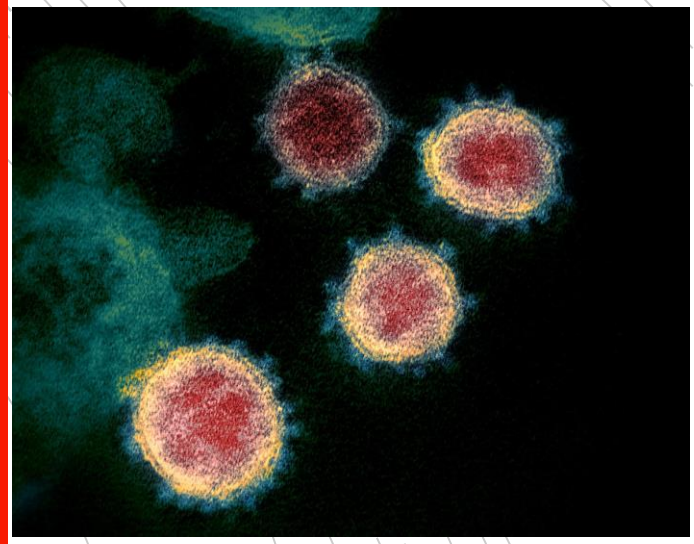
“Coronavirus Humanos”
(Origem, Evolução e Transmissibilidade, com enfoque no SARS CoV-2)

José MD Poças

(Diretor do SDI CHS Setúbal)

Aspetos introdutórios



frontiers in Immunology

REVIEW
published: 11 September 2020
doi: 10.3389/fimmu.2020.552909

Comparative Review of SARS-CoV-2, SARS-CoV, MERS-CoV, and Influenza A Respiratory Viruses

*Zeinab Abdelrahman[1,2], Mengyuan Li[1,2] and Xiaosheng Wang[1,2]**

[1] Biomedical Informatics Research Lab, School of Basic Medicine and Clinical Pharmacy, China Pharmaceutical University, Nanjing, China, [2] Cancer Genomics Research Center, School of Basic Medicine and Clinical Pharmacy, China Pharmaceutical University, Nanjing, China

Uma longa evolução na Natureza

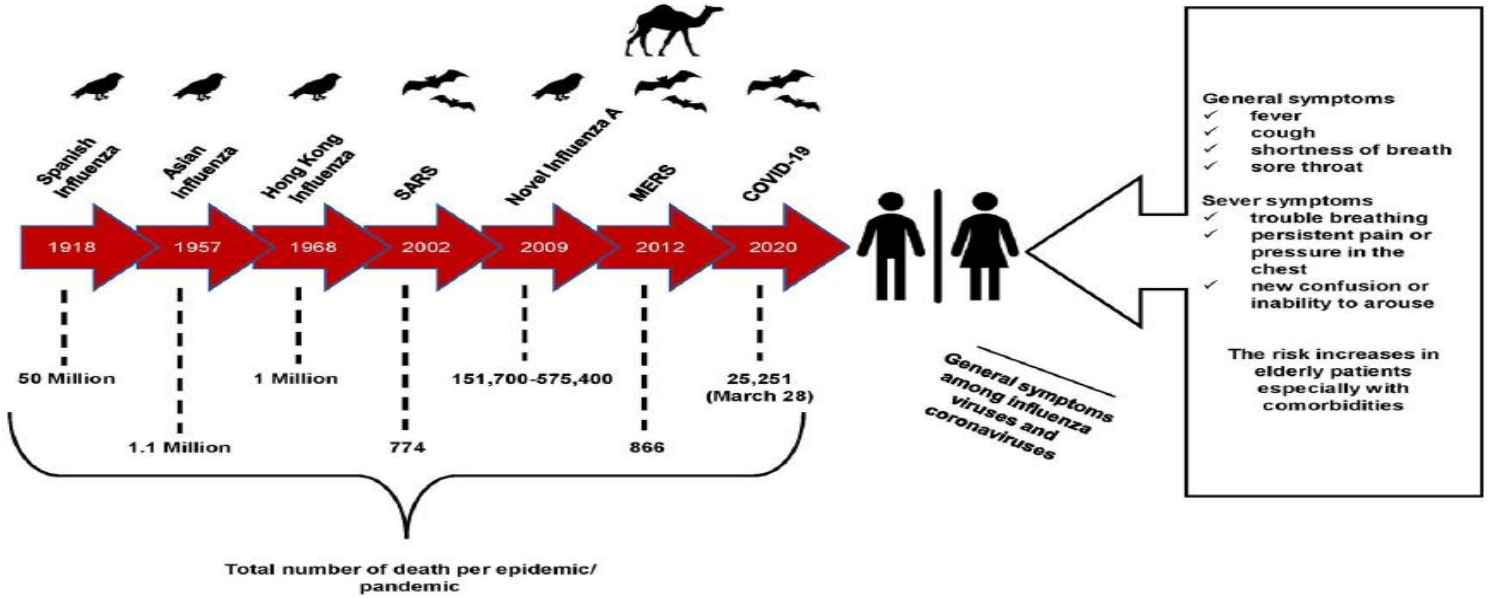
Trends in Microbiology

CellPress

Review

Molecular Evolution of Human Coronavirus Genomes

Diego Forni,[1] Rachele Cagliani,[1] Mario Clerici,[2,3] and Manuela Sironi[1,*]



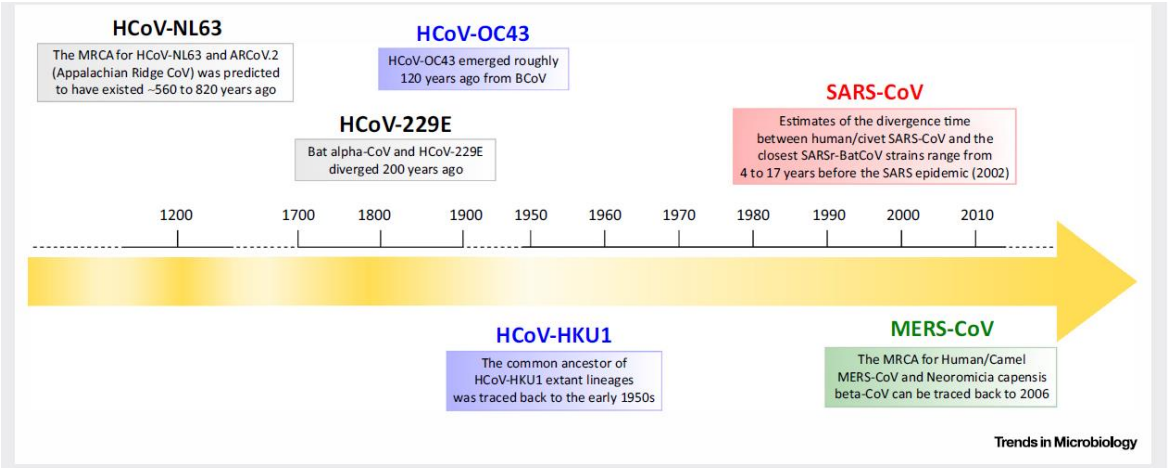
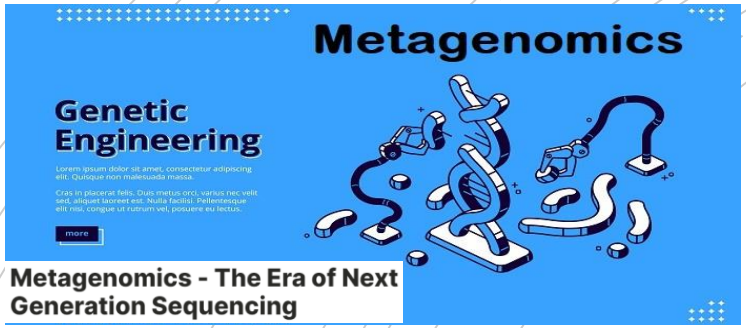


Figure I. Timeline for the Emergence of HCoVs.



O Isolamento do SARS CoV-2

Article

270 | Nature | Vol 579 | 12 March 2020

A pneumonia outbreak associated with a new coronavirus of probable bat origin

nature

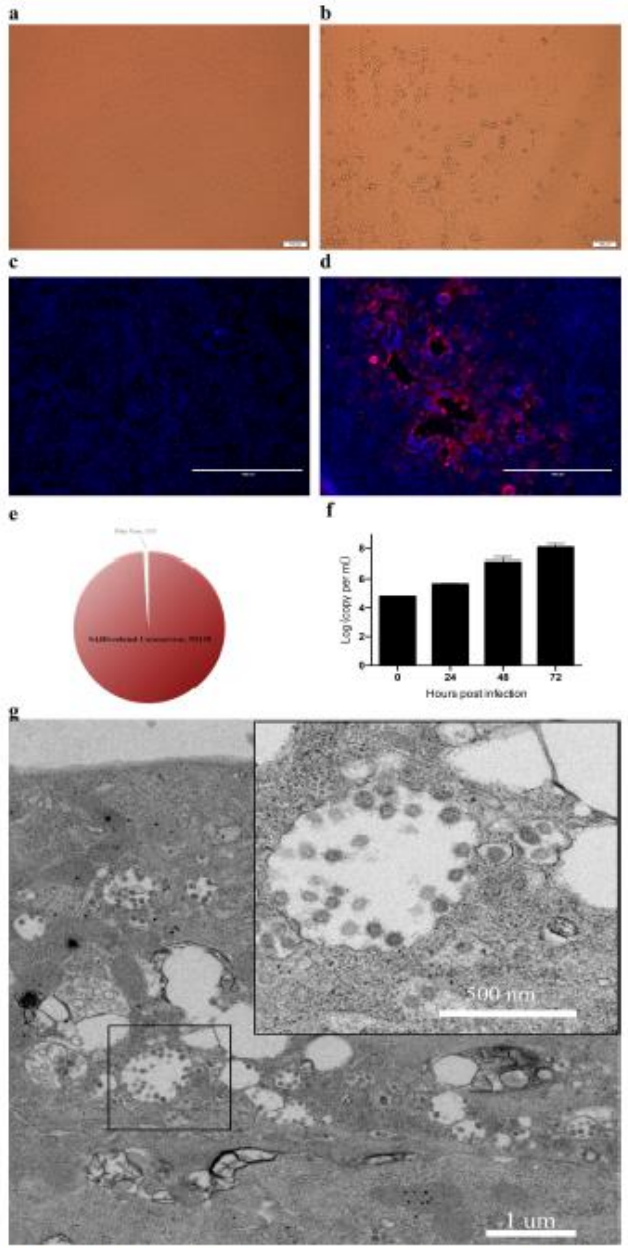
https://doi.org/10.1038/s41586-020-2012-7

Received: 20 January 2020

Accepted: 29 January 2020

Published online: 3 February 2020

Peng Zhou[1,5], Xing-Lou Yang[1,5], Xian-Guang Wang[2,5], Ben Hu[1], Lei Zhang[1], Wei Zhang[1], Hao-Rui Si[1,3], Yan Zhu[1], Bei Li[1], Chao-Lin Huang[2], Hui-Dong Chen[2], Jing Chen[1,3], Yun Luo[1,3], Hua Guo[1,3], Ren-Di Jiang[1,3], Mei-Qin Liu[1,3], Ying Chen[1,3], Xu-Rui Shen[1,3], Xi Wang[1,3], Xiao-Shuang Zheng[1,3], Kai Zhao[1,3], Quan-Jiao Chen[1], Fei Deng[1], Lin-Lin Liu[4], Bing Yan[1], Fa-Xian Zhan[4], Yan-Yi Wang[1], Geng-Fu Xiao[1] & Zheng-Li Shi[1]✉



Extended Data Fig. 6 | Isolation and antigenic characterization of 2019-nCoV. a, **b**, Vero E6 cells are shown at 24 h after infection with mock virus (**a**) or 2019-nCoV (**b**). **c**, **d**, Mock-virus-infected (**c**) or 2019-nCoV-infected (**d**) samples were stained with rabbit serum raised against recombinant SARSr-CoV Rp3 N protein (red) and DAPI (blue). The experiment was conducted twice independently with similar results. **e**, The ratio of the number of reads related to 2019-nCoV among the total number of virus-related reads in metagenomics analysis of supernatants from Vero E6 cell cultures. **f**, Virus growth in Vero E6 cells. **g**, Viral particles in the ultrathin sections were imaged using electron microscopy at 200 kV. The sample was from virus-infected Vero E6 cells. The inset shows the viral particles in an intra-cytosolic vacuole.

Clinical Infectious Diseases
MAJOR ARTICLE

Genomic Diversity of Severe Acute Respiratory Syndrome–Coronavirus 2 in Patients With Coronavirus Disease 2019

Zijie Shen,[1,2,a] Yan Xiao,[3,a] Lu Kang,[1,2,a] Wentai Ma,[1,2,a] Leisheng Shi,[1,2] Li Zhang,[1] Zhuo Zhou,[4] Jing Yang,[1,2] Jiaxin Zhong,[1,2] Donghong Yang,[5] Li Guo,[3] Guoliang Zhang,[6] Hongru Li,[7] Yu Xu,[5] Mingwei Chen,[8] Zhancheng Gao,[5] Jianwei Wang,[3] Lili Ren,[2,b] and Mingkun Li[1,9,b]

[1]Key Laboratory of Genomic and Precision Medicine, Beijing Institute of Genomics, Chinese Academy of Sciences, and China National Center for Bioinformation, Beijing, China, [2]University of Chinese Academy of Sciences, Beijing, China, [3]National Health Commission of the People's Republic of China Key Laboratory of Systems Biology of Pathogens and Christophe Mérieux Laboratory, Institute of Pathogen Biology, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China, [4]Biomedical Pioneering Innovation Center, Beijing Advanced Innovation Center for Genomics, Peking-Tsinghua Center for Life Sciences, Peking University Genome Editing Research Center, State Key Laboratory of Protein and Plant Gene Research, School of Life Sciences, Peking University, Beijing, China, [5]Department of Respiratory and Critical Care Medicine, Peking University People's Hospital, Beijing, China, [6]National Clinical Research Center for Infectious Diseases, Guangdong Key Laboratory for Emerging Infectious Diseases, Shenzhen Third People's Hospital, Southern University of Science and Technology, Shenzhen, China, [7]Fujian Provincial Hospital, Fujian, China, [8]Department of Respiratory and Critical Care Medicine, First Affiliated Hospital of Xi'an Jiaotong University, Xi'an, China, and [9]Center for Excellence in Animal Evolution and Genetics, Chinese Academy of Sciences, Kunming, China

Chapter 13
Emergence and Reemergence of Severe Acute Respiratory Syndrome (SARS) Coronaviruses

Preeti Baxi and Shailendra K. Saxena

O Vírus SARS CoV-2

Chemical Engineering Journal 405 (2021) 126893
Contents lists available at ScienceDirect
Chemical Engineering Journal
journal homepage: www.elsevier.com/locate/cej

SARS-CoV-2 in environmental perspective: Occurrence, persistence, surveillance, inactivation and challenges

S. Venkata Mohan[a,b,*], Manupati Hemalatha[a,b], Harishankar Kopperi[a], I. Ranjith[a], A. Kiran Kumar[a,c]

[a] Bioengineering and Environmental Sciences Lab, Department of Energy and Environmental Engineering (DEEE), CSIR-Indian Institute of Chemical Technology (CSIR-IICT), Hyderabad 500007, India
[b] Academy of Scientific and Innovative Research (AcSIR), CSIR-Indian Institute of Chemical Technology (CSIR-IICT) Campus, Hyderabad 500007, India
[c] CSIR-Indian Institute of Chemical Technology (CSIR-IICT) Dispensary, Hyderabad 500007, India

European Journal of Clinical Microbiology & Infectious Diseases
https://doi.org/10.1007/s10096-020-03899-4
REVIEW

The genetic sequence, origin, and diagnosis of SARS-CoV-2

Huihui Wang[1] · Xuemei Li[1] · Tao Li[1,2] · Shubing Zhang[1] · Lianzi Wang[1] · Xian Wu[1] · Jiaqing Liu[1]

Received: 12 March 2020 / Accepted: 7 April 2020

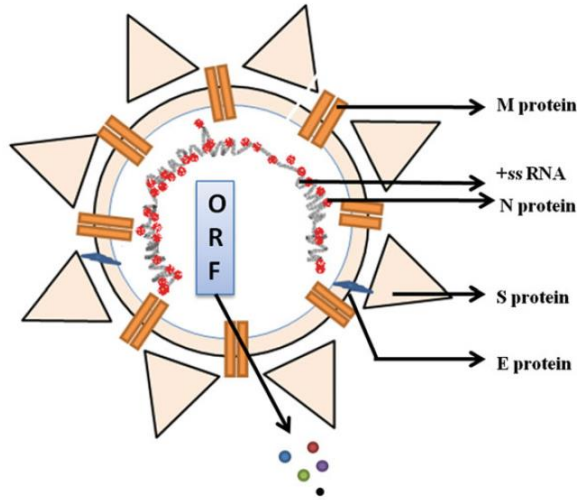


Fig. 13.3 Structure of coronavirus causing severe acute respiratory syndrome

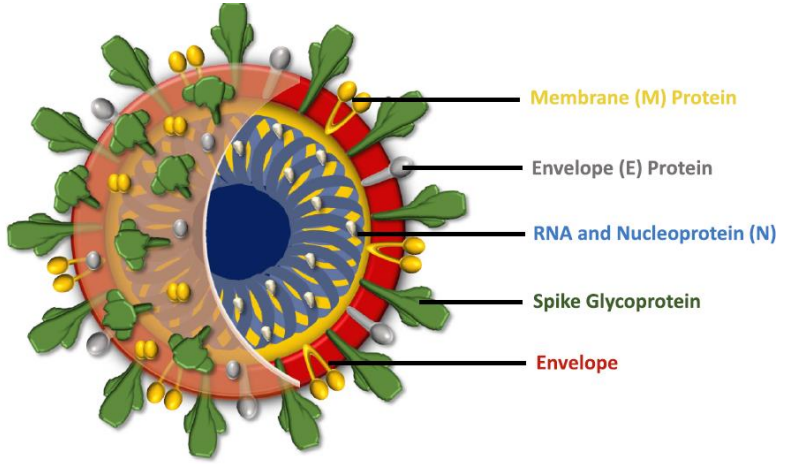


Fig. 1. Structure of Corona Virus (SARS-CoV-2).

Os coronavirus no mundo animal

Emerging Microbes & Infections
2020, VOL. 9
https://doi.org/10.1080/22221751.2020.1827984

EMI Taylor & Francis

REVIEW OPEN ACCESS

Zoonotic and reverse zoonotic events of SARS-CoV-2 and their impact on global health

Khalid Munir[a,b], Shoaib Ashraf[b,c], Isra Munir[d], Hamna Khalid[e], Mohammad Akram Muneer[b], Noreen Mukhtar[a], Shahid Amin[f], Sohaib Ashraf[c,g], Muhammad Ahmad Imran[g], Umer Chaudhry[h], Muhammad Usman Zaheer[i], Maria Arshad[j], Rukhsana Munir[k], Ali Ahmad[l] and Xin Zhao[m]

[a]PetLife Veterinary Professional Corporation, NJ, USA; [b]Department of Pathobiology, Riphah College of Veterinary Sciences, Riphah University, Lahore, Pakistan; [c]Wellman Center for Photomedicine, Massachusetts General Hospital, Harvard Medical School, Boston, MA, USA; [d]School of Dental Medicine, University of Pennsylvania, Philadelphia, PA, USA; [e]Department of Chemical and Biological Engineering, Villanova University, Villanova, PA, USA; [f]Animal Hospital of Loves Park, Loves Park, IL, USA; [g]Department of Microbiology, Shaikh Zayed Hospital Lahore, Lahore, Pakistan; [h]; Royal (Dick) School of Veterinary Studies and Roslin Institute, Edinburgh, UK; [i]Food and Agriculture Organization of the United Nations, Country Office, Islamabad, Pakistan; [j]District Headquarter Hospital, Lahore, Pakistan; [k]Consultant Emergency Medicine, Russells Hall Hospital, Dudley Group of Hospitals NHS Trust, Dudley, UK; [l]CHU Sainte-Justine Research Center, Department of Microbiology, Infectious Diseases and Immunology, University of Montreal, Montreal, Canada; [m]Department of Animal Sciences, McGill University, Sainte-Anne-de-Bellevue, Canada

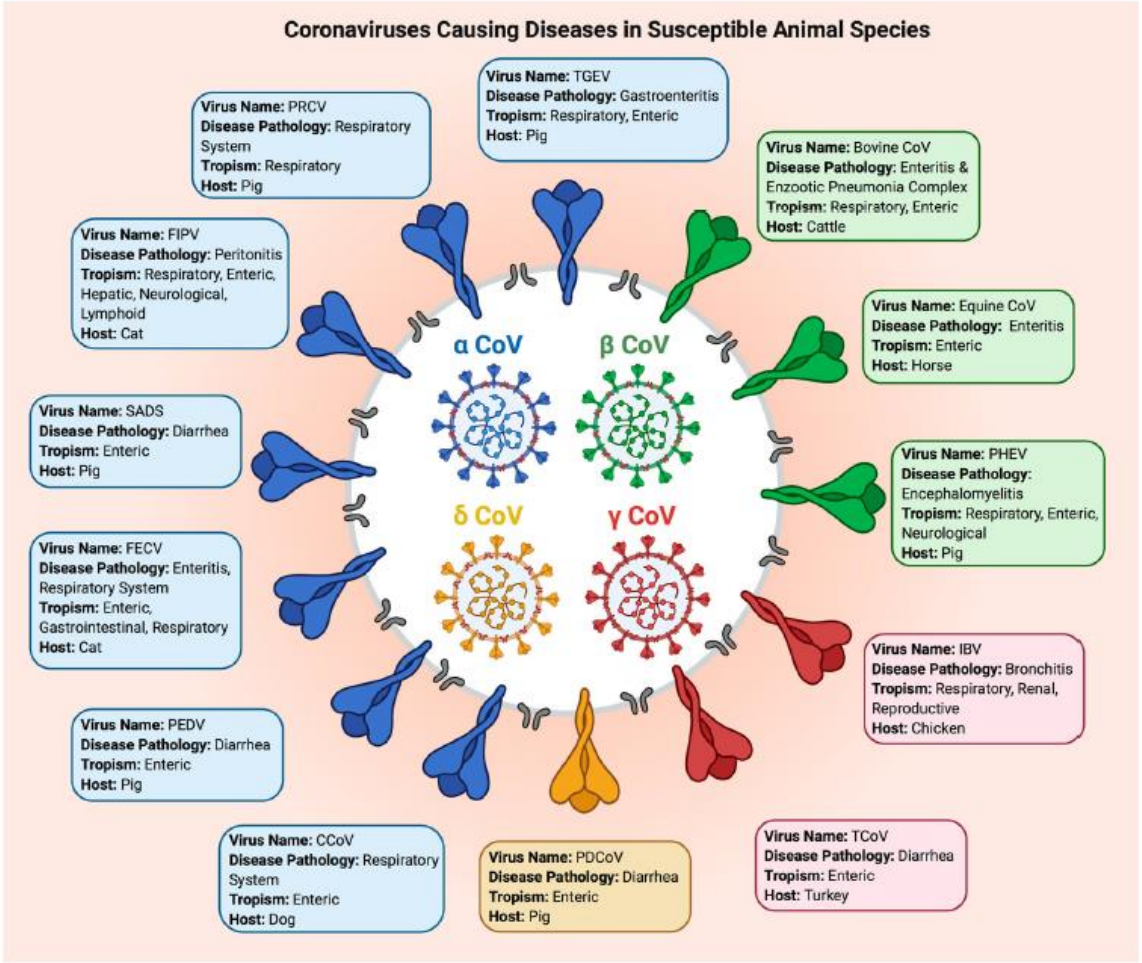
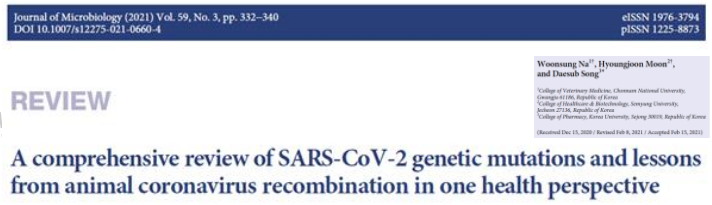


Figure 1. Selected important coronaviruses causing diseases in animal species. The figure shows different coronaviruses, their genera, main clinical symptoms, host species, and tissue/organ tropism. PEDV: Porcine Epidemic Diarrhea Virus; TGEV: Transmissible Gastroenteritis Virus; PRCV: Porcine Respiratory Coronavirus; FIPV: Feline Infectious Peritonitis Virus; FECoV: Feline Enteric Coronavirus; CCoV: Canine Coronavirus; PDCoV: Porcine Delta Coronavirus; TCoV: Turkey Coronavirus; IBV: Infectious Bronchitis Virus; PHEV: Porcine Hemagglutinating & Encephalomyelitis Virus; Equine CoV: Equine Coronavirus; BCoV: Bovine Coronavirus; Severe Acute Diarrhea Syndrome Coronavirus: SADS-CoV.

Aspetos Gerais sobre os Coronavirus Humanos


Journal of Microbiology (2021) Vol. 59, No. 3, pp. 332–340
DOI 10.1007/s12275-021-0660-4
eISSN 1976-3794
pISSN 1225-8873

Woonsung Na[1†], Hyoungjoon Moon[2†], and Daesub Song[3*]

REVIEW

A comprehensive review of SARS-CoV-2 genetic mutations and lessons from animal coronavirus recombination in one health perspective

- **Coronavírus**
  - **Descoberta- Anos 30 do século XX, compreendendo 39 espécies diferentes;**
  - **Vírus de cadeia simples de RNA com polarização+ c/ cerca de 70-80 micras cúbicas. Possuem elevada taxa de mutagenicidade e com possibilidade de recombinação genómica interespécies;**
  - **Existem 7 espécies são patogénicas para o Ser Humano, a 1ª identificada em 1966;**
  - **A homologia estrutural molecular entre o SARS CoV (1 e 2) é de 82% e do SARS CoV-2 de 96% com o dos morcegos** *Rhinolophus affinis e Malayanus,* **e de 85-92% com o do pangolim** *Manis javanica;*
  - **Os SARS CoV (1 e 2) penetram na célula do hospedeiro através do mesmo recetor celular (ACE2) que existem em muitos outros animais para além de mamíferos e para a qual algumas das novas variantes (VOCs) têm maior afinidade**

Table 1
Pairwise sequence identities between the SARS-CoV-2 (NC_045512.2) and other coronaviruses.

Accession No.	Virus	Isolate	Whole-genome	S gene	RBD[a]
MN996532.1	Bat-CoV	RaTG13	96.11	92.86	86.21
MG772933.1	Bat-SARS-CoV like	Bat-SL-CoVZC45	87.65	75.13	73.05
MG772934.1	Bat-SARS-CoV like	Bat-SL-CoVZXC21	87.43	74.69	72.9
AY390556.1	SARS-CoV	GZ02	78.95	72.56	72.6
NC_004718.3	SARS-CoV	Tor2	78.9	72.54	72.6
AY278489.2	SARS-CoV	GD01	78.9	72.54	64.82
AY278488.2	SARS-CoV	BJ01	78.89	72.48	63.17
JX869059.2	MERS-CoV	EMC	48.83	41.95	38.15

[a] RBD: receptor binding domain.

Int. J. Biol. Sci. 2020, Vol. 16 1686

IVYSPRING INTERNATIONAL PUBLISHER

International Journal of Biological Sciences

2020; 16(10): 1686-1697. doi: 10.7150/ijbs.45472

Review

Zoonotic origins of human coronaviruses

Zi-Wei Ye[1], Shuofeng Yuan[1], Kit-San Yuen[2], Sin-Yee Fung[2], Chi-Ping Chan[2], and Dong-Yan Jin[2]✉

1. Department of Microbiology, The University of Hong Kong, Pokfulam, Hong Kong.
2. School of Biomedical Sciences, The University of Hong Kong, Pokfulam, Hong Kong.

✉ Corresponding author: Dong-Yan Jin. E-mail: dyjin@hku.hk. School of Biomedical Sciences, 3/F Laboratory Block, 21 Sassoon Road, Pokfulam, Hong Kong.

Received: 2020.02.29; Accepted: 2020.03.03; Published: 2020.03.15

Resumo das características distintivas dos coronavírus humanos

viruses

MDPI

Review

COVID-19: Look to the Future, Learn from the Past

Zhangkai J. Cheng [1,2,*,†], Hui-Qi Qu [2,†], Lifeng Tian [2], Zhifeng Duan [2] and Hakon Hakonarson [2,3,4,5,*]

1 Institute of Medical Physics, School of Physics, University of Sydney, Sydney, NSW 2006, Australia
2 Center for Applied Genomics, The Children's Hospital of Philadelphia, Philadelphia, PA 19104, USA; quh@email.chop.edu (H.-Q.Q.); tianl@email.chop.edu (L.T.); bravewindheart@163.com (Z.D.)
3 Department of Pediatrics, The Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA
4 Division of Human Genetics, Children's Hospital of Philadelphia, Philadelphia, PA 19104, USA
5 Division of Pulmonary Medicine, Children's Hospital of Philadelphia, Philadelphia, PA 19104, USA
* Correspondence: jasontable@gmail.com (Z.J.C.); Hakonarson@email.chop.edu (H.H.)
† These authors contributed equally to this work.

Received: 31 August 2020; Accepted: 28 October 2020; Published: 29 October 2020

check for updates

Table 1. Comparison of clinical features and transmission routes of HCoVs

	HCoV-229E	HCoV-OC43	SARS-CoV	HCoV-NL63	HCoV-HKU1	MERS-CoV	SARS-CoV-2
Classification	alpha-CoV	beta-CoV, lineage A	beta-CoV, lineage B	alpha-CoV	beta-CoV, lineage A	beta-CoV, lineage C	beta-CoV, lineage B
Incubation period	2-5 days	2-5 days	2-11 days	2-4 days	2-4 days	2-13 days	3-6 days
Transmission	Respiratory droplets Fomites	Respiratory droplets Fomites	Respiratory droplets Fomites Fecal-oral	Respiratory droplets Fomites	Respiratory droplets Fomites	Respiratory droplets Fomites	Respiratory droplets Fomites Fecal-oral
Case fatality	N/A	N/A	9.6%	N/A	N/A	34.4%	3.5%
Clinical symptoms	Malaise Headache Nasal discharge Sneezing Sore throat Fever and cough	Malaise Headache Nasal discharge Sneezing Sore throat Fever and cough	Fever Myalgia Headache Malaise Dry cough Dyspnea Respiratory distress Diarrhea	Cough Rhinorrhea Tachypnea Fever Hypoxia Croup	Fever Running nose Cough Dyspnea	Fever Cough Chills Sore throat Myalgia Arthralgia Dyspnea Pneumonia Diarrhea and vomiting Acute renal impairment	Fever Dry cough Dyspnea Myalgia Headache Diarrhea
Epidemiology	Globally Peak in winter	Globally Peak in winter	2002-2003 in China Globally thereafter	Globally Peak in winter	Globally Peak in winter	2012 in Middle East 2015 in South Korea Endemic in Middle East	2019-2020 in China Globally thereafter
References	27-30	28	14, 15, 31	32-35	36, 37	17, 18, 39	40

Table 2. Comparison of four diseases.

Characteristics	SARS-CoV-2	SARS-CoV	MERS-CoV	Influenza
R_0	2.68	3	<1	1.3
Virulence	Low	High	High	Low
Case Fatality Rate	2%	10%	37%	0.1%
Natural Hosts	Bat	Bat	Bat	Animals, humans
Intermediate Hosts	Unknown	Civets	Camels	NA
Origin of Outbreak	Wuhan, China	Guangzhou, China	Saudi Arabia	NA
Incubation Period	2–16 days	2–7 days	4–8 days	1–4 days

Emerging Topics in Life Sciences (2020) 4 383–390
https://doi.org/10.1042/ETLS20200165

PORTLAND PRESS

Review Article

How SARS-CoV-2 (COVID-19) spreads within infected hosts — what we know so far

Sumana Sanyal
Sir William Dunn School of Pathology, University of Oxford, South Parks Road, Oxford OX1 3RE, U.K.
Correspondence: Sumana Sanyal (sumana.sanyal@path.ox.ac.uk)

Etiopatogenia

Journal of Autoimmunity 109 (2020) 102433
Contents lists available at ScienceDirect
Journal of Autoimmunity
journal homepage: www.elsevier.com/locate/jautimm

Review article

The epidemiology and pathogenesis of coronavirus disease (COVID-19) outbreak

Hussin A. Rothan[a], Siddappa N. Byrareddy[b,c,d,*]
[a] Department of Biology, College of Arts and Sciences, Georgia State University, Atlanta, GA, USA
[b] Department of Pharmacology and Experimental Neuroscience, University of Nebraska Medical Centre, Omaha, NE, USA
[c] Department of Genetics, Cell Biology and Anatomy, Omaha, NE, USA
[d] Department of Biochemistry and Molecular Biology, University of Nebraska Medical Centre, Omaha, NE, USA

CLINICAL UPDATE

thebmj

Virology, transmission, and pathogenesis of SARS-CoV-2

Muge Cevik, [1,2] Krutika Kuppalli, [3] Jason Kindrachuk, [4] Malik Peiris[5]

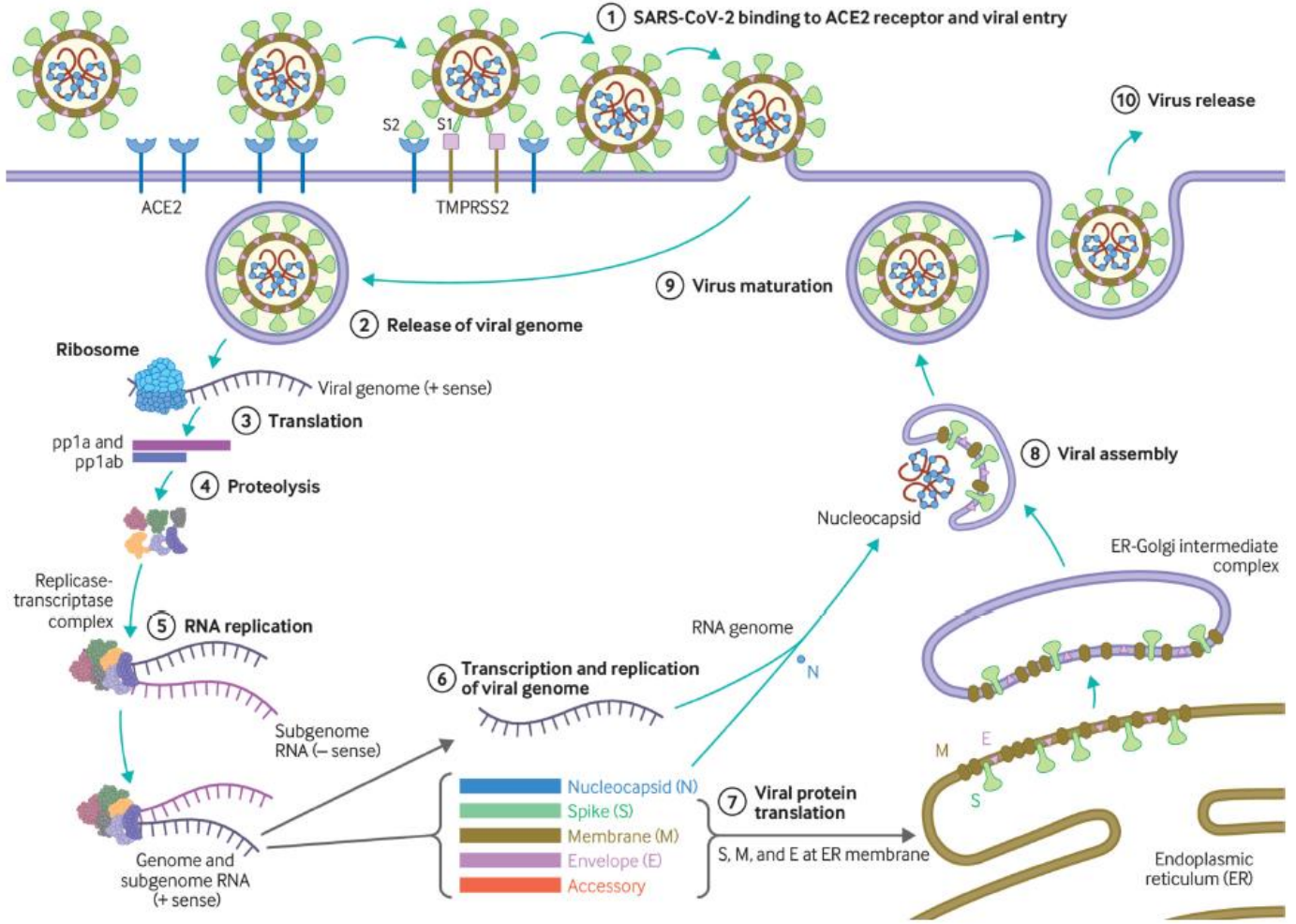


Fig 1 | (1) The virus binds to ACE 2 as the host target cell receptor in synergy with the host's transmembrane serine protease 2 (cell surface protein), which is principally expressed in the airway epithelial cells and vascular endothelial cells. This leads to membrane fusion and releases the viral genome into the host cytoplasm (2). Stages (3-7) show the remaining steps of viral replication, leading to viral assembly, maturation, and virus release

Mecanismo alternativo de penetração na célula dos hospedeiro a poder ser considerado

biomolecules

MDPI

Editorial

Why COVID-19 Transmission Is More Efficient and Aggressive Than Viral Transmission in Previous Coronavirus Epidemics?

