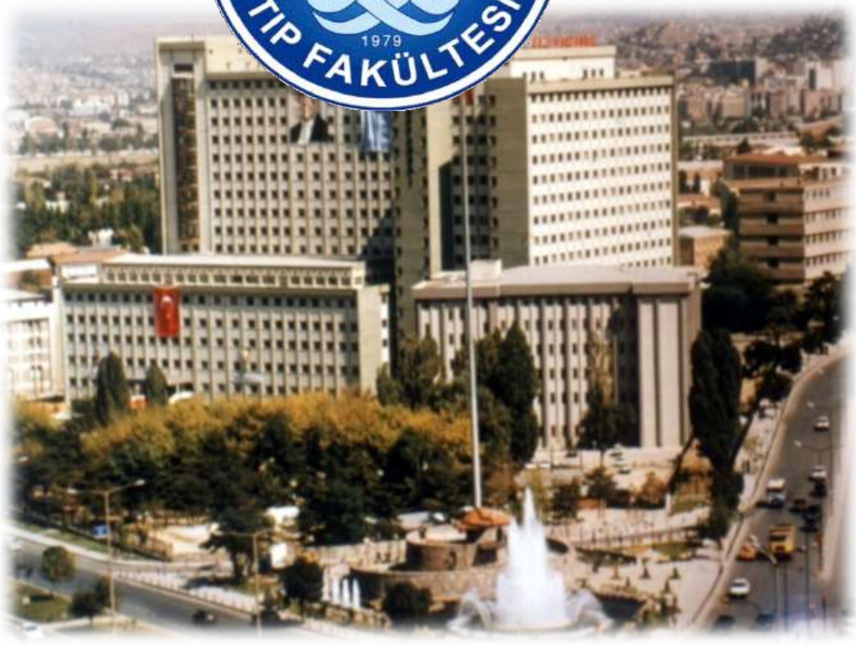
COVID-19 Aşılarının Gelecek Pandemilere Etkileri

GAZİ ÜNİVERSİTESİ
TIP FAKÜLTESİ
1979



esin
şenol

Dünya nüfusunun %40-70’i etkilenebilir!

DELTA –R:4-6 ; DEĞERİ İÇİN %60-80

The NEW ENGLAND JOURNAL of MEDICINE

Perspective

MAY 21, 2020

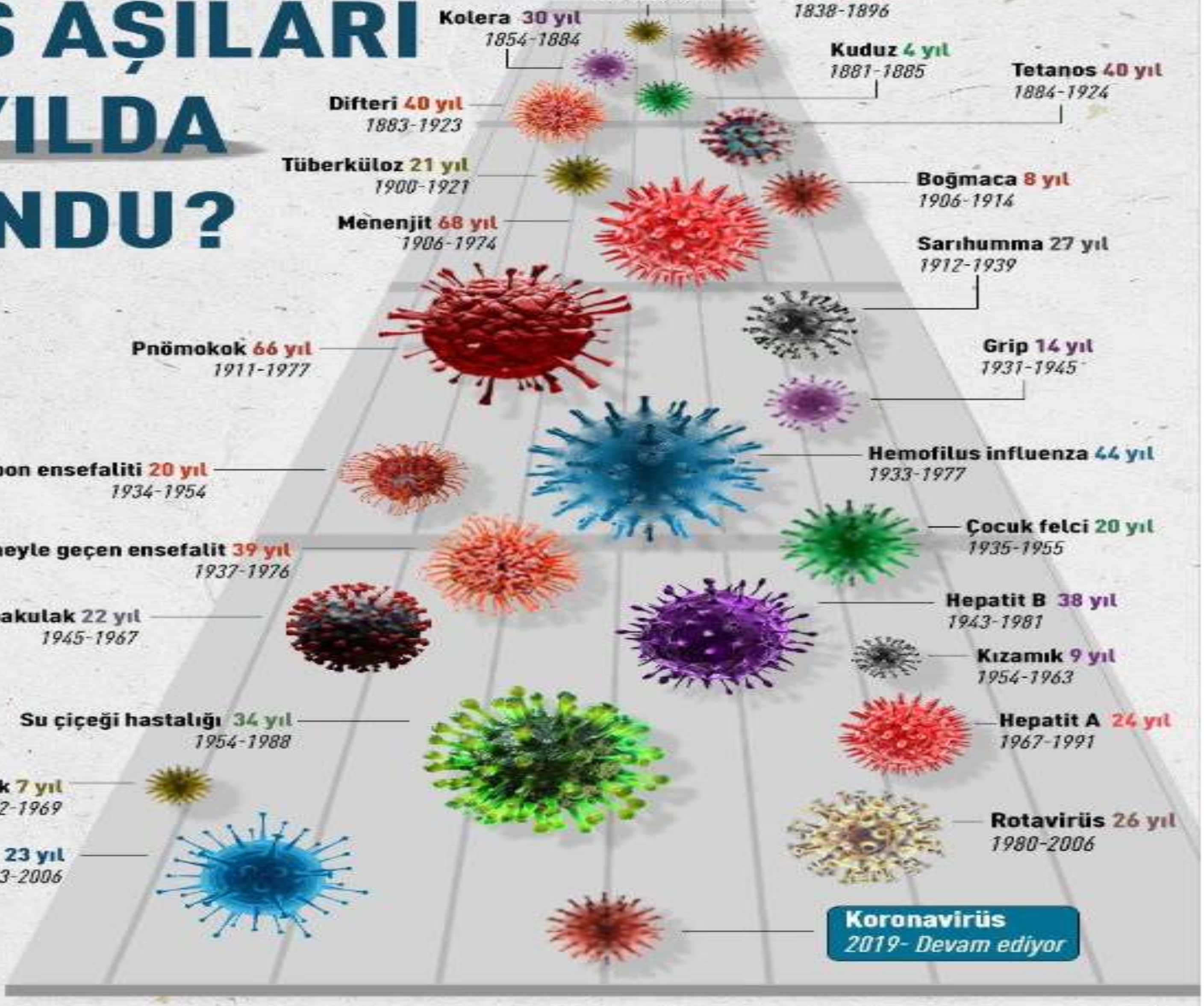
Developing Covid-19 Vaccines at Pandemic Speed

Nicole Lurie, M.D., M.S.P.H., Melanie Saville, M.D., Richard Hatchett, M.D., and Jane Halton, A.O., P.S.M.

The need to rapidly develop a vaccine against SARS-CoV-2 comes at a time of explosion in basic scientific understanding, including in areas such as genomics and structural biology that

The company continued development even when the outbreak ended, and stockpiles of investigational product were available for use in the recent outbreaks in

VİRÜS AŞILARI KAÇ YILDA BULUNDU?



Çiçek hastalığı 26 yıl
1770-1796

Tifo 58 yıl
1838-1896

Kolera 30 yıl
1854-1884

Kuduz 4 yıl
1881-1885

Tetanos 40 yıl
1884-1924

Difteri 40 yıl
1883-1923

Tüberküloz 21 yıl
1900-1921

Boğmaca 8 yıl
1906-1914

Menenjit 68 yıl
1906-1974

Sarıhumma 27 yıl
1912-1939

Pnömokok 66 yıl
1911-1977

Grip 14 yıl
1931-1945

Hemofilus influenza 44 yıl
1933-1977

Japon ensefaliti 20 yıl
1934-1954

Çocuk felci 20 yıl
1935-1955

Keneyle geçen ensefalit 39 yıl
1937-1976

Hepatit B 38 yıl
1943-1981

Kabakulak 22 yıl
1945-1967

Kızamık 9 yıl
1954-1963

Su çiçeği hastalığı 34 yıl
1954-1988

Hepatit A 24 yıl
1967-1991

Kızamıkçık 7 yıl
1962-1969

Rotavirüs 26 yıl
1980-2006

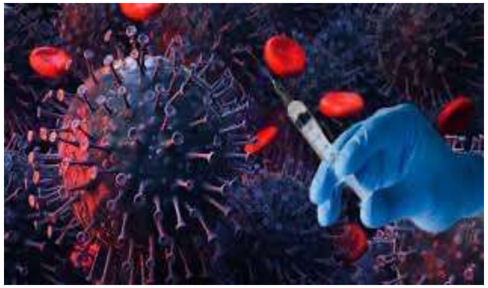
İnsan papilloma virüsü 23 yıl
1983-2006

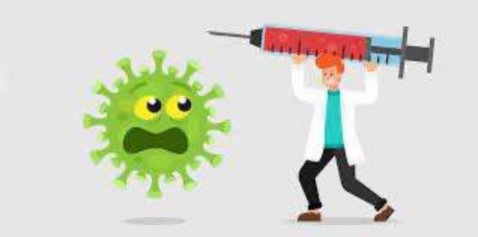
Koronavirüs
2019- Devam ediyor

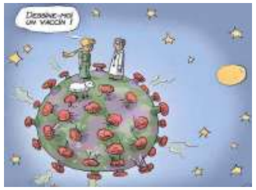
Sosyal Mesafe
Editör: Kübra Şafak
Grafik: Abdullah Özşahin

Kaynak: "Aşıların Maliyet Etkinliği"
Peter Hurford ve Marcus A. Davis

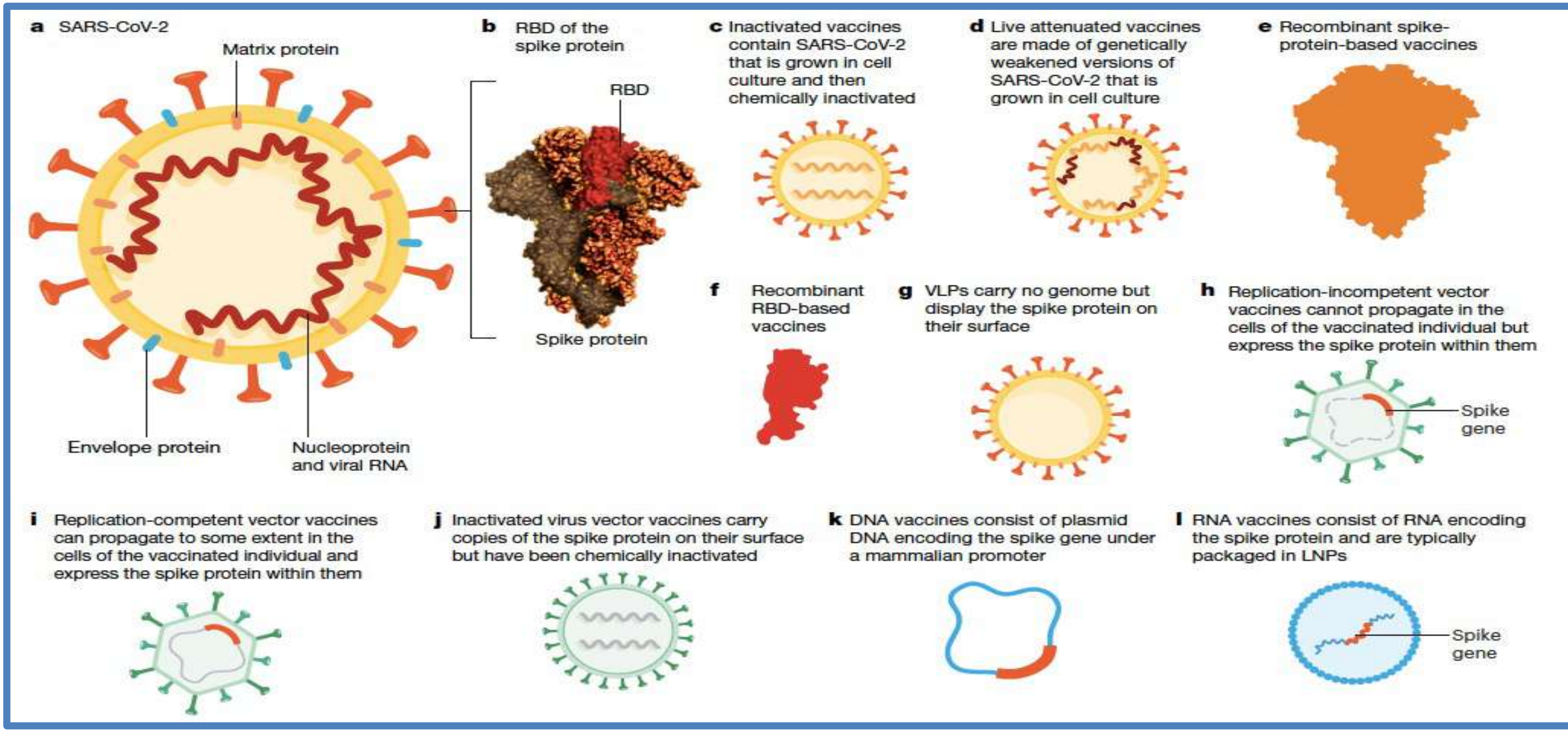
COVID-19 AŞILARI







COVID-19 AŞILARI



a SARS-CoV-2

b RBD of the spike protein

c Inactivated vaccines contain SARS-CoV-2 that is grown in cell culture and then chemically inactivated

d Live attenuated vaccines are made of genetically weakened versions of SARS-CoV-2 that is grown in cell culture

e Recombinant spike-protein-based vaccines

f Recombinant RBD-based vaccines

g VLPs carry no genome but display the spike protein on their surface

h Replication-incompetent vector vaccines cannot propagate in the cells of the vaccinated individual but express the spike protein within them

i Replication-competent vector vaccines can propagate to some extent in the cells of the vaccinated individual and express the spike protein within them

j Inactivated virus vector vaccines carry copies of the spike protein on their surface but have been chemically inactivated

k DNA vaccines consist of plasmid DNA encoding the spike gene under a mammalian promoter

l RNA vaccines consist of RNA encoding the spike protein and are typically packaged in LNPs

THE YEAR AHEAD

TIME

HOLLYWOOD'S NEW DIRECTION
BY JANICE MIN

AFTER TRUMP
BY MOLLY BALL

THE SOCIAL MEDIA MILITIA
BY SIMON SHUSTER
& BILLY PERRIGO

THE VACCINE REVOLUTION
BY WALTER ISAACSON

RACING TO BEAT THE VIRUS
BY ALICE PARK

Covid-19: UK launches world's first mass vaccination programme

Issued on: 08/12/2020 - 07:47

8 ARALIK 2020-UK

Vaccine Recommendations and Guidelines of the ACIP

Centers for Disease Control and Prevention

MMWR

Morbidity and Mortality Weekly Report

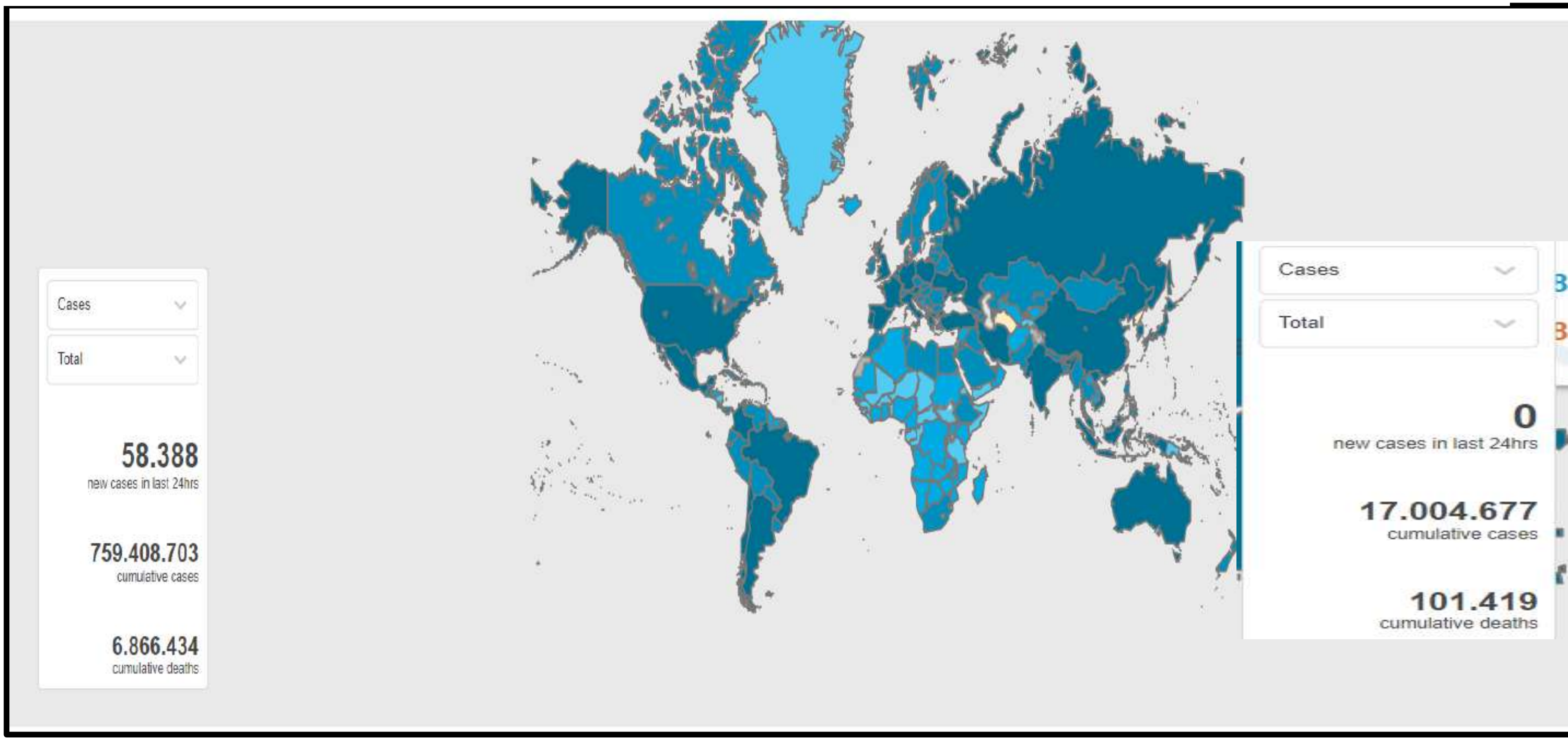
Early Release / Vol. 69

December 22, 2020

The Advisory Committee on Immunization Practices' Updated Interim Recommendation for Allocation of COVID-19 Vaccine — United States, December 2020

DÜNYADA DURUM-MART 2023
DÖRDÜNCÜ YIL

Globally, as of 6:21pm CET, 7 March 2023, there have been 759.408.703 confirmed cases of COVID-19, including 6.866.434 deaths, reported to WHO. As of 6 March 2023, a total of 13.229.471.213 vaccine doses have been administered.



