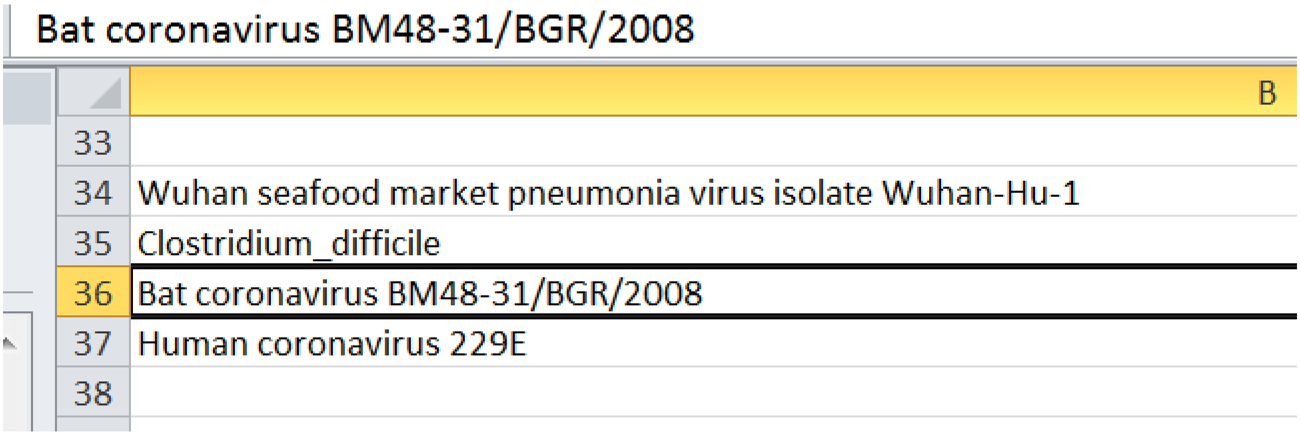
Twitter Thread by Billy Bostickson ■■&■ ■

Billy Bostickson ■■&■ ■
@BillyBostickson

@franciscodeasis @spectropan @ResearchGate @TheSeeker268 STRANGE TO SEE THIS IN Wuhan Hu-1
Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1
Clostridium_difficile
Bat coronavirus BM48-31/BGR/2008
Human coronavirus 229E



Bat coronavirus BM48-31/BGR/2008

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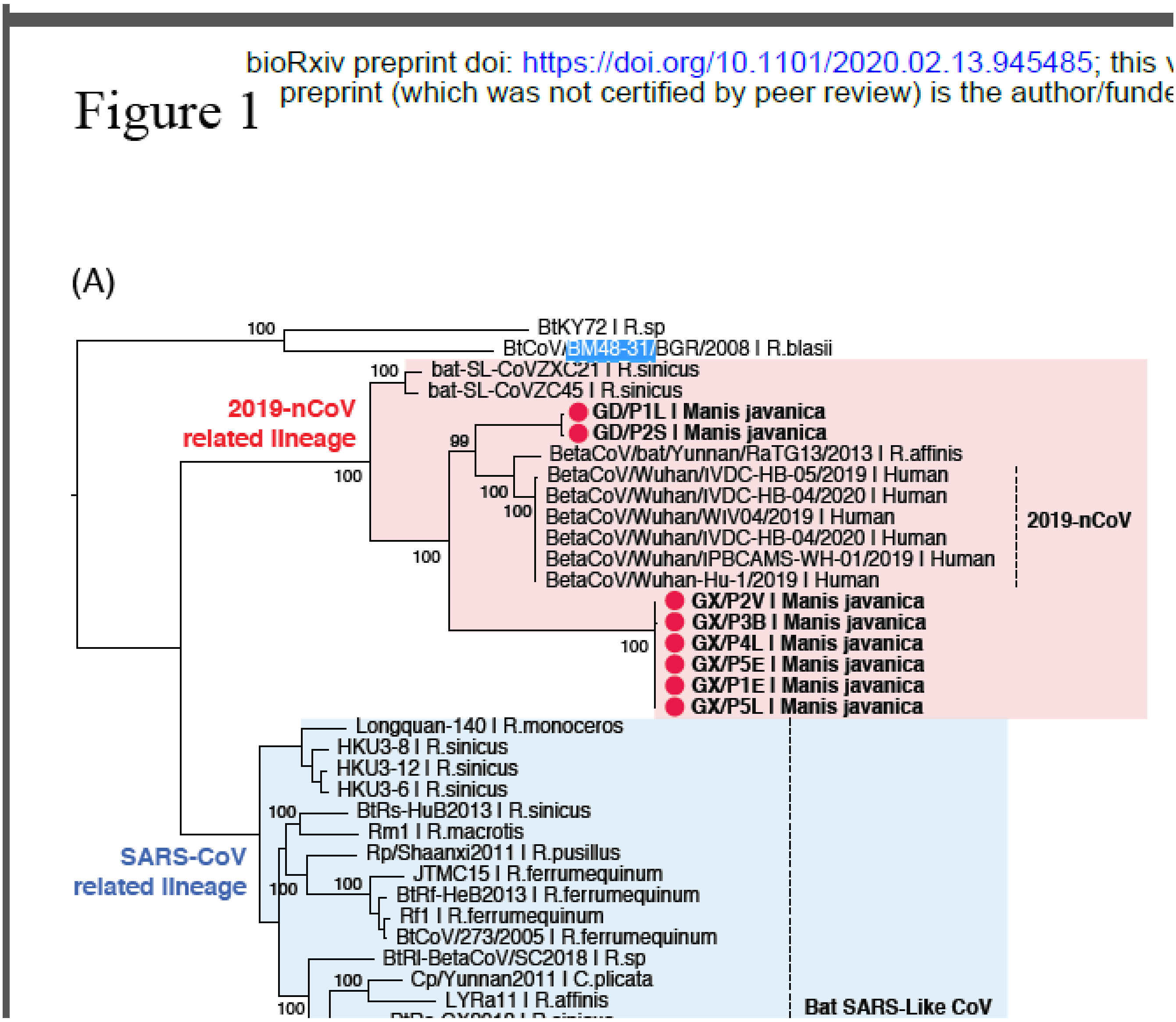
33	
34	Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1
35	Clostridium_difficile
36	Bat coronavirus BM48-31/BGR/2008
37	Human coronavirus 229E
38	

