UNIVERSIDADE DE SÃO PAULO
FACULDADE DE SAÚDE PÚBLICA

Universidade de São Paulo

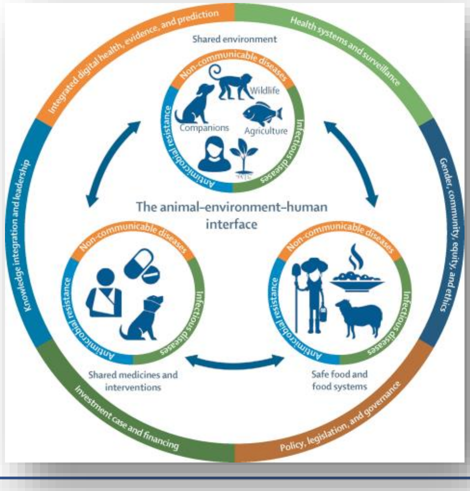
# Saúde Única
# “One Health Approach”

Prof. **Fredy Galvis Ovallos**

Departamento de Epidemiologia
FSP/USP

E-mail: fgalvis@usp.br

# Saúde Única



“É um enfoque para desenhar e implementar programas, políticas, legislação e pesquisa com a integração de diferentes setores trabalando juntos para a obtenção de melhores desfechos em saúde pública” (WHO, 2020)

- Segurança alimentar
- Controle de zoonoses (influenza, raiva, Febre do Nilo Ocidental)
- Resistência a antibióticos

# Saúde Única

Qual a importância do enfoque da Saúde Única?

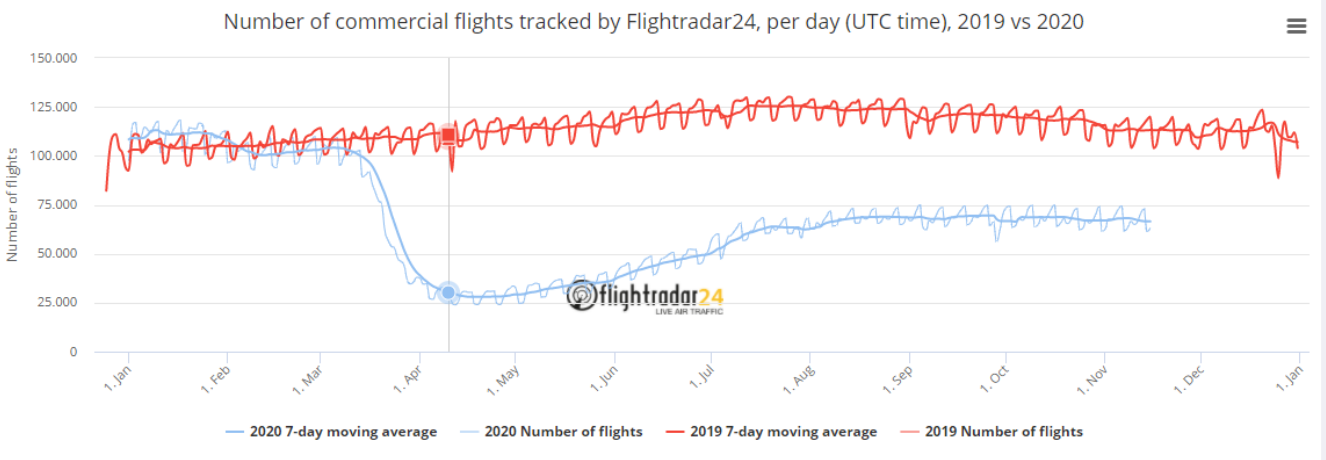
Muitos Patógenos Infectam tanto o homem como animais, sendo que existe um ecossistema compartilhado entre estes.

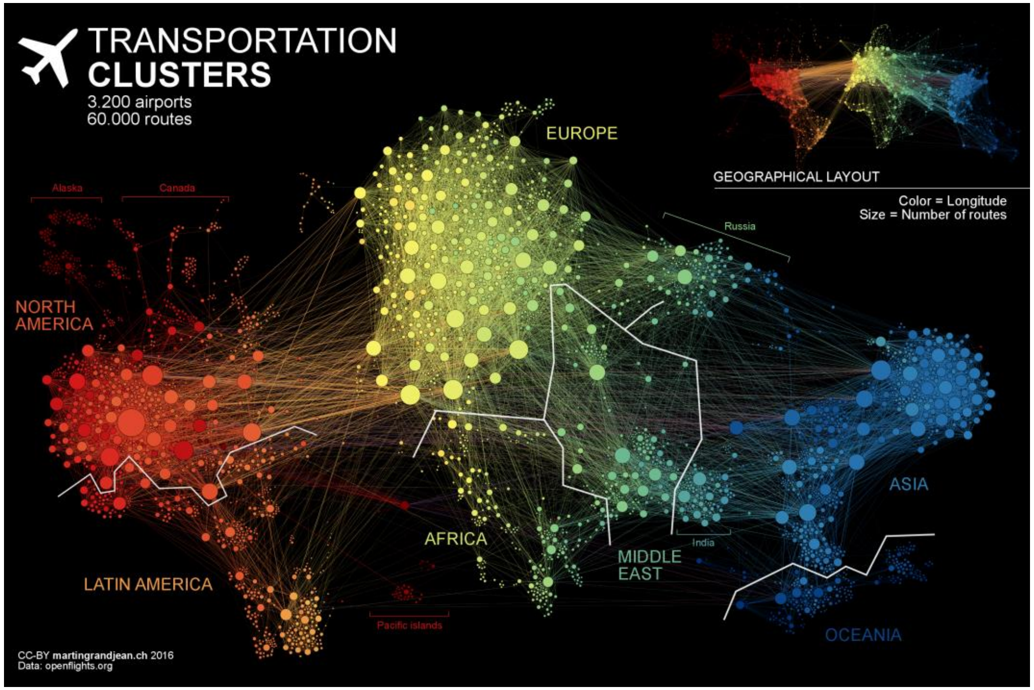
O compartilhamento de informações entre diferente atores contribui para a detecção precoce de potenciais riscos à população humana, desencadeando uma rápida e adequada resposta.

