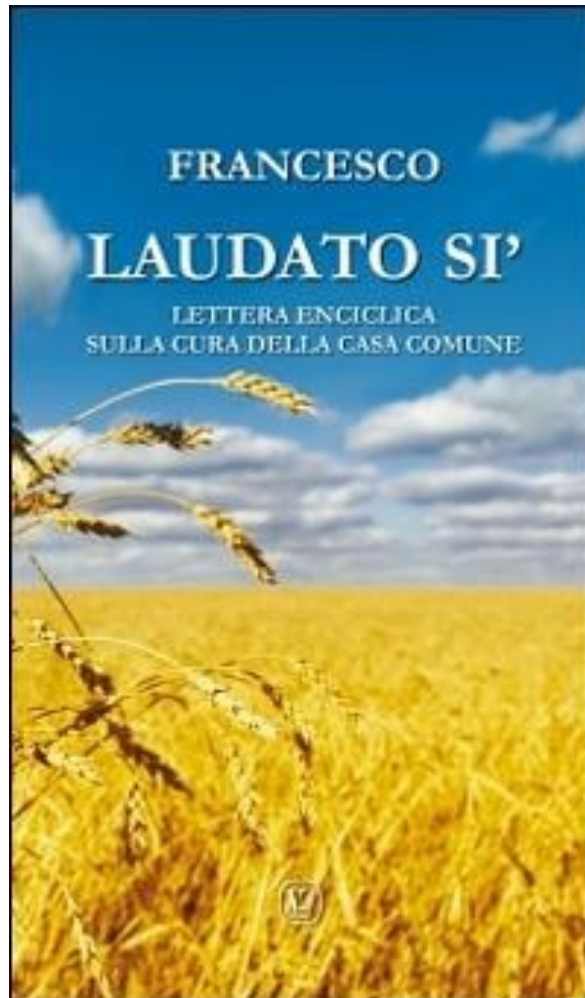






Amartya Sen Premio Nobel economia 1998

La strada della pandemia



1. Contatto Uomo Animale selvatico: salto di specie.

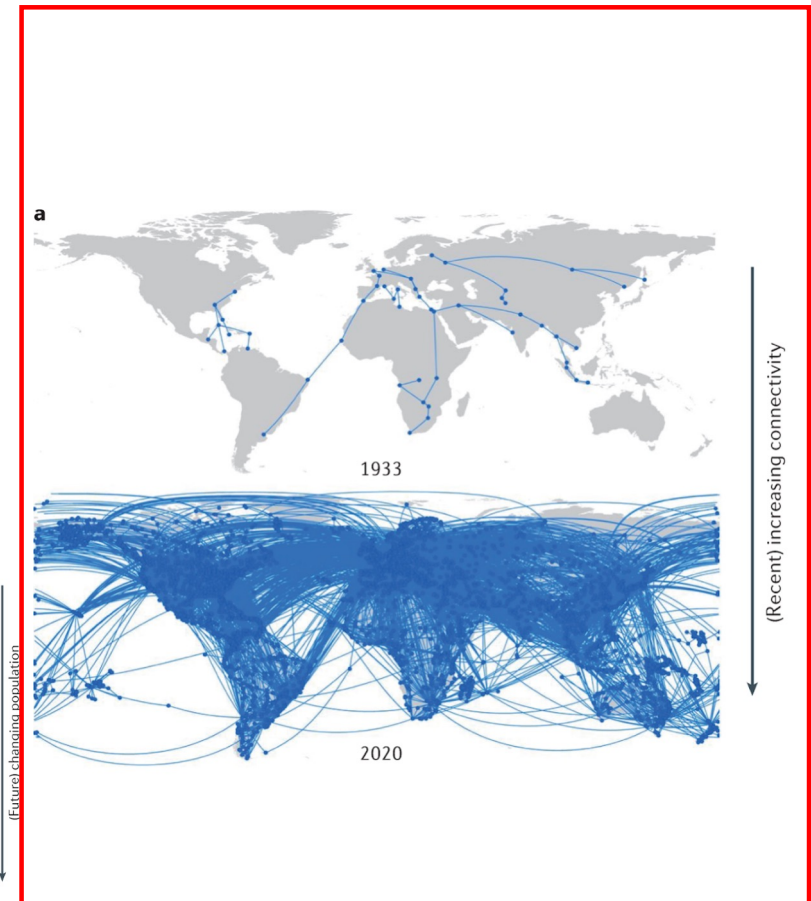
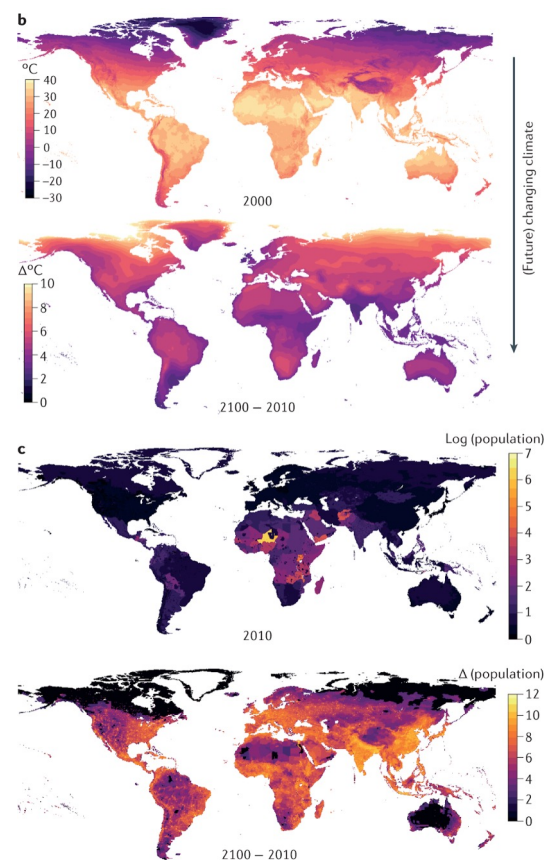
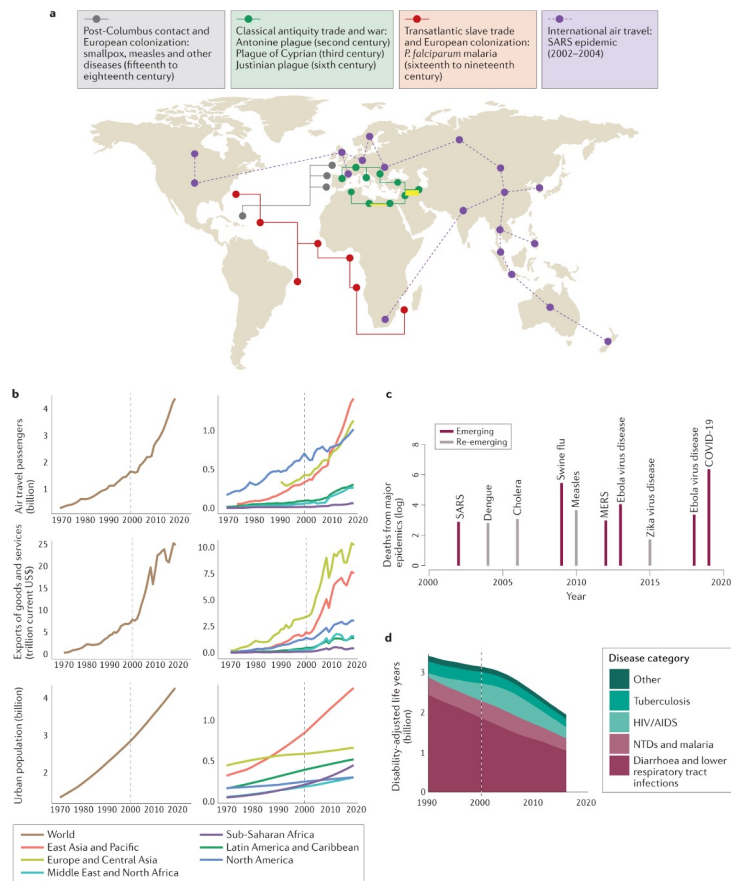
2. Globalizzazione, velocità degli spostamenti tra continenti c.d. Villaggio globale.

