Saúde Única e a pandemia da COVID-19 causada pelo novo coronavírus SARS-CoV-2

Origem zoonótica e contribuições da virologia

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Surroundings - wet market (Chinese city of Wuhan)

https://www.bangkokpost.com/world/1842104/why-wild-animals-are-a-key-ingredient-in-chinas-coronavirus-outbreak

31 dezembro/2019

Pneumonia em Hubei (China)

12 janeiro/2020

Novo coronavirus

26 março/2020
+530.000 casos
+24.000 mortes
+200 países

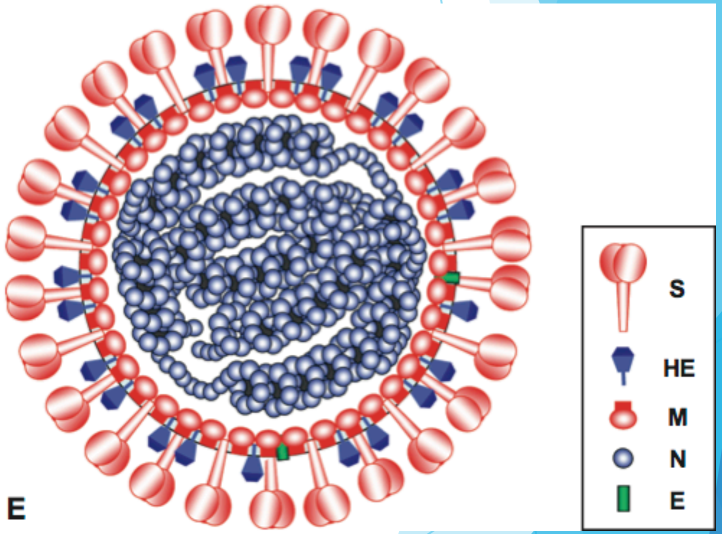
SARS-CoV-2 X COVID-19

O vírus

A doença

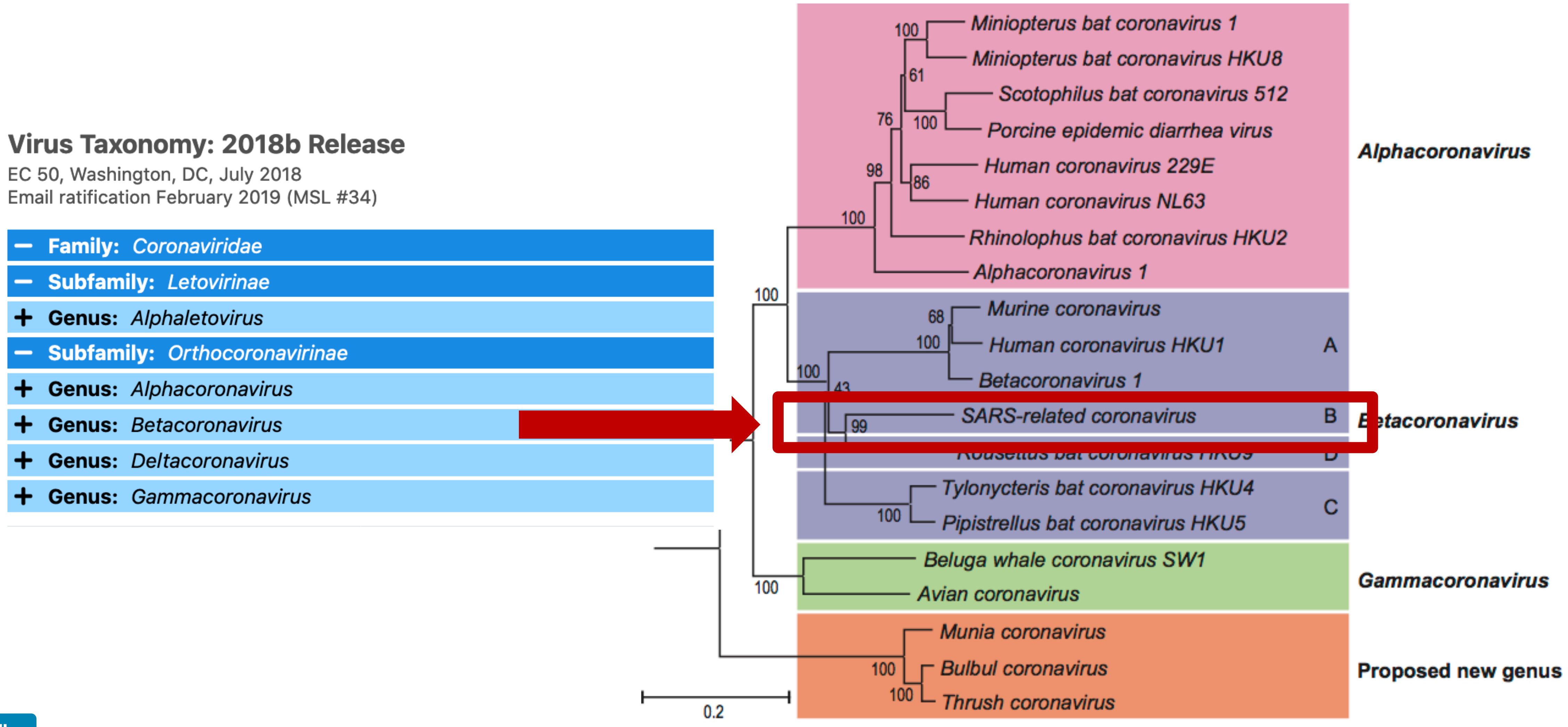
Coronavirus - CoV

- RNAfs+ linear
  - Mutações pontuais
  - Recombinação genética
  - Diversidade genética
- Envelopado
  - Sensibilidade
- 120–160 nm
- Classificação



Schematic representation of a (lineage A) betacoronavirus virion.

https://talk.ictvonline.org/ictv-reports/ictv_9th_report/positive-sense-rna-viruses-2011/w/posrna_viruses/223/coronaviridae-figures
https://health.clevelandclinic.org/the-new-coronavirus-what-is-it-and-should-you-worry/



Virus Taxonomy: 2018b Release

EC 50, Washington, DC, July 2018
Email ratification February 2019 (MSL #34)

- − **Family:** *Coronaviridae*
- − **Subfamily:** *Letovirinae*
- \+ **Genus:** *Alphaletovirus*
- − **Subfamily:** *Orthocoronavirinae*
- \+ **Genus:** *Alphacoronavirus*
- \+ **Genus:** *Betacoronavirus*
- \+ **Genus:** *Deltacoronavirus*
- \+ **Genus:** *Gammacoronavirus*

https://talk.ictvonline.org/ictv-reports/ictv_9th_report/positive-sense-rna-viruses-2011/w/posrna_viruses/223/coronaviridae-figures