# Fatores associados à interação entre Homem-Animais-ambiente

Crescimento e expansão das populações humanas a novas áreas geográficas (Pressão agrícola na Amazônia).

# Globalização: Aumento do transporte de animais e pessoas.





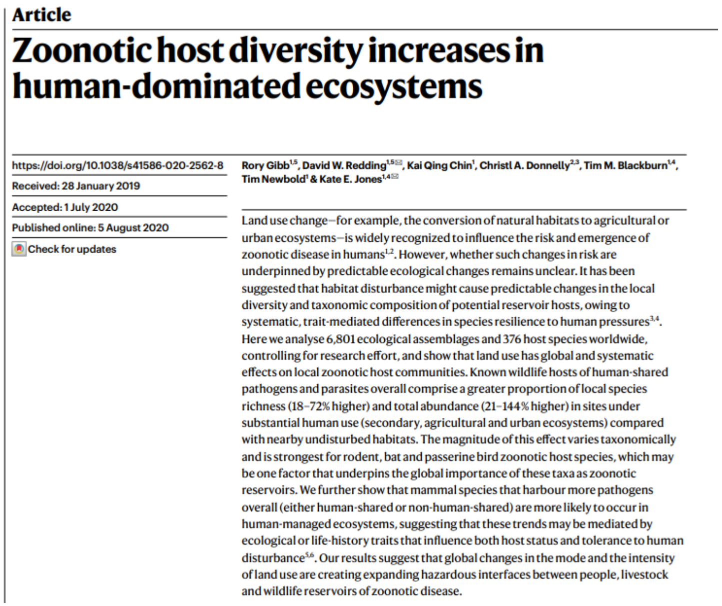
## Modificação da paisagem:

Nossa relação com animais vem mudando estando cada vez em contato o que aumenta a possibilidade de transmissão de patógenos de animais ao homem.

Fragmentação da paisagem

# Fatores associados à interação entre Homem-Animais-ambiente

Mudanças climáticas e no uso da terra (monocultura, redução da diversidade ecológica).



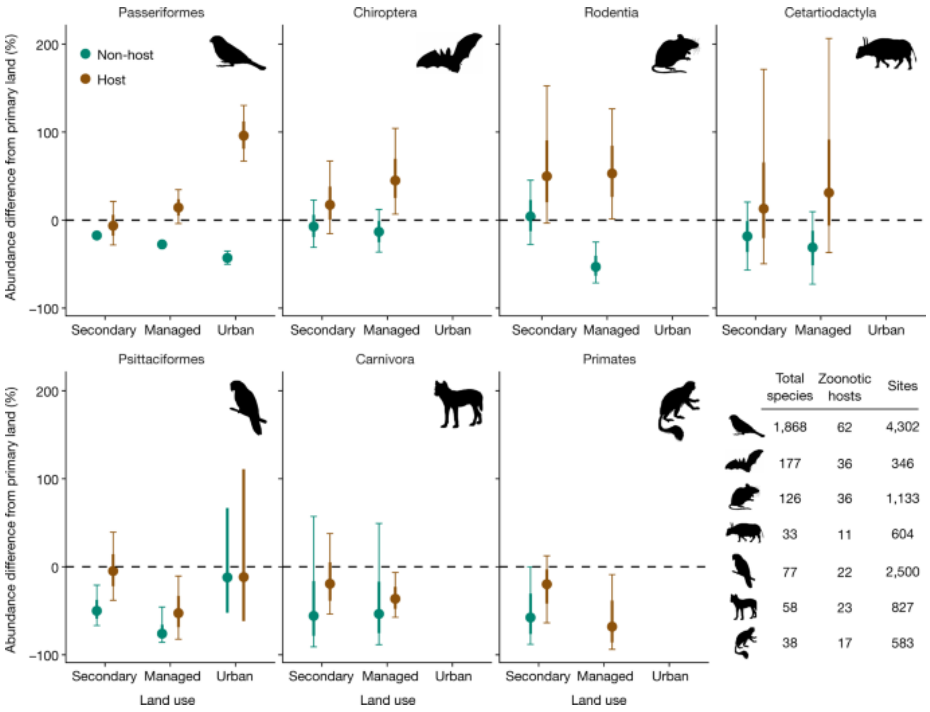
**Article**

## Zoonotic host diversity increases in human-dominated ecosystems

https://doi.org/10.1038/s41586-020-2562-8
Received: 28 January 2019
Accepted: 1 July 2020

