, and are driven to emerge by ecological, behavioural, or socioeconomic changes. Despite their substantial effects on global public health and growing understanding of the process by which they emerge, no pandemic has been predicted before infecting human beings. We review what is known about the pathogens that emerge, the hosts that they originate in, and the factors that drive their emergence. We discuss challenges to their control and new efforts to predict pandemics, target surveillance to the most crucial interfaces, and identify prevention strategies. New mathematical modelling, diagnostic, communications, and informatics technologies can identify and report hitherto unknown microbes in other species, and thus new risk assessment approaches are needed to identify microbes most likely to cause human disease. We lay out a series of research and surveillance opportunities and goals that could help to overcome these challenges and move the global pandemic strategy from response to pre-emption.

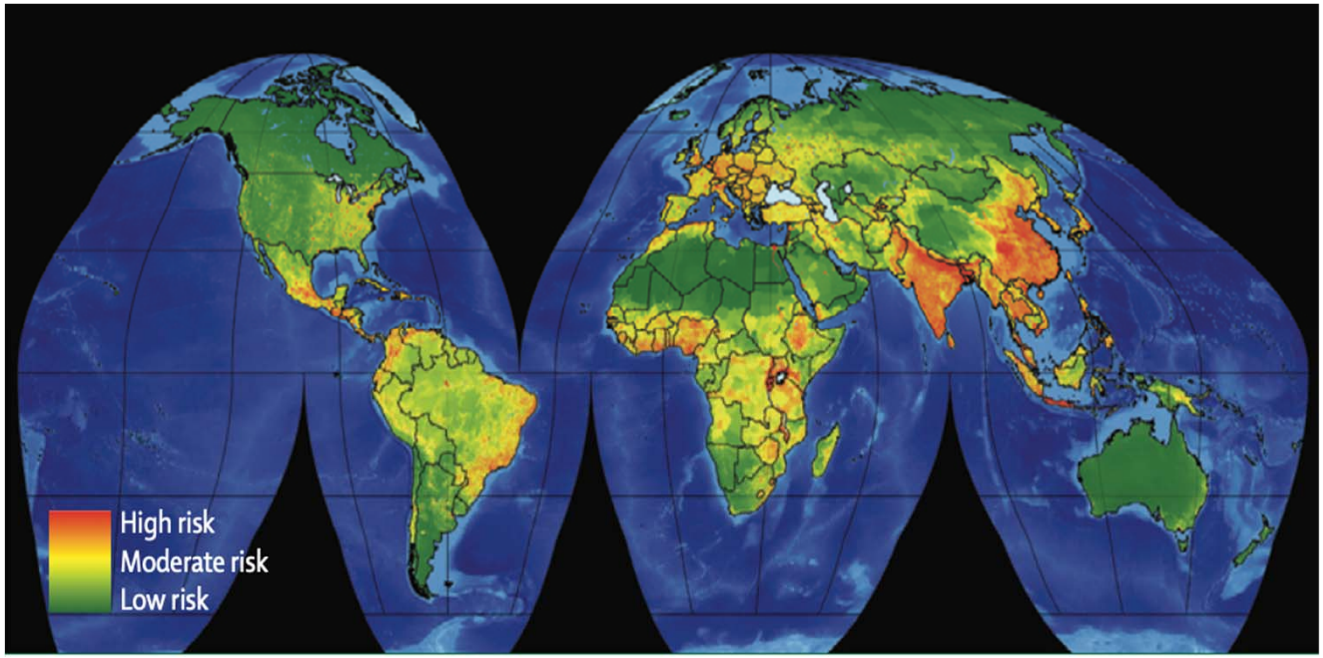
Prediction and prevention of the next pandemic zoonosis

Lancet 2012; 380: 1956–65

Stephen S Morse, Jonna A K Mazet, Mark Woolhouse, Colin R Parrish, Dennis Carroll, William B Karesh, Carlos Zambrana-Torrelio, W Ian Lipkin, Peter Daszak

A database of all known emerging infectious diseases since **1940** was used to identify the most likely origins of each separate emergence event.
Presence or absence of infections emerging from wildlife was analysed with logistic regression against a series of known drivers, including:

- **human population density**,
- **change in human population density**,
- **wildlife diversity** (mammalian species richness), gridded at 1 km2 resolution.



Global hotspots for emerging infectious diseases that originate in wildlife

The global distribution of model outputs gives a measure of the likelihood of a region to generate a new zoonotic emerging infectious disease that originates in wildlife. Because previous pandemics have mainly originated in wildlife, these maps identify hotspots where the next pandemic is most likely to originate.

Prediction and prevention of the next pandemic zoonosis

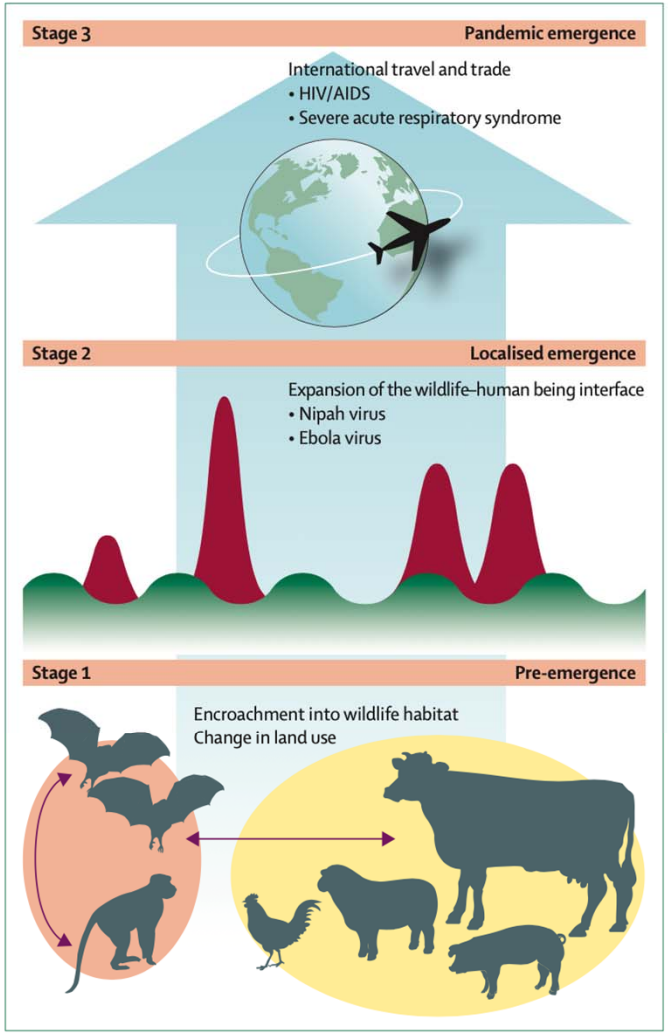
Lancet 2012; 380: 1956–65

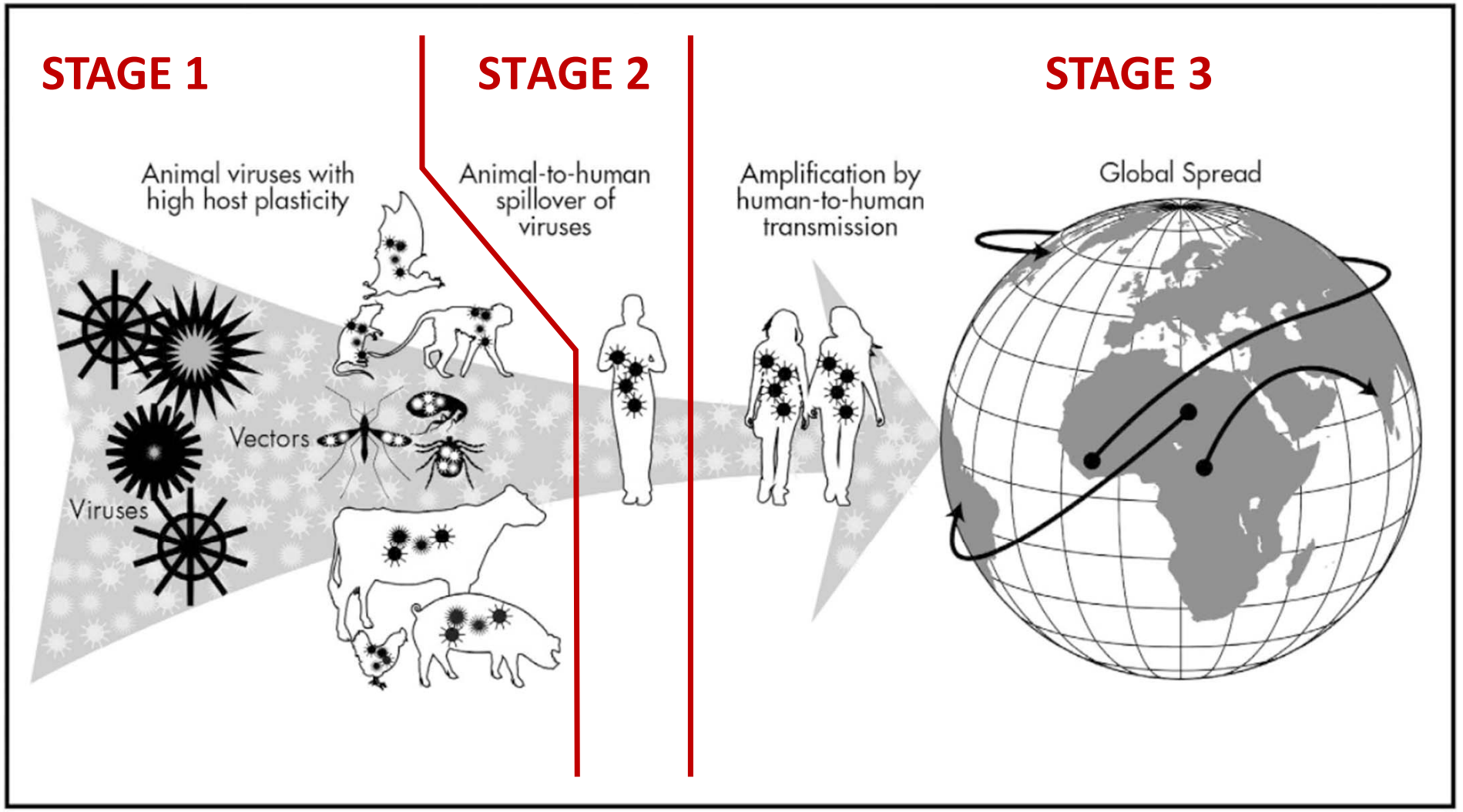
Stephen S Morse, Jonna A K Mazet, Mark Woolhouse, Colin R Parrish, Dennis Carroll, William B Karesh, Carlos Zambrana-Torrelio, W Ian Lipkin, Peter Daszak

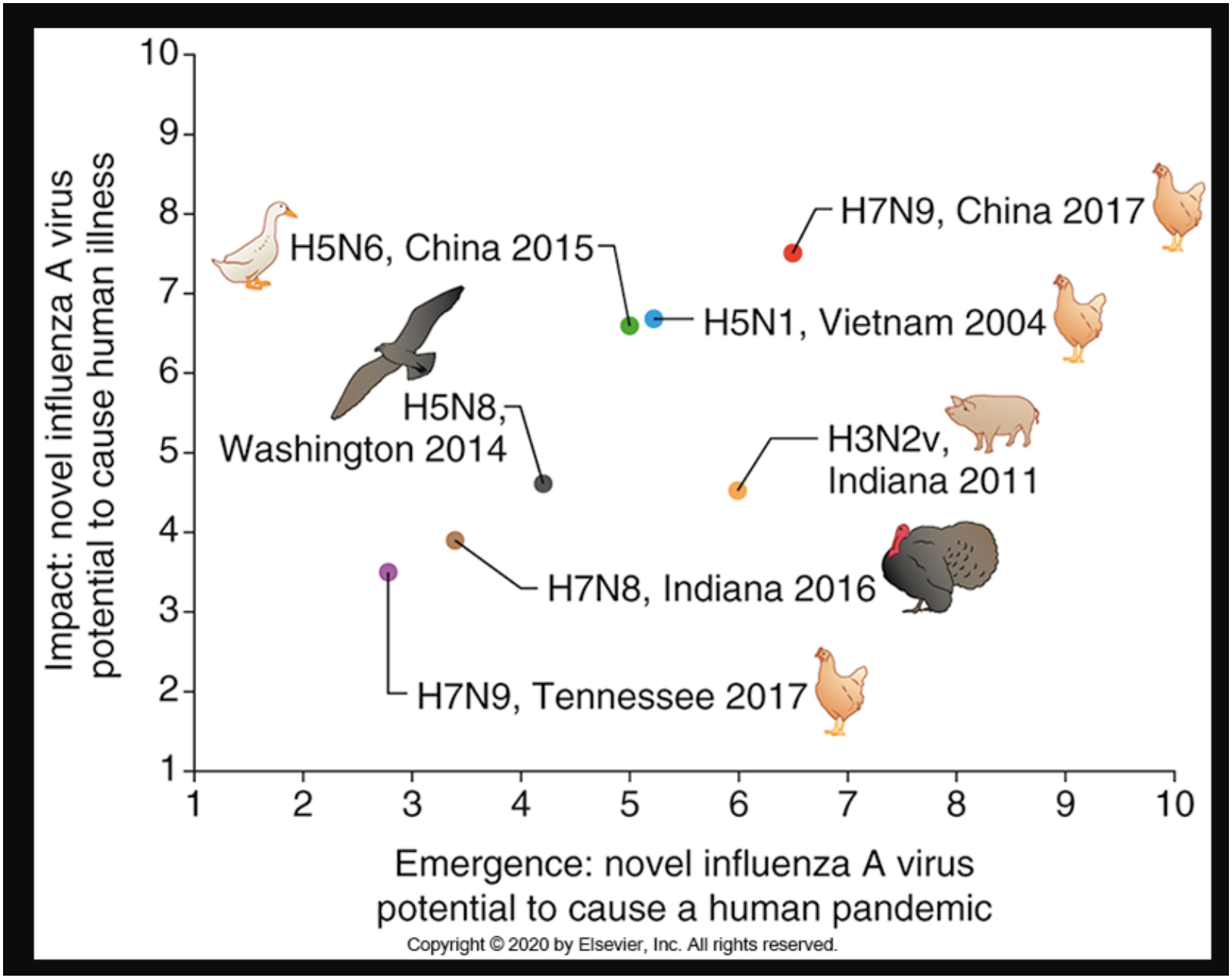
Stage 3 (full pandemic emergence): **sustained person-to-person transmission** and **large-scale spread**, often aided by global air travel (eg, HIV/AIDS, severe acute respiratory syndrome) or the international movement of reservoir hosts or vectors through trade (eg, West Nile virus). Stage 3 pandemics are rare because even pathogens capable of some person-to-person transmission might not be able to maintain long enough chains of transmission to spread (eg, Nipah virus in Bangladesh).

