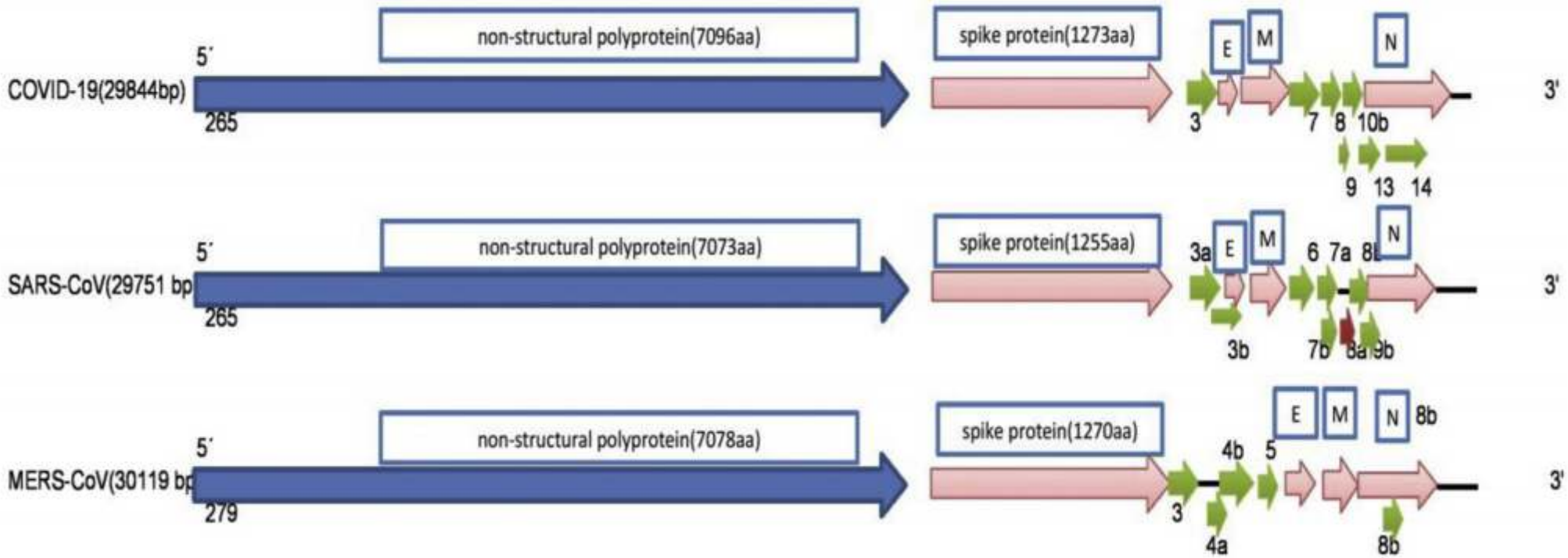
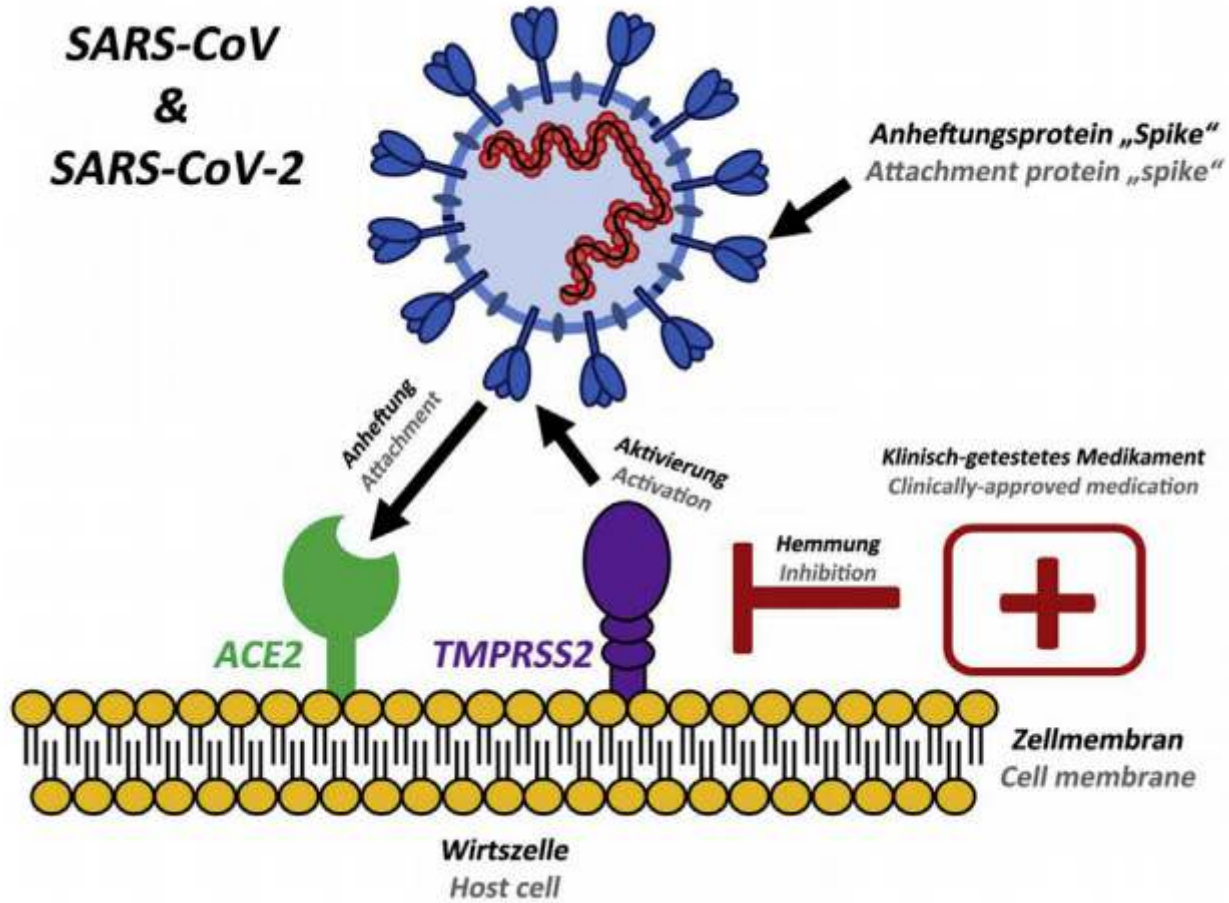
