

ESCAPING THE ERA OF PANDEMICS

Lessons not learned?
The power of communication and the need for a transformative change

Prof.Dr. Carlos Gonçalo das Neves

DVM PhD Dipl. ECZM (Wildlife Pop. Health) EBVS European Veterinary Specialist™

Director for Research and Internationalisation Research Professor President of the Wildlife Disease Association Member of the Lancet One Health Commission IUCN SSC Wildlife Specialist Group member







Acknowledgements:





Science and Policy for People and Nature









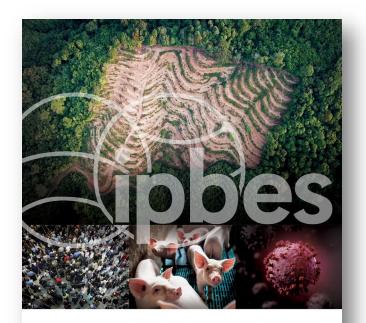




THE LANCET

Covid19 Commission





IPBES WORKSHOP ON BIODIVERSITY AND PANDEMICS

EXECUTIVE SUMMARY

Intergovernmental Platform on Biodiversity and Ecosystem Services



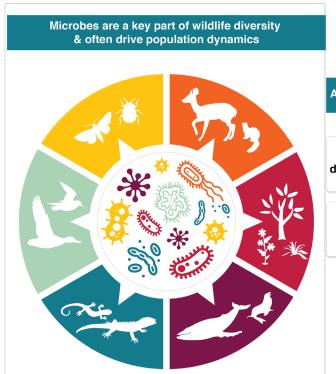
Escaping the 'Era of Pandemics':

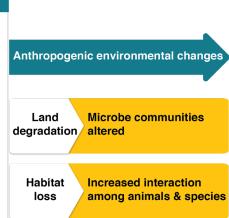
Experts Warn Worse Crises to Come

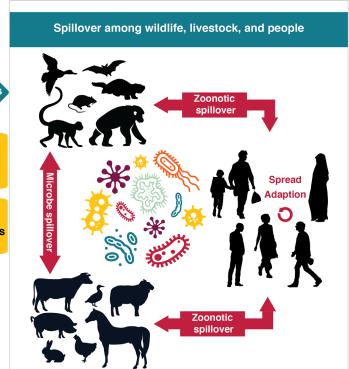
""The same human activities that drive climate change & biodiversity loss also drive pandemic risk through impacts on our environment"

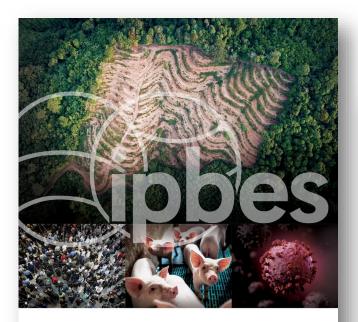


So...who is changing what?









IPBES WORKSHOP ON BIODIVERSITY AND PANDEMICS

EXECUTIVE SUMMARY

Intergovernmental Platform on Biodiversity and Ecosystem Services





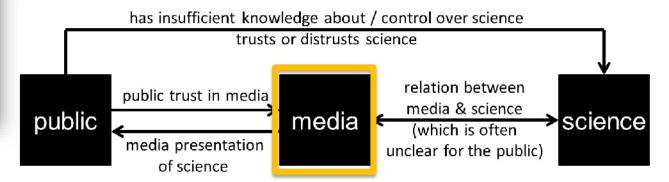


Trust in Science and Changing Landscapes of Communication

January 2019

ALLEA DISCUSSION PAPER # 3

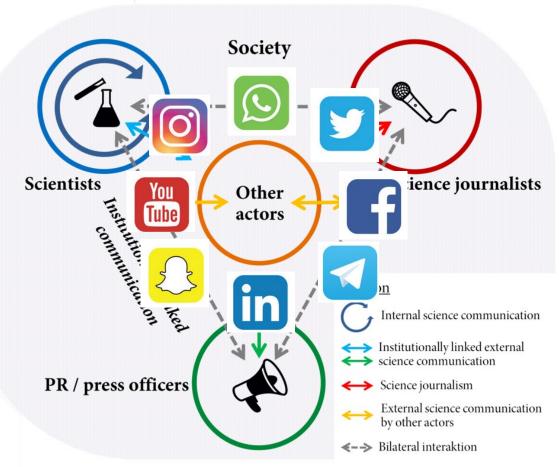
"Trust means deferring with comfort and confidence to others, about something beyond our knowledge or power, in ways that can potentially hurt us. In order to establish and maintain trust in science, such comfort and confidence relies on **communication by trustworthy and trusted mediators**."

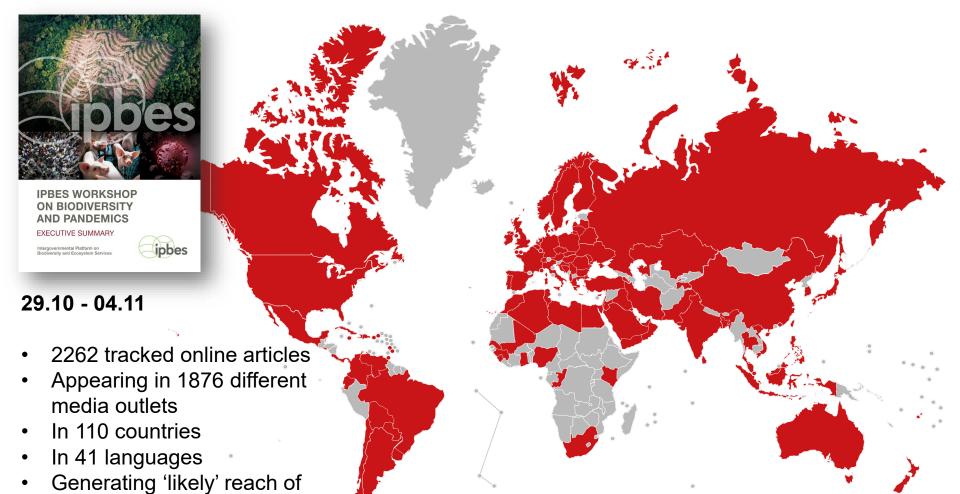


Source: Schäfer, M. S. (2016) Mediated Trust in Science: Concept, Measurement and Perspectives for the 'Science of Science Communication'. Journal of Science Communication 15(05), 1-7, p. 3.



#PandemicsReport



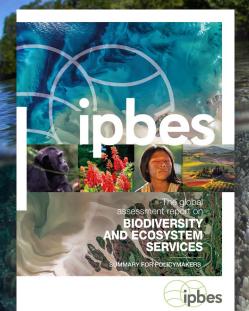


more than 157 million



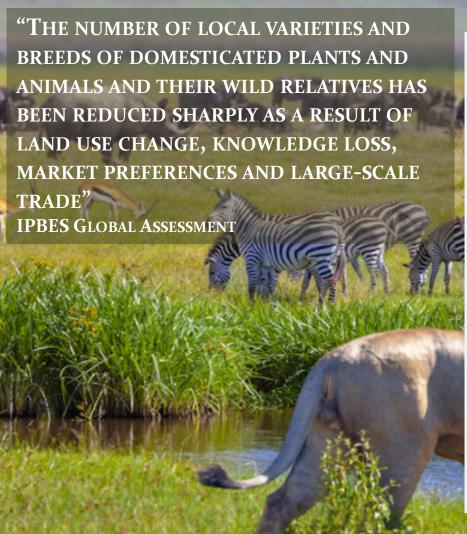
What are the links between biodiversity and pandemics?