Stage 2 (localised emergence): initial **spillover** of a wildlife or livestock pathogen to people. Causes range from handling of butchered wildlife to exposure to fomites in wildlife markets or livestock farms, or in the wild. Outcomes vary widely, from small clusters of human cases (eg, Menangle virus)[16] to large outbreaks, some with limited person-to-person transmission (eg, Ebola virus) and some without (eg, Hendra virus).

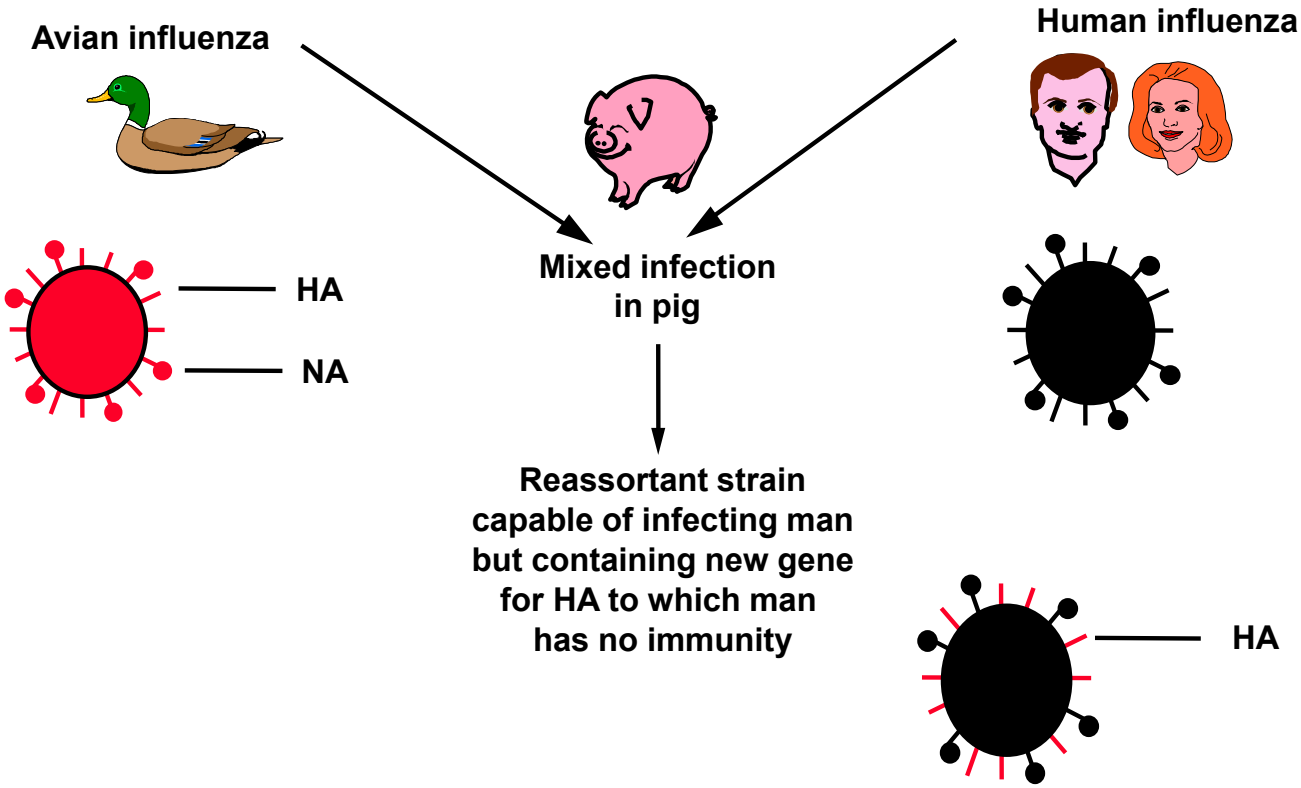
Stage 1 (pre-emergence): the putative pandemic pathogen **is still in its natural reservoir**. Ecological, social, or socioeconomic changes (eg, change in land use) alter the dynamics of pathogen transmission within the host or between hosts and allow the pathogen to expand within its host population, spread to a new region, or be transmitted to **another non-human host population or species**.

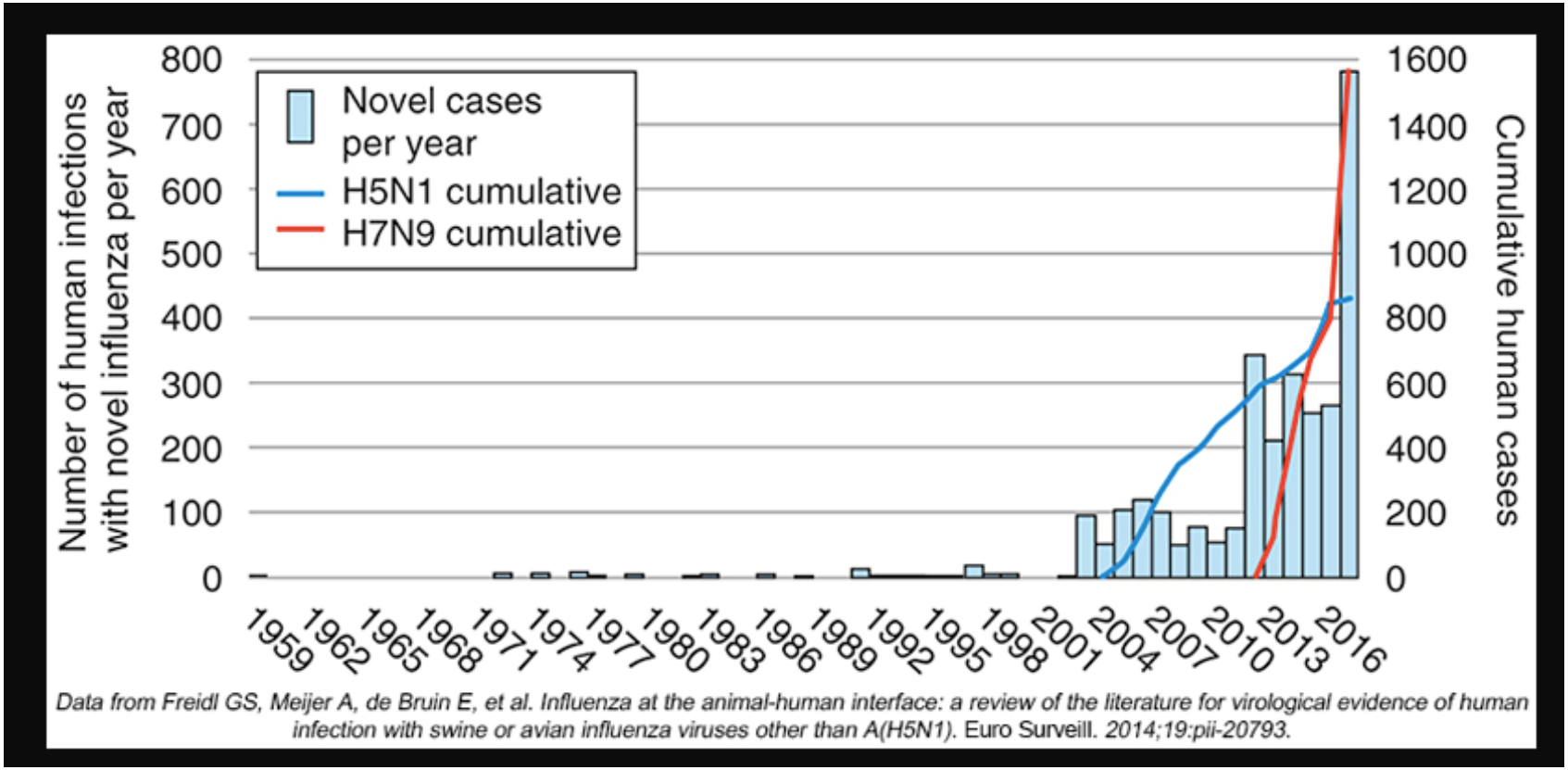



STAGE 1
STAGE 2
STAGE 3
Animal viruses with high host plasticity
Animal-to-human spillover of viruses
Amplification by human-to-human transmission
Global Spread
Vectors
Viruses


Impact: novel influenza A virus potential to cause human illness
10
9
8
7
6
5
4
3
2
1
H5N6, China 2015
H7N9, China 2017
H5N1, Vietnam 2004
H5N8, Washington 2014
H3N2v, Indiana 2011
H7N8, Indiana 2016
H7N9, Tennessee 2017
1
2
3
4
5
6
7
8
9
10
Emergence: novel influenza A virus potential to cause a human pandemic
Copyright © 2020 by Elsevier, Inc. All rights reserved.

Genetic reassortment hypothesis (influenza A virus)





Data from Freidl GS, Meijer A, de Bruin E, et al. Influenza at the animal-human interface: a review of the literature for virological evidence of human infection with swine or avian influenza viruses other than A(H5N1). Euro Surveill. *2014;19:pii-20793.*

The NEW ENGLAND JOURNAL of MEDICINE

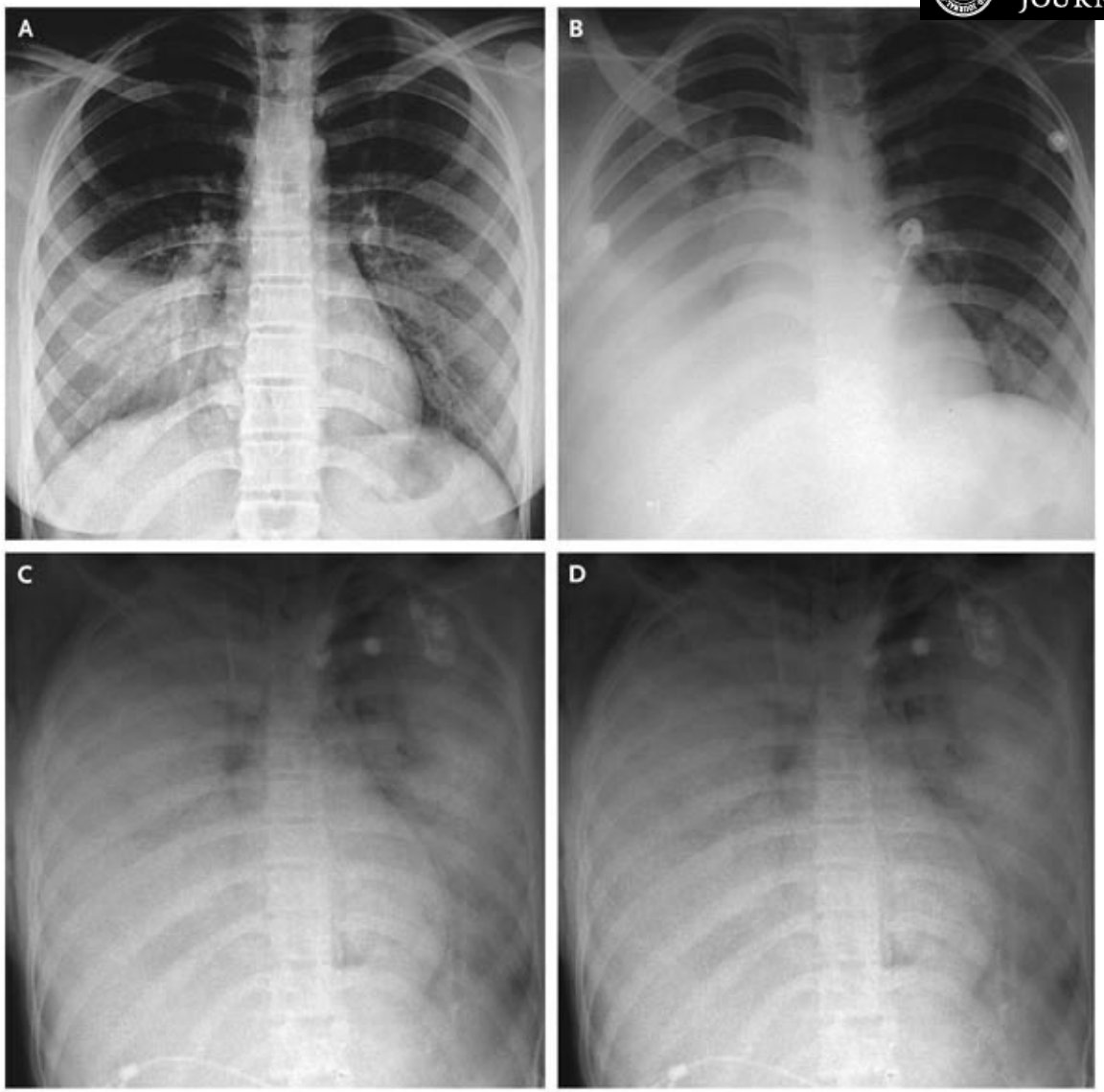
Oner AF et al. N Engl J Med 2006;355:2179-2185