Cases
Total

58.388
new cases in last 24hrs

759.408.703
cumulative cases

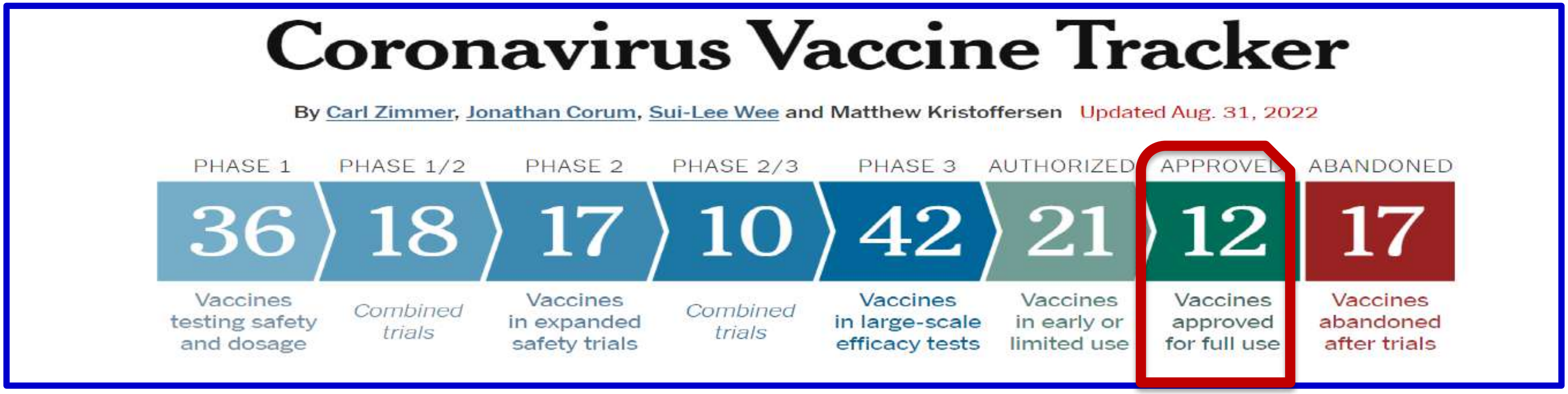
6.866.434
cumulative deaths

Cases
Total

0
new cases in last 24hrs

17.004.677
cumulative cases

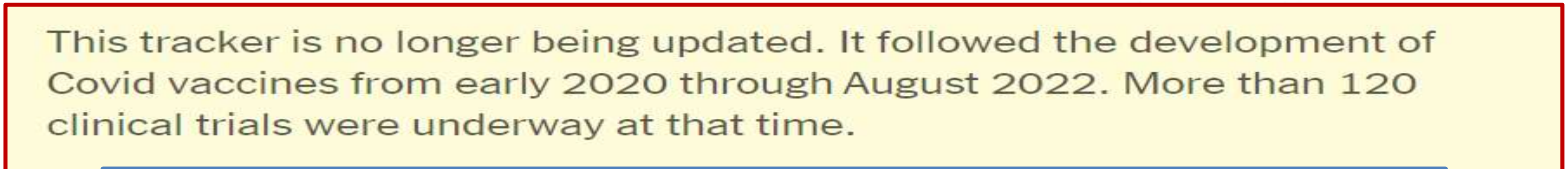
101.419
cumulative deaths



Coronavirus Vaccine Tracker

By Carl Zimmer, Jonathan Corum, Sui-Lee Wee and Matthew Kristoffersen Updated Aug. 31, 2022

PHASE 1	PHASE 1/2	PHASE 2	PHASE 2/3	PHASE 3	AUTHORIZED	APPROVED	ABANDONED
36	18	17	10	42	21	12	17
Vaccines testing safety and dosage	*Combined trials*	Vaccines in expanded safety trials	*Combined trials*	Vaccines in large-scale efficacy tests	Vaccines in early or limited use	Vaccines approved for full use	Vaccines abandoned after trials

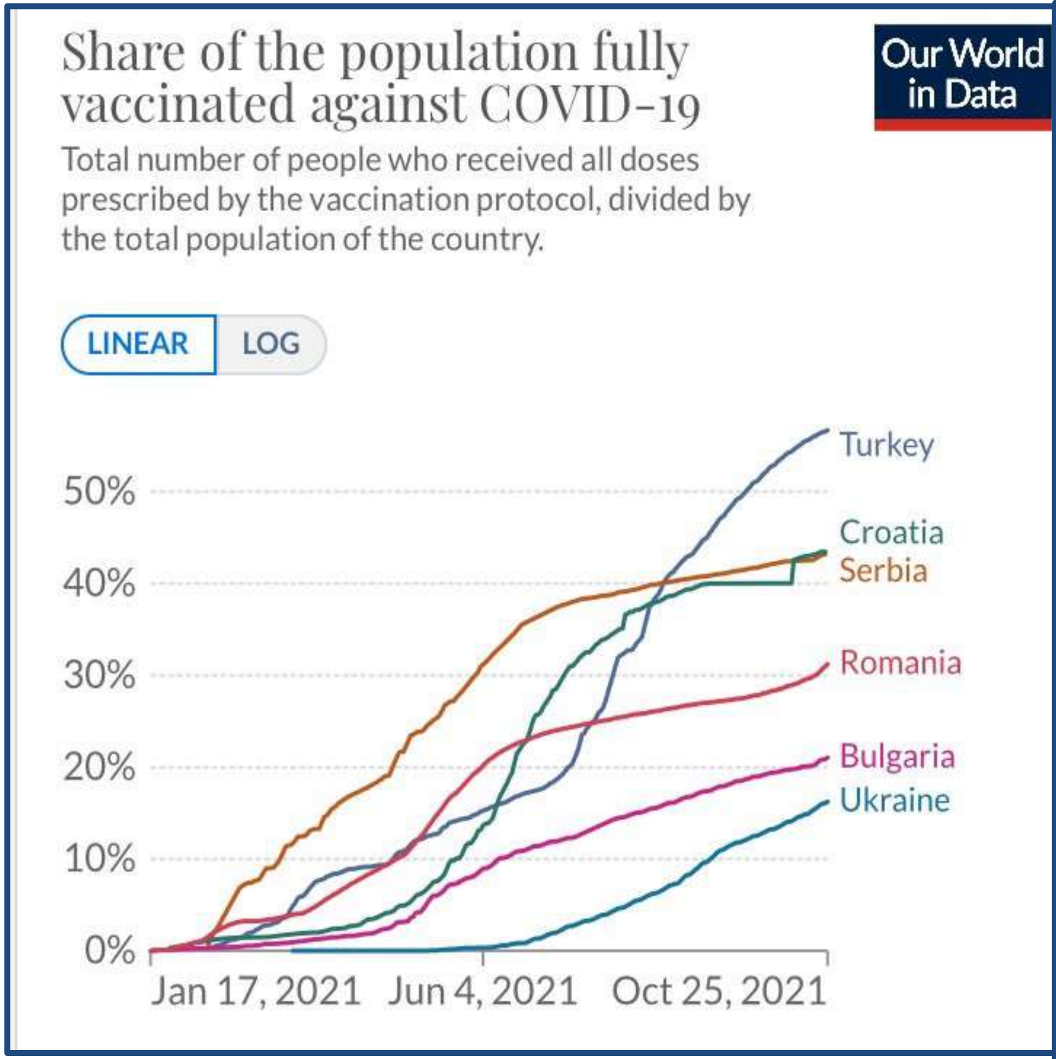


This tracker is no longer being updated. It followed the development of Covid vaccines from early 2020 through August 2022. More than 120 clinical trials were underway at that time.

Leading vaccines

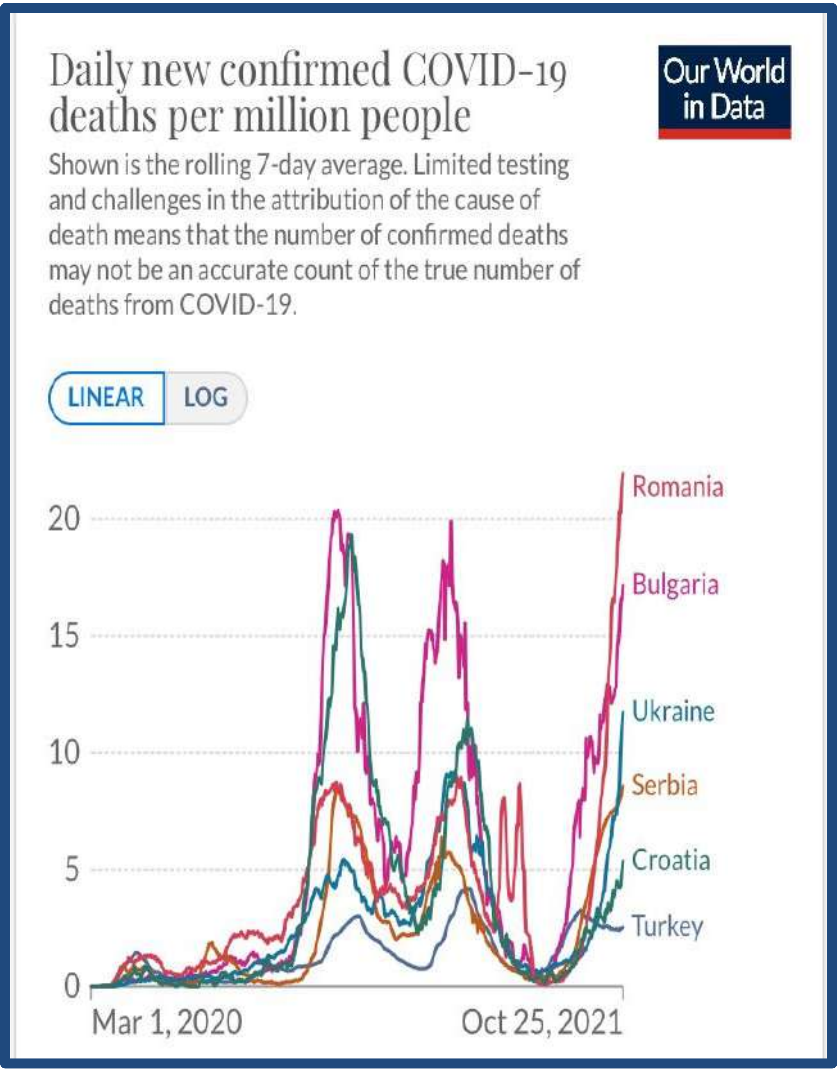
Developer	How It Works	Phase	Status
Pfizer-BioNTech	mRNA	3	Approved in U.S., other countries. Emergency use in many countries.
Sinopharm	Inactivated	3	Approved in China, Bahrain. Emergency use in many countries.
Oxford-AstraZeneca	ChAdOx1	2 3	Approved in Brazil, India. Emergency use in many countries.
Sinovac	Inactivated	3	Approved in China. Emergency use in many countries.
Moderna	mRNA	3	Approved in U.S., Canada, Switzerland. Emergency use in many countries.
Novavax	Protein	3	Approved in Canada, South Korea. Emergency use in several countries.
Bharat Biotech	Inactivated	3	Approved in India. Emergency use in other countries.
Johnson & Johnson	Ad26	3	Approved in Canada. Limited in U.S. Emergency use in many countries.
Baylor-Biological E	Protein	3	Emergency use in India, Botswana.
Gamaleya	Ad26, Ad5	3	Approved in Russia. Emergency use in many countries.

AŞILAMA VE ÖLÜM



Share of the population fully vaccinated against COVID-19

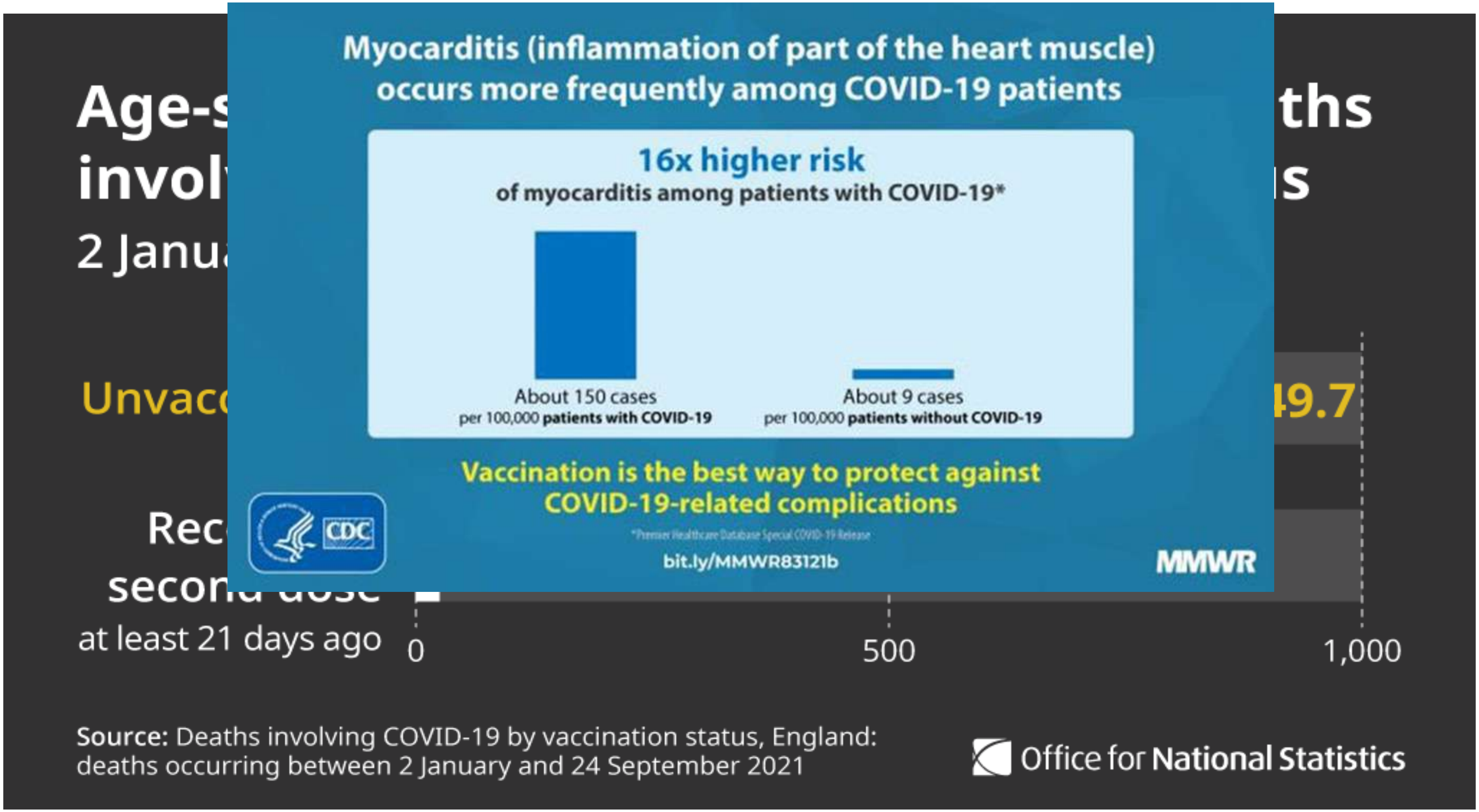
Total number of people who received all doses prescribed by the vaccination protocol, divided by the total population of the country.



Daily new confirmed COVID-19 deaths per million people

Shown is the rolling 7-day average. Limited testing and challenges in the attribution of the cause of death means that the number of confirmed deaths may not be an accurate count of the true number of deaths from COVID-19.

The age-adjusted risk of deaths involving #COVID19 was **32 times greater in unvaccinated** people than in fully vaccinated individuals between 2 Jan and 24 Sept 2021



Myocarditis (inflammation of part of the heart muscle) occurs more frequently among COVID-19 patients

16x higher risk

of myocarditis among patients with COVID-19*

About 150 cases per 100,000 **patients with COVID-19**

About 9 cases per 100,000 **patients without COVID-19**

Vaccination is the best way to protect against COVID-19-related complications

*Premier Healthcare Database Special COVID-19 Release

bit.ly/MMWR83121b

Source: Deaths involving COVID-19 by vaccination status, England: deaths occurring between 2 January and 24 September 2021

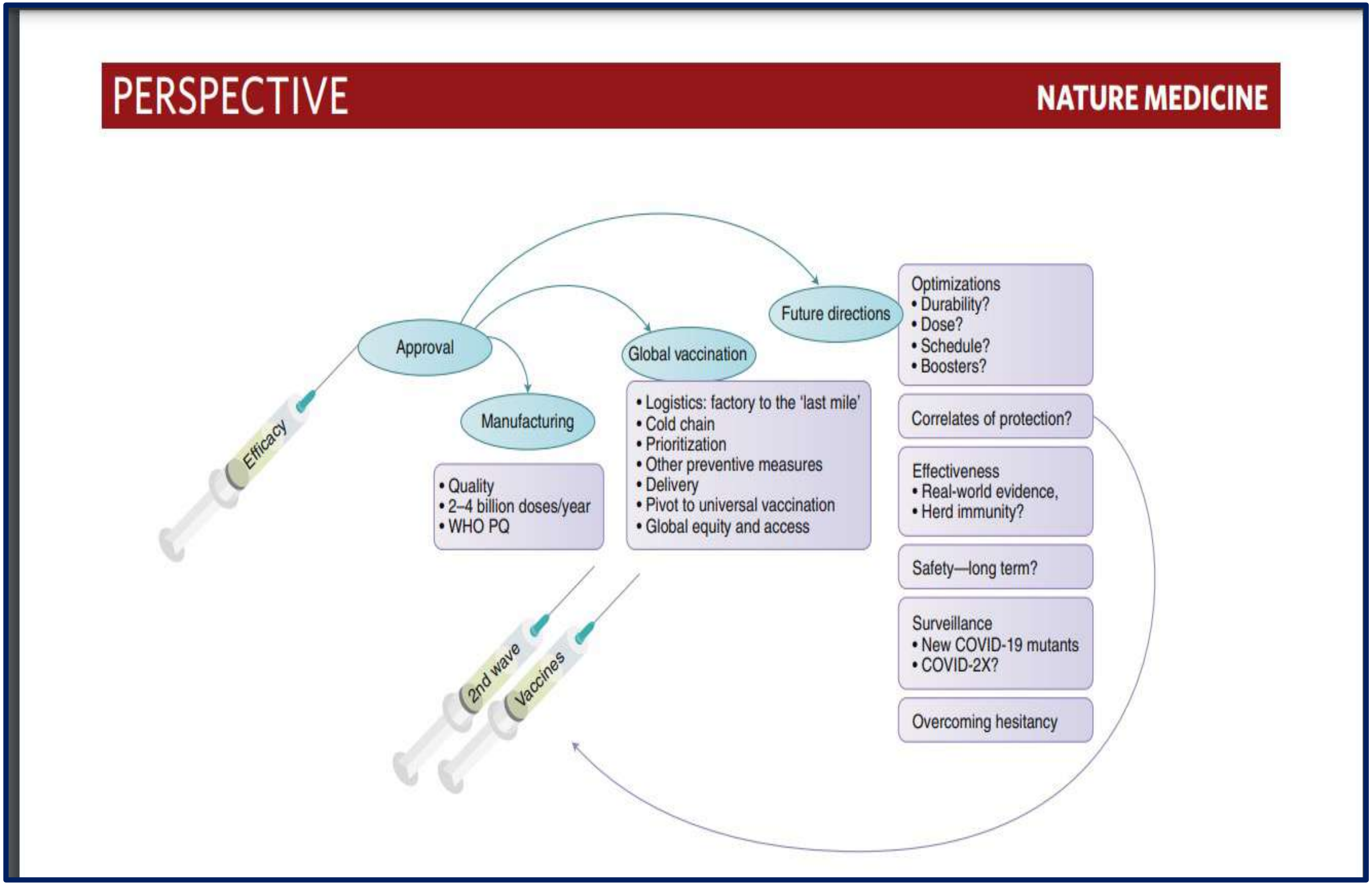
Office for **National Statistics**

Covid-19 overtakes 1918 Spanish flu as deadliest disease in American history

By Helen Branswell Sept. 20, 2021

Reprints

Nature Medicine | VOL 27 | February 2021 | 205–211 |
www.nature.com/naturemedicine



PERSPECTIVE

NATURE MEDICINE

- Quality
- 2–4 billion doses/year
- WHO PQ

- Logistics: factory to the 'last mile'
- Cold chain
- Prioritization
- Other preventive measures
- Delivery
- Pivot to universal vaccination
- Global equity and access

Optimizations
- Durability?
- Dose?
- Schedule?
- Boosters?

Correlates of protection?

Effectiveness
- Real-world evidence,
- Herd immunity?

Safety—long term?

Surveillance
- New COVID-19 mutants
- COVID-2X?

Overcoming hesitancy

New subvariants are masters of immune evasion

Vaccines and prior infection still prevent severe disease from new SARS-CoV-2 strains

By **Gretchen Vogel**

Once again, South Africa is at the forefront of the changing COVID-19 pandemic. Epidemiologists and virologists are watching closely as cases there rise sharply again, just 5 months after the Omicron variant caused a dramatic surge. This time, the drivers are two new subvariants of Omicron named BA.4 and BA.5, which the Network for Genomic Surveillance in South Africa first detected in January.

The new strains didn't have much of an impact initially, but over the past few weeks case numbers in South Africa jumped from roughly 1000 per day on 17 April to nearly 10,000 on 7 May. A third subvariant called BA.2.12.1 is spreading in the United States, driving increases along the East Coast.

It's still unclear whether the new subvariants will cause another global COVID-19 wave. But like the earlier versions of Omicron, they have a remarkable ability to evade immunity from vaccines, previous infection, or both—a disturbing portent for the future of the pandemic and a potentially serious complication for vaccine developers.

In most cases, vaccination or earlier infection still seem to provide protection from severe disease. "There's no reason to freak out," says John Moore, an immunologist at Weill Cornell Medicine. The new strains are "an additional hassle," he says, but "there's no indication that they're more dangerous or more pathogenic."

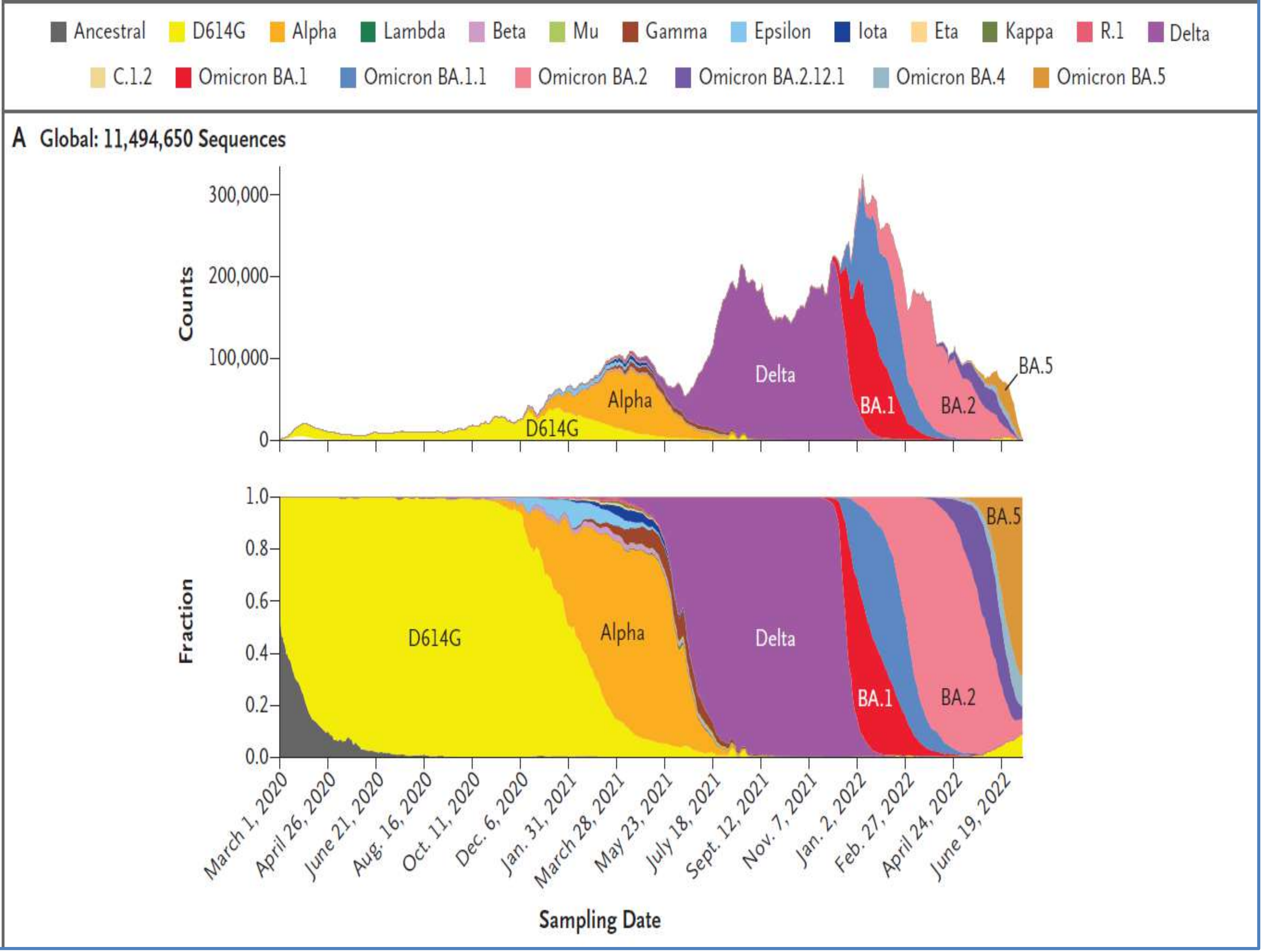
Hospitalizations in South Africa, for example, have increased, "but because it is starting from a very low level, it's not cause for alarm," says virologist Tulio de Oliveira of Stellenbosch University, who helped identify BA.4 and BA.5. Numbers of patients in intensive care units are as low as they have been since the start of the pandemic, he says. "At the moment, we expect something similar to the Omicron BA.1 wave," when hospitalization rates stayed manageable.

