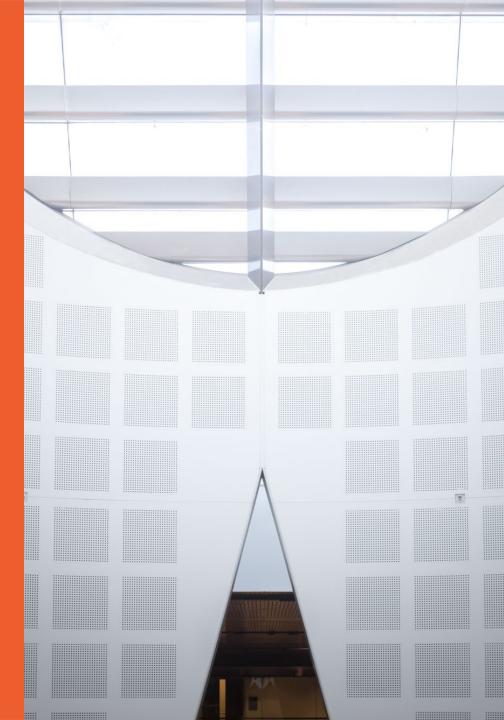
# Truth decay – Determining fact from fiction

Nick Enfield

Sydney Initiative for Truth (SIFT)

Sydney Social Sciences and Humanities Advanced Research Centre





News > World > Europe

## Pope Francis bans sale of cigarettes at the Vatican on health grounds

'The motive is very simple: the Holy See cannot be cooperating with a practice that is clearly harming the people'

Philip Pullella | 5 days ago | Q0 comments





WHO welcomes the Vatican's decision to ban the sale of cigarettes as of next year.

Tobacco kills more than 7 million people every year #NoTobacco ■ ◆



# TOBACCO KILLS PEOPLE EVERY YEAR

MORE THAN

MILLION

TOBACCO THREATENS HEALTH, ECONOMIES AND DEVELOPMENT.



12% OF DEATHS OF ALL PEOPLE AGED **OVER 30** ARE DUE TO TOBACCO.



TRILLION IN HEALTHCARE EXPENDITURE AND LOST PRODUCTIVITY FROM ILLNESS AND PREMATURE DEATH.

**#NOTOBACCO** 



#### WHO 🧼 @WHO

WHO welcomes the Vatican's decision to ban the sale of cigarettes as of next year.

Tobacco kills more than 7 million people every year #NoTobacco





I ask Nigel Farage why he's taken up cigarettes again. Farage: "I think the doctors have got it wrong on smoking"



The doctors have got it wrong on smoking.

# **Tobacco industry manipulation of research**

Lisa A. Bero (1)



The primary motivation of the tobacco industry has been to generate controversy about the health risks of its products. The industry has used several strategies including:

- 1. funding and publishing research that supports its position;
- 2. suppressing and criticising research that does not support its position;
- 3. changing the standards for scientific research;
- 4. disseminating interest group data or interpretation of risks via the lay (non-academic) press and directly to policymakers.

"body of fact" that exists in the mind of the general public. It is also the means of establishing a controversy. Within the business we recognize that a controversy exists. However, with the general public the consensus is that cigarettes are in some way harmful to the health.