Table 1. Epidemiologic Characteristics of the Patients.

Patient No.*	Age	Sex	Time from Last Known Exposure to Poultry to Onset of Illness	Time from Onset of Illness to Hospitalization	No. of Family Members without the Disease	Outcome
	yr		*days*			
1A	14	M	4	8	2	Died
2A	15	F	4	8	2	Died
3A	11	F	4	8	2	Died
4	9	F	7	5	7	Discharged
5B	14	F	5	10	6	Died
6B	5	M	5	10	6	Discharged
7	5	M	7	3	7	Discharged
8	8	F	4	1	10	Discharged

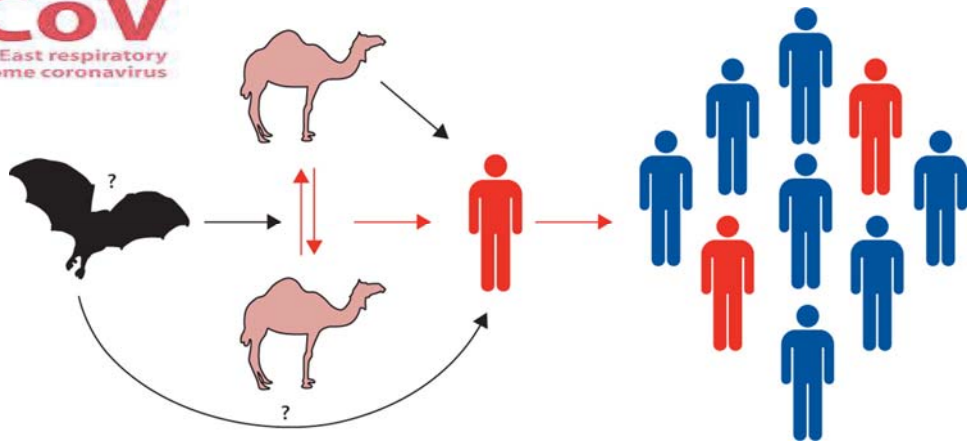
* Patients 1A, 2A, and 3A are siblings, and Patients 5B and 6B are siblings.

The NEW ENGLAND JOURNAL of MEDICINE

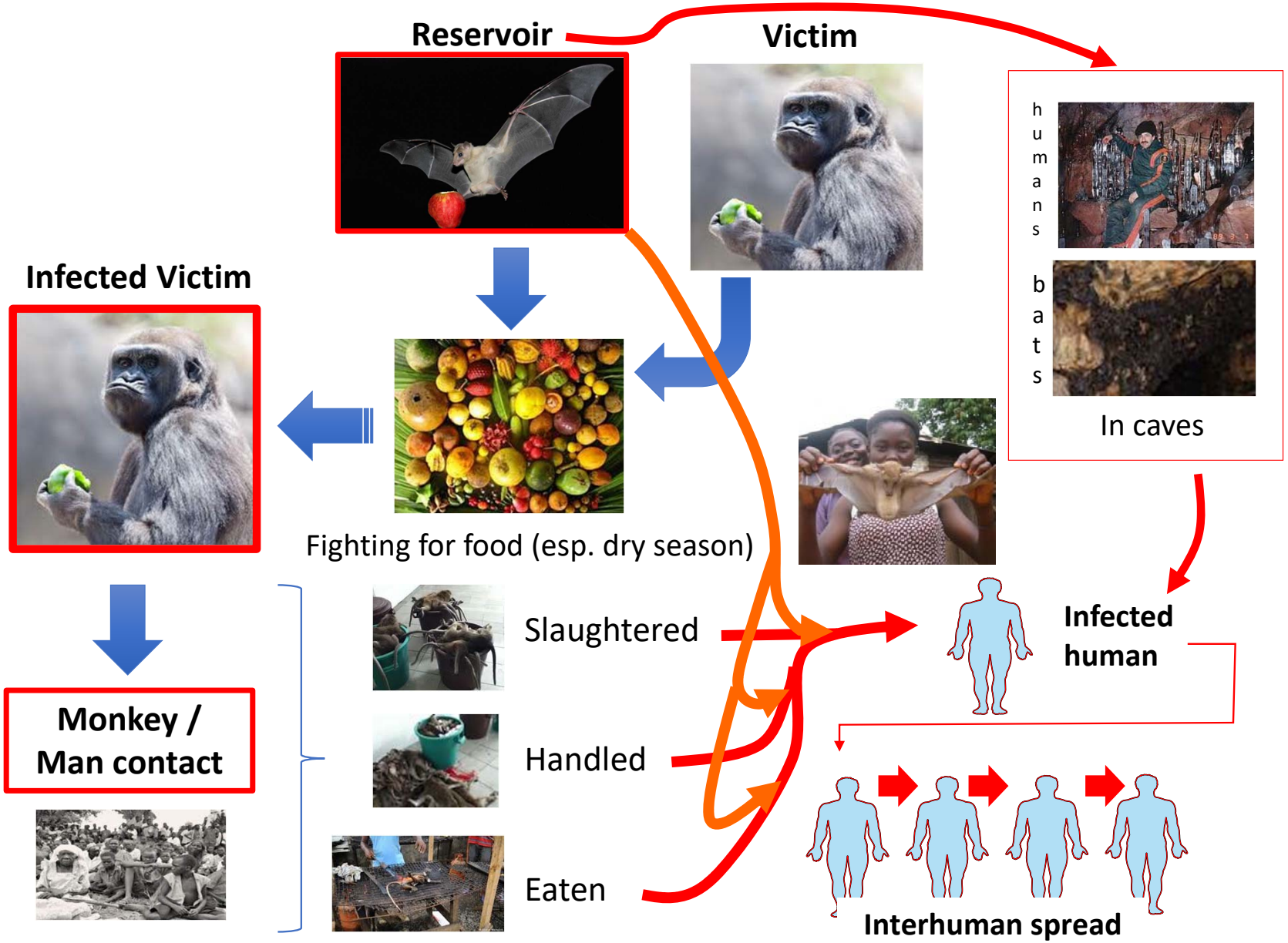


Oner AF et al. N Engl J Med 2006;355:2179-2185


MERS
-CoV
Middle East respiratory
syndrome coronavirus


?
?


Are we the reservoir of MERS CoV my dear??

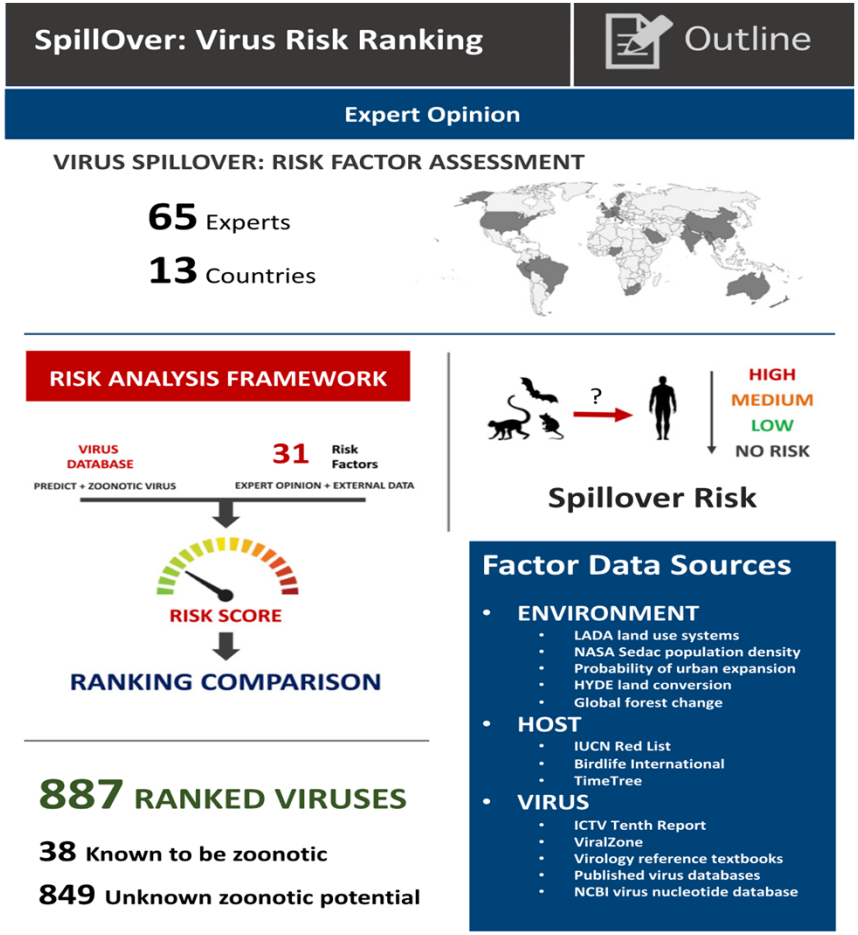

Reservoir
Victim
humans
bats
In caves
Infected Victim
Fighting for food (esp. dry season)
Monkey / Man contact
Slaughtered
Handled
Eaten
Infected human
Interhuman spread

Ranking the risk of animal-to-human spillover for newly discovered viruses

Zoë L. Grange, et al. PNAS 2021 Vol. 118 No. 15 e2002324118

Using data from testing 509,721 samples from 74,635 animals as part of a virus discovery project and public records of virus detections around the world, we ranked the spillover potential of 887 wildlife viruses.

SARS-CoV-2 is one of many potential viral threats to humans. There are just over **250 known zoonotic viruses—viruses that have previously spilled over from animals to humans** and caused disease in people.
While these viruses are of ongoing concern to human health, as repeated Ebola epidemics demonstrate, **the yet to be identified viruses pose an equal if not more serious threat to humanity**.
Approximately 1.67 million undescribed viruses are thought to exist in mammals and birds, up to half of which are estimated to have the potential to spill over into humans.