The new superspreaders do, however, showcase the restless virus' ability to find ways around the "immunity wall" built up over the past 2 years and to continue to circulate at high levels. Even if the new variants cause relatively little severe disease, "it's a numbers game," says Leif Erik Sander, an infectious disease expert at the Charité University Hospital in Berlin; enough new infections could still overwhelm health systems.

All three new strains share key mutations with the BA.2 strain of Omicron, which, like BA.1, emerged in southern Africa in October 2021. Initial studies by de Oliveira and Alex Sigal, an infectious disease expert at the Africa Health Research Institute in Durban, suggest BA.4 and BA.5 can elude the immunity of patients who were infected with the BA.1 strain, which in South Africa caused a much larger wave than BA.2. That may be in part because immunity has waned since South Africa's BA.1 wave peaked in December. People who were both vaccinated and infected had somewhat stronger protection, de Oliveira and Sigal reported in a 2 May preprint.

All three new variants have mutations that alter a key amino acid called L452, which may help explain their ability to dodge immunity. L452 is part of the receptor-binding domain, the part of the spike protein that locks onto cells, enabling infection. The domain is also a key target for protective antibodies.

The Delta variant that caused devastating surges around the world in 2021 had mutations in L452 as well, so many scientists


Ancestral
D614G
Alpha
Lambda
Beta
Mu
Gamma
Epsilon
Iota
Eta
Kappa
R.1
Delta
C.1.2
Omicron BA.1
Omicron BA.1.1
Omicron BA.2
Omicron BA.2.12.1
Omicron BA.4
Omicron BA.5
A Global: 11,494,650 Sequences
Counts
300,000
200,000
100,000
0
D614G
Alpha
Delta
BA.1
BA.2
BA.5
Fraction
1.0
0.8
0.6
0.4
0.2
0.0
D614G
Alpha
Delta
BA.1
BA.2
BA.5
March 1, 2020
April 26, 2020
June 21, 2020
Aug. 16, 2020
Oct. 11, 2020
Dec. 6, 2020
Jan. 31, 2021
March 28, 2021
May 23, 2021
July 18, 2021
Sept. 12, 2021
Nov. 7, 2021
Jan. 2, 2022
Feb. 27, 2022
April 24, 2022
June 19, 2022
Sampling Date

COVID19 AŞILARI VE RAPELLER

- AŞILAMA 14 MİLYON HAYAT KURTARDI
- BU KIŞ İÇİN RAPEL GEREKLİ
- GEÇEN KIŞ RAPEL YAPILSA ,ABD-300.000 kişinin hayatı kurtulacaktı
- ABD, NİSAN 2022 , >50 YAŞ ; 4 DOZ AŞILI OLANLAR İLE KARŞILAŞTIRILDIĞINDA
  - AŞISIZ;38 KAT
  - RAPELSİZ; 6 KAT
  - TEK RAPEL:4 KAT DAHA FAZLA ÖLDÜ
- HASTALIK GEÇİRMİŞ OLANDA DA EK DOZ HASTANEYE YATIŞI ÖNLEDİ
- GEREKSİNİM; TÜM VARYANTLARA ETKİLİ, UZUN SÜRELİ, BULAŞMAYI ÖNLEYEN AŞI

AŞI/BİLİM KARŞITLIĞI

Dogmatik düşünce, bilime güven duymamak

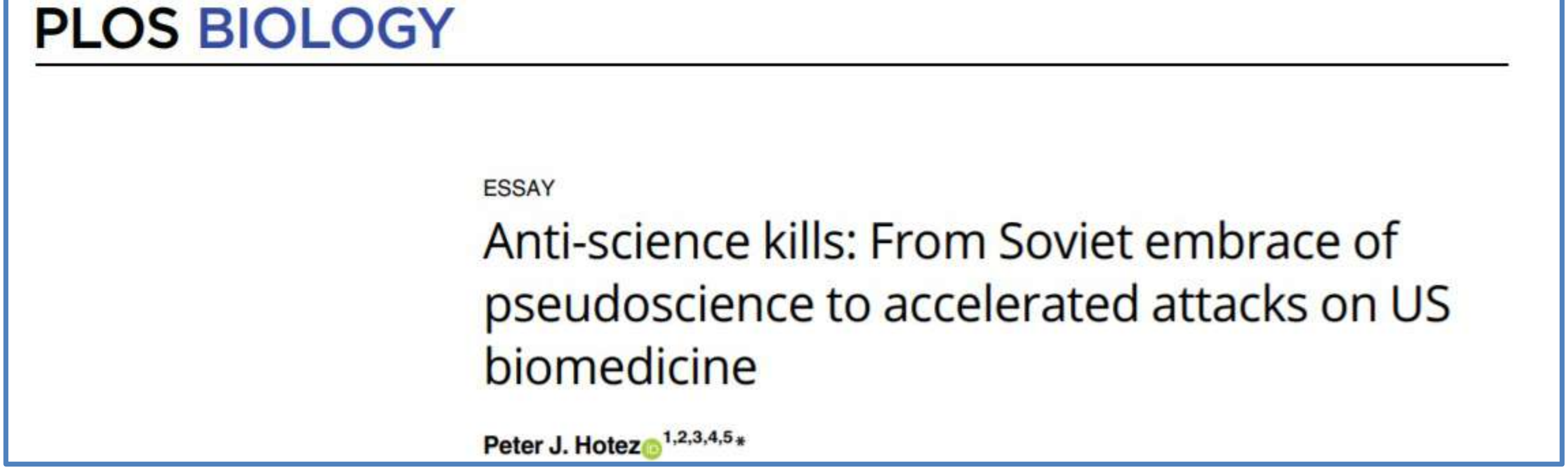
Batı Ortaçağı'nda hastalık kavramının algılanmasında temel öğeler*;

Majik düşünce (büyüsel), mistisizm (gizemcilik), obskürantizm (karanlıkçılık)

***Arda B: Batı Ortaçağında Hastalık Kavramı, Güneş Kitabevi , Ankara, 1997.**

Ten threats to global health in 2019

- Air pollution and climate change
- Noncommunicable diseases
- Threat of a global influenza pandemic
- Fragile and vulnerable settings, such as regions affected by drought and conflict
- Antimicrobial resistance
- Ebola and high-threat pathogens
- Weak primary care
- Vaccine Hesitancy
- Dengue
- HIV

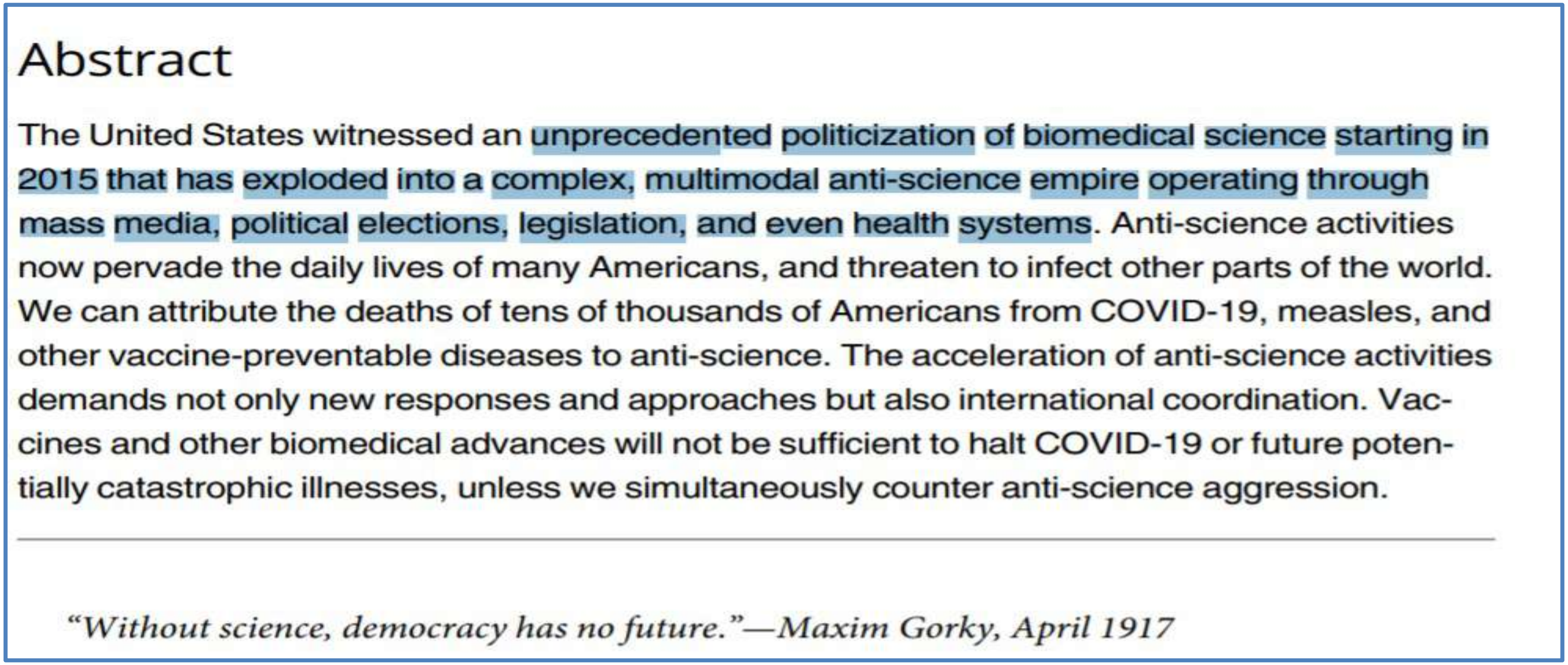


PLOS BIOLOGY

ESSAY

Anti-science kills: From Soviet embrace of pseudoscience to accelerated attacks on US biomedicine

Peter J. Hotez[1,2,3,4,5*]



Abstract

The United States witnessed an unprecedented politicization of biomedical science starting in 2015 that has exploded into a complex, multimodal anti-science empire operating through mass media, political elections, legislation, and even health systems. Anti-science activities now pervade the daily lives of many Americans, and threaten to infect other parts of the world. We can attribute the deaths of tens of thousands of Americans from COVID-19, measles, and other vaccine-preventable diseases to anti-science. The acceleration of anti-science activities demands not only new responses and approaches but also international coordination. Vaccines and other biomedical advances will not be sufficient to halt COVID-19 or future potentially catastrophic illnesses, unless we simultaneously counter anti-science aggression.

> *"Without science, democracy has no future."—Maxim Gorky, April 1917*

ÜLKEMİZDE AŞI REDDİ

- **Toplumun %55-75'i aşılara güven duymaktadır.**
- **Her tür aşıya karşı olanların oranı %2den azdır.**
- **Reddeden aile sayısı; 2015 'te yaklaşık ……5bin**

2016'da ………………12bin

2017'de ………………23bin

T.C. Sağlık Bakanlığı Sağlık İstatistikleri Yıllığı 2017 Haber Bülteni,2018.


Esin Davutoğlu Şenol, RAI Amsterdam'da.

Esin Davutoğlu Şenol paylaştı

14 Nisan 2019 ·

21. yy kesinlikle viral olacak ... Virüsler yüzyılı
domine edecek
İnfeksiyon Hastalıklarının , seyahatlerimiz ile
sınırlar aştığını, 20.yy da olduğu gibi
politikanın ve bilimin gündeminde ilk sırada
kalacağını göreceğiz..
Geleceğin Tıp" ı , kişiselleştirilmiş tıp , 4P
kuralı, mikrobiyom ,vektörler , direnç ve tabii
mikroplar ile şahane yolculuklarımız ve
maceralarımızı konuşacağız..
Tabii, inanca meyilli kişilerin ,infeksiyoncu
olmayan cemaatlerin yalan- dolan
rüzgarlarına kapılmaması zor olacak..
Ben bloğumda çok güzel
#kongresonrasınotlarım yapacağım
Tavsiyem, bilimden kopmayın, bilim dışı
verileri şüphe ile karşılayın ve bloğuma bakın
💪😘😀😀
#eccmid2019 #profdresinşenol

Esin Davutoğlu Şenol

22 Ağu 2013 ·

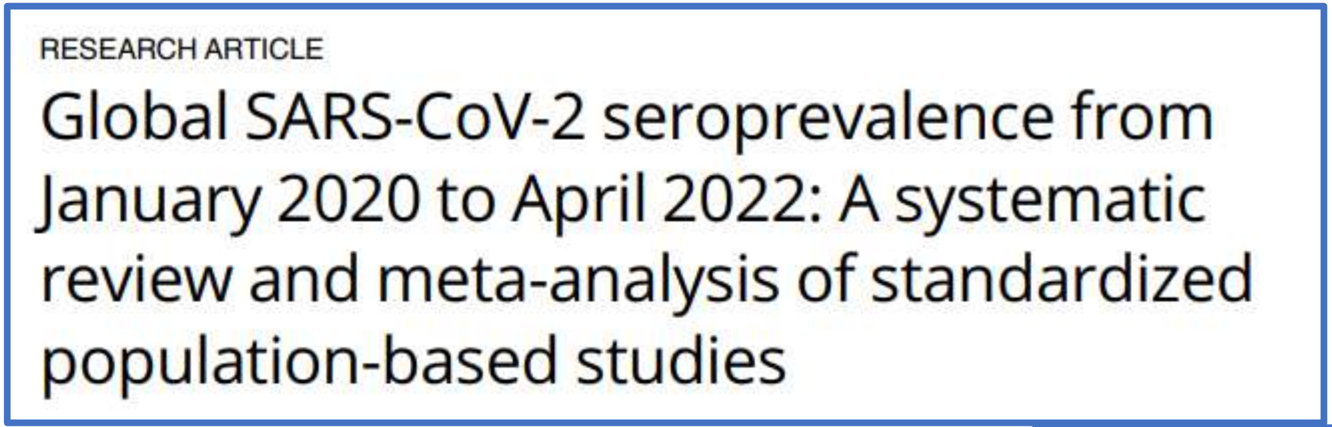
Daha nice yeni virusler çıkacak..Dünya
almıyor bu kalabalığı diye bağıracak

Klimik Derneği

22 Ağu 2013 ·

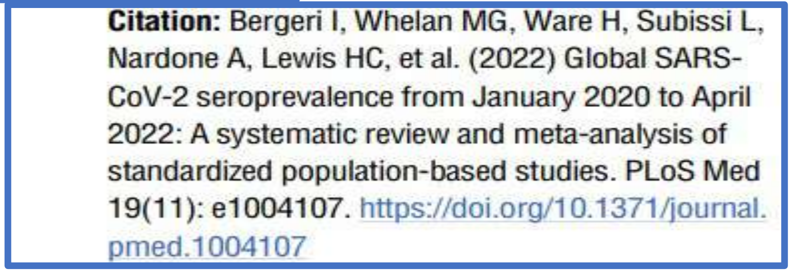
Suudi Arabistan'daki Yarasalarda 47 Kişiyi
Öldüren Gizemli Virus (MERS-CoV)
Saptandı http://www.klimik.... Devamını Gör

Suudi Arabistan'daki Yarasalarda 47 Kişiyi Öldüren Gizemli Virus (MERS-CoV) Saptandı

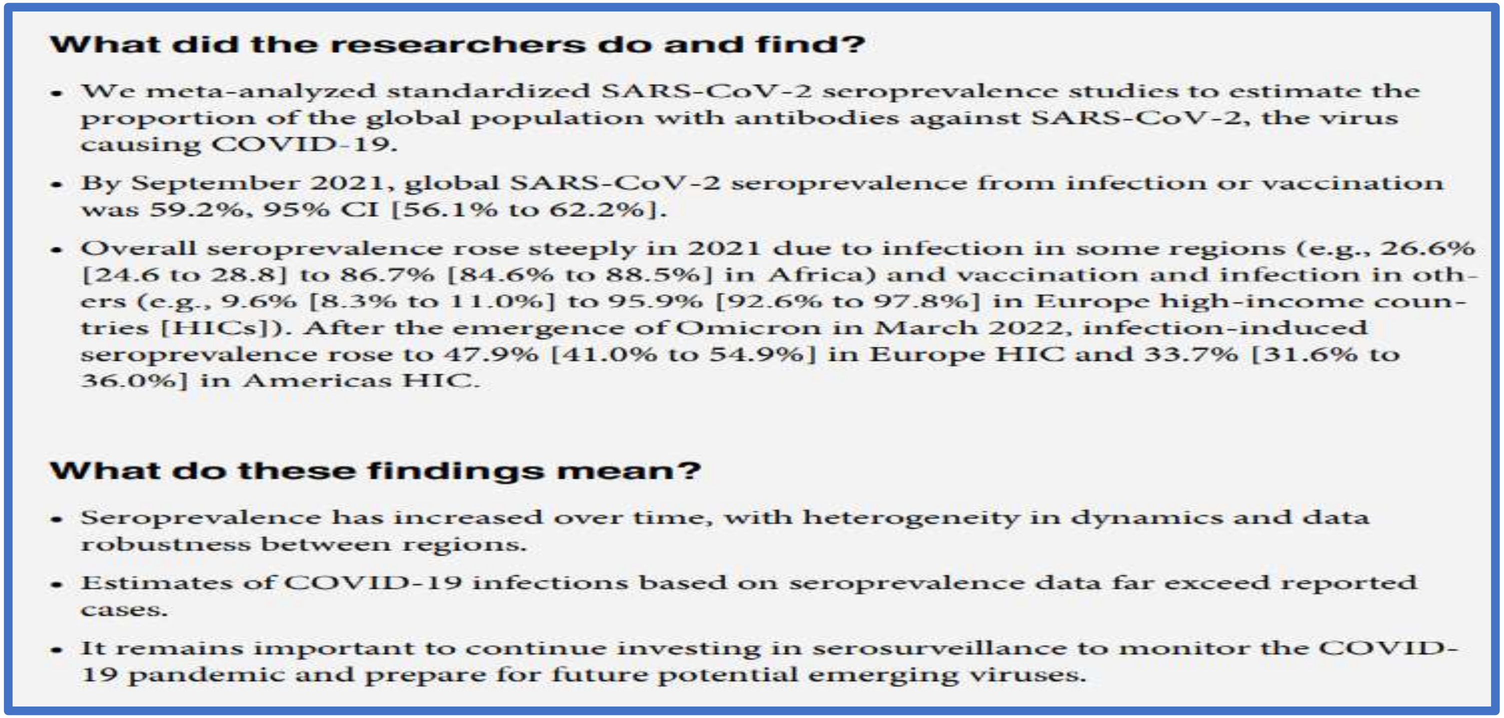


RESEARCH ARTICLE

Global SARS-CoV-2 seroprevalence from January 2020 to April 2022: A systematic review and meta-analysis of standardized population-based studies



Citation: Bergeri I, Whelan MG, Ware H, Subissi L, Nardone A, Lewis HC, et al. (2022) Global SARS-CoV-2 seroprevalence from January 2020 to April 2022: A systematic review and meta-analysis of standardized population-based studies. PLoS Med 19(11): e1004107. https://doi.org/10.1371/journal.pmed.1004107



What did the researchers do and find?

- We meta-analyzed standardized SARS-CoV-2 seroprevalence studies to estimate the proportion of the global population with antibodies against SARS-CoV-2, the virus causing COVID-19.
- By September 2021, global SARS-CoV-2 seroprevalence from infection or vaccination was 59.2%, 95% CI [56.1% to 62.2%].
- Overall seroprevalence rose steeply in 2021 due to infection in some regions (e.g., 26.6% [24.6 to 28.8] to 86.7% [84.6% to 88.5%] in Africa) and vaccination and infection in others (e.g., 9.6% [8.3% to 11.0%] to 95.9% [92.6% to 97.8%] in Europe high-income countries [HICs]). After the emergence of Omicron in March 2022, infection-induced seroprevalence rose to 47.9% [41.0% to 54.9%] in Europe HIC and 33.7% [31.6% to 36.0%] in Americas HIC.

What do these findings mean?

- Seroprevalence has increased over time, with heterogeneity in dynamics and data robustness between regions.
- Estimates of COVID-19 infections based on seroprevalence data far exceed reported cases.
- It remains important to continue investing in serosurveillance to monitor the COVID-19 pandemic and prepare for future potential emerging viruses.