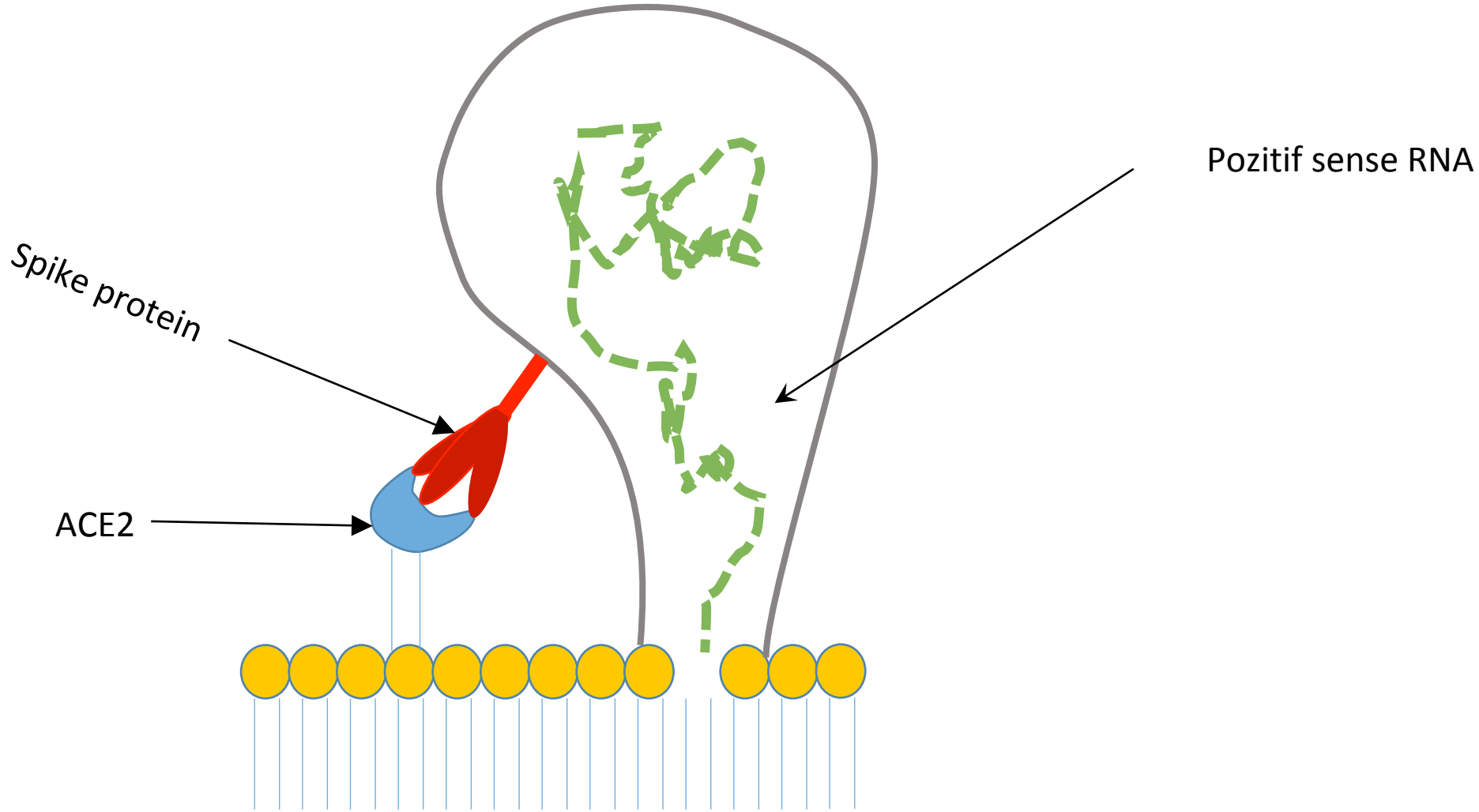
COVID-19