3. Difficoltà a riconoscere ciò che è nuovo. Ruolo dell'università e dell'informazione.

Infectious disease in an era of global change

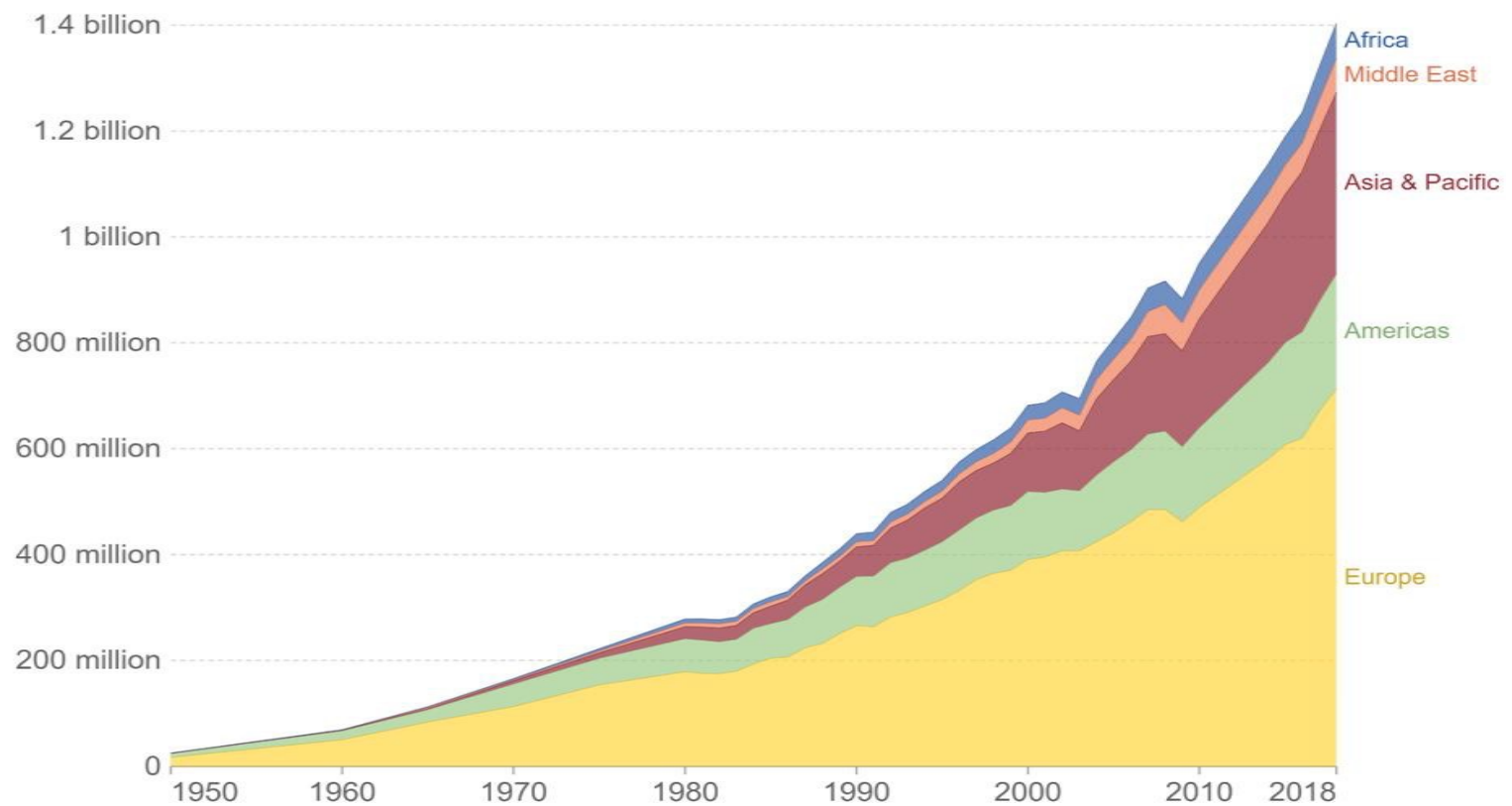
Rachel E. Baker , Ayesha S. Mahmud, Ian F. Miller, Malavika Rajeev, Fidisoa Rasambainarivo, Benjamin L. Rice, Saki Takahashi, Andrew J. Tatem, Caroline E. Wagner, Lin-Fa Wang, Amy Wesolowski & C. Jessica E. Metcalf 

Nature Reviews Microbiology **20**, 193–205 (2022) | [Cite this article](#)

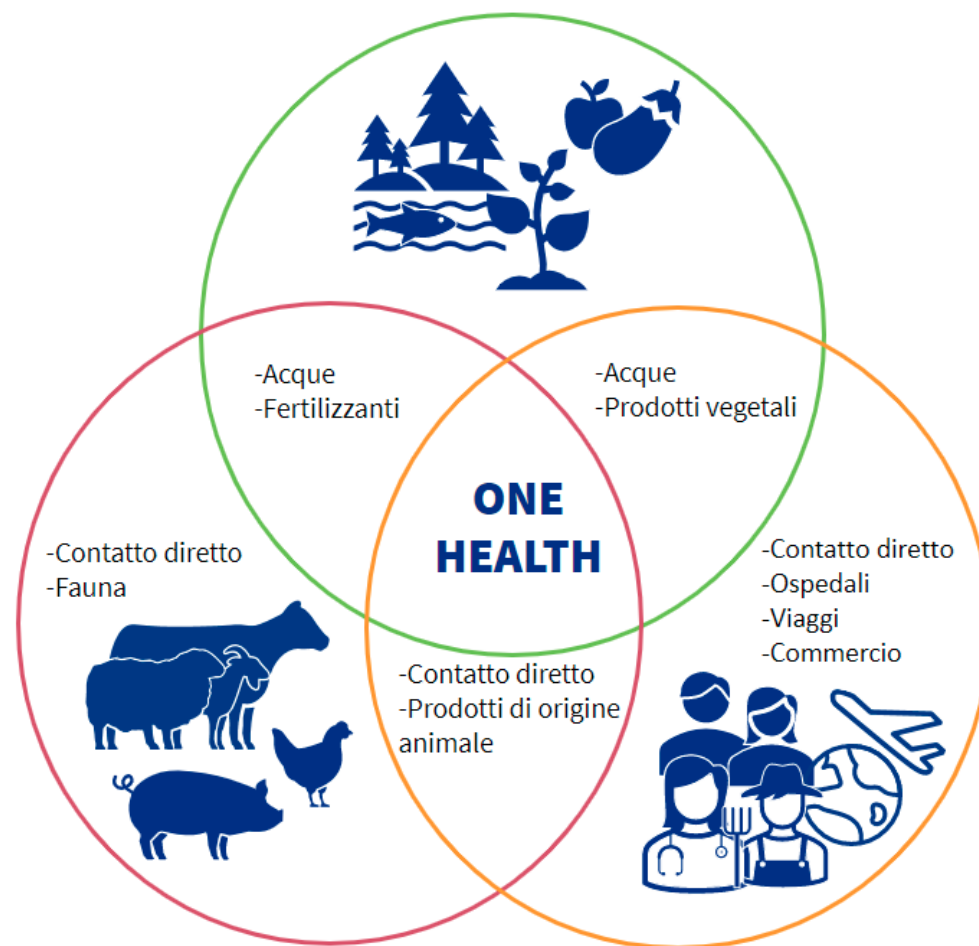


International Travels

From 1950 to 2018, 56-fold increase (1.4 billion international arrivals)



United Nations World Tourism Organization



-  Salute umana
-  Salute animale
-  Salute dell'ambiente

One Health: una sola salute per persone, animali e ambiente

- Approccio integrato alla salute.
- Riconosce che salute umana, animale e ambientale sono strettamente collegate.
- Promuove la collaborazione tra medicina, veterinaria, ecologia e altre discipline.
- Obiettivo: prevenire e affrontare le minacce sanitarie globali.  Orga... +1

Le Zoonosi

Oltre il 60% delle malattie infettive emergenti ha origine animale (zoonosi).