Fatma Elrashdy [1], Elrashdy M. Redwan [2,*] and Vladimir N. Uversky [2,3,4,*]

1 Department of Endemic Medicine and Hepatogastroenterology, Kasr Alainy School of Medicine, Cairo University, Cairo 11562, Egypt; fatmaelrashdy@kasralainy.edu.eg
2 Biological Science Department, Faculty of Science, King Abdulaziz University, P.O. Box 80203, Jeddah 21589, Saudi Arabia
3 Department of Molecular Medicine and USF Health Byrd Alzheimer's Research Institute, Morsani College of Medicine, University of South Florida, Tampa, FL 33612, USA
4 Institute for Biological Instrumentation of the Russian Academy of Sciences, Federal Research Center "Pushchino Scientific Center for Biological Research of the Russian Academy of Sciences", Pushchino, 142290 Moscow, Russia
* Correspondence: lradwan@kau.edu.sa (E.M.R.); vuversky@usf.edu (V.N.U.)

Received: 3 September 2020; Accepted: 8 September 2020; Published: 11 September 2020

check for updates

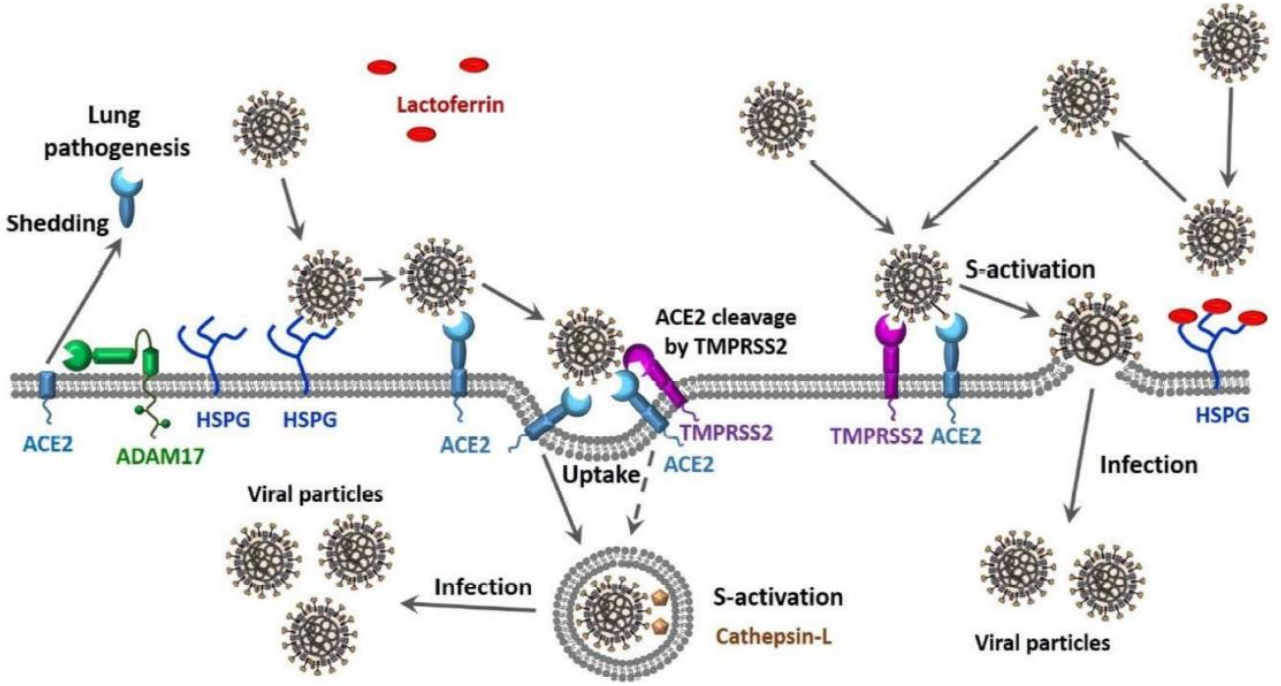


Figure 1. Suggested scenarios for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) cellular entry pathways and their potential effects on the viral load and transmission capability.

Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding

THE LANCET

Roujian Lu*, Xiang Zhao*, Juan Li*, Peihua Niu*, Bo Yang*, Honglong Wu*, Wenling Wang, Hao Song, Baoying Huang, Na Zhu, Yuhai Bi, Xuejun Ma, Faxian Zhan, Liang Wang, Tao Hu, Hong Zhou, Zhenhong Hu, Weimin Zhou, Li Zhao, Jing Chen, Yao Meng, Ji Wang, Yang Lin, Jianying Yuan, Zhihao Xie, Jinmin Ma, William J Liu, Dayan Wang, Wenbo Xu, Edward C Holmes, George F Gao, Guizhen Wu¶, Weijun Chen¶, Weifeng Shi¶, Wenjie Tan¶

A importância da distribuição dos recetores de ligação pelos diferentes órgãos na fisiopatologia da doença…

Biomedicine & Pharmacotherapy 131 (2020) 110678

Contents lists available at ScienceDirect

Biomedicine & Pharmacotherapy

journal homepage: www.elsevier.com/locate/biopha

Review

ACE2, TMPRSS2 distribution and extrapulmonary organ injury in patients with COVID-19

Mengzhen Dong [a,b,c], Jie Zhang [a,b,c], Xuefeng Ma [a,b,c], Jie Tan [a,b,c], Lizhen Chen [a,b,c], Shousheng Liu [a,b,c], Yongning Xin [a,b,c,*], Likun Zhuang [a,b,c,*]

[a] Department of Infectious Diseases, Qingdao Municipal Hospital, Qingdao University, Qingdao, China
[b] Institute of Hepatology, Qingdao Municipal Hospital, Qingdao University, Qingdao, China
[c] Digestive Disease Key Laboratory of Qingdao, Qingdao, China

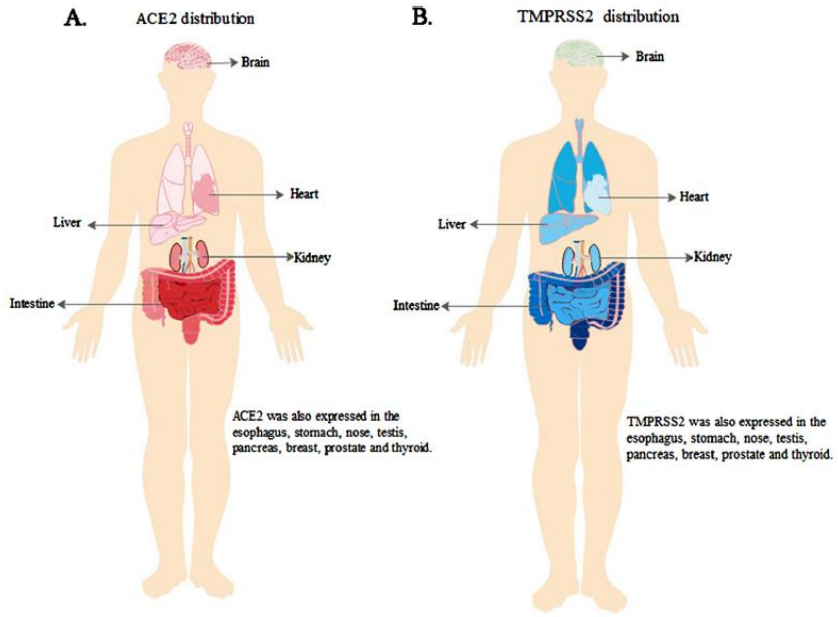


Fig. 2. Tissue distributions of ACE2 and TMPRSS2 in human.
(A–B) the schematic diagram of the expressions of ACE2 (A) and TMPRSS2 (B) in multiple human tissues. The colour strength is corresponding to the gene expression level. ACE2 and TMPRSS2 were expressed in the brain and heart; ACE2 expression is expressed at a relative low level in hepatocytes and mainly located in cholangiocytes, while TMPRSS2 is expressed in the hepatocytes and cholangiocytes; ACE2 and TMPRSS2 were highly expressed in kidney and intestinal epithelial cells. Both ACE2 and TMPRSS2 were also expressed in the esophagus, stomach, nose, testis, pancreas, breast, prostate and thyroid.

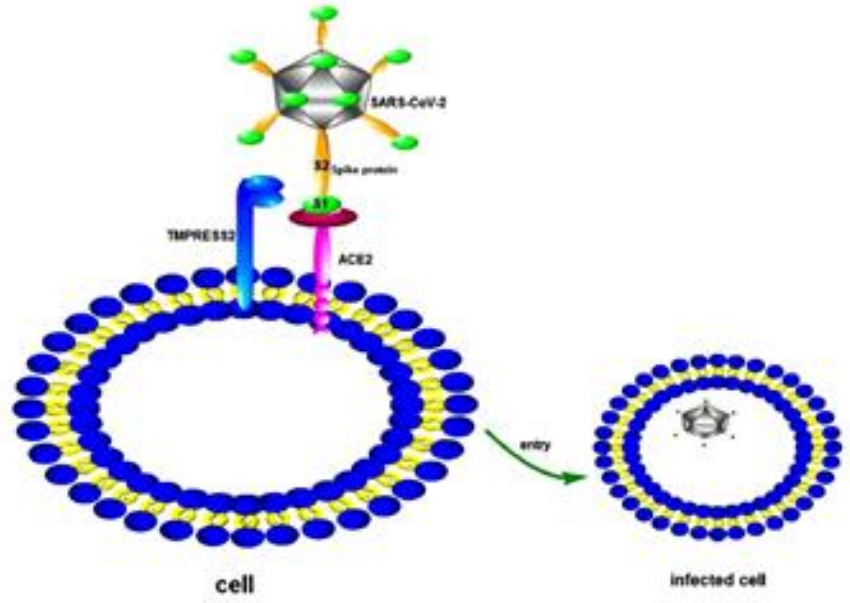


Fig. 1. Entry of SARS-CoV-2 into host cells.
SARS-CoV-2 infected the host cells by the spike protein of the virus and the functions of ACE2 and TMPRSS2 in host cells.

… recetores ACE2 de ligação, que existem dispersos por diversos animais

JOURNAL OF VIROLOGY, May 2006, p. 4211–4219 Vol. 80, No. 9
0022-538X/06/$08.00+0 doi:10.1128/JVI.80.9.4211–4219.2006

MINIREVIEW

Animal Origins of the Severe Acute Respiratory Syndrome Coronavirus: Insight from ACE2–S-Protein Interactions

Wenhui Li,[1]* Swee-Kee Wong,[1] Fang Li,[2] Jens H. Kuhn,[1,3] I-Chueh Huang,[1] Hyeryun Choe,[4] and Michael Farzan[1]*

Department of Microbiology and Molecular Genetics, Harvard Medical School and New England Primate Research Center, Southborough, Massachusetts[1]; Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School and Laboratory of Molecular Medicine, Children's Hospital, Boston, Massachusetts[2]; Department of Biology, Chemistry, Pharmacy, Freie Universität Berlin, Berlin, Germany[3]; and Department of Pediatrics, Harvard Medical School and Perlmutter Laboratory, Children's Hospital, Boston, Massachusetts[4]

Predominant S-protein amino acids:

S-protein residue #	SARS-CoV from 2003-2004 (e.g GD03)	⟸	SARS-CoV from palm civets (e.g. SZ3)	⟹	SARS-CoV from 2002-2003 (e.g. TOR2)
479	N		K		N
487	S		S		T

Most efficient ACE2 association:

S-protein residue #	Reservoir ACE2	⟹	Palm civet ACE2	⟹	Human ACE2
479	K?		K=N		N
487	S?		T		T

FIG. 4. Summary of genetic and biochemical studies of SARS-CoV S-protein residues 479 and 487. (Top) The most frequently observed residues at positions 479 and 487 in sequences of viral genomes obtained during the 2002-2003 human SARS-CoV epidemic and the sporadic infections of 2003-2004 and from palm civets in a Guangdong marketplace. Note that a single isolated palm civet genome (from >20 sequences) encodes a threonine at 487, whereas all sequences from the 2002-2003 epidemic (>100 sequences) encode this threonine. (Bottom) The S-protein residues that confer the most-efficient binding to the ACE2 proteins of the indicated species. The entry for reservoir species is speculative, based on the observation that the ACE2 of at least one animal (mouse) prefers lysine at residue 479 and the additional observation that all but one sequence from the Guangdong marketplace animals encode a serine at residue 487.

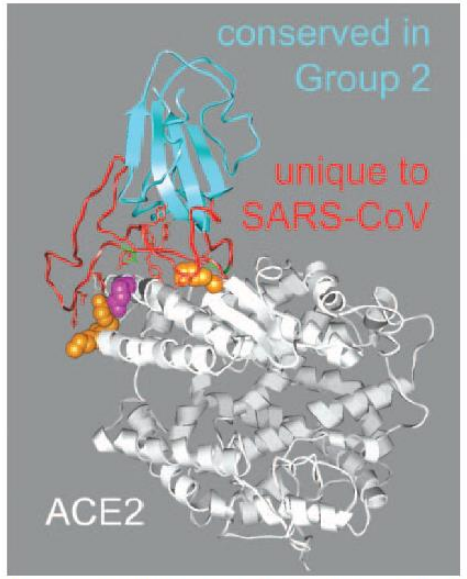


FIG. 2. Cocrystal of the SARS-CoV RBD bound to human ACE2. Cyan indicates a region of the RBD shared among group 2 coronaviruses, whereas red indicates the RBM, which is not homologous to that of other group 2 viruses. ACE2 is shown in white, with its cleft bearing the enzyme-active site facing forward and the membrane-associated C terminus at the bottom of the figure.

O SARS CoV-2 no mundo animal

Emerging Microbes & Infections
2020, VOL. 9
https://doi.org/10.1080/22221751.2020.1827984

EMi Taylor & Francis

REVIEW

OPEN ACCESS

Zoonotic and reverse zoonotic events of SARS-CoV-2 and their impact on global health

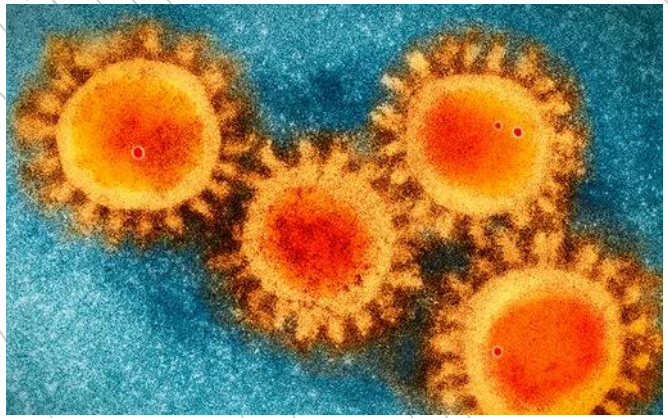
Khalid Munir[a,b*], Shoaib Ashraf[b,c*], Isra Munir[d], Hamna Khalid[e], Mohammad Akram Muneer[b], Noreen Mukhtar[a], Shahid Amin[f], Sohaib Ashraf[c,g], Muhammad Ahmad Imran[g], Umer Chaudhry[h], Muhammad Usman Zaheer[i], Maria Arshad[j], Rukhsana Munir[k], Ali Ahmad[l] and Xin Zhao[m]

[a]PetLife Veterinary Professional Corporation, NJ, USA; [b]Department of Pathobiology, Riphah College of Veterinary Sciences, Riphah University, Lahore, Pakistan; [c]Wellman Center for Photomedicine, Massachusetts General Hospital, Harvard Medical School, Boston, MA, USA; [d]School of Dental Medicine, University of Pennsylvania, Philadelphia, PA, USA; [e]Department of Chemical and Biological Engineering, Villanova University, Villanova, PA, USA; [f]Animal Hospital of Loves Park, Loves Park, IL, USA; [g]Department of Microbiology, Shaikh Zayed Hospital Lahore, Lahore, Pakistan; [h]; Royal (Dick) School of Veterinary Studies and Roslin Institute, Edinburgh, UK; [i]Food and Agriculture Organization of the United Nations, Country Office, Islamabad, Pakistan; [j]District Headquarter Hospital, Lahore, Pakistan; [k]Consultant Emergency Medicine, Russells Hall Hospital, Dudley Group of Hospitals NHS Trust, Dudley, UK; [l]CHU Sainte-Justine Research Center, Department of Microbiology, Infectious Diseases and Immunology, University of Montreal, Montreal, Canada; [m]Department of Animal Sciences, McGill University, Sainte-Anne-de-Bellevue, Canada

Table 1. Animal Species Susceptibility to SARS-CoV-2.

Species	Susceptibility	Infection type	Clinical signs	Transmission	References
Lion/Tigers	High	Natural	None or mild (mild respiratory disease and dry cough)	Animal to animal, human to animals; virus shed in feces and perhaps respiratory secretions	[65, 66, 70]
Dogs	Low	Natural/ Experimental	None or very mild (respiratory signs possible; comorbidities may increase the susceptibility or severity of signs)	None reported; dogs may shed virus in nasal secretions	[57, 64–70]
Domestic Cats	High	Natural/ Experimental	None or mild (mild respiratory signs such as sneezing, transparent ocular discharge, and lethargy; presence of other respiratory pathogens or comorbidities may increase the severity of the signs)	Cat to cat; cats shed virus in their nasal secretions and feces; air-borne transmission reported among cage mates	[53, 57, 64–66, 68, 70–73]
Poultry (chickens and ducks)	None	Experimental	None	None	[57, 80]
Pigs	None	Experimental	None	None	[57, 80]
Ferrets	High	Experimental	None or mild (sneezing, elevated temperature, reduced activity and occasional cough)	Ferret to ferret; ferrets shed virus in nasal secretions, saliva, urine and feces; air-borne transmission among cage mates reported	[52, 57, 59, 80]
Rhesus Macaques (*Macaca fascicularis* and *Macaca mulatta*)	High	Experimental	Moderate signs (irregular respiratory pattern, reduced appetite, hunched posture, pale appearance, dehydration, elevated temperature and weight loss as well as pulmonary infiltrates evident on lung radiograph)	Animal to animal; virus is shed in saliva, nasal secretions and feces	[51]
Fruit Bats (*Rousettus aegyptiacus*)	High	Experimental	None or mild (rhinitis)	Bat to bat; fruit bats shed virus via respiratory, oral and fecal routes	[80]
Farmed Minks	High	Natural	None or moderate to severe signs (gastrointestinal and respiratory signs, pneumonia and increased mortality rate)	Human to mink, mink to mink, mink to cat possible, mink to human possible; minks shed virus in respiratory and oral secretions as well as in feces	[66, 74]
Golden Syrian Hamsters	High	Experimental	Mild (progressive weight loss, lethargy, ruffled furs, rapid breathing and hunched back posture)	Hamster to hamster; hamsters shed virus in respiratory secretions and feces	[58]
Deer Mice (*Peromyscus maniculatus*)	High	Experimental	None or very mild (ruffled fur)	Mice to mice; mice shed virus in nasal secretions, saliva and feces	[60]

A Origem



Contents lists available at ScienceDirect

Travel Medicine and Infectious Disease

journal homepage: www.elsevier.com/locate/tmaid

Review

SARS-CoV-2 jumping the species barrier: Zoonotic lessons from SARS, MERS and recent advances to combat this pandemic virus

Kuldeep Dhama [a, **], Shailesh Kumar Patel [a], Khan Sharun [b], Mamta Pathak [a], Ruchi Tiwari [c], Mohd Iqbal Yatoo [d], Yashpal Singh Malik [e], Ranjit Sah [f], Ali A. Rabaan [g], Parmod Kumar Panwar [h], Karam Pal Singh [a], Izabela Michalak [i], Wanpen Chaicumpa [j], Dayron F. Martinez-Pulgarin [k], D. Katterine Bonilla-Aldana [k,l], Alfonso J. Rodriguez-Morales [k,m,n,*]

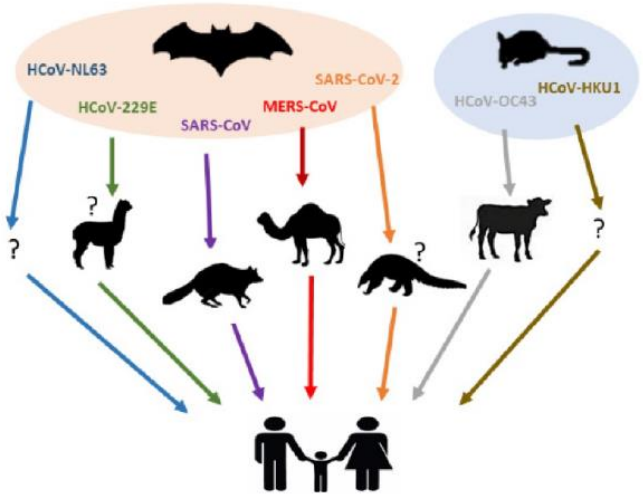


Figure 1. Animal hosts of HCoVs. Blue, green, purple, red, orange, grey, brown arrows represent the transmission of HCoV-NL63, HCoV-229E, SARS-CoV, MERS-CoV, SARS-CoV-2, HCoV-OC43 and HCoV-HKU1 from their natural hosts (bats or rodents) to the intermediate hosts (camelids, civets, dromedary camels, pangolins or bovines), and eventually to the human population. No concrete evidence exists on the intermediated host(s) of HCoV-NL63 and HCoV-HKU1, which was shown as a question mark (?).

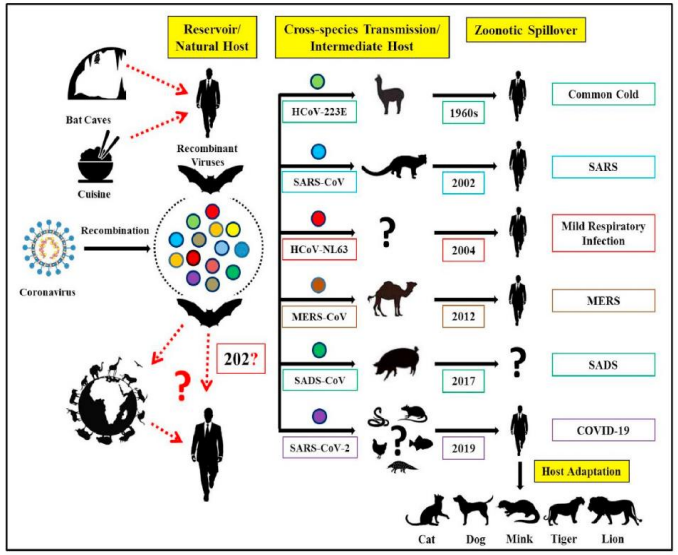


Fig. 1. Cross-species transmission of known zoonotic coronaviruses from bats to animals before spillover to humans and probable prospects of further transmission to mammalian hosts.

Reservatórios Animais e Hospedeiros Intermediários

Le Infezioni in Medicina, Suppl. 1, 6-17, 2020

REVIEW

Emerging coronaviruses: first SARS, second MERS and third SARS-CoV-2. Epidemiological updates of COVID-19

Mehrdad Halajiᵃ·ᵇ, Abbas Farahaniᵃ, Reza Ranjbarᵃ, Mohammad Heiatᵃ, Farhad Safarpoor Dehkordiᵃ

ᵃDepartment of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran; ᵇIsfahan Kidney Diseases Research Center, Isfahan University of Medical Sciences, Isfahan, Iran; ᶜInfectious and Tropical Diseases Research Center, Hormozgan Health Institute, Hormozgan University of Medical Sciences, Bandar Abbas, Iran; ᵈMolecular Biology Research Center, Systems Biology and Poisonings Institute, Baqiyatallah University of Medical Sciences, Tehran, Iran; ᵉBaqiyatallah Research Center for Gastroenterology and Liver Disease, Baqiyatallah University of Medical Sciences, Tehran, Iran; ᶠHalal Research Center of IRI, FDA, Tehran, Iran

VETERINARY QUARTERLY
2020, VOL. 40, NO. 1, 169–182
https://doi.org/10.1080/01652176.2020.1766725

Taylor & Francis

REVIEW

OPEN ACCESS

COVID-19: animals, veterinary and zoonotic links

Ruchi Tiwariᵃ, Kuldeep Dhamaᵇ, Khan Sharunᶜ, Mohd. Iqbal Yatooᵈ, Yashpal Singh Malikᵉ, Rajendra Singhᵇ, Izabela Michalakᶠ, Ranjit Sahᵍ, D. Katterine Bonilla-Aldanaʰ·ⁱ and Alfonso J Rodriguez-Moralesʲ·ᵏ

ᵃDepartment of Veterinary Microbiology and Immunology, College of Veterinary Sciences, UP Pt. Deen Dayal Upadhayay Pashu Chikitsa Vigyan Vishwavidyalay Evum Go-Anusandhan Sansthan (DUVASU), Mathura, India; ᵇDivision of Pathology, ICAR-Indian Veterinary Research Institute, Izatnagar, Bareilly, Uttar Pradesh, India; ᶜDivision of Surgery, ICAR-Indian Veterinary Research Institute, Izatnagar, Bareilly, Uttar Pradesh, India; ᵈSher-E, Kashmir University of Agricultural Sciences and Technology of Kashmir, Shalimar, Srinagar, Jammu and Kashmir, India; ᵉDivision of Biological Standardization, ICAR-Indian Veterinary Research Institute, Izatnagar, Bareilly, Uttar Pradesh, India; ᶠFaculty of Chemistry, Department of Advanced Material Technologies, Wroclaw University of Science and Technology, Wroclaw, Poland; ᵍDepartment of Microbiology, Tribhuvan University Teaching Hospital, Institute of Medicine, Kathmandu, Nepal; ʰSemillero de Zoonosis, Grupo de Investigación BIOECOS, Fundación Universitaria Autónoma de las Américas, Sede Pereira, Pereira, Risaralda, Colombia; ⁱPublic Health and Infection Research Group, Faculty of Health Sciences, Universidad Tecnologica de Pereira, Pereira, Colombia; ʲGrupo de Investigacion Biomedicina, Faculty of Medicine, Fundacion Universitaria Autonoma de las Americas, Pereira, Risaralda, Colombia

frontiers in Veterinary Science

MINI REVIEW
published: 11 December 2020
doi: 10.3389/fvets.2020.596391

An Overview of SARS-CoV-2 and Animal Infection

Mohamed A. A. Mahdy[1], Waleed Younis[2] and Zamzam Ewaida[3]*

[1] Department of Anatomy and Embryology, Faculty of Veterinary Medicine, South Valley University, Qena, Egypt, [2] Department of Microbiology, Faculty of Veterinary Medicine, South Valley University, Qena, Egypt, [3] Qena University Hospital, South Valley University, Qena, Egypt

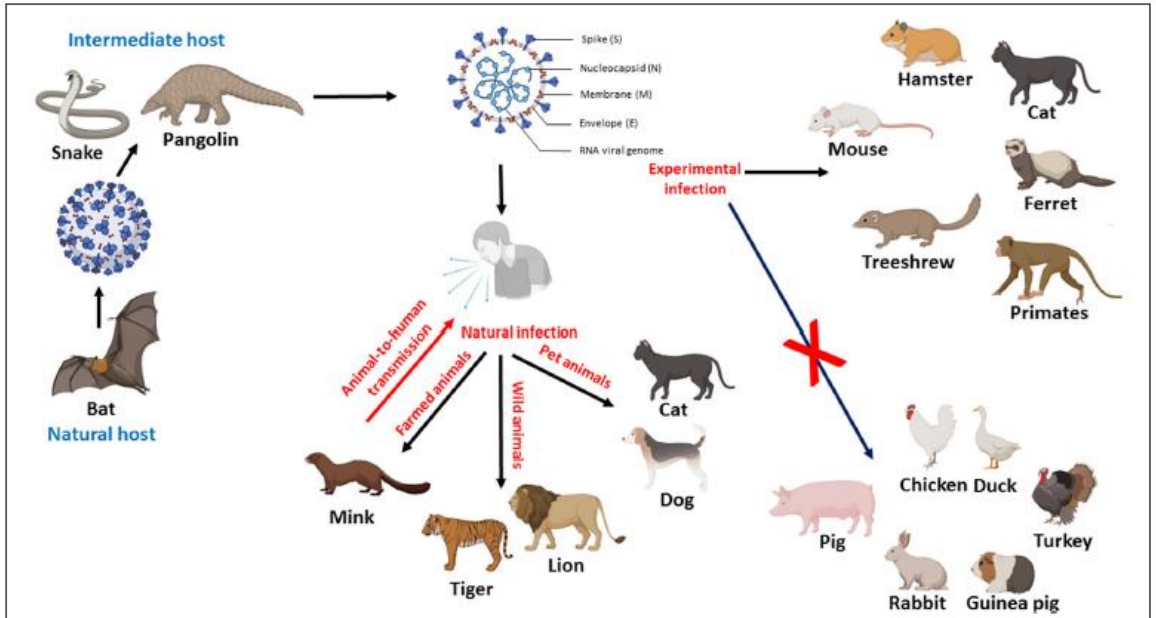


FIGURE 1 | Diagram showing the possible role of animals in the transmission of SARS-CoV-2, potential intermediate hosts, natural and experimental infection of animals. Figure was created with BioRender.com.

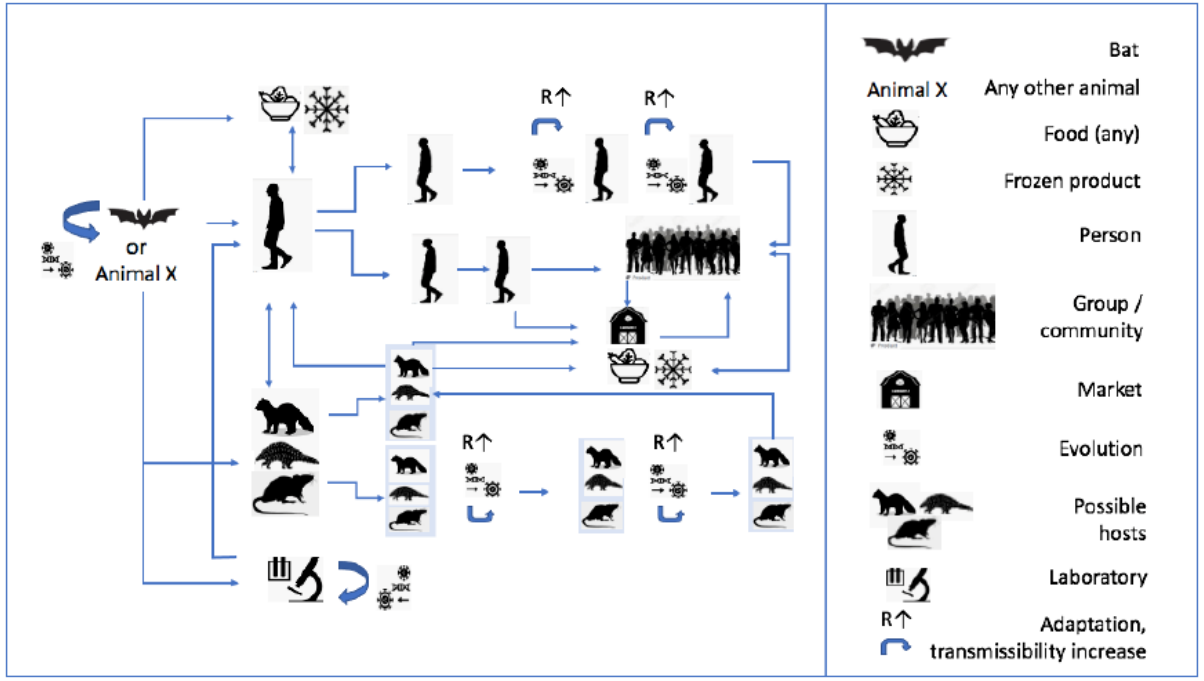
WHO-convened Global Study of Origins of SARS-CoV-2: China Part

Joint WHO-China Study
14 January-10 February 2021

Joint Report

World Health Organization

O que diz o Relatório da OMS e as dúvidas levantadas acerca da origem real do vírus



Science of the Total Environment 750 (2021) 141711

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

SARS-CoV-2 has been circulating in northern Italy since December 2019: Evidence from environmental monitoring

Giuseppina La Rosa [a,*], Pamela Mancini [a], Giusy Bonanno Ferraro [a], Carolina Veneri [a], Marcello Iaconelli [a], Lucia Bonadonna [a], Luca Lucentini [a], Elisabetta Suffredini [b]

[a] Department of Environment and Health, Istituto Superiore di Sanità, Rome, Italy
[b] Department of Food Safety, Nutrition and Veterinary Public Health, Istituto Superiore di Sanità, Rome, Italy

HIGHLIGHTS

- SARS-CoV-2 was already circulating in northern Italy at the end of 2019.
- Virus concentration in wastewater samples ranged from <LOD to 5.6×10^4 g.c./L.
- Nested and real-time RT-PCR assays were shown to be specific for SARS-CoV-2.
- Nested RT-PCR and real-time RT-(q)PCR showed an overall agreement of 65.0%.
- Sewage monitoring can contribute to the early detection of SARS-CoV-2 circulation.