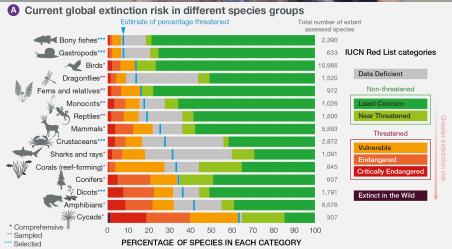
BIODIVERSITY IS FUNDAMENTAL TO HUMAN LIFE ON EARTH, AND IT IS BEING DESTROYED BY US AT A RATE UNPRECEDENTED IN HISTORY.



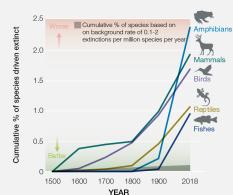
"Many of nature's contributions to people are essential for human health and their decline thus threatens a good quality of life"



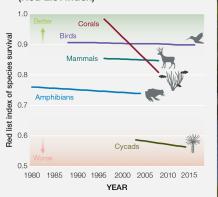








Declines in species survival since 1980 (Red List Index)



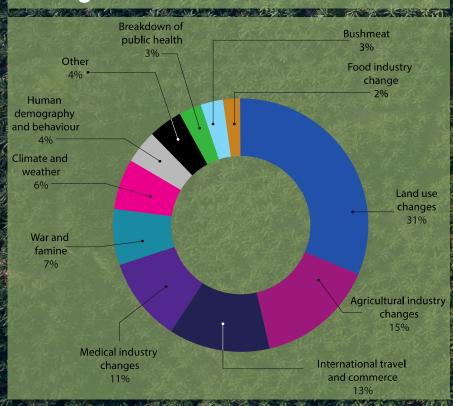
Land-use change, agricultural expansion, & urbanization cause more than

of emerging disease events

#PandemicsReport



Land Use Change Drives Disease Emergence



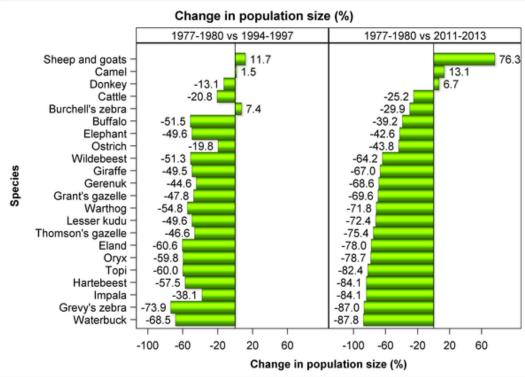
Land use change could lead to disease emergence by:

- Increasing opportunities for wildlife-human-domestic animal contacts → pathogen spillover from wildlife (to humans or domestic animals) (pathogen pool hypothesis)
- Altering host-pathogen ecological dynamics → crossspecies transmission (perturbation hypothesis)

Loh & Zambrana-Torrelio 2015. Vector Bourne Zoonotic Dis

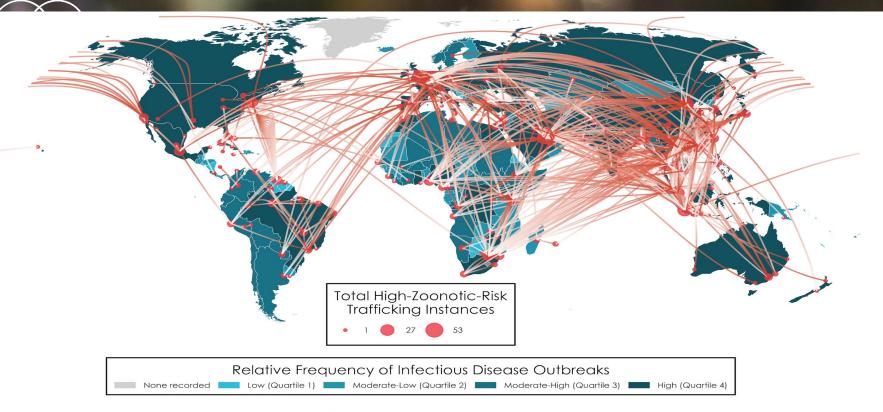


EXTREME DECLINES IN
WILDLIFE AND
CONTEMPORANEOUS INCREASE
IN LIVESTOCK HAS ALSO AN
IMPACT ON EXCHANGE OF
PATHOGENS AND ENHANCED
RISK FOR EIDS



Ogutu JO, Piepho HP, Said MY, Ojwang GO, Njino LW, et al. (2016) Extreme Wildlife Declines and Concurrent Increase in Livestock Numbers in Kenya: What Are the Causes?. PLOS ONE 11(9): e0163249. https://doi.org/10.1371/journal.pone.0163249















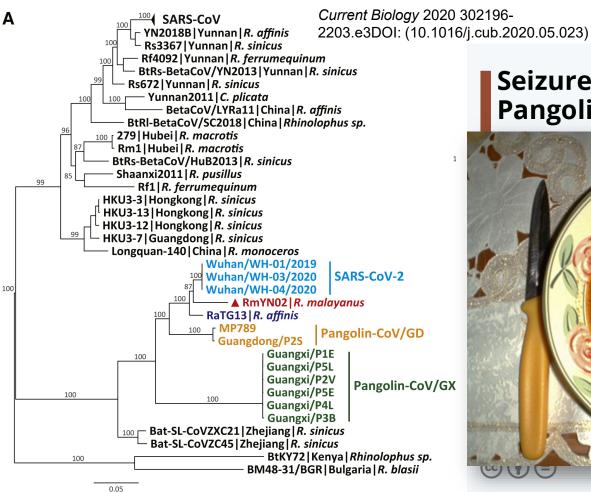








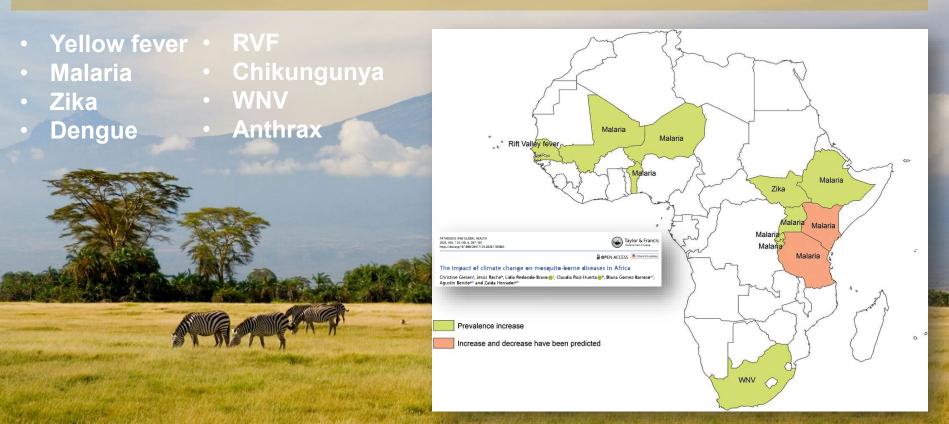




Seizures of Trafficked Pangolins on the Rise



CLIMATE CHANGE COULD DRIVE MORE THAN 50% OF AFRICAN BIRD & MAMMAL SPECIES TO EXTINCTION BY 2100. FURTHERMORE IT ENABLES THE SPREAD OF DISEASES TO NEW SPECIES AND INCREASES RISK FOR HUMANS