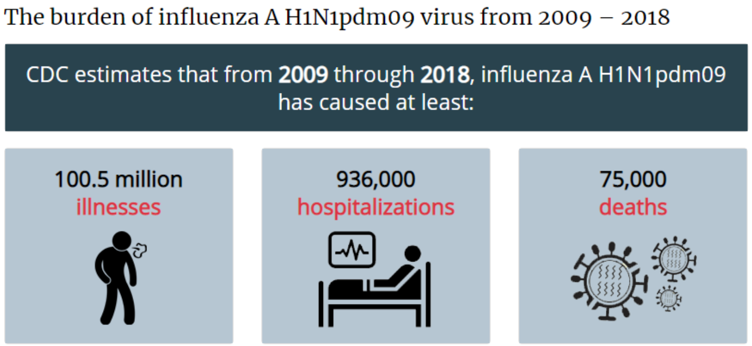
Rory Gibb[1,5], David W. Redding[1,5 ✉], Kai Qing Chin[1], Christl A. Donnelly[2,3], Tim M. Blackburn[1,4], Tim Newbold[1] & Kate E. Jones[1,4 ✉]

Land use change—for example, the conversion of natural habitats to agricultural or urban ecosystems—is widely recognized to influence the risk and emergence of zoonotic disease in humans[1,2]. However, whether such changes in risk are underpinned by predictable ecological changes remains unclear. It has been suggested that habitat disturbance might cause predictable changes in the local diversity and taxonomic composition of potential reservoir hosts, owing to systematic, trait-mediated differences in species resilience to human pressures[3,4]. Here we analyse 6,801 ecological assemblages and 376 host species worldwide, controlling for research effort, and show that land use has global and systematic effects on local zoonotic host communities. Known wildlife hosts of human-shared pathogens and parasites overall comprise a greater proportion of local species richness (18–72% higher) and total abundance (21–144% higher) in sites under substantial human use (secondary, agricultural and urban ecosystems) compared with nearby undisturbed habitats. The magnitude of this effect varies taxonomically and is strongest for rodent, bat and passerine bird zoonotic host species, which may be one factor that underpins the global importance of these taxa as zoonotic reservoirs. We further show that mammal species that harbour more pathogens overall (either human-shared or non-human-shared) are more likely to occur in human-managed ecosystems, suggesting that these trends may be mediated by ecological or life-history traits that influence both host status and tolerance to human disturbance[5,6]. Our results suggest that global changes in the mode and the intensity of land use are creating expanding hazardous interfaces between people, livestock and wildlife reservoirs of zoonotic disease.



“Land use change directly and indirectly drives the loss, turnover and homogenization of biodiversity (including through invasions and rare species losses), modifies the structure of the landscape in ways that modulate epidemiological processes (for example, fragmentation and resource provisioning) and can increase contact between humans and wildlife (for example, through agricultural practices and hunting)”.

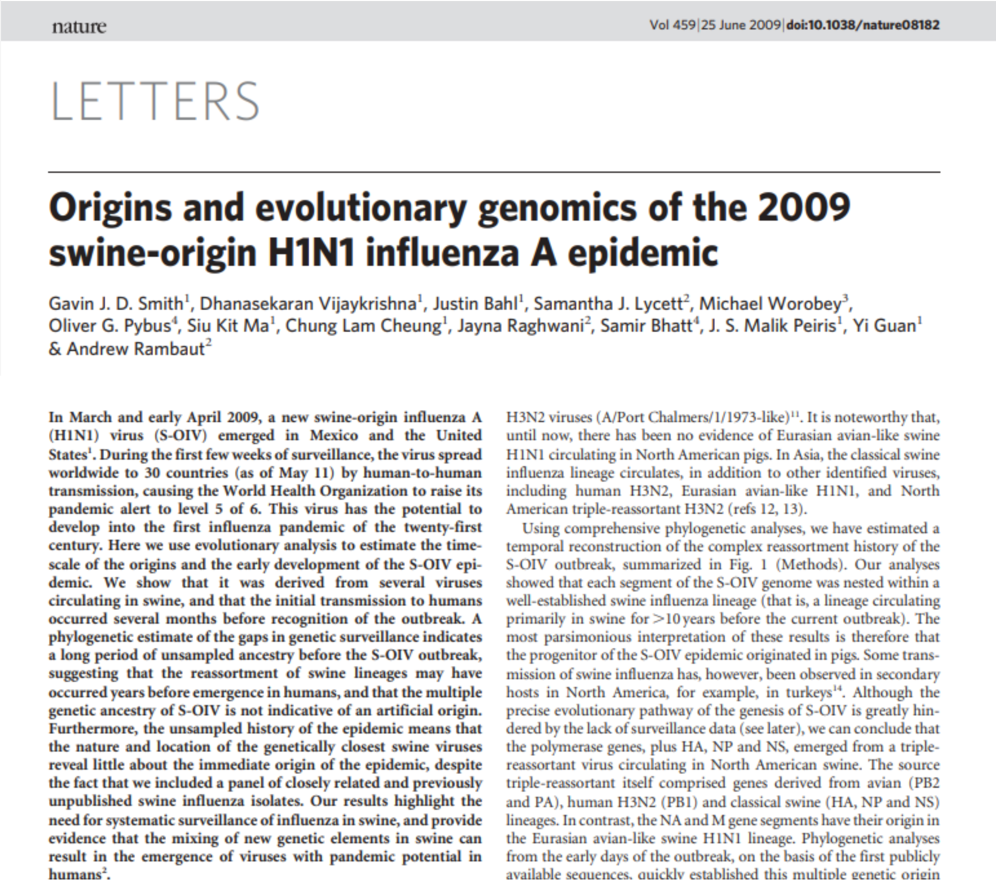
# H1N1



The burden of influenza A H1N1pdm09 virus from 2009 – 2018

CDC estimates that from **2009** through **2018**, influenza A H1N1pdm09 has caused at least:

| | | |
|---|---|---|
| 100.5 million<br>illnesses | 936,000<br>hospitalizations | 75,000<br>deaths |



nature

Vol 459 | 25 June 2009 | **doi:10.1038/nature08182**

## LETTERS

## Origins and evolutionary genomics of the 2009 swine-origin H1N1 influenza A epidemic

Gavin J. D. Smith[1], Dhanasekaran Vijaykrishna[1], Justin Bahl[1], Samantha J. Lycett[2], Michael Worobey[3], Oliver G. Pybus[4], Siu Kit Ma[1], Chung Lam Cheung[1], Jayna Raghwani[2], Samir Bhatt[4], J. S. Malik Peiris[1], Yi Guan[1] & Andrew Rambaut[2]

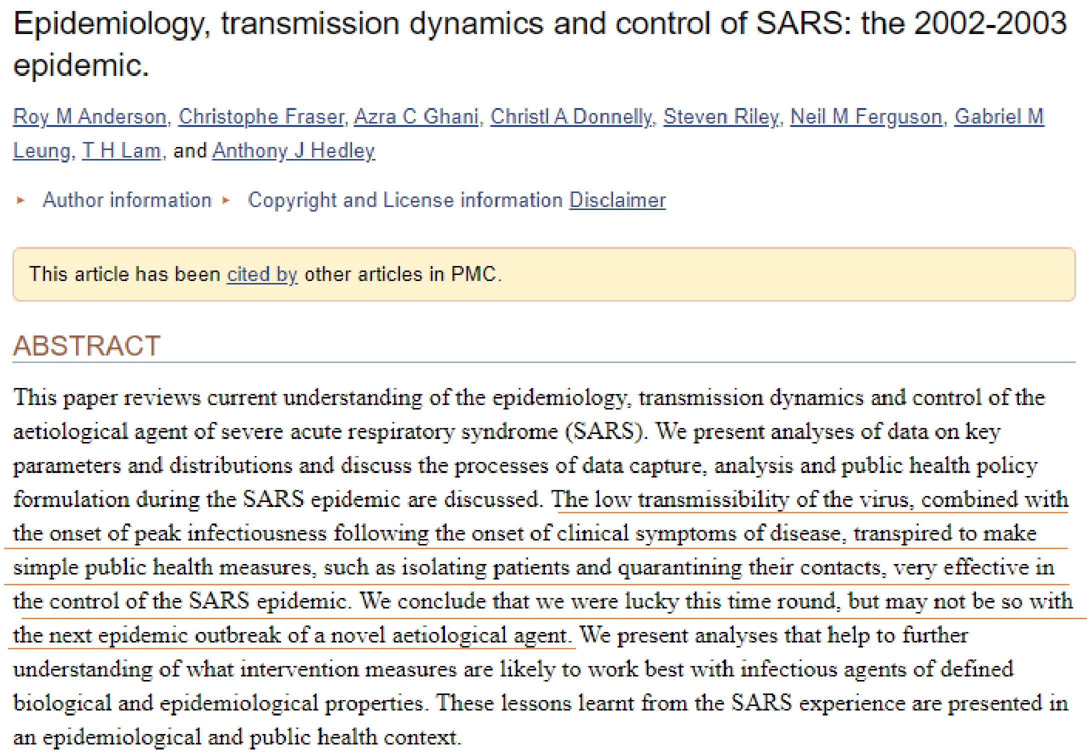
**In March and early April 2009, a new swine-origin influenza A (H1N1) virus (S-OIV) emerged in Mexico and the United States[1]. During the first few weeks of surveillance, the virus spread worldwide to 30 countries (as of May 11) by human-to-human transmission, causing the World Health Organization to raise its pandemic alert to level 5 of 6. This virus has the potential to develop into the first influenza pandemic of the twenty-first century. Here we use evolutionary analysis to estimate the timescale of the origins and the early development of the S-OIV epidemic. We show that it was derived from several viruses circulating in swine, and that the initial transmission to humans occurred several months before recognition of the outbreak. A phylogenetic estimate of the gaps in genetic surveillance indicates a long period of unsampled ancestry before the S-OIV outbreak, suggesting that the reassortment of swine lineages may have occurred years before emergence in humans, and that the multiple genetic ancestry of S-OIV is not indicative of an artificial origin. Furthermore, the unsampled history of the epidemic means that the nature and location of the genetically closest swine viruses reveal little about the immediate origin of the epidemic, despite the fact that we included a panel of closely related and previously unpublished swine influenza isolates. Our results highlight the need for systematic surveillance of influenza in swine, and provide evidence that the mixing of new genetic elements in swine can result in the emergence of viruses with pandemic potential in humans[2].**

H3N2 viruses (A/Port Chalmers/1/1973-like)[11]. It is noteworthy that, until now, there has been no evidence of Eurasian avian-like swine H1N1 circulating in North American pigs. In Asia, the classical swine influenza lineage circulates, in addition to other identified viruses, including human H3N2, Eurasian avian-like H1N1, and North American triple-reassortant H3N2 (refs 12, 13).