Haluk VAHABOĞLU


non-structural polyprotein(7096aa)
spike protein(1273aa)
5´
COVID-19(29844bp)
265
E
M
N
3
7
8
10b
9
13
14
3'
non-structural polyprotein(7073aa)
spike protein(1255aa)
5´
SARS-CoV(29751 bp
265
3a
E
M
6
7a
N
3b
7b
3'
non-structural polyprotein(7078aa)
spike protein(1270aa)
5´
MERS-CoV(30119 bp
279
E
M
N
8b
4b
5
3
4a
8b
3'


SARS-CoV
&
SARS-CoV-2
Anheftungsprotein „Spike“
Attachment protein „spike“
Anheftung
Attachment
Aktivierung
Activation
Klinisch-getestetes Medikament
Clinically-approved medication
Hemmung
Inhibition
ACE2
TMPRSS2
Zellmembran
Cell membrane
Wirtszelle
Host cell


Spike protein
ACE2
Pozitif sense RNA

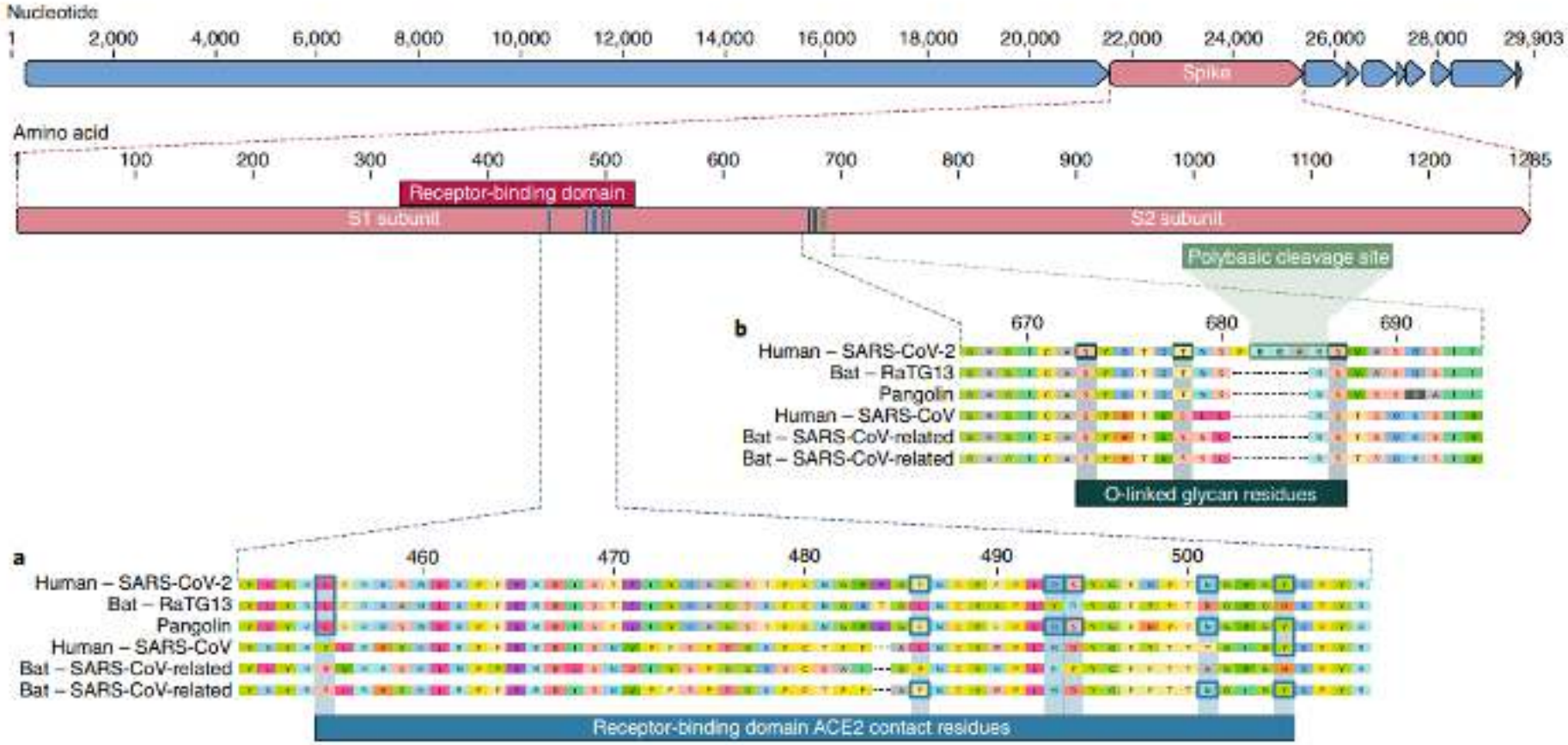


Fig. 1 | Features of the spike protein in human SARS-CoV-2 and related coronaviruses. a, Mutations in contact residues of the SARS-CoV-2 spike protein. The spike protein of SARS-CoV-2 (red bar at top) was aligned against the most closely related SARS-CoV-like coronaviruses and SARS-CoV itself. Key residues in the spike protein that make contact to the ACE2 receptor are marked with blue boxes in both SARS-CoV-2 and related viruses, including SARS-CoV (Urbani strain). **b**, Acquisition of polybasic cleavage site and O-linked glycans. Both the polybasic cleavage site and the three adjacent predicted O-linked glycans are unique to SARS-CoV-2 and were not previously seen in lineage B betacoronaviruses. Sequences shown are from NCBI GenBank, accession codes MN908947, MN996532, AY278741, KY417146 and MK211376. The pangolin coronavirus sequences are a consensus generated from SRR10168377 and SRR10168378 (NCBI BioProject PRJNA573298)[29,30].

Nature Medicine **volume 26**, pages450–452(2020)

- Natural selection in an animal host before zoonotic transfer
  - Neither the bat betacoronaviruses nor the pangolin betacoronaviruses sampled thus far have polybasic cleavage sites