Trasmissione tra
animali e uomo

Circa il 60% delle
malattie emergenti
è zoonotico

Fattori di Emergenza



Urbanizzazione



Deforestazione



Commercio
globale



Cambiamento
climatico

Ruolo dell'Ambiente



QUALITÀ
DELL'ACQUA



INQUINAMENTO



BIODIVERSITÀ



ECOSISTEMI SANI
COME BARRIERA AI
PATOGENI

Contribuisce a diversi Obiettivi di Sviluppo Sostenibile (SDGs):

- Salute e benessere (SDG 3)
- Acqua pulita (SDG 6)
- Consumo responsabile (SDG 12)
- Lotta al cambiamento climatico (SDG 13)
- Vita sulla Terra (SDG 15)



FAOHome +1

- Migliore prevenzione delle epidemie.
- Riduzione dei costi sanitari. Es. Antibiotico resistenza
- Protezione dell'ambiente.
- Maggiore sicurezza alimentare.
- Sviluppo sostenibile.  FAOHome +1

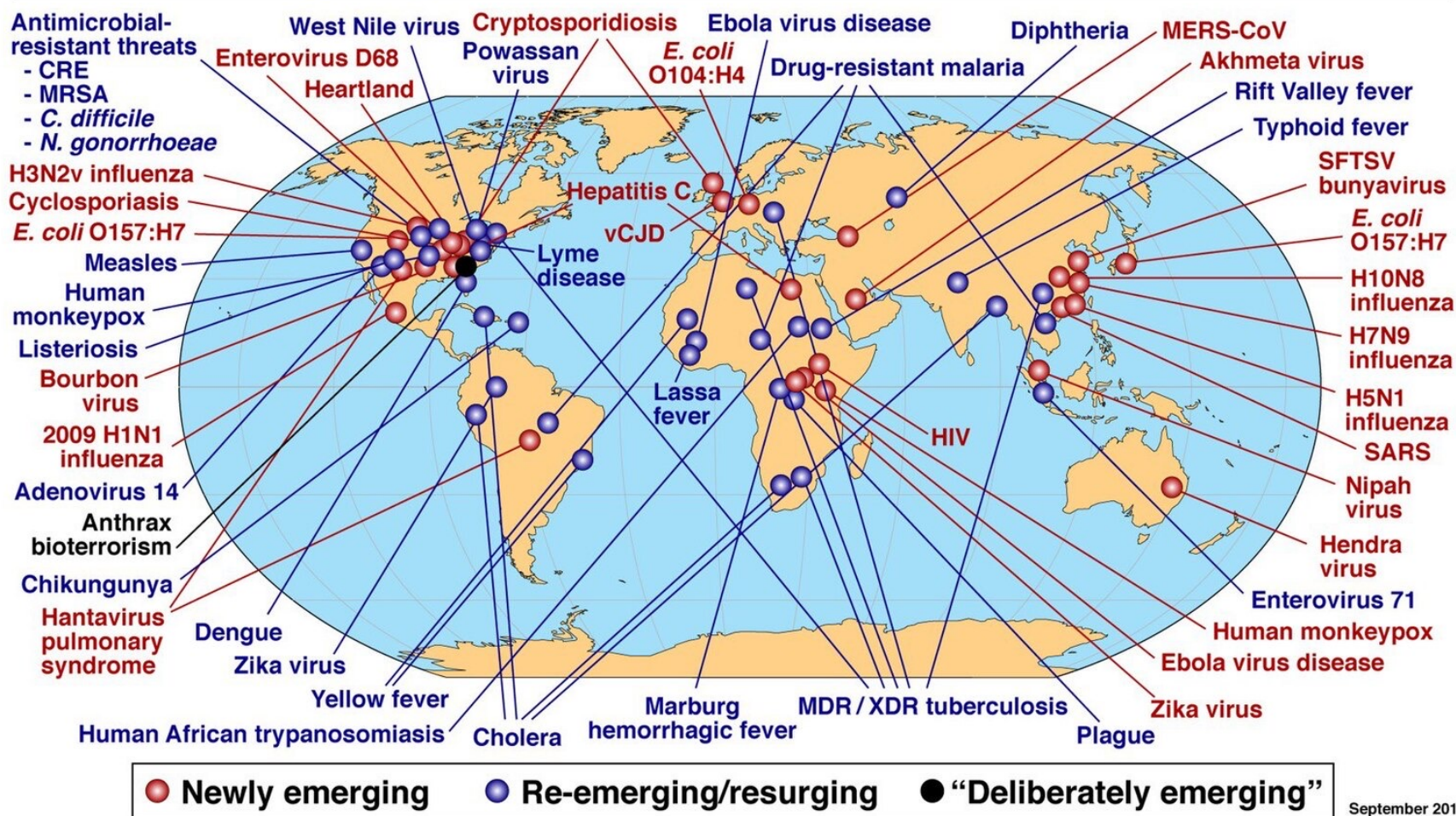


William H. Stewart addressing the World Health Organization, 1966. Photograph courtesy the National Library of Medicine

"The time has come to close the book on infectious diseases. We have basically wiped out infection in the United States."

—William Stewart, US Surgeon General, 1967

Global Examples of Emerging and Re-Emerging Infectious Diseases





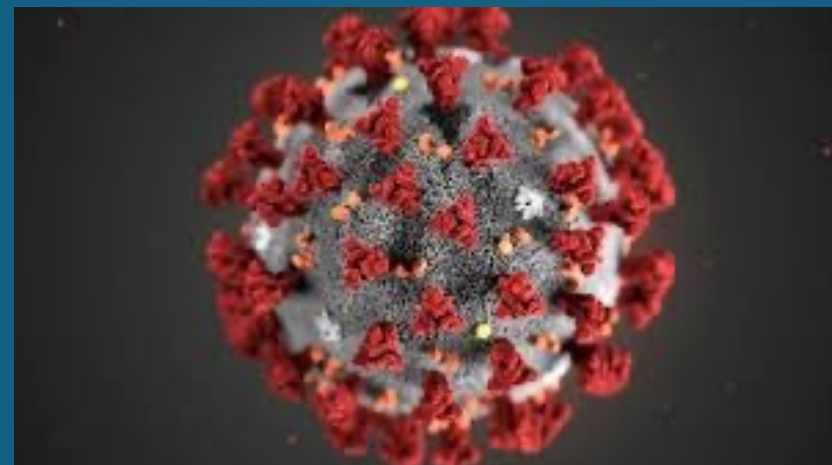
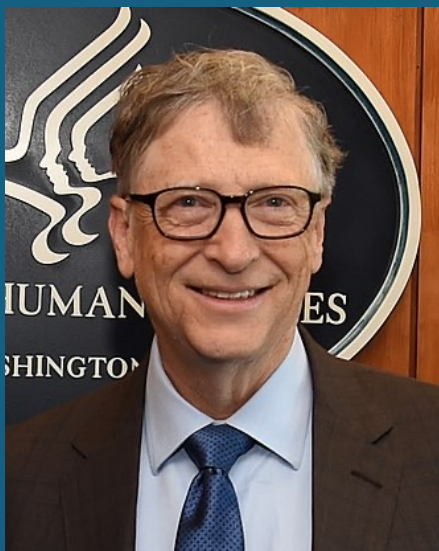
ENDEMIC



EPIDEMIC



PANDEMIC



"Quando ero un ragazzo, il disastro di cui ci preoccupavamo era la guerra nucleare. Oggi la più grande catastrofe possibile non è più quella. Se qualcosa ucciderà 10 milioni di persone nelle prossime decadi, è più probabile che sia un virus molto contagioso e non una guerra. Non missili ma microbi". Queste parole, pronunciate da **Bill Gates** nel 2015 durante una conferenza, suonano oggi, in queste settimane di emergenza coronavirus, come una profezia.