GRAPHICAL ABSTRACT

METHODS

Archival sewage samples:

- Pre-epidemic period: 40 samples (October 2019 - February 2020)
- Non-epidemic period: 24 samples (September 2018 - June 2019)

- Sample concentration (WHO, 2003, with modifications)
- Viral nucleic acids extraction with magnetic silica beads
- Real-time RT-PCR (newly designed assay) + Nested RT-PCR and sequencing

RESULTS

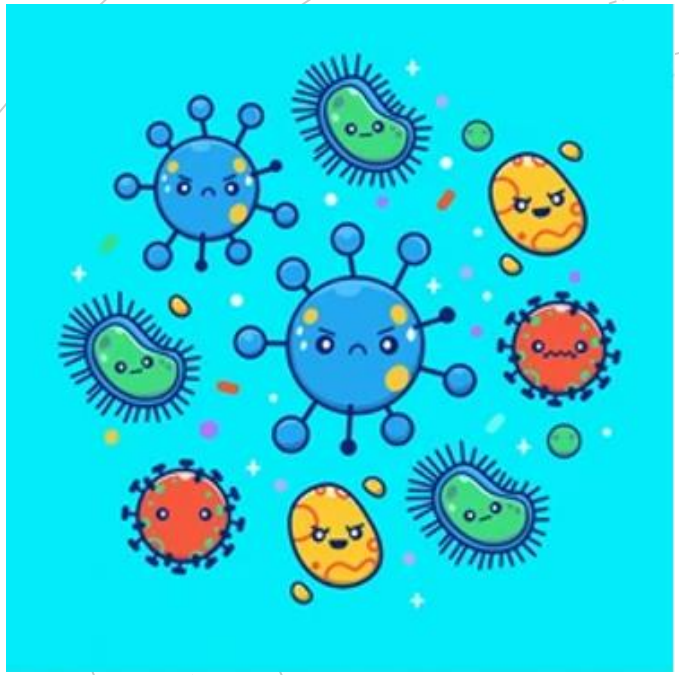
- **First occurrence of SARS-CoV-2 in sewage:**

City	Date of sampling
Milan	December 18, 2019
Turin	December 18, 2019
Bologna	January 29, 2020

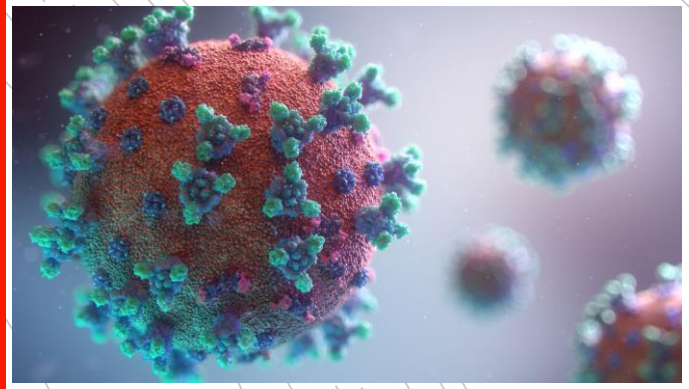
- **Agreement between the two assays:** 65.0% (26/40 paired results)
- **Virus concentration:** from <LOD to 5.6×10^4 g.c./L; most of the samples were below the analytical LOQ

CONCLUSIONS

- **SARS-CoV-2 has been circulating in northern Italy since December 2019**
- **WBE could contribute to the early detection of a possible second wave of infection**



A Evolução



Mechanisms of disease

THE LANCET

Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection

YiJun Ruan, Chia Lin Wei, Ling Ai Ee, Vinsensius B Vega, Herve Thoreau, Se Thoe Su Yun, Jer-Ming Chia, Patrick Ng, Kuo Ping Chiu, Landri Lim, Zhang Tao, Chan Kwai Peng, Lynette Oon Lin Ean, Ng Mah Lee, Leo Yee Sin, Lisa F P Ng, Ren Ee Chee, Lawrence W Stanton, Philip M Long, Edison T Liu

A caracterização da estrura molecular na base da árvore filogenética e da classificação taxonómica

REVIEWS

NATURE REVIEWS | MICROBIOLOGY

Characteristics of SARS-CoV-2 and COVID-19

Ben Hu[1,3], Hua Guo[1,2,3], Peng Zhou[1] and Zheng-Li Shi[1]✉

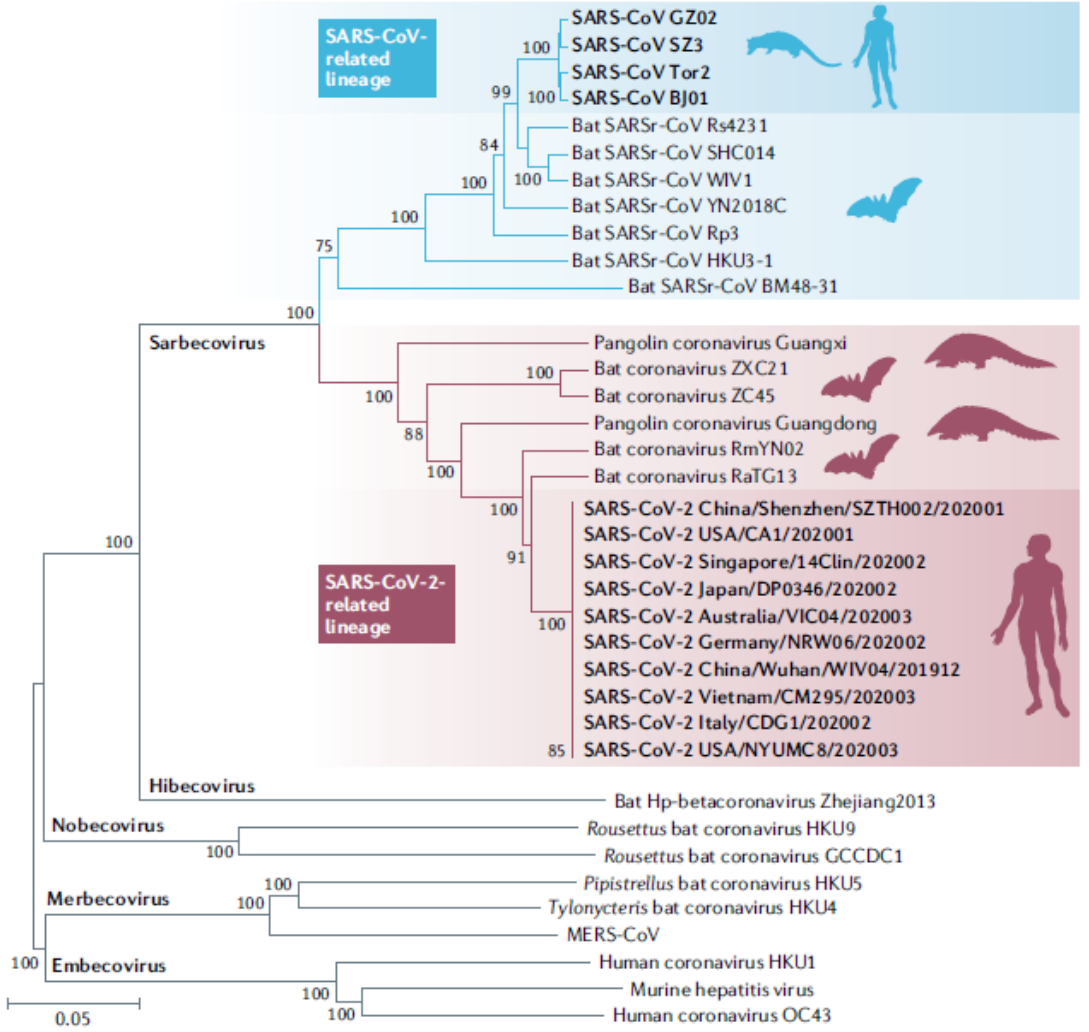


Fig. 2 | **Phylogenetic tree of the full-length genome sequences of SARS-CoV-2, SARSr-CoVs and other betacoronaviruses.** The construction was performed by the neighbour joining method with use of the program MEGA6 with bootstrap values being calculated from 1,000 trees. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) clusters with closely related viruses in bats and pangolins and together with SARS-CoV and bat SARS-related coronaviruses (SARSr-CoVs) forms the sarbecoviruses. The sequences were downloaded from the GISAID database and GenBank. MERS-CoV, Middle East respiratory syndrome coronavirus.

Clinical Infectious Diseases
MAJOR ARTICLE

Genomic Diversity of Severe Acute Respiratory Syndrome–Coronavirus 2 in Patients With Coronavirus Disease 2019

Zijie Shen,[1,2,a] Yan Xiao,[3,a] Lu Kang,[1,2,a] Wentai Ma,[1,2,a] Leisheng Shi,[1,2] Li Zhang,[1] Zhuo Zhou,[4] Jing Yang,[1,2] Jiaxin Zhong,[1,2] Donghong Yang,[5] Li Guo,[3] Guoliang Zhang,[6] Hongru Li,[7] Yu Xu,[5] Mingwei Chen,[8] Zhancheng Gao,[5] Jianwei Wang,[2] Lili Ren,[3,b] and Mingkun Li[1,9,b]

[1]Key Laboratory of Genomic and Precision Medicine, Beijing Institute of Genomics, Chinese Academy of Sciences, and China National Center for Bioinformation, Beijing, China, [2]University of Chinese Academy of Sciences, Beijing, China, [3]National Health Commission of the People's Republic of China Key Laboratory of Systems Biology of Pathogens and Christophe Mérieux Laboratory, Institute of Pathogen Biology, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China, [4]Biomedical Pioneering Innovation Center, Beijing Advanced Innovation Center for Genomics, Peking-Tsinghua Center for Life Sciences, Peking University Genome Editing Research Center, State Key Laboratory of Protein and Plant Gene Research, School of Life Sciences, Peking University, Beijing, China, [5]Department of Respiratory and Critical Care Medicine, Peking University People's Hospital, Beijing, China, [6]National Clinical Research Center for Infectious Diseases, Guangdong Key Laboratory for Emerging Infectious Diseases, Shenzhen Third People's Hospital, Southern University of Science and Technology, Shenzhen, China, [7]Fujian Provincial Hospital, Fujian, China, [8]Department of Respiratory and Critical Care Medicine, First Affiliated Hospital of Xi'an Jiaotong University, Xi'an, China, and [9]Center for Excellence in Animal Evolution and Genetics, Chinese Academy of Sciences, Kunming, China

Uma grande capacidade de mutagenicidade e uma consequente variabilidade genómica

RESEARCH ARTICLE
Ecological and Evolutionary Science

Rampant C→U Hypermutation in the Genomes of SARS-CoV-2 and Other Coronaviruses: Causes and Consequences for Their Short- and Long-Term Evolutionary Trajectories

P. Simmonds[a]

[a]Nuffield Department of Medicine, University of Oxford, Oxford, United Kingdom

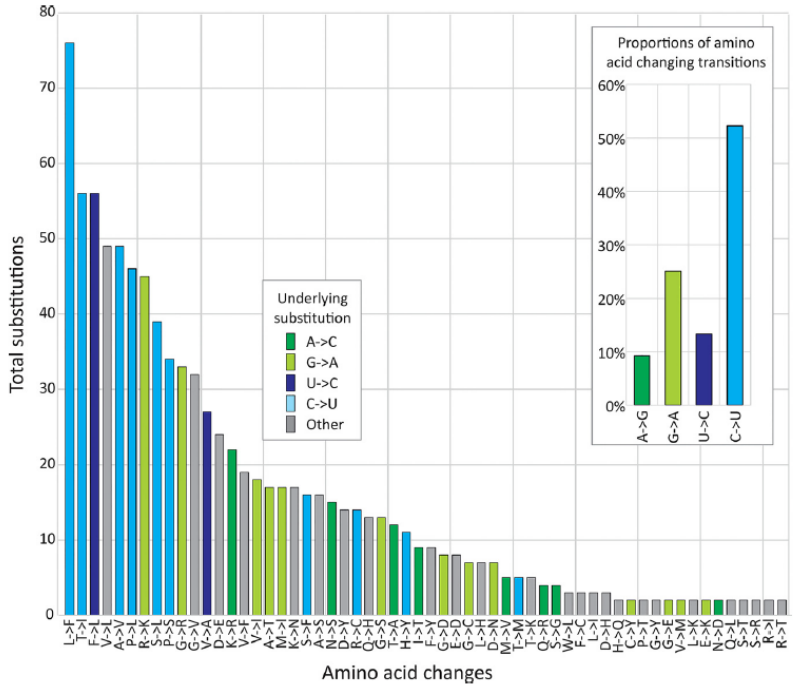


FIG 5 Amino acid changes induced by different nucleotide substitutions. Numbers of individual amino acids changes observed in the combined SARS-CoV-2 data set (864 sequences) at a 5% variability threshold. Bars are colored based on the underlying nucleotide changes. Inset graph shows the relative proportions of transitions leading to amino acid changes.

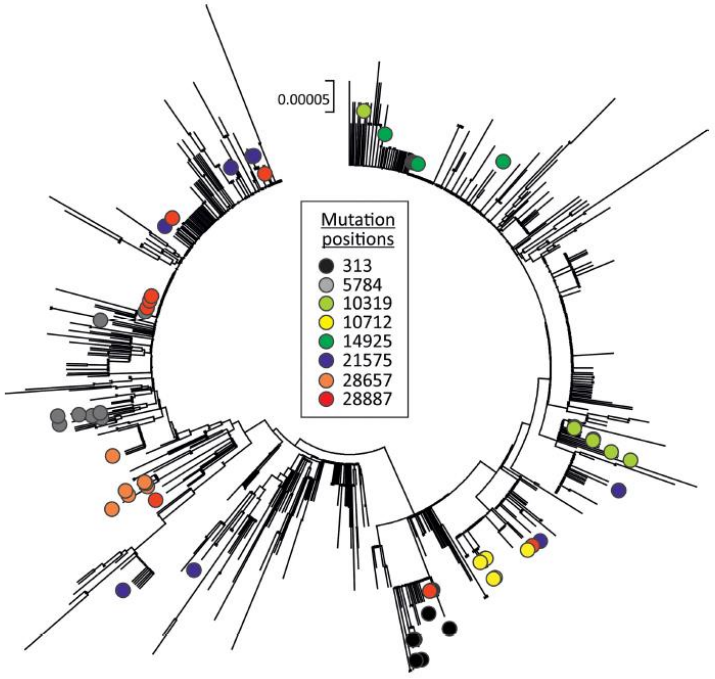
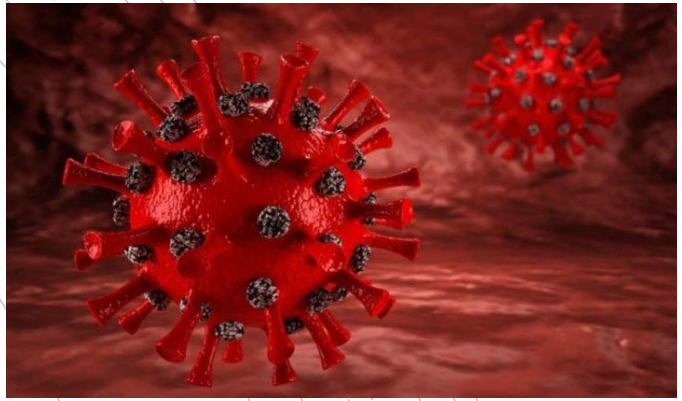


FIG 4 Phylogeny of SARS-CoV-2 and positions of sequences with C→U changes. A neighbor-joining tree of 865 SARS-CoV-2 complete genome sequences was constructed in MEGA6 (41). Labels show the position of sequences containing a selection of C→U transitions at the genome positions indicated in the key.

A Transmissibilidade



Trends in Immunology

CellPress
REVIEWS

Review

Mechanisms of SARS-CoV-2 Transmission and Pathogenesis

Andrew G. Harrison,[1,2] Tao Lin,[1,2] and Penghua Wang[1,*]

A dinâmica da replicação viral, a resposta imunológica e as manifestações clínicas

CLINICAL UPDATE

thebmj

Virology, transmission, and pathogenesis of SARS-CoV-2

Muge Cevik, [1,2] Krutika Kuppalli, [3] Jason Kindrachuk, [4] Malik Peiris[5]

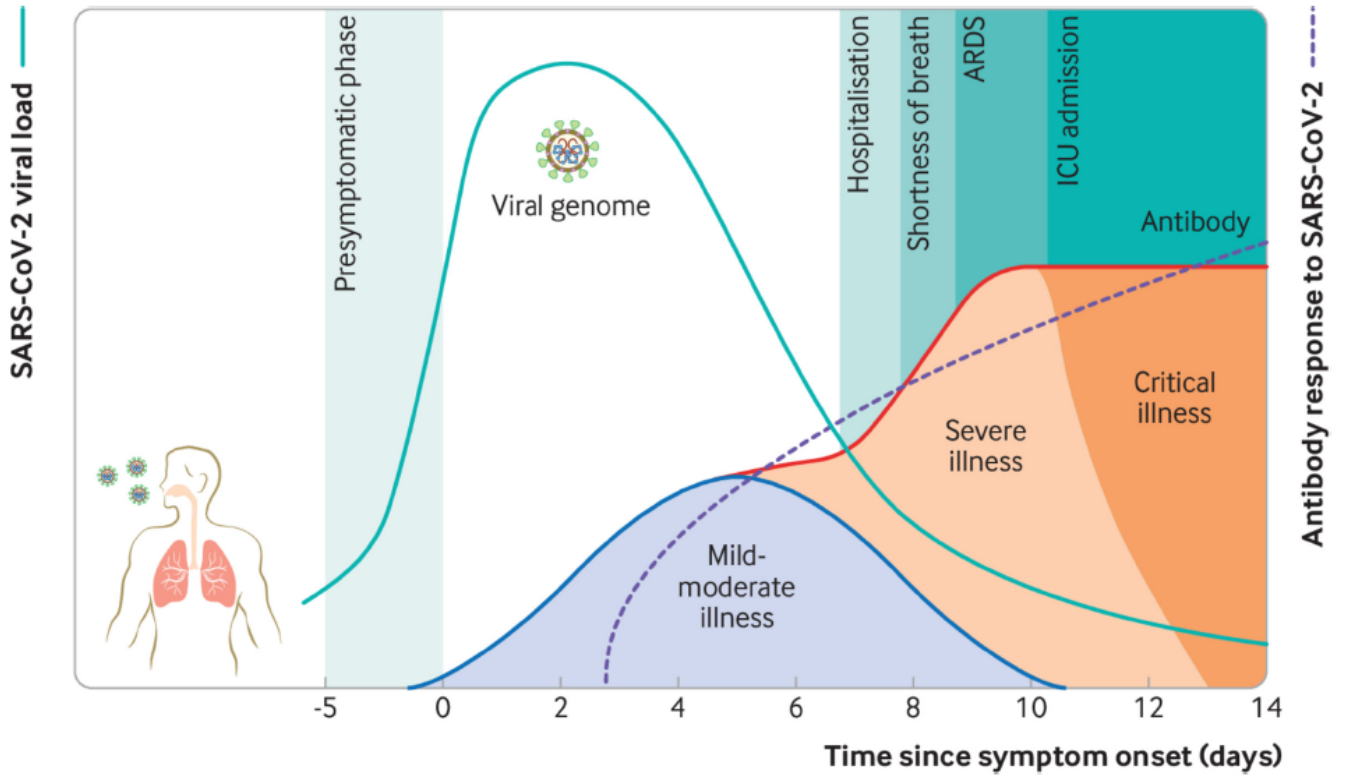
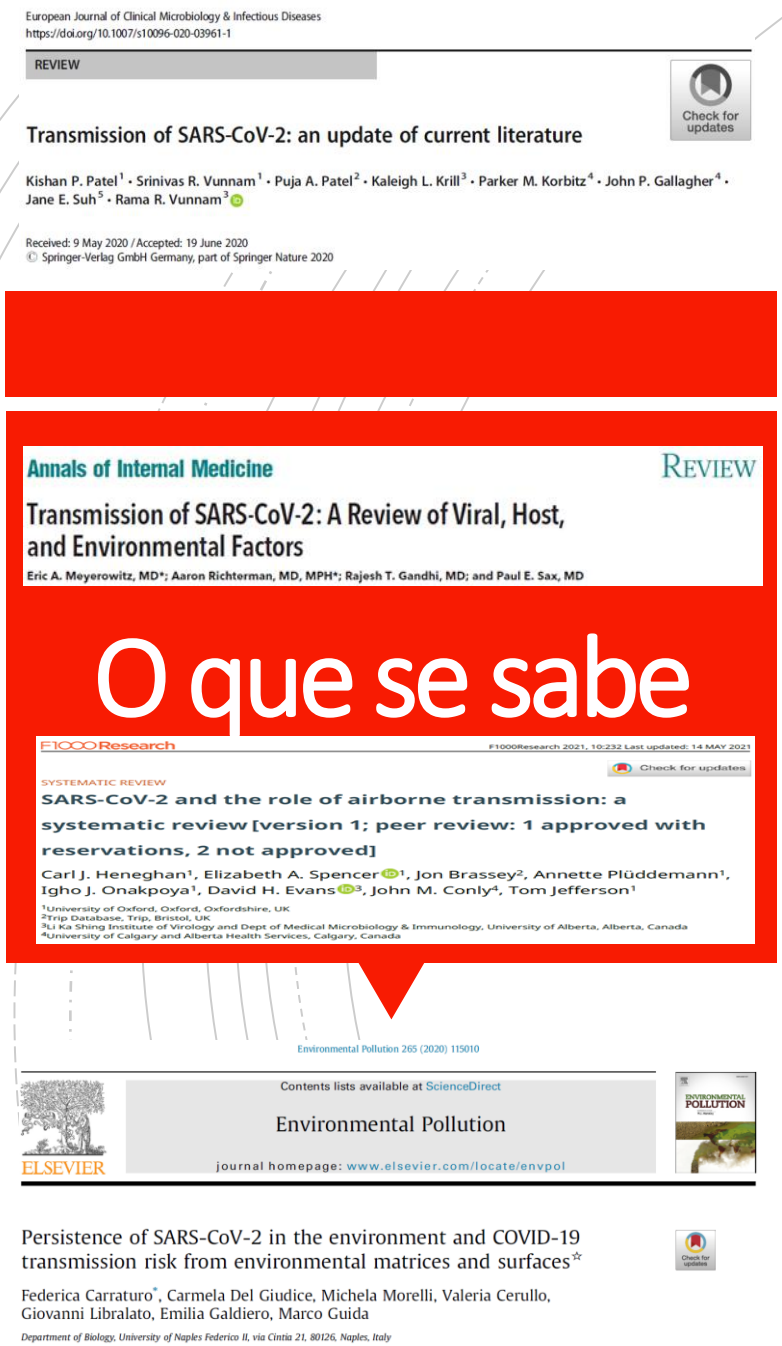


Fig 2 | After the initial exposure, patients typically develop symptoms within 5-6 days (incubation period). SARS-CoV-2 generates a diverse range of clinical manifestations, ranging from mild infection to severe disease accompanied by high mortality. In patients with mild infection, initial host immune response is capable of controlling the infection. In severe disease, excessive immune response leads to organ damage, intensive care admission, or death. The viral load peaks in the first week of infection, declines thereafter gradually, while the antibody response gradually increases and is often detectable by day 14 (figure adapted with permission from https://www.sciencedirect.com/science/article/pii/S009286742030475X; https://www.thelancet.com/journals/lanres/article/PIIS2213-2600(20)30230-7/fulltext)


European Journal of Clinical Microbiology & Infectious Diseases
https://doi.org/10.1007/s10096-020-03961-1

REVIEW

Transmission of SARS-CoV-2: an update of current literature

Kishan P. Patel[1] · Srinivas R. Vunnam[1] · Puja A. Patel[2] · Kaleigh L. Krill[3] · Parker M. Korbitz[4] · John P. Gallagher[4] · Jane E. Suh[5] · Rama R. Vunnam[3]

Received: 9 May 2020 / Accepted: 19 June 2020
© Springer-Verlag GmbH Germany, part of Springer Nature 2020

Annals of Internal Medicine

REVIEW

Transmission of SARS-CoV-2: A Review of Viral, Host, and Environmental Factors

Eric A. Meyerowitz, MD*; Aaron Richterman, MD, MPH*; Rajesh T. Gandhi, MD; and Paul E. Sax, MD

O que se sabe

F1000Research

F1000Research 2021, 10:232 Last updated: 14 MAY 2021

Check for updates

SYSTEMATIC REVIEW

SARS-CoV-2 and the role of airborne transmission: a systematic review [version 1; peer review: 1 approved with reservations, 2 not approved]

Carl J. Heneghan[1], Elizabeth A. Spencer[1], Jon Brassey[2], Annette Plüddemann[1], Igho J. Onakpoya[1], David H. Evans[3], John M. Conly[4], Tom Jefferson[1]

[1]University of Oxford, Oxford, Oxfordshire, UK
[2]Trip Database, Trip, Bristol, UK
[3]Li Ka Shing Institute of Virology and Dept of Medical Microbiology & Immunology, University of Alberta, Alberta, Canada
[4]University of Calgary and Alberta Health Services, Calgary, Canada

Environmental Pollution 265 (2020) 115010

Contents lists available at ScienceDirect

Environmental Pollution

journal homepage: www.elsevier.com/locate/envpol

ELSEVIER

Persistence of SARS-CoV-2 in the environment and COVID-19 transmission risk from environmental matrices and surfaces☆

Federica Carraturo*, Carmela Del Giudice, Michela Morelli, Valeria Cerullo, Giovanni Libralato, Emilia Galdiero, Marco Guida

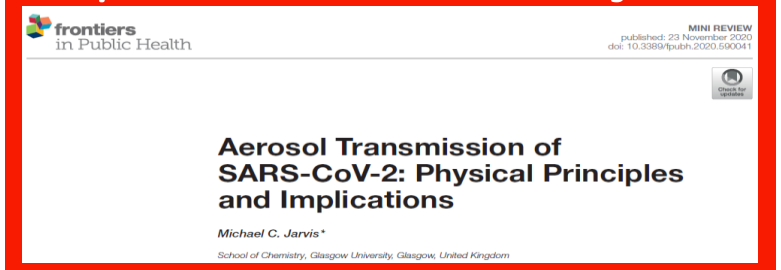
Department of Biology, University of Naples Federico II, via Cintia 21, 80126, Naples, Italy

- **Sobrevida do vírus**
  - **Aerossóis- até 3h (intermitente)**
  - **Superfícies: 6 – 72h (até 9 dias no plástico e no aço; talvez até 28 dias em ambientes muito contaminados...)**
  - **Nas máscaras faciais- 4 a 7 dias**
- **Inativação**
  - **30 mn a 60ªc; 5 mn a 70°C; 1 mn a 80ªc; PH ideal: 5 – 9; sobrevive à congelação**
- **Contagiosidade**
  - **Do dia – 2 ao dia + 10 (até dia + 20 nos doentes imunodeprimidos) ou com doença crítica**
  - **"*Shedding* viral"- Até 2 meses**
  - **Estima-se que cerca de 40 a 75% das infeções sejam assintomáticas**
  - **R (t): 2-3**
- **Período de incubação**
  - **2 a 14 dias (mediana de 5 dias)**
- **Meios de transmissão**
  - **Predominante- Aerossóis (< 5-10 micras cúbicas)**
  - **Possível- Vertical; contacto direto com objetos contaminados**
  - **Não comprovado: Sexual; sanguínea; fecal-oral; saliva; aleitamento**
- **Produtos orgânicos onde o vírus já foi isolado**
  - **Secreções das vias respiratórias; saliva, fezes, LCR, esperma, lágrimas, sangue e placenta (não na urina e secreções vaginais, sendo ainda discutível no leite materno)**
- **Fatores de suscetibilidade**
  - **Variantes genéticas do vírus (VOCs): (> Inglesa, Sul-Africana, Brasileira e Indiana)**
  - **Carga viral e gravidade clínica do hospedeiro (< a partir de doentes assintomáticos)**
  - **Distância entre pessoas (até 2 m) e duração do contacto (> 15 mn)**
  - **Arejamento dos espaços (> no interior do que no exterior de edifícios ou de meios de transporte)**
  - **Utilização de precauções (máscara, higiene das mãos e etiqueta respiratória)**

Ten scientific reasons in support of airborne transmission of SARS-CoV-2

www.thelancet.com Vol 397 May 1, 2021 THE LANCET

"Cerca de 60% das infeções na comunidade resultam da transmissão aérea na fase presintomática da doença"



frontiers in Public Health

MINI REVIEW
published: 23 November 2020
doi: 10.3389/fpubh.2020.590041

Aerosol Transmission of SARS-CoV-2: Physical Principles and Implications

Michael C. Jarvis*

School of Chemistry, Glasgow University, Glasgow, United Kingdom

Environment International 144 (2020) 106039

Contents lists available at ScienceDirect

Environment International

journal homepage: www.elsevier.com/locate/envint

Aerosol transmission of SARS-CoV-2? Evidence, prevention and control

Song Tang[a,b,1], Yixin Mao[a,1], Rachael M. Jones[c,1], Qiyue Tan[a], John S. Ji[d,e], Na Li[a], Jin Shen[a], Yuebin Lv[a], Lijun Pan[a], Pei Ding[a], Xiaochen Wang[a], Youbin Wang[a], C. Raina MacIntyre[f,g], Xiaoming Shi[a,b,*]

[a] China CDC Key Laboratory of Environment and Population Health, National Institute of Environmental Health, Chinese Center for Disease Control and Prevention, Beijing 100021, China
[b] Center for Global Health, School of Public Health, Nanjing Medical University, Nanjing, Jiangsu 211166, China
[c] Department of Family and Preventive Medicine, School of Medicine, University of Utah, Salt Lake City, UT 84108, USA
[d] Environmental Research Center, Duke Kunshan University, Kunshan, Jiangsu 215316, China
[e] Nicholas School of the Environment, Duke University, Durham, NC 27708, USA
[f] Kirby Institute, Faculty of Medicine, The University of New South Wales, Sydney, Australia
[g] College of Public Service & Community Solutions and College of Health Solutions, Arizona State University, USA

JOHNS HOPKINS BLOOMBERG SCHOOL of PUBLIC HEALTH

As vias possíveis e transmissão

Trends in Immunology

CellPress REVIEWS

Review

Mechanisms of SARS-CoV-2 Transmission and Pathogenesis

Andrew G. Harrison,[1,2] Tao Lin,[1,2] and Penghua Wang[1,*]

Biochemical Society Transactions (2020) 48 2307–2316
https://doi.org/10.1042/BST20200693

PORTLAND PRESS

Review Article

Transmission and prevention of SARS-CoV-2

Zhongyi Wang[1,*], Yingying Fu[1,*], Zhendong Guo[2,*], Jiaming Li[1], Jingjing Li[1], Hongliang Cheng[1], Bing Lu[1] and Qiang Sun[1]

[1]Laboratory of Cell Engineering, Beijing Institute of Biotechnology, 20 Dongdajie Road, Beijing 100071, China; [2]Changchun Veterinary Research Institute, Chinese Academy of Agriculture Sciences, 666 Liuying West Road, Changchun, Jilin, China

Correspondence: Bing Lu (13693506666@163.com) or Qiang Sun (sunq@bmi.ac.cn)

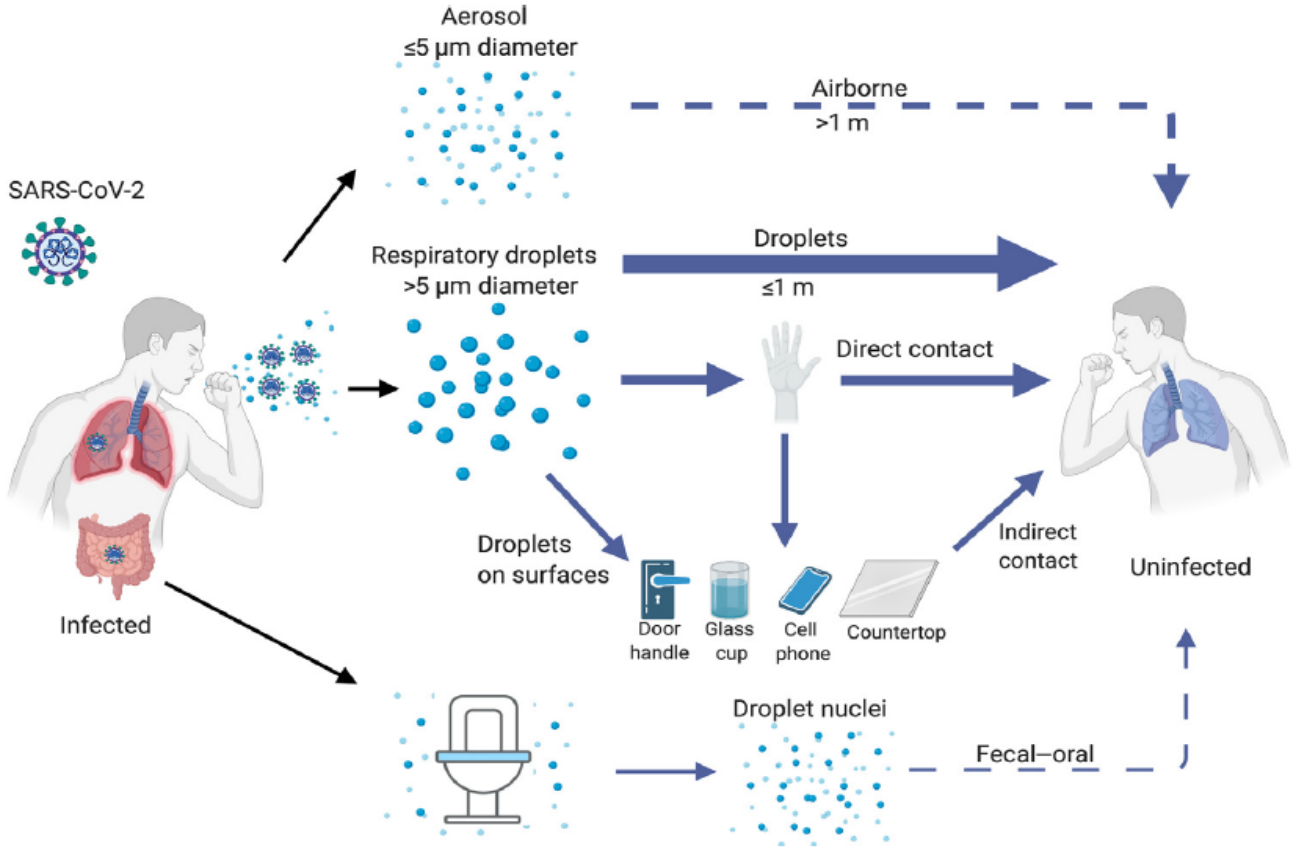


Figure 2. Proposed Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Transmission Routes. The ongoing COVID-19 pandemic has resulted in numerous accounts of different transmission routes between humans. Droplet transmission (>5 μm) is the most pronounced and heavily implicated mode of transmission reported during the pandemic. Direct contact spread from one infected individual to a second, naïve person has also been considered a driver of human-to-human transmission, especially in households with close interactions between family members. The contagiousness of SARS-CoV-2 after disposition on fomites (e.g., door handles) is under investigation, but is likely a compounding factor for transmission events, albeit less frequently than droplet or contact-driven transmission. Both airborne and fecal–oral human-to-human transmission events were reported in the precursor SARS-CoV epidemic but have yet to be observed in the current crises. Solid arrows show confirmed viral transfer from one infected person to another, with a declining gradient in arrow width denoting the relative contributions of each transmission route. Dashed lines show the plausibility of transmission types that have yet to be confirmed. SARS-CoV-2 symbol in 'infected patient' indicates where RNA/infectious virus has been detected [43,44,47–49,57,59,60]. Figure generated with BioRender.

As viagens de avião como modelo da transmissão aérea de infeção

JAMA Network Open

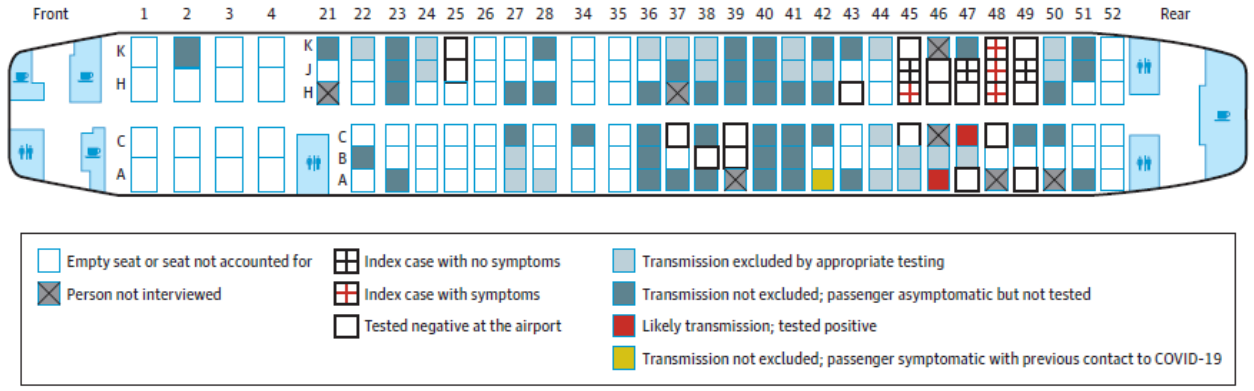
Research Letter | Public Health

Assessment of SARS-CoV-2 Transmission on an International Flight and Among a Tourist Group

Sebastian Hoehl, MD; Onur Karaca; Niko Kohmer, MD; Sandra Westhaus, PhD; Jürgen Graf, MD; Udo Goetsch, MD; Sandra Ciesek, MD

JAMA Network Open. 2020;3(8):e2018044. doi:10.1001/jamanetworkopen.2020.18044 August 18, 2020

Figure 1. Seating of the Index Cases and Other Passengers on the Aircraft (Boeing 737-900)



COVID-19 indicates coronavirus disease 2019.

Physics of Fluids ARTICLE scitation.org/journal/phf

Simulation of aerosol transmission on a Boeing 737 airplane with intervention measures for COVID-19 mitigation

Cite as: Phys. Fluids **33**, 033312 (2021); doi: 10.1063/5.0044720
Submitted: 19 January 2021 · Accepted: 13 February 2021 ·
Published Online: 16 March 2021

Khaled Talaat,[1] Mohamed Abuhegazy,[2,a)] Omar A. Mahfoze,[3] Osman Anderoglu,[1] and Svetlana V. Poroseva[2]

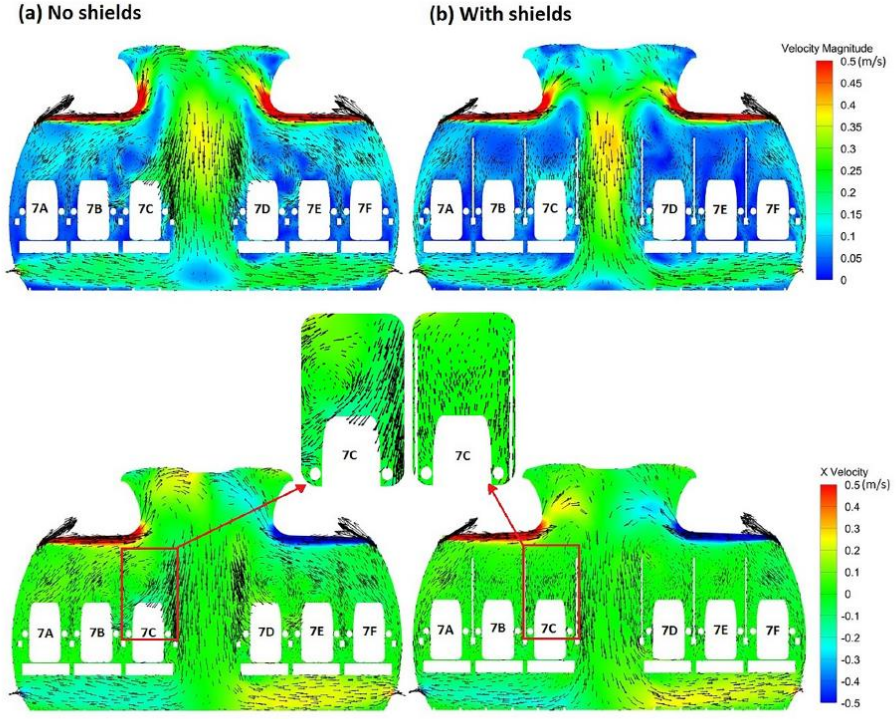


FIG. 2. Distribution of the velocity magnitude and lateral velocity component through a section of the cabin for (a) the model with no shields and (b) the model with shields.