Using comprehensive phylogenetic analyses, we have estimated a temporal reconstruction of the complex reassortment history of the S-OIV outbreak, summarized in Fig. 1 (Methods). Our analyses showed that each segment of the S-OIV genome was nested within a well-established swine influenza lineage (that is, a lineage circulating primarily in swine for >10 years before the current outbreak). The most parsimonious interpretation of these results is therefore that the progenitor of the S-OIV epidemic originated in pigs. Some transmission of swine influenza has, however, been observed in secondary hosts in North America, for example, in turkeys[14]. Although the precise evolutionary pathway of the genesis of S-OIV is greatly hindered by the lack of surveillance data (see later), we can conclude that the polymerase genes, plus HA, NP and NS, emerged from a triple-reassortant virus circulating in North American swine. The source triple-reassortant itself comprised genes derived from avian (PB2 and PA), human H3N2 (PB1) and classical swine (HA, NP and NS) lineages. In contrast, the NA and M gene segments have their origin in the Eurasian avian-like swine H1N1 lineage. Phylogenetic analyses from the early days of the outbreak, on the basis of the first publicly available sequences, quickly established this multiple genetic origin

# SARS

*Beta-Coronavirus*
*Paguma larvata*



## Epidemiology, transmission dynamics and control of SARS: the 2002-2003 epidemic.

Roy M Anderson, Christophe Fraser, Azra C Ghani, Christl A Donnelly, Steven Riley, Neil M Ferguson, Gabriel M Leung, T H Lam, and Anthony J Hedley

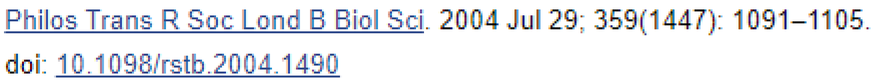
▸ Author information ▸ Copyright and License information Disclaimer

This article has been cited by other articles in PMC.

### ABSTRACT

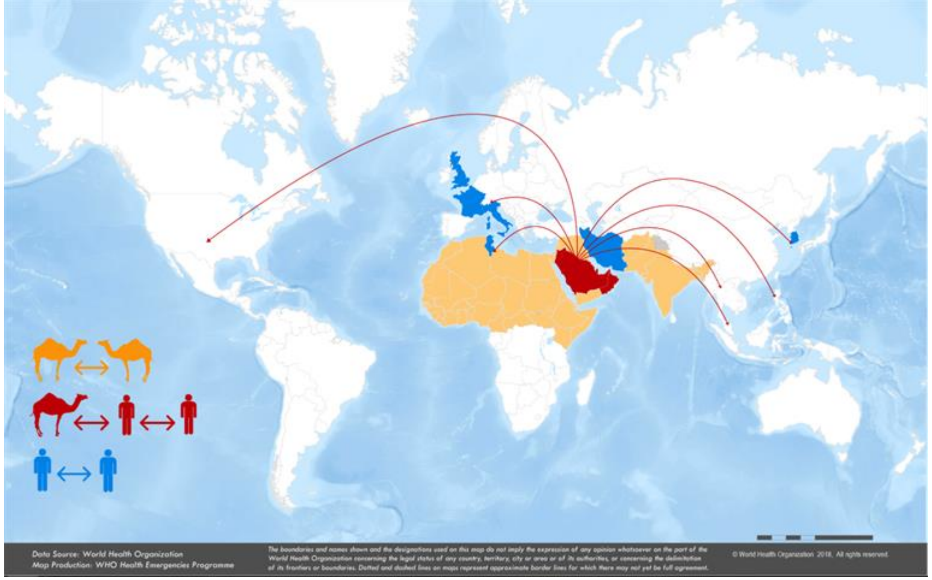
This paper reviews current understanding of the epidemiology, transmission dynamics and control of the aetiological agent of severe acute respiratory syndrome (SARS). We present analyses of data on key parameters and distributions and discuss the processes of data capture, analysis and public health policy formulation during the SARS epidemic are discussed. The low transmissibility of the virus, combined with the onset of peak infectiousness following the onset of clinical symptoms of disease, transpired to make simple public health measures, such as isolating patients and quarantining their contacts, very effective in the control of the SARS epidemic. We conclude that we were lucky this time round, but may not be so with the next epidemic outbreak of a novel aetiological agent. We present analyses that help to further understanding of what intervention measures are likely to work best with infectious agents of defined biological and epidemiological properties. These lessons learnt from the SARS experience are presented in an epidemiological and public health context.

Guangdong China
2002: 791 Casos
31 mortes
8.000 casos 774 mortes
Controlado em 2003.



Philos Trans R Soc Lond B Biol Sci. 2004 Jul 29; 359(1447): 1091–1105.
doi: 10.1098/rstb.2004.1490

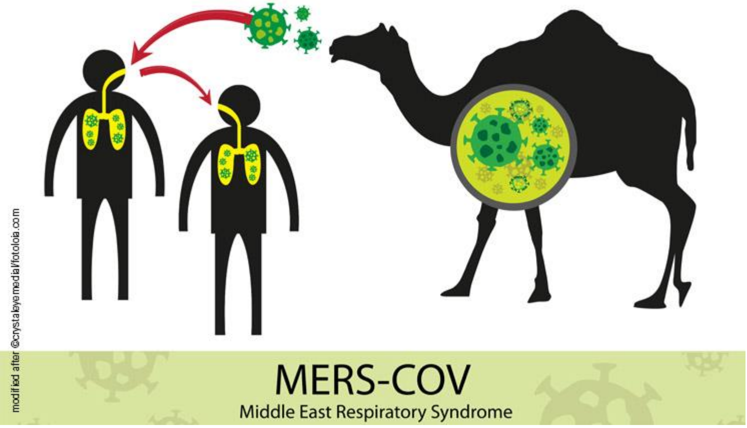
# MERS



Data Source: World Health Organization
Map Production: WHO Health Emergencies Programme