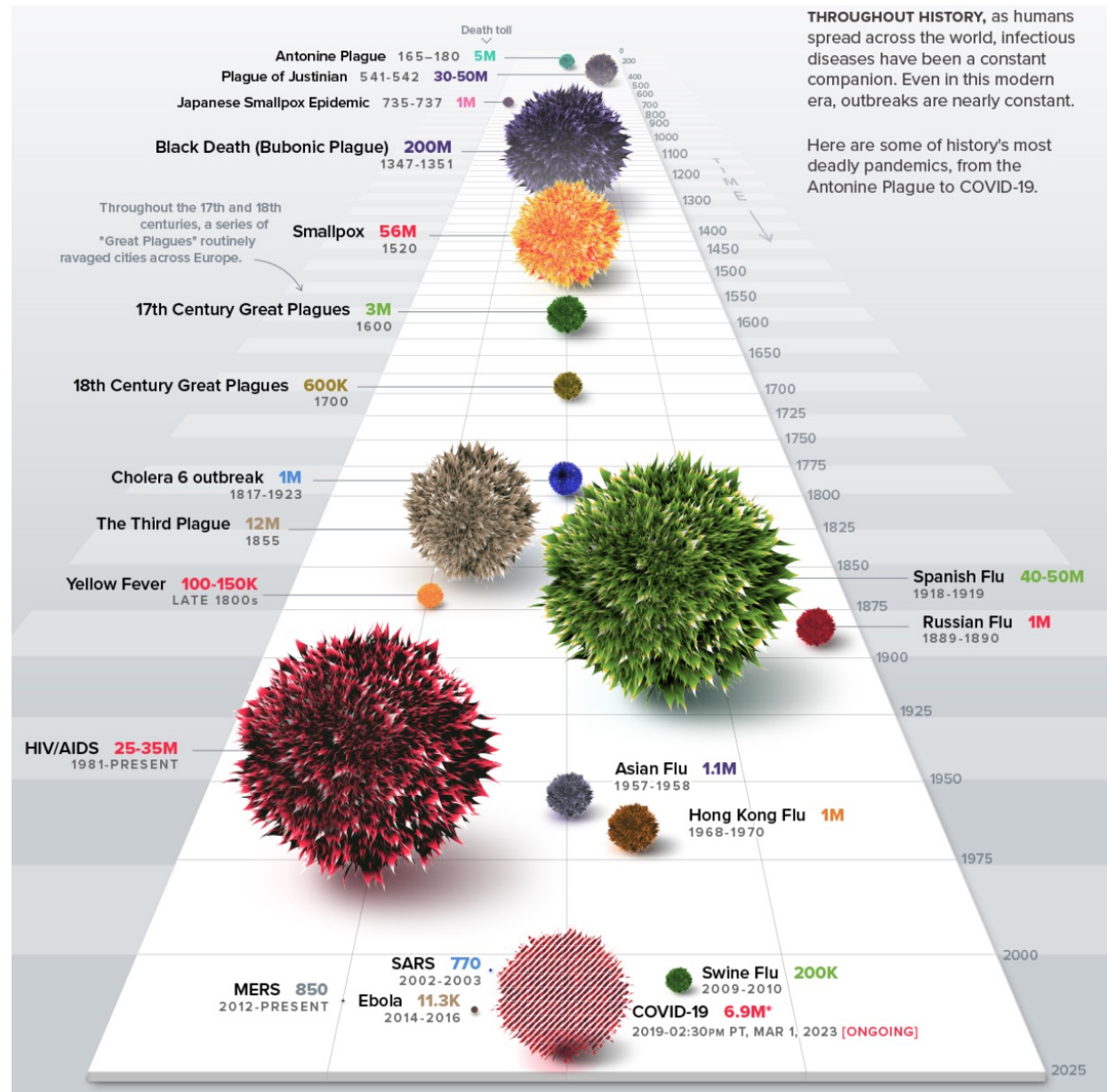
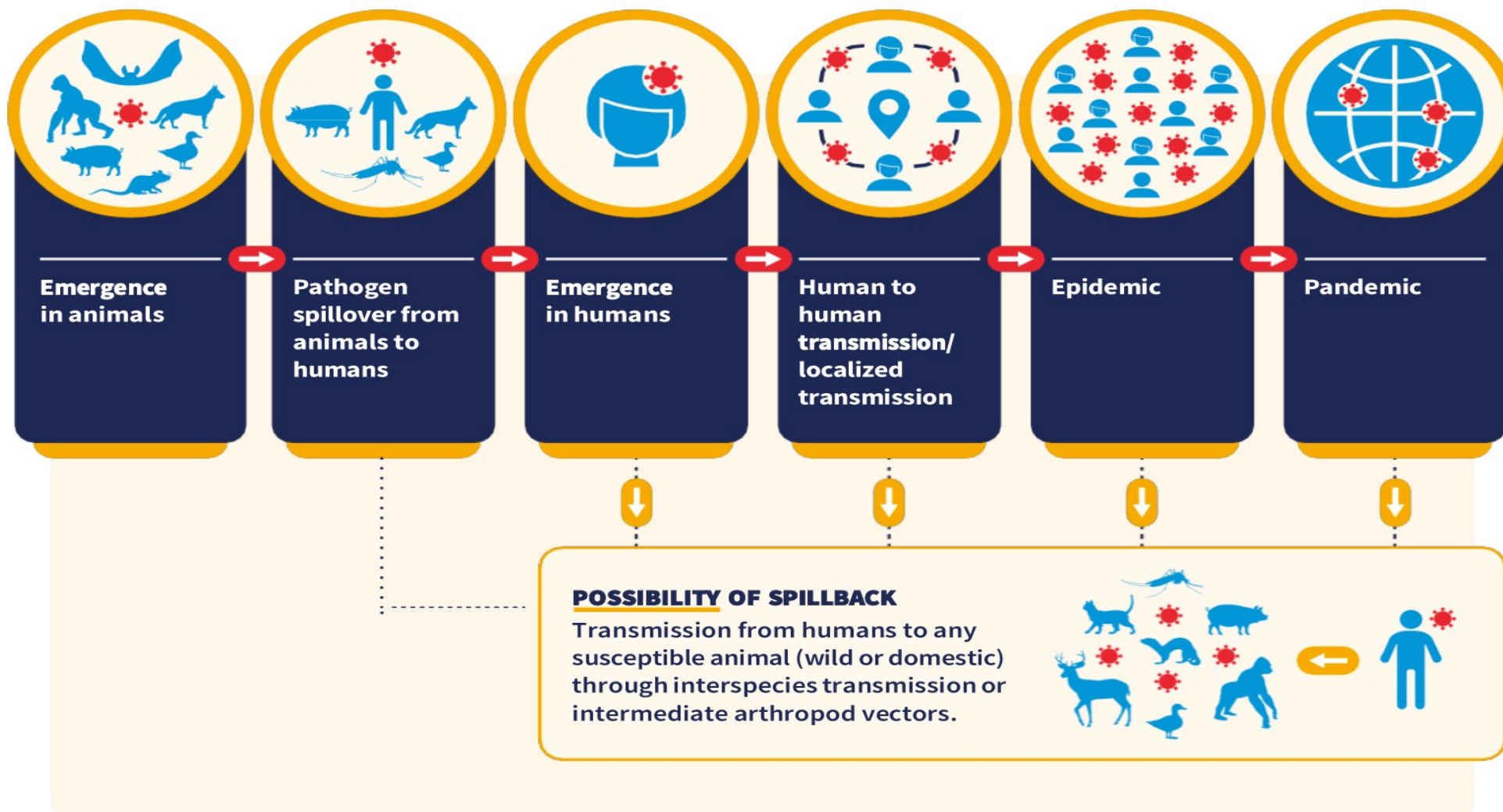


Figure 1: Stages of emergence, zoonotic spillover and potential spillback



The first zoonotic transmission likely involve lineage B viruses and occurred in late-November/early-December 2019 and no earlier than the beginning of November 2019, while the introduction of lineage A likely occurred within weeks of the first event. These findings define the narrow window between when SARS-CoV-2 first jumped into humans and when the first cases of COVID-19 were reported. Hence, as with SARS-CoV-1 in 2002 and 2003, SARS-CoV-2 emergence likely resulted from multiple zoonotic events.