BREAKING

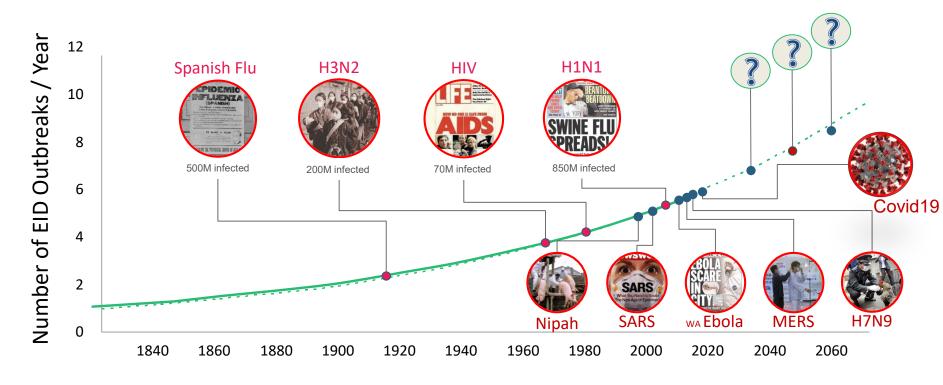
NEWS

PATHOGEN X

Pandemic emerging diseases are a growing threat

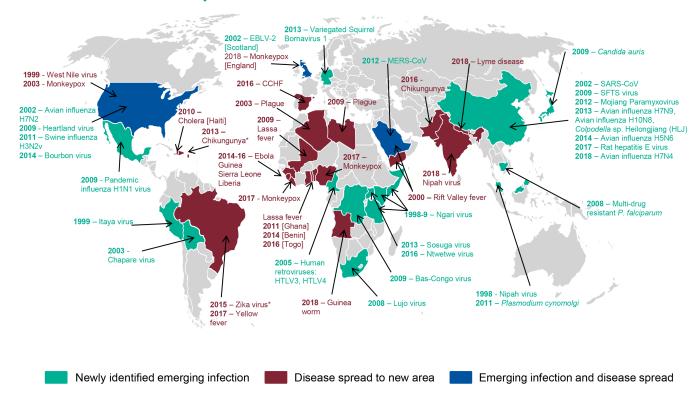
Pandemic emerging diseases are a growing threat

Pandemic emerging diseases are a growing threat



Allen et al. (2017) Nature Communications

Global map of significant and new emerging infections in humans: spread to new areas since 1998



*Incursion followed by regional spread

24

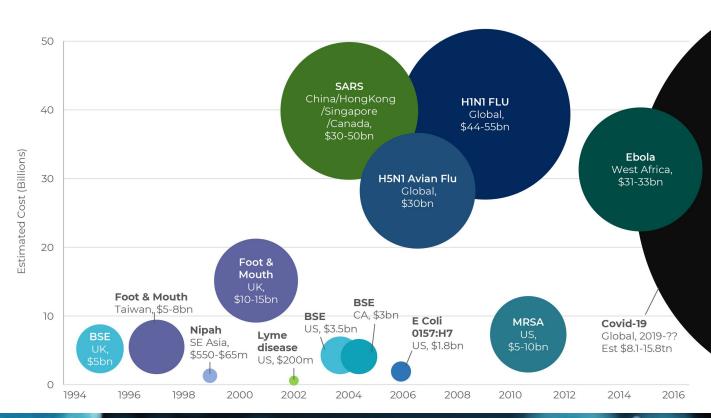


Pandemics and other emerging zoonoses cause widespread human suffering, and likely more than a trillion dollars in economic damages annually



• Global strategies to prevent pandemics ~ \$22 - 31.2 billion annually - two orders of magnitude less than the damages pandemics produce

Costs of Pandemics



Costs of **Pandemics**

POLICY FORUM

Ecology and economics for pandemic prevention

Investments to prevent tropical deforestation and to limit wildlife trade will protect against future zoonosis outbreaks

By Andrew P. Dobson¹, Stuart L. Pimm², Lee Hannah³, Les Kaufman⁴, Jorge A. Ahumada³, Amy W. Ando⁵, Aaron Bernstein⁶, Jonah Busch⁷, Peter Daszak⁶, Jens Engelmann⁹, Margaret F. Kinnaird10, Binbin V. Li11, Ted Loch-Temzelides12, Thomas Lovejov13, Katarzyna Nowak14, Patrick R. Roehrdanz³, Mariana M. Vale¹⁵

or a century, two new viruses per year have spilled from their natural hosts into humans (1), The MERS, SARS, and 2009 H1N1 epidemics, and the HIV and coronavirus disease 2019 (COVID-19) pandemics, testify to their damage. Zoonotic viruses infect neople directly most often when they handle live primates, bats, and other wildlife (or their meat) or indirectly from farm animals such as chickens and pigs. The risks are higher than ever (2, 3) as increasingly intimate associations between humans and wildlife disease reservoirs accelerate the potential for viruses to spread globally. Here, we assess the cost of monitoring and preventing disease spillover driven by of tropical forests and by the burgeoning wildlife trade. Currently, we invest relaively little toward preventing deforestation and regulating wildlife trade, despite wellesearched plans that demonstrate a high eturn on their investment in limiting zoonoses and conferring many other benefits. As public funding in response to COVID-19 continues to rise, our analysis suggests that the associated costs of these preventive efforte would be substantially loss than the economic and mortality costs of responding to these pathogens once they have emerged.

Tropical forest edges are a major launchnad for novel human viruses. Edges arise as humans build roads or clear forests for timber production and agriculture. Humans and their livestock are more likely

Email: dobber@orinceton.edu.stuartnimm@me.com

to contact wildlife when more than 25% of the original forest cover is lost (4), and such contacts determine the risk of disease transmission. Pathogen transmission depends on the contact rate, the abundance of susceptible humans and livestock, and the abundance of infected wild hosts, Contact rates vary with the perimeter (the length of the forest edge) between forest and nonforest. Deforestation tends to create checkerboards, whereupon we see a maximum perimeter at a 50% level of forest conversion. Thereafter, the abundance of domestic animals and humans rapidly exceeds that of wild animals so although we expect transmission to decline, the magnitude of any resultant outbreak is higher (4) Habitat fragmentation compliand livestock and crop monocultures have led to increasing virus spillovers. Hunting, transport, farming, and trade of wildlife for food, pets, and traditional medicine compound these routes of transmission and closely track deforestation. For example, bats are the probable reservoirs of Ebola, Nipah, SARS, and the virus behind COVID-19. Fruit bats (Pteropodidae in the Old World, the genus Artibeus in the New World) are more likely to feed near human cettlements when their forcet habitate are disturbed: this has been a key factor in viral emergence in West Africa, Malaysia.

Rangladesh, and Australia (5-7). The clear link between deforestation and virus emergence suggests that a major effort to retain intact forest cover would have a large return on investment even if its only benefit was to reduce virus emergence events. The largest-scale example of directed deforestation reduction comes from Brazil between 2005 and 2012. Deforestation in the Amazon dropped by 70%, vet production of the region's dominant soy crop still there are ongoing discussions on phasing increased (8). International contributions. out this industry. The justification is that

about \$1 billion supported land-use zoning. market and credit restrictions, and stateof-the-science satellite monitoring. Brazil's program reduced forest fragmentation and edge at a lower cost than could have been achieved by carbon-pricing approaches (9).

Several estimates of the effectiveness and cost of strategies to reduce tropical deforestation are available (8, 9). At an annual cost of \$9.6 billion, direct forest-protection payments to outcompete deforestation economically could achieve a 40% reduction in areas at highest risk for virus spillover [see supplementary materials (SM)]. Multiple payment-for-ecosystem-services programs demonstrate the effectiveness of this approach. At the low end, widespread adoption of the earlier Brazil policy model could achieve the same reduction for only \$1.5 billion annually by removing subsidies that favor deforestation, restricting private land clearing, and supporting territorial rights of indigenous peoples. All require national motivation and political will. Strong public support for similar deforestation-prevention policies may emerge in other countries recovering from COVID-19's devastation.