@Daoyu15 @franciscodeasis @spectropan @ResearchGate @TheSeeker268 A Bulgarian Bat Virus mentioned in Lam et al:
Identification of 2019-nCoV related coronaviruses in Malayan pangolins in southern China
https://t.co/XRV8YfQ62F



bioRxiv preprint doi: https://doi.org/10.1101/2020.02.13.945485; this v
preprint (which was not certified by peer review) is the author/funde

Figure 1

@Daoyu15 @franciscodeasis @spectropan @ResearchGate @TheSeeker268 Bat coronavirus BM48-31/BGR/2008

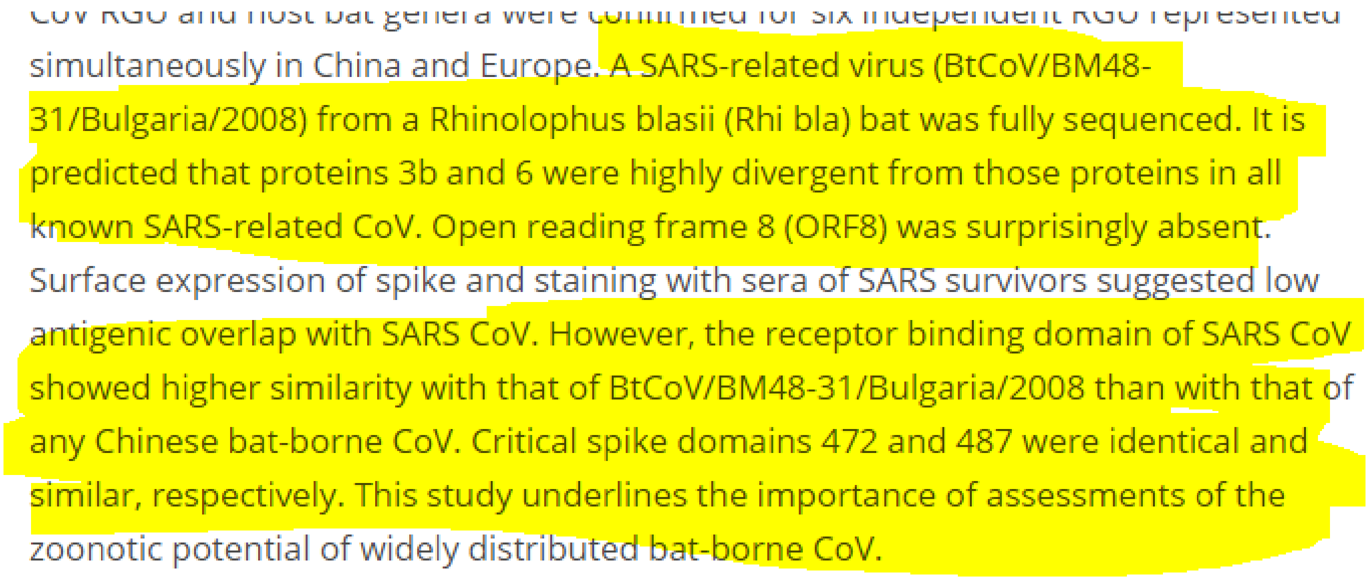
Drosten

https://t.co/TB7hfDmsD0
and
https://t.co/JiVyAkL3H5

Publications

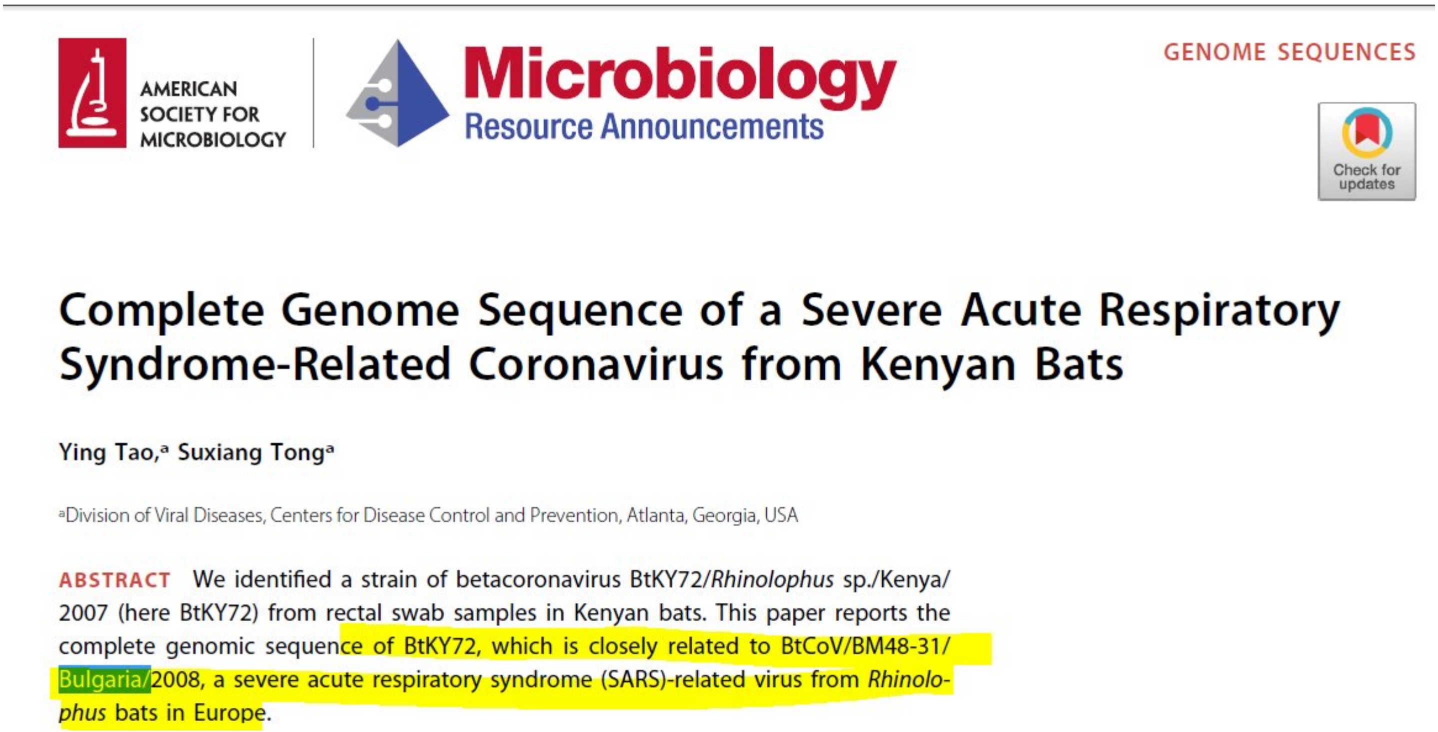
1. **"Genomic characterization of severe acute respiratory syndrome-related coronavirus in European bats and classification of coronaviruses based on partial RNA-dependent RNA polymerase gene sequences."**
Drexler J.F., Gloza-Rausch F., Glende J., Corman V.M., Muth D., Goettsche M., Seebens A., Niedrig M., Pfefferle S., Yordanov S., Zhelyazkov L., Hermanns U., Vallo P., Lukashev A., Muller M.A., Deng H., Herrler G., Drosten C.
J. Virol. 84:11336-11349(2010) [PubMed] [Europe PMC] [Abstract]

@Daoyu15 @franciscodeasis @spectropan @ResearchGate @TheSeeker268 Genomic characterization of severe acute respiratory syndrome-related coronavirus in European bats and classification of coronaviruses based on partial RNA-dependent RNA polymerase gene sequences.
https://t.co/apTzRc4RnK



CoV RGO and host bat genera were confirmed for six independent RGO represented simultaneously in China and Europe. A SARS-related virus (BtCoV/BM48-31/Bulgaria/2008) from a Rhinolophus blasii (Rhi bla) bat was fully sequenced. It is predicted that proteins 3b and 6 were highly divergent from those proteins in all known SARS-related CoV. Open reading frame 8 (ORF8) was surprisingly absent. Surface expression of spike and staining with sera of SARS survivors suggested low antigenic overlap with SARS CoV. However, the receptor binding domain of SARS CoV showed higher similarity with that of BtCoV/BM48-31/Bulgaria/2008 than with that of any Chinese bat-borne CoV. Critical spike domains 472 and 487 were identical and similar, respectively. This study underlines the importance of assessments of the zoonotic potential of widely distributed bat-borne CoV.