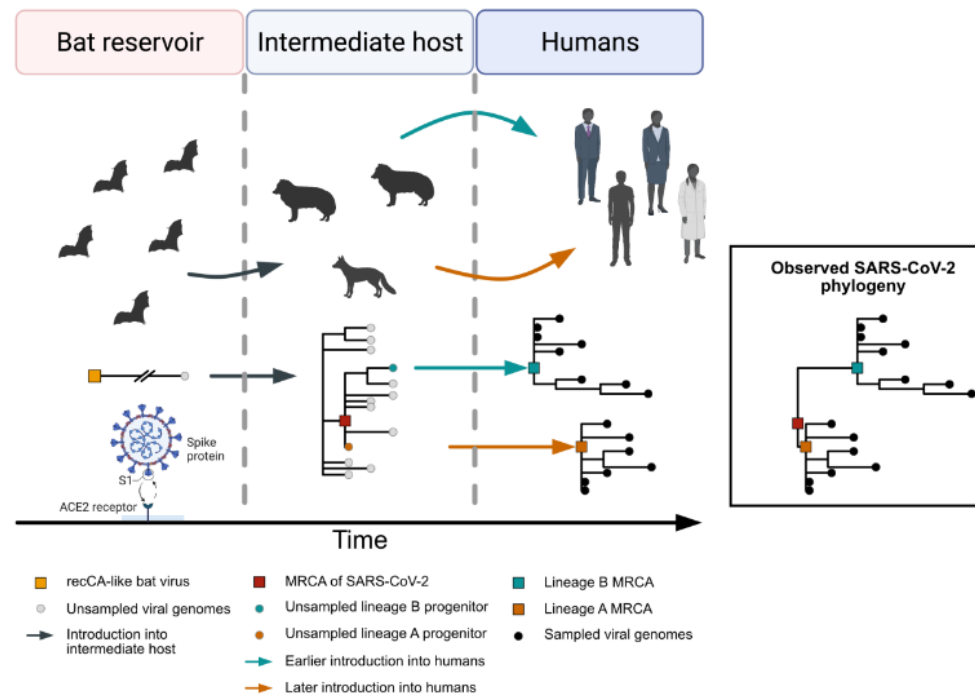
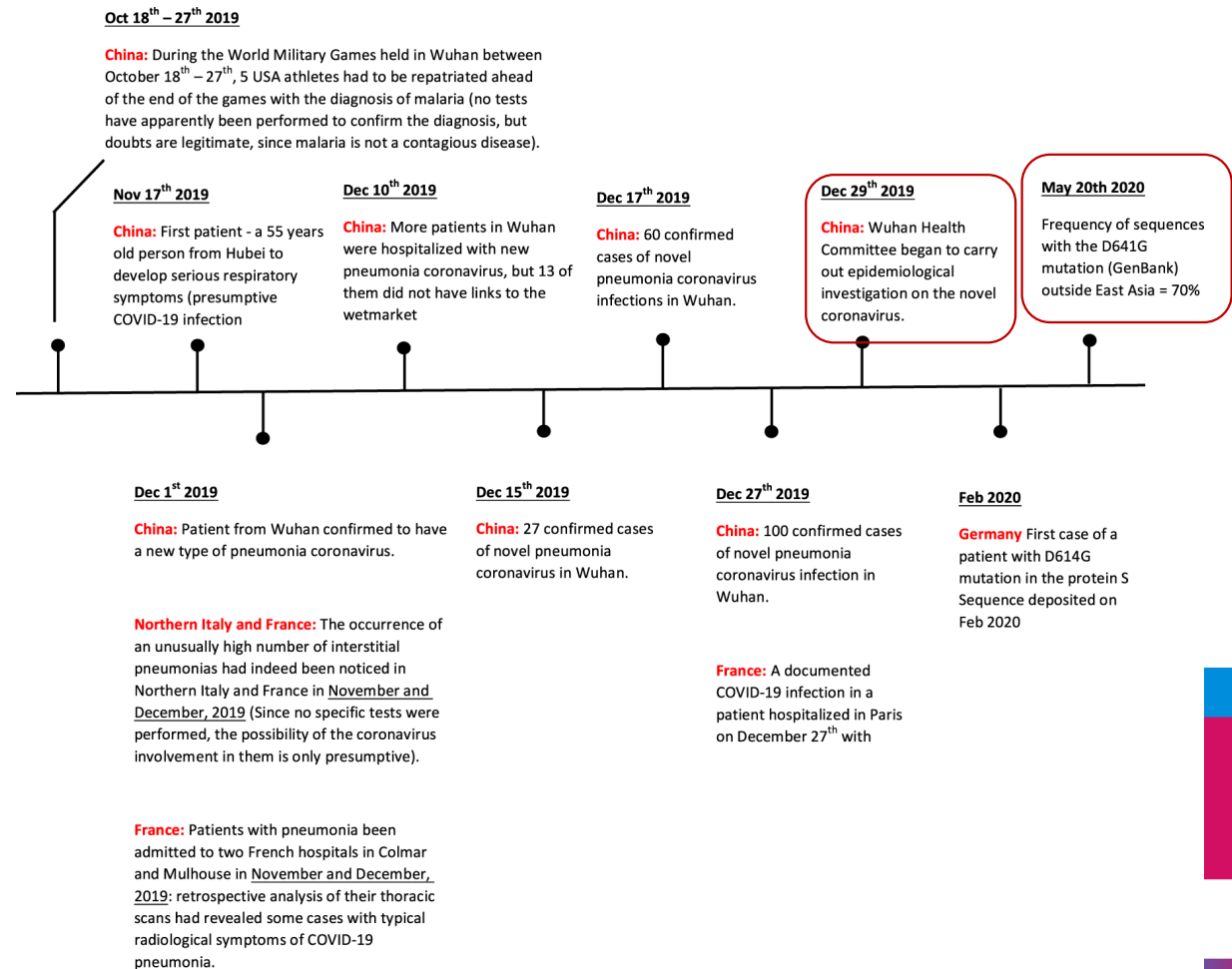


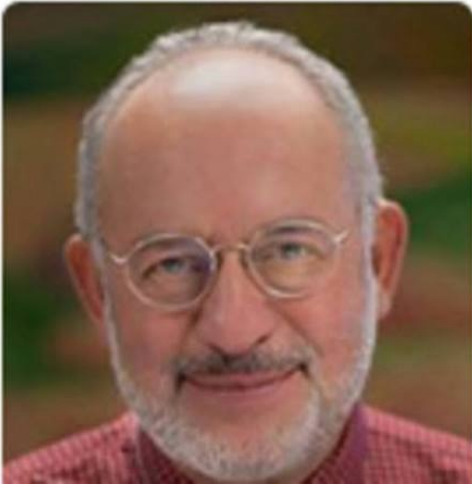
Figure 8. Schematic depicting the multiple zoonotic origin of SARS-CoV-2. A recCA-like virus was circulating in bats, and likely after gaining the ability to bind ACE2, jumped into an intermediate host. Therein, lineages A and B appeared and were separately introduced into humans shortly thereafter. An example phylogeny of viruses in the intermediate host is depicted, leading to separate phylogenies for lineages A and B. The resulting SARS-CoV-2 phylogeny from the combined lineage A and B viruses is presented in the black box. This scenario depicts a lineage A ancestral haplotype. See Figure S25 for intermediate and lineage B ancestral haplotypes.

At the very beginning...

*“On 31 December 2019, the **WHO** China Country Office was informed of cases of pneumonia of unknown etiology (unknown cause) detected in Wuhan City, Hubei Province of China. As of 3 January 2020, a total of 44 patients with pneumonia of unknown etiology have been reported to WHO by the national authorities in China. Of the 44 cases reported, 11 are severely ill, while the remaining 33 patients are in stable condition”*

*- Pneumonia of unknown cause – China/ World Health Organization -**





Edgar K. Marcuse

Progetto *Public Engagement Pilot Project on Pandemic influenza*
PEPPPI 2005

- **Garantire il funzionamento della società:** Mantenere attivi i servizi essenziali (infrastrutture, ordine pubblico, sanità).
- **Ridurre la mortalità dei più vulnerabili:** Proteggere le categorie a più alto rischio di ospedalizzazione e decesso.
- **Rifiuto di criteri casuali:** I cittadini escludono l'uso di lotterie o il principio del "chi prima arriva, meglio alloggia" per l'assegnazione delle dosi.  Amazon.com +1

PERSPECTIVE

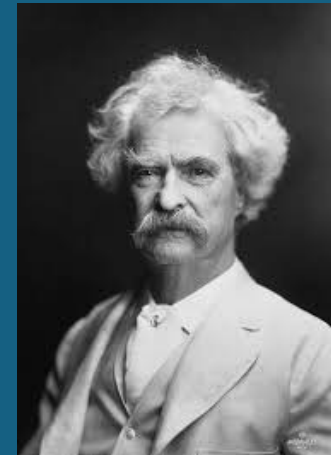
<https://doi.org/10.1038/s41591-022-01728-z>

nature
medicine



An epidemic of uncertainty: rumors, conspiracy theories and vaccine hesitancy

Ed Pertwee ¹✉, Clarissa Simas ¹ and Heidi J. Larson ^{1,2}



“una bugia fa in tempo a viaggiare per mezzo mondo,
mentre la verità si sta mettendo le scarpe”.

Mark Twain

COVID 19 - Search Results - Pub

pubmed.ncbi.nlm.nih.gov/?term=COVID+19&sort=date

NIH National Library of Medicine
National Center for Biotechnology Information

Log in

COVID 19

Search

Advanced

Create alert

Create RSS

User Guide

Save

Email

Send to

Sort by: Most recent

Display options

MY CUSTOM FILTERS

Edit custom filters

RESULTS BY YEAR

516,118 results

Page 1 of 51,612

☐

1

Isolation and pathogenicity of a highly virulent recombinant GI1c subtype PEDV strain.

Cite

Fan J, Liu Y, Fu W, Chen L, Li Y, Wang Z, Li D, Zhao P, Du W, Rao D, Zhang N, Song C, Yu L. BMC Vet Res. 2026 Jul 13. doi: 10.1186/s12917-026-05714-2. Online ahead of print. PMID: 42443885

Porcine epidemic diarrhoea virus (PEDV) is a highly contagious enteric **coronavirus** causing acute watery diarrhoea and high mortality in neonatal piglets, threatening the global swine industry. ...

☐

2

Societal worries and mental disorders in the general population: insights from the Netherlands Mental Health Survey and Incidence Study (NEMESIS).

Top Have M, Tuithof M, Van Dorsselaer S, Kerteling S, Shields, Zeeman L, Luik A

«Con il coronavirus si è affacciato un problema nuovo, e la scienza lo affronta andando per tentativi, sempre tenendo conto che la soluzione giusta non è una soluzione vera in termini assoluti. Ogni teoria vive sempre sotto assedio, e oggi le teorie hanno una vita più breve rispetto al passato, e dunque non c'è nulla di male nel vedere gli scienziati che si contraddicono: tentano di imparare, di capire».