1969 memo from Brown & Williamson, a then-subsidiary of British American Tobacco



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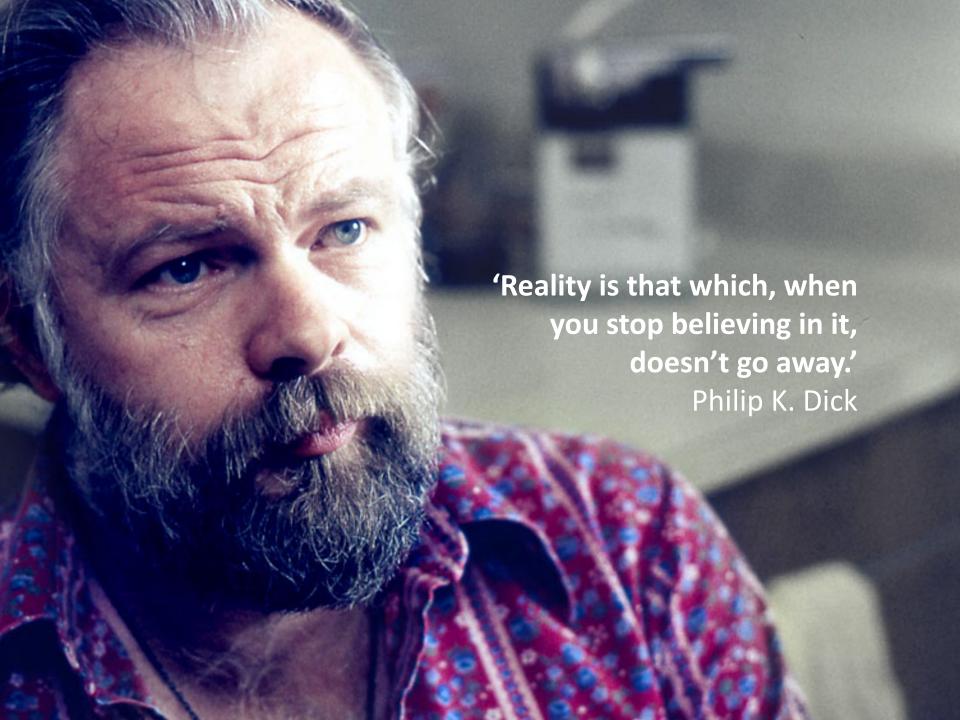
12% OF DEATHS OF ALL PEOPLE AGED OVER 30 ARE DUE TO TOBACCO.

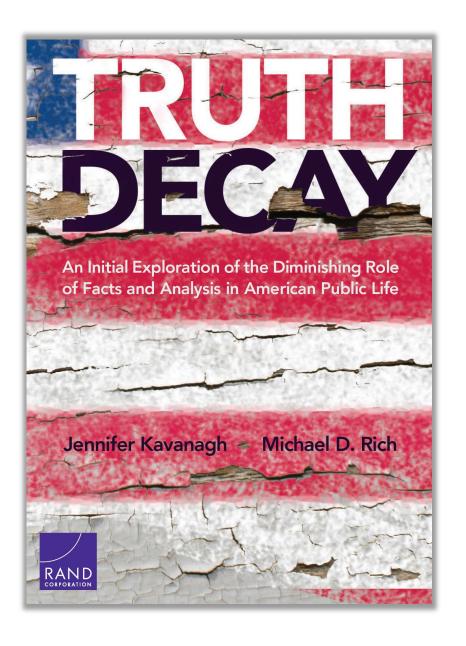


GLOBAL ANNUAL COSTS FROM TOBACCO USE ARE **US\$1.4**TRILLION IN HEALTHCARE EXPENDITURE AND LOST
PRODUCTIVITY FROM ILLNESS AND PREMATURE DEATH.

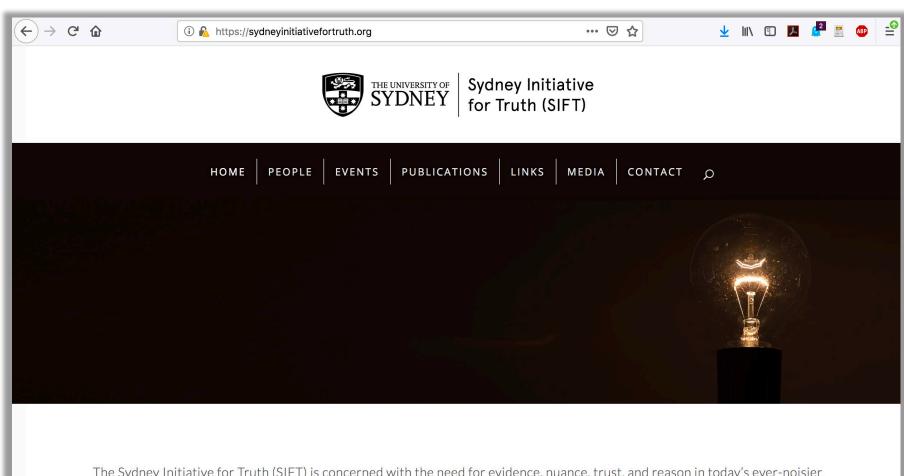
**#NOTOBACCO** 

Around 400 people will have died from tobacco-related illness during the course of this talk today.