  - For a precursor virus to acquire both the polybasic cleavage site and mutations in the spike protein suitable for binding to human ACE2, an animal host would probably have to have a high population density (to allow natural selection to proceed efficiently) and an ACE2-encoding gene that is similar to the human orthologue
- Natural selection in humans following zoonotic transfer
  - This scenario presumes a period of unrecognized transmission in humans between the initial zoonotic event and the acquisition of the polybasic cleavage site
- Selection during passages
  - The acquisition of both the polybasic cleavage site and predicted O-linked glycans also argues against culture-based scenarios

Leading Edge
Commentary

Cell

A Genomic Perspective on the Origin and Emergence of SARS-CoV-2

Yong-Zhen Zhang[1] and Edward C. Holmes[1,2,*]
[1]Shanghai Public Health Clinical Center and School of Life Science, Fudan University, Shanghai, China
[2]Marie Bashir Institute for Infectious Diseases and Biosecurity, School of Life and Environmental Sciences and School of Medical Sciences, The University of Sydney, Sydney, Australia
*Correspondence: edward.holmes@sydney.edu.au
https://doi.org/10.1016/j.cell.2020.03.035

It seems inevitable that SARS-CoV-2 will become the fifth endemic coronavirus in the human population (along with HKU1,NL63, OC43, and 229E) and one that is currently spreading in a totally susceptible population.

Pulmonary post-mortem findings in a series of COVID-19 cases from northern Italy: a two-centre descriptive study

Luca Carsana, Aurelio Sonzogni, Ahmed Nasr, Roberta Simona Rossi, Alessandro Pellegrinelli, Pietro Zerbi, Roberto Rech, Riccardo Colombo, Spinello Antinori, Mario Corbellino, Massimo Galli, Emanuele Catena, Antonella Tosoni, Andrea Gianatti, Manuela Nebuloni

The Lancet Infectious Diseases, 2020

- macrophages in the alveolar lumina (in 24 cases)
- lymphocytes in the interstitium (in 31 cases)
- **necrosis of pneumocytes (in all cases),**
- hyaline membranes (in 33 cases),
- interstitial and intra-alveolar oedema (in 37 cases),
- **type 2 pneumocyte hyperplasia (in all cases),**