The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

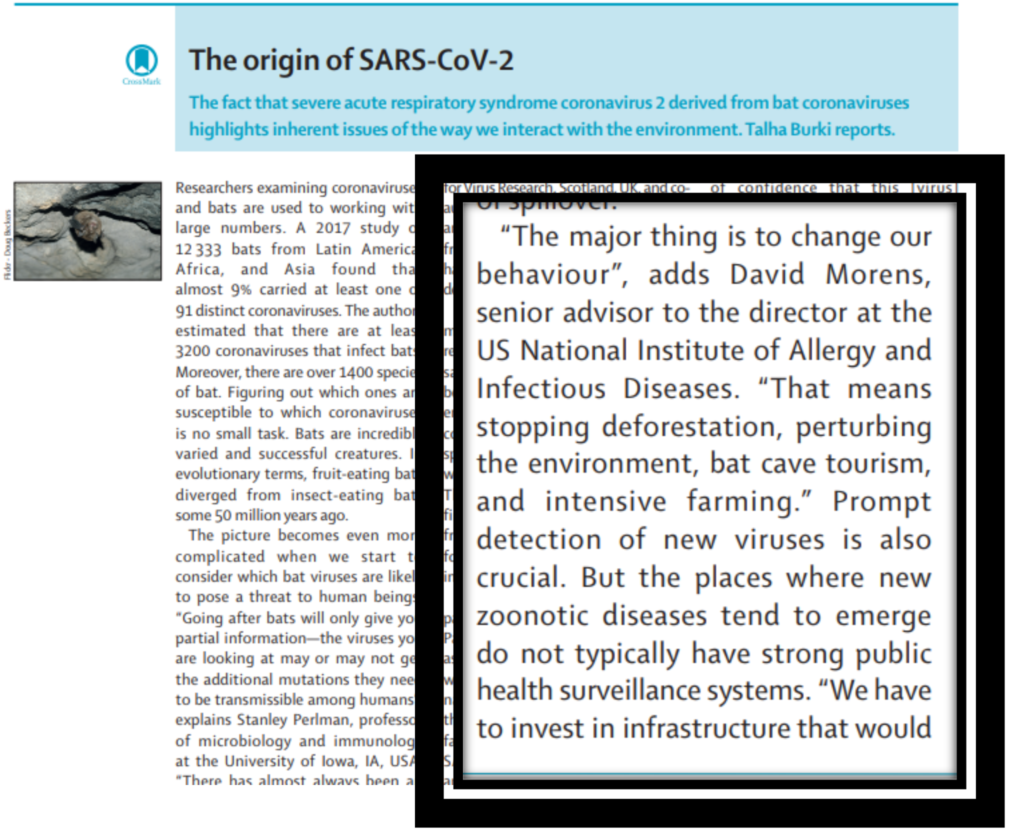
© World Health Organization 2018. All rights reserved.



modified after ©crystaleyemedia/fotolia.com

Reportado em 2012
na Arábia Saudita

# COVID-19



## The origin of SARS-CoV-2

The fact that severe acute respiratory syndrome coronavirus 2 derived from bat coronaviruses highlights inherent issues of the way we interact with the environment. Talha Burki reports.

Flickr - Doug Beckers

Researchers examining coronaviruse
and bats are used to working wit
large numbers. A 2017 study o
12 333 bats from Latin America
Africa, and Asia found tha
almost 9% carried at least one o
91 distinct coronaviruses. The author
estimated that there are at leas
3200 coronaviruses that infect bats
Moreover, there are over 1400 specie
of bat. Figuring out which ones ar
susceptible to which coronaviruse
is no small task. Bats are incredibl
varied and successful creatures. I
evolutionary terms, fruit-eating bat
diverged from insect-eating bat
some 50 million years ago.
The picture becomes even mor
complicated when we start t
consider which bat viruses are likel
to pose a threat to human beings
"Going after bats will only give yo
partial information—the viruses yo
are looking at may or may not ge
the additional mutations they nee
to be transmissible among humans
explains Stanley Perlman, professo
of microbiology and immunolog
at the University of Iowa, IA, USA
"There has almost always been a

for Virus Research, Scotland, UK, and co- of confidence that this virus

or spillover.

"The major thing is to change our behaviour", adds David Morens, senior advisor to the director at the US National Institute of Allergy and Infectious Diseases. "That means stopping deforestation, perturbing the environment, bat cave tourism, and intensive farming." Prompt detection of new viruses is also crucial. But the places where new zoonotic diseases tend to emerge do not typically have strong public health surveillance systems. "We have to invest in infrastructure that would

# Outros exemplos

- Raiva
- *Salmonella*
- Vírus do Nilo Ocidental
- Brucellosis
- Doença de Lyme
- Ebola
- Vírus Mayaro
- Febre amarela

# A transição demográfica e as doenças infecciosas

“A transição demográfica

- Crescimento da população
- urbanização rápida
- Desorganizada
- Desmatamento
- Globalização
- Mudanças climáticas
- Instabilidade política

tem importante efeito na dinâmica de doenças infecciosas que são mais dificeis de predizer”