RAND Corporation 2018



The Sydney Initiative for Truth (SIFT) is concerned with the need for evidence, nuance, trust, and reason in today's ever-noisier infosphere.

SIFT's interdisciplinary researchers aim to understand and remedy the 'post truth' crisis. Through philosophy, linguistics, political science, public health, media, environmental science, and data science, we are investigating a range of issues around truth, including the quality of public discourse, commercial influence in research, historical trends in 'truth decay', cognitive biases, political and media spin, fake news, power and claims to truth, the role of language, and the decline of trust in expertise.

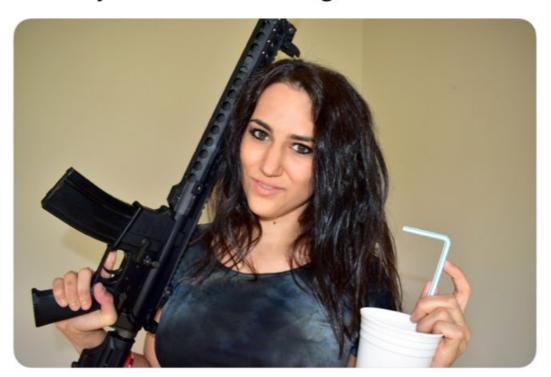
Principle 1.
Statements are sometimes for informing, other times for signaling allegiance





#### **Tweet**

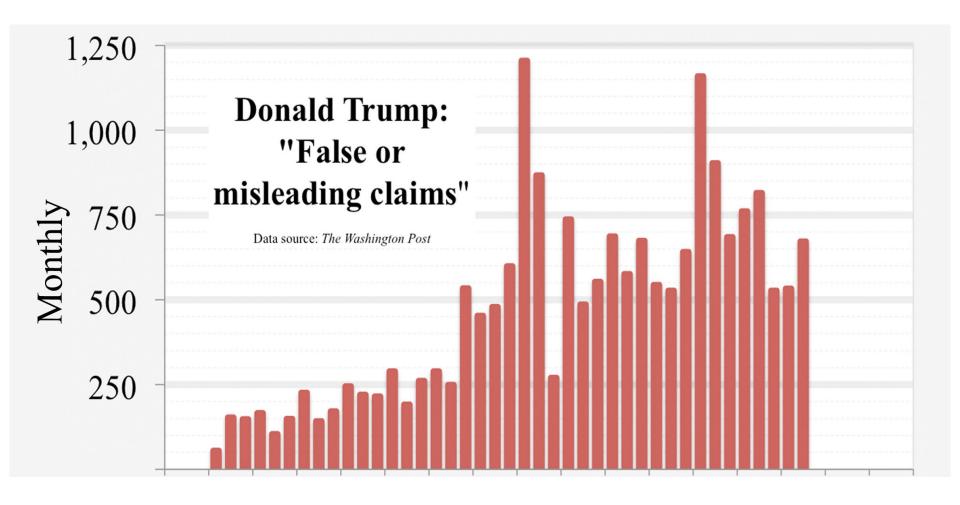
Hey, GOVERNMENT, you can't take my AR-15, so what makes you think you can take my plastic straw? I don't need your permission, you are subordinate to me, and that's the world you're stuck living in.



@Armastrangelo June 29, 2018







Trump has now made more than 18,000 false statements during his presidency

(Washington Post, Toronto Star, factcheck.org)

#### US Black youth unemployment, 2016

Trump: "58%"

Bureau of Labor Statistics: "21%"

"The press takes him literally, but not seriously; his supporters take him seriously, but not literally."

Salena Zito, Atlantic Sept 2016

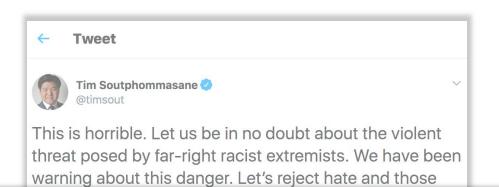






Christchurch terror attack: 49 dead, Australian man arrested
New Zealand police confirmed 49 people lost their lives in shootings at two
Christchurch mosques.