PLOS BIOLOGY

ESSAY

Superspreading events in the transmission dynamics of SARS-CoV-2: Opportunities for interventions and control

Benjamin M. Althouse[1,2,3]*, Edward A. Wenger[1]*, Joel C. Miller[4], Samuel V. Scarpino[5,6,7,8,9,10], Antoine Allard[11,12], Laurent Hébert-Dufresne[11,13,14], Hao Hu[15]*

1 Institute for Disease Modeling, Bellevue, Washington, United States of America, 2 University of Washington, Seattle, Washington, United States of America, 3 New Mexico State University, Las Cruces, New Mexico, United States of America, 4 School of Engineering and Mathematical Sciences, La Trobe University, Bundoora, Victoria, Australia, 5 Network Science Institute, Northeastern University, Boston, Massachusetts, United States of America, 6 Department of Marine & Environmental Sciences, Northeastern University, Boston, Massachusetts, United States of America, 7 Department of Physics, Northeastern University, Boston, Massachusetts, United States of America, 8 Department of Health Sciences, Northeastern University, Boston, Massachusetts, United States of America, 9 ISI Foundation, Turin, Italy, 10 Santa Fe Institute, Santa Fe, New Mexico, United States of America, 11 Département de Physique, de Génie Physique et d'Optique, Université Laval, Québec, Québec, Canada, 12 Centre Interdisciplinaire en Modélisation Mathématique, Université Laval, Québec, Québec, Canada, 13 Vermont Complex Systems Center, University of Vermont, Burlington, Vermont, United States of America, 14 Department of Computer Science, University of Vermont, Burlington, Vermont, United States of America, 15 Bill & Melinda Gates Foundation, Seattle, Washington, United States of America

OPEN ACCESS

A enorme importância dos debominados *"superspreaders"* ... não só na COVID-19!!!

Table. Factors that increase the risk for superspreading events and implications for prevention and control of COVID-19*

Factor	Disease	Epidemiologic role	Implications for control of COVID-19
Pathogen	Tuberculosis	Certain strains of *Mycobacterium tuberculosis* are more infectious, and patients ill with these strains should be prioritized for examination of a larger circle of contacts (*21*,*22*)	Continued monitoring for genetic change and for changes in the epidemiology of transmission
Host	Influenza	Viral shedding and risk for transmission among asymptomatic and presymptomatic persons can result in influenza transmission (*23*), particularly in closed settings with minimal ventilation (H. Nishiura et al., unpub. data, https://doi.org/10.1101/2020.02.28.20029272)	Identification of factors associated with increased transmissibility and rapid intervention to prevent transmission from similar patients prospectively; further characterization of risk for asymptomatic transmission
Environment	SARS	Airborne transmission of SARS can result in environmental spread of disease in community (*24*) and healthcare settings (*25*)	Assess changes in plumbing and ventilation that may be needed to reduce risk for spread; increase social distancing; reduce mass gatherings in closed environments; ensure effective triage, isolation, and general infection control in healthcare facilities
Behavior	Ebola	Inaccurate perceptions of Ebola risk can result in behaviors that increase the probability of transmission (*26*,*27*)	Promote handwashing, cough etiquette, and safer care-seeking behavior, including mask-wearing by persons who are ill, and ensure that timely and accurate messaging about risk and behavioral preventive measures are tailored to and reach affected populations
Response	MERS	Timely implementation of control measures can reduce outbreak duration and number of transmission events (*28*)	Rapidly identify and isolate cases to reduce transmission; implement large-scale NPIs in affected areas within 1 week

*COVID-19, coronavirus disease; MERS, Middle East respiratory syndrome; NPIs, nonpharmaceutical interventions; SARS, severe acute respiratory syndrome.

EMERGING INFECTIOUS DISEASES CDC PERSPECTIVE Vol. 26, No. 6, June 2020

Identifying and Interrupting Superspreading Events—Implications for Control of Severe Acute Respiratory Syndrome Coronavirus 2

Thomas R. Frieden,[1] Christopher T. Lee[1]

Can J Anesth/J Can Anesth
https://doi.org/10.1007/s12630-020-01729-x

REVIEW ARTICLE/BRIEF REVIEW

Asymptomatic carriage and transmission of SARS-CoV-2: What do we know?

Patients asymptomatiques du SARS-CoV-2 et transmission du virus : Où en sont nos connaissances?

Susan Lee, MAS, MD, FRCPC · Paula Meyler, MD, FRCPC · Michelle Mozel, MSc · Tonia Tauh, MD, FRCPC · Richard Merchant, MD, FRCPC

Received: 29 April 2020 / Revised: 21 May 2020 / Accepted: 25 May 2020

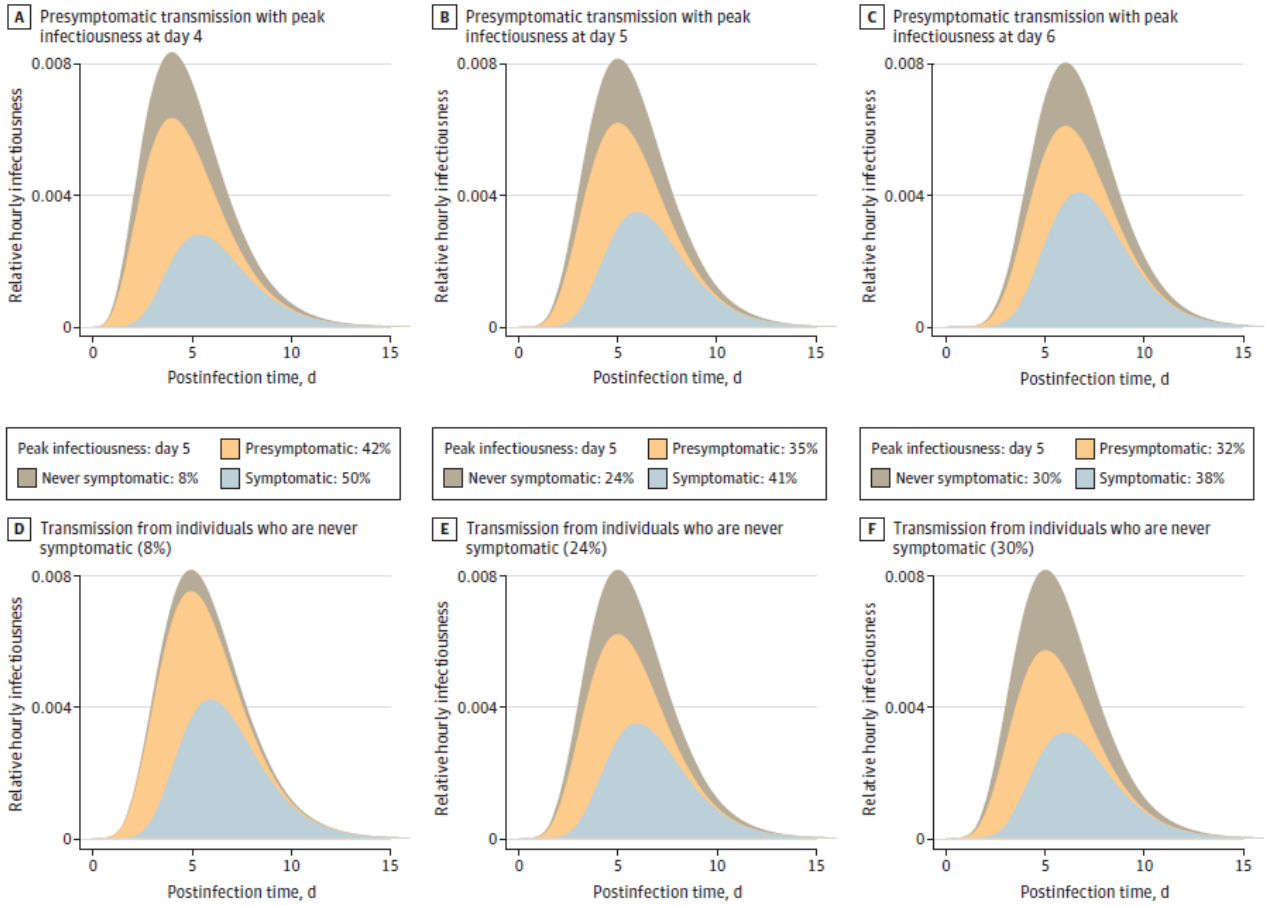
"Cerca de 50% das infeções resultam da contaminação a partir de pessoas infetadas assintomáticas"

JAMA Network Open

Original Investigation | Infectious Diseases

SARS-CoV-2 Transmission From People Without COVID-19 Symptoms

Michael A. Johansson, PhD; Talia M. Quandelacy, PhD, MPH; Sarah Kada, PhD; Pragati Venkata Prasad, MPH; Molly Steele, PhD, MPH; John T. Brooks, MD; Rachel B. Slayton, PhD, MPH; Matthew Biggerstaff, ScD, MPH; Jay C. Butler, MD



The top curve in each panel represents the average relative hourly infectiousness, such that while the lower curves change under different assumptions, the total hourly infectiousness equals 1 in all cases. Within each curve, the colored area indicates the proportion of transmission from each class of individuals. The portion attributed to individuals with symptoms (light blue) can also be interpreted as the maximum proportion of transmission that can be controlled by immediate isolation of all symptomatic cases. Panels A, B, and C show different levels of presymptomatic transmission. We calibrated infectiousness to peak at day 4 (A), 5 (B; median incubation period), or 6 (C) days. Panels D, E, and F show different proportions of transmission from individuals who are never symptomatic: 8% (C; eg, 10% never symptomatic and 75% relative infectivity), 24% (D; baseline, 30% never symptomatic and 75% relative infectivity), and 30% (E; eg, 30% never symptomatic and 100% relative infectivity).

Período de infecciosidade de uma pessoa infetada

Journal of Infection 81 (2020) 847–856

Contents lists available at ScienceDirect

Journal of Infection

journal homepage: www.elsevier.com/locate/jinf

Review

The duration of infectiousness of individuals infected with SARS-CoV-2

Kieran A. Walsh[a,1,*], Susan Spillane[a,1], Laura Comber[a], Karen Cardwell[a,b], Patricia Harrington[a], Jeff Connell[c], Conor Teljeur[a], Natasha Broderick[a], Cillian F. de Gascun[c], Susan M. Smith[b], Máirín Ryan[a,d,2], Michelle O'Neill[a,2]

[a] Health Information and Quality Authority, Smithfield, Dublin 7, Ireland
[b] Health Research Board Centre for Primary Care Research, Department of General Practice, Royal College of Surgeons in Ireland, 123 St. Stephens Green, Dublin 2, Ireland
[c] National Virus Reference Laboratory, University College Dublin, Belfield, Dublin 4, Ireland
[d] Department of Pharmacology & Therapeutics, Trinity College Dublin, Trinity Health Sciences, James Street, Dublin 8, Ireland

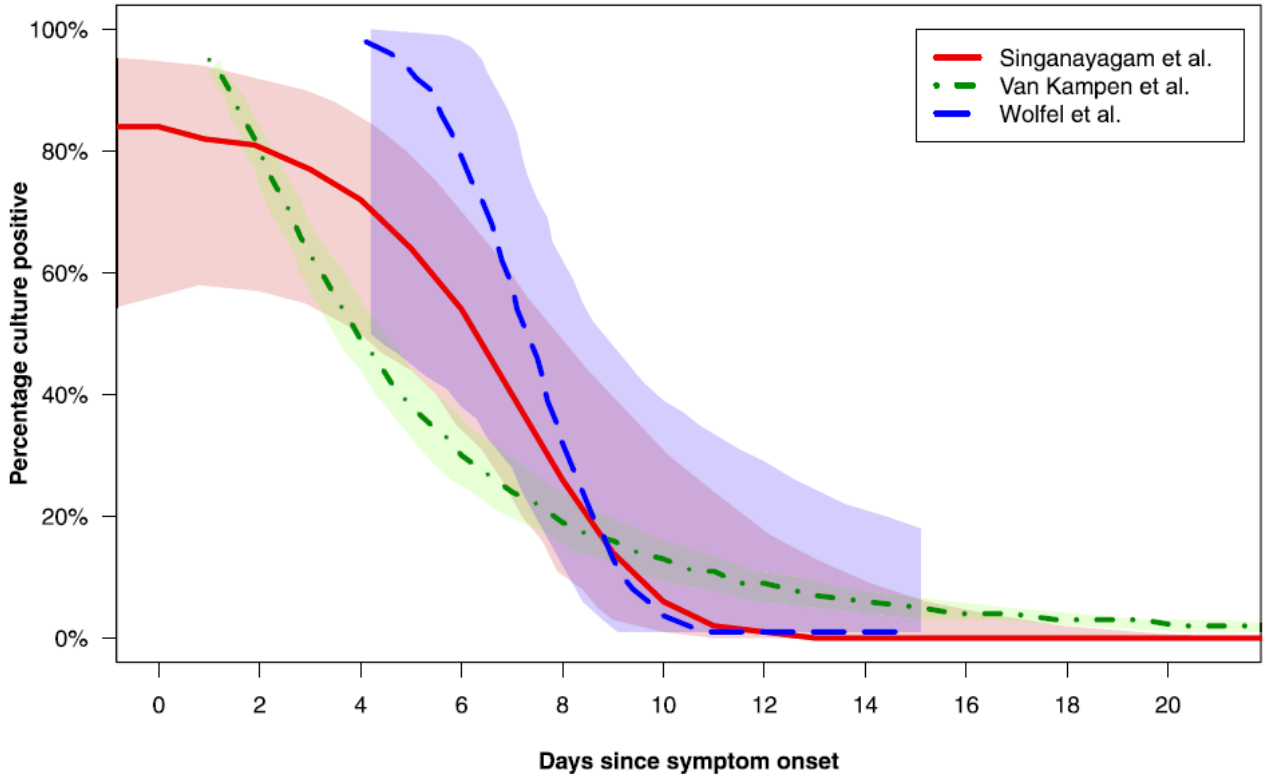


Fig. 3. Probability curves presented in 3 studies (Singanayagam et al., van Kampen et al., Wölfel et al.) which attempted to model the probability of successful virus culture versus duration of days of symptoms.[31–33] *Curves are presented with adaptation from the original presentation in the respective manuscripts in order to provide information for the first 20 days post symptom onset and to permit visual comparison of curves via overlay on a single plot. Lines (solid, dashed or dotted) depict estimated probability of positive virus culture* versus *days post symptom onset, while shaded areas depict 95% confidence intervals around these estimates.*

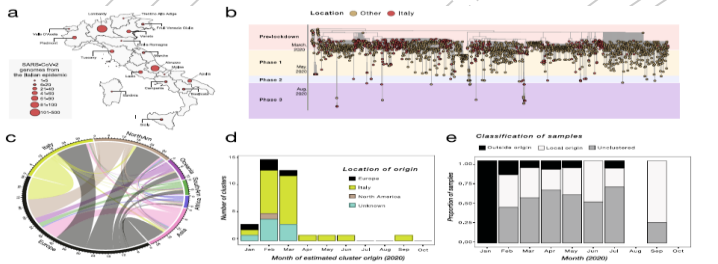


Fig. 3 Phylogenetic characterization of Italian SARS-CoV-2 sequences. **a** Map of Italy showing the number of SARS-CoV-2 genome sequences by region. The size of the circles indicates the number of new genomes available since the beginning of the epidemic in Italy. **b** Time-resolved maximum likelihood tree of 1421 SARS-CoV-2 sequences including 714 from Italy (red circles). **c** Chord diagram of estimated numbers of migration flows between the geographic areas. **d** Frequency of estimated geographical origins for identified transmission clusters involving Italy and originating in the months of January through October of 2020. **e** Frequency of Italian sequences (sampled from January through October) classified as unclustered (gray) or belonging to clusters with Italian (white) or non-Italian origins (black).

A eficácia das medidas de saúde pública … e o impacto do comportamento individual!!!

communications biology | COMMUNICATIONS BIOLOGY | (2021)4:489

ARTICLE

https://doi.org/10.1038/s42003-021-02025-0

SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy

Marta Giovanetti[1,2,3,22], Eleonora Cella[4,22], Francesca Benedetti[5,22], Brittany Rife Magalis[6,22], Vagner Fonseca[2,7,8], Silvia Fabris[3], Giovanni Campisi[9], Alessandra Ciccozzi[3], Silvia Angeletti[10], Alessandra Borsetti[11], Vittoradolfo Tambone[12], Caterina Sagnelli[13], Stefano Pascarella[14], Alberto Riva[15], Giancarlo Ceccarelli[16], Alessandro Marcello[17], Taj Azarian[4], Eduan Wilkinson[7], Tulio de Oliveira[7], Luiz Carlos Junior Alcantara[1,2], Roberto Cauda[18], Arnaldo Caruso[9], Natalie E. Dean[19], Cameron Browne[20], Jose Lourenco[21], Marco Salemi[6,8], Davide Zella[5,8] & Massimo Ciccozzi[3,8]

Apple Mobility Data Tool to Track User Movement, COVID-19 Spread

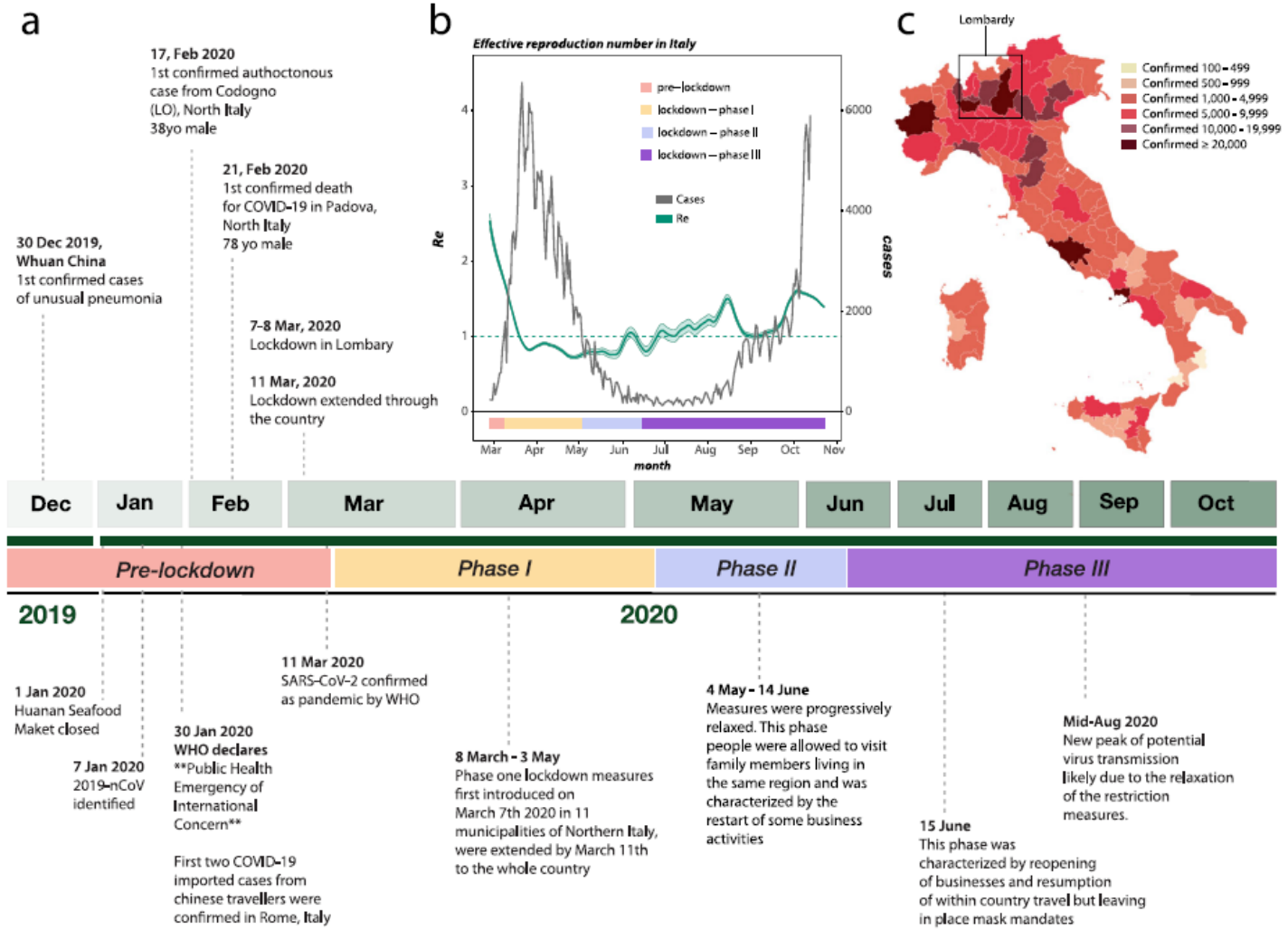


Fig. 1 History of SARS-CoV-2 epidemic in Italy. **a** Timeline of key events following the first confirmed cases of SARS-CoV-2 infection in Italy. **b** Epidemic curve showing the progression of reported daily viral infection numbers in Italy from the beginning of the epidemic in March (black) and changes in *Re* estimations in the same period (green), with lockdown phases indicated along the bottom. **c** Map of cumulative SARS-CoV-2 cases per 100,000 inhabitants in Italy up to Oct 2020.

Science of the Total Environment 736 (2020) 139487

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Optimal temperature zone for the dispersal of COVID-19

Zhongwei Huang, Jianping Huang *, Qianqing Gu, Pengyue Du, Hongbin Liang, Qing Dong

Collaborative Innovation Center for West Ecological Safety (CIWES), College of Atmospheric Sciences, Lanzhou University, Lanzhou 730000, China

A importância dos fatores meteriológicos: a temperatura, a humidade e o teor de ozono

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

On airborne transmission and control of SARS-Cov-2

Maosheng Yao [a,*], Lu Zhang [a], Jianxin Ma [b], Lian Zhou [c]

[a] College of Environmental Sciences and Engineering, Peking University, Beijing 100871, China
[b] Center for Disease Control and Prevention of Chaoyang District of Beijing, Beijing 100020, China
[c] Jiangsu Provincial Center for Disease Prevention and Control, Nanjing 210009, Jiangsu, China

Decreasing viability: SARS-Cov-2?

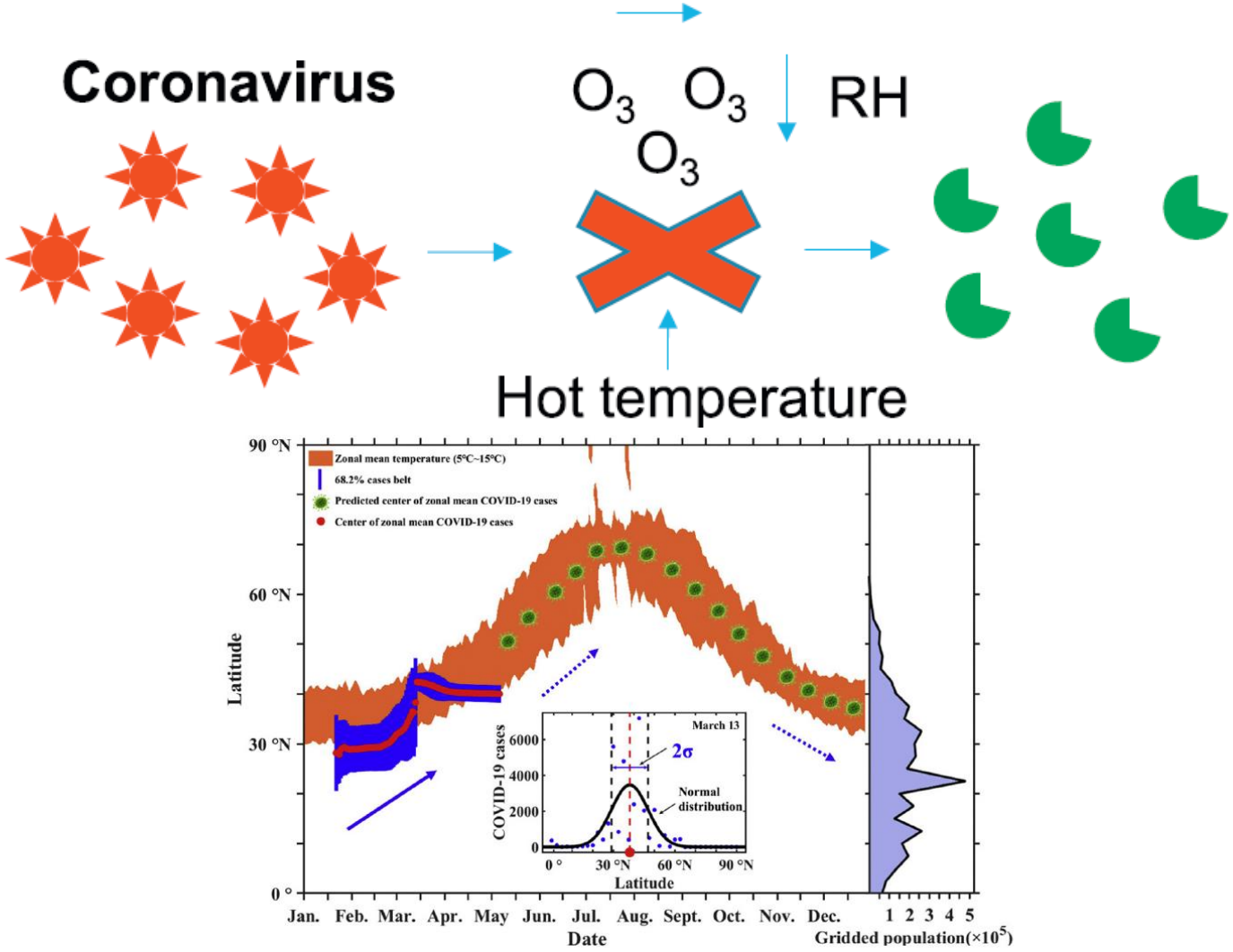


Fig. 3. (a) Relationship between cumulative cases of coronavirus disease 2019 (COVID-19) and temperatures from January 22, 2020 to May 6, 2020. The orange zone represents the latitudinal zone with a mean surface temperature between 5 °C and 15 °C in 2019 according to a reanalysis of the National Centers for Environmental Prediction data. Blue lines (red points) represent the standard derivation (center) of the fitted normal distribution curve of zonal mean cumulative COVID-19 cases each day. The illustration is an example of the normal distribution fitted on March 13, 2020. Notably, daily COVID-19 cases in several countries such as China, the United States, and Canada were counted separately for each province. (b) Zonal mean of the gridded populations from 1980 to 2010 developed by the Center for Global Environmental Research at the National Institute for Environmental Studies, Japan.

ACS OMEGA
http://pubs.acs.org/journal/acsodf
Perspective

Fomite Transmission, Physicochemical Origin of Virus–Surface Interactions, and Disinfection Strategies for Enveloped Viruses with Applications to SARS-CoV-2

Nicolas Castaño,‡ Seth C. Cordts,‡ Myra Kurosu Jalil,‡ Kevin S. Zhang,‡ Saisneha Koppaka, Alison D. Bick, Rajorshi Paul, and Sindy K. Y. Tang*

Cite This: ACS Omega 2021, 6, 6509−6527 Read Online

O que é capaz de descontaminar objetos ou superfícies

Received: 29 August 2020 | Revised: 28 October 2020 | Accepted: 12 November 2020
DOI: 10.1002/hsr2.213
REVIEW
Health Science Reports WILEY

Physicochemical susceptibility of SARS-CoV-2 to disinfection and physical approach of prophylaxis

Fatemeh Saadatpour | Fatemeh Mohammadipanah

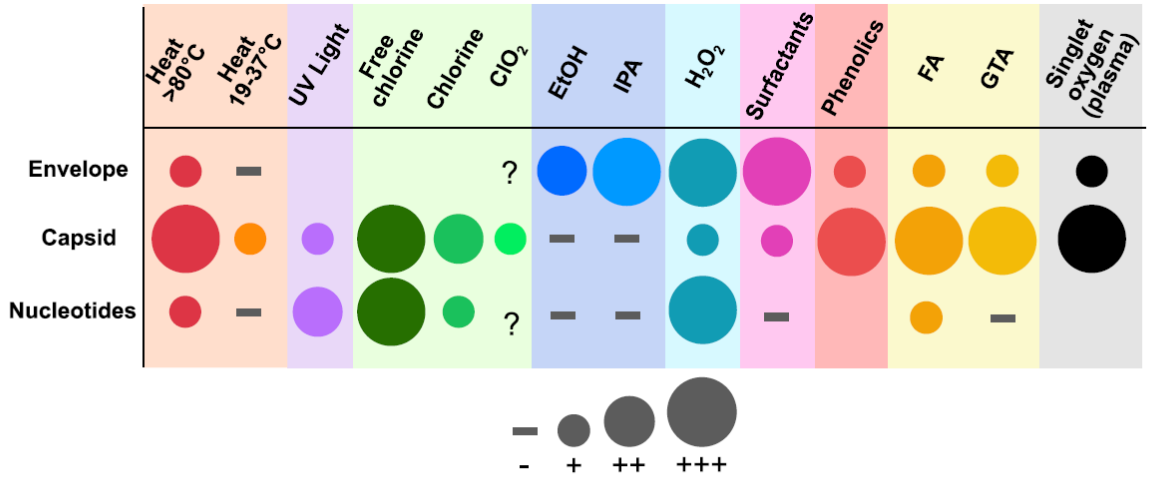


Figure 4. Viral structures targeted by different disinfectants. Symbol abbreviations: +, light damage; ++, moderate damage; +++, severe damage; − no damage; ?, uncertain/debated. Chemical abbreviations: ClO_2, chlorine dioxide; EtOH, ethanol; IPA, isopropanol; H_2O_2, hydrogen peroxide; FA formaldehyde; GTA, glutaraldehyde.[83] References: heat,[148,155,177] UV light,[148,177–180] chlorines,[148,181] EtOH and IPA, H_2O_2,[157] surfactants,[1] phenolics,[157] FA and GTA,[182,183] and singlet oxygen.[148,179,184]

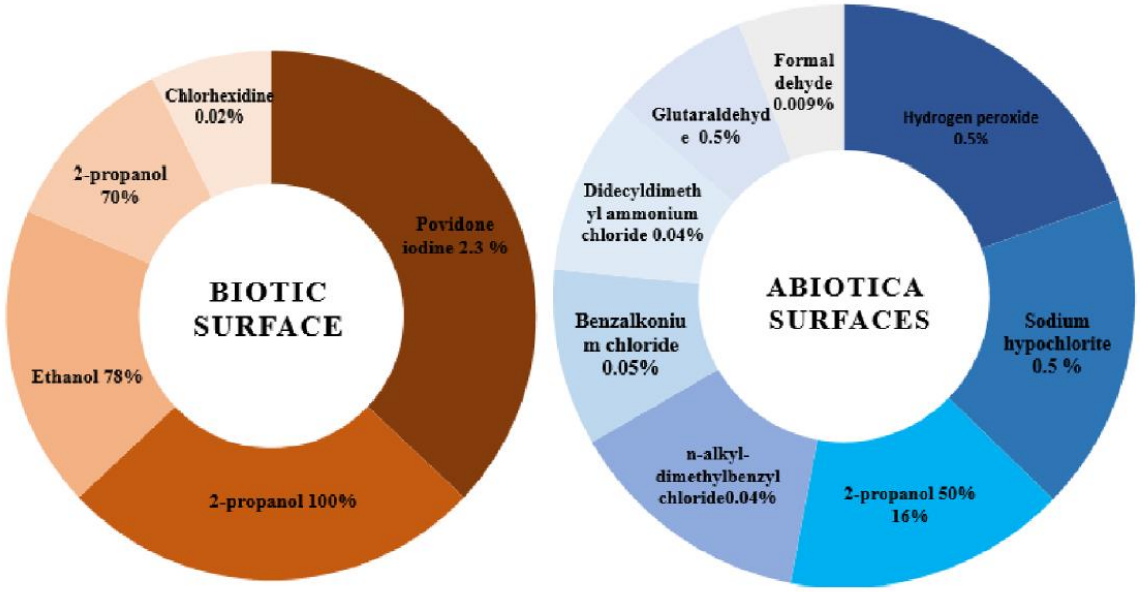
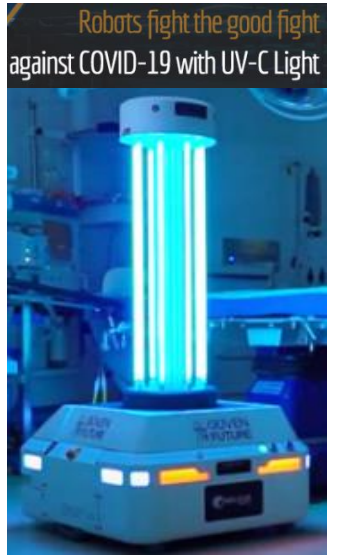


FIGURE 2 Hierarchy of the virucidal efficacy of the pure chemical compounds on H-CoV. Left: Antiseptics agents (on skin) and Right: Biocides (on abiotic surface and tools)

Uma panóplia de diferentes tecnologias que surgiram com a pandemia, nem sempre com eficácia inequivocamente comprovada…!!!

ESTERILIZADOR PLASMA PERÓXIDO DE HIDRÓGENO

Gerador de ozónio



UNIDADE DE DESCONTAMINAÇÃO PORTÁTIL

Hospitais e Clínicas estão Preparados para o Coronavírus?

Exaustão de Ar com FIltro Hepa

A Transmissão Vertical

nature COMMUNICATIONS

ARTICLE

https://doi.org/10.1038/s41467-020-17436-6 OPEN

Transplacental transmission of SARS-CoV-2 infection

Alexandre J. Vivanti[1,8], Christelle Vauloup-Fellous[2,8], Sophie Prevot[3], Veronique Zupan[4], Cecile Suffee[5], Jeremy Do Cao[6], Alexandra Benachi[1] & Daniele De Luca[4,7]

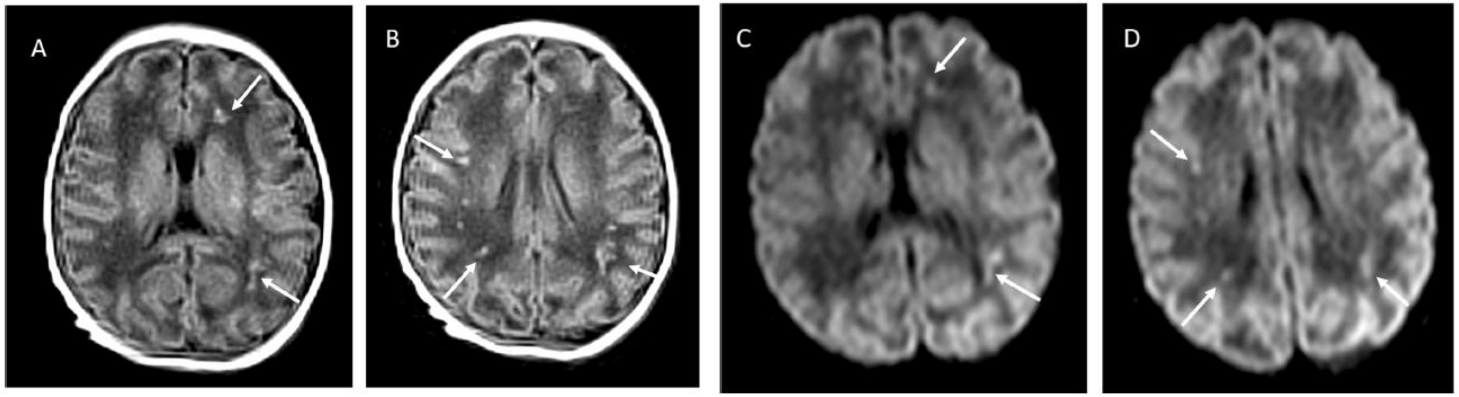
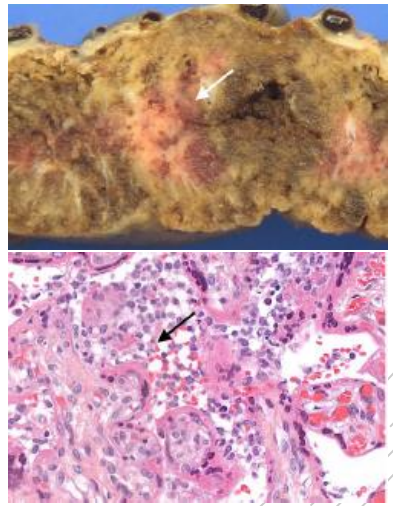


Fig. 2 Cerebral MRI performed at 11 days of life. a, **b** and **c**, **d** T1 and diffusion-weighted sequences, respectively. Images are taken at two different levels and show hyperintensities of the periventricular and subcortical frontal or parietal white matter (arrows).