Dario Antiseri 2020

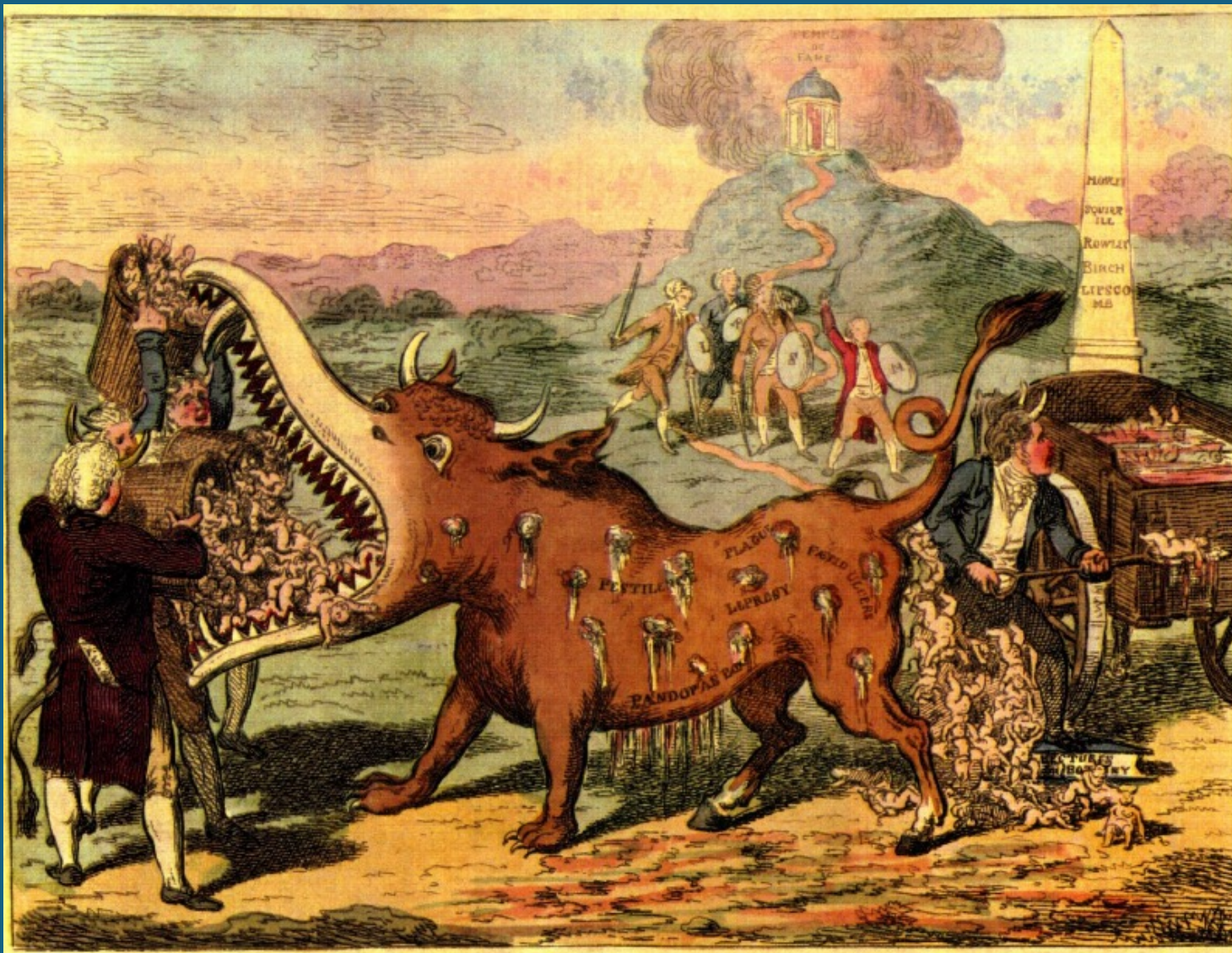
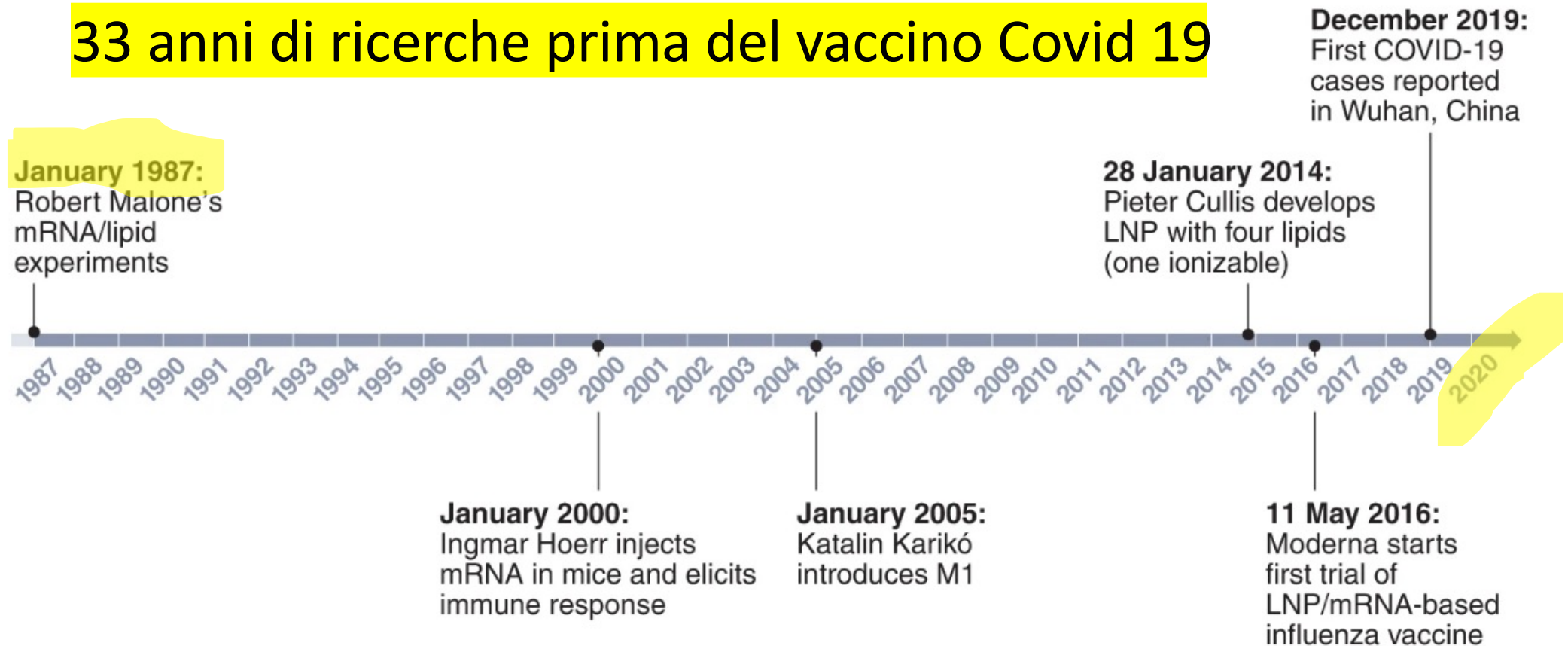


Fig. 1: The long road to mRNA vaccines.

From: [The COVID-19 vaccine patent race](#)

33 anni di ricerche prima del vaccino Covid 19



As early as 1987, experiments using liposome-mediated mRNA transfection suggested that mRNA could be used as a drug.

U. Storz Nature Biotech 2002



Katalin Karikó Drew Weissman

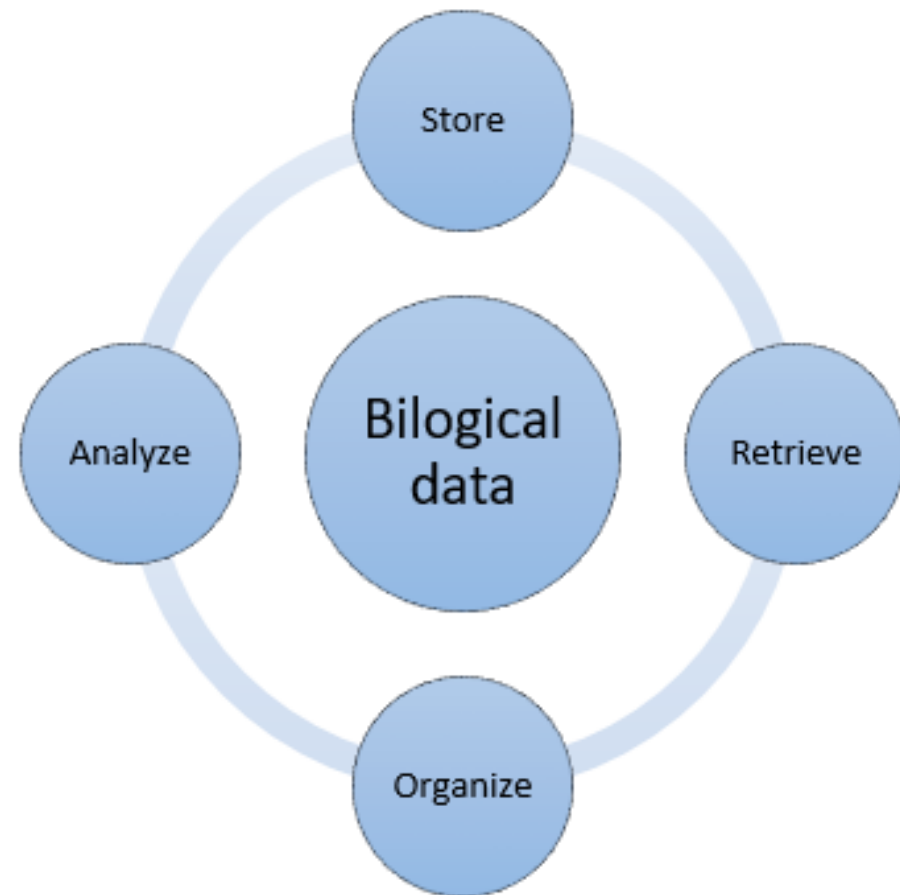
> [J Immunol.](#) 1996 Aug 1;157(3):1271-8.