Ranking the risk of animal-to-human spillover for newly discovered viruses

Zoë L. Grange, et al. PNAS 2021 Vol. 118 No. 15 e2002324118

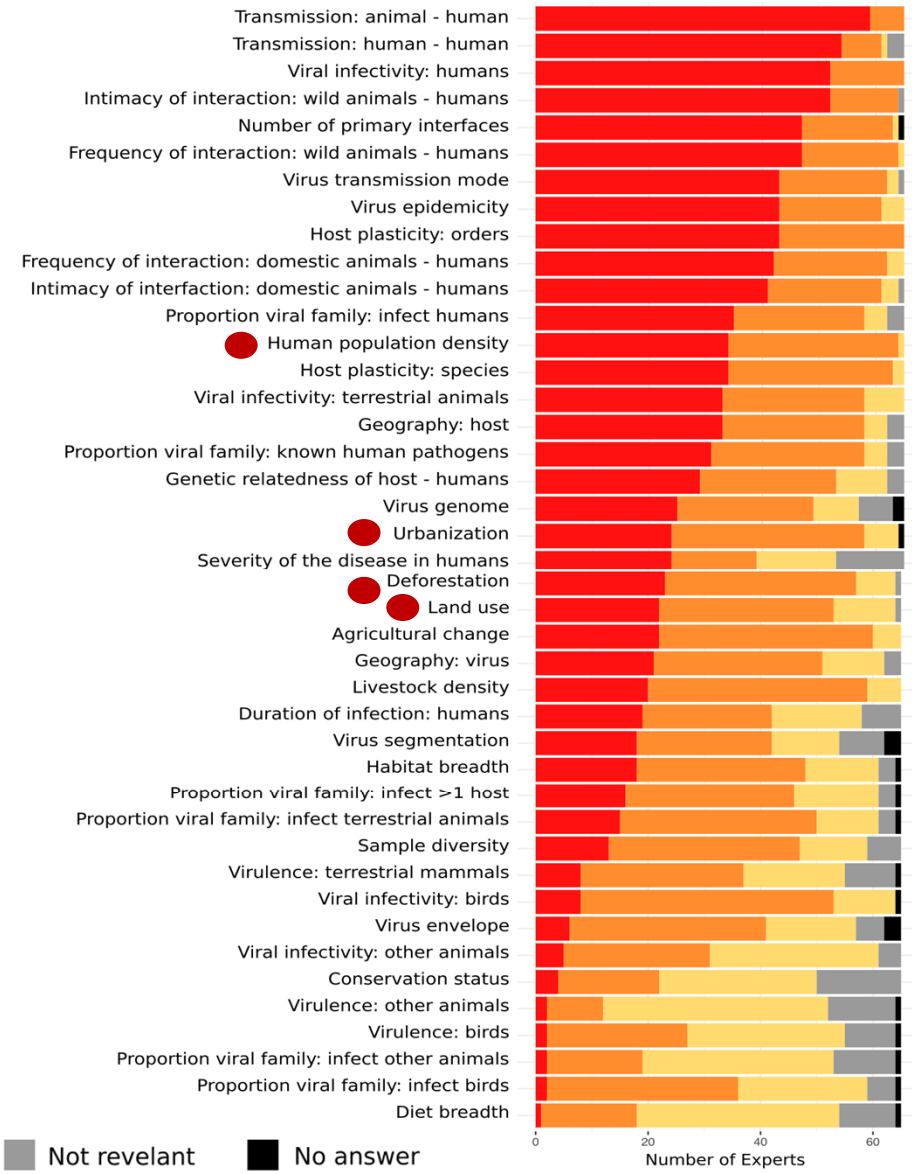
Our team sampled wildlife at high- risk human disease transmission interfaces in over 30 countries, resulting in the discovery of **hundreds of previously undetected viruses**.

The risk each virus poses to human health **is not equal**. Two viruses may be nearly identical, one zoonotic and the other not.

Several factors about the virus,

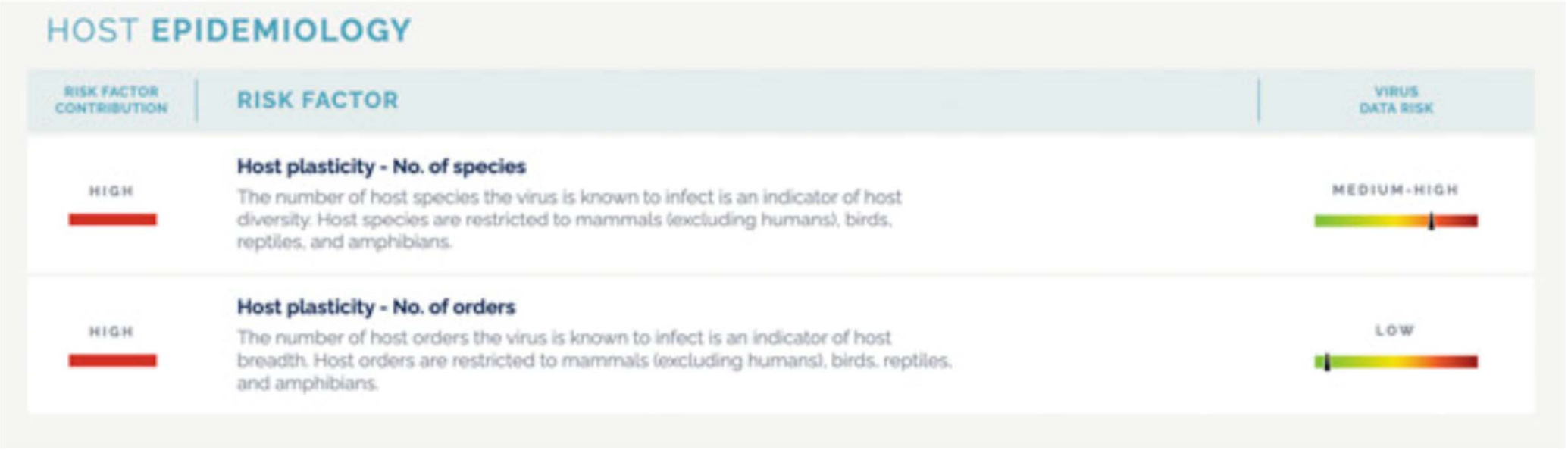
- **host** (the organism in which a virus can live and multiply),
- **environment** (the location and ecology where the host lives), and
- **related human behavior**

influence the likelihood that a virus will become zoonotic and spread within human populations



Ranking the risk of animal-to-human spillover for newly discovered viruses

Zoë L. Grange, et al. PNAS 2021 Vol. 118 No. 15 e2002324118

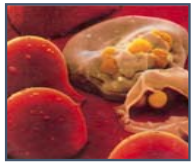


Ranking the risk of animal-to-human spillover for newly discovered viruses

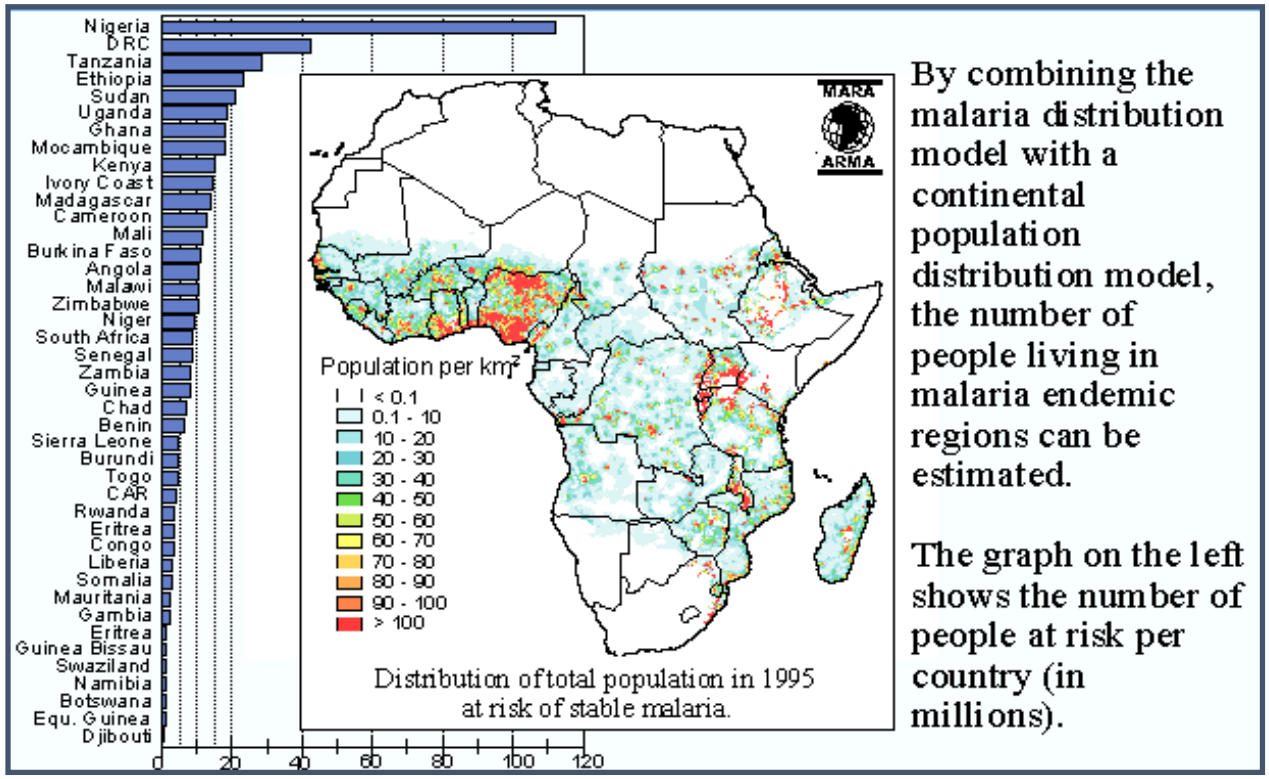
Zoë L. Grange, et al. PNAS 2021 Vol. 118 No. 15 e2002324118

ENVIRONMENTAL **FACTORS**

RISK FACTOR CONTRIBUTION	RISK FACTOR	VIRUS DATA RISK
MEDIUM	**Land use in host ecosystem** Primary land use system (urban, forest, crops etc.) where the virus has been detected in a host species.	HIGH
MEDIUM	**Livestock density in host ecosystem** Density of livestock animals where the virus has been detected in a host species.	HIGH
HIGH	**Human population density in host ecosystem** Density of people per sqKm where the virus has been detected in a host species.	HIGH
MEDIUM	**Deforestation in host ecosystem** Presence of deforestation where the virus has been detected in a host species. Deforestation is defined as >20% canopy cover change between 2000 and 2017.	HIGH
MEDIUM	**Urbanization in host ecosystem** Presence of urbanization where the virus has been detected in a host species. Urbanization is defined as a location having a >75% probability of urban expansion.	HIGH
MEDIUM	**Agricultural system change in host ecosystem** Presence of agricultural change where the virus has been detected in a host species. Agricultural system change is defined as an increase in pasture/cropland areas between 1970 and 2005.	HIGH



Il 90% dei casi è nell'Africa sub sahariana, dove la malaria è la prima causa di morte nei soggetti in età pediatrica e negli adolescenti.



By combining the malaria distribution model with a continental population distribution model, the number of people living in malaria endemic regions can be estimated.

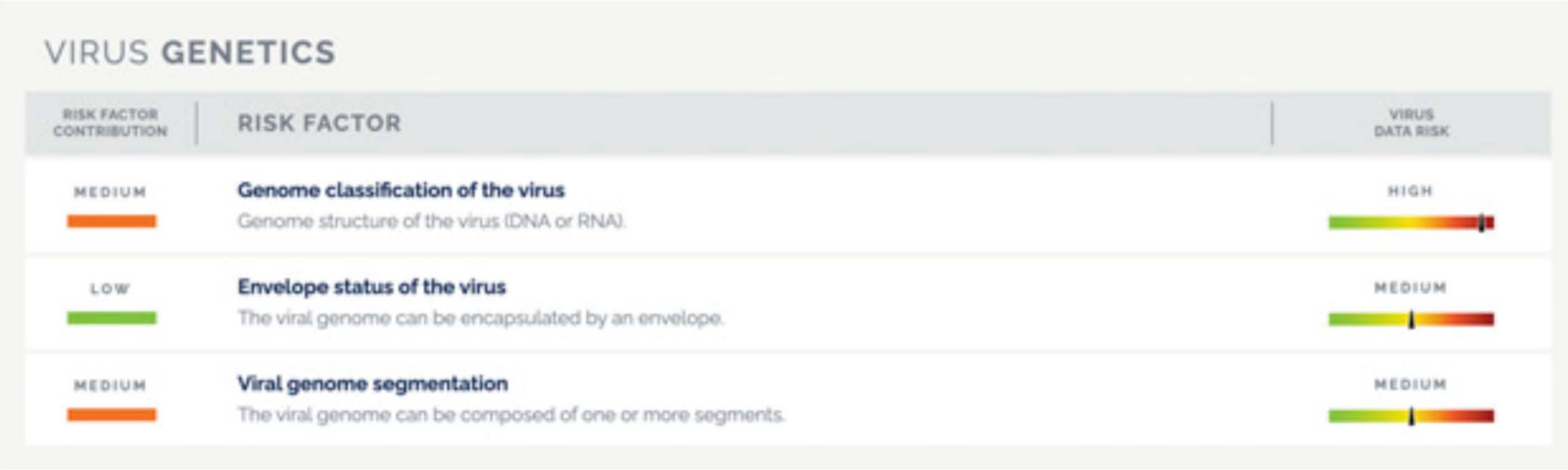
The graph on the left shows the number of people at risk per country (in millions).