S sbs.com.au March 2019

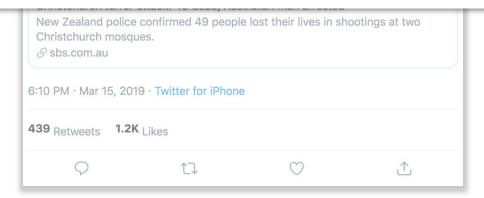


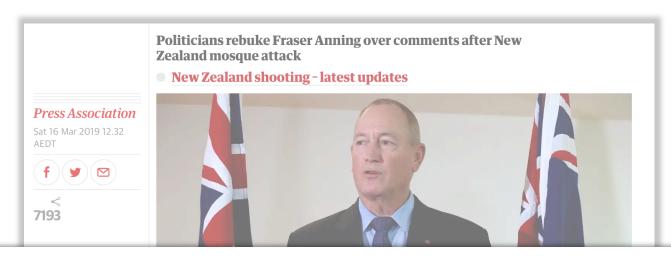


Australia's former Race Discrimination Commissioner Dr Tim Soutphommasane told the BBC he had seen a "return of race politics" in the past five years.

He notes a "crucial" development was the government's attempts to weaken hate speech laws in 2014 and 2017.

"That encouraged far-right extremists and others to believe that free speech permitted hate speech - that they had a right to be bigots," he said.





"The real cause of bloodshed on New Zealand streets today is the immigration program which allowed Muslim fanatics to migrate to New Zealand in the first place."

▲ Fraser Anning tweeted: 'Does anyone still dispute the link between Muslim immigration and violence?' Photograph: David Clark/AAP

An Australian senator has been strongly criticised after he blamed the New Zealand shooting on Muslim immigration.

Following the attack, which left 49 people dead at two mosques in Christchurch, Fraser Anning tweeted: "Does anyone still dispute the link between Muslim immigration and violence?"

In a statement shared by an Australian journalist on Twitter, the <u>Queensland</u> senator also wrote: "As always, leftwing politicians and the media will rush to claim that the causes of today's shootings lie with gun laws or those who hold nationalist views, but this is all cliched nonsense.

"The real cause of bloodshed on New Zealand streets today is the immigration program which allowed Muslim fanatics to migrate to New Zealand in the first place."

Principle 1.
Statements are sometimes for informing, other times for signaling allegiance

Principle 2.
Our own cognitive limitations play a role in truth decay

**Confirmation bias** 

2, 4, 6
8, 10, 12 
20, 22, 24 

20, 22, 24

Rule:

'Start with n and add 2 each time'?

2, 4, 6
3, 6, 9 
20, 40, 60 
20, 40, 60

Rule:

'Start with n and add n each time'?

2, 4, 6

3, 4, 57

4, 3, 60 🗶

Rule:

2, 4, 6

3, 4, 57

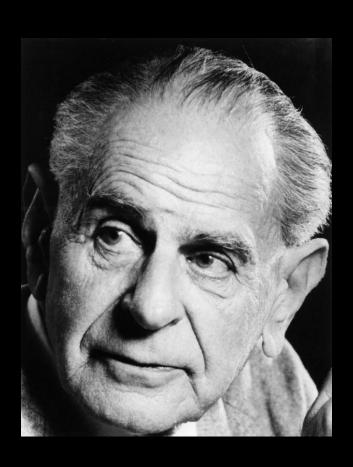


4, 3, 60 🗶



Rule: 'Start with n and add a higher number each time'.

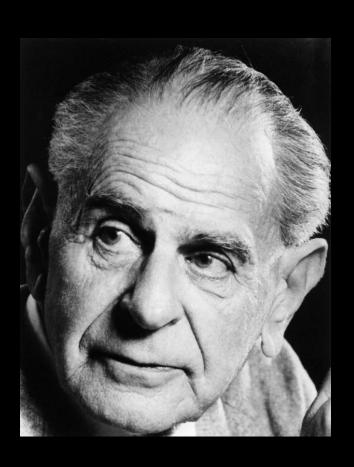
## **Confirmation Bias**



We never confirm a hypothesis, we can only show that it has not been falsified.

**Karl Popper** 

## **Confirmation Bias**



We never confirm a hypothesis, we can only show that it has not been falsified.

**Karl Popper** 

So we must always *try* to find evidence *against* our beliefs.