Effect of *Mycobacterium tuberculosis* on HIV replication. Role of immune activation

D Goletti ¹, D Weissman, R W Jackson, N M Graham, D Vlahov, R S Klein, S S Munsiff, L Ortona, R Cauda, A S Fauci

Una nuova scienza
al servizio di
One Health

La Bioinformatica





SHORT COMMUNICATION

JOURNAL OF
MEDICAL VIROLOGY WILEY

Evidence for mutations in SARS-CoV-2 Italian isolates potentially affecting virus transmission

Domenico Benvenuto¹ | Ayse Banu Demir² | Marta Giovanetti³ |
Martina Bianchi⁴ | Silvia Angeletti⁵ | Stefano Pascarella⁴ | Roberto Cauda^{6,7} |
Massimo Ciccozzi¹ | Antonio Cassone⁸

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Email: domenico benvenuto95@gmail.com

Abstract

Italy is the first western country suffering heavy severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission and disease impact after coronavirus disease-2019 pandemic started in China. Even though the presence of mutations on spike glycoprotein and nucleocapsid in Italian isolates has been reported, the potential impact of these mutations on viral transmission has not been evaluated. We have compared SARS-CoV-2 genome sequences from Italian patients with virus sequences from Chinese patients. We focussed upon three nonsynonymous mutations of genes coding for S(one) and N(two) viral proteins present in Italian isolates and absent in Chinese ones, using various bioinformatics tools. Amino acid analysis and changes in three-dimensional protein structure suggests the mutations reduce protein stability and, particularly for S1 mutation, the enhanced torsional ability of the molecule could favor virus binding to cell receptor(s). This theoretical interpretation awaits experimental and clinical confirmation.

KEYWORDS

bioinformatics, COVID-19, molecular evolution, mutation, SARS coronavirus

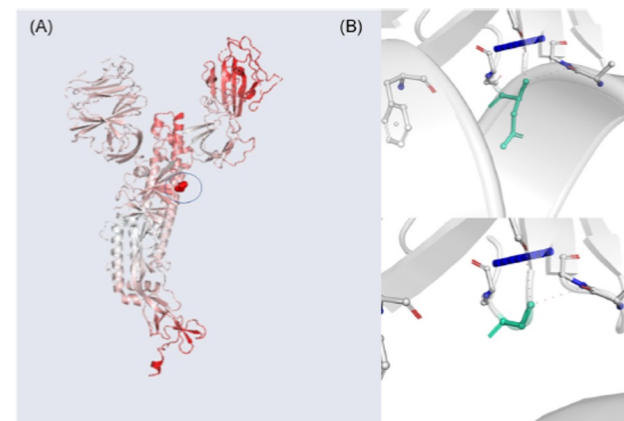


FIGURE 1 A. A model of spike glycoprotein monomer displaying the amino acids colored according to the vibrational entropy change upon mutation, red regions are those gaining in flexibility. The amino acid mutation is blue circled; (B) the top image shows the molecular interaction between the side chain of the wild-type amino acid and the side chains of the surrounding amino acid; the bottom image shows the molecular interaction between the side chain of the mutated amino acid and the side chains of the surrounding amino acid

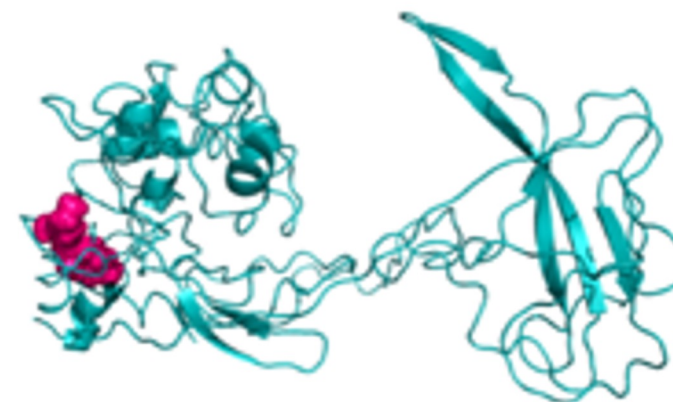


FIGURE 2 Cartoon model of the nucleocapsid of the SARS-CoV-2 where the mutated amino acids have been shown in purple

Ecoepidemiology and Complete Genome Comparison of Different Strains of Severe Acute Respiratory Syndrome-Related *Rhinolophus* Bat Coronavirus in China Reveal Bats as a Reservoir for Acute, Self-Limiting Infection That Allows Recombination Events[†]

Susanna K. P. Lau,^{1,2,3,4,†} Kenneth S. M. Li,^{4,†} Yi Huang,⁴ Chung-Tong Shek,⁵ Herman Tse,^{1,2,3,4} Ming Wang,⁶ Garnet K. Y. Choi,⁴ Huifang Xu,⁶ Carol S. F. Lam,⁴ Rongtong Guo,⁶ Kwok-Hung Chan,⁴ Bo-Jian Zheng,⁴ Patrick C. Y. Woo,^{1,2,3,4,*} and Kwok-Yung Yuen^{1,2,3,4,*}



FIG. 1. Map showing the locations of bat sampling and tagging in Hong Kong. Squares represent the locations where bats were positive for SARSr-Rh-BatCoV, dark circles represent locations where bats were positive for Rh-BatCoV HKU2, and triangles represent locations where the bats were positive for both Rh-BatCoV HKU2 and SARSr-Rh-BatCoV. The percentages indicate the proportion of bats positive for SARSr-Rh-BatCoV, Rh-BatCoV HKU2, or SARSr-Rh-BatCoV/Rh-BatCoV HKU2 at each location. Blank circles represent locations negative for SARSr-Rh-BatCoV and Rh-BatCoV HKU2. The red circle represents the location of Shenzhen Dongman market (SZDM) in China where civet SARSr-CoV was first identified. The arrow indicates the direction of migration of Chinese imported bats demonstrated in the trade market.