Deforestation in Africa


2014 EBOLA OUTBREAK
Bamako
Mali
GUINEA
Dabola
Conakry
Freetown
SIERRA LEONE
Atlantic
Ocean
Monrovia
LIBERIA

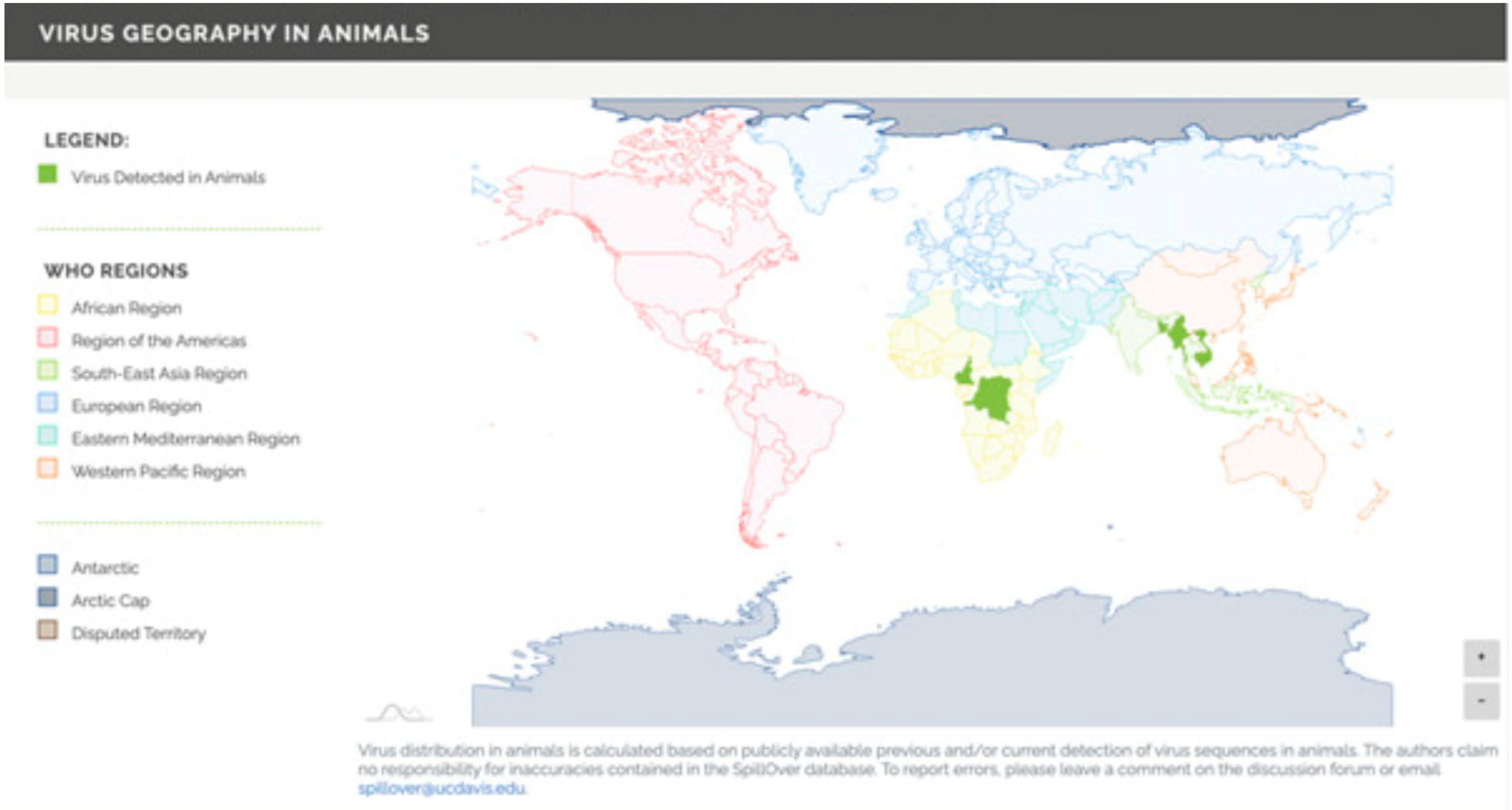
Ranking the risk of animal-to-human spillover for newly discovered viruses

Zoë L. Grange, et al. PNAS 2021 Vol. 118 No. 15 e2002324118



Ranking the risk of animal-to-human spillover for newly discovered viruses

Zoë L. Grange, et al. PNAS 2021 Vol. 118 No. 15 e2002324118



Ranking the risk of animal-to-human spillover for newly discovered viruses

Zoë L. Grange, et al. PNAS 2021 Vol. 118 No. 15 e2002324118

Selection of Risk Factors.

$$Risk\ Factor\ Influence(0-3) = \frac{\sum(Spillover\ Risk\ (0-3) \times Level\ of\ Expertise\ (1-16))i}{\sum Level\ of\ Expertise\ (1-16)i}.$$

A Database of Wildlife-Origin Viruses

Virus Risk Assessment

$$Virus\ Data\ Risk = \frac{Risk\ Factor\ Influence \times Risk\text{-}Level\ Score}{3} = \frac{(2.175) \times (5)}{3} = 3.624.$$

Development of the SpillOver: Viral Risk Ranking Tool.

A virus spillover risk ranking comparison of the top 50 wildlife viruses in the spillover database, including viruses known to be zoonotic and those with unknown zoonotic potential, which were detected in a broad-scale virus discovery effort in Africa and Southeast and South Asia from 2009 to 2019

		Virus			
Risk ranking position	Risk ranking score*	Virus	Genus	Family	Detection in hosts
1	91.18	Lassa virus†	*Mammarenavirus*	Arenaviridae	Regional
2	87.14	SARS-CoV-2†	*Betacoronavirus*	Coronaviridae	Semiglobal
3	87.00	Ebola virus†	*Ebolavirus*	Filoviridae	Regional
4	86.49	Seoul virus†	*Hantavirus*	Bunyaviridae	Global
5	86.49	Nipah virus†	*Henipavirus*	Paramyxoviridae	Semiglobal
6	86.38	Hepatitis E virus†	*Orthohepevirus*	Hepeviridae	Global
7	85.70	Marburg virus†	*Marburgvirus*	Filoviridae	Regional
8	85.04	SARS-CoV†	*Betacoronavirus*	Coronaviridae	National—large
9	84.78	Simian immunodeficiency virus†	*Lentivirus*	Retroviridae	Semiglobal
10	84.69	Rabies virus†	*Lyssavirus*	Rhabdoviridae	Global
11	84.61	Lymphocytic choriomeningitis virus†	*Mammarenavirus*	Arenaviridae	Global
12	83.99	Simian foamy virus†	*Spumavirus*	Retroviridae	Global
13	80.98	Coronavirus 229E (bat strain)	*Alphacoronavirus*	Coronaviridae	Regional
14	80.01	Rousettus bat coronavirus HKU9	*Betacoronavirus*	Coronaviridae	Global
15	79.71	SARS-related betacoronavirus Rp3	*Betacoronavirus*	Coronaviridae	National—large
16	78.97	European bat lyssavirus 1†	*Lyssavirus*	Rhabdoviridae	Regional
17	78.81	Andes virus†	*Hantavirus*	Bunyaviridae	National—small
18	78.63	Murine coronavirus	*Betacoronavirus*	Coronaviridae	Global
19	78.57	Puumala virus†	*Hantavirus*	Bunyaviridae	Regional
20	78.03	Chaerephon bat coronavirus/Kenya/KY22/2006	*Alphacoronavirus*	Coronaviridae	Regional
21	77.32	Coronavirus PREDICT_CoV-35	*Alphacoronavirus*	Coronaviridae	Semiglobal
22	77.21	Borna disease virus†	*Bornavirus*	Bornaviridae	Semiglobal
23	76.42	Longquan Aa mouse coronavirus	*Betacoronavirus*	Coronaviridae	Semiglobal
24	76.14	Monkeypox virus†	*Orthopoxvirus*	Poxviridae	Semiglobal
25	75.78	European bat lyssavirus 2†	*Lyssavirus*	Rhabdoviridae	Regional
26	75.51	Laguna Negra virus†	*Hantavirus*	Bunyaviridae	Regional
27	75.05	Eidolon bat coronavirus/Kenya/KY24/2006	*Betacoronavirus*	Coronaviridae	Regional
28	74.65	Cowpox virus†	*Orthopoxvirus*	Poxviridae	Regional
29	74.64	Coronavirus PREDICT CoV-24	*Betacoronavirus*	Coronaviridae	Semiglobal
30	74.60	Macaque Foamy virus	*Spumavirus*	Retroviridae	Global
31	73.80	Rodent coronavirus	*Alphacoronavirus*	Coronaviridae	Regional
32	73.36	Sin Nombre virus†	*Hantavirus*	Bunyaviridae	Regional
33	73.23	Human mastadenovirus G	*Mastadenovirus*	Adenoviridae	Semiglobal
34	72.94	Coronavirus PREDICT CoV-22	*Betacoronavirus*	Coronaviridae	Semiglobal
35	72.91	Reston virus†	*Ebolavirus*	Filoviridae	Semiglobal
36	72.49	Bombali virus	*Ebolavirus*	Filoviridae	Regional
37	72.46	Coronavirus HKU1	*Betacoronavirus*	Coronaviridae	National—small
38	72.17	Kenya bat coronavirus/BtKY56/BtKY55	*Betacoronavirus*	Coronaviridae	Regional
39	72.08	Paramyxovirus PREDICT PMV-10	Unassigned	Paramyxoviridae	Regional
40	71.73	Bat coronavirus 1	*Alphacoronavirus*	Coronaviridae	Semiglobal
41	71.64	BtVs-BetaCoV/SC2013	*Betacoronavirus*	Coronaviridae	National—large
42	71.54	Australian bat lyssavirus†	*Lyssavirus*	Rhabdoviridae	National—large
43	71.37	Bat coronavirus Hipposideros/GhanaKwam/20/	*Betacoronavirus*	Coronaviridae	Regional
44	71.24	Coronavirus PREDICT CoV-68	*Betacoronavirus*	Coronaviridae	Regional
45	71.14	Mamastrovirus 1	*Mamastrovirus*	Astroviridae	Semiglobal
46	71.13	Dobrava-Belgrade virus†	*Hantavirus*	Bunyaviridae	Regional
47	71.06	Scotophilus bat coronavirus 512	*Alphacoronavirus*	Coronaviridae	Regional
48	80.00	Paramyxovirus PREDICT PMV-13	Unassigned	Paramyxoviridae	Semiglobal
49	70.98	Paramyxovirus PREDICT PMV-15	Unassigned	Paramyxoviridae	Regional
50	70.96	Coronavirus PREDICT CoV-16	*Betacoronavirus*	Coronaviridae	Regional

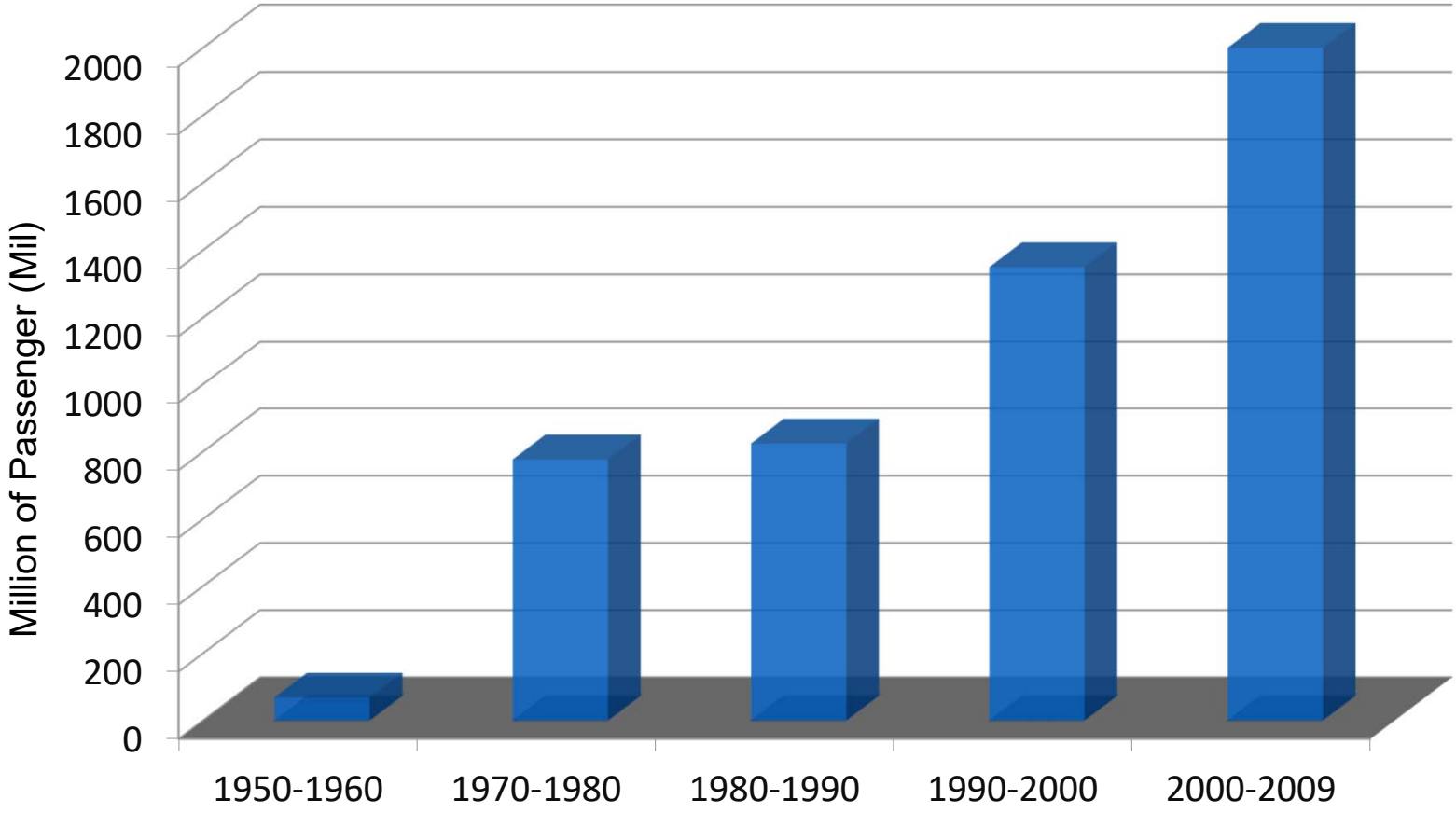
Why Have we Seen Such a Dramatic Increase in Epidemic Infectious Diseases?