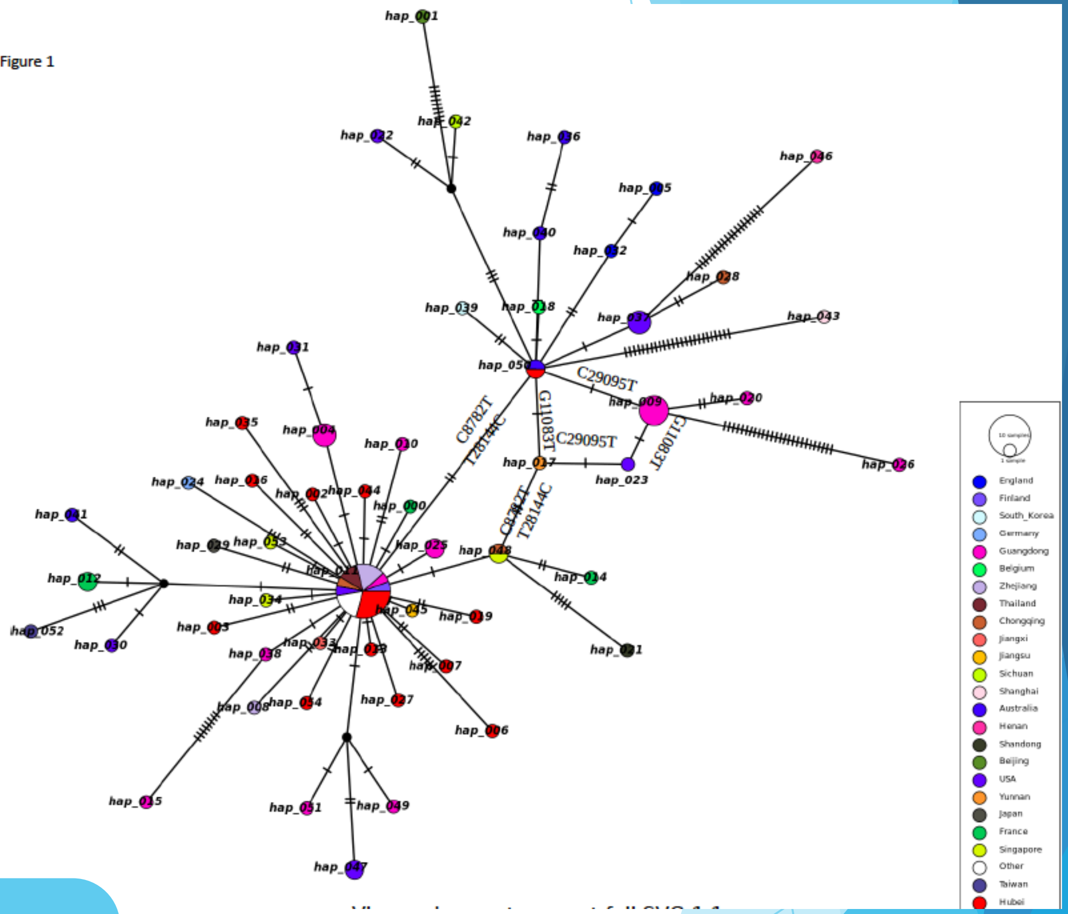
Coronavirus - CoV

Recombinação entre RNAs homólogos

Genótipos

Adaptação a novas espécies de hospedeiros

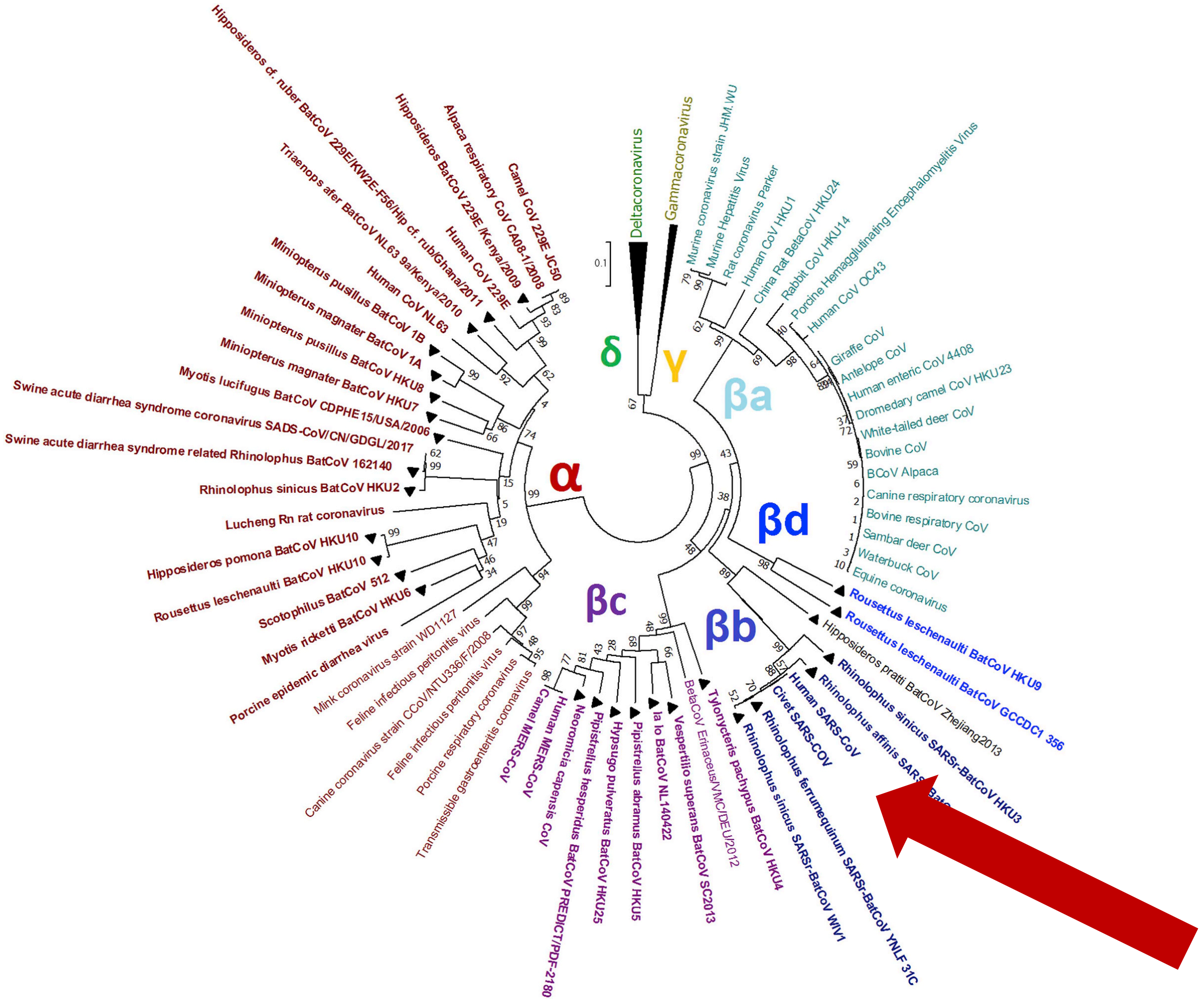
Figure 1



Clinical Infectious Diseases, ciaa219, https://doi.org/10.1093/cid/ciaa219

Infection, Genetics and Evolution 71 (2019) 21–30

Coronavirus - CoV - Diversidade genética




Infection, Genetics and Evolution 71 (2019) 21–30

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ELSEVIER

Review

Molecular epidemiology, evolution and phylogeny of SARS coronavirus

Hayes K.H. Luk[a], Xin Li[a], Joshua Fung[a], Susanna K.P. Lau[a,b,c,d,*], Patrick C.Y. Woo[a,b,c,d,*]

Fig. 2. The diversity of CoVs as demonstrated with a phylogenetic tree targeting the 303 bp partial RdRp sequence (position 15,293–15,596 with respect to Human SARS-CoV TOR2). The neighbor-joining phylogenetic tree was constructed with maximum composite likelihood method by MEGA 7.0. The test of phylogeny was statistically supported by the bootstraps value calculated from 1000 trees. Bat CoVs were labeled with black triangles. The branches of Gammacoronavirus and Deltacoronavirus were compressed.