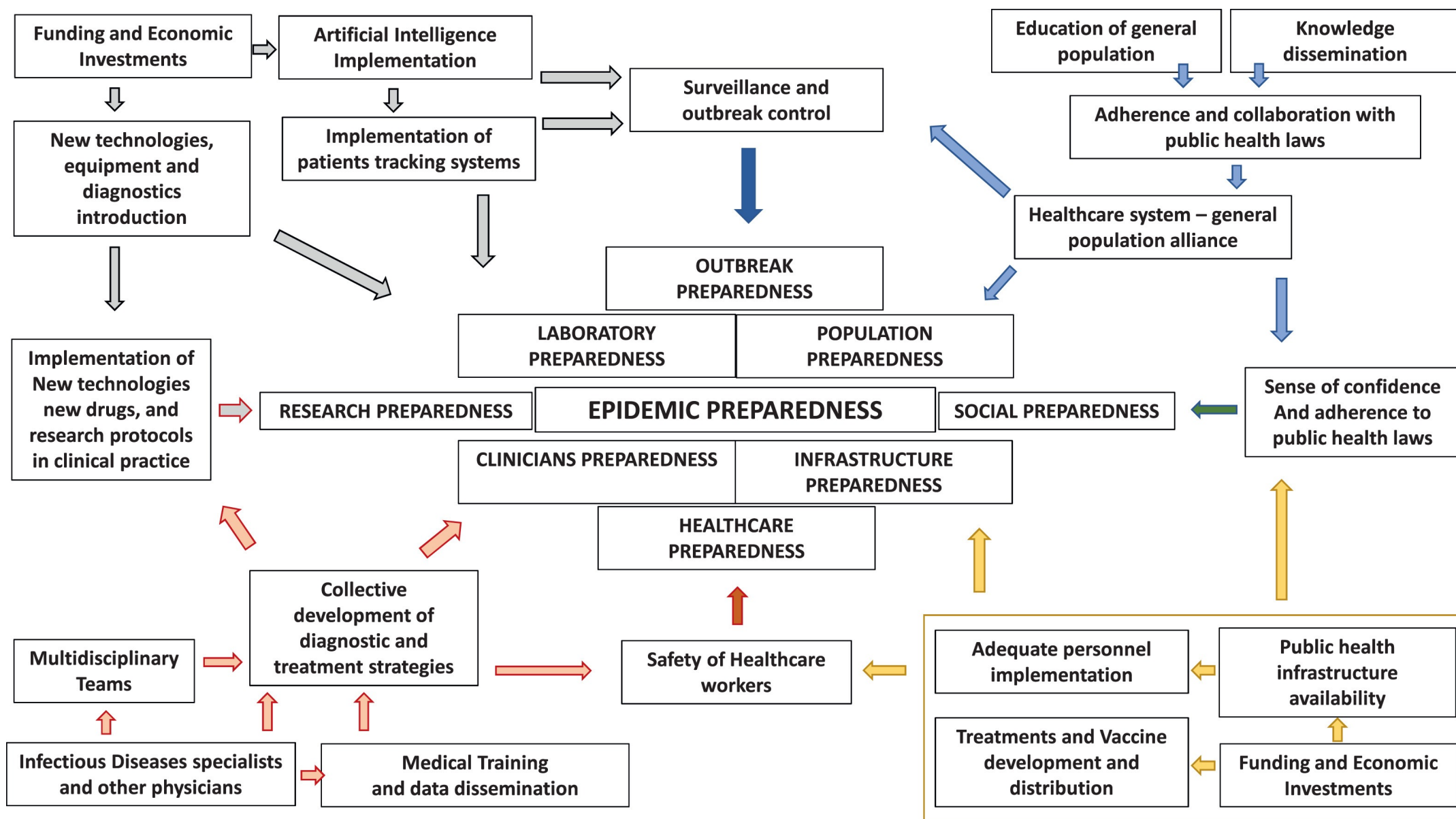


FIG. 6. Estimation of the time of interspecies transmission of SARSr-CoV. Squares denote the MRCA of all SARSr-CoV (1972), the MRCA of human/civet SARSr-CoV and the closest SARSr-Rh-BatCoV (1995), and the MRCA of human and civet SARSr-CoV (2001), respectively.

Pandemic preparedness for the real world

**Why we must invest in equitable, ethical and effective
approaches to help prepare for the next pandemic**

March 2023



Sorveglianza Integrata



RACCOLTA DATI CONDIVISA



MONITORAGGIO DI
ANIMALI, UOMO E
AMBIENTE



IDENTIFICAZIONE PRECOCE
DEI FOCOLAI

The Copenhagen Recommendations

Report
from the Invitational EU Conference on
The Microbial Threat
Copenhagen, Denmark
9 - 10 September 1998

Edited by:
Vibeke Thamdrup Rosdahl, Division Director, Statens Serum Institut and
Knud Borge Pedersen, Director, Danish Veterinary Laboratory

www.microbial.threat.dk

Workshop no. 4: Elements of good practice in the use of antimicrobial agents

List of participants

Chairman: Jeremy Metters, Department of Health, United Kingdom
Co-Chairman: Otto Cars, University Hospital, Uppsala, Sweden
Secretary: Niels Frimodt-Møller, State Serum Institute, Denmark

Isabelle Bauraind, Ministry of Social Affairs Public Health and Environment, Belgium
André Bryskier, Hoechst Marion Roussel, France
Robin Bywater, Fedesa, Belgium
Antonio Saenz Calvo, Instituto de Salud Carlos III, Spain
Roberto Cauda, Università Cattolica del Sacro Cuore, Roma, Italy
Pierre Choraine, Federation des Veterinaires d'Europe, Belgium
Teresa Coucello, Direção-Geral da Saúde, Portugal
Helen Giamarellou, Athens University School of Medicine, Greece
J. Gilley, British Medical Association, United Kingdom
Bart Gordts, A.Z. Sint Jan, Belgium
Beatriz Pérez Gorricho, Hospital del Niño Jesús, Madrid, Spain
Danielle Hansen-Koenig, Direction de la Sante, Luxembourg
Mary Horgan, Cork University Hospital, Ireland
Sven Erik Jorsal, Danish Veterinary Laboratory, Denmark
G. Kreutz, Bundesinstitut für Arzneimittel und Medizinprodukte, Germany
Karl G. Kristinsson, National University Hospital, Iceland
B. J. Kullberg, Academic Hospital Nijmegen, The Netherlands
Jens K. Møller, Aarhus University Hospital, Denmark
Sigvard Mölstad, University Hospital MAS, Malmö, Sweden
Jan Nagler, Cabinet of the Minister of Public Health, Belgium
Leena Nünistö, Health & Social Welfare Department, Vantaa, Finland
M. Powell, Medicines Control Agency, United Kingdom
Peter Rudman, Agriculture House, United Kingdom
Pascal Sanders, Centre National d'Etudes Vétérinaires et Alimentaires, Fougères, France
Melico Silvestre, Hospitais da Universidade de Coimbra, Portugal
David J. Taylor, University of Glasgow Veterinary School, United Kingdom
A. van den Bogaard, University of Limburg, The Netherlands
Agnes Wechsler-Fördös, Rudolfstiftung, Austria

Topic:

The antibiotic policies in the different EU Member States as well as within each member state differ considerably. A number of different elements could be used in order to change the usage of antimicrobial agents and the occurrence of resistant micro-organisms. This might include: pre- and postgraduate training, availability of data on consumption and resistance, local and nation-wide recommendations, reimbursement policy of selected antibiotics, committees, guidelines etc. The workshop should not prepare guidelines for the good practice.

USO INAPPROPRIATO
degli antibiotici da parte
dei pazienti



USO NON NECESSARIO
degli antibiotici in
agricoltura e allevamento



OVERPRESCRIZIONE
degli antibiotici da parte
dei medici



CAUSE dell'ANTIBIOTICO- RESISTENZA



SCARSA IGIENE
e carenze nelle pratiche di prevenzione



DIFFUSIONE DELLE INFEZIONI
negli ospedali e nelle strutture cliniche

MANCATA ATTUAZIONE DI TEST DIAGNOSTICI
che possano informare e guidare la prescrizione

Alcuni antibiotici
usati per il
trattamento degli

ANIMALI



sono gli stessi che vengono
utilizzati per le

PERSONE



Un approccio

ONE HEALTH

può ridurre
l'antibiotico
resistenza



Antimicrobico-Resistenza

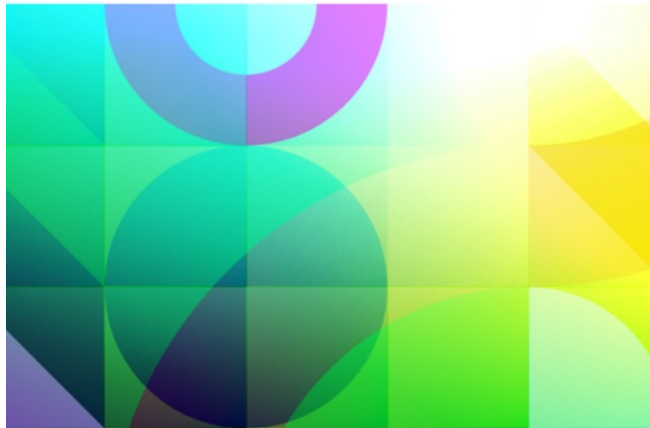
Uso eccessivo
di antibiotici

Impatto su
medicina e
veterinaria

Minaccia
crescente per la
salute globale

- Organizzazione Mondiale della Sanità (WHO)
- Organizzazione delle Nazioni Unite per l'Alimentazione e l'Agricoltura (FAO)
- Organizzazione Mondiale per la Salute Animale (WOAH)
- Programma delle Nazioni Unite per l'Ambiente (UNEP)

ONE HEALTH, ONE ETHICS



One Health, One Ethics

Contemporary Issues in Bioethics | Vol. 2

In its current mandate, the CNECV has chosen the One Health approach as a priority, intending to develop knowledge and disseminate information, as well as to deepen reflection and foster public debate, going beyond theoretical-conceptual discussions to concrete and concerted action at local, regional and global level.

The concept of One Health expresses an indissoluble unity between human, animal, and ecosystem health. It is also an ethical attitude or integrated relationship between humans and other beings and their habitat. In One Health, ethics plays a crucial role in decision-making processes and the formulation of guidelines, based on principles of responsibility, respect for vulnerability, and global justice.

The deterioration of the environment and ecosystems, fuelled by climate change, has contributed to the worsening of multiple diseases of environmental and animal origin, leading to the emergence of