Mother		Neonate	
Sample	**Viral load (Log)**	**Sample**	**Viral load (Log)**
Nasopharyngeal swab	4.22	Blood	1.15
Vaginal swab	0.63	Nasopharyngeal swab (DOL1)	2.21
Placenta	11.15	Rectal swab	4.71
Amniotic fluid	2.09	Nasopharyngeal swab (DOL3)	7.30
Blood	4.87	Nasopharyngeal swab (DOL18)	4.54



The Lancet Regional Health - Western Pacific 4 (2020) 100045

Contents lists available at ScienceDirect

The Lancet Regional Health - Western Pacific

journal homepage: www.elsevier.com/locate/lanwpc

Research paper

A study of breastfeeding practices, SARS-CoV-2 and its antibodies in the breast milk of mothers confirmed with COVID-19

Sicong Peng[a,1], Huaping Zhu[a,1], Lixia Yang[c], Li Cao[a], Xiaona Huang[d], Michelle Dynes[e], Anuradha Narayan[d], Jianbo Xia[b], Yang Chen[a], Pei Zhang[a], Hongyan Liu[a], Hua Li[a], Shiwen Xia[a,*]

[a] Department of Neonatology, Maternal and Child Health Hospital of Hubei Province, Wuhan, Hubei 430070, China
[b] Department of Laboratory Medicine, Maternal and Child Health Hospital of Hubei Province, Wuhan, Hubei, China
[c] Department of Neonatology, Xiaochang First People's Hospital, Xiaochang, Hubei, China
[d] Health, Nutrition and WASH, UNICEF China, Beijing, China
[e] UNICEF East Asia and Pacific Regional Office, Bangkok, Thailand

Research Letter

August 19, 2020

Evaluation for SARS-CoV-2 in Breast Milk From 18 Infected Women

Christina Chambers, PhD, MPH[1]; Paul Krogstad, MD[2]; Kerri Bertrand, MPH[1]; et al

Author Affiliations | Article Information

JAMA. 2020;324(13):1347-1348. doi:10.1001/jama.2020.15580

A transmissão pela amamentação

frontiers in Pediatrics

BRIEF RESEARCH REPORT

Detection of SARS-CoV-2 in Milk From COVID-19 Positive Mothers and Follow-Up of Their Infants

Enrico Bertino[1], Guido Eugenio Moro[2], Giuseppe De Renzi[3], Giuseppina Viberti[3], Rossana Cavallo[4,5], Alessandra Coscia[1], Carlotta Rubino[1], Paola Tonetto[1], Stefano Sottemano[1], Maria Francesca Campagnoli[6], Antonella Soldi[1], Michael Mostert[1], Francesco Cresi[1*], David Lembo[7] and Collaborative Research Group on SARS-CoV-2 in Human Milk

Ann. N.Y. Acad. Sci. ISSN 0077-8923

ANNALS OF THE NEW YORK ACADEMY OF SCIENCES

Special Issue: Annals *Reports*

Review

Transmission of SARS-CoV-2 through breast milk and breastfeeding: a living systematic review

Elizabeth Centeno-Tablante,[1,a] Melisa Medina-Rivera,[1,a] Julia L. Finkelstein,[1] Pura Rayco-Solon,[2] Maria Nieves Garcia-Casal,[3] Lisa Rogers,[3] Kate Ghezzi-Kopel,[4] Pratiwi Ridwan,[1] Juan Pablo Peña-Rosas,[3] and Saurabh Mehta[1]

[1]Division of Nutritional Sciences, Cornell University, Ithaca, New York. [2]Department of Maternal, Newborn, Child and Adolescent Health and Ageing, World Health Organization, Geneva, Switzerland. [3]Department of Nutrition and Food Safety, World Health Organization, Geneva, Switzerland. [4]Albert R. Mann Library, Cornell University, Ithaca, New York

- **O que é que se deve dizer acerca desta importante problemática**
  - **O vírus pode ser detetado no leite materno através de testes PCR;**
  - **A presença de vírus infetante, através de culturas, não foi demonstrada;**
  - **A transmissão da infeção por via digestiva não está confirmada;**
  - **A presença de imunoglobulinas anti SARS CoV-2 (IgA, IgM e IgG) bem como da lactoferrina, podem ter efeito protetor por inibirem a replicação do vírus no leite da mãe;**
  - **A transmissão que possa eventualmente ocorrer da mãe para o RN dever-se-á, com muito maior probabilidade, à inalação de aerossóis ou por contacto com partículas infetantes presentes na pele da mãe ou em objetos contaminados, do que pelo próprio leite;**
  - **As vantagens da amamentação superam largamente os seus potenciais riscos;**
  - **Suspender a amamentação deve resultar de uma opção dos pais, a quem se devem fornecer os conhecimentos cientificamente comprovados necessários à sua decisão informada (sobretudo por parte da mãe) e, nunca, decorrente de qualquer parecer médico.**

Urologia Internationalis

Original Paper

Urol Int 2020;104:678–683
DOI: 10.1159/000510531

Received: June 23, 2020
Accepted: July 27, 2020
Published online: August 11, 2020

Investigation of SARS-CoV-2 in Semen of Patients in the Acute Stage of COVID-19 Infection

Bircan Kayaaslan[a] Gulay Korukluoglu[b] Imran Hasanoglu[a] Ayse Kaya Kalem[a] Fatma Eser[a] Esragul Akinci[c] Rahmet Guner[a]

[a]Infectious Disease and Clinical Microbiology, Ankara Yildirim Beyazit University, Ankara City Hospital, Ankara, Turkey; [b]Clinical Microbiology, Virology, National Virology Laboratory, Turkish Public Health Institution, Ankara, Turkey; [c]Infectious Disease and Clinical Microbiology, University of Health Sciences, Ankara City Hospital, Ankara, Turkey

International Journal of Surgery 84 (2020) 156–158

Contents lists available at ScienceDirect

International Journal of Surgery

journal homepage: www.elsevier.com/locate/ijsu

Correspondence

SARS-CoV-2 in semen: Potential for sexual transmission in COVID-19

Khan Sharun[1]

A Problemática da transmissão sexual

PLOS ONE

RESEARCH ARTICLE

Female reproductive tract has low concentration of SARS-CoV2 receptors

Jyoti Goad[1,2], Joshua Rudolph[3], Aleksandar Rajkovic[1,2]*

1 Department of Pathology, University of California, San Francisco, San Francisco, California, United States of America, 2 Department of OB-GYN, University of California, San Francisco, San Francisco, California, United States of America, 3 Department of Medicine, Lung Biology Center, University of California, San Francisco, San Francisco, California, United States of America

Received: 12 May 2020 | Revised: 30 May 2020 | Accepted: 8 June 2020

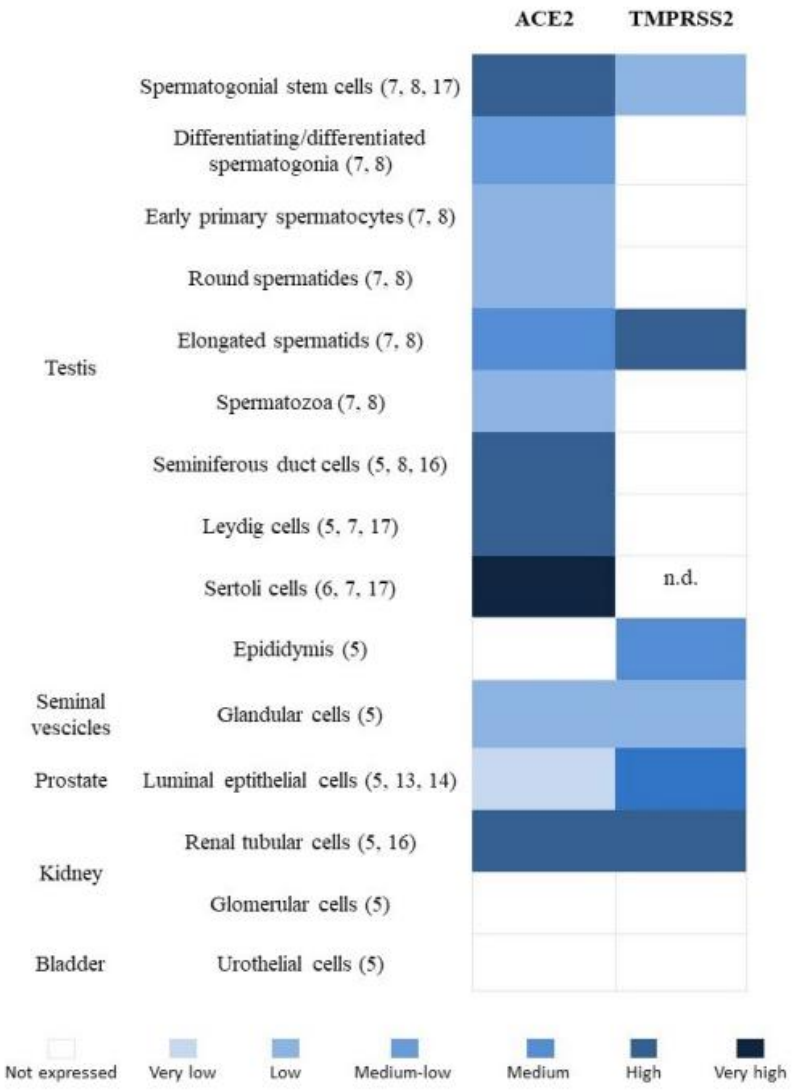
DOI: 10.1111/andr.12839

OPINION ARTICLE

ANDROLOGY WILEY

SARS-CoV-2 in the semen: Where does it come from?

Claudia Massarotti[1] | Andrea Garolla[2] | Elena Maccarini[1] | Paola Scaruffi[1] | Sara Stigliani[1] | Paola Anserini[1] | Carlo Foresta[2]



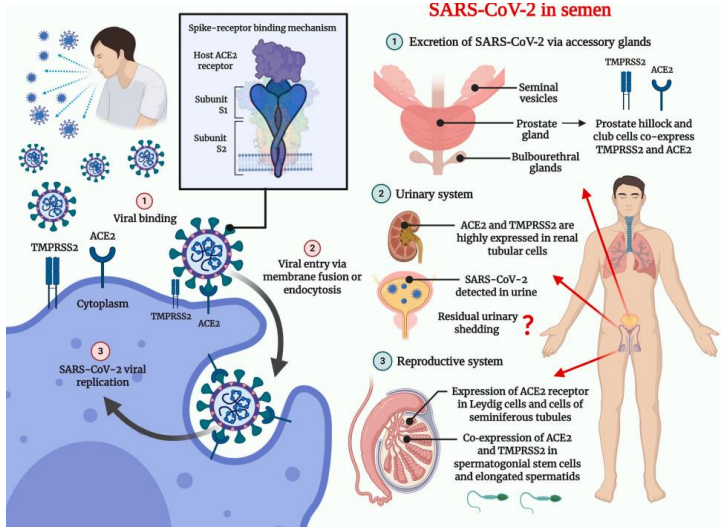


FIGURE 1 Levels of *ACE2* and *TMPRSS2* expression in human cells of the male urogenital system. n.d., not determined

Environmental Research 188 (2020) 109861

Contents lists available at ScienceDirect

Environmental Research

journal homepage: www.elsevier.com/locate/envres

Review article

Influence of airborne transmission of SARS-CoV-2 on COVID-19 pandemic. A review

José L. Domingo [a,*], Montse Marquès [a], Joaquim Rovira [a,b]

[a] Laboratory of Toxicology and Environmental Health, School of Medicine, Universitat Rovira I Virgili, Sant Llorens 21, 43201, Reus, Catalonia, Spain
[b] Environmental Engineering Laboratory, Departament D'Enginyeria Química, Universitat Rovira I Virgili, Av. Paisos Catalans 26, 43007, Tarragona, Catalonia, Spain

Em resumo

Contents lists available at ScienceDirect

Travel Medicine and Infectious Disease

journal homepage: www.elsevier.com/locate/tmaid

Review

SARS-CoV-2 jumping the species barrier: Zoonotic lessons from SARS, MERS and recent advances to combat this pandemic virus

Kuldeep Dhama [a,**], Shailesh Kumar Patel [a], Khan Sharun [b], Mamta Pathak [a], Ruchi Tiwari [c], Mohd Iqbal Yatoo [d], Yashpal Singh Malik [e], Ranjit Sah [f], Ali A. Rabaan [g], Parmod Kumar Panwar [h], Karam Pal Singh [a], Izabela Michalak [i], Wanpen Chaicumpa [j], Dayron F. Martinez-Pulgarin [k], D. Katterine Bonilla-Aldana [k,l], Alfonso J. Rodriguez-Morales [k,m,n,*]

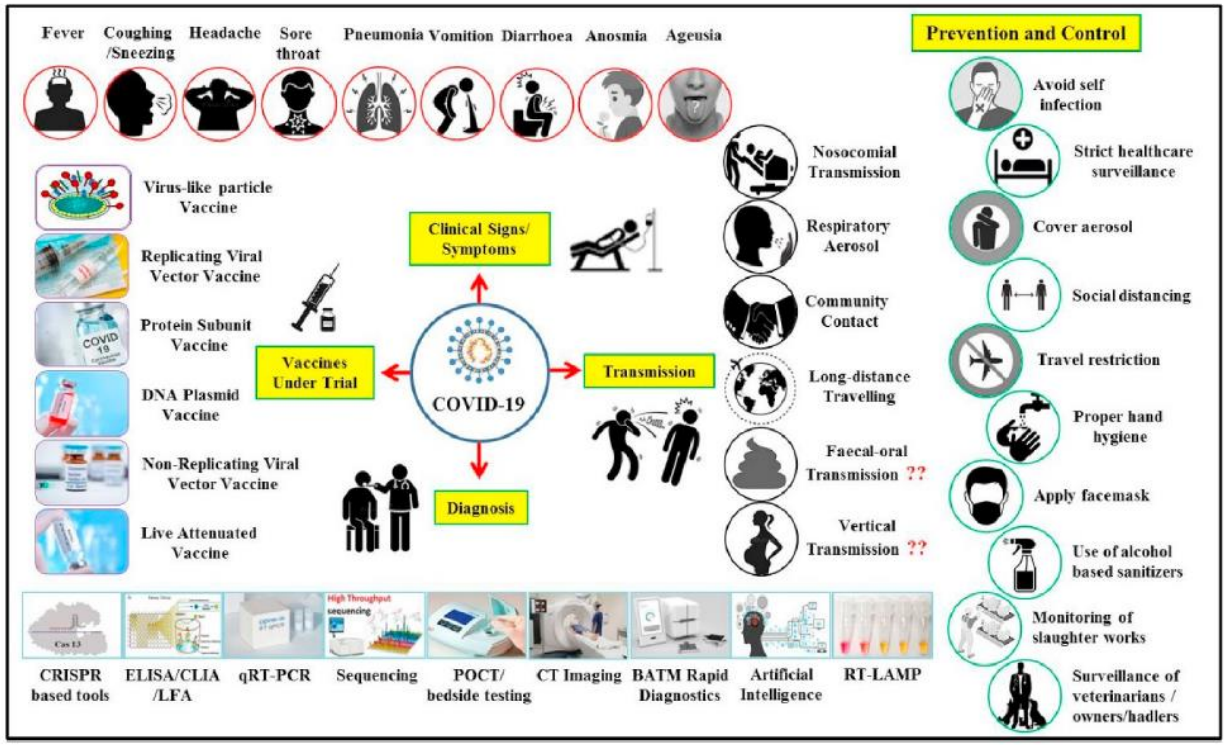
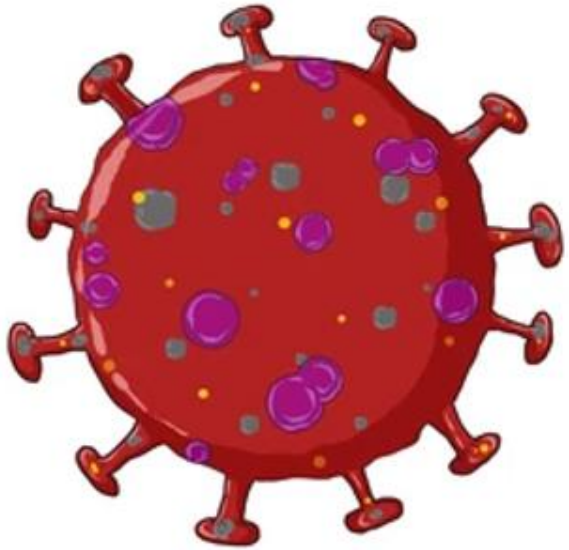
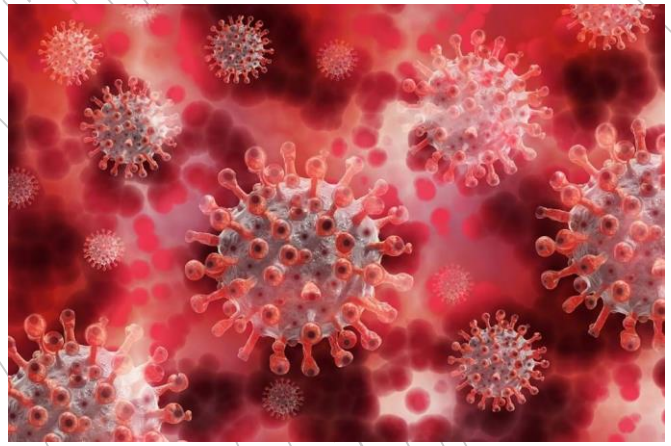


Fig. 2. Schematic illustration of clinical signs, modes of transmission, advances in diagnosis, and vaccine designing along with salient prevention and control strategies to counter COVID-19.



Algumas das muitas dúvidas que estão, ainda hoje, por serem cabalmente respondidas



Journal of Infection and Public Health 14 (2021) 474–477

Contents lists available at ScienceDirect

Journal of Infection and Public Health

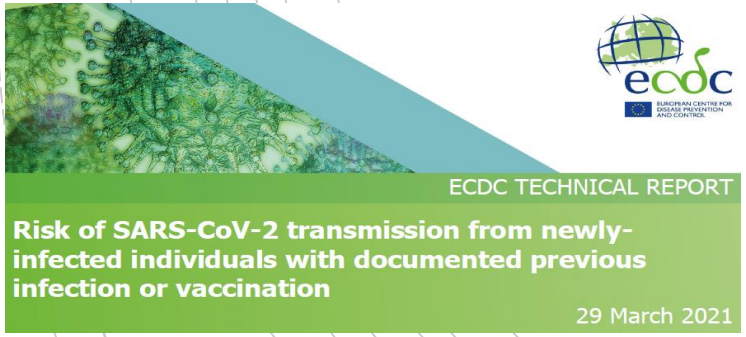
journal homepage: http://www.elsevier.com/locate/jiph

Reinfection, recurrence, or delayed presentation of COVID-19? Case series and review of the literature

Fatehi Elzein[a,*], Ahmed Ibrahim[a], Fatima Alshahrani[b], Mervat Mahrous[c,d], Esam Murshid[c], Turki Aldhehyan[a], Ghadah Almutiri[a], Meshal Altowairqi[a], Medina Ahmed[f], Mohammed Alsaeed[a], Eid Alsufyani[a], Nouf Alnawshan[e]

[a] Internal Medicine Department, Prince Sultan Military Medical City (PSMMC), Riyadh, Saudi Arabia
[b] Infectious Diseases Unit, College of Medicine, King Saud University Medical City, Saudi Arabia
[c] PSMMC, Department of Oncology, Riyadh, Saudi Arabia
[d] Faculty of Medicine, Minia University, Egypt
[e] PSMMC, Department of Neurology, Riyadh, Saudi Arabia
[f] PSMMC, Department of Microbiology, Saudi Arabia

A complexa problemática das reinfeções…



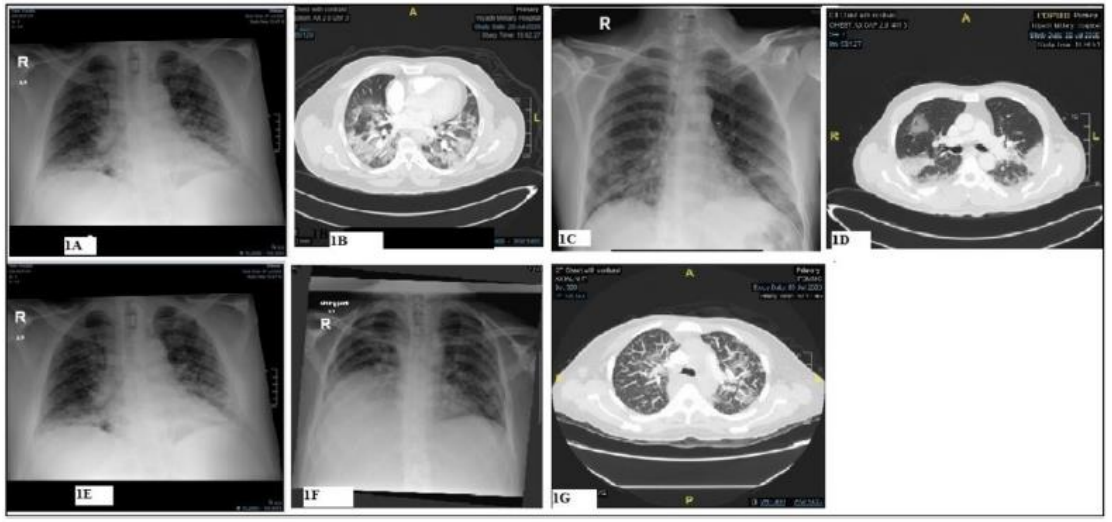


Fig. 1. Chest X-ray and CT scan of patient 1 (A & B), patient 2 (C & D), patient 3 (E) and patient 4 (F & G).

European Journal of Clinical Microbiology & Infectious Diseases (2021) 40:1–12
https://doi.org/10.1007/s10096-020-04057-6

REVIEW

Is recurrence possible in coronavirus disease 2019 (COVID-19)? Case series and systematic review of literature

Anna Gidari[1] · Marco Nofri[1] · Luca Saccarelli[2] · Sabrina Bastianelli[1] · Samuele Sabbatini[3] · Silvia Bozza[3] · Barbara Camilloni[3] · Igino Fusco-Moffa[4] · Claudia Monari[3] · Edoardo De Robertis[2] · Antonella Mencacci[3] · Daniela Francisci[1]

Received: 24 July 2020 / Accepted: 30 September 2020 / Published online: 10 October 2020

Recurrent SARS-CoV-2 RNA positivity after COVID-19: a systematic review and meta-analysis

nature

Characteristics of COVID-19 Recurrence: A Systematic Review and Meta-Analysis

TUNG HOANG

Annals of Global Health

… e das recorrências!

Taylor & Francis

INFECTIOUS DISEASES, 2021; VOL. 53, NO. 5, 315–324
https://doi.org/10.1080/23744235.2020.1871066

REVIEW ARTICLE

A systematic review on the recurrence of SARS-CoV-2 virus: frequency, risk factors, and possible explanations

Seyed Mohammad Piri[a]*, Maryam Edalatfar[a]*, Sina Shool[b]*, Mohammad Naser Jalalian[c] and Soheil Tavakolpour[d,e]

[a]Sina Trauma and Surgery Research Center, Tehran University of Medical Sciences, Tehran, Iran; [b]Faculty of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran; [c]Faculty of Medicine, Tehran University of Medical Sciences, Tehran, Iran; [d]Infectious Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran; [e]Dana-Farber Cancer Institute, Harvard Medical School, Boston, MA, USA

European Journal of Clinical Microbiology & Infectious Diseases
https://doi.org/10.1007/s10096-020-04088-z

REVIEW

Recurrence of SARS-CoV-2 viral RNA in recovered COVID-19 patients: a narrative review

Thi Loi Dao[1,2,3] · Van Thuan Hoang[1,2,3] · Philippe Gautret[1,2]

Received: 10 September 2020 / Accepted: 23 October 2020

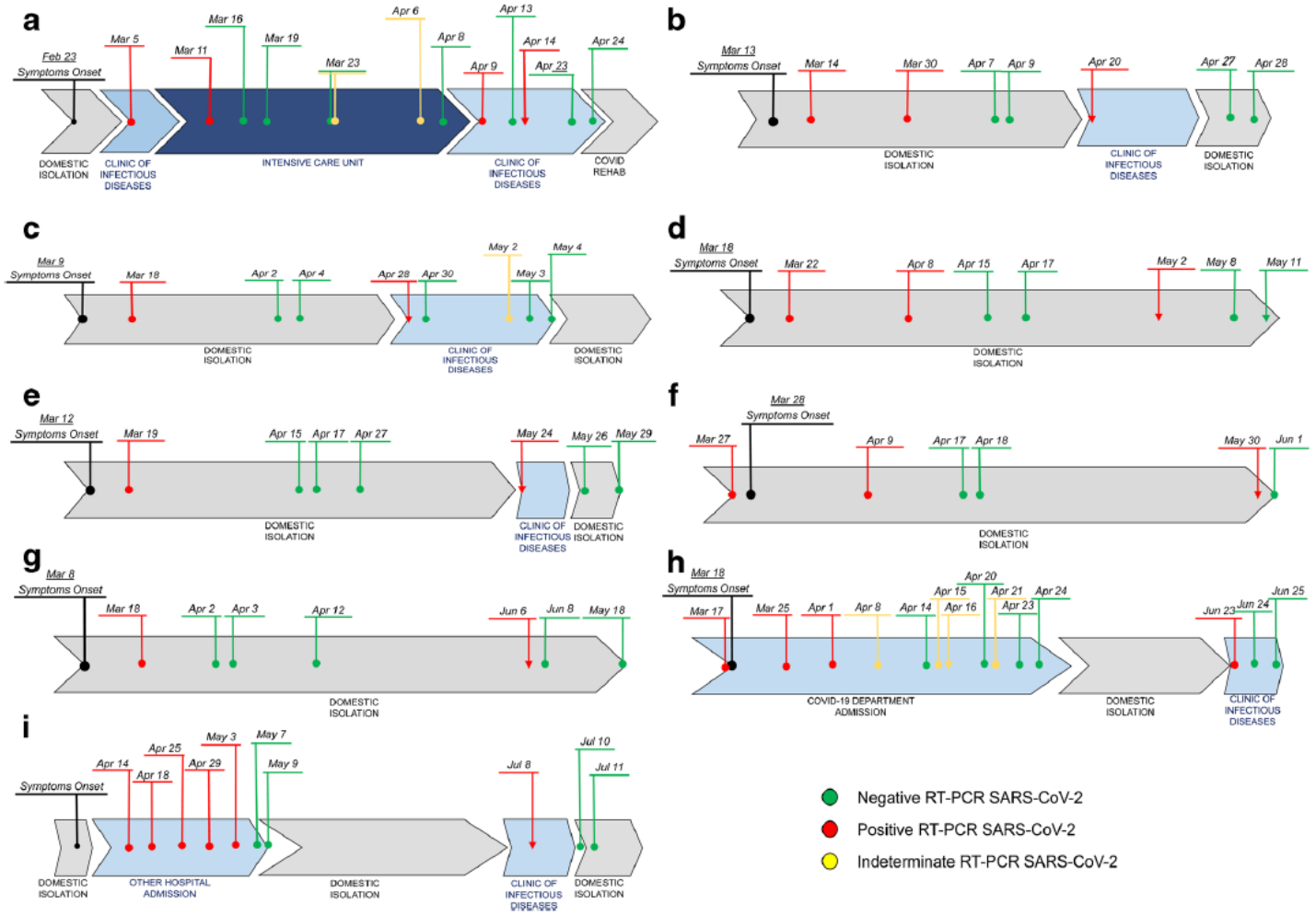
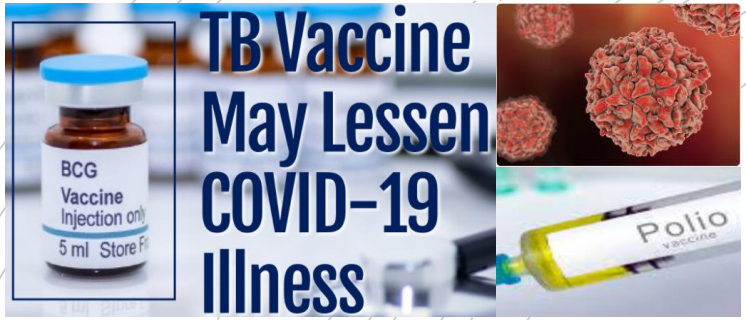


Fig. 1 Respiratory sample timeline of each described case. Above the timeline: time of onset of symptoms and collection of samples. Under the timeline: movement of patient (e.g., hospitalization, discharge, domestic isolation). Black: onset of symptoms. Red: positive sample for severe acute respiratory syndrome (SARS-CoV-2). Green: negative sample for SARS-CoV-2. Yellow: indeterminate sample for SARS-CoV-2. Point: exam performed with traditional RT-PCR. Arrow: exam performed with Xpert® Xpress SARS-CoV-2, Cepheid



Check for updates
CORONAVIRUS
Covid-19: Do many people have pre-existing immunity?
It seemed a truth universally acknowledged that the human population had no pre-existing immunity to SARS-CoV-2, but is that actually the case? **Peter Doshi** explores the emerging research on immunological responses
thebmj

Qual a importância da imunização adquirida a infeções anteriores por outros coronavírus?

Signal Transduction and Targeted Therapy
nature
International journal of science
www.nature.com/sigtrans
RESEARCH HIGHLIGHT OPEN

COVID-19: cross-immunity of viral epitopes may influence severity of infection and immune response

Junaid Kashir[1,2], Khaled AlKattan[1] and Ahmed Yaqinuddin[1]

Signal Transduction and Targeted Therapy (2021)6:102 ; https://doi.org/10.1038/s41392-021-00490-x

RESEARCH

RESEARCH ARTICLE SUMMARY

Science
AAAS

CORONAVIRUS

Viral epitope profiling of COVID-19 patients reveals cross-reactivity and correlates of severity

Ellen Shrock*, Eric Fujimura*, Tomasz Kula†, Richard T. Timms†, I-Hsiu Lee, Yumei Leng, Matthew L. Robinson, Brandon M. Sie, Mamie Z. Li, Yuezhou Chen, Jennifer Logue, Adam Zuiani, Denise McCulloch, Felipe J. N. Lelis, Stephanie Henson, Daniel R. Monaco, Meghan Travers, Shaghayegh Habibi, William A. Clarke, Patrizio Caturegli, Oliver Laeyendecker, Alicja Piechocka-Trocha, Jonathan Z. Li, Ashok Khatri, Helen Y. Chu, MGH COVID-19 Collection & Processing Team, Alexandra-Chloé Villani, Kyle Kays, Marcia B. Goldberg, Nir Hacohen, Michael R. Filbin, Xu G. Yu, Bruce D. Walker, Duane R. Wesemann, H. Benjamin Larman, James A. Lederer, Stephen J. Elledge‡

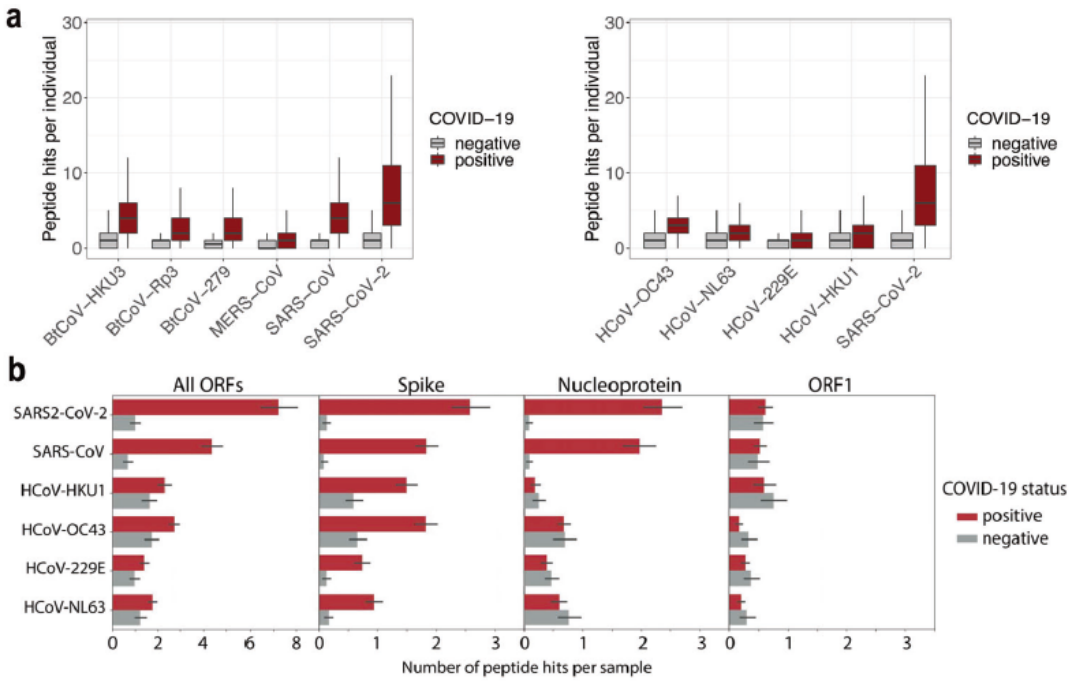


Fig. 1 Representative indicators of the findings by Shrock et al.,[1] suggesting significant overlap between SARS-CoV-2 proteins with other coronaviruses in human patients. **a** Box plots illustrating the number of peptide hits from the indicated coronaviruses in confirmed COVID-19 patients and pre-COVID-19 era controls (negative for SARS-CoV-2). Cross-reactivity toward SARS-CoV-2 peptides was observed in pre-COVID-19 era samples, while COVID-19 patients also exhibited cross-reactivity with other common hCoVs, SARS-CoV, and MERS-CoV. **b** Bar graphs depicting the average number of peptides derived from SARS-CoV-2, SARS-CoV, and each of the four most common hCoVs significantly enriched per sample following IgG immunoprecipitation in the experiments of Shrock et al.[1] The ORF1 region of SARS-CoV-2 exhibited greatest comparative matches between patients diagnosed with COVID-19 versus those that tested negative, indicating a potentially large degree of overlap between previous CoV and SARS-CoV-2 infection, whereby previous CoV perhaps reduced the severity of SARS-CoV-2 infection. Figure adapted from Shrock et al.,[1] with permission

Qual a real importância da infeção nas crianças e adolescentes (2-20 anos) na dinâmica epidemiológica ao nível da comunidade?

Household transmission of SARS-CoV-2 and risk factors for susceptibility and infectivity in Wuhan: a retrospective observational study

Fang Li*, Yuan-Yuan Li*, Ming-Jin Liu*, Li-Qun Fang, Natalie E Dean, Gary W K Wong, Xiao-Bing Yang, Ira Longini, M Elizabeth Halloran, Huai-Ji Wang, Pu-Lin Liu, Yan-Hui Pang, Ya-Qiong Yan, Su Liu, Wei Xia, Xiao-Xia Lu, Qi Liu, Yang Yang, Shun-Qing Xu

www.thelancet.com/infection Vol 21 May 2021 THE LANCET

Interpretation Within households, children and adolescents were less susceptible to SARS-CoV-2 infection but were more infectious than older individuals. Presymptomatic cases were more infectious and individuals with asymptomatic infection less infectious than symptomatic cases. These findings have implications for devising interventions for blocking household transmission of SARS-CoV-2, such as timely vaccination of eligible children once resources become available.

Our study has implications for forecasting and control of the global pandemic of SARS-CoV-2. Differential susceptibility and infectivity between age groups, as well as other epidemiological parameters estimated in this study, are key inputs for modelling studies projecting the future trajectory of the pandemic. The relatively high infectivity of children in households should be considered carefully when making decisions around school reopenings, as infected children can pass the virus to their family members. Finally, given the vulnerability of infants to infection, their caregivers should be prioritised for vaccination.

THE LANCET

www.thelancet.com/infection Vol 21 May 2021

Implications of all the available evidence
The high infectivity of children with SARS-CoV-2 infection highlights the need for careful planning of school reopening. Additionally, the susceptibility of infants supports caregivers of infants being prioritised for vaccination. When feasible, cases could be isolated and household contacts quarantined away from their homes to prevent household transmission, particularly when presymptomatic.