WILDLIFE TRADE SPILLOVER

Global demand for wildlife causes neonle to enter forests to collect wildlife for sale in markets in urban and rural areas. In cities, where neonle have diverse ontions for protein, bushmeat is a luxury bought to show status, and occasionally for cultural reasons. COVID-19 is the huge price society now pays for such encounters with wild species.

Wildlife markets and the legal and illegal wildlife trade bring live and dead wild animals into contact with hunters, traders, commerce. Trade follows global consumer demand. The United States is one of the bigfor the massive exotic pet industry (10). The transit conditions, lack of health screen ing at import, and warehouses that store animals before and after import are similar to live animal markets, all conducive to

Some countries have wildlife farming industries intended to prevent overhunting of wild species while meeting market demands for protein and appealing to cultural traditions. In China wildlife farming is a ~\$20 billion industry employing some 15 million people (II). With the February 2020 announcement by the Standing Committee of the National People's Congress of a ban on wildlife consumption for food and related trade in China complemented by an Amazon Fund of it creates risks for disease emergence and

Summary of prevention costs, benefits, and break-even probability change

ITEM	VALUES (2020 \$)
Expenditures on preventive measures	
Annual funding for monitoring wildlife trade (CITES+)	\$250-\$750 M
Annual cost of programs to reduce spillovers	\$120-\$340 M
Annual cost of programs for early detection and control	\$217-\$279 M
Annual cost of programs to reduce spillover via livestock	\$476-\$852 M
Annual cost of reducing deforestation by half	\$1.53-\$9.59 B
Annual cost of ending wild meat trade in China	\$19.4 B
TOTAL GROSS PREVENTION COSTS (C)	\$22.0-\$31.2 B
Ancillary benefit of prevention	
Social cost of carbon	\$36.5/tonne
Annual CO ₂ emissions reduced from 50% less deforestation	118 Mt
Ancillary benefits from reduction in CO ₂ emissions	\$4.31B
TOTAL PREVENTION COSTS NET OF CARBON BENEFITS (C)	\$17.7-\$26.9 B
TOTAL TREE ENTITION COCTO TIET OF CARDON BETTER TO (C)	Q17.7 Q20.3 D
	\$17.7 \Q20.3 B
Damages from COVID-19 Lost GDP in world from COVID-19	\$5.6 T
Damages from COVID-19	
Damages from COVID-19 Lost GDP in world from COVID-19 Value of a statistical life (V) adjusted for COVID-19	\$5.6 T \$5.34 M or \$10.0 M
Damages from COVID-19 Lost GDP in world from COVID-19 Value of a statistical life (V) adjusted for COVID-19 mortality structure Total COVID-19 world mortality (O _o) forecast	\$5.6 T \$5.34 M or \$10.0 M
Damages from COVID-19 Lost GDP in world from COVID-19 Value of a statistical life (V) adjusted for COVID-19 mortality structure Total COVID-19 world mortality ($Q_{\rm p}$) forecast by 28 July 2020, 50th percentile with 95% error bounds	\$5.6 T \$5.34 M or \$10.0 M
Damages from COVID-19 Lost GDP in world from COVID-19 Value of a statistical life (V) adjusted for COVID-19 mortality structure Total COVID-9 world mortality (Q_0) forecast by 28 July 2020, 50th percentile with 95% error bounds Value of deaths in world from COVID-19 = $Q_0 \times V$	\$5.6 T \$5.34 M or \$10.0 M 590,643 [473,209,1,019,078]
Damages from COVID-19 Lost GDP in world from COVID-19 Value of a statistical life (V) adjusted for COVID-19 mortality structure Total COVID-19 world mortality (Q_0) forecast by 28 July 2020, 50th percentile with 95% error bounds Value of deaths in world from COVID-19 = $Q_0 \times V$ Lowest (\$5.34 M × 2.5th percentile mortality forecast)	\$5.6 T \$5.34 M or \$10.0 M 590,643 [473,209,1,019,078] \$2.5 T
Damages from COVID-19 Lost GDP in world from COVID-19 Value of a statistical life (V) adjusted for COVID-19 mortality structure Total COVID-19 world mortality (Q_0) forecast by 28 July 2020, 50th percentile with 95% error bounds Value of deaths in world from COVID-19 = $Q_0 \times V$ Lowest (\$5.34 M × 2.5th percentile mortality forecast) Middle (\$10 M × 50th percentile mortality forecast)	\$5.6 T \$5.34 M or \$10.0 M 590.643 [473.209,1.019.078] \$2.5 T \$5.9 T
Damages from COVID-19 Lost GDP in world from COVID-19 Value of a statistical life (V) adjusted for COVID-19 mortality structure Total COVID-19 world mortality (Q_0) forecast by 28 July 2020, 50th percentile with 95% error bounds Value of deaths in world from COVID-19 = $Q_0 \times V$ Lowest (\$5.34 M × 2.5th percentile mortality forecast) Middle (\$10 M × 50th percentile mortality forecast) Highest (\$10 M × 9.75th percentile mortality forecast)	\$5.6 T \$5.34 M or \$10.0 M 590.643 [473.209,1.019.078] \$2.5 T \$5.9 T
Damages from COVID-19 Lost GDP in world from COVID-19 Value of a statistical life (V) adjusted for COVID-19 mortality structure Total COVID-19 world mortality (Q_o) forecast by 28 July 2020, 50th percentile with 95% error bounds Value of deaths in world from COVID-19 = $Q_o \times V$ Lowest (\$5.34 M × 2.5th percentile mortality forecast) Middle (\$10 M × 50th percentile mortality forecast) Highest (\$10 M × 97.5th percentile mortality forecast)	\$5.6 T \$5.34 M or \$10.0 M 590.643 [473.209,1.019.078] \$2.5 T \$5.9 T \$10.2 T

The break-even change in annual probability of pandemic satisfies $C = \Delta P \times D$. where P_0 = benchmark probability of pandemic; P_1 = probability of pandemic with prevention efforts in place; $\Delta P = P_0 - P_1$; and $\% \Delta P = (\Delta P/P_0) \times 100$.

If $P_0 = 0.01$, C = \$30.7 B, and D = \$11.5 T (most likely scenario, ignoring ancillary benefits of CO₂ reductions), prevention results in net benefits if it decreases P by 26.7% to $P_1 = 0.00733$. Using other values of C, D, and P results in $\%\Delta P$ ranging from 11.8% to 75.7%; only one scenario has a $\%\Delta P$ exceeding 50%. See supplementary materials.

2,**2B**

19.4B

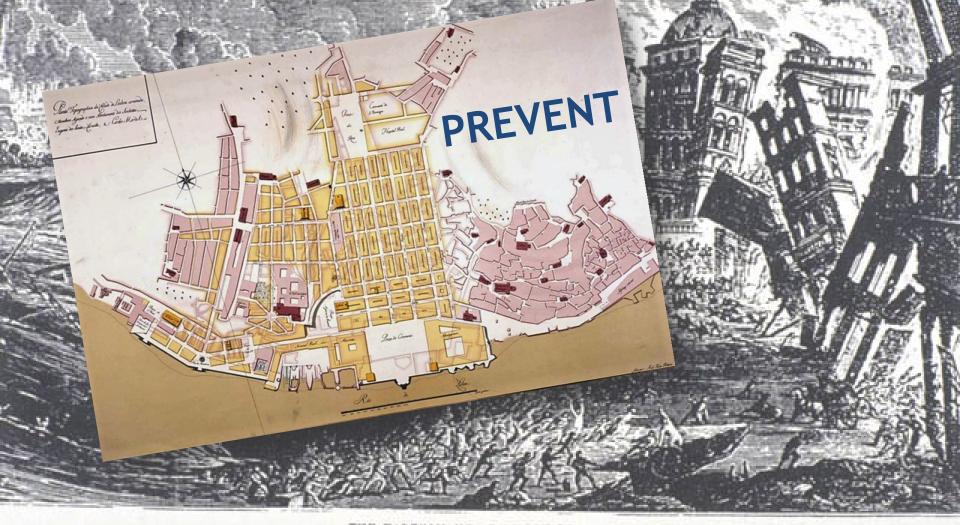
Investments to prevent deforestation and to limit wildlife trade will protect against future zoonosis outbreaks