Major Drivers

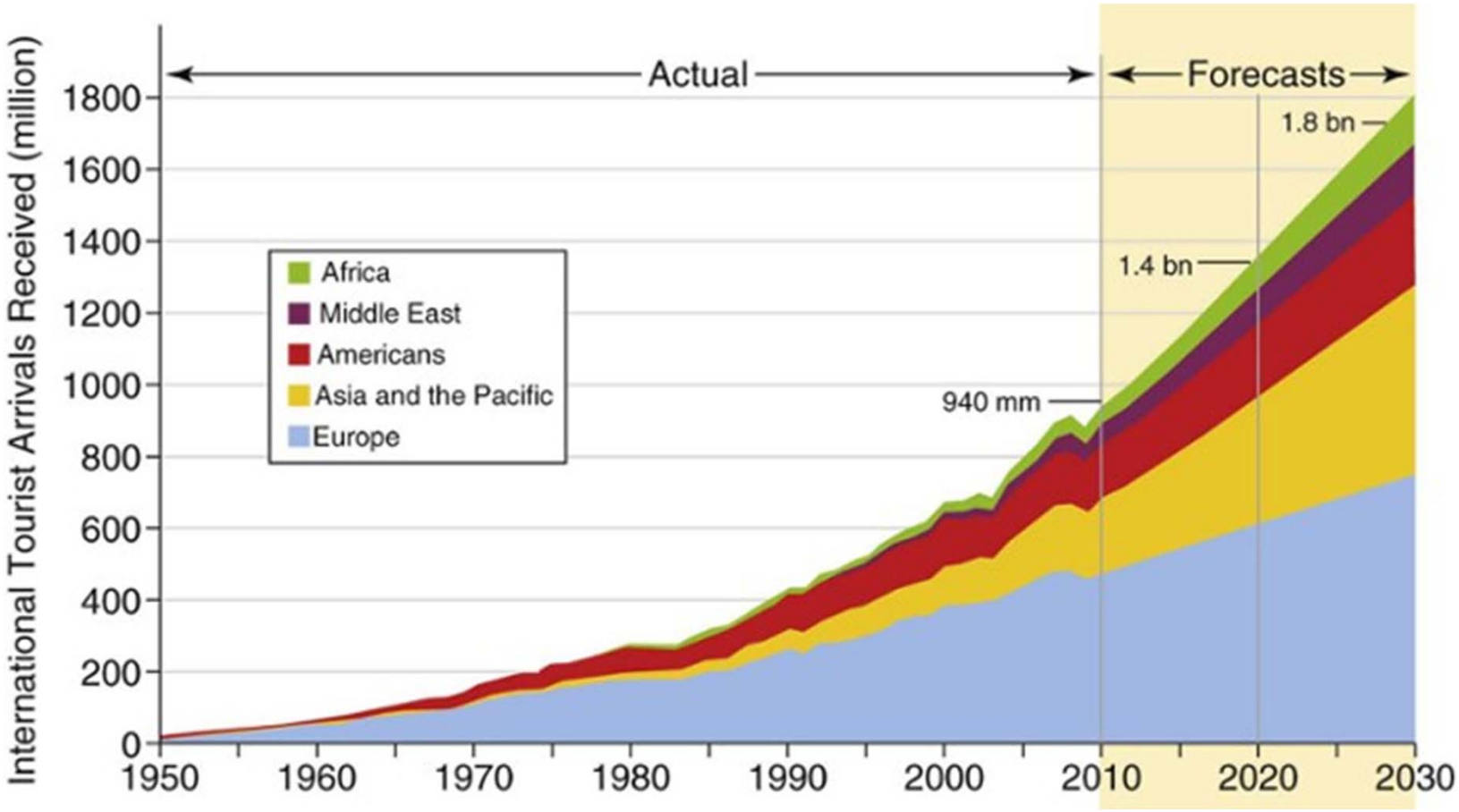
- Demographic Changes (Pop Growth)
  - Environmental Change
    - Uncontrolled Urbanization
    - Agricultural/Land Use Practices
    - Deforestation
  - Animal Husbandry
- Modern Transportation (Globalization)
  - Increased Movement of People, Animals, Commodities
- Lack of Public Health Infrastructure

The global air network

Average annual number of global airline passengers by decade, 1950-2010



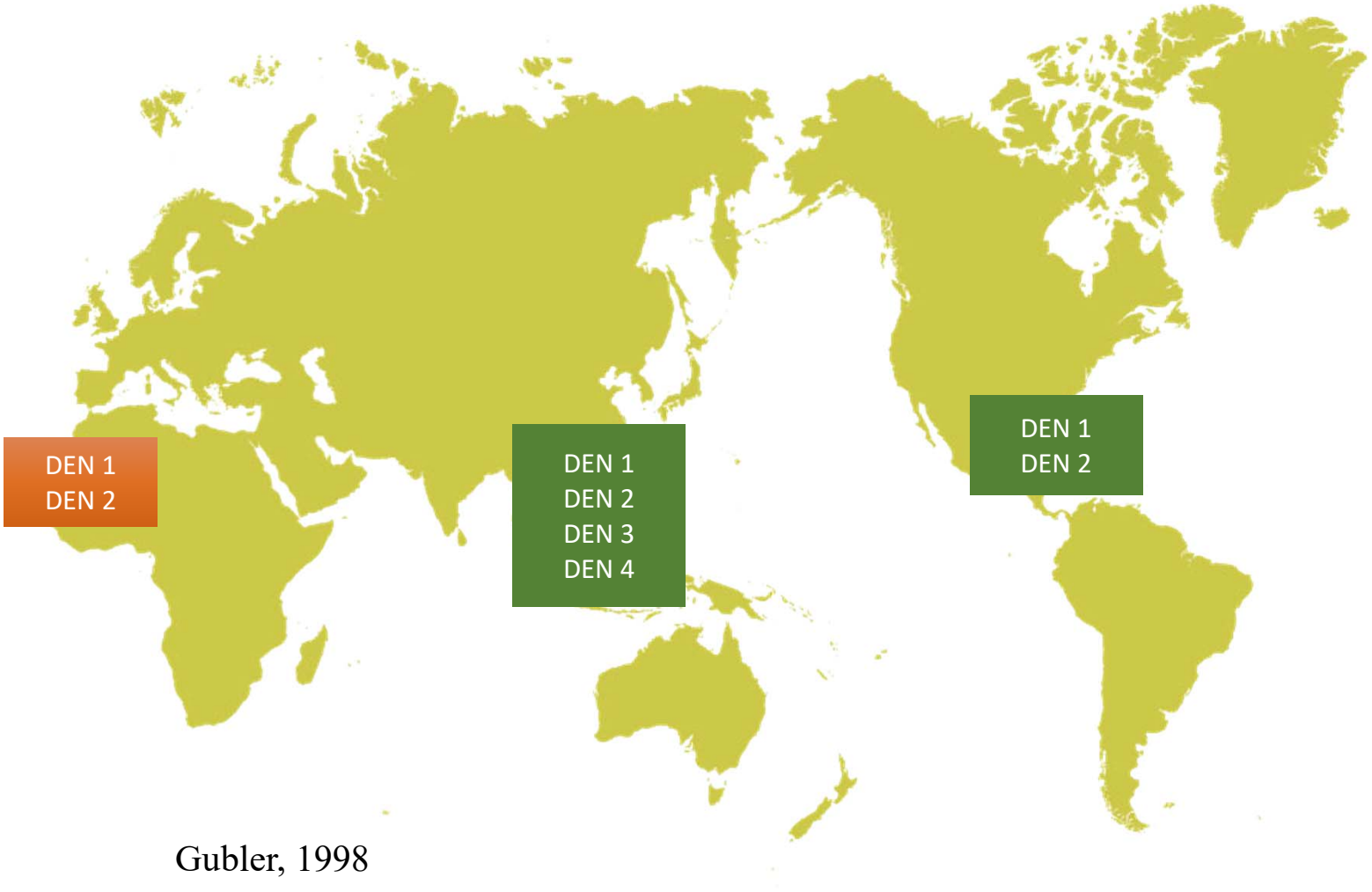
IATA 2010



International tourist arrivals, actual trends and forecast, 1950-2030

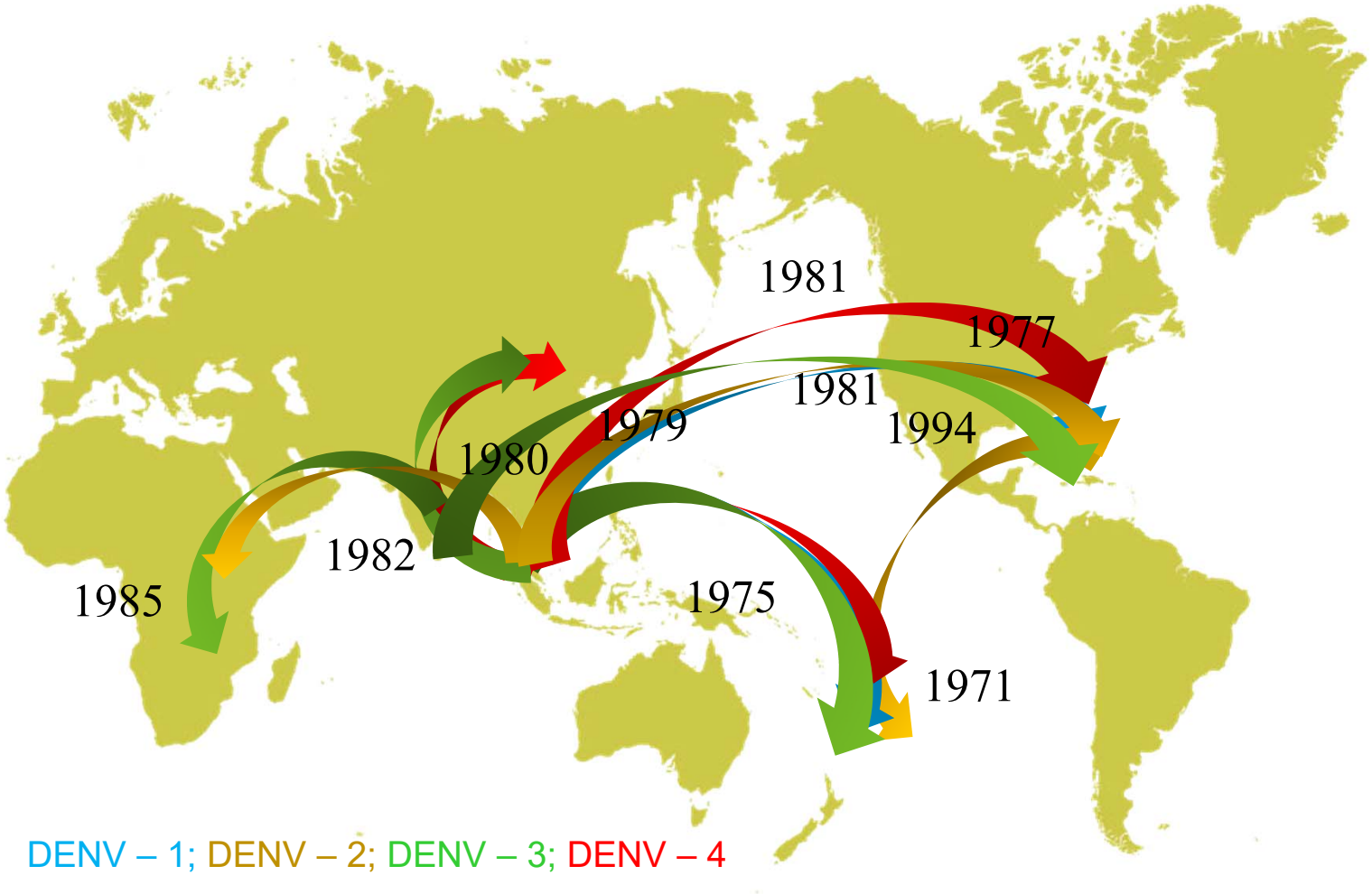
Commercial Air Traffic Over a 24 Hour Period