Pathology (December 2020) 52(7), pp. 801–808

FOCUS ON SARS-COV-2

SARS-CoV-2 in children: spectrum of disease, transmission and immunopathological underpinnings

PHOEBE C. M. WILLIAMS[1,2], ANNALEISE R. HOWARD-JONES[3], PETER HSU[4,5], PAMELA PALASANTHIRAN[1,2], PAUL E. GRAY[1,2], BRENDAN J. MCMULLAN[1,2], PHILIP N. BRITTON[3,5,6], ADAM W. BARTLETT[1,2]

[1]*Department of Immunology and Infectious Diseases, Sydney Children's Hospital, Randwick, NSW, Australia;* [2]*School of Women's and Children's Health, UNSW Sydney, NSW, Australia;* [3]*Department of Infectious Diseases and Microbiology, The Children's Hospital at Westmead, NSW, Australia;* [4]*Department of Allergy and Immunology and Kids Research, The Children's Hospital at Westmead, NSW, Australia;* [5]*Discipline of Child and Adolescent Health, University of Sydney, NSW, Australia;* [6]*Marie Bashir Institute, University of Sydney, NSW, Australia*

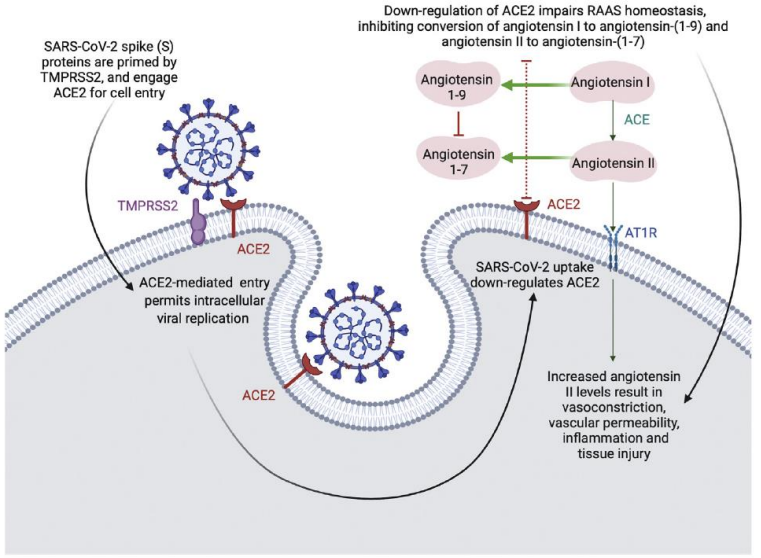


Fig. 1 Host cell interaction with SARS-CoV-2. ACE, angiotensin converting enzyme; AT1R, angiotensin 1 receptor; RAAS, renin-angiotensin-aldosterone system; TMPRSS2, transmembrane protease serine 2.

Science of the Total Environment 744 (2020) 140946

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Review

SARS-CoV-2 in the environment: Modes of transmission, early detection and potential role of pollutions

Khaled Al Huraimel, Mohamed Alhosani, Shabana Kunhabdulla, Mohammed Hashem Stietiya *

Division of Consultancy, Research & Innovation (CRI), Sharjah Environment Company – Bee'ah, Sharjah, United Arab Emirates

Qual a real dimensão do contributo da poluição ambiental ?

Science of the Total Environment 729 (2020) 138474

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

Factors determining the diffusion of COVID-19 and suggested strategy to prevent future accelerated viral infectivity similar to COVID

Mario Coccia

CNR – National Research Council of Italy, Research Institute on Sustainable Economic Growth, Collegio Carlo Alberto, Via Real Collegio, 30-10024 Moncalieri, Torino, Italy
Yale School of Medicine, 310 Cedar Street, Lauder Hall, New Haven, CT 06510, USA

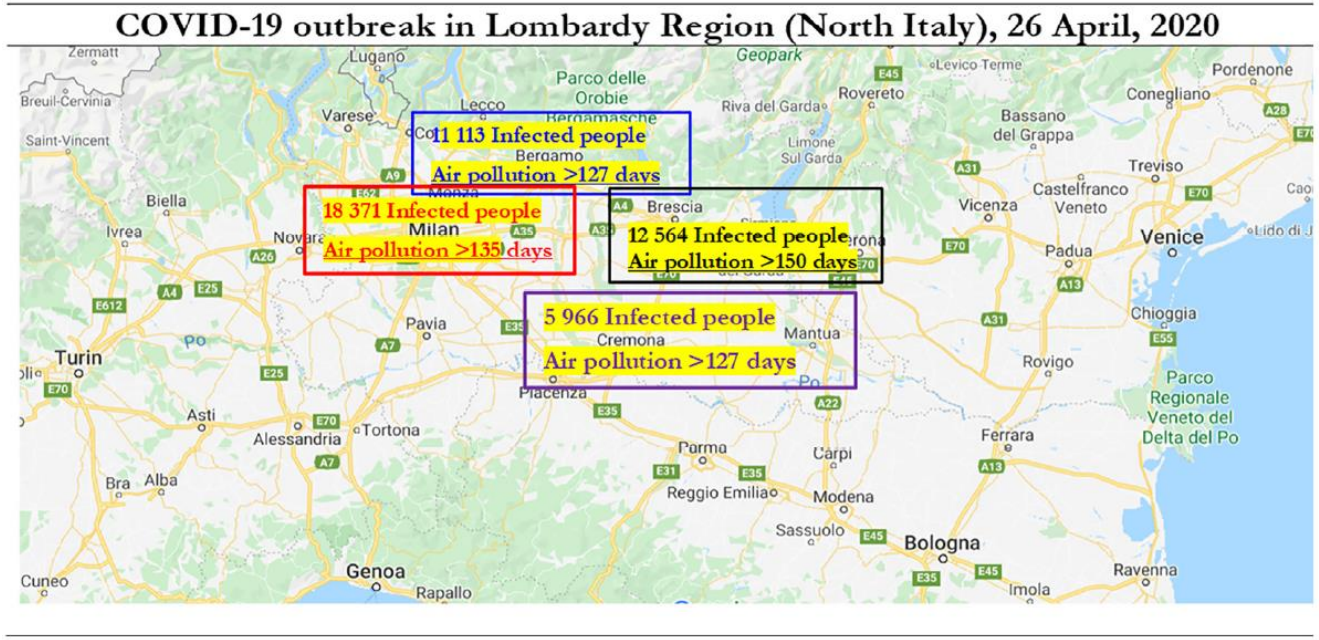
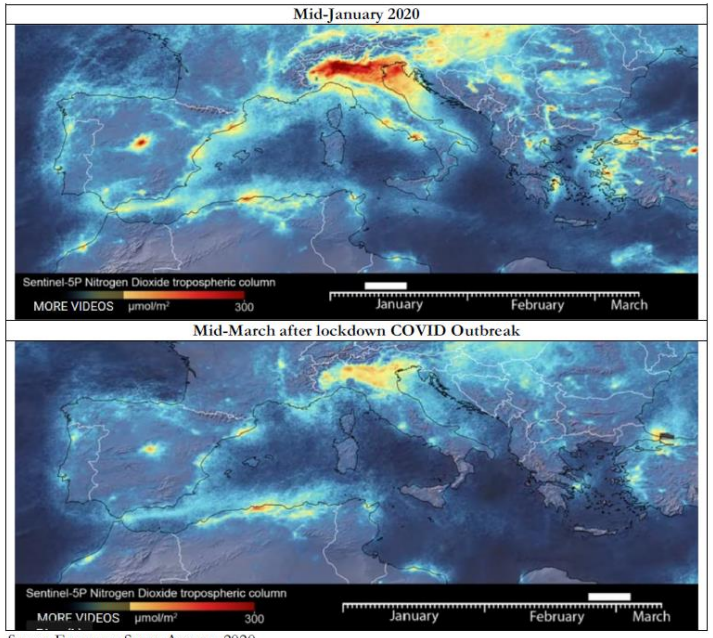
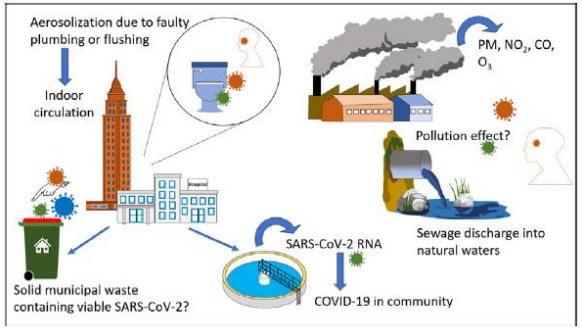


Fig. 3. COVID-19 Outbreak (number of infected individual on 26 April 2020) and days exceeding the limits set for PM_{10} or ozone.



Sources: European Space Agency, 2020.

Fig. 4. Reduction Nitrogen Dioxide before (January 2020) and during lockdown (February–March 2020) because of COVID-19 Outbreak in Italy.
Sources: European Space Agency (2020).



International Journal of Environmental Research and Public Health

MDPI

Review

Can Air-Conditioning Systems Contribute to the Spread of SARS/MERS/COVID-19 Infection? Insights from a Rapid Review of the Literature

Francesco Chirico [1,2,*], Angelo Sacco [3], Nicola Luigi Bragazzi [4] and Nicola Magnavita [1,5]

1 Post-Graduate School of Occupational Health, Università Cattolica del Sacro Cuore, 00168 Roma, Italy; nicola.magnavita@unicatt.it
2 Health Service Department, State Police, Ministry of Interior, 20125 Milan, Italy
3 Local Healthcare Unit Roma 2, 00155 Roma, Italy; angelo.sacco@alice.it
4 Laboratory for Industrial and Applied Mathematics (LIAM), Department of Mathematics and Statistics, York University, Toronto, ON M3J 1P3, Canada; bragazzi@yorku.ca
5 Department of Woman/Child & Public Health, Fondazione Policlinico A. Gemelli IRCCS, 00168 Roma, Italy; nicola.magnavita@policlinicogemelli.it
* Correspondence: medlavchirico@gmail.com; Tel.: +39-3346-904-194

Received: 21 July 2020; Accepted: 18 August 2020; Published: 20 August 2020

check for updates

Podem os sistemas de ventilação no interior dos edifícios facilitar a transmissibilidade?

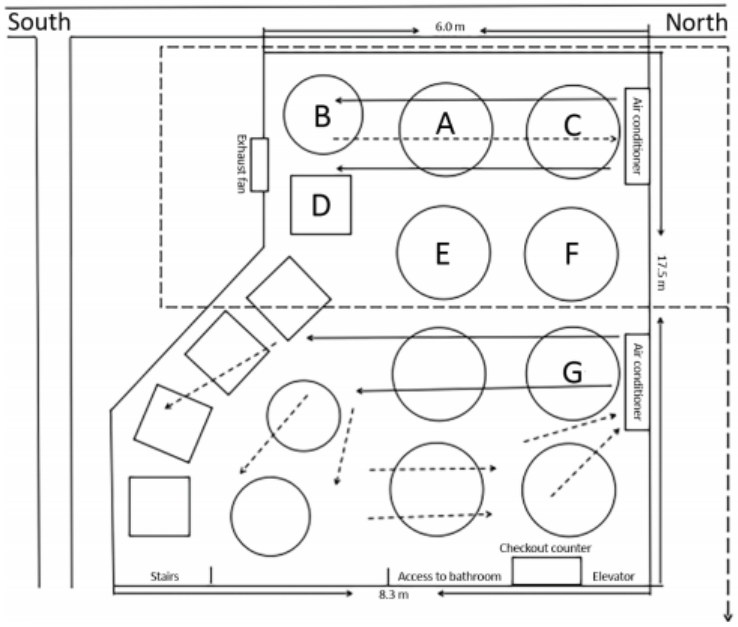


Figure. Sketch showing arrangement of restaurant tables and air conditioning airflow at site of outbreak of 2019 novel coronavirus disease, Guangzhou, China, 2020. Red circles indicate seating of future case-patients; yellow-filled red circle indicates index case-patient.

COVID-19 Outbreak Associated with Air Conditioning in Restaurant, Guangzhou, China, 2020

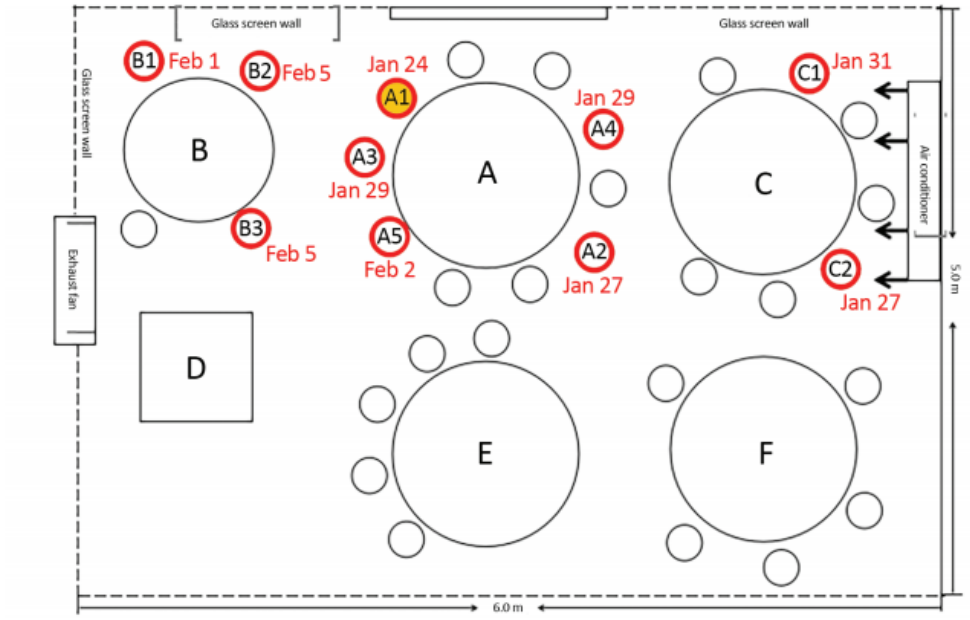
Jianyun Lu,[1] Jieni Gu,[1] Kuibiao Li,[1] Conghui Xu,[1] Wenzhe Su, Zhisheng Lai, Deqian Zhou, Chao Yu, Bin Xu, Zhicong Yang

CDC Centers for Disease Control and Prevention
CDC 24/7: Saving Lives, Protecting People™

EMERGING INFECTIOUS DISEASES®

EID Journal > Volume 26 > Number 7—July 2020 > Main Article

Volume 26, Number 7—July 2020



Aspetos polémicos da transmissibilidade ao nível ambiental e suas possíveis implicações futuras


Science of the Total Environment 743 (2020) 140444

Contents lists available at ScienceDirect

Science of the Total Environment

journal homepage: www.elsevier.com/locate/scitotenv

SARS-CoV-2 from faeces to wastewater treatment: What do we know? A review

Paola Foladori [a,*], Francesca Cutrupi [a], Nicola Segata [b], Serena Manara [b], Federica Pinto [b], Francesca Malpei [c], Laura Bruni [d], Giuseppina La Rosa [e]

[a] Department of Civil, Environmental and Mechanical Engineering, University of Trento, via Mesiano 77, 38123 Trento, Italy
[b] Department of Cellular Computational and Integrative Biology-CIBIO, Via Sommarive 9, 38123 Trento, Italy
[c] Department of Civil and Environmental Engineering, Politecnico di Milano, Piazza L. da Vinci, 32, 20133 Milano, Italy
[d] ADEP, Agenzia per la Depurazione (Wastewater Treatment Agency), Autonomous Province of Trento, via Gilli 3, 38121 Trento, Italy
[e] Department of Environment and Health, National Institute of Health, Rome, Italy.

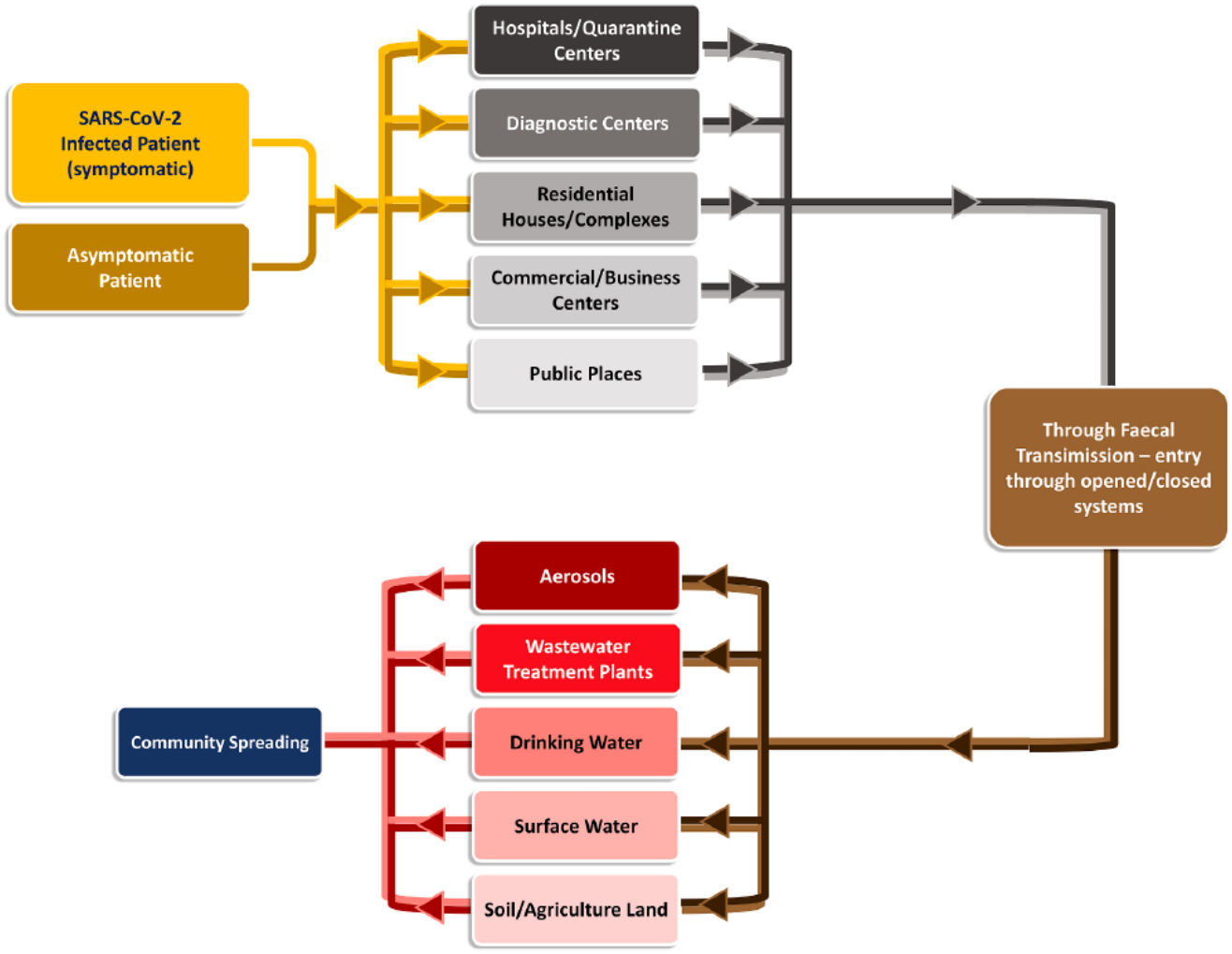


Fig. 2. Possible Transmission Route of SARS-CoV-2.

THE LANCET

Articles

Changes in symptomatology, reinfection, and transmissibility associated with the SARS-CoV-2 variant B.1.1.7: an ecological study

Mark S Graham*, Carole H Sudre*, Anna May, Michela Antonelli, Benjamin Murray, Thomas Varsavsky, Kerstin Kläser, Liane S Canas, Erika Molteni, Marc Modat, David A Drew, Long H Nguyen, Lorenzo Polidori, Somesh Selvachandran, Christina Hu, Joan Capdevila, COVID-19 Genomics UK (COG-UK) Consortium†, Alexander Hammers, Andrew T Chan, Jonathan Wolf, Tim D Spector, Claire J Steves‡, Sebastien Ourselin‡

Quais as implicações da crescente diversidade genética na futura eficácia do tratamento, das vacinas e no próprio diagnóstico?

RESEARCH

Science

AAAS

CORONAVIRUS

Recurrent deletions in the SARS-CoV-2 spike glycoprotein drive antibody escape

Kevin R. McCarthy[1,2,3]*, Linda J. Rennick[1,2], Sham Nambulli[1,2], Lindsey R. Robinson-McCarthy[4], William G. Bain[5,6,7], Ghady Haidar[8,9], W. Paul Duprex[1,2]*

Genetic Variants of SARS-CoV-2 May Lead to False Negative Results with Molecular Tests for Detection of SARS-CoV-2 - Letter to Clinical Laboratory Staff and Health Care Providers

U.S. FOOD & DRUG ADMINISTRATION

pathogens

MDPI

http://www.mdpi.com/journal/pathogens

Brief Report

Emergence of Drift Variants That May Affect COVID-19 Vaccine Development and Antibody Treatment

Takahiko Koyama [1,*], Dilhan Weeraratne [2], Jane L. Snowdon [2] and Laxmi Parida [1]

1 TJ Watson Research Center, IBM, Yorktown Heights, NY 10598, USA
2 Center for Artificial Intelligence, Research, and Evaluation, IBM, Cambridge, MA 02142, USA
* Correspondence: tkoyama@us.ibm.com

Received: 4 April 2020; Accepted: 24 April 2020; Published: 26 April 2020

check for updates

Int. J. Biol. Sci. 2021, Vol. 17 1476

IVYSPRING INTERNATIONAL PUBLISHER

International Journal of Biological Sciences

2021; 17(6): 1476-1485. doi: 10.7150/ijbs.59137

Review

The Genetic Variant of SARS-CoV-2: would It Matter for Controlling the Devastating Pandemic?

Shuxin Guo[1,2], Kefang Liu[2] and Jun Zheng[1,3]✉

1. Faculty of Health Sciences, University of Macau, Macau SAR, China
2. Chinese Academy of Sciences Key Laboratory of Pathogenic Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, 100101 Beijing, China
3. Institute of Translational Medicine, University of Macau, Macau SAR, China

✉ Corresponding author: junzheng@um.edu.mo

Received: 2021.02.07; Accepted: 2021.03.12; Published: 2021.04.10

vaccines Vaccines 2021, 9, 243. MDPI

Review

Emerging SARS-CoV-2 Variants and Impact in Global Vaccination Programs against SARS-CoV-2/COVID-19

Carmen Elena Gómez *, Beatriz Perdiguero and Mariano Esteban *

Centro Nacional de Biotecnología, Department of Molecular and Cellular Biology, Consejo Superior de Investigaciones Científicas (CNB-CSIC), Campus de Cantoblanco, 28049 Madrid, Spain; perdigue@cnb.csic.es
* Correspondence: cegomez@cnb.csic.es (C.E.G.); mesteban@cnb.csic.es (M.E.);
Tel.: +34-915854560 (C.E.G.); +34-915854553 (M.E.)

Variants of concern (VOC)

Na prática, o que se sabe?

Lancet Infect Dis 2021
Published Online
April 12, 2021

THE LANCET
Infectious Diseases

Articles

Genomic characteristics and clinical effect of the emergent SARS-CoV-2 B.1.1.7 lineage in London, UK: a whole-genome sequencing and hospital-based cohort study

Dan Frampton*, Tommy Rampling*, Aidan Cross*, Heather Bailey*, Judith Heaney, Matthew Byott, Rebecca Scott, Rebecca Sconza, Joseph Price, Marios Margaritis, Malin Bergstrom, Moira J Spyer, Patricia B Miralhes, Paul Grant, Stuart Kirk, Chris Valerio, Zaheer Mangera, Thaventhran Prabhahar, Jeronimo Moreno-Cuesta, Nish Arulkumaran, Mervyn Singer, Gee Yen Shin, Emilie Sanchez, Stavroula M Paraskevopoulou, Deenan Pillay, Rachel A McKendry, Mariyam Mirfenderesky, Catherine F Houlihan†, Eleni Nastouli†

GUEST EDITOR'S PAGE JACC: BASIC TO TRANSLATIONAL SCIENCE VOL. 6, NO. 3, 2021
MARCH 2021:305–8

What Are the Clinical Implications of the SARS-CoV-2 Variants

5 Things Every Cardiologist Should Know

Adriana M. Rauseo, MD, Jane A. O'Halloran, MD, PhD

JACC Journals

Table 1. Main characteristics of the emergent severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) variants. Data updated on February 16 2021 (https://outbreak.info (accessed on 9 March 2021)).

Variants	B.1.1.7	B.1.351	P.1
1st detection	September 2020	8 October 2020	2 January 2021
Detection site	United Kingdom	South Africa	Japan/Brazil
Mutations in S protein	7 mutations: **N501Y**, A570D, **D614G**, P681H, T716I, S982A, D1118H 2 deletions: H69-V70del, Y144del	9 mutations: L18F, D80A, D215G, R246I, K417N, E484K, **N501Y**, **D614G**, A701V 1 deletion: LAL 242-244 del	12 mutations: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, **N501Y**, **D614G**, H655Y, T1027I, V1176F
Countries reported cases	82	40	19
Countries with sequences	64	35	14

SARS-CoV-2 variants of concern

Table 1. *Cont.*

Variants	B.1.1.7	B.1.351	P.1
Potential risk	- Higher transmission - Higher disease severity - Modest reduction in the neutralization efficacy of sera from convalescent patients or vaccinees	- Higher transmission - Higher reinfection rates - Significant reduction in the neutralization efficacy of sera from convalescent patients or vaccinees	- Higher transmission - Higher reinfection rates - Significant reduction in the neutralization efficacy of sera from convalescent patients or vaccinees

REVIEWS

NATURE REVIEWS | IMMUNOLOGY

Check for updates

Immunological considerations for COVID-19 vaccine strategies

Mangalakumari Jeyanathan[1,2,3,5], Sam Afkhami[1,2,3,5], Fiona Smaill[2,3], Matthew S. Miller[1,3,4], Brian D. Lichty[1,2] and Zhou Xing[1,2,3]

Ir-se-á atingir a denominada imunidade de grupo?...

NEWS FEATURE · 18 MARCH 2021

Five reasons why COVID herd immunity is probably impossible

Even with vaccination efforts in full force, the theoretical threshold for vanquishing COVID-19 looks to be out of reach.

COMMENT

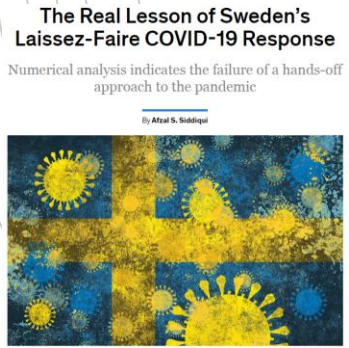
NATURE REVIEWS | IMMUNOLOGY

Check for updates

COVID-19 herd immunity: where are we?

Arnaud Fontanet[1,2] and Simon Cauchemez[3]

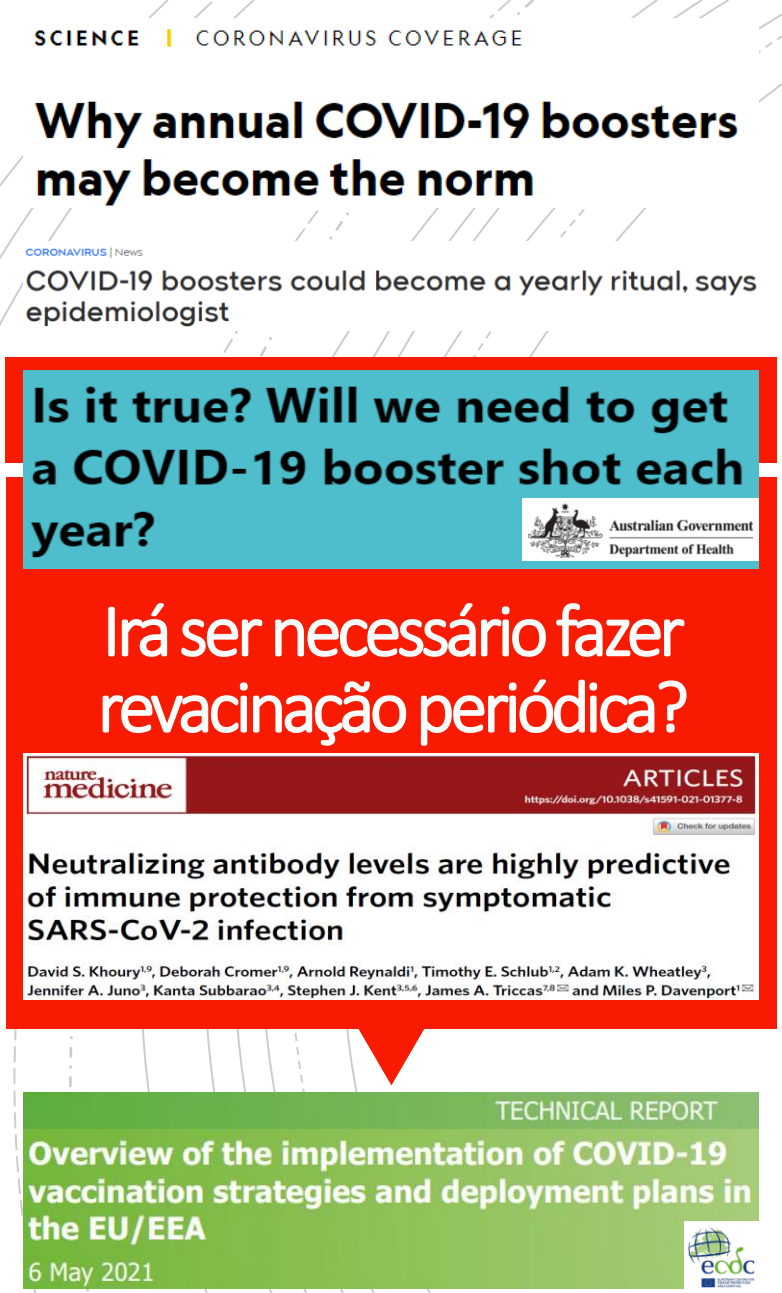
… As lições que devemos retirar da estratégia sueca!



Coronavirus: Swedish King Carl XVI Gustaf says coronavirus approach 'has failed'

17 December 2020

Coronavirus pandemic



- **O que se sabe acerca da imunidade relativa conferida pela doença ou pela imunização**
  - Nenhuma vacina é 100% eficaz na prevenção da doença ou da transmissão do vírus;
  - Existe uma boa correlação entre o nível de anticorpos neutralizantes, a proteção contra a infeção e as formas graves da doença, tal como com a robustez da resposta ao nível da imunidade celular;
  - O teor de ACs produzidos pela pessoa infetada é diretamente proporcional à intensidade da sintomatologia da infeção, atingindo-se o seu pico antes do 1º mês após o seu início e aos 3 meses após a vacinação;
  - A infeção produz entre 80-100% de proteção contra novas infeções durante 6 meses (< em pessoas > 65 anos);
  - A eficácia da imunização varia entre 65-95% de proteção contra novas infeções aos 2 meses (conforme o tipo de vacina);
  - As pessoas infetadas devem ser vacinadas cerca de 6 meses depois da doença (1 ou 2 doses?)

Qual a abordagem clínica mais correta dp denominado *"Long pos COVID Syndrome"* ...!!!

nature medicine | VOL 27 | APRIL 2021 | 601–615 FOCUS | REVIEW ARTICLE
https://doi.org/10.1038/s41591-021-01283-z

Post-acute COVID-19 syndrome

Ani Nalbandian[1,24], Kartik Sehgal[2,3,4,24] ✉, Aakriti Gupta[1,5,6], Mahesh V. Madhavan[1,5], Claire McGroder[7], Jacob S. Stevens[8], Joshua R. Cook[9], Anna S. Nordvig[10], Daniel Shalev[11], Tejasav S. Sehrawat[12], Neha Ahluwalia[13], Behnood Bikdeli[4,5,6,14], Donald Dietz[15], Caroline Der-Nigoghossian[16], Nadia Liyanage-Don[17], Gregg F. Rosner[1], Elana J. Bernstein[18], Sumit Mohan[8], Akinpelumi A. Beckley[19], David S. Seres[20], Toni K. Choueiri[2,3,4], Nir Uriel[1], John C. Ausiello[9], Domenico Accili[9], Daniel E. Freedberg[21], Matthew Baldwin[7], Allan Schwartz[1], Daniel Brodie[7], Christine Kim Garcia[7], Mitchell S. V. Elkind[10,22], Jean M. Connors[4,23], John P. Bilezikian[9], Donald W. Landry[8] and Elaine Y. Wan[1] ✉

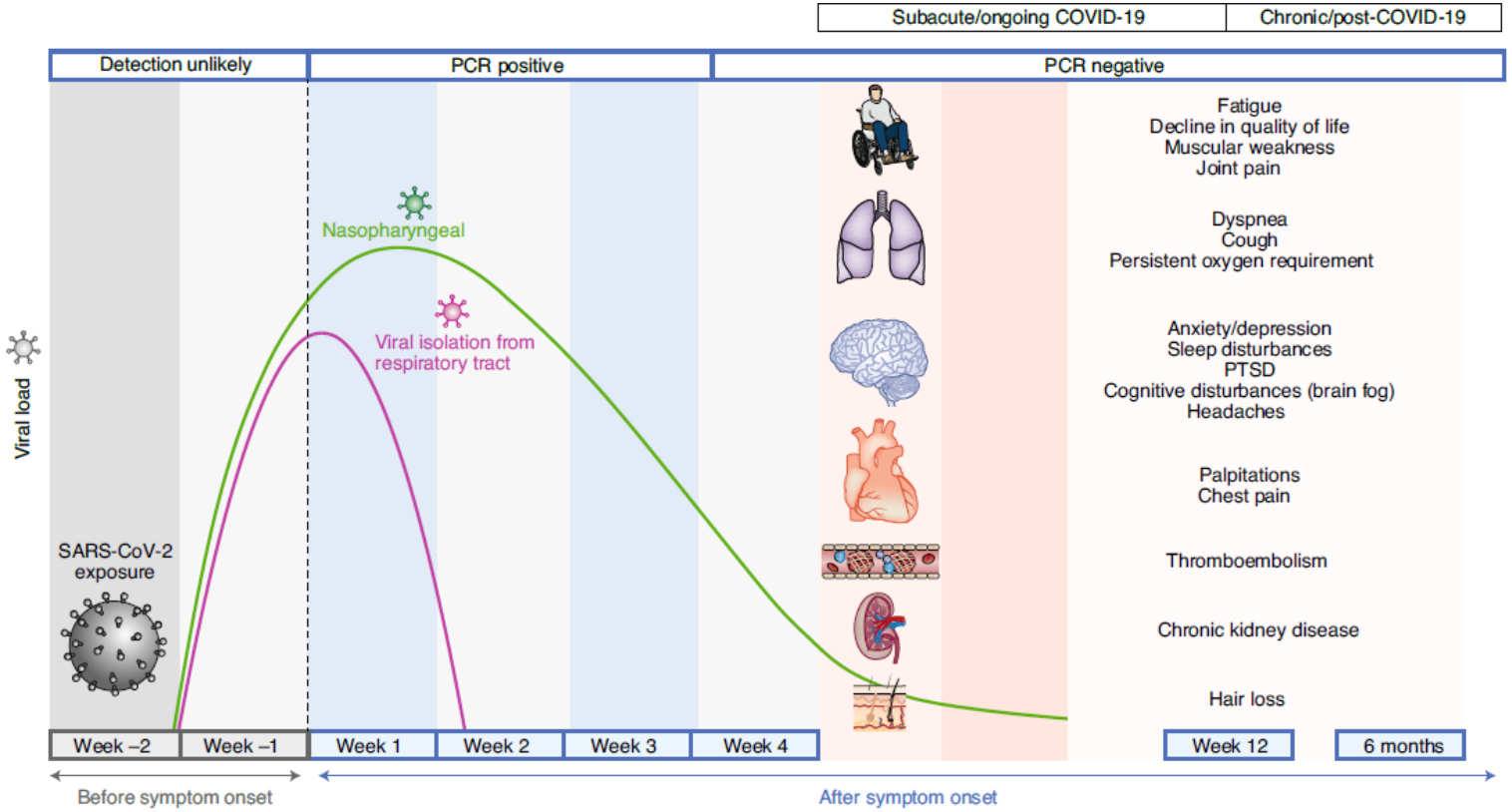


Fig. 1 | Timeline of post-acute COVID-19. Acute COVID-19 usually lasts until 4 weeks from the onset of symptoms, beyond which replication-competent SARS-CoV-2 has not been isolated. Post-acute COVID-19 is defined as persistent symptoms and/or delayed or long-term complications beyond 4 weeks from the onset of symptoms. The common symptoms observed in post-acute COVID-19 are summarized.