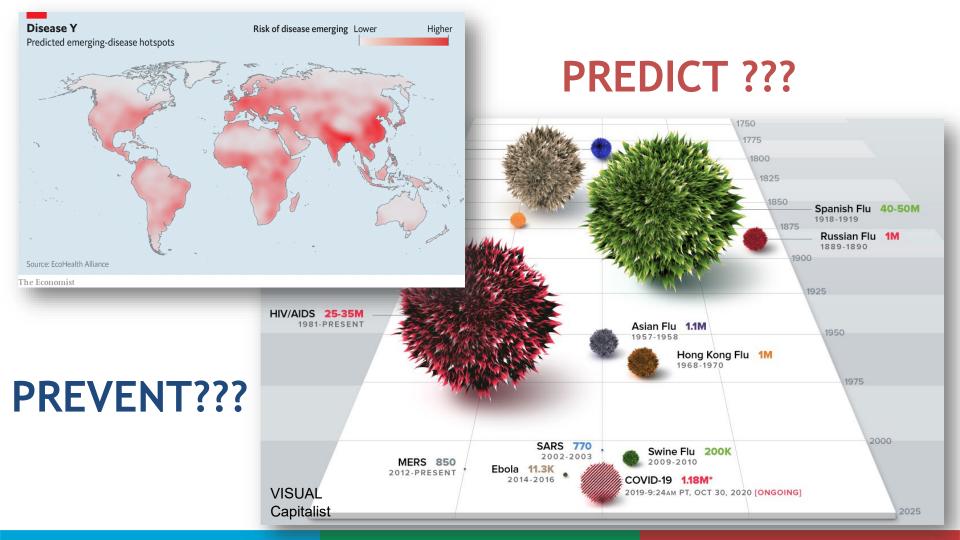
24 JULY 2020 • VOL 369 ISSUE 6502 379

Highest (\$10 M × 97.5th percentile mortality forecast)





THE EARTHQUAKE AT LISBON IN 175

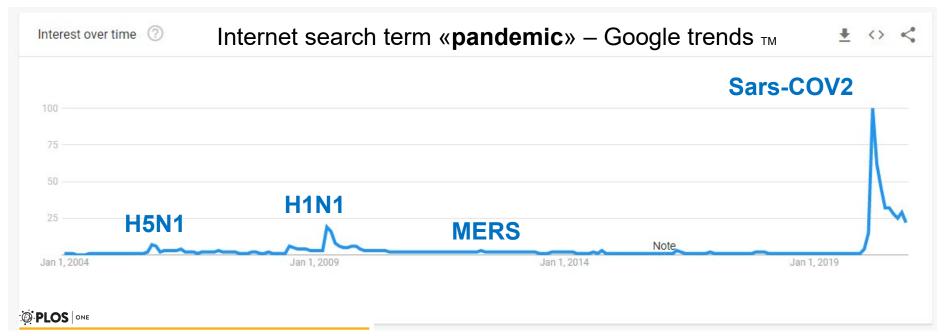


- "that those who come from infested areas shall not enter until after a period of isolation for the purpose of disinfection."
- "those sick shall hold themselves inside their houses and are not to leave under any circumstances"
- "circulation is to be restricted and regulated"





Lest we forget ??



RESEARCH ARTICLE

The Effects of Media Reports on Disease Spread and Important Public Health Measurements

Shannon Collinson^{1,2}, Kamran Khan^{3,4}, Jane M. Heffernan^{1,2}*

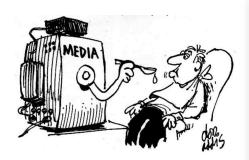
1 Modelling Infection and Immunity Lab, Centre for Disease Modelling, York University, Toronto, Canada, 2 Mathematics & Statistics, York University, Toronto, Canada, 2 Lik & Shing Knowledge Institute, St. Michael's Hospital, Toronto, Canada, 4 Department of Medicine, Division of Infectious Diseases, University of Toronto, Toronto, Canada



ORIGINAL RESEARCH published: 21 August 2020

How the Media Places Responsibility for the COVID-19 Pandemic—An Australian Media Analysis

Trevor Thomas, Annabelle Wilson, Emma Tonkin, Emma R. Miller and Paul R. Ward*



The POWER To inform... To prioritize... To influence...

All laters and smalls must contain a full name, actives and telephone numbonly your name and ocaily will be published, unless otherwise requested. We reserve the right to detil letters, Send them in via - small to mailbot 'lleesstermecury coult.'

Please note: We are unable to enter into correspondence about why contributions have not been used.

Saluting

everyone

affected

Victoria Park War Memorial.

father, Otto Roenisch, who, vi-

by the government as a Ger

enemy alien, was interned at St

whole of the First World War a

And I also remember my o

father, Paul Harton Roenisch, w

although severely restricted in

name, won a commendation fr

Montgomery for "outstanding s

vice and great devotion to o

during the campaign in France'

Rowan Roenisch Leice

quality of its players

adly died in 1991

afterwards repatriated to Sil

children here in England.

remembered especially my grand

my father experienced

WITH Armistice Day just passed, i that occurred in the Great European War in October 1917. It was during the 3rd Battle of

Ypres (Passchendael). My father took part as a lance con noral in the 2nd London Regiment

of the Royal Fusiliers and in a disastrous engagement on October 26, got wounded by shrapnel in his lung and was invalided home to England The shrapnel could not be removed, and remained in him for the rest of

The action was vividly described by Major W E Grey, who authored the official history of the regiment in 1929. It covers the four days that the preparing for the actual attack on That did not start from the men

going "over the top" from their trenches as we are aboves shown. They assembled in advance in noman's land and launched the attack from there, having crept out of the trenches in the dead of night 24 But let Major Grev tell the story.

*From the time of leaving Ithe base camp behind the lines on the morning of Tuesday 23rd October until it returned thither in the early hours of Saturday 27th October, th Battalion had had neither hot food nor drink of any sort whate "Assembly fin no man's land] says

Capt Harper, was a terrible job... bu thanks largely to the magnificent over 24 hours before the assault

talion at zero hour, disorganised by and Lewis guns fouled with mud sible to maintain the correct alighand many rendered useless, has to ment for two consecutive yards. be added the miserable fact that the "The men stumbled and slipped WE missed the Ham event at the This surely shows just how strong creeping protective [artillery] bar- in the stinking slime.

undergo the terrific ordeal of sitting, advancing troops were enveloped in Out of the reach of their compan-or lying, in stinking mud-holes for a curtain of smoke and flames, as ions, they were gradually sucked *Promptly at 5.30am a gallant bat- Gaps appeared in their ranks, and rible.*

"The yielding nature of the ground

shell after shell burst around them. down to a death, indescribably hor- A NEW football season has begut talion jumped off - waded rather - little heaps of dead and wounded romits assembly position... To a bat- marked their progress.

And my father was still a teerager, that Leicester City have worn it here it 18 games played to date-

Neville Hunnings, Evington the casualities of the earlier waiting [i.e. myled may all against a Straight hours, soaked to the skin, its rifles advance, and made it almost imposeral top defenders unavailable for some of these matches.