**Betford et al. 2019. Nature. 2019 Nov;575(7781):130-136. doi: 10.1038/s41586-019-1717-y.**

# Novos enfoques

Áreas chaves para integração na resposta a epidemias no século XXI

| Área | Áreas chave ou disciplinas |
|---|---|
| Governabilidade e infraestrutura | Organizações Locais, nacionais e internacionais, Transparência das múltiplas parte interessadas, melhoria no compartilhamento de informações, logística e administração de crises. |
| Engajamento e comunicação | Engajamento de resposta lideranças comunitárias e diplomacia em saúde (Ex: Situação médicos e enfermeiras na epidemia da cólera 1830 vs Covid 19) |
| Ciências sociais | Antropologia, ciências políticas. (Humanização da resposta) |
| Ética | Consentimento, desenho de ensaios clínicos |
| Tecnologias emergentes | Genômica de patógenos, metagenômica, ciência de dados, geografia humana etc. (smartphones, dados de conexão, monitoramento da mobilidade) |
| Pesquisa e desenvolvimento | Diagnóstico, terapia e vacinas |
| Saúde única | Ecologia e ciências ambientais, veterinária e agricultura |

**Betford et al. 2019. Nature. 2019 Nov;575(7781):130-136. doi: 10.1038/s41586-019-1717-y.**

# Novos enfoques

## Resistência a antibióticos

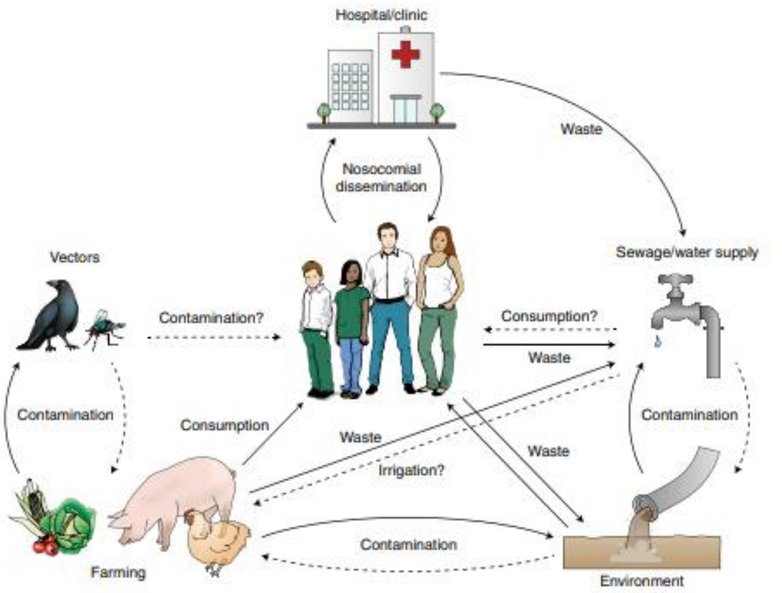
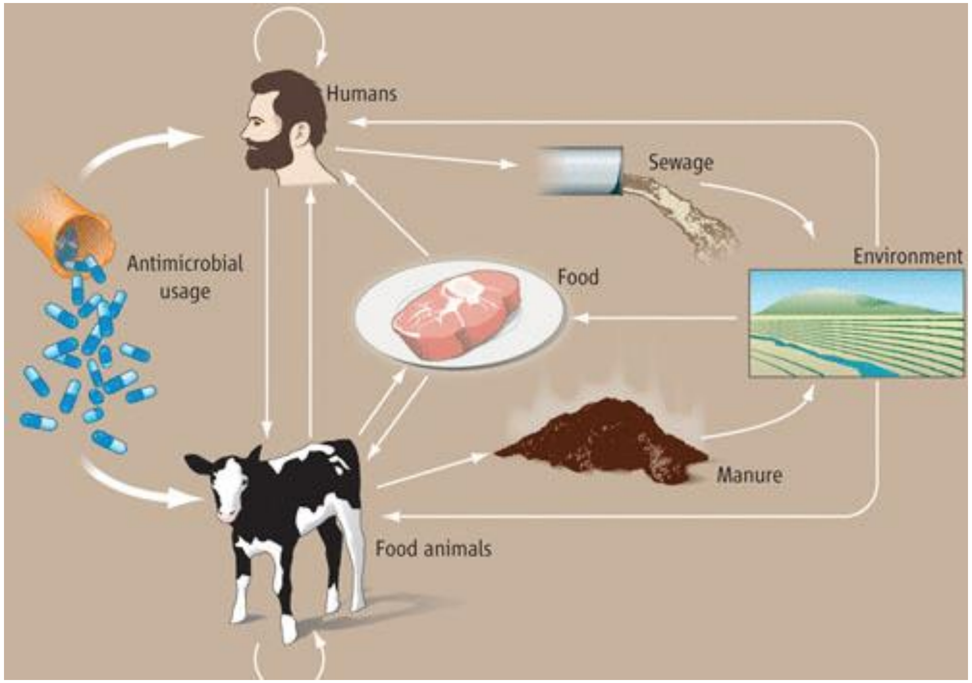


**Fig. 1 | Complex AMR interactions across one-health sectors.** A potential schematic for complex transmission paths between human, environmental, agricultural and clinical reservoirs of AMR genes and drug-resistant pathogens. Dashed lines indicate putative transmission paths.