Diagnostic Microbiology and Infectious Disease 98 (2020) 115094

Contents lists available at ScienceDirect

Diagnostic Microbiology and Infectious Disease

journal homepage: www.elsevier.com/locate/diagmicrobio

Review

Clinical, molecular, and epidemiological characterization of the SARS-CoV-2 virus and the Coronavirus Disease 2019 (COVID-19), a comprehensive literature review

Esteban Ortiz-Prado [a,*], Katherine Simbaña-Rivera [a], Lenin Gómez- Barreno [a], Mario Rubio-Neira [b], Linda P. Guaman [c], Nikolaos C Kyriakidis [d], Claire Muslin [a], Ana María Gómez Jaramillo [e], Carlos Barba-Ostria [a], Doménica Cevallos-Robalino [f], Hugo Sanches-SanMiguel [a], Luis Unigarro [g], Rasa Zalakeviciute [h,i], Naomi Gadian [j], Andrés López-Cortés [k,l]

Implicações para as possíveis estratégias de tratamento com antivíricos

Journal of Clinical Microbiology®

MINIREVIEW

Emergence of a Novel Coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2: Biology and Therapeutic Options

Suliman Khan,[a,b] Rabeea Siddique,[a,b] Muhammad Adnan Shereen,[c] Ashaq Ali,[d] Jianbo Liu,[a] Qian Bai,[a,b] Nadia Bashir,[c] Mengzhou Xue[a,b]

[a]Department of Cerebrovascular Diseases, Second Affiliated Hospital of Zhengzhou University, Zhengzhou, China
[b]Henan Medical Key Laboratory of Translational Cerebrovascular Diseases, Zhengzhou, China
[c]State Key Laboratory of Virology, College of Life Sciences, Wuhan University, Wuhan, China
[d]Wuhan institute of Virology, Chinese Academy of Sciences, Wuhan, China
[e]Department of Respiratory Medicine, Second Affiliated Hospital of Zhengzhou University, Zhengzhou, China

NATURE REVIEWS | MICROBIOLOGY

Check for updates

Characteristics of SARS-CoV-2 and COVID-19

Ben Hu[1,3], Hua Guo[1,2,3], Peng Zhou[1] and Zheng-Li Shi[1]✉

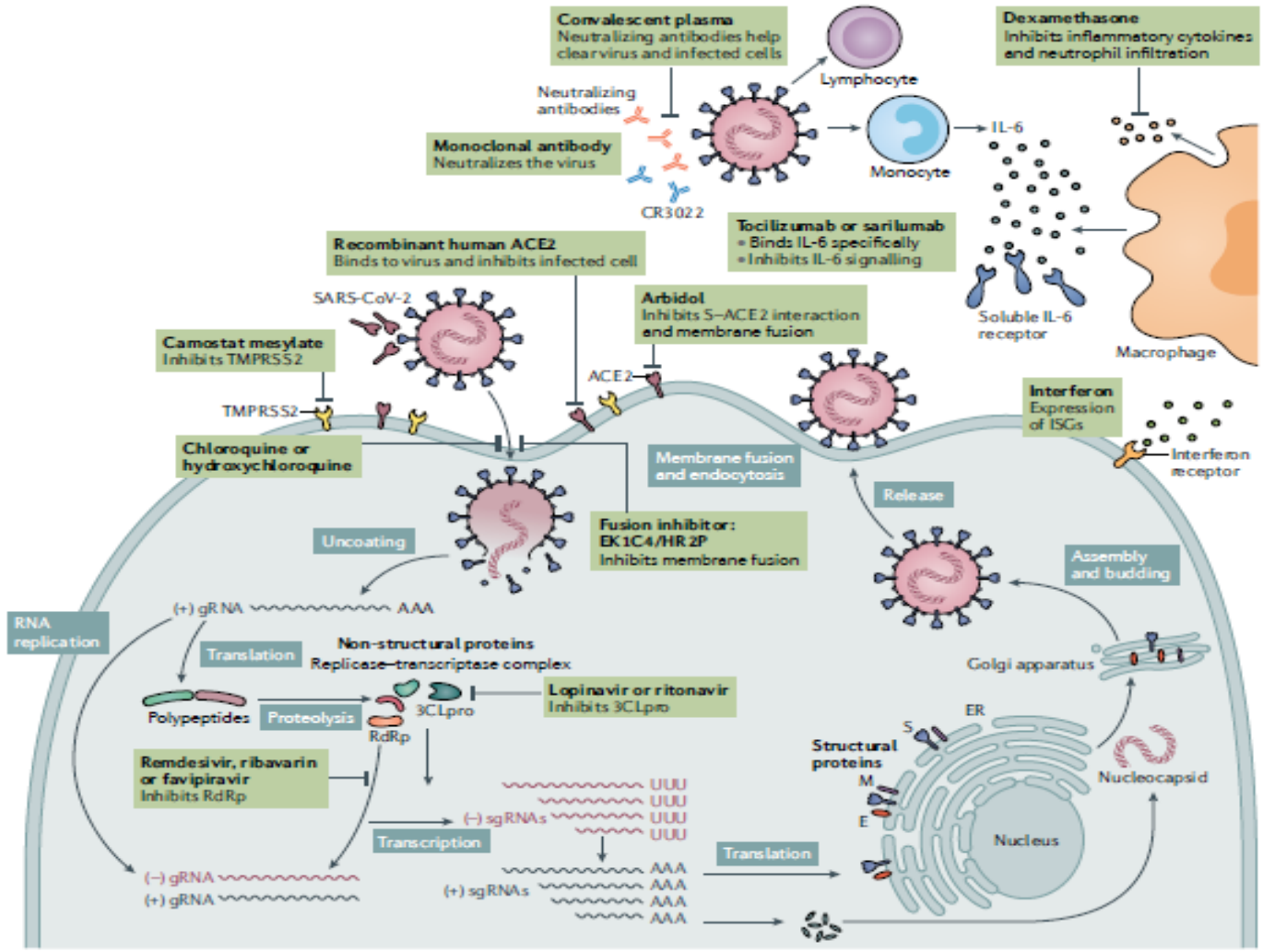


Fig. 5 | **SARS-CoV-2 replication and potential therapeutic targets.** Potential antivirals target the different steps of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) replication, ranging from receptor binding, entry and fusion to replication. Furthermore, immunoglobulin-based and immunomodulatory drugs are potential therapeutics as well. Note that robust data on clinical efficacy are lacking for most of these treatments so far. 3CLpro, 3C-like protease; ACE2, angiotensin-converting enzyme 2; CR3022, a SARS-CoV-specific human monoclonal antibody; E, envelope protein; EK1C4, lipopeptide derived from EK1 which is a pan-coronavirus fusion inhibitor targeting the HR1 domain of the spike protein; ER, endoplasmic reticulum; gRNA, genomic RNA; HR2P, heptad repeat 2-derived peptides of SARS-CoV-2 spike protein; IL-6, interleukin-6; ISG, interferon-stimulated gene; M, membrane protein; RdRp, RNA-dependent RNA polymerases; sgRNA, subgenomic RNA; S, spike protein; TMPRSS2, transmembrane protease serine protease 2.

Implicações para as possíveis estratégias de tratamento com imunomodelador

Human Immunology xxx (xxxx) xxx

Contents lists available at ScienceDirect

journal homepage: www.elsevier.com/locate/humimm

Review

Chemotherapy vs. Immunotherapy in combating nCOVID19: An update

Abhigyan Choudhury, Gargi Mukherjee, Suprabhat Mukherjee *,1

Integrative Biochemistry & Immunology Laboratory, Department of Animal Science, Kazi Nazrul University, Asansol 713 340, West Bengal, India

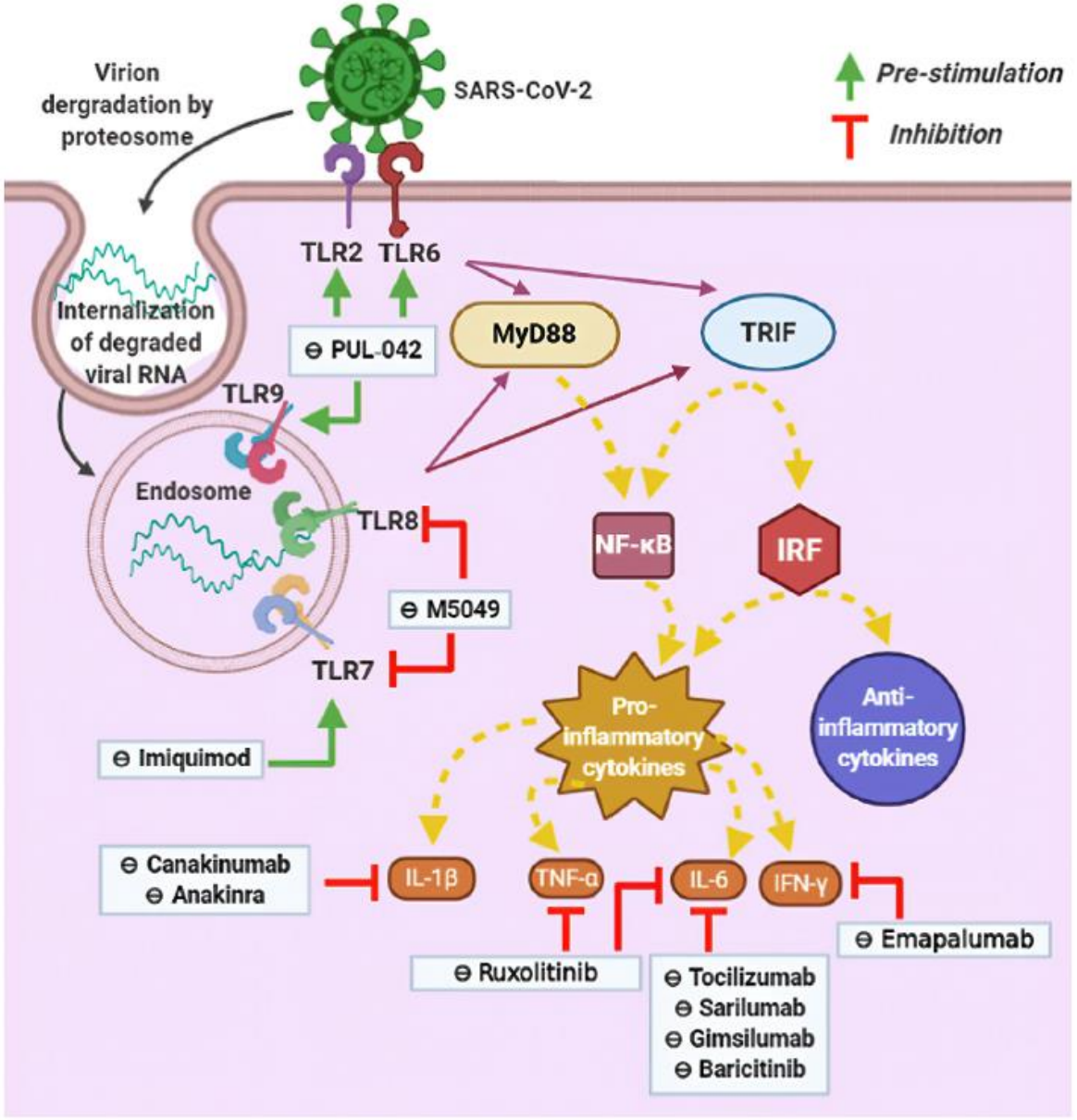
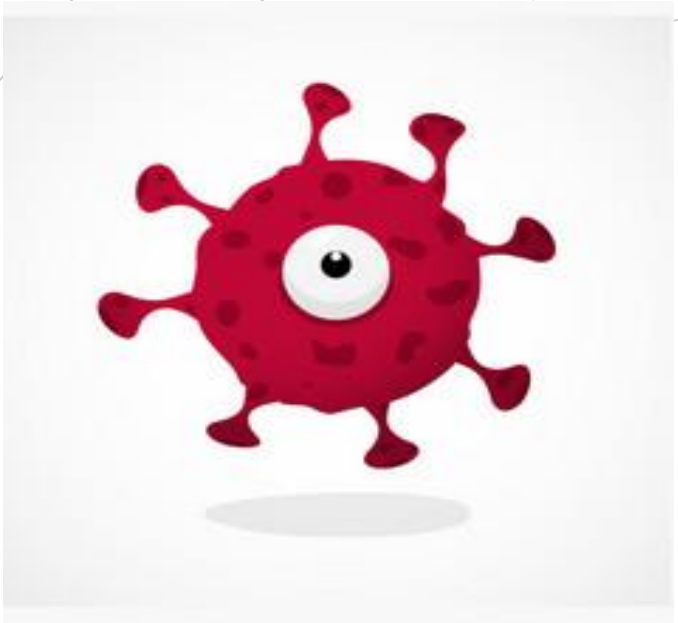
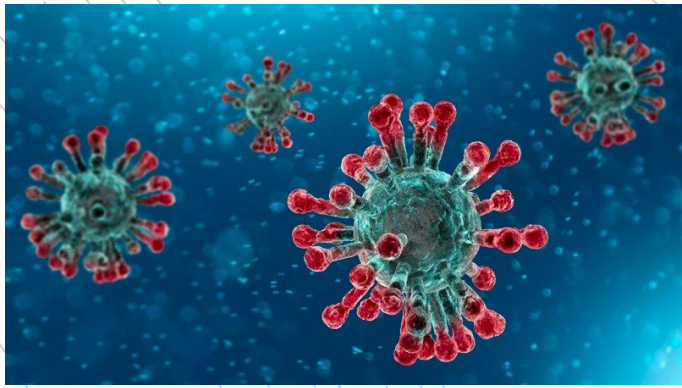


Fig. 2. Immunotherapeutic targets. The figure illustrates the various pathways of immunomodulation achieved by the different immunotherapeutic molecules.



Conclusões



The One Health Triad

A única perspetiva correta de abordarmos a problemática das zoonoses e das doenças transmitidas por vetores é a decorrente da filosofia *One Health Medicine*

Emerging Microbes & Infections
2020, VOL. 9
https://doi.org/10.1080/22221751.2020.1827984

EMi Taylor & Francis

REVIEW OPEN ACCESS Check for updates

Zoonotic and reverse zoonotic events of SARS-CoV-2 and their impact on global health

Khalid Munir[a,b*], Shoaib Ashraf [b,c*], Isra Munir[d], Hamna Khalid[e], Mohammad Akram Muneer[b], Noreen Mukhtar[a], Shahid Amin[f], Sohaib Ashraf[c,g], Muhammad Ahmad Imran[g], Umer Chaudhry[h], Muhammad Usman Zaheer[i], Maria Arshad[j], Rukhsana Munir[k], Ali Ahmad [l] and Xin Zhao [m]

[a]PetLife Veterinary Professional Corporation, NJ, USA; [b]Department of Pathobiology, Riphah College of Veterinary Sciences, Riphah University, Lahore, Pakistan; [c]Wellman Center for Photomedicine, Massachusetts General Hospital, Harvard Medical School, Boston, MA, USA; [d]School of Dental Medicine, University of Pennsylvania, Philadelphia, PA, USA; [e]Department of Chemical and Biological Engineering, Villanova University, Villanova, PA, USA; [f]Animal Hospital of Loves Park, Loves Park, IL, USA; [g]Department of Microbiology, Shaikh Zayed Hospital Lahore, Lahore, Pakistan; [h]; Royal (Dick) School of Veterinary Studies and Roslin Institute, Edinburgh, UK; [i]Food and Agriculture Organization of the United Nations, Country Office, Islamabad, Pakistan; [j]District Headquarter Hospital, Lahore, Pakistan; [k]Consultant Emergency Medicine, Russells Hall Hospital, Dudley Group of Hospitals NHS Trust, Dudley, UK; [l]CHU Sainte-Justine Research Center, Department of Microbiology, Infectious Diseases and Immunology, University of Montreal, Montreal, Canada; [m]Department of Animal Sciences, McGill University, Sainte-Anne-de-Bellevue, Canada

ONE MEDICINE
ONE HEALTH™

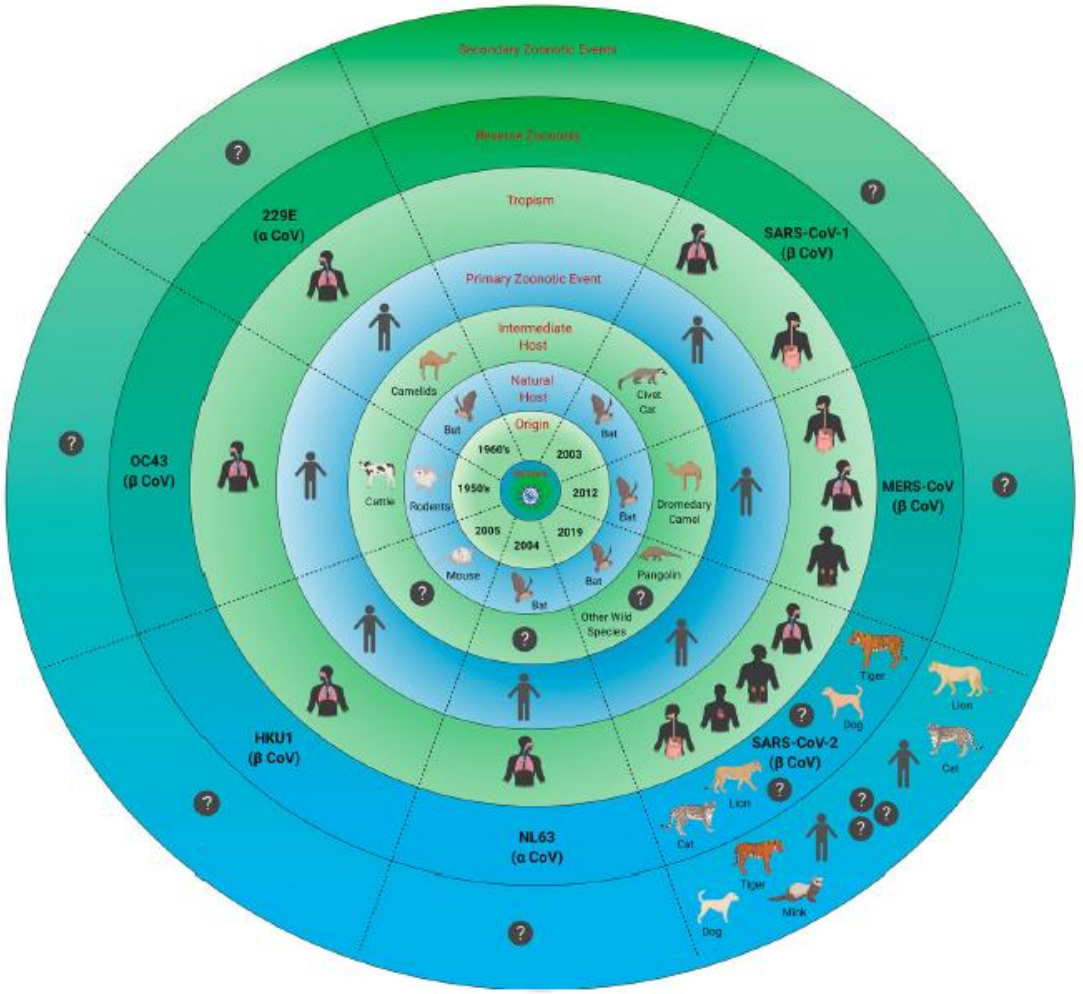


Figure 2. Human coronaviruses. The figure shows seven human coronaviruses, their origins, natural reservoirs, intermediate hosts, tissue/organ tropism and reverse zoonosis along with primary and potential secondary and tertiary zoonotic events. An interrogative sign (?) indicates unknown or unidentified.

Figure 3. SARS-CoV-2 and the One-World – One-Health concept. It emphasizes that human health is dependent and intricately connected with that of animals (domestic and wild), birds and plants. A disturbance in the ecosystem results in human diseases (zoonotic or reverse-zoonotic). The letter X denotes a zoonotic event; the color red, white and yellow depict potential primary, secondary and tertiary zoonotic events, respectively.

Mensagem em estilo de Homenagem ao meu Mestre, Professor Doutor Armindo Filipe

One Health 10 (2020) 100127

Contents lists available at ScienceDirect

One Health

journal homepage: www.elsevier.com/locate/onehlt

The SARS-CoV-2 outbreak from a one health perspective

Maged Gomaa Hemida[a,b,*], Mohammed M. Ba Abduallah[c]

[a] Department of Microbiology, College of Veterinary Medicine, King Faisal University, Saudi Arabia
[b] Department of Virology, Faculty of Veterinary Medicine, Kafrelsheikh University, Egypt
[c] Department of Biological Sciences, College of Science, King Faisal University, Saudi Arabia

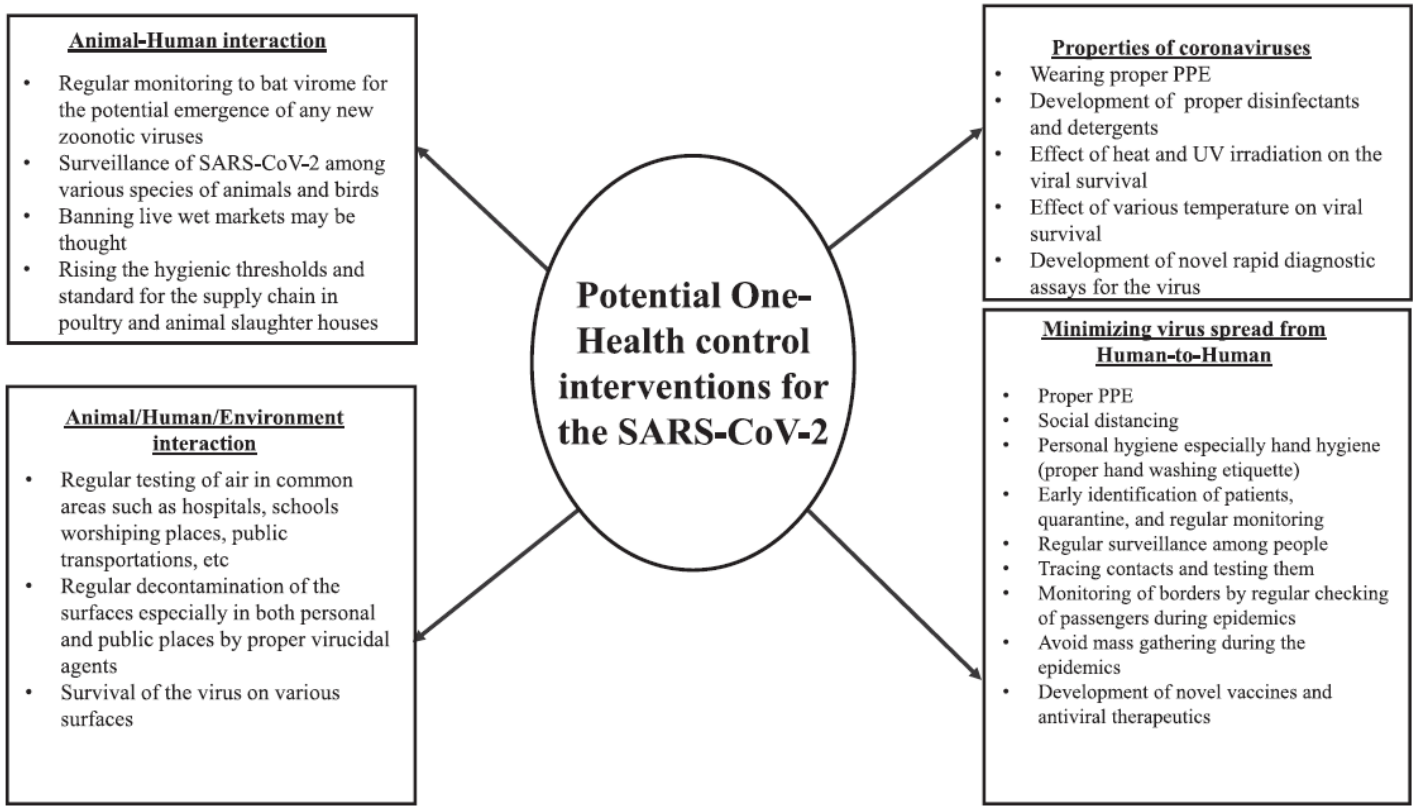


Fig. 2. Some control interventions for the SARS-CoV -2 based on the One Health concept.
Some potential control measures for the SARS-CoV-2 outbreak. (a) Some strategies based on the physicochemical and biological properties of the virus (b) Some strategies based on the animal/human interaction (c) Some strategies based on the animal/environment/human interaction (d) some strategies bases on reduction the virus spread from person to person.

Denmark drops plans for mass mink cull after Covid mutation fears

The New York Times

MPs refused to support forced killing of millions of mink after concerns raised over disease risk and threat to livelihoods

Soluções radicais polémicas de hoje …

Denmark announces cull of 15 million mink over Covid mutation fears

THE IRISH Sun

Mutated virus infects 12 humans, sparking concerns that effectiveness of future vaccine could be affected

Science | AAAS

Bird flu strain taking a toll on humans

nature International journal of science

nature THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

Outbreak of chicken flu rattles Hong Kong

David Cyranoski

… tal como no passado … e … no futuro???

U.S.News & WORLD REPORT

East Asia Pacific

Hong Kong, China on Bird Flu Alert

By Ivan Broadhead
January 02, 2012 07:00 PM

É fundamental promover a deteção precoce da emergênca de novos agentes microbianos na preparação da resposta adequada a futuras pandemias

Journal of Clinical Virology 131 (2020) 104594

Contents lists available at ScienceDirect

Journal of Clinical Virology

journal homepage: www.elsevier.com/locate/jcv

Coronavirus discovery by metagenomic sequencing: a tool for pandemic preparedness

Ellen C. Carbo [a,*], Igor A. Sidorov [a], Jessika C. Zevenhoven-Dobbe [a], Eric J. Snijder [a], Eric C. Claas [a], Jeroen F.J. Laros [b,c,d], Aloys C.M. Kroes [a], Jutte J.C. de Vries [a]

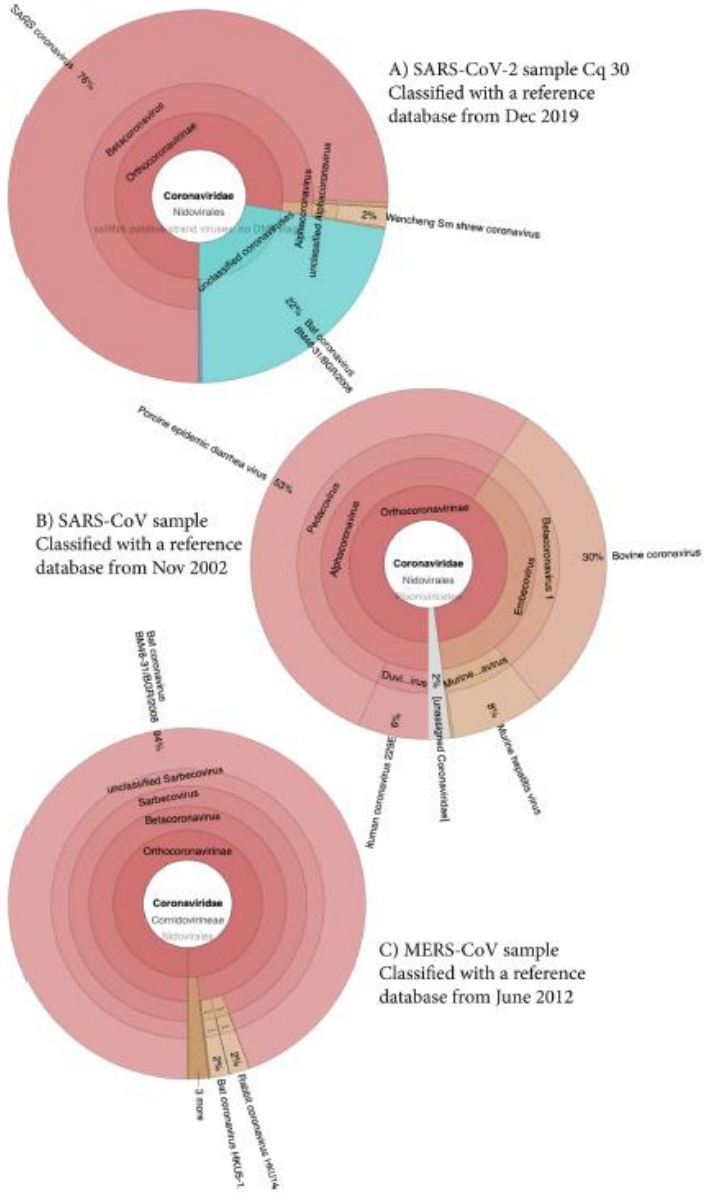
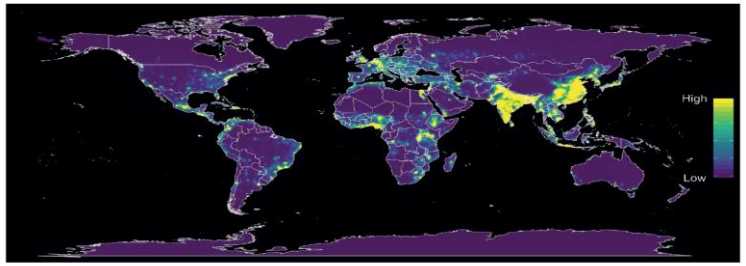


Fig. 1. Centrifuge classification results of viral reads of SARS-CoV-2, SARS-CoV, and MERS-positive samples, using viral metagenomic databases created before the emergence of these viruses. A) SARS-CoV-2, B) SARS-CoV, C) MERS.

Global hotspot map of estimated risk in zoonotic disease emergence



Allen *et al.* (2017)[23] analysed emerging infectious diseases (EID) of wildlife origin based on a broad set of predictors, such as the distribution of tropical forested regions, human population density, mammal species richness, agricultural land use, and others. The resulting heat map shows the global spatial patterns of estimated risk of zoonotic EID events after factoring out reporting bias.

O conhecimento da epidemiologia molecular ao nível mundial em cada momento é de decisiva importância para o controlo eficaz da propagação dos microrganismos com potencial pandémico

...

Journal of Microbiology (2021) Vol. 59, No. 3, pp. 332–340
DOI 10.1007/s12275-021-0660-4
eISSN 1976-3794
pISSN 1225-8873

REVIEW

A comprehensive review of SARS-CoV-2 genetic mutations and lessons from animal coronavirus recombination in one health perspective

AMERICAN SOCIETY FOR MICROBIOLOGY | Journal of Clinical Microbiology®

MINIREVIEW

SHERLOCK and DETECTR: CRISPR-Cas Systems as Potential Rapid Diagnostic Tools for Emerging Infectious Diseases

Mujahed I. Mustafa,[a] Abdelrafie M. Makhawi[a]

[a]Department of Biotechnology, University of Bahri, Khartoum, Sudan

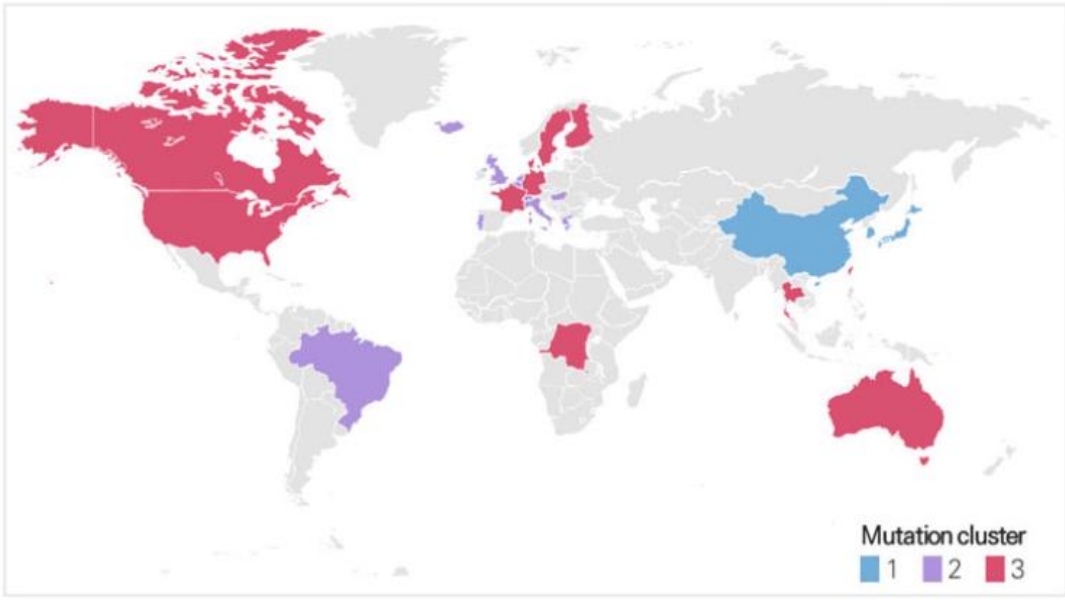
HORIZON 2020

News

VEO: 15 million for development early detection system for infectious diseases outbreaks

VEO report on mutations and variation in publicly shared SARS-CoV-2 raw sequencing data, Report No. 3, 26 Apr. 2021

Mutation cluster



China
Korea
Japan
India
Singapore

England
Iceland
Netherlands
Greece
Portugal
Brazil
Italy
Switzerland
Belgium
Hungary

USA
Taiwan
Australia
Canada
Thailand
Spain
Denmark
Congo
Germany
Sweden
Finland
France
Luxemburg

Fig. 1. Clustering analysis of SARS-CoV-2 in 28 countries (modified from Toyoshima *et al.*, 2020). Clustering analysis of SARS-CoV-2 among 28 countries. A global mapping of the three clusters.

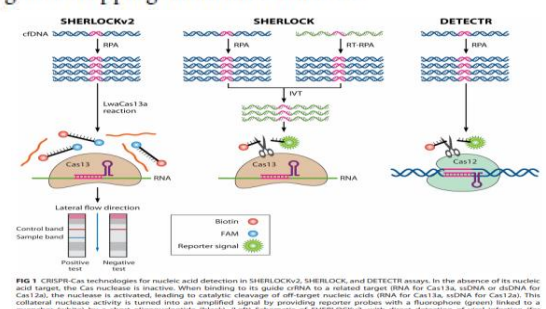
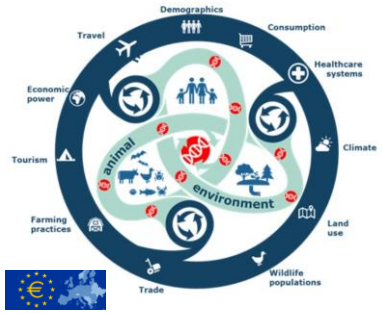
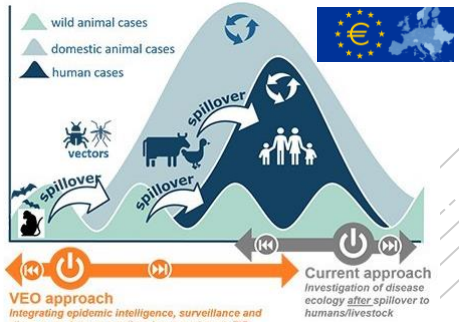


FIG 1 CRISPR-Cas technologies for nucleic acid detection in SHERLOCKv2, SHERLOCK, and DETECTR assays. In the absence of its nucleic acid target, the Cas nuclease is inactive. When binding to its guide crRNA to a related target (RNA for Cas13a, ssDNA or dsDNA for Cas12a), the nuclease is activated, leading to catalytic cleavage of off-target nucleic acids (RNA for Cas13a, ssDNA for Cas12a). This collateral nuclease activity is turned into an amplified signal by providing reporter probes with a fluorophore (green) linked to a quencher (white) by a short oligonucleotide (black). (Left) Schematic of SHERLOCKv2, with direct detection of viral infection (for example) in bodily fluids. (Middle) Schematic of the SHERLOCK system. Nucleic acid is extracted from clinical samples (for example), and the target is amplified by recombinase polymerase amplification (RPA) with either RNA or DNA as the input (reverse transcriptase recombinase polymerase amplification [RT-RPA] or RPA, respectively). RPA products are detected in a reaction mixture containing T7 RNA polymerase, Cas13, a target-specific crRNA, and an RNA reporter that fluoresces when cleaved. (Right) Schematic of the DETECTR system.



Key challenge: global changes in global trends acting as drivers of infectious disease emergence and spread in the One Health domain. Using open data potentially informative of such drivers could greatly add to the surveillance and prediction of EIDs.