Trump imitated a disabled reporter. Now he pretends not to see a child in a wheelchair, as though frightened he might catch his condition.

1:08 PM - 28 Jul 2017

12,883 Retweets 52,240 Likes







13K



52K



Video Clip 1 Video Clip 2

Principle 2.
Our own cognitive limitations play a role in truth decay

Principle 3.
The truth matters because facts are reasons for action













Principle 3.
The truth matters because facts are reasons for action



"These smug pilots have lost touch with regular passengers like us.

Who thinks I should fly the plane?"

Our information is filtered through people

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- What are their motivations and incentives?
- What do they say, and which words do they use?
- Do you want to believe it? Why (not)?
- What actions could their words be used to justify?
- What do they *not* say?

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Never doubt that reality is always there, to provide sound reasons for action

### The Sydney Morning Herald

# How Sydney cancer scientist Jennifer Byrne became a research fraud super sleuth

#### By Kate Aubusson

**Updated** 26 January 2017 – 2:23pm, first published 25 January 2017 – 1:22pm













It was a gut feeling that had Professor Jennifer Byrne flipping open her computer on a Saturday night and firing up the medical equivalent of a Google search.

What she found made her sick to her stomach.

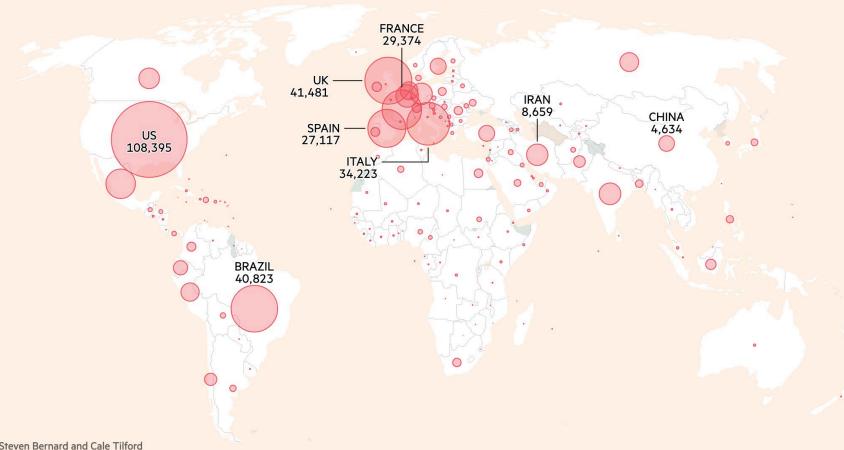


Professor Jennifer Byrne, Head of the Children's Cancer Research Unit at The Children's Hospital at Westmead, has uncovered alleged research fraud.

### Mapping the coronavirus outbreak

As of 2.51pm June 13 BST

Confirmed cases **Deaths 7,570,154 418,622** 



Graphic: Steven Bernard and Cale Tilford Sources: ECDC; Covid Tracking Project; FT research @ FT

### CORRESPONDENCE

## **Transmission of 2019-nCoV Infection from an Asymptomatic Contact in Germany**

TO THE EDITOR: The novel coronavirus (2019-nCoV) from Wuhan is currently causing concern in the medical community as the virus is spreading around the world. Since identification of the virus in late December 2019, the number of cases from China that have been imported into other countries is on the rise, and the epidemiologic picture is changing on a daily basis. We are reporting a case of 2019-nCoV infection acquired outside Asia in which transmission appears to have occurred during the incubation period in the index patient.

A 33-year-old otherwise healthy German businessman (Patient 1) became ill with a sore throat, chills, and myalgias on January 24, 2020. The following day, a fever of 39.1°C (102.4°F) developed, along with a productive cough. By the evening of the next day, he started feeling better and went back to work on January 27.

Before the onset of symptoms, he had attended meetings with a Chinese business partner at his company near Munich on January 20 and 21. The business partner, a Shanghai resident, had visited Germany between January 19 and 22. During her stay, she had been well with no signs or symptoms of infection but had become ill on her flight back to China, where she tested positive for 2019-nCoV on January 26 (index patient in Fig. 1) (see Supplementary Appendix, available at NEJM.org, for details on the timeline of symptom development leading to hospitalization).