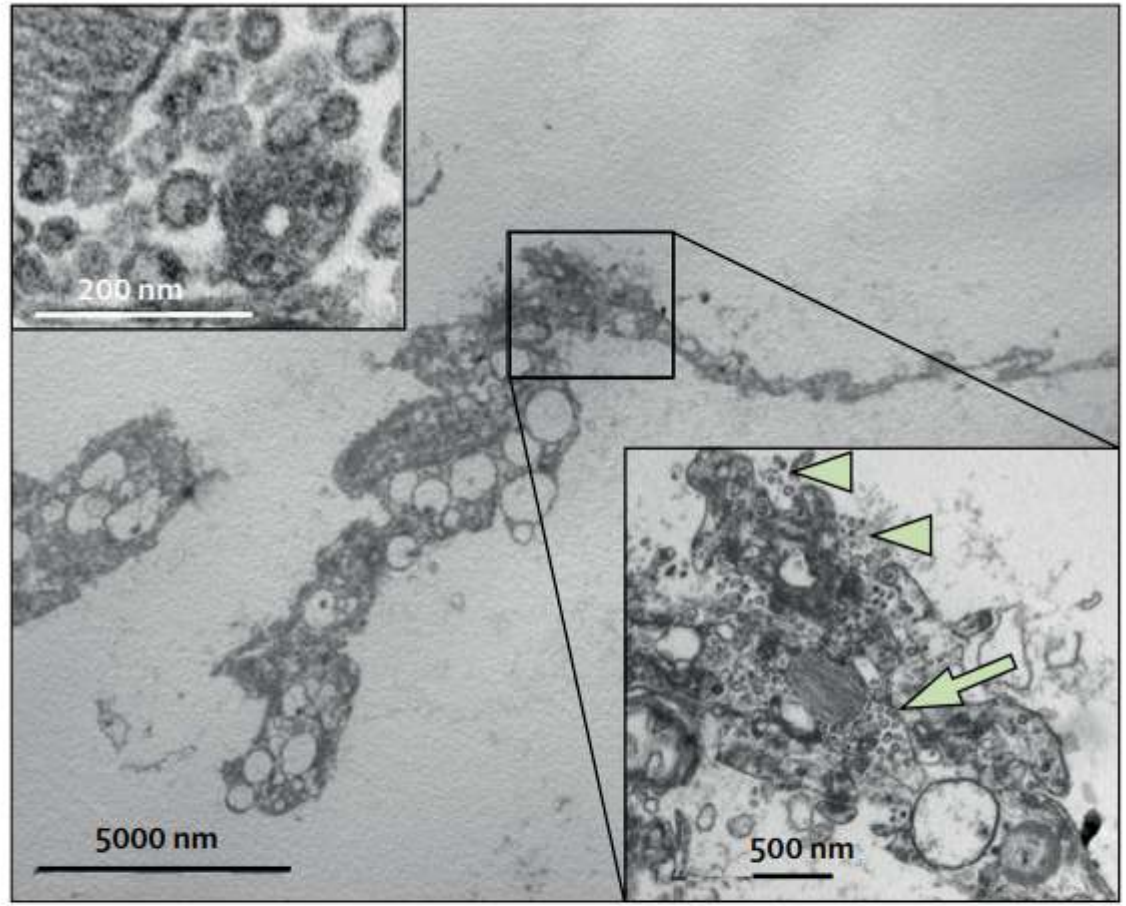


Figure 2: **Electron microscopy of a representative case**
Flat type 2 pneumocyte without lamellar electron-dense bodies of surfactant free in the alveolar space, containing numerous virions (inset bottom right) in cytoplasmic vacuoles (arrow) and along the plasma membrane (arrow heads). Virions had an average diameter of 82 nm, and viral projection about 13 nm in length (inset upper left, original magnification × 85 000).

Modern Pathology (2020) 33:1007–1014
https://doi.org/10.1038/s41379-020-0536-x

USCAP

ARTICLE

Pathological study of the 2019 novel coronavirus disease (COVID-19) through postmortem core biopsies

Sufang Tian[1] · Yong Xiong[2] · Huan Liu[1] · Li Niu[1] · Jianchun Guo[1] · Meiyan Liao[3] · Shu-Yuan Xiao[1,4]

- Advanced DAD and
- Superimposed bacterial pneumonia

Journal of
Clinical Medicine

MDPI

Editorial

COVID-19 Deaths: Are We Sure It Is Pneumonia? Please, Autopsy, Autopsy, Autopsy!

Cristoforo Pomara [1,2,*], Giovanni Li Volti [3,*] and Francesco Cappello [4,5,*]

- Are we sure that is it correct to treat COVID-19 as a severe pneumonia?
- Are we sure people are dying “with” and not “because of” COVID-19?