The Journal of Infectious Diseases

PERSPECTIVE

The Concept of Classical Herd Immunity May Not Apply to COVID-19

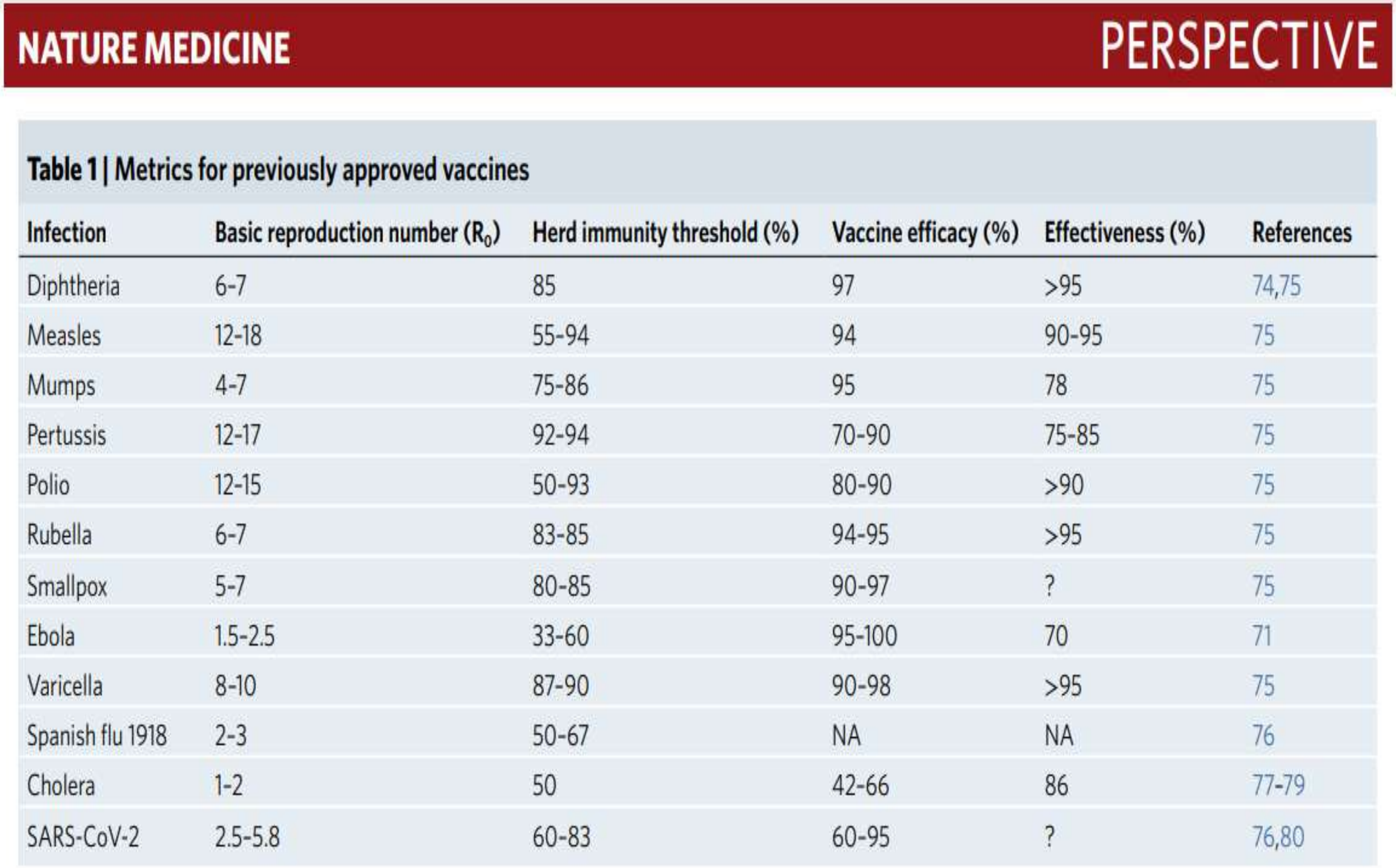
David M. Morens,[1] Gregory K. Folkers,[1] and Anthony S. Fauci[1]

[1]National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, USA

Keywords. COVID-19; SARS-CoV-2; herd immunity; history.

Nature Medicine | VOL 27 | February 2021 | 205–211 |

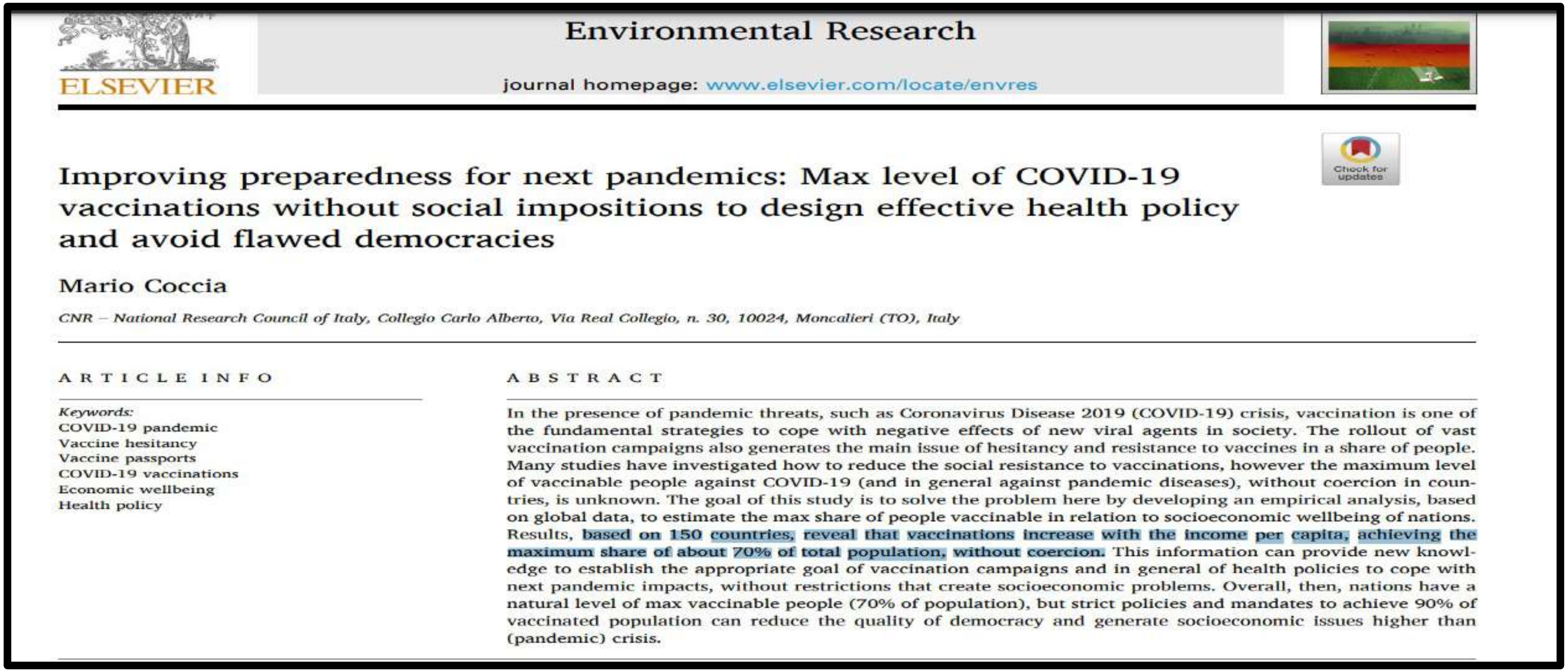
www.nature.com/naturemedicine



NATURE MEDICINE PERSPECTIVE

Table 1 | Metrics for previously approved vaccines

Infection	Basic reproduction number (R_0)	Herd immunity threshold (%)	Vaccine efficacy (%)	Effectiveness (%)	References
Diphtheria	6-7	85	97	>95	74,75
Measles	12-18	55-94	94	90-95	75
Mumps	4-7	75-86	95	78	75
Pertussis	12-17	92-94	70-90	75-85	75
Polio	12-15	50-93	80-90	>90	75
Rubella	6-7	83-85	94-95	>95	75
Smallpox	5-7	80-85	90-97	?	75
Ebola	1.5-2.5	33-60	95-100	70	71
Varicella	8-10	87-90	90-98	>95	75
Spanish flu 1918	2-3	50-67	NA	NA	76
Cholera	1-2	50	42-66	86	77-79
SARS-CoV-2	2.5-5.8	60-83	60-95	?	76,80



Environmental Research

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Improving preparedness for next pandemics: Max level of COVID-19 vaccinations without social impositions to design effective health policy and avoid flawed democracies

Mario Coccia

CNR – National Research Council of Italy, Collegio Carlo Alberto, Via Real Collegio, n. 30, 10024, Moncalieri (TO), Italy

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ABSTRACT

In the presence of pandemic threats, such as Coronavirus Disease 2019 (COVID-19) crisis, vaccination is one of the fundamental strategies to cope with negative effects of new viral agents in society. The rollout of vast vaccination campaigns also generates the main issue of hesitancy and resistance to vaccines in a share of people. Many studies have investigated how to reduce the social resistance to vaccinations, however the maximum level of vaccinable people against COVID-19 (and in general against pandemic diseases), without coercion in countries, is unknown. The goal of this study is to solve the problem here by developing an empirical analysis, based on global data, to estimate the max share of people vaccinable in relation to socioeconomic wellbeing of nations. Results, based on 150 countries, reveal that vaccinations increase with the income per capita, achieving the maximum share of about 70% of total population, without coercion. This information can provide new knowledge to establish the appropriate goal of vaccination campaigns and in general of health policies to cope with next pandemic impacts, without restrictions that create socioeconomic problems. Overall, then, nations have a natural level of max vaccinable people (70% of population), but strict policies and mandates to achieve 90% of vaccinated population can reduce the quality of democracy and generate socioeconomic issues higher than (pandemic) crisis.

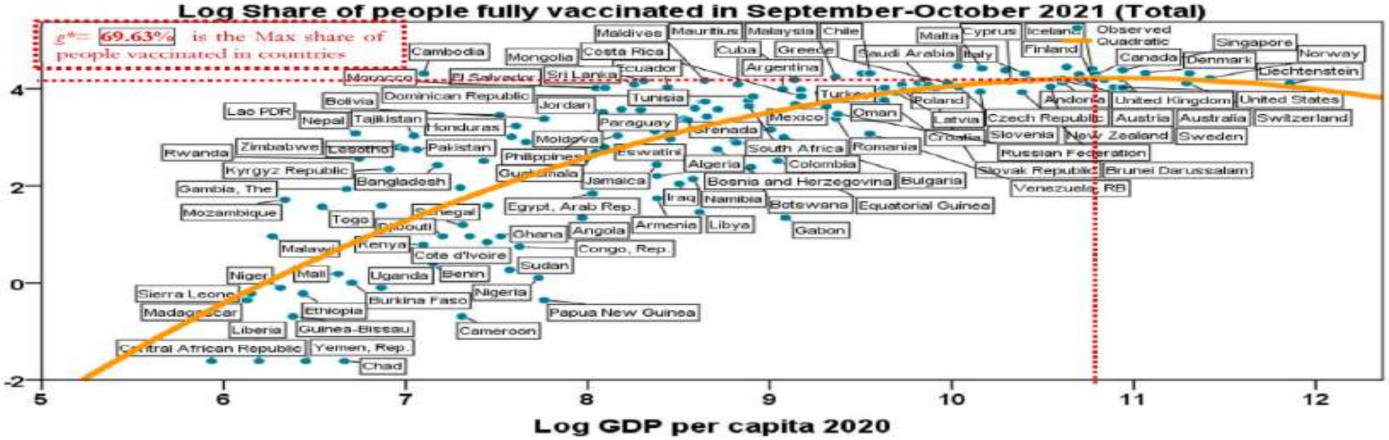


Fig. 2. The maximum level of vaccinated people (69.63%) based on full sample of countries.

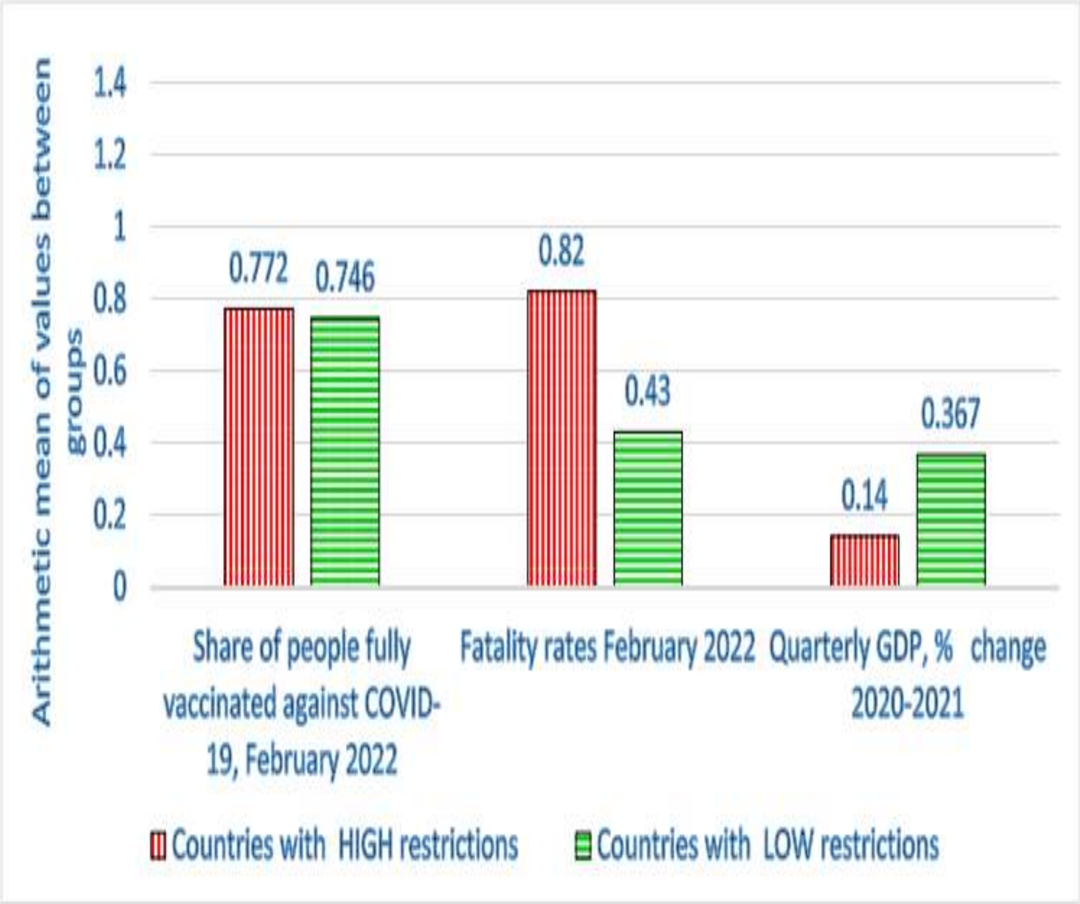
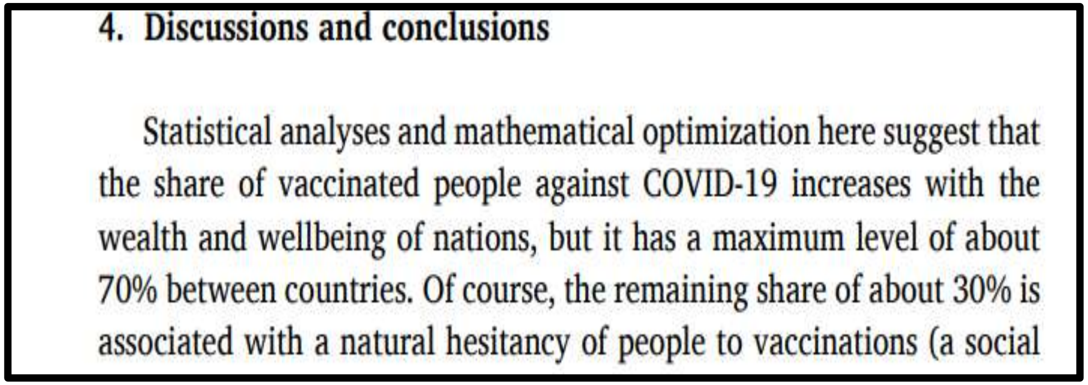


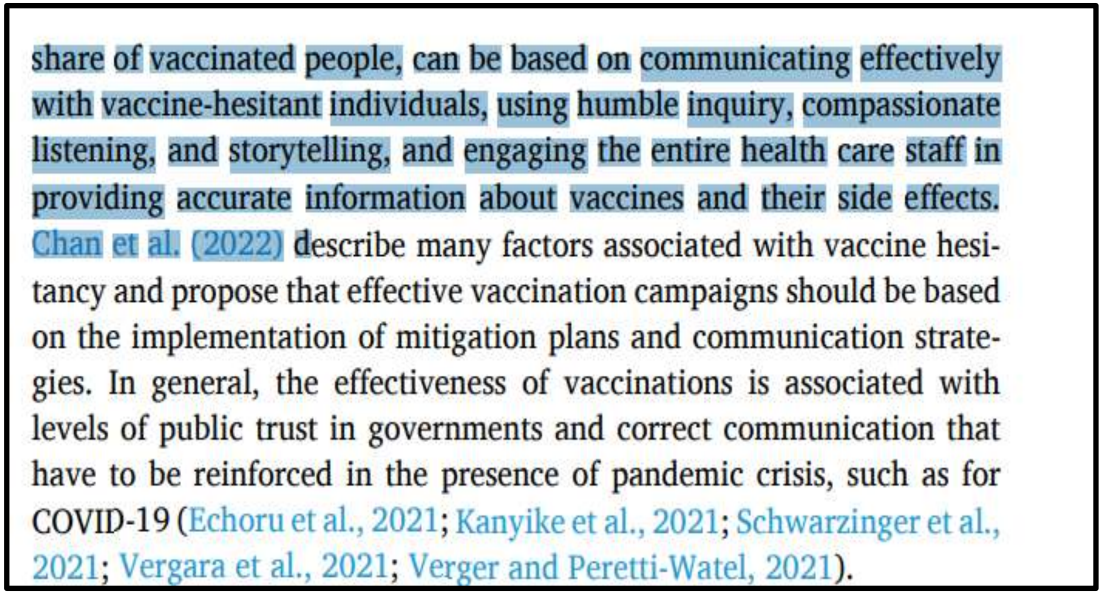
Fig. 3. Comparative analysis of health and economic indicators between countries with *high* and *low* restrictions to cope with COVID-19 pandemic crisis.



4. Discussions and conclusions

Statistical analyses and mathematical optimization here suggest that the share of vaccinated people against COVID-19 increases with the wealth and wellbeing of nations, but it has a maximum level of about 70% between countries. Of course, the remaining share of about 30% is associated with a natural hesitancy of people to vaccinations (a social

sosyal, ekonomik, politik ve psikolojik faktörler



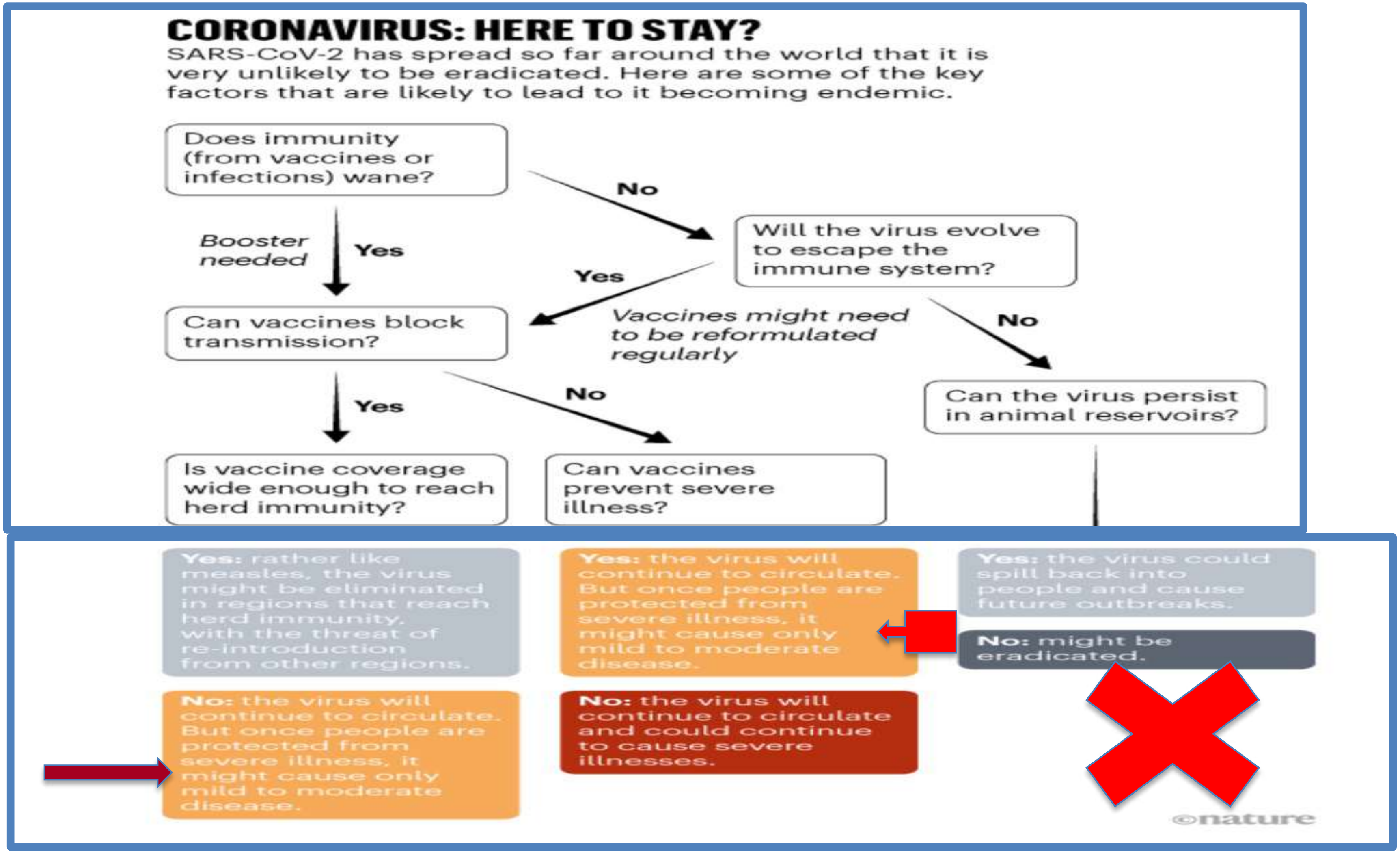
share of vaccinated people, can be based on communicating effectively with vaccine-hesitant individuals, using humble inquiry, compassionate listening, and storytelling, and engaging the entire health care staff in providing accurate information about vaccines and their side effects. Chan et al. (2022) describe many factors associated with vaccine hesitancy and propose that effective vaccination campaigns should be based on the implementation of mitigation plans and communication strategies. In general, the effectiveness of vaccinations is associated with levels of public trust in governments and correct communication that have to be reinforced in the presence of pandemic crisis, such as for COVID-19 (Echoru et al., 2021; Kanyike et al., 2021; Schwarzinger et al., 2021; Vergara et al., 2021; Verger and Peretti-Watel, 2021).