On January 27, she informed the company about her illness. Contact tracing was started, and the above-mentioned colleague was sent to the Division of Infectious Diseases and Tropical Medicine in Munich for further assessment. At presentation, he was afebrile and well. He reported no previous or chronic illnesses and had no his-

Jan 2020

Peer-reviewed in top journal, high media impact; but flawed: conclusion accidentally true, never retracted

### Impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand

Neil M Ferguson, Daniel Laydon, Gemma Nedjati-Gilani, Natsuko Imai, Kylie Ainslie, Marc Baguelin, Sangeeta Bhatia, Adhiratha Boonyasiri, Zulma Cucunubá, Gina Cuomo-Dannenburg, Amy Dighe, Ilaria Dorigatti, Han Fu, Katy Gaythorpe, Will Green, Arran Hamlet, Wes Hinsley, Lucy C Okell, Sabine van Elsland, Hayley Thompson, Robert Verity, Erik Volz, Haowei Wang, Yuanrong Wang, Patrick GT Walker, Caroline Walters, Peter Winskill, Charles Whittaker, Christl A Donnelly, Steven Riley, Azra C Ghani.

On behalf of the Imperial College COVID-19 Response Team

WHO Collaborating Centre for Infectious Disease Modelling MRC Centre for Global Infectious Disease Analysis Abdul Latif Jameel Institute for Disease and Emergency Analytics Imperial College London

## Uncanny similarity of unique inserts in the 2019-nCoV spike protein to HIV-1 gp120 and Gag

Prashant Pradhan<sup>\$1,2</sup>, Ashutosh Kumar Pandey<sup>\$1</sup>, Akhilesh Mishra<sup>\$1</sup>, Parul Gupta<sup>1</sup>, Praveen Kumar Tripathi<sup>1</sup>, Manoj Balakrishnan Menon<sup>1</sup>, James Gomes<sup>1</sup>, Perumal Vivekanandan<sup>\*1</sup>and Bishwajit Kundu<sup>\*1</sup>

<sup>1</sup>Kusuma School of biological sciences, Indian institute of technology, New Delhi-110016, India.

<sup>2</sup>Acharya Narendra Dev College, University of Delhi, New Delhi-110019, India

\$Equal contribution

\* Corresponding authors- email: <u>bkundu@bioschool.iitd.ac.in</u>

vperumal@bioschool.iitd.ac.in

Jan 2020

Non-peer-reviewed preprint, massive media impact, analysis flawed, quickly retracted

### SARS-like WIV1-CoV poised for human emergence

Vineet D. Menachery<sup>a</sup>, Boyd L. Yount Jr.<sup>a</sup>, Amy C. Sims<sup>a</sup>, Kari Debbink<sup>a,b</sup>, Sudhakar S. Agnihothram<sup>c</sup>, Lisa E. Gralinski<sup>a</sup>, Rachel L. Graham<sup>a</sup>, Trevor Scobey<sup>a</sup>, Jessica A. Plante<sup>a</sup>, Scott R. Royal<sup>a</sup>, Jesica Swanstrom<sup>a</sup>, Timothy P. Sheahan<sup>a</sup>, Raymond J. Pickles<sup>c,d</sup>, Davide Corti<sup>e,f,g</sup>, Scott H. Randell<sup>d</sup>, Antonio Lanzavecchia<sup>e,f</sup>, Wayne A. Marasco<sup>h</sup>, and Ralph S. Baric<sup>a,c,1</sup>

<sup>a</sup>Department of Epidemiology, University of North Carolina at Chapel Hill, Chapel Hill, NC 27599; <sup>b</sup>Department of Microbiology and Immunology, University of North Carolina at Chapel Hill, NC 27599; <sup>c</sup>Division of Microbiology, National Center for Toxicological Research, Food and Drug Administration, Jefferson, AR 72079; <sup>d</sup>Department of Cell Biology and Physiology and Marsico Lung Institute/Cystic Fibrosis Center, University of North

Carolina at Chapel Hill, Chapel Hill, NC 27599; "Institute for Research in Biomedicine Rellinzona Switzerland: "Institute of Microb Technische Hochschule Zurich, Zurich, Switzerland; "Humabs BioMed SA, Bellinz Dana-Farber Cancer Institute—Department of Medicine, Harvard Medicial School,