Global distribution of dengue virus serotypes, **1970**

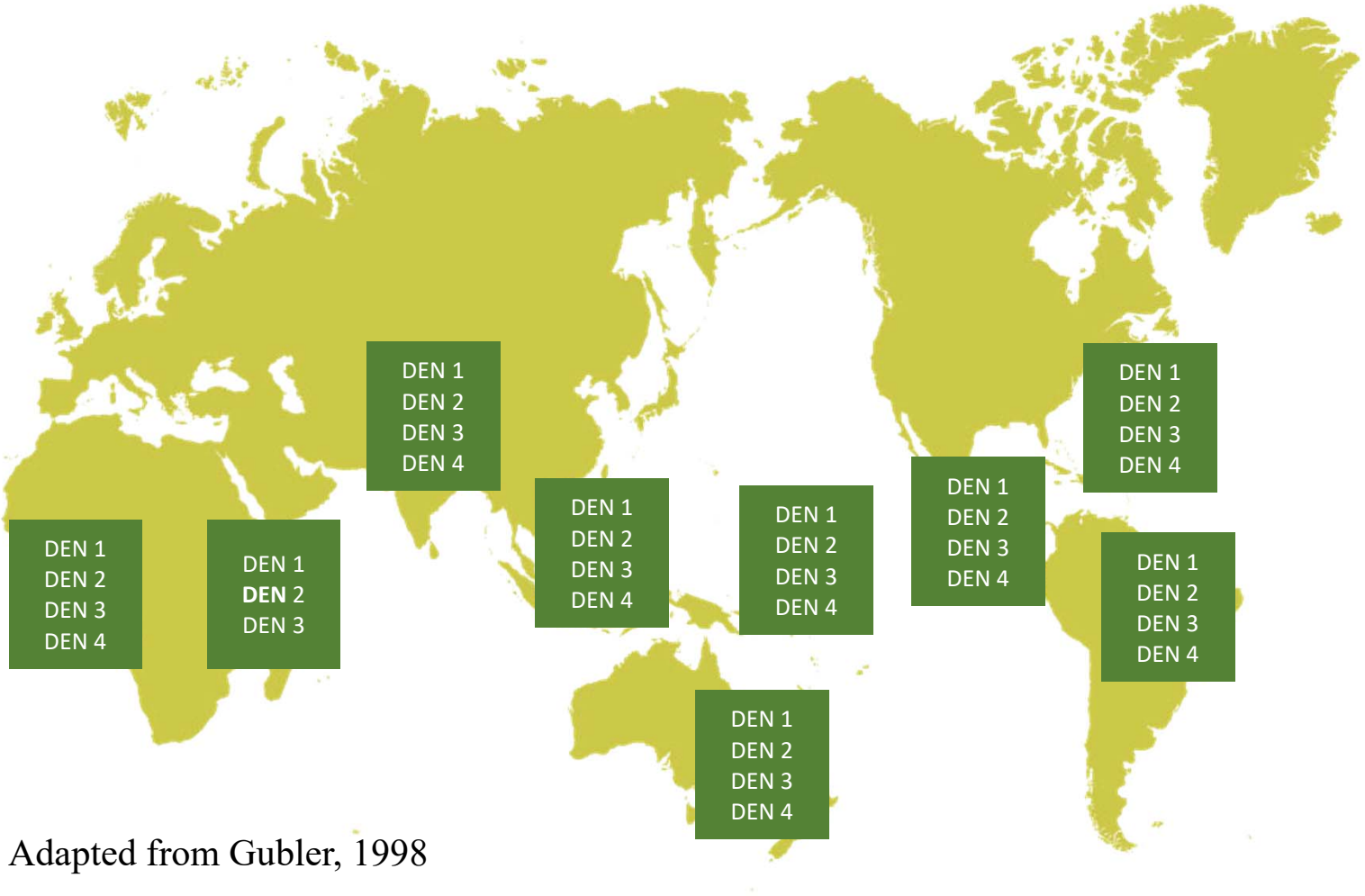


Gubler, 1998

Global distribution of dengue virus serotypes, 1970-2000

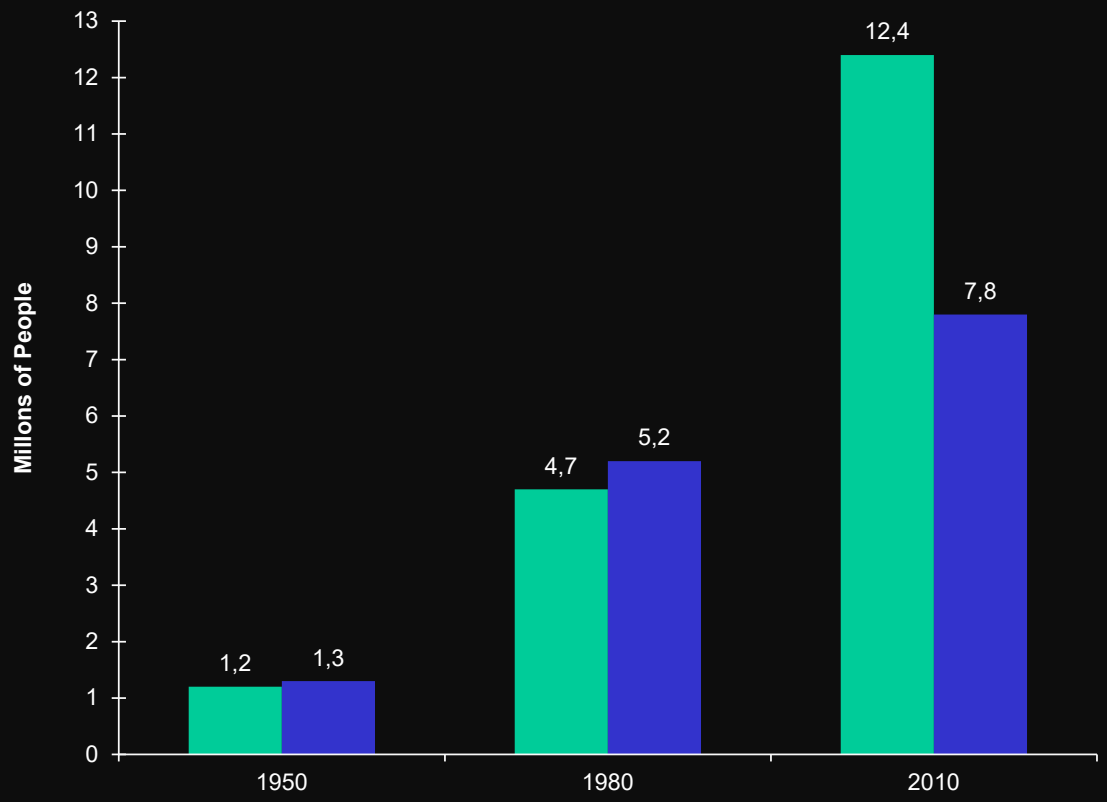


Global distribution of dengue virus serotypes, 2012

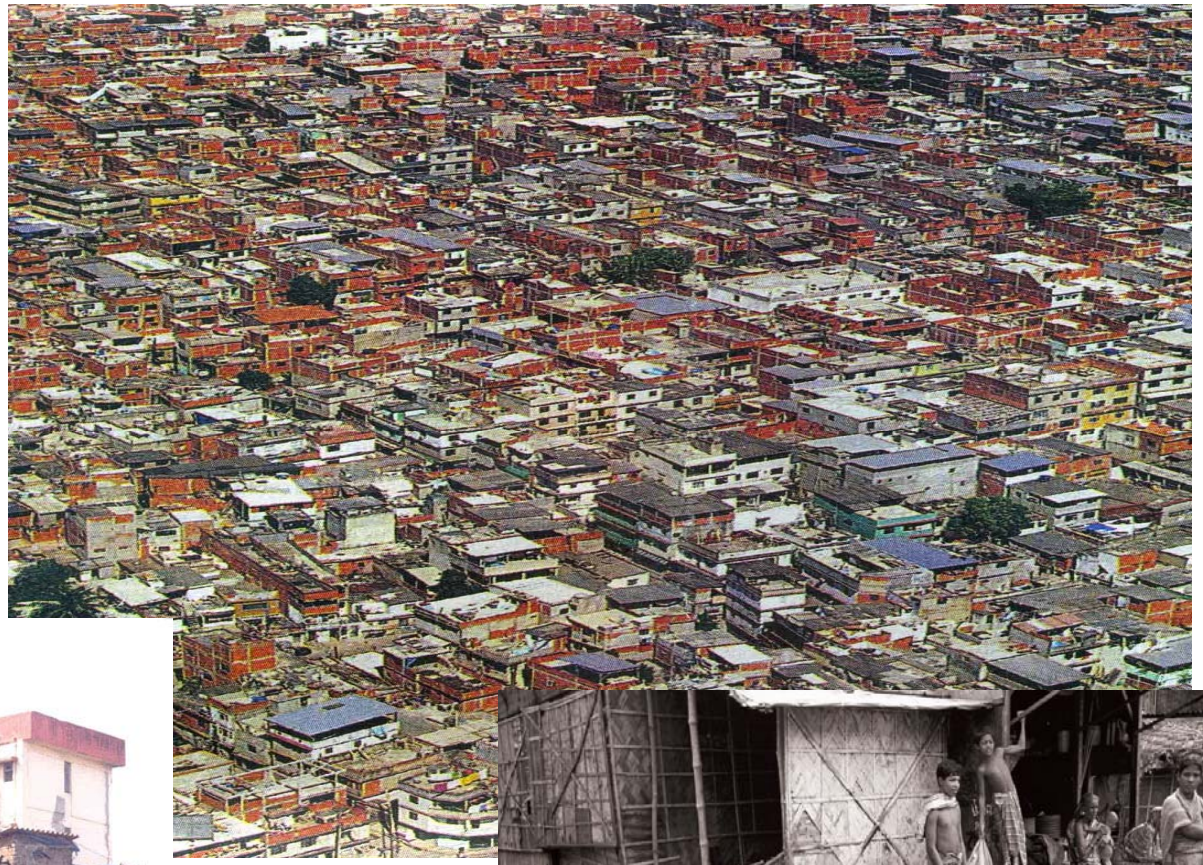


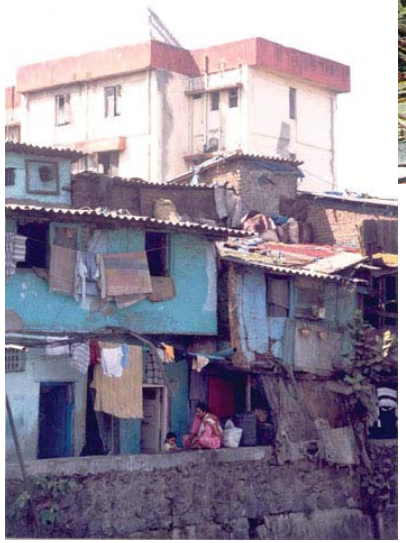
Adapted from Gubler, 1998

Urban Growth in Asian(1) and American(2) Cities, 1950-2010



1. Mean population of Dhaka, Bangkok, Jakarta, Manila and Saigon.
2. Mean population of Rio de Janeiro, Sao Paulo, San Juan, Caracas and Guayaquil.