RAPID COMMUNICATION

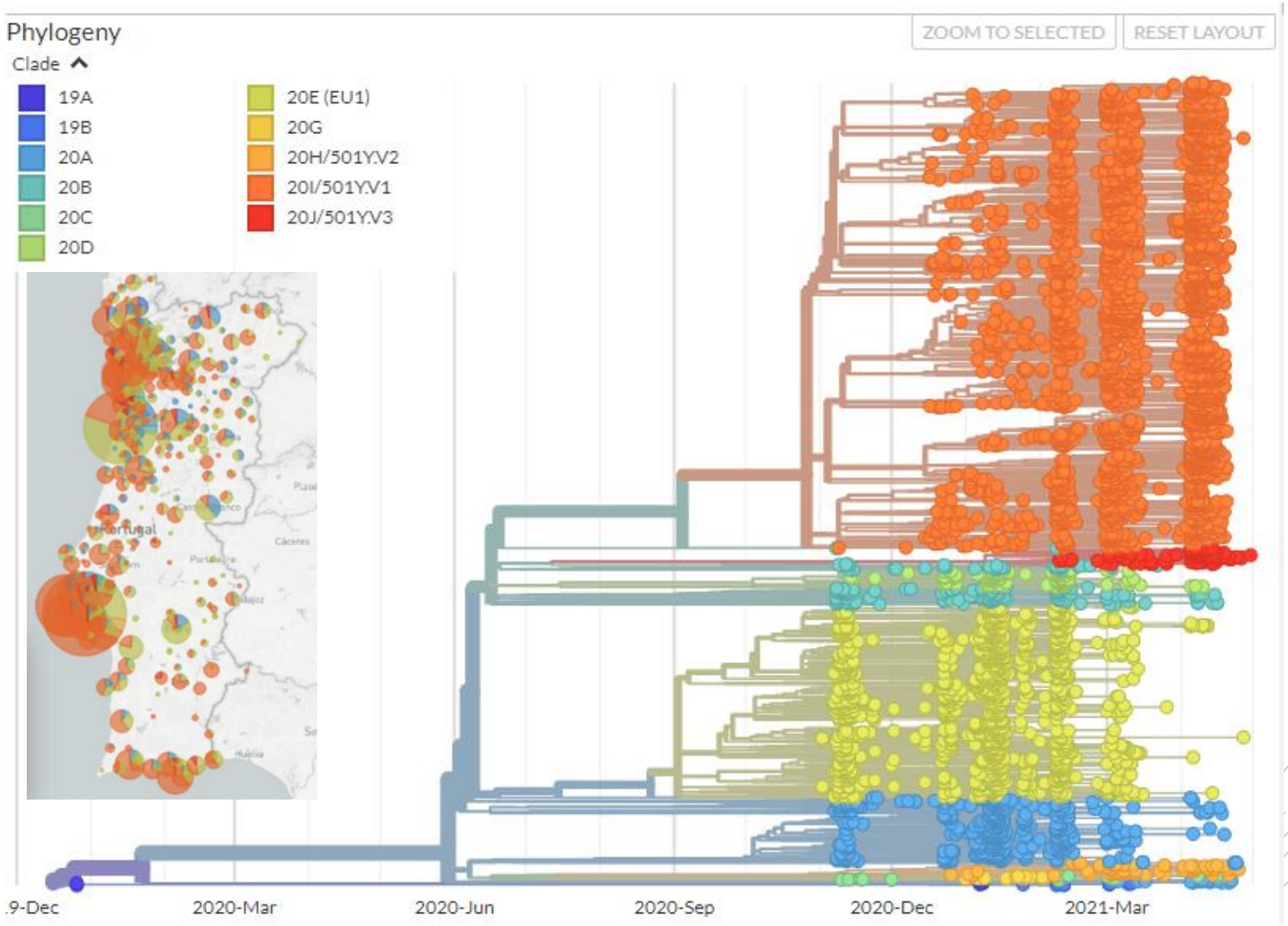
Tracking SARS-CoV-2 lineage B.1.1.7 dissemination: insights from nationwide spike gene target failure (SGTF) and spike gene late detection (SGTL) data, Portugal, week 49 2020 to week 3 2021

Eurosurveillance

Vítor Borges[1,2], Carlos Sousa[2,3], Luís Menezes[4], António Maia Gonçalves[5], Miguel Pichão[6], José Pedro Almeida[7], Margarida Vieita[7], Rafael Santos[7], Ana Rita Silva[3], Mariana Costa[3], Luís Carneiro[3], Pedro Casaca[8], Pedro Pinto-Leite[8], André Peralta-Santos[8], Joana Isidro[1], Sílvia Duarte[9], Luís Vieira[9], Raquel Guiomar[10], Susana Silva[11], Baltazar Nunes[11], João P Gomes[1]

1. Bioinformatics Unit, Department of Infectious Diseases, National Institute of Health Dr. Ricardo Jorge (INSA), Lisbon, Portugal
2. These authors contributed equally to this work
3. Molecular Diagnostics Laboratory, Unilabs, Oporto, Portugal
4. Executive Office, Unilabs, Oporto, Portugal
5. Medical Office, Unilabs, Oporto, Portugal
6. IT Office, Unilabs, Oporto, Portugal
7. Data Intelligence, Unilabs, Oporto, Portugal
8. 8 Division of Epidemiology and Statistics, Directorate of Information and Analysis, Directorate-General of Health, Lisbon, Portugal
9. 9 Innovation and Technology Unit, Department of Human Genetics; National Institute of Health Dr. Ricardo Jorge (INSA), Lisbon, Portugal
10. National Reference Laboratory for Influenza and other Respiratory Viruses, Department of Infectious Diseases; National Institute of Health Dr. Ricardo Jorge (INSA), Lisbon, Portugal
11. Epidemiological Research Unit Department of Epidemiology, National Institute of Health Dr. Ricardo Jorge (INSA), Lisbon, Portugal

… tal como se passou a fazer em Portugal com amostras de doentes…



REPÚBLICA PORTUGUESA SAÚDE · SNS SERVIÇO NACIONAL DE SAÚDE · Instituto Nacional de Saúde Doutor Ricardo Jorge

Diversidade genética do novo coronavírus SARS-CoV-2 (COVID-19) em Portugal

Mais informações em https://insaflu.insa.pt/covid19/

SAÚDE / CORONAVÍRUS OBSERVADOR

Águas residuais começam testadas à Covid-19

… e também através de análises periódicas das águas residuais urbanas

REPÚBLICA PORTUGUESA
GABINETE DO MINISTRO DO AMBIENTE E DA AÇÃO CLIMÁTICA

NOTA DE IMPRENSA

Investigação em águas residuais pretende criar sistema de alerta precoce do vírus SARS-CoV-2

Ciências ULisboa
Faculdade de Ciências da Universidade de Lisboa

COVIDETECT: 1.ª FASE DO PROJETO CONCLUÍDA

Proieto COVIDETECT

ÁGUAS DO DOURO E PAIVA
Grupo Águas de Portugal

APDA
ASSOCIAÇÃO PORTUGUESA DE DISTRIBUIÇÃO E DRENAGEM DE ÁGUAS

/ Sociedade / Noticias /

Share Tweet LinkedIn

Sistema de alerta precoce do vírus SARS-CoV-2 em águas residuais está a avançar

E, ainda, uma temida ameaça que afinal não se concretizou…

Review

THE LANCET HIV

Overview of SARS-CoV-2 infection in adults living with HIV

Juan Ambrosioni*, José Luis Blanco*, Juliana M Reyes-Urueña, Mary-Ann Davies, Omar Sued, Maria Angeles Marcos, Esteban Martínez, Silvia Bertagnolio, Jose Alcamí, Jose M Miro, COVID-19 in HIV Investigators†

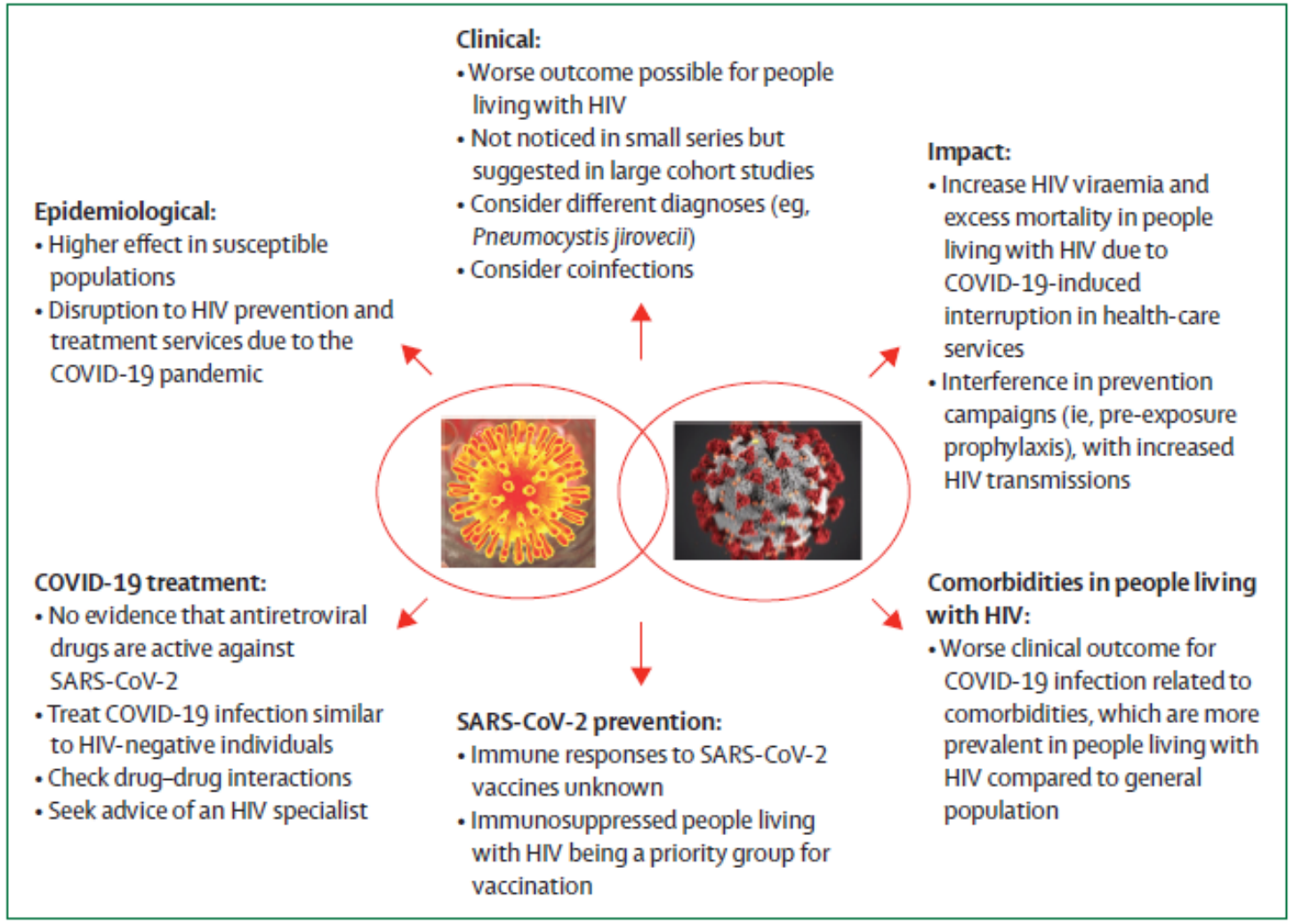


Figure 2: **Interaction of the HIV and SARS-CoV-2 pandemics and unanswered questions**

… mas que é uma realidade sobre a qual há ainda alguns pontos não completamente esclarecidos

AIDS RESEARCH AND HUMAN RETROVIRUSES
Volume 37, Number 4, 2021

DOI: 10.1089/aid.2020.0284

Human Immunodeficiency Virus and Severe Acute Respiratory Syndrome Coronavirus 2 Coinfection: A Systematic Review of the Literature and Challenges

Raj H. Patel,[1] Arpan Acharya,[2] Hitendra S. Chand,[3] Mahesh Mohan,[4] and Siddappa N. Byrareddy[2,5,6]

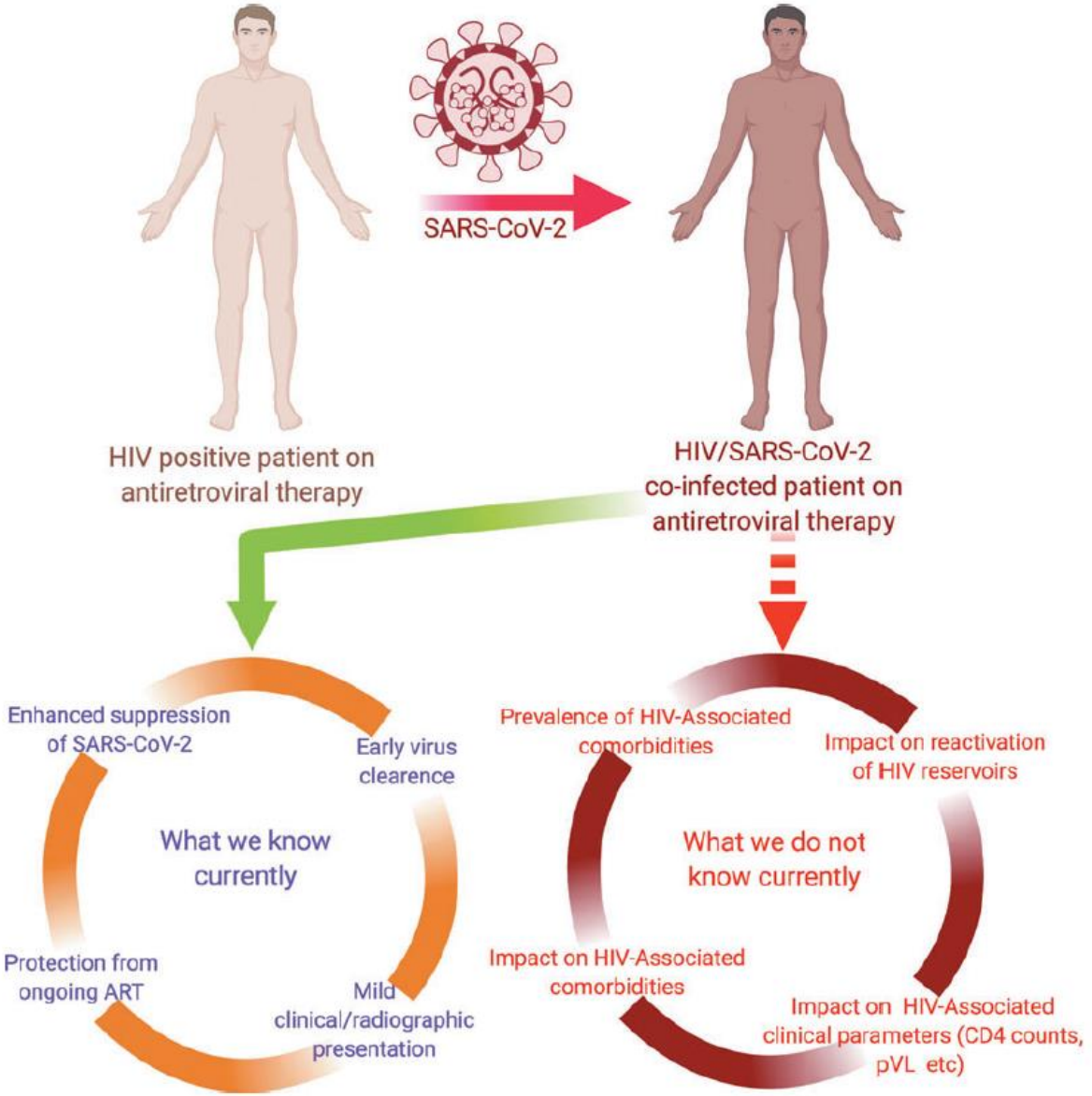


FIG. 2. Similarities and differences between HIV patients and HIV/SARS-CoV-2 coinfection patients on antiretroviral therapy. HIV, human immunodeficiency virus; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

AIDS RESEARCH AND HUMAN RETROVIRUSES
Volume 37, Number 4, 2021
© Mary Ann Liebert, Inc.
DOI: 10.1089/aid.2020.0161

What HIV in the Brain Can Teach Us About SARS-CoV-2 Neurological Complications?

Lena Al-Harthi,[1] Edward Campbell,[2] Julie A. Schneider,[3] and David A. Bennett[3]

Uma "estranha" coincidência"?

AIDS RESEARCH AND HUMAN RETROVIRUSES
Volume 00, Number 00, 2021
© Mary Ann Liebert, Inc.
DOI: 10.1089/aid.2021.0005

Pressing Questions and Challenges in the HIV-1 and SARS-CoV-2 Syndemic

Monty Montano[1,2]

Journal of NeuroVirology
https://doi.org/10.1007/s13365-020-00897-2

REVIEW

Studying the neuropsychological sequelae of SARS-CoV-2: lessons learned from 35 years of neuroHIV research

Andrew Levine[1] · Ned Sacktor[2] · James T. Becker[3]

Received: 15 June 2020 / Revised: 11 August 2020 / Accepted: 18 August 2020

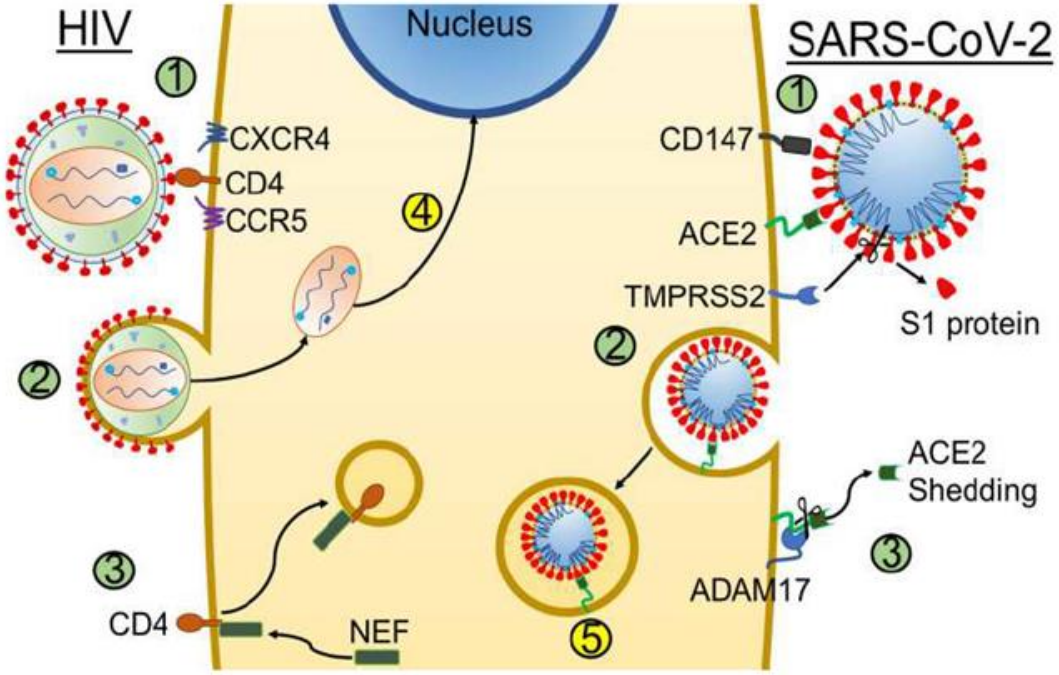


Figure 2 Comparative overview of viral entry and receptor downregulation. Schematic representation of a host cell potentially co-infected with HIV (left side) and SARS-CoV-2 (right side). [1] Binding of HIV or SARS-CoV-2 to key receptors. Both SARS-CoV-2 require initial interaction with specific receptors at the cell membrane: HIV binds to CD4 and co-receptors CCR5 and CXCR4 (left) and SARS-CoV-2 binds to host cell receptors CD147 or ACE2 (right). Binding of SARS-CoV-2 to ACE2 receptor requires initial cleavage of the viral S1 glycoprotein assisted by human protease TMPRSS2 so that viral S2 protein can be internalized along with the rest of the virion (right). [2] Entry of virus into cell. HIV fusion with the cell membrane leads to disassembly of the virion in the cytoplasm, leading to the release of viral genetic material, reverse transcription and [4] eventual integration of viral DNA into the host cell DNA, whereas SARS-CoV-2 enters the cell through endocytosis after binding to ACE2 or CD147. [3] Downregulation of CD4 by NEF or ACE2 by ADAM17. Viral internalization (infection) leads to downregulation of the initial entry receptor for HIV (CD4, mediated by the viral Nef polypeptide) and ACE2 for SARS-CoV-2, which is cleaved by the host ADAM17. [5] Fusion of the endosome and the virus. The viral membrane and endosome membrane fuse, releasing SARS-CoV-2's genome into the host cell. Illustration credit: Nicholas J. Evans.

AIDS RESEARCH AND HUMAN RETROVIRUSES
Volume 37, Number 4, 2021
© Mary Ann Liebert, Inc.
DOI: 10.1089/aid.2020.0161

What HIV in the Brain Can Teach Us About SARS-CoV-2 Neurological Complications?

Lena Al-Harthi,[1] Edward Campbell,[2] Julie A. Schneider,[3] and David A. Bennett[3]

Ou não?

AIDS RESEARCH AND HUMAN RETROVIRUSES
Volume 00, Number 00, 2021
© Mary Ann Liebert, Inc.
DOI: 10.1089/aid.2021.0005

Pressing Questions and Challenges in the HIV-1 and SARS-CoV-2 Syndemic

Monty Montano[1,2]

Journal of NeuroVirology
https://doi.org/10.1007/s13365-020-00897-2

REVIEW

Check for updates

Studying the neuropsychological sequelae of SARS-CoV-2: lessons learned from 35 years of neuroHIV research

Andrew Levine[1] · Ned Sacktor[2] · James T. Becker[3]

Received: 15 June 2020 / Revised: 11 August 2020 / Accepted: 18 August 2020

Sites of Immune Response and Potential Implications in the Development of COVID-19

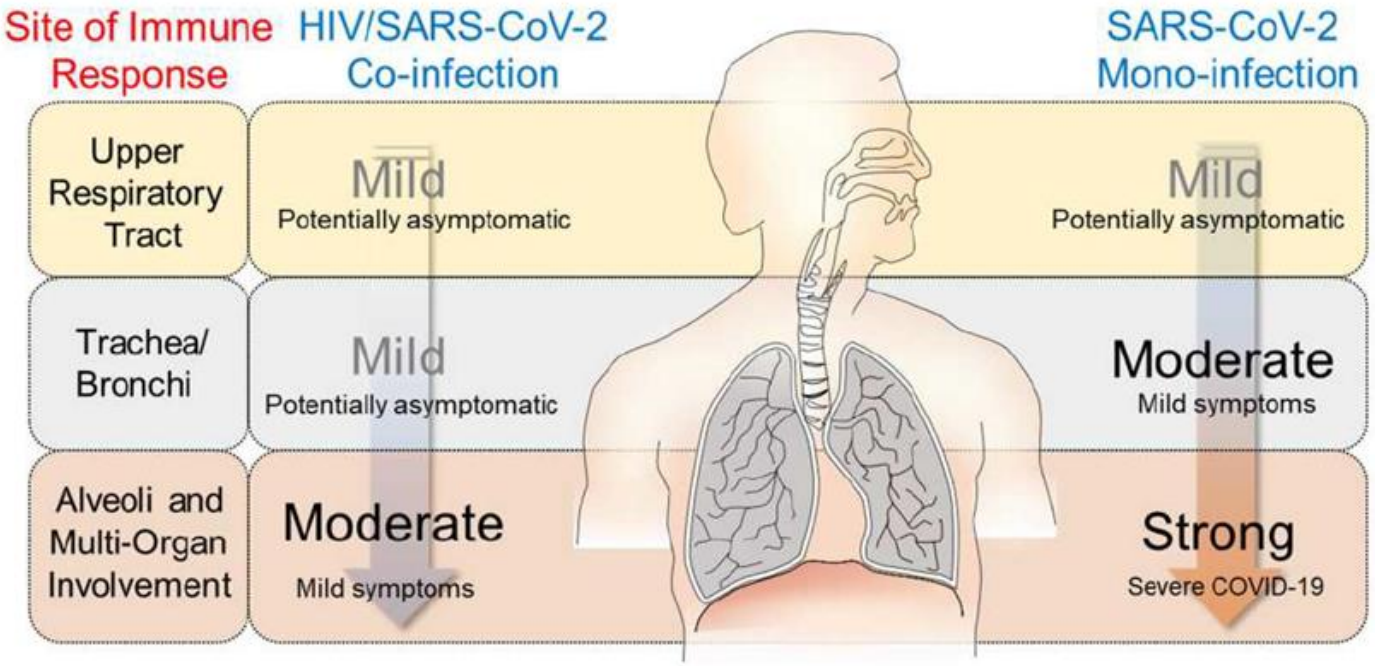
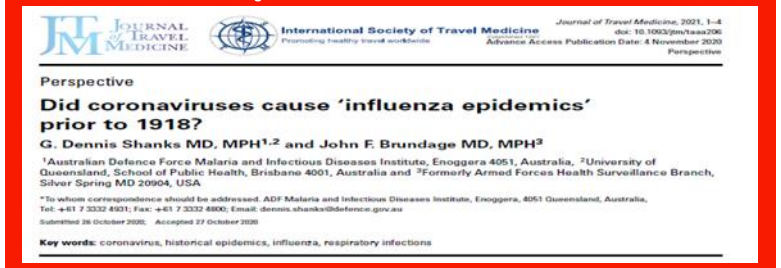


Figure 3 Hypothetical differences in immune response in HIV/SARS CoV-2 co-infection and SARS-CoV-2 mono-infection and potential implications in the development of COVID-19. A milder immune response is observed in HIV/SARS CoV-2 co-infection, potentially due to a chronically lower immunocompetency in patients living with managed HIV. While the patients are not immunodeficient, they are immunosuppressed. This may reduce the severity of the inflammation that occurs with infection, and lead to a better prognosis for PLWH who become infected with SARS-CoV-2. In turn this would mean a weakened cytokine storm would occur when the virus has reached the lungs and entered the blood, spreading to other organs. The weakened cytokine storm would entail lower systemic inflammation and cause less damage to other organs.

Uma procadora pergunta relativa ao passado …



Journal of Travel Medicine

International Society of Travel Medicine

Journal of Travel Medicine, 2021, 1–4
doi: 10.1093/jtm/taaa206
Advance Access Publication Date: 4 November 2020
Perspective

Perspective

Did coronaviruses cause 'influenza epidemics' prior to 1918?

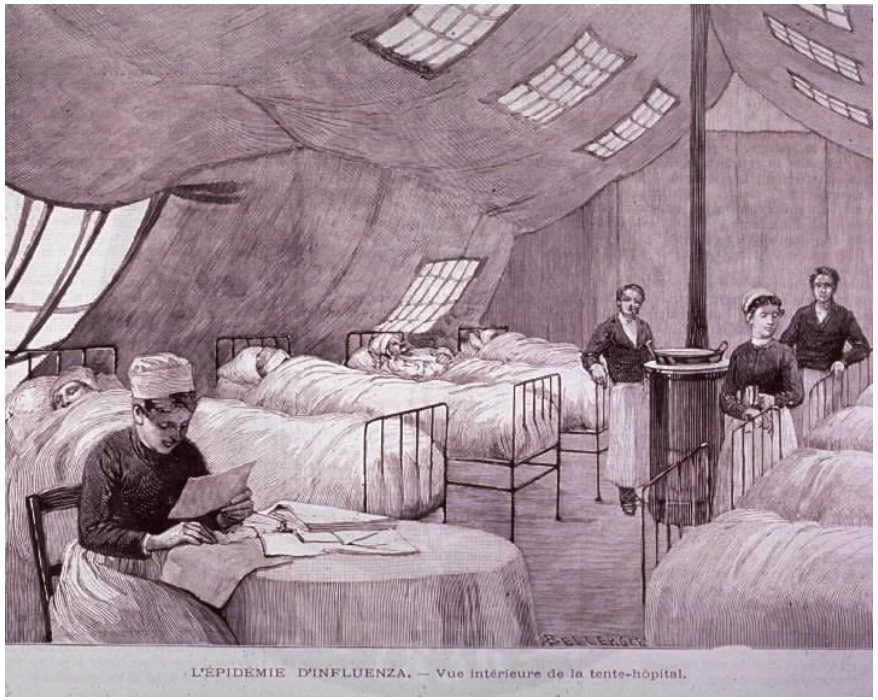
G. Dennis Shanks MD, MPH[1,2] and John F. Brundage MD, MPH[3]

[1]Australian Defence Force Malaria and Infectious Diseases Institute, Enoggera 4051, Australia, [2]University of Queensland, School of Public Health, Brisbane 4001, Australia and [3]Formerly Armed Forces Health Surveillance Branch, Silver Spring MD 20904, USA

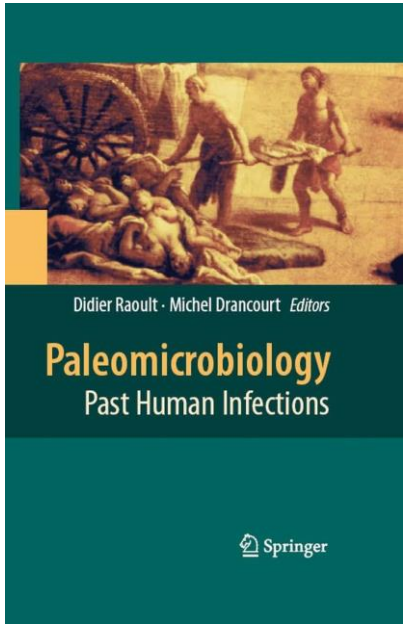
*To whom correspondence should be addressed. ADF Malaria and Infectious Diseases Institute, Enoggera, 4051 Queensland, Australia. Tel: +61 7 3332 4931; Fax: +61 7 3332 4800; Email: dennis.shanks@defence.gov.au

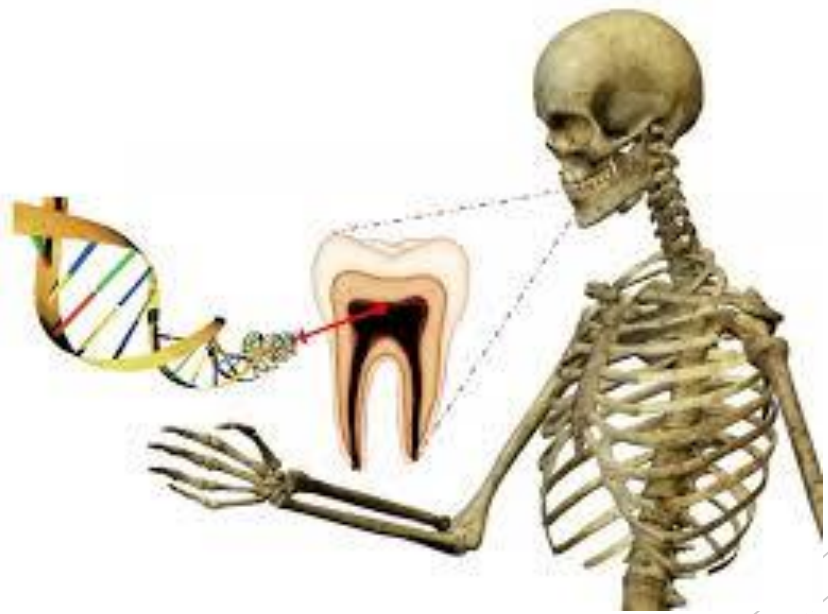
Submitted 26 October 2020; Accepted 27 October 2020

Key words: coronavirus, historical epidemics, influenza, respiratory infections

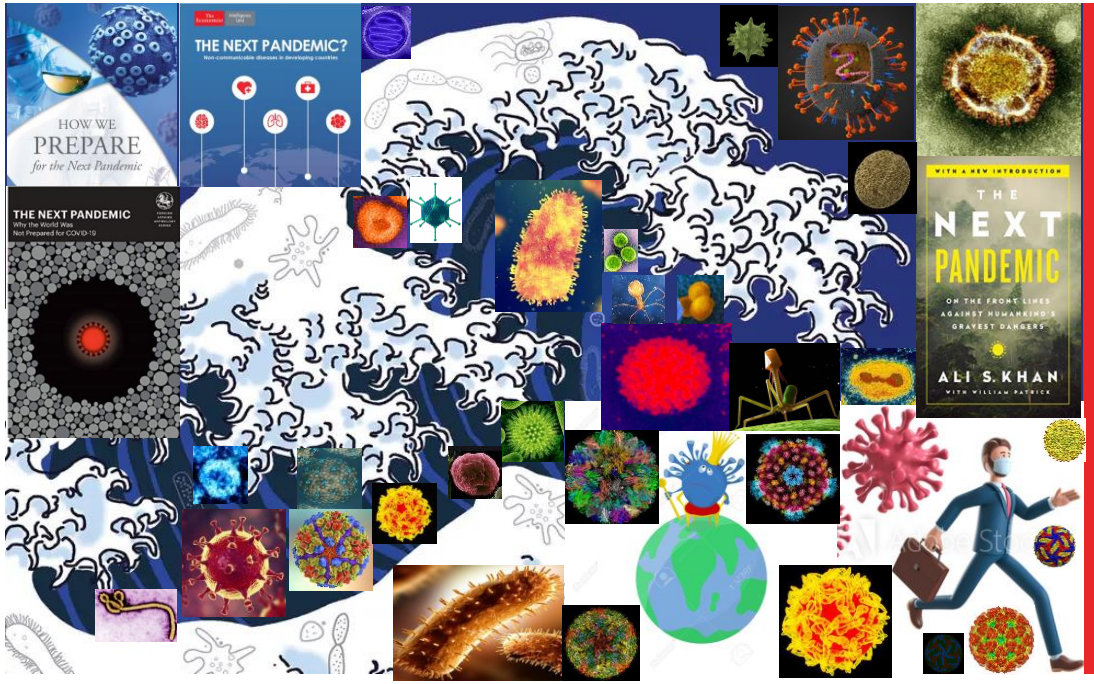


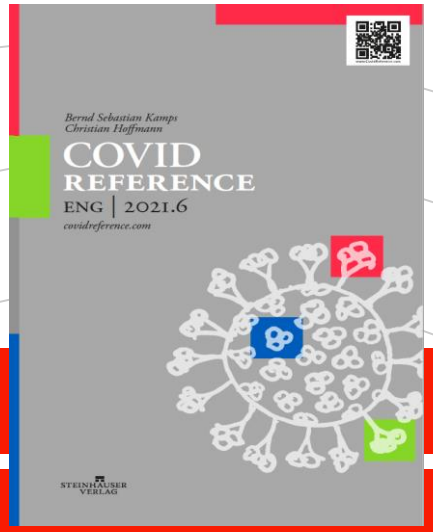
L'ÉPIDEMIE D'INFLUENZA. — Vue intérieure de la tente-hôpital.





… como pretexto para fazer uma outra, quase a terminar: Quando, Qual e a partir de Onde se deflagrará a próxima Pandemia?





Fim...

Para consultar, ler e meditar!!!

viruses

MDPI

Review

COVID-19: Look to the Future, Learn from the Past

Zhangkai J. Cheng [1,2,*,†], Hui-Qi Qu [2,†], Lifeng Tian [2], Zhifeng Duan [2] and Hakon Hakonarson [2,3,4,5,*]

1 Institute of Medical Physics, School of Physics, University of Sydney, Sydney, NSW 2006, Australia
2 Center for Applied Genomics, The Children's Hospital of Philadelphia, Philadelphia, PA 19104, USA; quh@email.chop.edu (H.-Q.Q.); tianl@email.chop.edu (L.T.); bravewindheart@163.com (Z.D.)
3 Department of Pediatrics, The Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA
4 Division of Human Genetics, Children's Hospital of Philadelphia, Philadelphia, PA 19104, USA
5 Division of Pulmonary Medicine, Children's Hospital of Philadelphia, Philadelphia, PA 19104, USA
* Correspondence: jasontable@gmail.com (Z.J.C.); Hakonarson@email.chop.edu (H.H.)
† These authors contributed equally to this work.

Received: 31 August 2020; Accepted: 28 October 2020; Published: 29 October 2020

check for updates

UN environment programme

COVID-19 RESPONSE

ILRI INTERNATIONAL LIVESTOCK RESEARCH INSTITUTE

CGIAR

PREVENTING THE NEXT PANDEMIC

Zoonotic diseases and how to break the chain of transmission

A Scientific Assessment with Key Messages for Policy-Makers
A Special Volume of UNEP's *Frontiers* Report Series

"REFLEXÕES EM TEMPOS DE PANDEMIA: HISTÓRIAS DE VIDA, DE PRAZER, DE SOFRIMENTO E DE MORTE"

Autor: José MD Poças

Não podemos deixar esquecer a dimensão Humana desta Pandemia!!!

Um convite de índole pessoal para a cerimónia de apresentação do meu próximo livro