Cenotaph, but arrived at 11.25am on this squad is that Brendan Rodgers

crepting protective (untility) have in the suitabiling direction of the protection o

loyal as can be. Around him are improving professionals, loyal career players and fast-learning enthusiastic young players.

One doesn't need to name them all. I admire this group of men anchoring themselves towards the league. Yes, it's early days yet but there is enough hope that this team can

be. He is a top sportsman playing not for himself but for the team.

by wars hand John Hoffman autstile our house, playing Dark Isle on long-term and there is a feeling the one who suffered during the wars they can sustain a season-long chal of the 20th century. Usually, every year, John plays

and marches with the Leicester-shire Seaforth Highlanders at the For me, whilst John played, I

Outbreak on fur farms shows other victims THE widespread outbreaks

Covid-19 on Danish mink farms i more evidence that the exploitation of animals poses a health threat to humans - not to mention the animal cruelty involved ("Denmark trave

Once again it is being shown that ramming animals together results n diseases that can be passed on to

Eurthermore these diseases can mutate as has happened in Denmark. It's been reported that a mutation may not respond to the vaccines currently being developed fo

Excited about team and killed in the hope of halting the spread of the variant strain of the rus Hosewer these unfortunate animals receive little publicity. Let's hope that when this pandemic i wer (if it ever is) all countries wil cruel fur farming for ever Elizabeth Allison, Avlestone

NEWSLETTERS



England legend Shearer impressed with City's title credentials

ALAN Shearer is tipping Leicester Premier League title race, writes Andy Turner.
Although the England legend and

Match of the Day pundit believes champions Liverpool and Manchester City will be the main top honours, he reckons the Foxes deserve to be the current pace setters in the Premier League.

the top of the table after a 1-0 home the Day 2 analysis.

Man City and Liverpool shared the spoils in a 1-1 draw at the Etihad, leaving the Reds in thirs place behind Tottenham, both of whom are a single point behind

Manchester City as the stand-out think one of them will win the title - bad day - including all of the sides I going forward and defensively. but Leicester and Tottenham might have something to say about that," said Shearer, as part of his Match of don't see it changing any time soon.

"Southampton also spent some weekend and it is pretty refreshing

to see some different teams up interesting and it's something that might last a bit longer too. "The big thing that has stood out already about this season is how inpredictable it has been compared to previous years.

have just mentioned.
"That makes it exciting, and I partly because of the intense schedule and the number of injurier

common theme. It is Leicester who ever done - I know he missed one of moment. They are among the teams who have got injury problems but they are still playing some magnificent football. "I was really impressed by the

Foxes in their win over Wolves on "Every team has had at least one Sunday, in everything they did players in Wilfred Ndidi, Ricardo wouldn't know it from watching

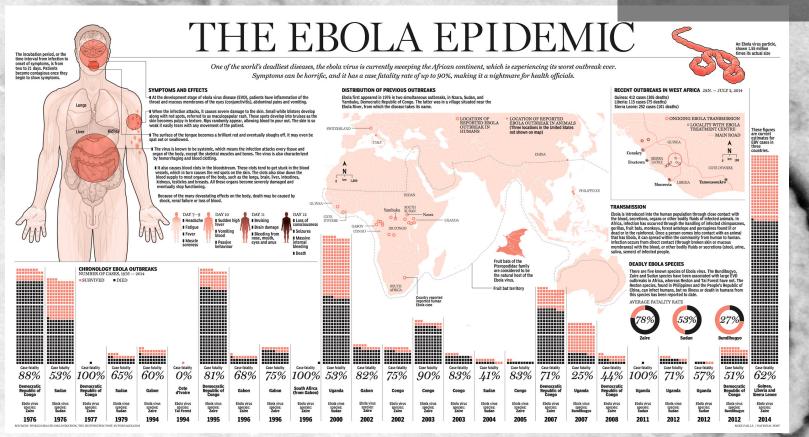
"Jamie Vardy is 33 in Januar with which is turning into another but he is looking as sharp as he's

some of his attacking play was "Then you have Nampalys Mendy who was unbelievably good in

midfield, and what a find Wesley Fofana looks at centre-half. slip-ups, losing at home to West Ham and Aston Villa last month "But now they are on a run of six and they will be full of confidence when they take on Liverpool at after the international break!

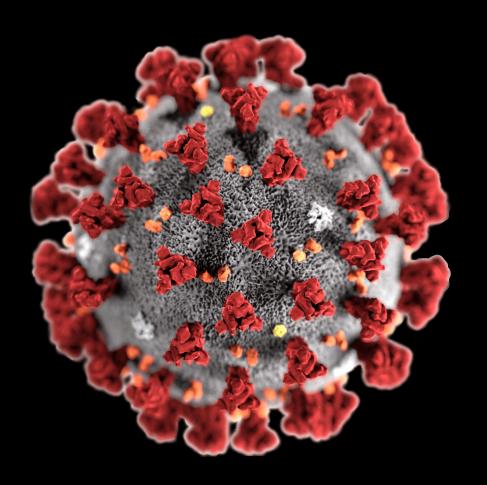
pressreader Problems on 11 604 275 4656

EBOLA



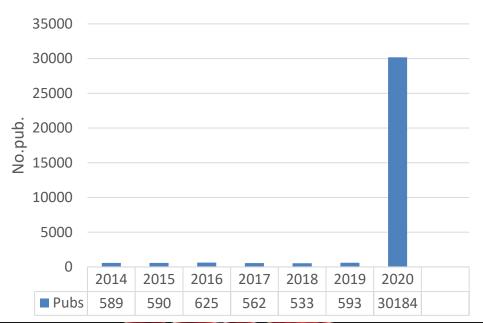






WHAT ABOUT... SARS-COV 2?

CORONAVIRUS Pubmed Publ.



The NEW ENGLAND JOURNAL of MEDICINE

BRIEF REPORT

A Novel Coronavirus from Patients with Pneumonia in China, 2019

Na Zhu, Ph.D., Dingvu Zhang, M.D., Wenling Wang, Ph.D., Xingwang Li, M.D. Bo Yang, M.S., Jingdong Song, Ph.D., Xiang Zhao, Ph.D., Baoying Huang, Ph.D., Weifeng Shi, Ph.D., Roujian Lu, M.D., Peihua Niu, Ph.D., Faxian Zhan, Ph.D., Xuejun Ma, Ph.D., Dayan Wang, Ph.D., Wenbo Xu, M.D., Guizhen Wu, M.D., George F. Gao. D.Phil., and Wenjie Tan, M.D., Ph.D., for the China Novel Coronavirus Investigating and Research Team

SUMMARY

In December 2019, a cluster of patients with pneumonia of unknown cause was. From the NHC Key Laboratory of Biosafelinked to a seafood wholesale market in Wuhan, China. A previously unknown betacoronavirus was discovered through the use of unbiased sequencing in samples from patients with pneumonia. Human airway epithelial cells were used to isolate a (N.Z., W.W., J.S., X.Z., B.H., R.L., P.N., novel coronavirus, named 2019-nCoV, which formed a clade within the subgenus sarbecovirus, Orthocoronavirinae subfamily. Different from both MERS-CoV and SARS-CoV, 2019-nCoV is the seventh member of the family of coronaviruses that infect humans. Enhanced surveillance and further investigation are ongoing. (Funded by the National Key Research and Development Program of China and the National Major Project for Control and Prevention of Infectious Disease in China.)