Edited by Peter Palese, Icahn School of Medicine at Mount Sinai, New York, NY,

Outbreaks from zoonotic sources represent a threat to both human disease as well as the global economy. Despite a wealth of metagenomics studies, methods to leverage these datasets to identify future threats are underdeveloped. In this study, we describe an approach that combines existing metagenomics data with reverse genetics to engineer reagents to evaluate emergence and pathogenic potential of circulating zoonotic viruses. Focusing on the severe acute respiratory syndrome (SARS)-like viruses, the results indicate that the WIV1-coronavirus (CoV) cluster has the ability to directly infect and may undergo limited transmission in human populations. However, in vivo attenuation suggests additional adaptation is required for epidemic disease. Importantly, available SARS monoclonal antibodies offered success in limiting viral infection absent from available vaccine approaches. Together, the data highlight the utility of a platform to identify and prioritize prepandemic strains harbored in animal reservoirs and document the threat posed by WIV1-CoV for emergence in human populations.

SARS | CoV | emergence | Spike | WIV1

2016



### Identification of Diverse Alphacoronaviruses and Genomic Characterization of a Novel Severe Acute Respiratory Syndrome-Like Coronavirus from Bats in China

Biao He,<sup>a,d</sup> Yuzhen Zhang,<sup>b</sup> Lin Xu,<sup>a,d</sup> Weihong Yang,<sup>b</sup> Fanli Yang,<sup>a</sup> Yun Feng,<sup>b</sup> Lele Xia,<sup>a</sup> Jihua Zhou,<sup>b</sup> Weibin Zhen,<sup>c</sup> Ye Feng,<sup>a,d</sup> Huancheng Guo,<sup>a,d</sup> Hailin Zhang,<sup>b</sup> Changchun Tu<sup>a,d</sup>

Key Laboratory of Jilin Province for Zoonosis Prevention and Control, Institute of Military Veterinary, Academy of Military Medical Sciences, Changchun, Jilin Province, China<sup>12</sup>, Yunnan Institute of Endemic Diseases Control and Prevention, Dall, Yunnan Province, China<sup>12</sup>, Baoshan Prefecture Center for Diseases Control and Prevention, Baoshan, Yunnan Province, China<sup>13</sup>, Jiangsu Co-Innovation Center for Prevention and Control of Important Animal Infectious Diseases and Zoonoses, Yangzhou, Jiangsu Province, China<sup>14</sup>

#### **ABSTRACT**

Although many severe acute respiratory syndrome-like coronaviruses (SARS-like CoVs) have been identified in bats in China, Europe, and Africa, most have a genetic organization significantly distinct from human/civet SARS CoVs in the receptor-binding domain (RBD), which mediates receptor binding and determines the host spectrum, resulting in their failure to cause human infections and making them unlikely progenitors of human/civet SARS CoVs. Here, a viral metagenomic analysis of 268 bat rectal swabs collected from four counties in Yunnan Province has identified hundreds of sequences relating to alpha- and betacoronaviruses. Phylogenetic analysis based on a conserved region of the RNA-dependent RNA polymerase gene revealed that alphacoronaviruses had diversities with some obvious differences from those reported previously. Full genomic analysis of a new SARS-like CoV from Baoshan (LYRa11) showed that it was 29,805 nucleotides (nt) in length with 13 open reading frames (ORFs), sharing 91% nucleotide identity with human/civet SARS CoVs and the most recently reported SARS-like CoV Rs3367, while sharing 89% with other bat SARS-like CoVs. Notably, it showed the highest sequence identity with the S gene of SARS CoVs and Rs3367, especially in the RBD region. Antigenic analysis showed that the S1 domain of LYRa11 could be efficiently recognized by SARS-convalescent human serum, indicating that LYRa11 is a novel virus antigenically close to SARS CoV. Recombination analyses indicate that LYRa11 is likely a recombinant descended from parental lineages that had evolved into a number of bat SARS-like CoVs.

2016

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- What would their words justify?
- What do they *not* say?

Never doubt that reality is always there, to provide sound reasons for action

## An optimistic coda

We can be the gatekeepers

Thank you

N. J. Enfield
Sydney Initiative for Truth (SIFT)
The University of Sydney

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