NEWS FEATURE · 16 FEBRUARY 2021

The coronavirus is here to stay — here's what that means

A *Nature* survey shows many scientists expect the virus that causes COVID-19 to become endemic, but it could pose less danger over time.

Nicky Phillips



CORONAVIRUS: HERE TO STAY?

SARS-CoV-2 has spread so far around the world that it is very unlikely to be eradicated. Here are some of the key factors that are likely to lead to it becoming endemic.

Yes: rather like measles, the virus might be eliminated in regions that reach herd immunity, with the threat of re-introduction from other regions.

No: the virus will continue to circulate. But once people are protected from severe illness, it might cause only mild to moderate disease.

Yes: the virus will continue to circulate. But once people are protected from severe illness, it might cause only mild to moderate disease.

No: the virus will continue to circulate and could continue to cause severe illnesses.

Yes: the virus could spill back into people and cause future outbreaks.

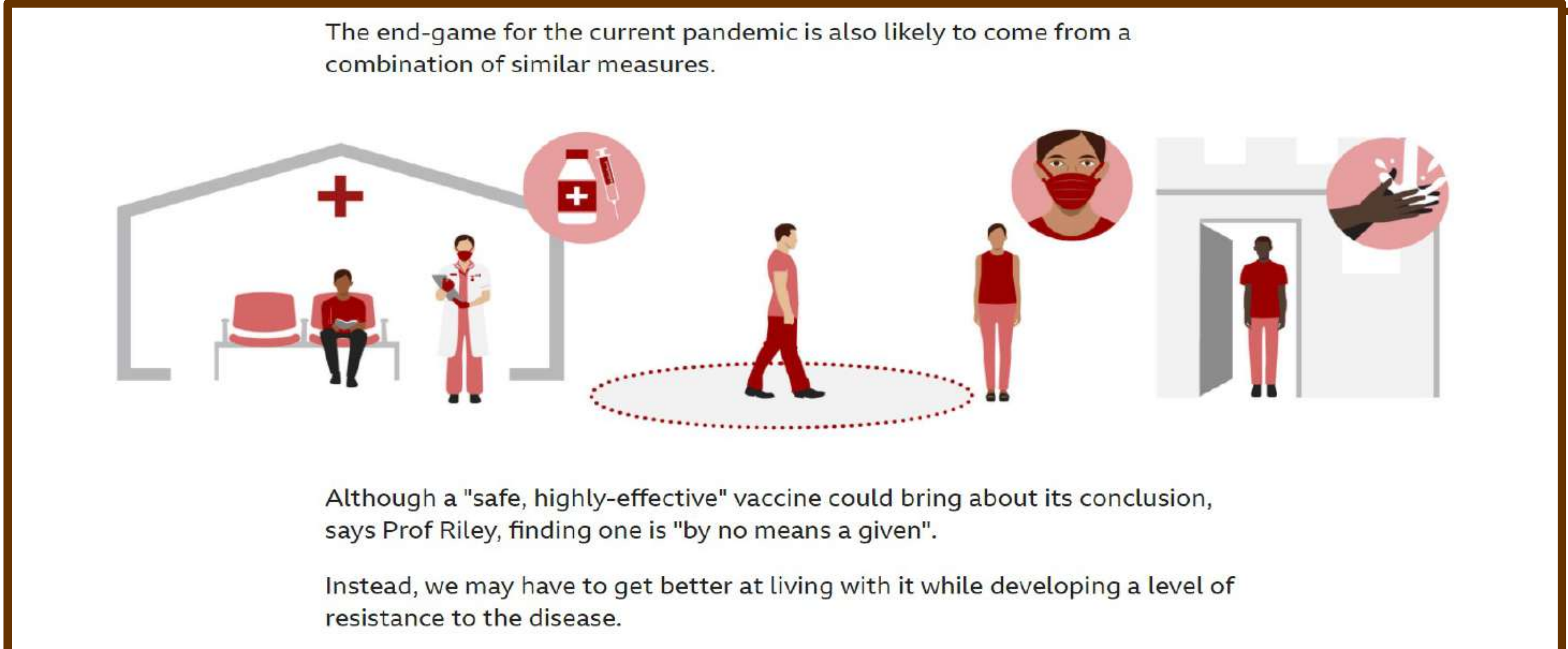
No: might be eradicated.

©nature

How do pandemics end?

By the Visual Journalism Team 7 October 2020 | News

We are in the grip of a pandemic like none other in living memory. While people are pinning their hopes on a vaccine to wipe it out, the fact is most of the infections faced by our ancestors are still with us.



The end-game for the current pandemic is also likely to come from a combination of similar measures.

Although a "safe, highly-effective" vaccine could bring about its conclusion, says Prof Riley, finding one is "by no means a given".

Instead, we may have to get better at living with it while developing a level of resistance to the disease.

Vaccine manufacturing facilities have had to rapidly ramp up their capabilities to produce RNA vaccines.

HOW COVID UNLOCKED THE POWER OF RNA

Vaccine research and development might never be the same again. By Elie Dolgin

It was a Friday afternoon in March 2013 when Andy Geall got the call. Three people in China had just become infected with a new strain of avian influenza. The global head of vaccines research at Novartis, Rino Rappuoli, wanted to know whether Geall and his colleagues were ready to put their new vaccine technology to the test.

A year earlier, Geall's team at Novartis's US research hub in Cambridge, Massachusetts, had packaged strings of RNA nucleotides inside of small fat droplets, known as lipid nanoparticles (LNPs), and used them to successfully vaccinate rats against a respiratory virus[1]. Could they now do the same for the novel flu strain? And could they do it as fast as possible?

As Geall, head of the RNA group, recalls: "I said, 'Yeah, sure. Just send us the sequence.'" By Monday, the team had begun synthesizing the RNA. By Wednesday, they were assembling the vaccine. By the weekend, they were testing it in cells — a week later, in mice[2].

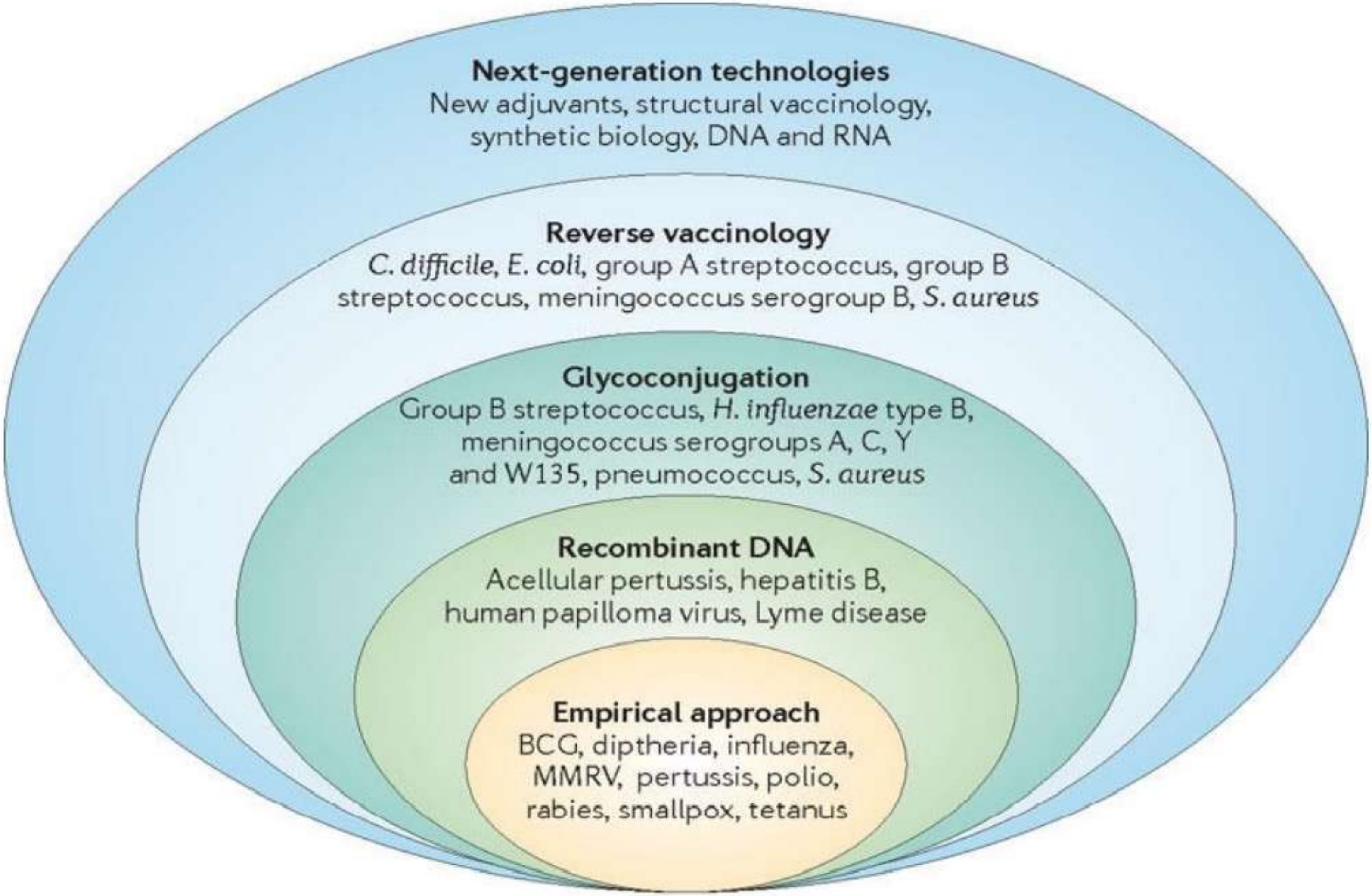
The development happened at a breakneck speed[3]. The Novartis team had achieved in one month what typically took a year or more.

But at the time, the ability to manufacture clinical-grade RNA was limited. Geall and his colleagues would never find out whether this vaccine, and several others that they developed, would work in people. In 2015, Novartis sold its vaccines business.

Five years and one global pandemic later, RNA vaccines are proving their worth. Last month, two RNA vaccine candidates — one from US pharmaceutical giant Pfizer and BioNTech in Mainz, Germany, and another from Moderna in Cambridge, Massachusetts — won emergency approval from regulators in several countries to fight COVID-19.

The era of RNA vaccines has arrived — and dozens of companies are getting in the game. "All of the major pharmas are, in one way or the other, now testing out the technology," says Jeffrey Ulmer, former head of preclinical research and development at GlaxoSmithKline's vaccine division in Rockville, Maryland, and before that a member of Geall's team at Novartis.

The idea of using RNA in vaccines has been around for nearly three decades. More streamlined than conventional approaches, the genetic technology allows researchers to fast-track many stages of vaccine research and development. The intense interest now could lead to solutions for particularly recalcitrant diseases, such as tuberculosis, HIV and malaria. And the speed at which they can be made could improve seasonal-flu vaccines.



Next-generation technologies
New adjuvants, structural vaccinology, synthetic biology, DNA and RNA

Reverse vaccinology
C. difficile, *E. coli*, group A streptococcus, group B streptococcus, meningococcus serogroup B, *S. aureus*

Glycoconjugation
Group B streptococcus, *H. influenzae* type B, meningococcus serogroups A, C, Y and W135, pneumococcus, *S. aureus*

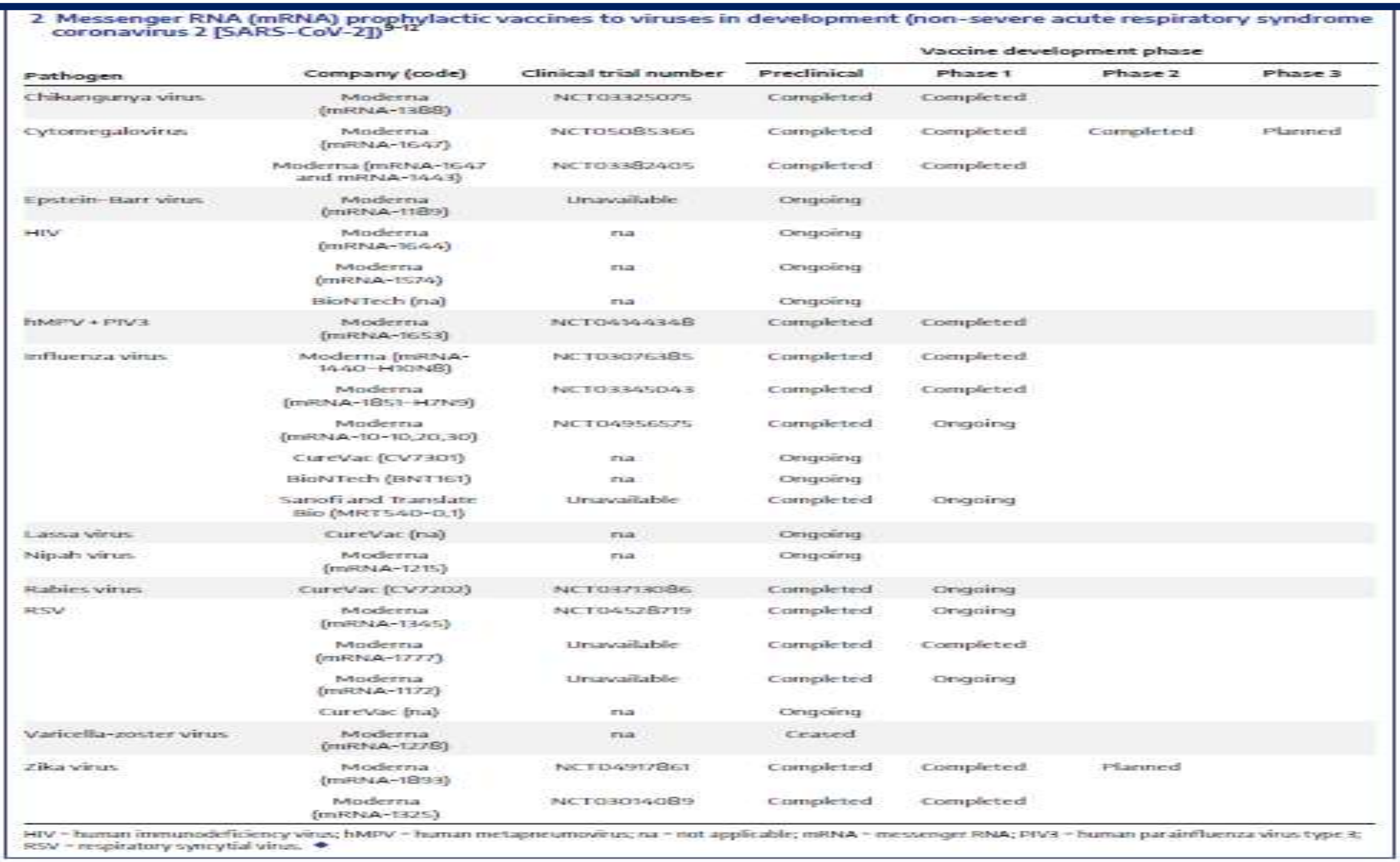
Recombinant DNA
Acellular pertussis, hepatitis B, human papilloma virus, Lyme disease

Empirical approach
BCG, diptheria, influenza, MMRV, pertussis, polio, rabies, smallpox, tetanus

Nature Reviews | Immunology

mRNA vaccines: a transformative technology with applications beyond COVID-19

mRNA vaccines can be used for broader infectious diseases prevention and cancer therapy



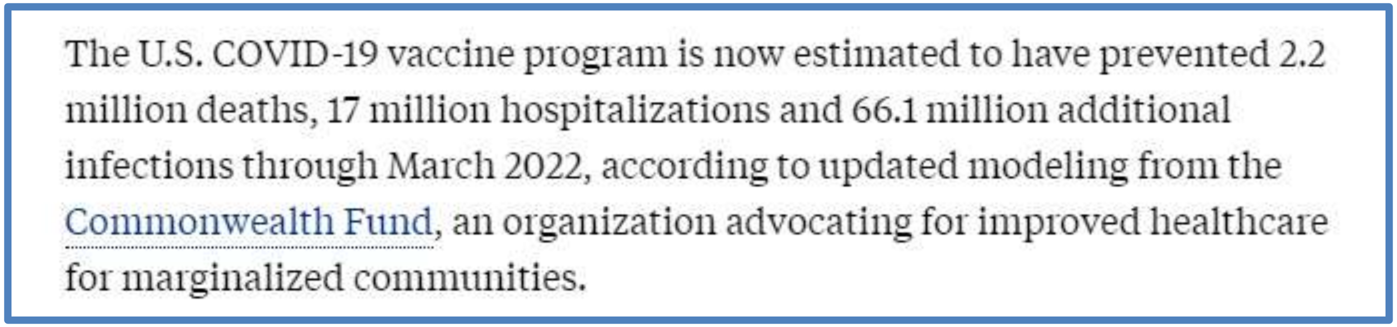
2 Messenger RNA (mRNA) prophylactic vaccines to viruses in development (non-severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2])[9-12]

			Vaccine development phase			
Pathogen	**Company (code)**	**Clinical trial number**	**Preclinical**	**Phase 1**	**Phase 2**	**Phase 3**
Chikungunya virus	Moderna (mRNA-1388)	NCT03325075	Completed	Completed		
Cytomegalovirus	Moderna (mRNA-1647)	NCT05085366	Completed	Completed	Completed	Planned
	Moderna (mRNA-1647 and mRNA-1443)	NCT03382405	Completed	Completed		
Epstein–Barr virus	Moderna (mRNA-1189)	Unavailable	Ongoing			
HIV	Moderna (mRNA-1644)	na	Ongoing			
	Moderna (mRNA-1574)	na	Ongoing			
	BioNTech (na)	na	Ongoing			
hMPV + PIV3	Moderna (mRNA-1653)	NCT04144348	Completed	Completed		
Influenza virus	Moderna (mRNA-1440–H10N8)	NCT03076385	Completed	Completed		
	Moderna (mRNA-1851–H7N9)	NCT03345043	Completed	Completed		
	Moderna (mRNA-10-10,20,30)	NCT04956575	Completed	Ongoing		
	CureVac (CV7301)	na	Ongoing			
	BioNTech (BNT161)	na	Ongoing			
	Sanofi and Translate Bio (MRT540-0,1)	Unavailable	Completed	Ongoing		
Lassa virus	CureVac (na)	na	Ongoing			
Nipah virus	Moderna (mRNA-1215)	na	Ongoing			
Rabies virus	CureVac (CV7202)	NCT03713086	Completed	Ongoing		
RSV	Moderna (mRNA-1345)	NCT04528719	Completed	Ongoing		
	Moderna (mRNA-1777)	Unavailable	Completed	Completed		
	Moderna (mRNA-1172)	Unavailable	Completed	Ongoing		
	CureVac (na)	na	Ongoing			
Varicella-zoster virus	Moderna (mRNA-1278)	na	Ceased			
Zika virus	Moderna (mRNA-1893)	NCT04917861	Completed	Completed	Planned	
	Moderna (mRNA-1325)	NCT03014089	Completed	Completed		

HIV – human immunodeficiency virus; hMPV – human metapneumovirus; na – not applicable; mRNA – messenger RNA; PIV3 – human parainfluenza virus type 3; RSV – respiratory syncytial virus. ◆

COVID vaccine program prevented millions of US deaths, study finds

The COVID vaccine program is estimated to have prevented 2.2 million deaths.



The U.S. COVID-19 vaccine program is now estimated to have prevented 2.2 million deaths, 17 million hospitalizations and 66.1 million additional infections through March 2022, according to updated modeling from the Commonwealth Fund, an organization advocating for improved healthcare for marginalized communities.

WHO/ECDC: Nearly half a million lives saved by COVID-19 vaccination in less than a year

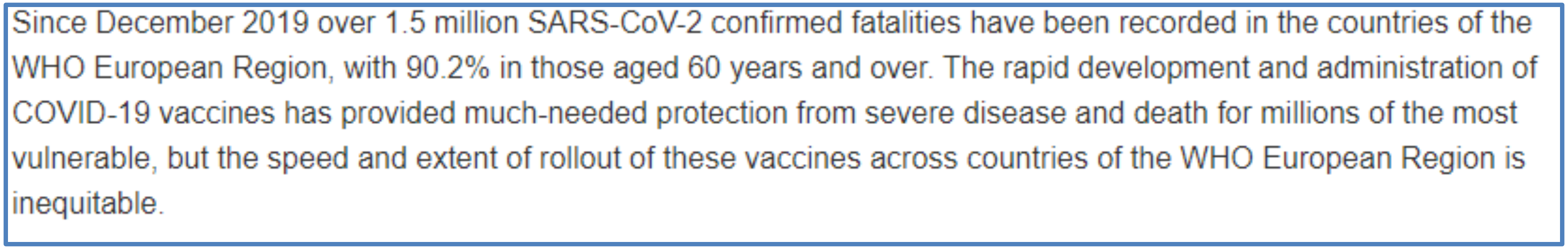
Press release

25 Nov 2021

A new study by the WHO Regional Office for Europe and European Centre for Disease Prevention and Control (ECDC) published in Eurosurveillance estimates that 470,000 lives have been saved among those aged 60 years and over since the start of COVID-19 vaccination roll-out in 33 countries across the WHO European Region.