ESTUDOS FILOGENÉTICOS

Hospedeiro ancestral

Hospedeiro intermediário

Humanos

Bat, *Rhinolophus affinis*
Alexandre Hassanin

α e β

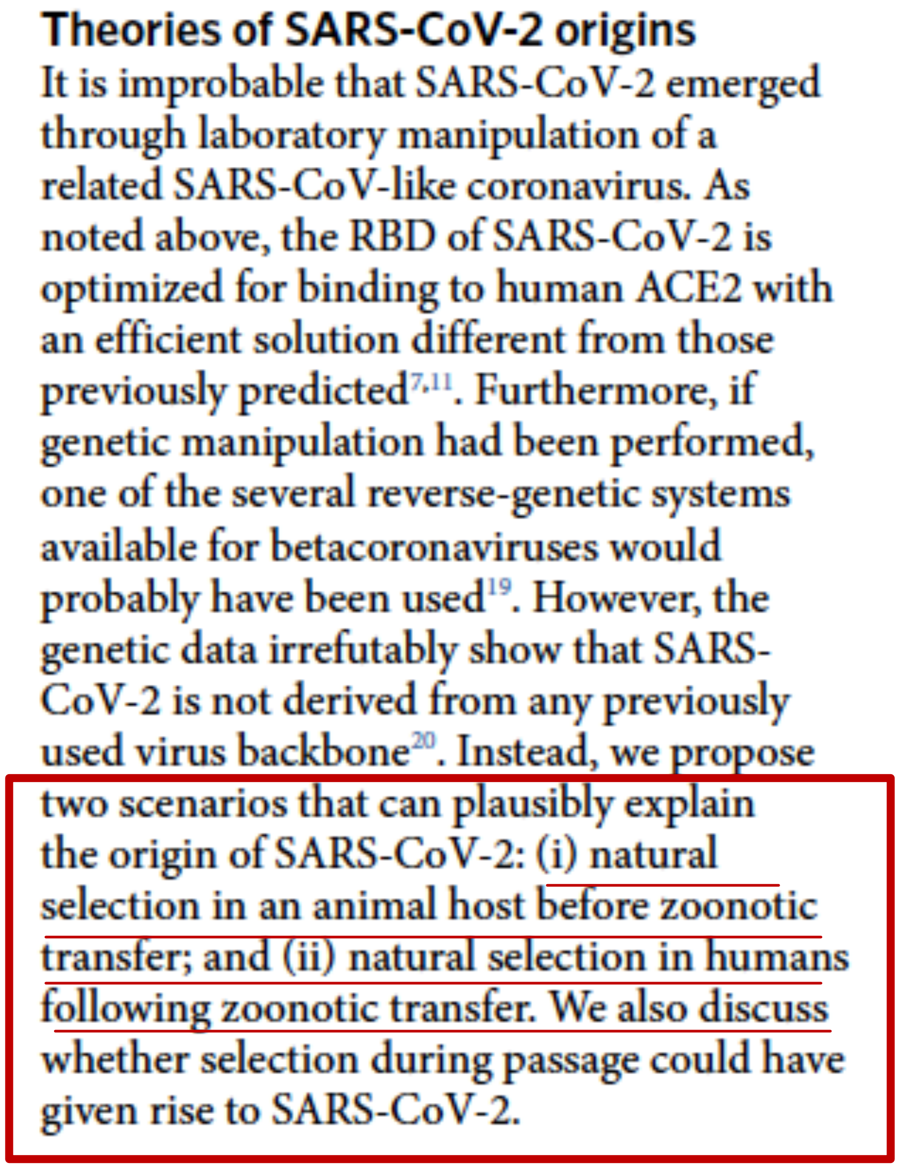
?

~~Serpente~~
Civeta?
Pangolim?
...

https://theconversation.com/coronavirus-origins-genome-analysis-suggests-two-viruses-may-have-combined-134059
https://olhardigital.com.br/coronavirus/noticia/xiaomi-esta-desenvolvendo-uma-mascara-de-protecao-facial-inteligente/97019

The proximal origin of SARS-CoV-2

NATURE MEDICINE | www.nature.com/naturemedicine



Theories of SARS-CoV-2 origins

It is improbable that SARS-CoV-2 emerged through laboratory manipulation of a related SARS-CoV-like coronavirus. As noted above, the RBD of SARS-CoV-2 is optimized for binding to human ACE2 with an efficient solution different from those previously predicted[7,11]. Furthermore, if genetic manipulation had been performed, one of the several reverse-genetic systems available for betacoronaviruses would probably have been used[19]. However, the genetic data irrefutably show that SARS-CoV-2 is not derived from any previously used virus backbone[20]. Instead, we propose two scenarios that can plausibly explain the origin of SARS-CoV-2: (i) natural selection in an animal host before zoonotic transfer; and (ii) natural selection in humans following zoonotic transfer. We also discuss whether selection during passage could have given rise to SARS-CoV-2.

Evidências genéticas:
NÃO foi sintetizado em laboratório

Seleção natural em hospedeiro animal ANTES?

Seleção natural em hospedeiro humano APÓS?

https://doi.org/10.1038/s41591-020-0820-9

Questões “virais” (ou vitais?)

- Presença da RNA ou de anticorpos?
- Infecção? (SARS-CoV-2)
- Doença? (COVID-19)
- Transmissão?

E mais

PRESSÃO DE SELEÇÃO

VARIABILIDADE GENÉTICA

CAPACIDADE TÉCNICA

VARIÁVEIS AMBIENTAIS

VARIÁVEIS SÓCIO-ECONÔMICAS

ONE HEALTH

WHAT'S NEXT?

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