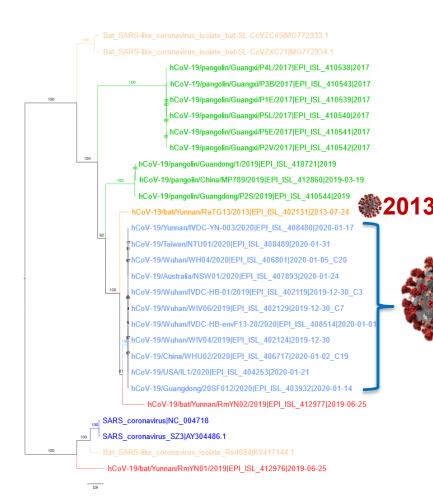
MERGING AND REEMERGING PATHOGENS ARE GLOBAL CHALLENGES FOR public health.1 Coronaviruses are enveloped RNA viruses that are distributed broadly among humans, other mammals, and birds and that cause respiratory, enteric, hepatic, and neurologic diseases.^{2,3} Six coronavirus species are known stitute for Viral Disease Control and Preto cause human disease.4 Four viruses - 229E, OC43, NL63, and HKU1 - are prevalent and typically cause common cold symptoms in immunocompetent individuals, The two other strains — severe acute respiratory syndrome coronavirus Gao at the National Institute for Viral (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) — are zoonotic in origin and have been linked to sometimes fatal illness.5 SARS-CoV was the causal agent of the severe acute respiratory syndrome outbreaks in 2002 and 2003 in Guangdong Province, China.6-8 MERS-CoV was the pathogen responsible for severe respiratory disease outbreaks in 2012 in the Middle East.9 Given the high prevalence and wide distribution of coronaviruses, the large genetic diversity and frequent recombination of their genomes, and increasing human-animal interface Drs. Zhu, Zhang, w. wang, Li, an contributed equally to this article. activities, novel coronaviruses are likely to emerge periodically in humans owing to frequent cross-species infections and occasional spillover events. 5,10

In late December 2019, several local health facilities reported clusters of patients with pneumonia of unknown cause that were epidemiologically linked to a NEngl | Med 2020:382:727-33. seafood and wet animal wholesale market in Wuhan. Hubei Province, China, 11 On DOI: 10.1056/NEIMog2001017 December 31, 2019, the Chinese Center for Disease Control and Prevention (China Copyright © 2020 Mossachusetts Medical Society. CDC) dispatched a rapid response team to accompany Hubei provincial and Wuhan city health authorities and to conduct an epidemiologic and etiologic investigation. We report the results of this investigation, identifying the source of the pneumonia

ty, National Institute for Viral Disease Control and Prevention, Chinese Center for Disease Control and Prevention X.M., D.W., W.X., G.W., G.F.G., W.T.), and the Department of Infectious Diseases Beijing Ditan Hospital, Capital Medical University (X.L.) - both in Beijing; Wuhan linvintan Hospital (D.Z.), the Division for Viral Disease Detection. Hubei Provincial Center for Disease Control and Prevention (B.Y., F.Z.), and the Center for Biosafety Mega-Science, Chinese Academy of Sciences (W.T.) - all in Wuhan; and the Shandong First Medical University and Shandong Academy of Medical Sciences, Jinan, China (W.S.). Address reprint requests to Dr. Tan at the NHC Key Laboratory of Biosafety, National Invention, China CDC, 155 Changbai Road, Changping District, Beijing 102206, China; or at tanwi@ivdc.chinacdc.cn, Dr. Disease Control and Prevention, China CDC. Beiling 102206. China, or at gaof@ im.ac.cn. or Dr. Wu at the NHC Key Laboratory of Biosafety, National Institute for Viral Disease Control and Prevention. China CDC, Beijing 102206, China, or at wugz@ivdc.chinacdc.cn.

Drs. Zhu, Zhang, W. Wang, Li, and Yang

This article was published on January 24, 2020, and updated on January 29, 2020,



REPORTS

Bats Are Natural Reservoirs of SARS-Like Coronaviruses

Wendong Li.⁷² Zhengü Shi,²⁴ Meng Yu,³ Wuze Ren,² Craig Smith,⁴ Jonathan H. Epstein,⁵ Hanzhong Wang,⁵ Cary Crameri,³ Zhihong Hu,² Huajun Zhang,² Jianhong Zhang,² Jennifer McSachern,³ Hume Field,⁴ Peter Daszak,⁵ Bryan T. Eaton,3 Shuyi Zhang,16* Lin-Fa Wang3

Severe acute respiratory syndrome (SARS) emerged in 2002 to 2002 in southern China. The origin of its devilogical agent, the SARS contensives (SARS-CW). Coronaviruse (SARS-CW) contensives (SARS-CW) contensives (SARS-CW) contensives (SARS-CW) depth or responsible for the SARS-culteral. Here viruses, bettered SARS-like coronaviruses (SL-CW)3, display greater greated virusited that SARS-CW footated from humans or from civet. The human civilization civil civet isolates of SARS-COV nestle phylogenetically within the spectrum of St-CoVs, indicating that the virus responsible for the SARS outbreak was a member of this coronavirus group.

Severe acute respiratory syndrome (SARS) studies have revealed no widespread infection was caused by a newly emerged corenevinus, in wild or farmed civets (6, 7). Experimental new known as SARS consumints (SARS-CoV) infection of civets with two different humans (1, 2, 11 repire of the early success of etisical studies and molecular characterization ical symptoms, rendering them unlikely to be of this virus (3, 4), efforts to identify the ori- the natural reservoir boots (8). Those data su CoV, it will be difficult to prevent and control and other common species in animal markets future outbreaks of SARS.

Studies conducted previously on animals market cycle in naive species than an in-Straines constanted previously on animals market eyels in naive species from an instruct eyels in the same animal market in Guarge, sampled from the animal markets in Guarge, doing, Chrin, indicated that masked palm eives the claim of the natural neserovir of the virus.

Buts are reserveir houts of several nonnexis been infected by SARS-CoV (5). This led to which have recently emerged in Australia and which have recently emerged in Australia and a large-scale culling of civets to prevent fur. East Asia, respectively (9-17). Buts may be to taggi-mate cutting to tree to prevent their SARS outbreaks. However, subsequent their SARS outbreaks. However, subsequent display clinical symptoms (22). These chancerists before Key Lobertony of Sciences (CAS), Beijing, Ohns. State Key Lebentony of but products in food and traditional medicine.

markets in southern China and elsewhere is Asia (13) led us to survey bats in the search for the natural reservoir of SARS-CoV. In this study, conducted from Murch to December of 2004, we sampled 408 bats representing nine species, six genera, and three families from four locations in China

was more likely a reflection of an "artificia

(Guanedone, Guanexi, Hubei, and Tianiin) af ter trapping them in their native habitat (Tabl-1). Blood, fecal, and threat swabs were col-

28 OCTOBER 2005 VOL 310 SCIENCE WWW.scien



RESEARCH ARTICLE

Discovery of a rich gene pool of bat SARSrelated coronaviruses provides new insights into the origin of SARS coronavirus

Ben Hu^{1, ©}, Lei-Ping Zeng^{1, ©}, Xing-Lou Yang^{1, ©}, Xing-Yi Ge¹, Wei Zhang¹, Bei Li¹, Jia-Zheng Xie¹, Xu-Rui Shen¹, Yun-Zhi Zhang^{2,3}, Ning Wang¹, Dong-Sheng Luo¹, Xiao-Shuang Zheng¹, Mei-Niang Wang¹, Peter Daszak⁴, Lin-Fa Wang⁵, Jie Cui¹*, Zheng-