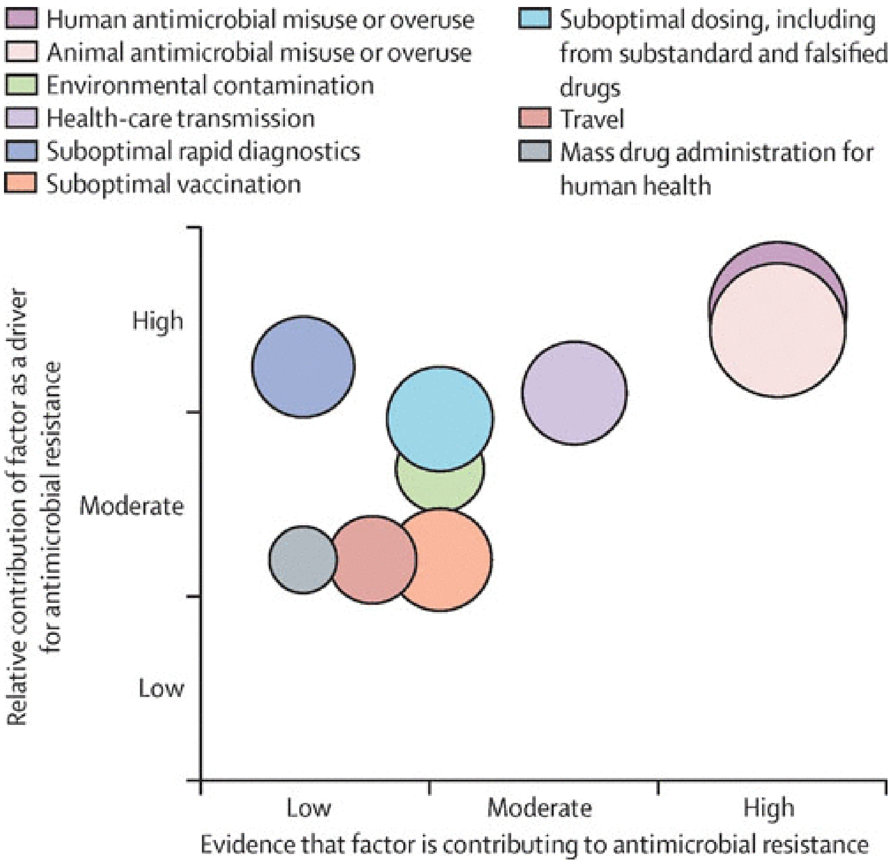


doi: 10.1038/s41564-018-0208-5. PMID: 30046173.

doi:10.1128/microbiolspec.ARBA-0009-2017

# Novos enfoques

## Resistência a antibióticos



doi:10.1128/microbiolspec.ARBA-0009-2017.

# Novos enfoques

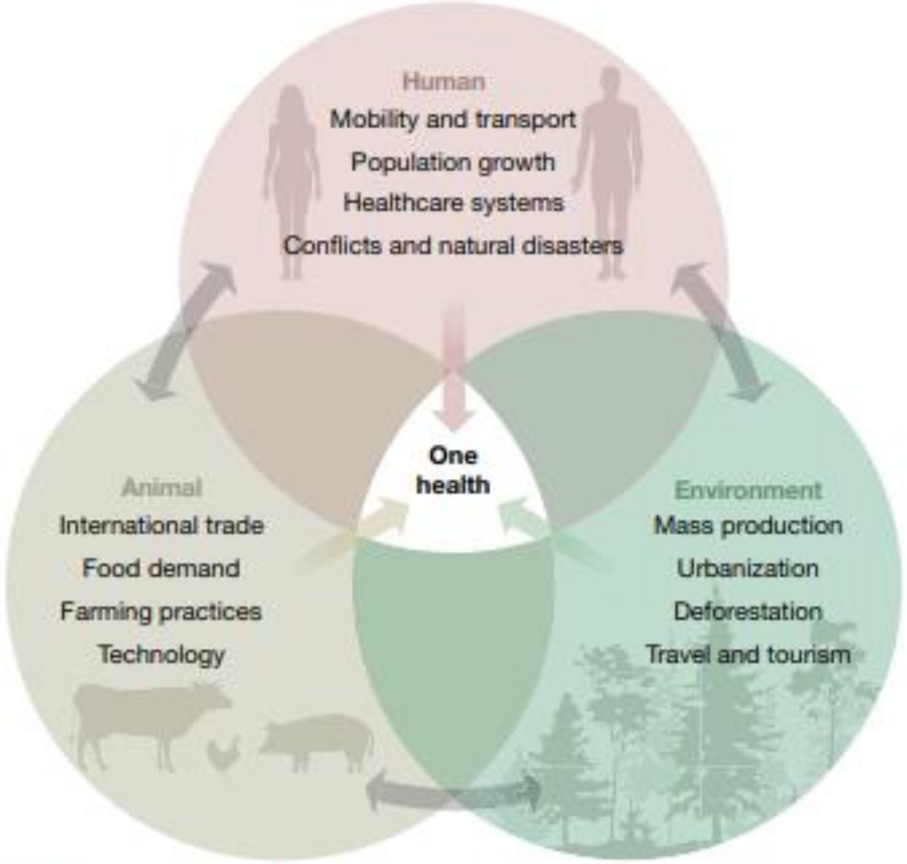


**Fig. 1 | An ecosystem of interactions.** The tightly interconnected nature of human, animal and environmental health makes the emergence and decline of epidemics difficult to predict. One Health integrates multiple perspectives in a framework that emphasizes the need to consider any particular aspect in this broader context.

# Saúde única na Vigilância em saúde

- “One Health surveillance describes the systematic collection, validation, analysis, interpretation of data and dissemination of information collected on humans, animals and the environment to inform decisions for more effective, evidence- and system-based health interventions”