JOURNAL OF VIROLOGY, Dec. 2005, p. 15511–15524 Vol. 79, No. 24
0022-538X/05/$08.00+0 doi:10.1128/JVI.79.24.15511–15524.2005
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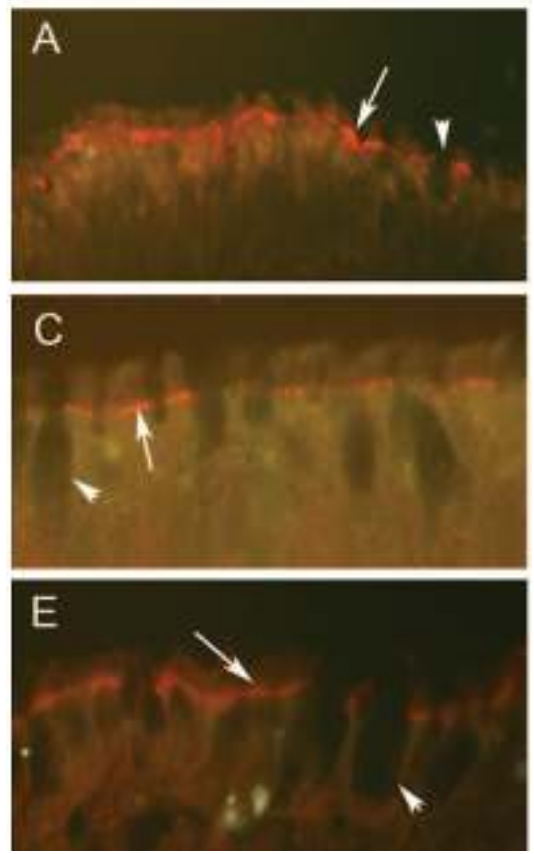
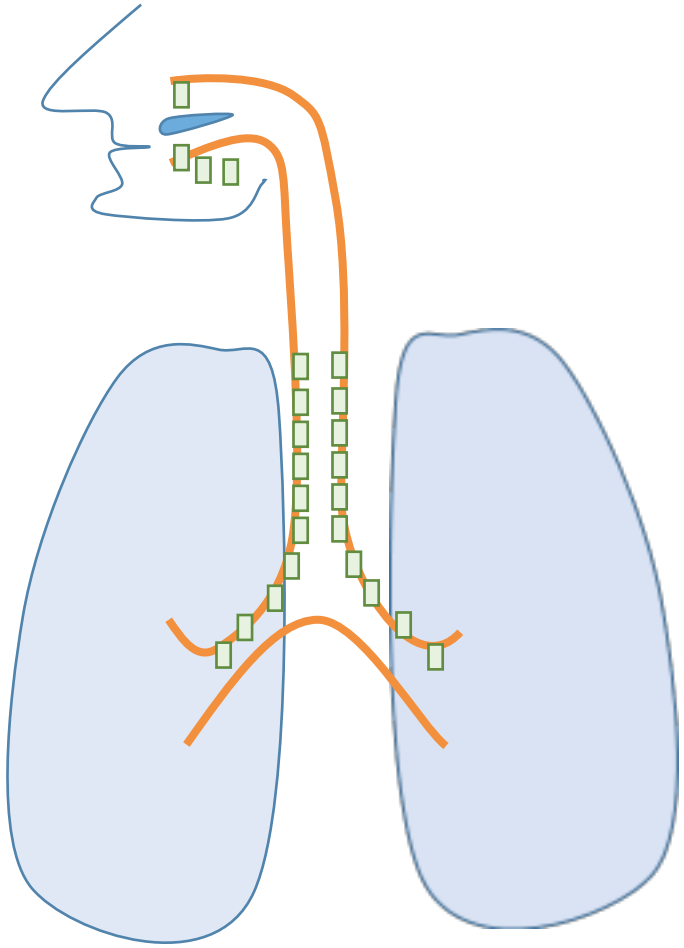
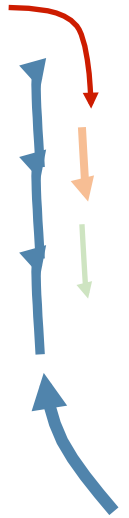
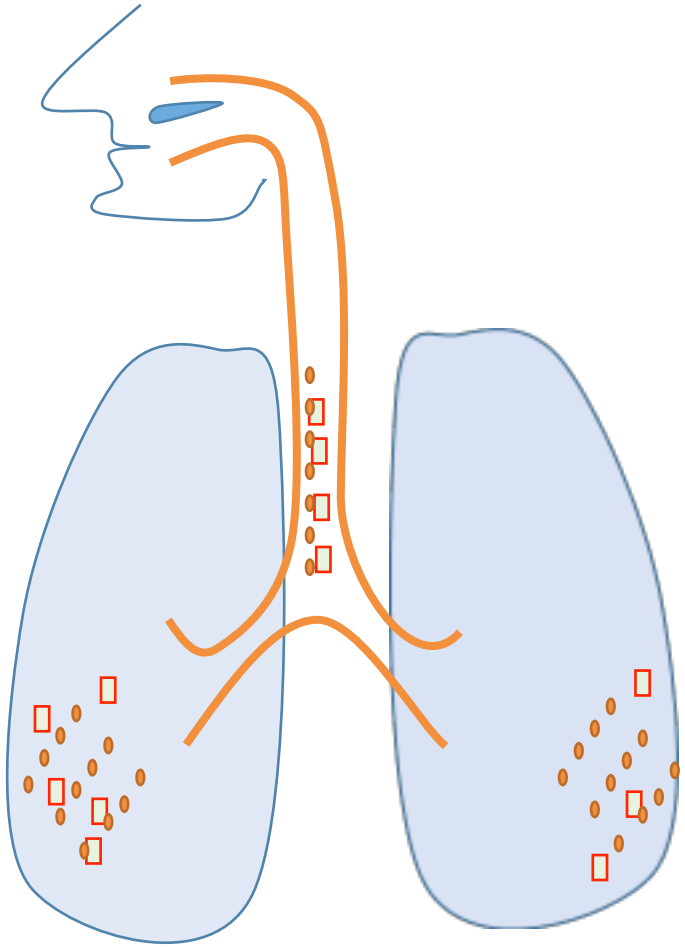
Severe Acute Respiratory Syndrome Coronavirus Infection of Human Ciliated Airway Epithelia: Role of Ciliated Cells in Viral Spread in the Conducting Airways of the Lungs