This estimate does not include lives saved by vaccinating people less than 60 years nor lives saved from the indirect effect of vaccination because of a reduction in transmission.

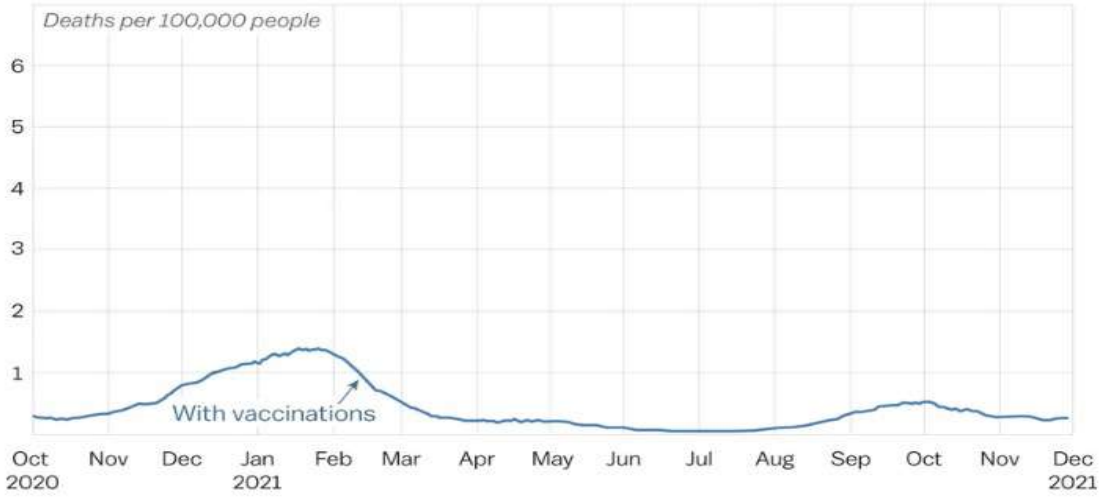
Dr Hans Henri P. Kluge, WHO Regional Director for Europe says, "COVID-19 has exacted a devastating death toll in our Region, but we can now categorically say that without COVID-19 vaccines as a tool to contain this pandemic, many more people would have died.



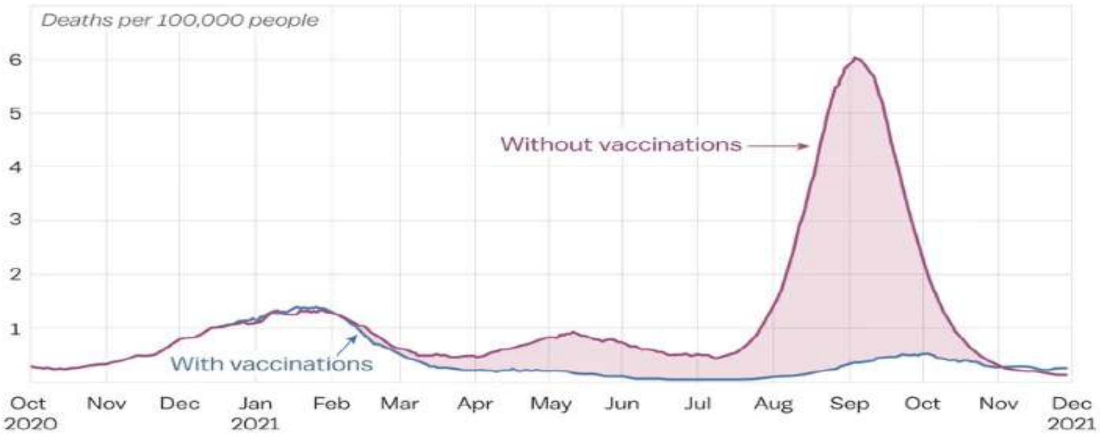
Since December 2019 over 1.5 million SARS-CoV-2 confirmed fatalities have been recorded in the countries of the WHO European Region, with 90.2% in those aged 60 years and over. The rapid development and administration of COVID-19 vaccines has provided much-needed protection from severe disease and death for millions of the most vulnerable, but the speed and extent of rollout of these vaccines across countries of the WHO European Region is inequitable.

US Covid-19 deaths, with and without vaccines

A graph of pre-omicron US Covid-19 deaths tells a bleak story, with loss of life peaking in early 2021 and again when the delta variant surged in the fall.



But if you compare the actual death toll to an estimate of the lives that would have been lost without vaccines, the losses are put into new perspective.



Note: Estimates through November 2021

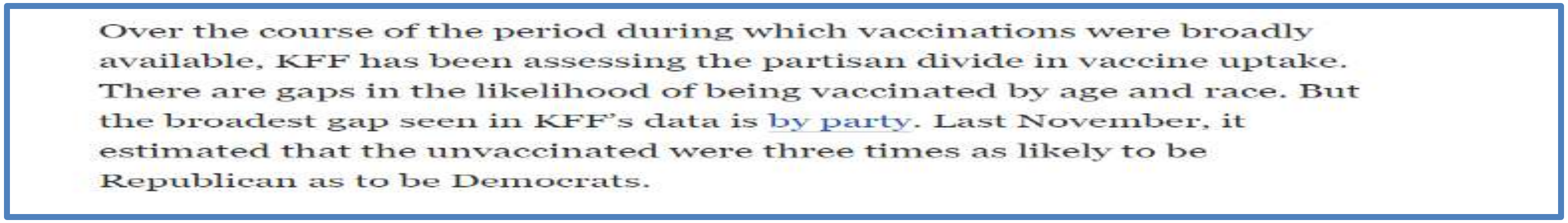
Source: Eric C. Schneider et al., *The U.S. COVID-19 Vaccination Program at One Year: How Many Deaths and Hospitalizations Were Averted?* (Commonwealth Fund, December 2021)

The Washington Post
Democracy Dies in Darkness

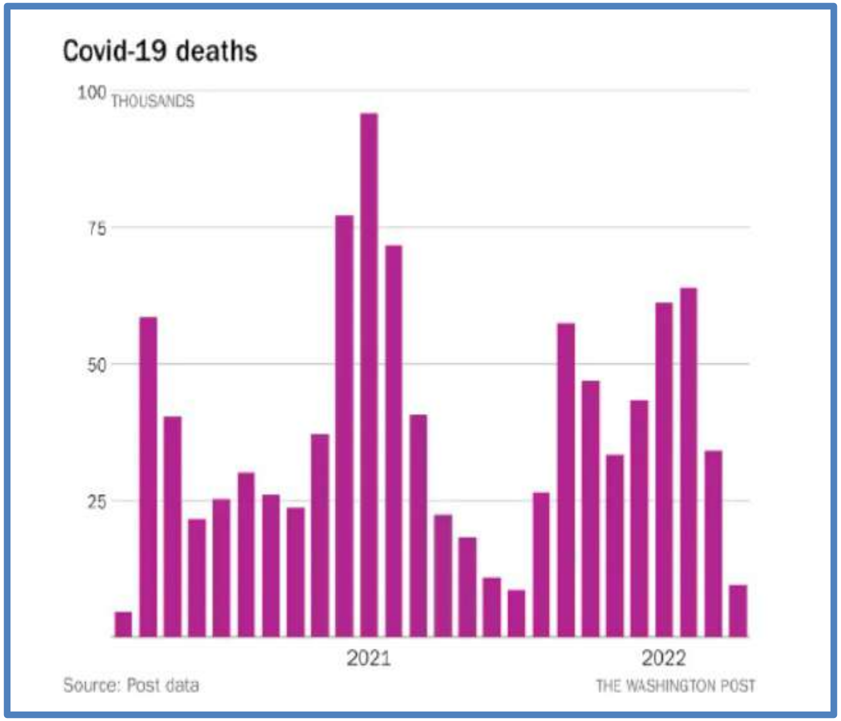
Politics Fact Checker Biden administration The 202s Polling Redistricting tracker Elections

POLITICS

Quarter of U.S. covid deaths were probably preventable with vaccination



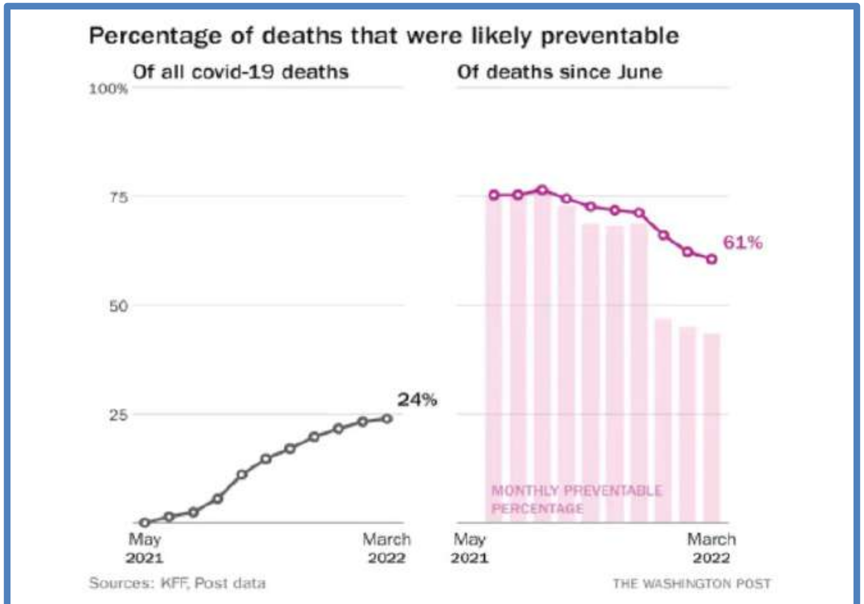
Over the course of the period during which vaccinations were broadly available, KFF has been assessing the partisan divide in vaccine uptake. There are gaps in the likelihood of being vaccinated by age and race. But the broadest gap seen in KFF's data is by party. Last November, it estimated that the unvaccinated were three times as likely to be Republican as to be Democrats.



Covid-19 deaths

Source: Post data

THE WASHINGTON POST



Percentage of deaths that were likely preventable

Sources: KFF, Post data

THE WASHINGTON POST

Since this analysis is based on national data, the researchers didn't break down the number of preventable deaths per state. But we would

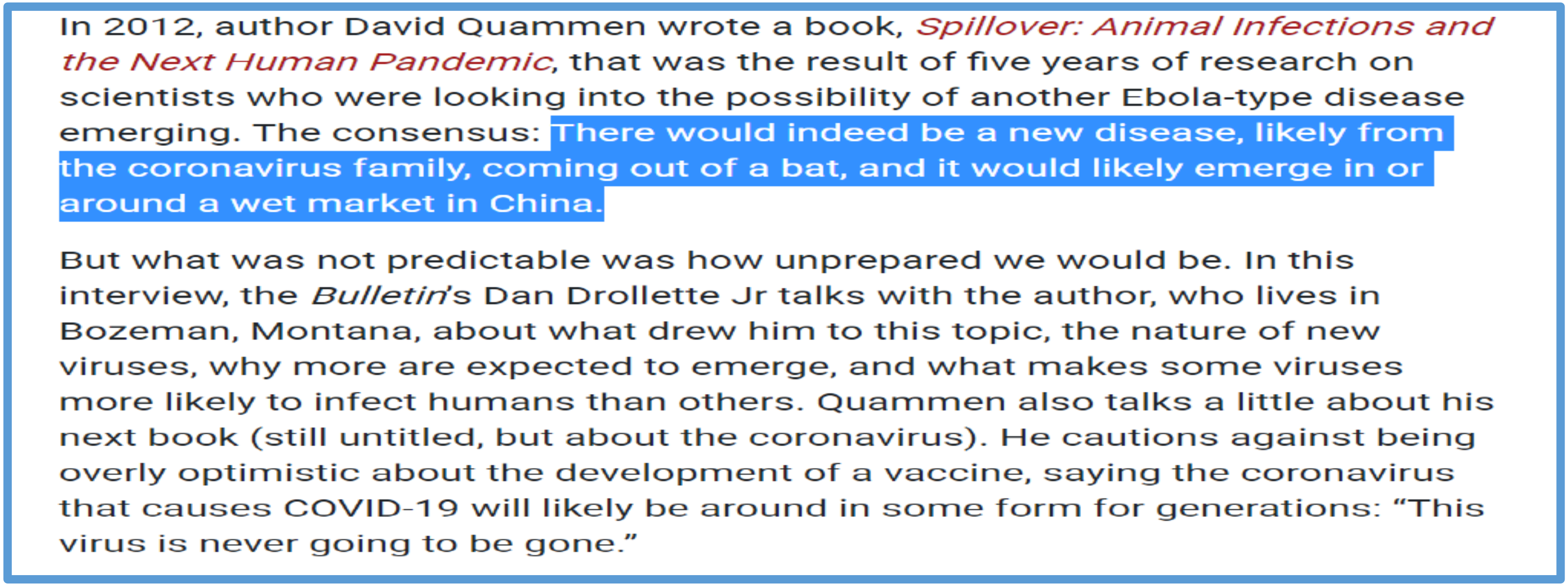
Yakın tarihli salgınlar ile mücadelerimizden öğrendiklerimiz şöyle, HIV pandemisinden bildiğimiz şey hiçbir zaman tek bir önlemin yeterli olmayacağı ve ekonomik ve sosyal olarak korumamız gereken gruplar olduğu.

David Quammen, while accompanying a wolf collaring and tracking operation in Yellowstone National Park for a National Geographic article. Image courtesy of Ronan Donovan

Adam Kucharski'den

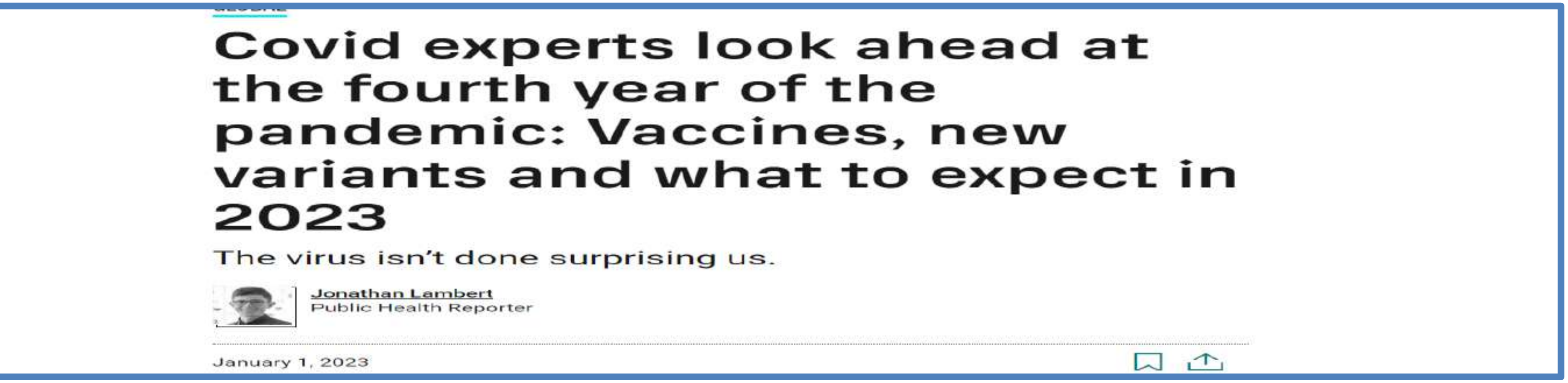
" Bir pandemi gören yalnızca bir pandemi görür .Bizi şimdi kıyıya çıkaran şeyler bir daha ki sefere işimize yaramayabilir"

Portrait of David Quammen in the backcountry of Yellowstone National Park. Image courtesy of Ronan Donovan



In 2012, author David Quammen wrote a book, *Spillover: Animal Infections and the Next Human Pandemic*, that was the result of five years of research on scientists who were looking into the possibility of another Ebola-type disease emerging. The consensus: There would indeed be a new disease, likely from the coronavirus family, coming out of a bat, and it would likely emerge in or around a wet market in China.

But what was not predictable was how unprepared we would be. In this interview, the *Bulletin*'s Dan Drollette Jr talks with the author, who lives in Bozeman, Montana, about what drew him to this topic, the nature of new viruses, why more are expected to emerge, and what makes some viruses more likely to infect humans than others. Quammen also talks a little about his next book (still untitled, but about the coronavirus). He cautions against being overly optimistic about the development of a vaccine, saying the coronavirus that causes COVID-19 will likely be around in some form for generations: “This virus is never going to be gone.”

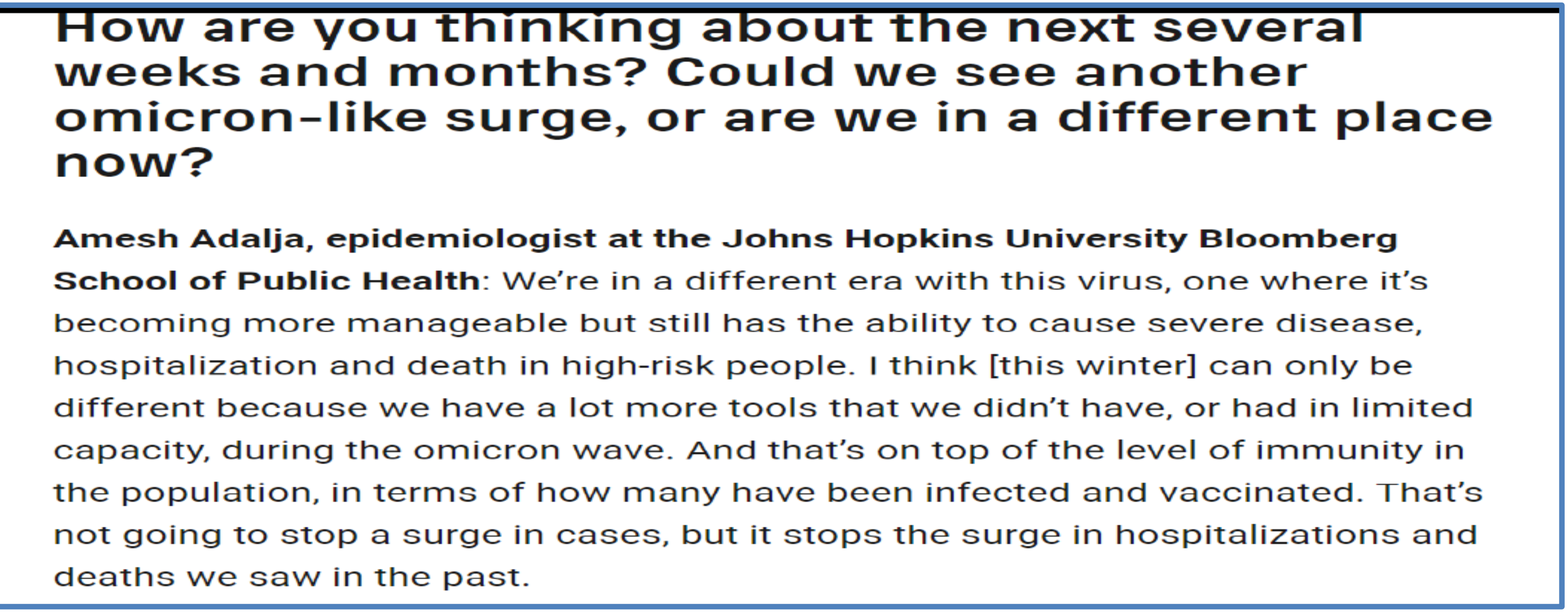


Covid experts look ahead at the fourth year of the pandemic: Vaccines, new variants and what to expect in 2023

The virus isn't done surprising us.

Jonathan Lambert
Public Health Reporter

January 1, 2023



How are you thinking about the next several weeks and months? Could we see another omicron-like surge, or are we in a different place now?

Amesh Adalja, epidemiologist at the Johns Hopkins University Bloomberg School of Public Health: We're in a different era with this virus, one where it's becoming more manageable but still has the ability to cause severe disease, hospitalization and death in high-risk people. I think [this winter] can only be different because we have a lot more tools that we didn't have, or had in limited capacity, during the omicron wave. And that's on top of the level of immunity in the population, in terms of how many have been infected and vaccinated. That's not going to stop a surge in cases, but it stops the surge in hospitalizations and deaths we saw in the past.