LETTER

doi:10.1038/nature12711

Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor

Xing-Yi Ge³*, Jia-Lu Li¹*, Xing-Lou Yang³*, Aleksei A. Chmurn², Guangjian Zhu², Jonathan H. Epstein², Jonna K. Maze², Ben Hu¹, Wei Zhang¹, Cheng Peng², Yu- Ji Zhang², Chu-Ming Luo³, Bing Tan³, Ning Wang¹, Yan Zhu¹, Gary Crameri², Shu-Yi Zhang³, Lin-Fa Wang⁴, Peter Daszal², Szheng-U Shi³

of both viruses¹⁶, attempts to isolate the progenitor virus of SARS-GoV from bats have been unsuccessful. Diverse SARS-like corona-viruses (SL-OVs) have now been reported from bats in China, all positive samples vas confirmed by sequencing. The species origin of all positive samples vas confirmed to be R. stratus of the confirmed by the con Europe and Africa¹⁰⁰, but none is considered a direct progenitor of SABS-CoV because of their phylogenetic dispurity from this visus observed in samples collected in October (30% in 2011 and 48.7% in 2012 than those in April (7.1% in 2011) Away (7.1% in 2012) Extended to the control of th recenter molecule, the human anciotensin converting enzyme II. Data Table 1) Analysis of the Spreading RRD sequences indicated the receptor mosecure, use numan any normal control of the control of in Yunnan. China: RsSHQ014 and Rs3367. These viruses are far more doubly related to SARS-CoV than any previously identified but coro-naviruses, particularly in the receptor binding domain of the spike

Their full-length genome sequences were determined, and both were protein. Most importantly, we report the first recorded isolation of found to be 29,787 base pairs in size (excluding the poly(A) tail). The protein. Most importantly, we report tori make recorded isolation of a live SL-CoV (MSL SL-CoV-MSVI) from bat faced is amples in Vero E6 cells, which has typical coronaries more phology, 99.9% and collective to a support to the coverage of the coverage o horseshoe bats for cell entry. Perliminary in vitro testing indicates
that WIVI also has a broad species tropism. Our results provide the
tities were observed at the protein level between these new SL-CoVs strongest evidence to date that Chinese horseshoe bats are natural and SARS-CoVs (Extended Data Tables 3 and 4). To understand the reservoirs of SARS-CoV, and that intermediate hosts may not be
evolutionary origin of these two novel SL-CoV strains, we conducted
necessary for direct human infection by some bat SL-CoVs. They also
recombination analysis with the Recombination Detection Program

Middle East respiratory syndrome coronavirus (MERS-CoV)² demon-strate that CoVs are a significant public health threat SABS-CoV was points were located at nucleotides 20,827, 26,553 and 28,885 in the shown to use the human ACE2 molecule as its entry receptor, and this is considered a hallmark of its cross-species transmissibility." The receptor in the hallmark of its cross-species transmissibility." The receptor in the properties of the properties of the properties of the properties of the hallmark of its cross-species of the properties of the hallmark of its cross-species of the properties of the hallmark of its cross-species of the properties of the hallmark of its cross-species of and State State of the SARS COV splint (to venturate region) cannot be added State State of the SARS COV splint (to venturate region) cannot be added State State of the SARS COV splint (S) protein is falled by the SARS COV splint (s) provided from the SARS COV seed from the St. CoV is have major recognized differences from s.N.St. CoV in the RID aggreted that fix NAC, or fixSPCOVA is the checondent of a conditional form of the fix proteins, including more or two decisions. Regulating the RID of one St. CoV is posterin with SARS CoV is conformed the ability to use human ACE2 and registate efficients in major. In some cover, to do see, no

The 2002-3 pandemic caused by severe acute respiratory syndrome in Kunming, Yunnan Province, China (Extended Data Table 1). A total or 117 anal swabs or faceal samples were collected from individual bats events in recent history'. An ongoing outbreak of Middle East respiratory syndrome coronavirus² suggests that this group of viruses remains a key threat and that their distribution is wider than previously roogs. RNA polymerace (RdRP) medis A and C, which are conserved among nited. Although bits have been suggested to be the natural reservoirs and photocoronaviruse and betacoronaviruses.²

high-risk vidilite groups in emerging disease botspots as a strategy
(RI, Ryo, Star St., RH, LH) and BMS-31 and human driver
for pandenic preparedness. r pandemic preparedness. representative SAIS-CoV strains (BJ01, Sz.3, 1 or 2 and Gz02). Three 2002–3 pandemic of SARS and the onosing emergence of the breakpoints were detected with strong P values (<10⁻²⁰) and supported

numan ACE: and represent entering in mice. - Frowever, to once, no

Over and previously inclinates 32-COV is an interest to Proposition entering.

Over and previously inclinates 32-COV is an interest to Proposition entering to SARSorigin has been shown to use ACE2.

CoV (85% and 96% for ReSHCD14 and Br3367, respectively). Second, We concluded a 12-month lensitudinal survey (April 2011-September there are no deletions and they have perfect sequence alignment will 2012) of St. CoVs in a colony of Rhinolophus sinicus at a single location the SARS-CoV RBD region (Extended Data Figs 1 and 2). Structural

www.new.new.get.get.com/comments.com/fig/1007085/y/11V200g/.W/min Intended Visrogic of the Comment Accoming on control Wilder ECDOT. John "Cost leight-fill and Cost." (See Fill See Fi

China, 2011

Li Yang, 'Zhiqiang Wu, 'Xianwen Ren, 'Fan Yang, ' Guimei He, Junpeng Zhang, Jie Dong, Lilian Sun, Yafang Zhu, Jiang Du, Shuyi Zhang, and Qi Jin

To clarify the evolutionary relationships among betavoronaviruses that infect bats, we analyzed samples collected during 2010-2011 from 14 insectivorous hat species in China. We identified complete genomes of 2 novel hetecoronsviruses in Rhipplophus pussibus and Chaerenhon plicate bats, which showed close genetic relationships with severe acute respiratory syndrome coronaviruses.

Novel SARS-like mucleic acid purification method (6). The extracted RNA and DNA were amplified by sequence-independent Betacoronaviruses PCR. The amplified viral nucleic acid libraries of the bat species were then sequenced with the Illumina/Solexa in Bats, GAII sequencer (Illumina, San Diego, CA, USA). Those reads generated by the Illumina/Solexa GAII with length of 80 bases were directly aligned to the protein sequences in the National Center for Biotechnology Information nonredundant protein database by the blastx program in the BLAST software package, version 2.2.22 (www.ncbi nlm.nih.gov/blast) with parameters "-e 1e-5 -F T -b 10 av 10 " No assembly was performed before alignment Sequence similarity-based taxonomic assignments were conducted as described (7). We found 1,075 reads of betacoronavirus in Rhinolophus pusillus bats in Shaanxi and 92 reads of betacoronavirus in Chaerephon plicata bats in Yunnan.

We estimated the approximate locations of those reads on the CoV genome and their relative distances on



What can governments do to prevent future pandemics?







Governments could establish an intergovernmental council on pandemic prevention to help escape the 'era of pandemics'

- Building a new intergovernmental health and trade partnership to reduce zoonotic disease risks in the international wildlife trade, building on collaborations among international organisations.
- Institutionalizing the 'One Health' approach in national governments to build pandemic preparedness, enhance pandemic prevention programs, and to investigate and control outbreaks across sectors.

#PandemicsReport



Enabling transformative change to reduce the types of consumption, globalized agricultural expansion and trade that have led to pandemics

Educating communities from all sectors in emerging infectious diseases hotspots

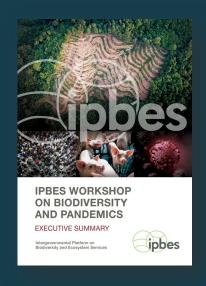
- Making better use of indigenous knowledge
- Incorporate pandemic risk into planning
- Supporting One Health scientific research to design and test better strategies to prevent pandemics





ipbes #PandemicsReport





https://ipbes.net/pandemics media@ipbes.net #PandemicsReport

Carlos.dasneves@vetinst.no