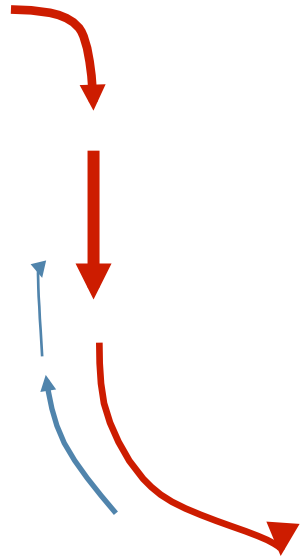
Amy C. Sims,[1]* Ralph S. Baric,[1,2] Boyd Yount,[1] Susan E. Burkett,[3] Peter L. Collins,[4] and Raymond J. Pickles[2,3]











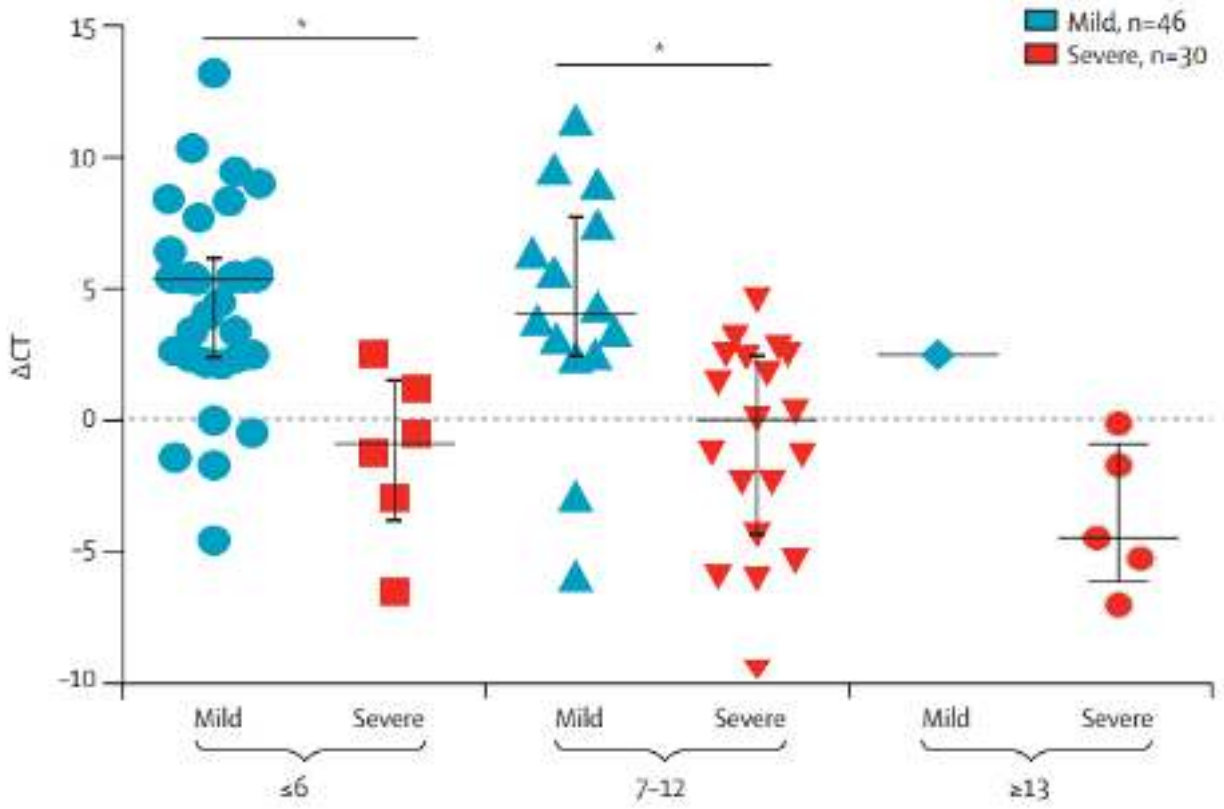
$$y = \beta_0 + \beta_1 x_1 + \varepsilon$$