MICROBIOLOGY

Computer scan uncovers 100,000 new viruses

Clues to future outbreaks may be hidden in existing genomic databases

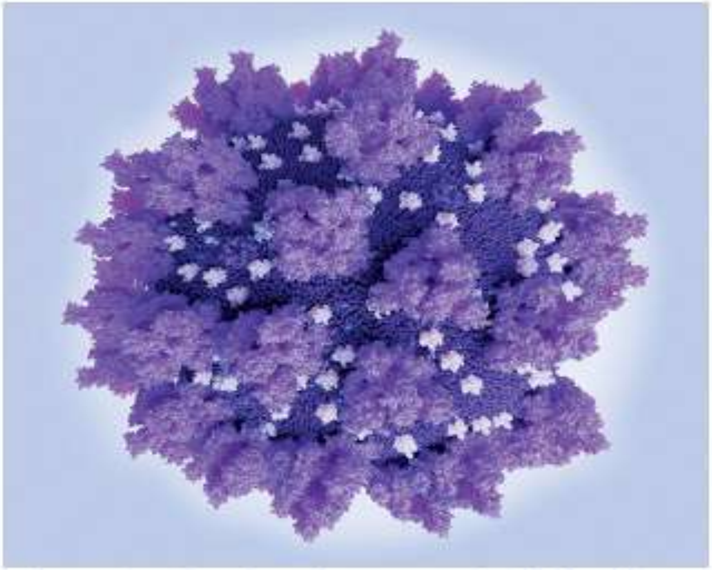
By Elizabeth Pennisi

It took just one virus to cripple the world's economy and kill millions of people; yet virologists estimate that trillions of still-unknown viruses exist, many of which might be lethal or have the potential to spark the next pandemic. Now, they have a new—and very long—list of possible suspects to interrogate. By sifting through unprecedented amounts of existing genomic data, scientists have uncovered more than 100,000 novel viruses, including nine coronaviruses and more than 300 related to the hepatitis Delta virus, which can cause liver failure.

"It's a foundational piece of work," says J. Rodney Brister, a bioinformatician at the National Library of Medicine. The study, published last week in *Nature*, expands the number of known viruses that use RNA instead of DNA for their genes by an order of magnitude. It "demonstrates our outrageous lack of knowledge about this group of organisms," says disease ecologist Peter Daszak, president of the EcoHealth Alliance, a nonprofit research group in New York City that is raising money to launch a global survey of viruses.

Scientists predict the study will also help launch so-called petabyte genomics—the analyses of previously unfathomable quantities of DNA and RNA data. (One petabyte is 10^{15} bytes.) That wasn't exactly what computational biologist Artem Babaian had in mind when he came up with the project while in between jobs in early 2020. Instead, he was simply curious about how many coronaviruses—aside from the virus that had just launched the COVID-19 pandemic—could be found in sequences in existing genomic databases.

So, he and independent supercomputing expert Jeff Taylor scoured cloud-based genomic data that had been deposited to a global sequence database and uploaded by the U.S. National Institutes of Health. As of now, the database contains 16 petabytes of archived sequences, which come from genetic surveys of everything from fugu fish, the risky Japanese delicacy, to farm soils to human guts. (A database with a 5-megabase digital photo of every person in the United States would take up about the same amount of space.) The sequences also capture the genomes of viruses infecting different organisms in samples, but the viruses usually go undetected.



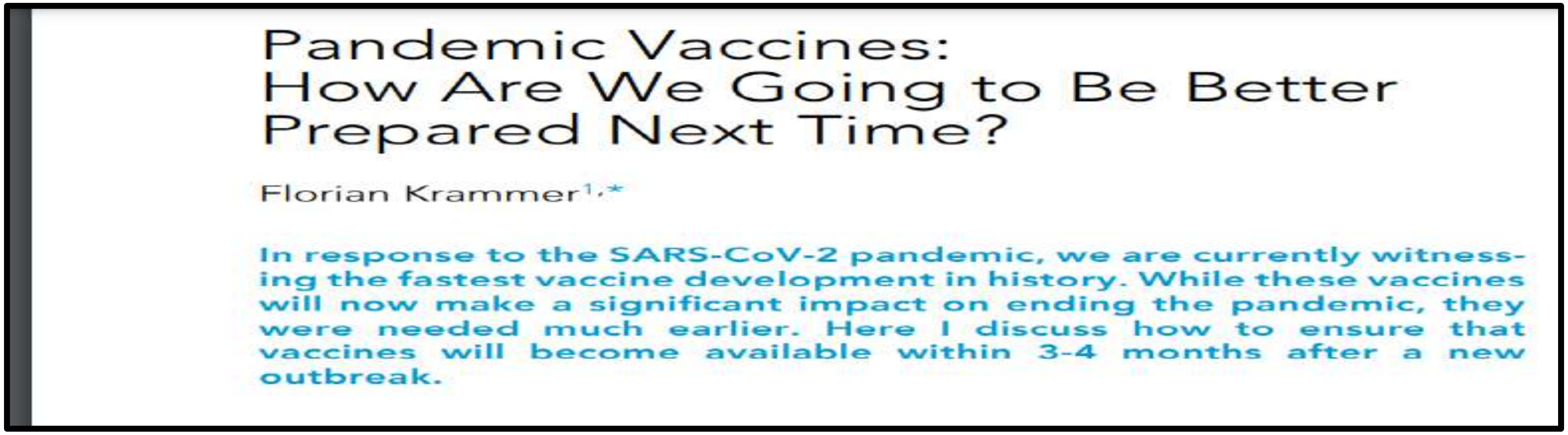
In a vast repository of genetic sequences, scientists found nine unknown coronaviruses, relatives of SARS-CoV-2 (computer model).

IMAGE: JUAN GAERTNER/SCIENCE SOURCE

To sift through the reams of data, Babaian and Taylor devised a set of computer search tools specialized for cloud-based data. With the help of several bioinformaticians, some whom became collaborators on the project, they tweaked the new software to make their analysis "way faster than anyone thought possible," recalls Babaian, who is now at the University of Cambridge.

They soon expanded the viral hunt beyond coronaviruses and looked at all the data in the cloud. Babaian and his colleagues' programs hunted among the cloud's sequences for matches to the central core of the gene for RNA-dependent RNA polymerase, which is key to the replication of all RNA viruses. Such viruses include not only coronaviruses, but also those that cause flu, polio, measles, and hepatitis.

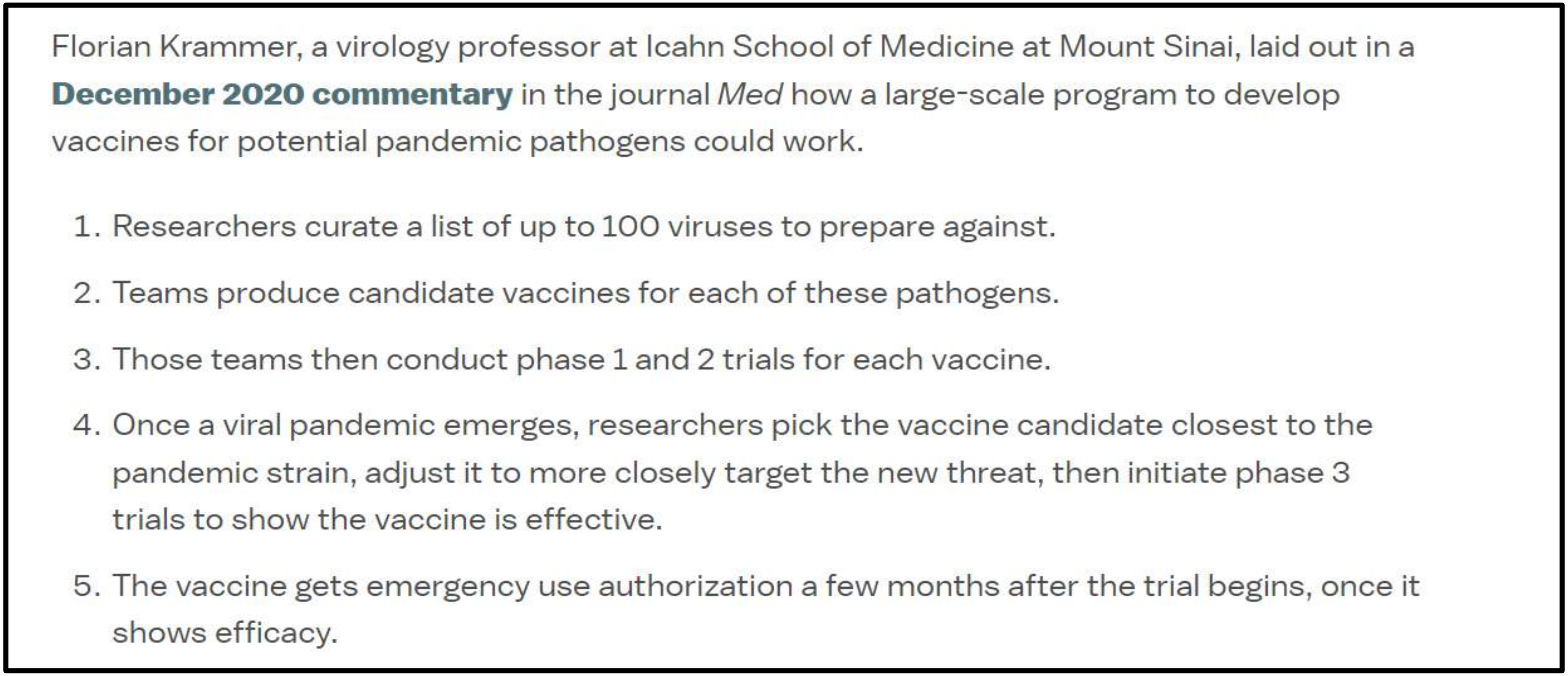
Babaian's approach was fast enough to work through 1 million data sets a day—at a com-



Pandemic Vaccines:
How Are We Going to Be Better Prepared Next Time?

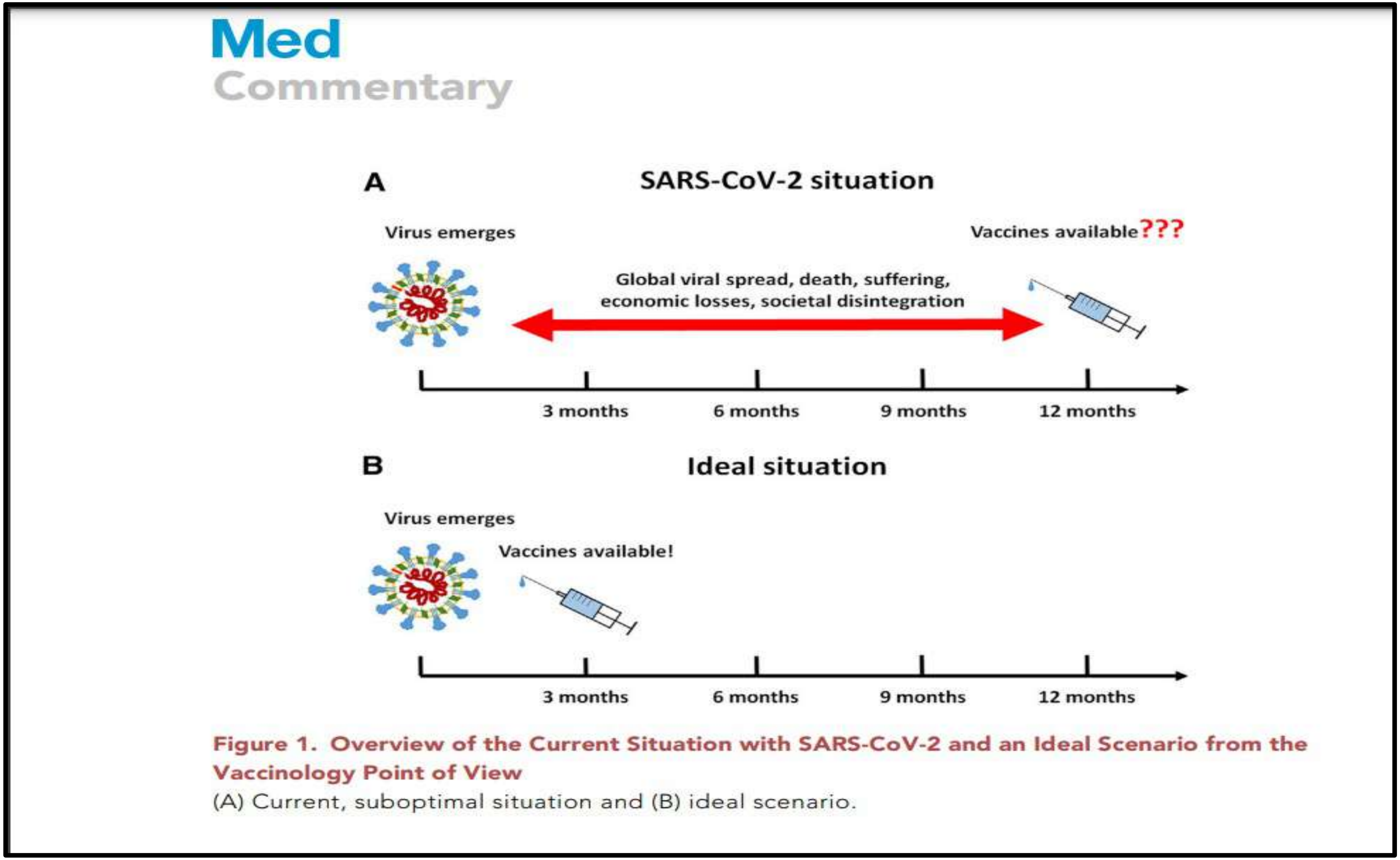
Florian Krammer[1,*]

In response to the SARS-CoV-2 pandemic, we are currently witnessing the fastest vaccine development in history. While these vaccines will now make a significant impact on ending the pandemic, they were needed much earlier. Here I discuss how to ensure that vaccines will become available within 3-4 months after a new outbreak.



Florian Krammer, a virology professor at Icahn School of Medicine at Mount Sinai, laid out in a **December 2020 commentary** in the journal *Med* how a large-scale program to develop vaccines for potential pandemic pathogens could work.

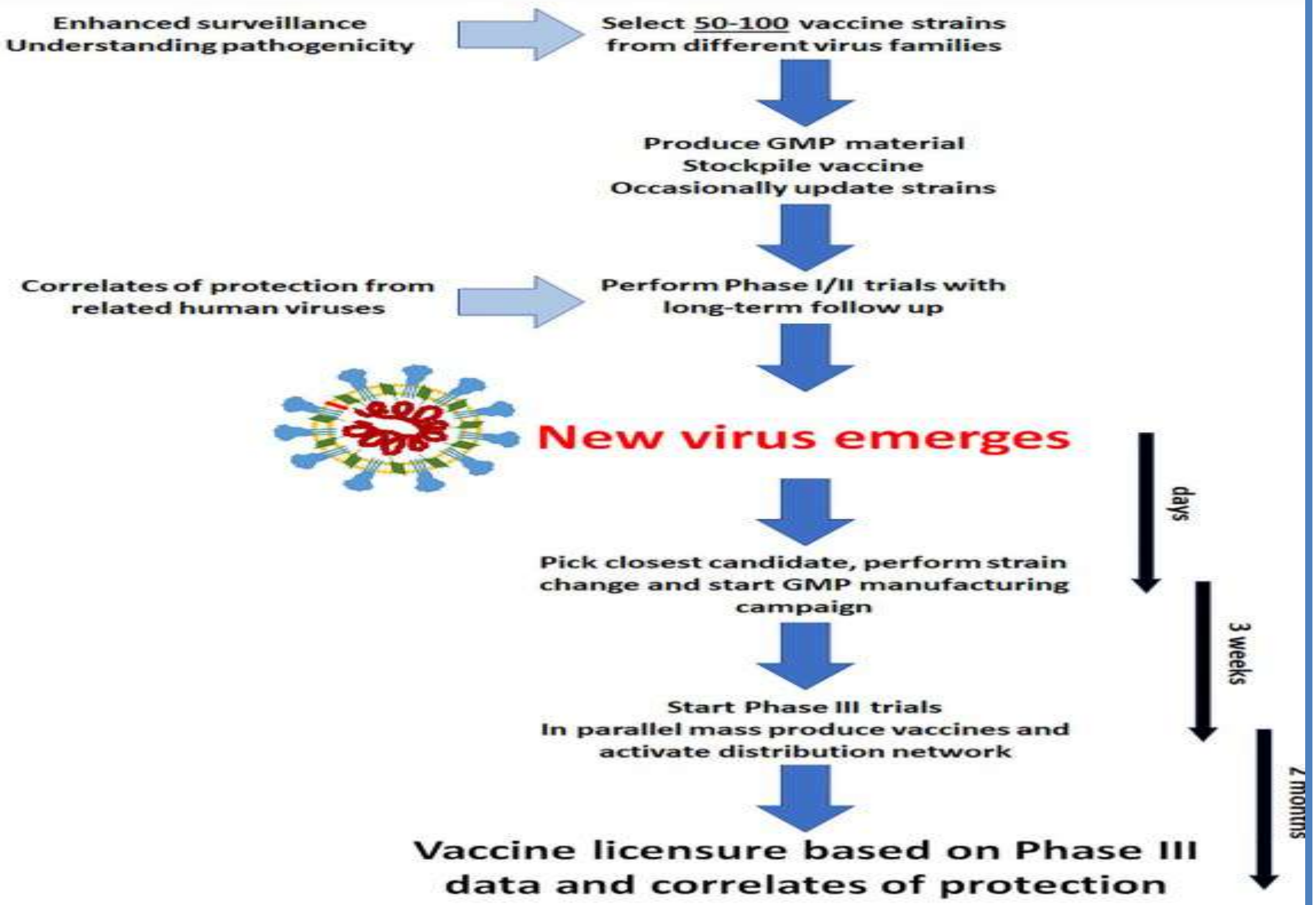
1. Researchers curate a list of up to 100 viruses to prepare against.
2. Teams produce candidate vaccines for each of these pathogens.
3. Those teams then conduct phase 1 and 2 trials for each vaccine.
4. Once a viral pandemic emerges, researchers pick the vaccine candidate closest to the pandemic strain, adjust it to more closely target the new threat, then initiate phase 3 trials to show the vaccine is effective.
5. The vaccine gets emergency use authorization a few months after the trial begins, once it shows efficacy.



Med
Commentary

Figure 1. Overview of the Current Situation with SARS-CoV-2 and an Ideal Scenario from the Vaccinology Point of View

(A) Current, suboptimal situation and (B) ideal scenario.



Enhanced surveillance
Understanding pathogenicity

Select 50-100 vaccine strains from different virus families

Produce GMP material
Stockpile vaccine
Occasionally update strains

Correlates of protection from related human viruses

Perform Phase I/II trials with long-term follow up

New virus emerges

Pick closest candidate, perform strain change and start GMP manufacturing campaign

Start Phase III trials
In parallel mass produce vaccines and activate distribution network

Vaccine licensure based on Phase III data and correlates of protection

Figure 2. Schematic of a Vaccinology-Based Strategy Toward Better Pandemic Preparedness

Pandemic Preparedness in a Changing World

SARS-like viruses may jump from animals to people hundreds of thousands of times a year

NEWS

Study pinpoints Asian regions that could spark the next coronavirus pandemic

By Kai Kupferschmidt

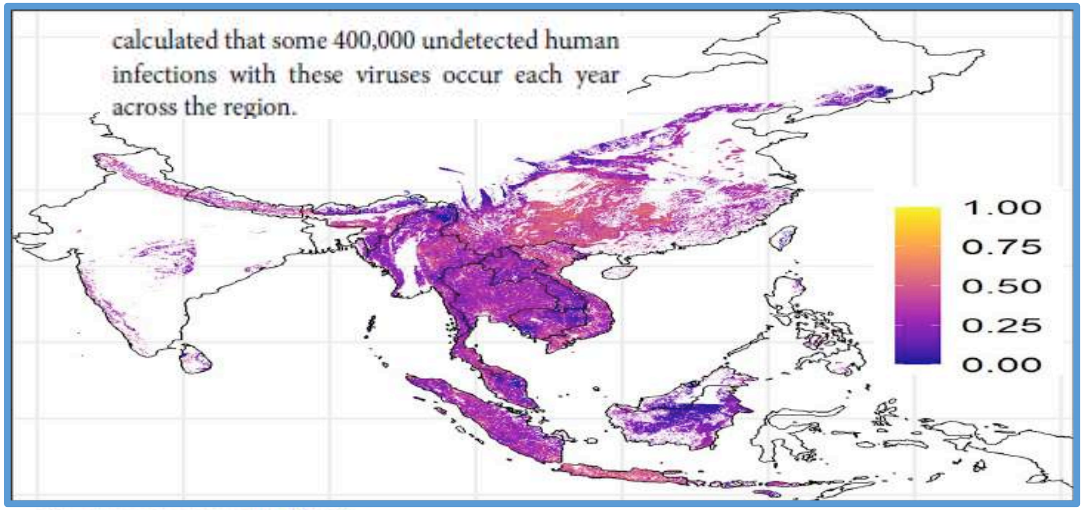
most likely to emerge," Daszak says. The maps could guide efforts to reduce the likelihood of spillover by changing behaviors in high-risk communities and targeting surveillance to detect new outbreaks earlier, he says. Daszak, a vocal advocate of the hypothesis that SARS-CoV-2 came from the wild instead of a research lab, says the maps could also guide efforts to find the virus' natural origin. (Several studies are underway or being planned to look for SARS-CoV-2 and its relatives in *Rhinolophus* [horseshoe] bats and other animals.)

But the researchers went one step further. Small surveys done before COVID-19 erupted

"I think if the seroprevalence estimate is way off, the whole thing collapses," says David Fisman, an epidemiologist at the University of Toronto, who calls the modeling "shaky." The high number of hidden infections "doesn't ring true," Fisman says, because you would expect regular spillovers to be recognized, as they are for rabies and the Nipah virus.

But Rasmussen says many infections could remain hidden if they are short-lived and don't lead to onward transmission because the viruses are not well adapted to humans. They might not infect enough cells—or cells of the right type—to be transmitted to another person, or they

23 yarasa türü
500 milyon insana sıçrama



calculated that some 400,000 undetected human infections with these viruses occur each year across the region.