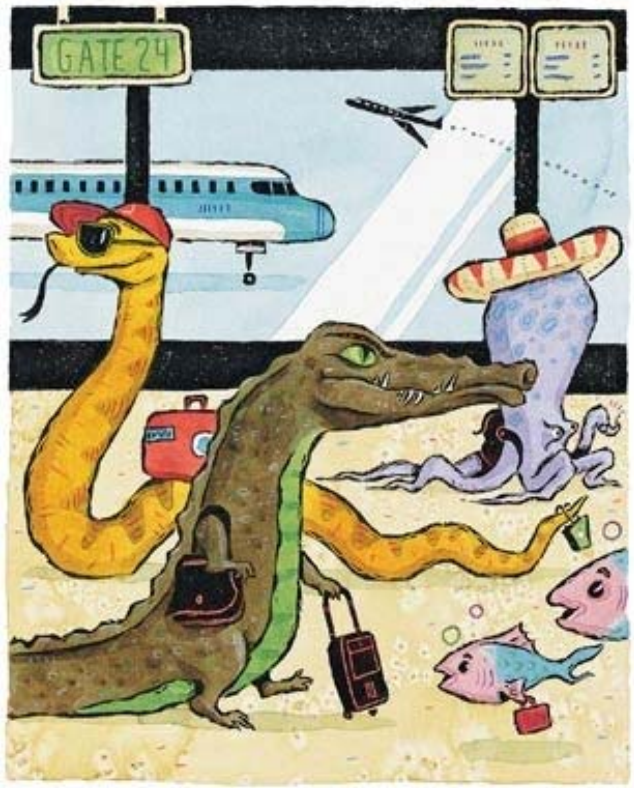


Exotic Mosquito Species Recently Introduced and Established in the US

- *Aedes* (*Stegomyia*) *albopictus*
- *Ochlerotatus* (*Aedes Finlaya*) *togoi*
- *Ochlerotatus* (*Aedes Finlaya*) *japonicus*
- *Aedes bahamensis*
- *Culex biscayensis*

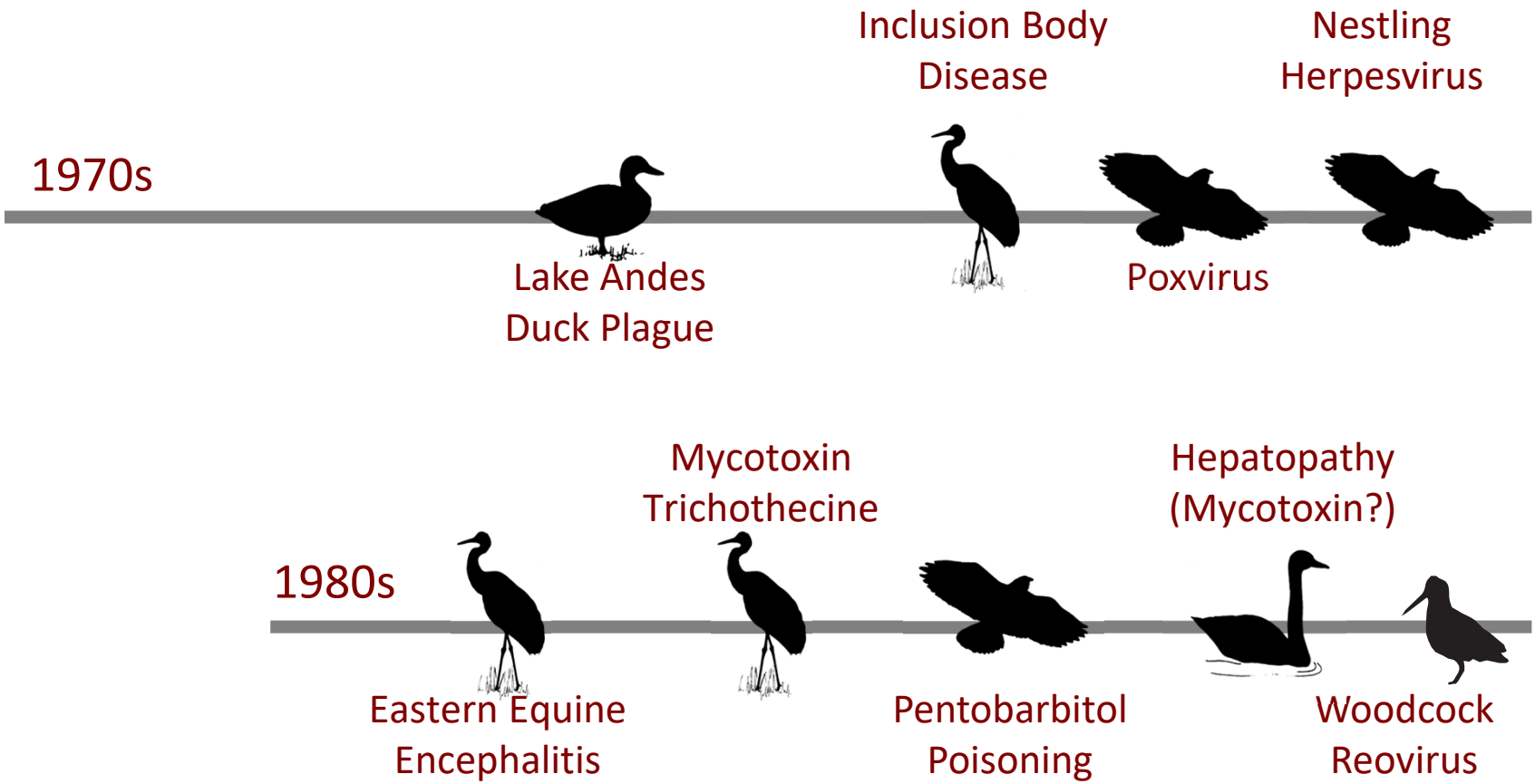
Live Animal Importation into the USA - 2002

- 47,000 mammals
  - 28 species of rodents
- 379,000 birds
- 2 million reptiles
  - & Poisonous snakes
- 49 million amphibians
- 223 million fish

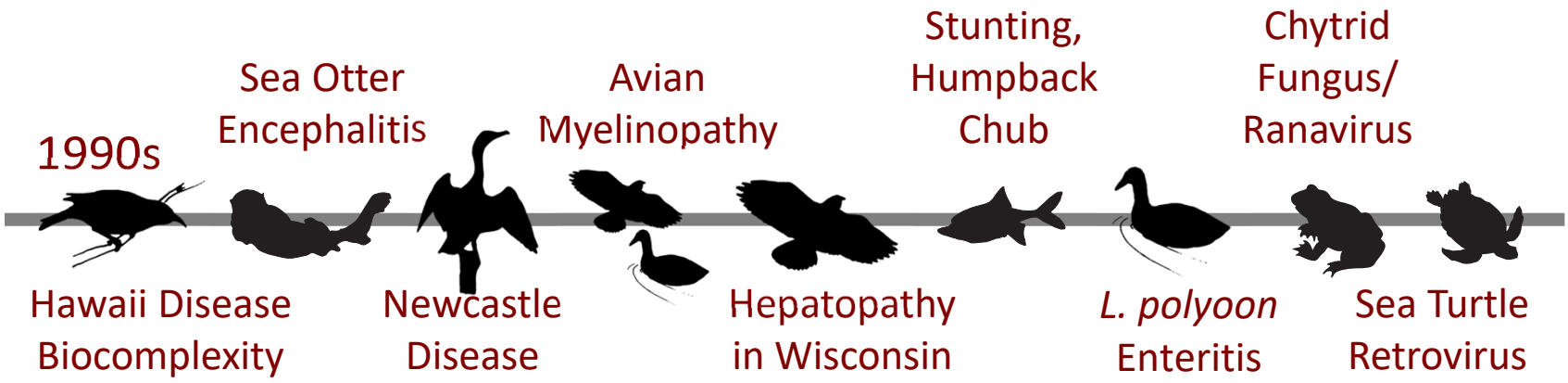


Data from U.S. Fish & Wildlife Service

Emerging Diseases Identified by NWHC



Emerging Diseases Identified by NWHC



Tuesday, Oct 16, 2012

http://www.dailymail.co.uk/science

The Armageddon virus: Why experts fear a disease that leaps from animals to humans could devastate mankind in the next five years

- **Warning comes after man died from a Sars-like virus that had previously only been seen in bats**
- **Earlier this month a man from Glasgow died from a tick-borne disease that is widespread in domestic and wild animals in Africa and Asia**

Pathogens of Tomorrow

From Whence They Will Come?

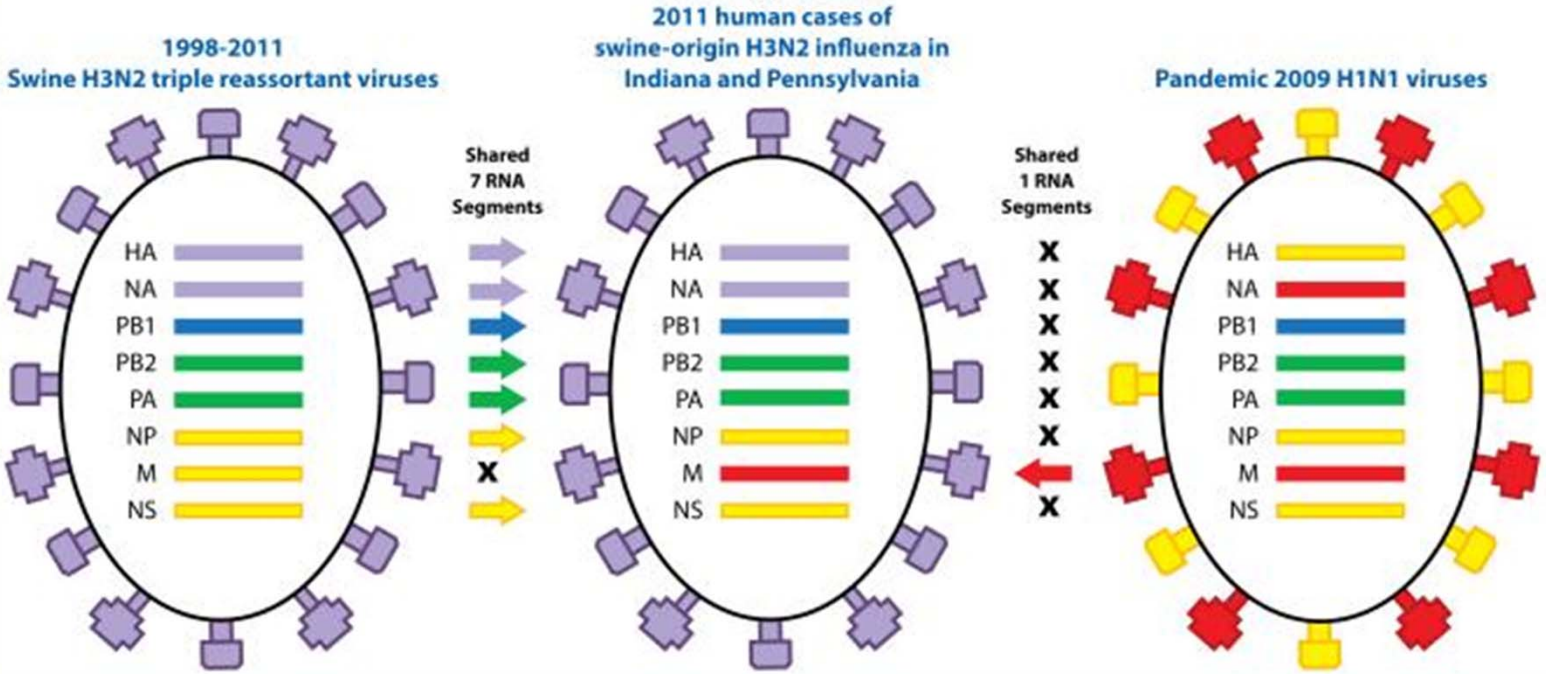
From Asia

From Animals

Mostly Viruses

The human cases of swine-origin H3N2 influenza in Indiana and Pennsylvania resulted from existing influenza viruses exchanging genetic material through a process called "reassortment"

(Influenza A viruses have 8 RNA segments: HA, NA, PB1, PB2, PA, NP, M, NS)



Hemagglutinin (HA) protein*

Neuraminidase (NA) protein*

RNA segments shared between viruses

X RNA segments not shared between viruses

Human origin HA and NA (antigenically and genetically different from those of current human H3N2 viruses)

Human PB1

Avian - North American

Classical swine - North American

Swine - Eurasian

The human cases of swine-origin H3N2 influenza in Indiana and Pennsylvania contain the "M" RNA segment from the 2009 H1N1 virus and 7 RNA segments from swine H3N2 triple-reassortant viruses.

* *The RNA segments for HA and NA determine the structure of the HA and NA proteins on the surface of influenza viruses.*

National Center for Immunization and Respiratory Diseases
Influenza Division

CDC

CS227100

TORINO:

Stefano Bonora

Francesco G. De Rosa

Andrea Calcagno

Antonio D'Avolio

Mauro Sciandra

Marco Siccardi

Cristina Tettoni

Sabrina Audagnotto

Letizia Marinaro

Jessica Cusato

Laura Trentini

Marco Simiele

Amedeo De Nicolò

Anna Lucchini

Filippo Lipani

Roberto Bertucci

Chiara Montrucchio

Chiara Alcantarini

Marino Bonasso

Ilaria De Benedetto

Stefano Biffi

Paolo Tiralongo

Micol Ferrara

Alice Trentalange

Lucio Boglione

Pino Cariti

Ilaria Motta

Silvia Corcione

Ambra Barco

Tommaso Lupia

Simone Mornese Pinna

Enrica Borgogno

Silvia Scabini

Giancarlo Orofino

Valeria Ghisetti

Valeria Avataneo

Alessandra Manca

Ilaria Zedda

Alice Ianniello

Elisa De Vivo

Luca Paglietti

Miriam Antonucci

Mattia Trunfio

Elena Salvador

Walter Rugge

Acknowledgments

THE UNIVERSITY
of LIVERPOOL

LIVERPOOL:

David Back

Saye Khoo

Andy Owen

Marco Siccardi

SSAT
ST STEPHEN'S AIDS TRUST

LONDON:

Marta Boffito

Margherita Bracchi

Nicole Pagani

ROMA:

Andrea Antinori

Adriana Ammassari

Giuseppe Ippolito