$$y = logit(p/(1-p))$$

Tablo 1. PCR testi ile SARS-CoV-2 pozitif izlediğimiz hastalar										
YAS	IMUGEAH				USA (New York)			ITALYA		ÇİN
	ÖLDÜ	SAĞ	ORAN		erkek	kadın				
[0,40]	3	380	% 0.78							
(40,50]	1	156	% 0.64		%8.2	%2.5		%0.6		%3.7
(50,60]	3	142	% 2.07		%12.2	%6.9		%2.7		%12.7
(60,70]	8	69	% 10.39		%18.7	%12.0		%8.6		%30.2
(70,80]	5	41	% 10.87		%35.8	%27.4		%35.6		%30.5
(80,90]	8	23	% 25.81		%60.6	%48.1		%52.3		%20.3
(90,100]	1	6	% 14.29		%63.6	%46.4				

[1] *Richardson, S., Hirsch, J. S., Narasimhan, M., Crawford, J. M., McGinn, T., Davidson, K. W., ... & Cookingham, J. (2020). Presenting characteristics, comorbidities, and outcomes among 5700 patients hospitalized with COVID-19 in the New York City area. Jama.*
[2] *Onder, G., Rezza, G., & Brusaferro, S. (2020). Case-fatality rate and characteristics of patients dying in relation to COVID-19 in Italy. Jama, 323(18), 1775-1776.*
[3] *Data Çin CDC kaynaklarından Onder et al. Tarafından derlenmiştir*

Virüs yükü



Lancet Infect Dis 2020 https://doi.org/10.1016/ S1473-3099(20)30232-2

$$y = \beta\downarrow 0 + \beta\downarrow 1 \ yas + \beta\downarrow 2 \ viral \ y\ddot{u}k + \varepsilon$$

- YAŞ = rejenerasyon yeteneğini
- Viral yük =
  - Alınan enfektif materyal miktarı
  - ACE_2 + TMPRSS2 taşıyan hücre sayısı ve lokalizasyonu

CT Manifestations of Coronavirus Disease (COVID-19) Pneumonia and Influenza Virus Pneumonia: A Comparative Study

Liaoyi Lin, MD[1], Gangze Fu, MD, Shuangli Chen, MD, Jiejie Tao, MD, Andan Qian, MD, Yunjun Yang, PhD, Meihao Wang, PhD

- The properties of the largest lesion,
- presence of ground-glass opacity,
- presence of consolidation,
- mosaic attenuation,
- bronchial wall thickening,
- centrilobular nodules,
- interlobular septal thickening,
- crazy paving pattern,
- air bronchogram,

did not show significant differences ($p > 0.05$)

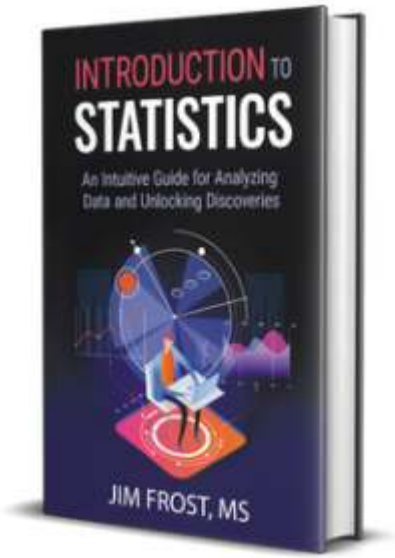
In addition, no significant difference was seen in CT score, length of the largest lesion, mean density, volume, or mass of the lesions between the two groups ($p > 0.05$)

Flu Shots, How Effective Are They?

By Jim Frost

Treatment	Flu count	Group size
Shot	49	5103
Placebo	74	2549

$$1 - \frac{0.009602}{0.029031} = 0.669$$



Absolute RD= 0.019 (0.026; 0.012)

bioRxiv preprint doi: https://doi.org/10.1101/2020.05.13.092619. this version posted May 22, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder. It is made available under a CC-BY-NC-ND 4.0 International license.

half-maximal neutralizing titers ranging from undetectable in 33% to below 1:1000 in 79%, while only 1% showed titers >1:5000. Antibody cloning revealed expanded clones of RBD-

	G (-)ive		G (+)ive	
	Yaşadı	**Öldü**	**Yaşadı**	**Öldü**
PCR				
Negative	2 (22%)	7 (78%)	4 (80%)	1 (20%)
Positive	2 (25%)	6 (75%)	2 (22%)	7 (78%)