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Building genomic sequencing capacity in Africa to respond to the SARS-CoV-2 pandemic

Tulio de Oliveira[1,2,3,4*], Eduan Wilkinson[1], Cheryl Baxter[1,3], Houriiyah Tegally[1], Jennifer Giandhari[2], Yeshnee Naidoo[1], Sureshnee Pillay[2]

Genomics surveillance aims to transform public health interventions by monitoring genetic changes that impact pathogenicity, diagnostics, therapeutics, and vaccines. Monitoring the genetic changes in SARS-CoV-2 has played an important role in shaping the scientific response to the pandemic and allowed the identification of several variants of interest (VOI) and five variants of concern (VOC) to date. Although Africa accounts for only about 2.5% and 4.1% of the world's reported COVID-19 cases and deaths, respectively (*1*, *2*), two of the VOC were identified by scientists from South Africa. Here, we reflect on some of the investments and capacity development initiatives that have resulted in an exponential growth in genomic sequencing capabilities across the continent over the past 2 years.

Early in the SARS-CoV-2 pandemic, genomic surveillance was available in just a few African countries with only 5,245 SARS-CoV-2 genome sequences being made publicly available in 2020 (3). In 2020 and 2021, significant investments in equipment and training were made to extend the geographic coverage of sequencing within many laboratories in Africa, thus increasing surveillance capacity on the continent. These investments resulted in an exponential increase in the number of SARS-CoV-2 genome sequences produced (Figure 1). Interestingly, it took 375 days to produce the first 10,000 SARS-CoV-2 genomes, 87 days to produce the next 10,000, and just 24 days to produce the most recent 10,000 genomes. To date, almost 100,000 SARS-CoV-2 genome sequences from Africa have been shared, and 54 African countries are now contributing to SARS-CoV-2 genome sequencing.

In 2020, the World Health Organization (WHO) and the Africa Centres for Disease Control and Prevention (Africa CDC)

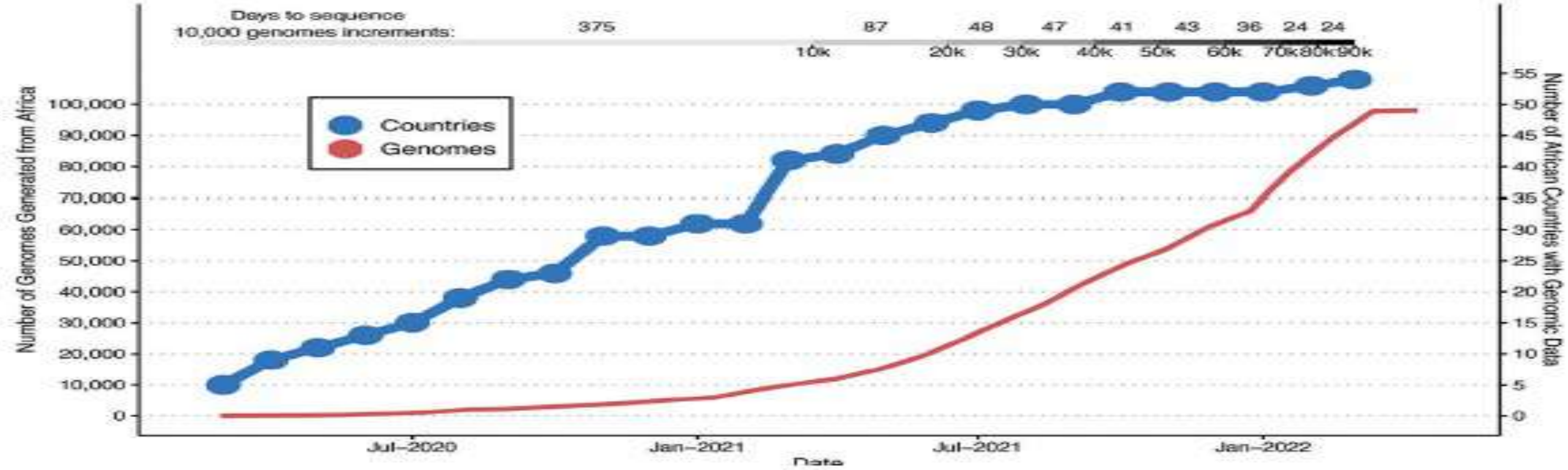

FIGURE 1. Increase in the number of SARS-CoV-2 sequences (solid red line) and African countries (blue circles) contributing genomic sequences to the Global Initiative on Sharing All Influenza Data (GISAID) between January 2020 and March 2022. Note that countries contributing to genomic sequences include 52 African countries and two overseas territories (Reunion and Mayotte).

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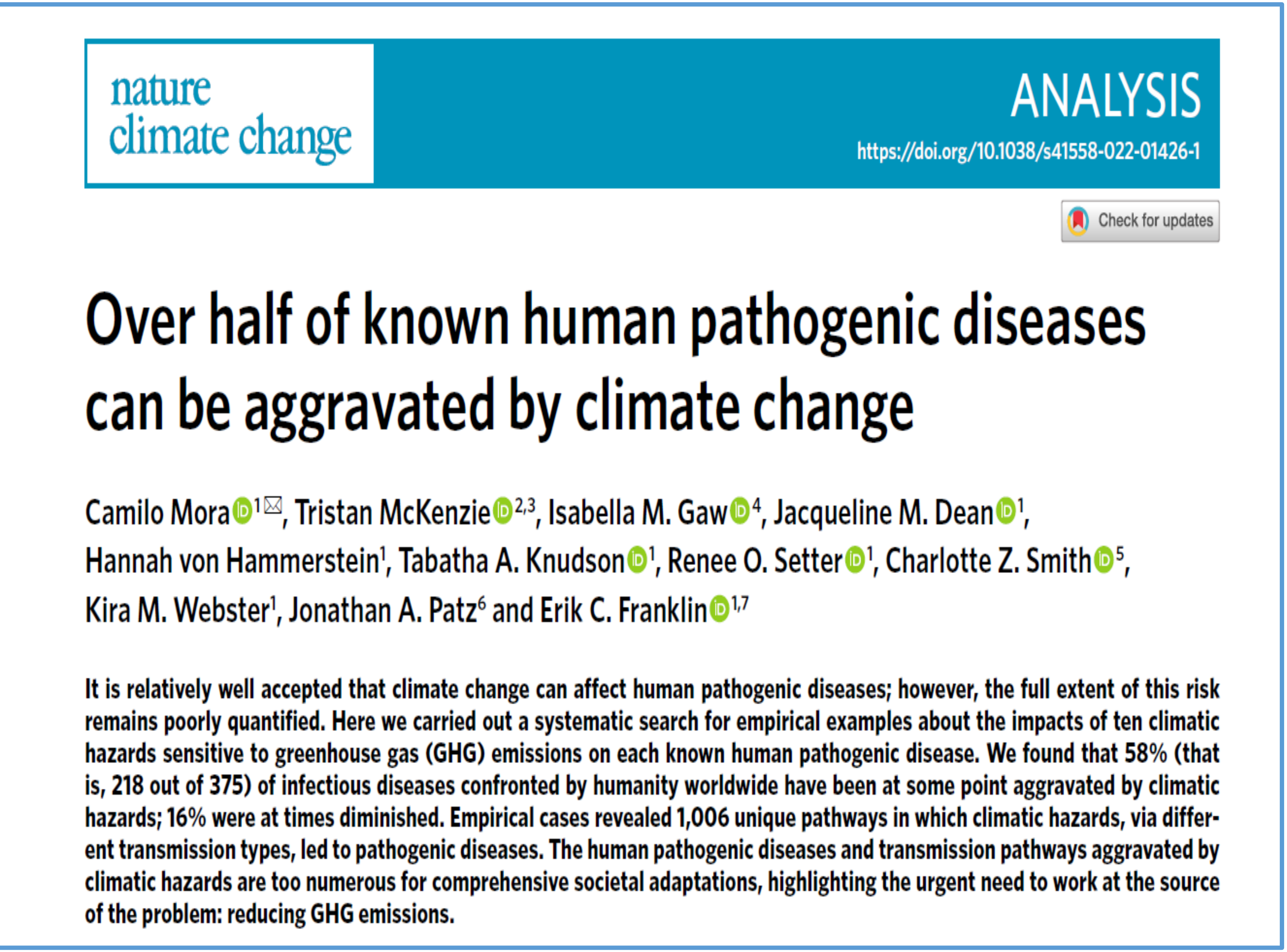
[1] Centre for Epidemic Response and Innovation (CERI), School of Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, South Africa
[2] KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP), Nelson R. Mandela School of Medicine, University of KwaZulu-Natal, Durban, South Africa
[3] Centre for the AIDS Programme of Research in South Africa (CAPRISA), Durban, South Africa
[4] Department of Global Health, University of Washington, Seattle, Washington, USA
*Corresponding author: tulio@sun.ac.za



nature climate change

ANALYSIS

https://doi.org/10.1038/s41558-022-01426-1

Over half of known human pathogenic diseases can be aggravated by climate change

Camilo Mora[1], Tristan McKenzie[2,3], Isabella M. Gaw[4], Jacqueline M. Dean[1], Hannah von Hammerstein[1], Tabatha A. Knudson[1], Renee O. Setter[1], Charlotte Z. Smith[5], Kira M. Webster[1], Jonathan A. Patz[6] and Erik C. Franklin[1,7]

It is relatively well accepted that climate change can affect human pathogenic diseases; however, the full extent of this risk remains poorly quantified. Here we carried out a systematic search for empirical examples about the impacts of ten climatic hazards sensitive to greenhouse gas (GHG) emissions on each known human pathogenic disease. We found that 58% (that is, 218 out of 375) of infectious diseases confronted by humanity worldwide have been at some point aggravated by climatic hazards; 16% were at times diminished. Empirical cases revealed 1,006 unique pathways in which climatic hazards, via different transmission types, led to pathogenic diseases. The human pathogenic diseases and transmission pathways aggravated by climatic hazards are too numerous for comprehensive societal adaptations, highlighting the urgent need to work at the source of the problem: reducing GHG emissions.

İklim krizi, denizlerdeki ısınma, yaşamakta olduğumuz pandeminin bireysel, toplumsal ve çevresel hasarları de eklendiğinde önümüzdeki dönem için iki alt başlık olduğunu rahatlıkla söyleyebiliriz.

1.Virüs ile ilişkili değişimlerin en kötüsü gerçekleşmez ise, yeni ve farklı , bağışıklıktan önemli derecede kaçan bir varyant, COVID-19'un birkaç yıl içinde ve en iyi ihtimalle sonsuza kadar "endemik" bir hastalık olarak bizimle kalacağıdır.

2.Bu yüzyılda, hatta yüksek olasılıkla önümüzdeki dekatta , mutlaka yeni bir pandeminin olacağıdır.

Zoonotik sıçramaları ve çevre değişimini dikkate alınarak yapılan modelleme çalışmaları,bu yüzyılda doğmuş bir insanın COVID-19 gibi bir salgın yaşama olasılığının %38 olduğunu gösteriyor.

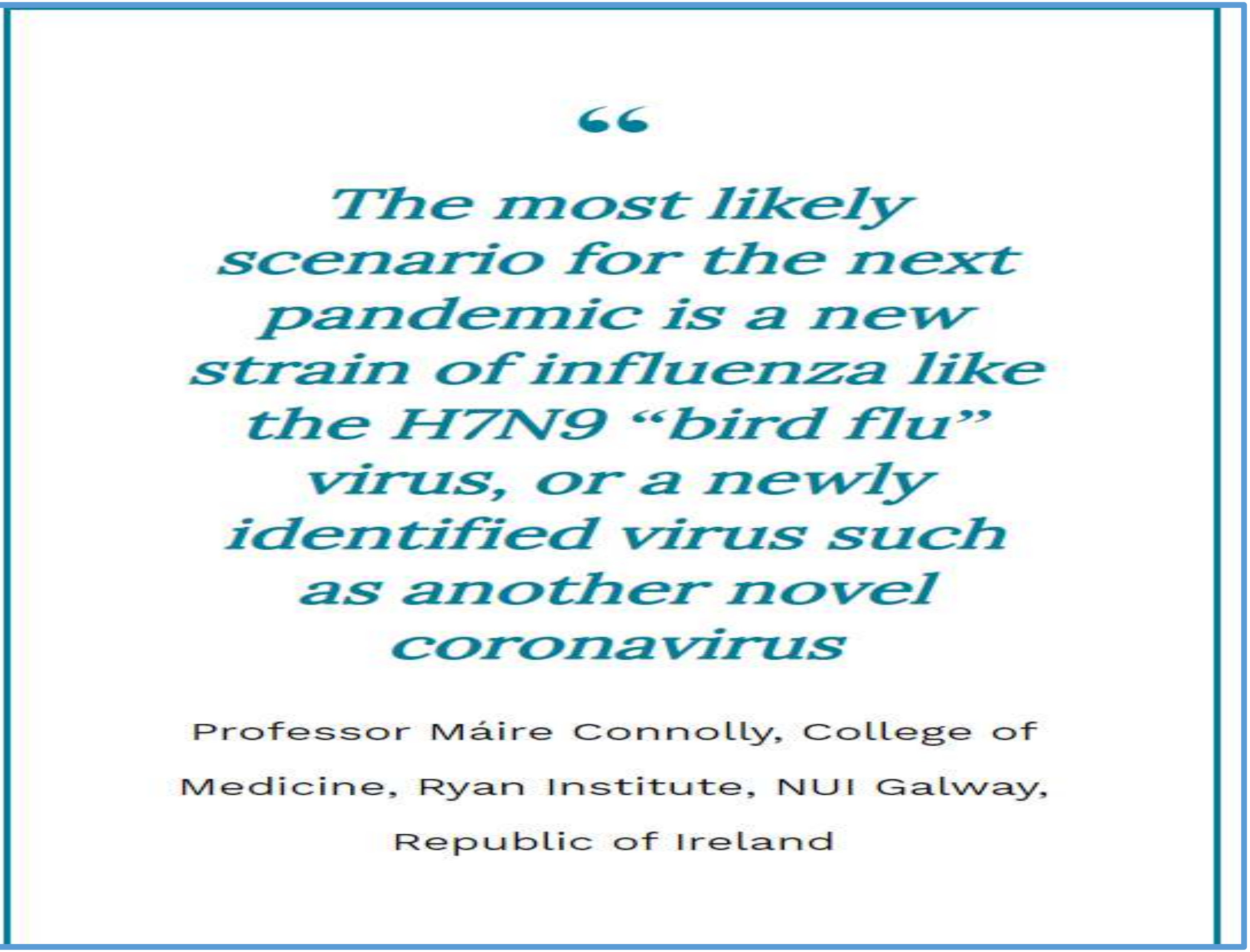
Marania M, Katulb GG, Pan W,et al.Intensity and frequency of extreme novel epidemics PNAS 2021 Vol. 118 No. 35 e2105482118

- Dünyada ekonomisi en büyük olan ülkelerin biraraya geldiği G7 zirvesinde olası bir salgına hazırlıkta , dünyada alanında önemli , lider bilim insanları heyeti tarafından "100 Gün Misyonu" başlıklı bir rapor sunuldu.. (17)
- Buna göre ,uluslararası koordinasyon ve işbirliği ile yol haritaları belirlenip, küresel işbirliği güçlendirilmeli ve X hastalığı için tanı, tedavi ve aşılar ilk 100 gün içinde hazırlanabilir olmalıdır.
- Sürekli ve adanmış bir liderlik, bağımsız kurum ve kuruluşların oluşturulması ve güçlendirilmesi, zayıf halka olabilecek bölgelerle işbirliği, zoonozların monitorizayonu ve birinci basamak koruyucu sağlık hizmetlerinin güçlendirilmesi önceliklidir.

https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1038969/100_Days_Mission_-_First_Implementation_Report__1_.pdf

Araştırmaların bu hastalıkların tanı, tedavi ve aşı geliştirme konusuna odaklanması öneriliyor.

- COVID-19
- Kırım Kongo Kanamalı Ateşi
- Ebola ve Marburg Virus Hastalığı
- Lassa Ateşi
- MERS-CoV ve SARS
- Nipah ve henipaviral hastalık
- Rift Valley Ateşi
- Zika
- “Disease X”;X Hastalığı (henüz bilinmeyen, uluslararası salgına yol açabilecek bir hastalık)



> “The most likely scenario for the next pandemic is a new strain of influenza like the H7N9 “bird flu” virus, or a newly identified virus such as another novel coronavirus

Professor Máire Connolly, College of Medicine, Ryan Institute, NUI Galway, Republic of Ireland

SARS/MERS-CoV Aşıları

188 patent-%50 si- S protein: RBD-S1 subunit

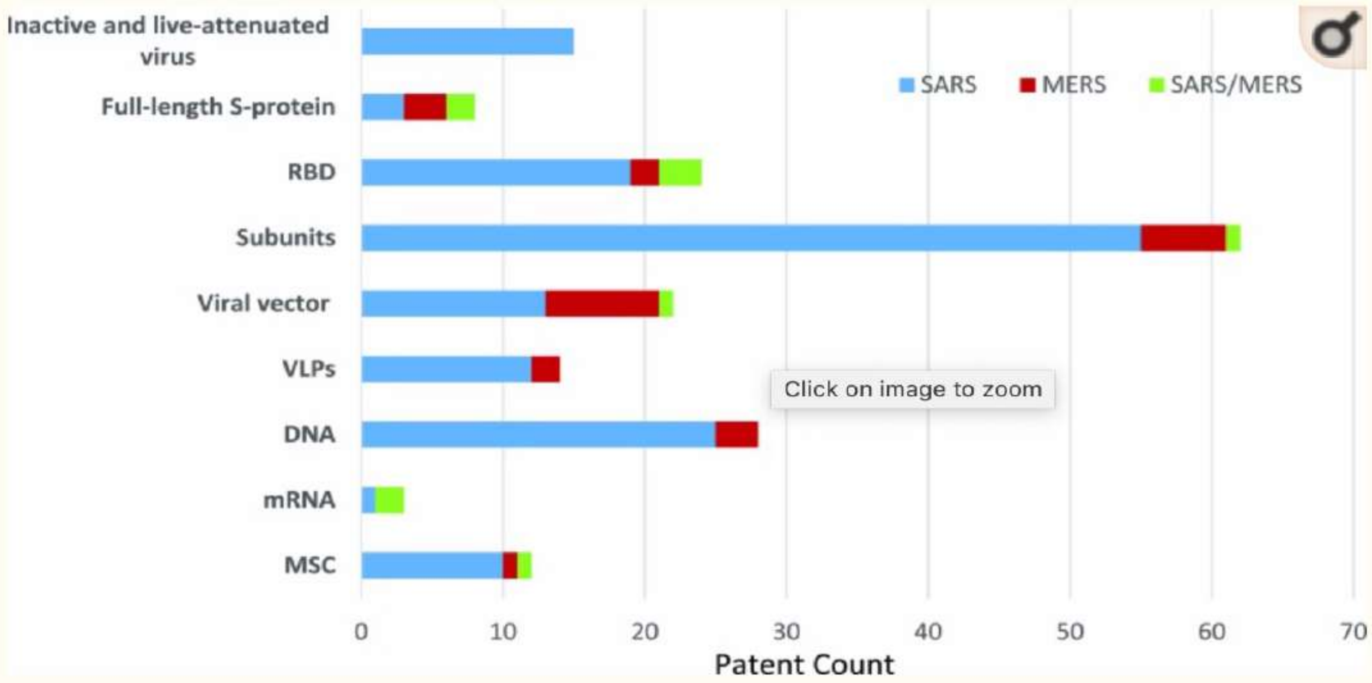


Figure 7

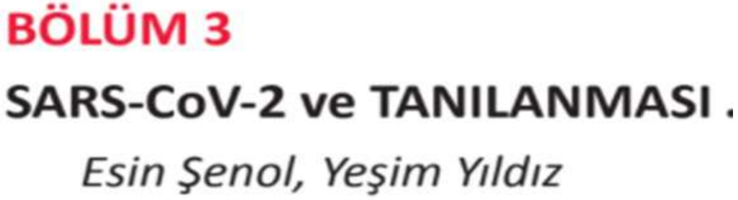
Distribution of vaccine-related patent associated to SARS and MERS.


TÜSAD Eğitim Kitapları Serisi – 25

COVID-19 PANDEMİSİNDEN ÖĞRENDİKLERİMİZ, GELECEK ÖNGÖRÜLERİ VE YARININ PLANLANMASI

Editörler: Prof. Dr. Güntülü Ak
Prof. Dr. Ülkü Yılmaz

- **7 Ocak 2020’**de, bu hastaların bronkoalveolar lavaj sıvısından , qRT-PCR ile etken izole edilmiş ve daha önce insanlardan izole edilmemiş yeni bir Coronavirus olarak tanımlanarak ilk **genom dizisi** 10 Ocak’ta virological.org’da yayınlanmıştır


BÖLÜM 3

SARS-CoV-2 ve TANILANMASI .

Esin Şenol, Yeşim Yıldız

Yakın tarihli salgınlar ile mücadelerimizden öğrendiklerimiz şöyle, HIV pandemisinden bildiğimiz şey hiçbir zaman tek bir önlemin yeterli olmayacağı ve ekonomik ve sosyal olarak korumamız gereken gruplar olduğu.

İSTİKRARLI BİR DÖNEME GEÇİŞİMİZİN 2 İLA 10 YIL SÜRECEĞİNİ öngörüyor:

“Son derecede dinamik ve tahmin edilemez.”

David Quammen, while accompanying a wolf collaring and tracking operation in Yellowstone National Park for a National Geographic article. Image courtesy of Ronan Donovan

Adam Kucharski’den
“ Bir pandemi gören yalnızca bir pandemi görür .
Bizi şimdi kıyıya çıkaran şeyler bir daha ki sefere işimize yaramayabilir”

DİNLEDİĞİNİZ İÇİN TEŞEKKÜRLER…

SORULARINIZ?

Prof. Dr. Esin Şenol