@Daoyu15 @franciscodeasis @spectropan @ResearchGate @TheSeeker268 Complete Genome Sequence of a SARS - Related Coronavirus from Kenyan Bats
Tao and Tong
https://t.co/pz17H1Abvm



GENOME SEQUENCES

Complete Genome Sequence of a Severe Acute Respiratory Syndrome-Related Coronavirus from Kenyan Bats

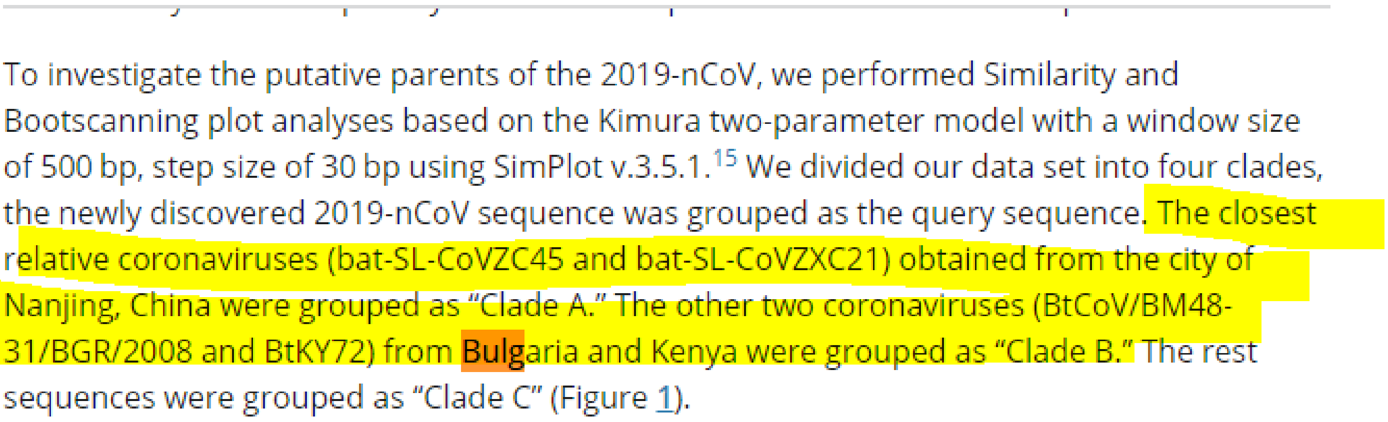
Ying Tao,[a] Suxiang Tong[a]

[a]Division of Viral Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia, USA

ABSTRACT We identified a strain of betacoronavirus BtKY72/*Rhinolophus* sp./Kenya/2007 (here BtKY72) from rectal swab samples in Kenyan bats. This paper reports the complete genomic sequence of BtKY72, which is closely related to BtCoV/BM48-31/Bulgaria/2008, a severe acute respiratory syndrome (SARS)-related virus from *Rhinolophus* bats in Europe.

@Daoyu15 @franciscodeasis @spectropan @ResearchGate @TheSeeker268 Cross■species transmission of the newly identified coronavirus 2019■nCoV
First published: 22 January 2020 https://t.co/3DuybjzTkW

https://t.co/RlDSE2xuDK



To investigate the putative parents of the 2019-nCoV, we performed Similarity and Bootscanning plot analyses based on the Kimura two-parameter model with a window size of 500 bp, step size of 30 bp using SimPlot v.3.5.1.[15] We divided our data set into four clades, the newly discovered 2019-nCoV sequence was grouped as the query sequence. The closest relative coronaviruses (bat-SL-CoVZC45 and bat-SL-CoVZXC21) obtained from the city of Nanjing, China were grouped as "Clade A." The other two coronaviruses (BtCoV/BM48-31/BGR/2008 and BtKY72) from Bulgaria and Kenya were grouped as "Clade B." The rest sequences were grouped as "Clade C" (Figure 1).

@Daoyu15 @franciscodeasis @spectropan @ResearchGate @TheSeeker268 Bulgarian Bat Virus BM48-31/BGR/2008
Referenced by Dorsten, Koopmans in
Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR
https://t.co/t3sC0yTjNw

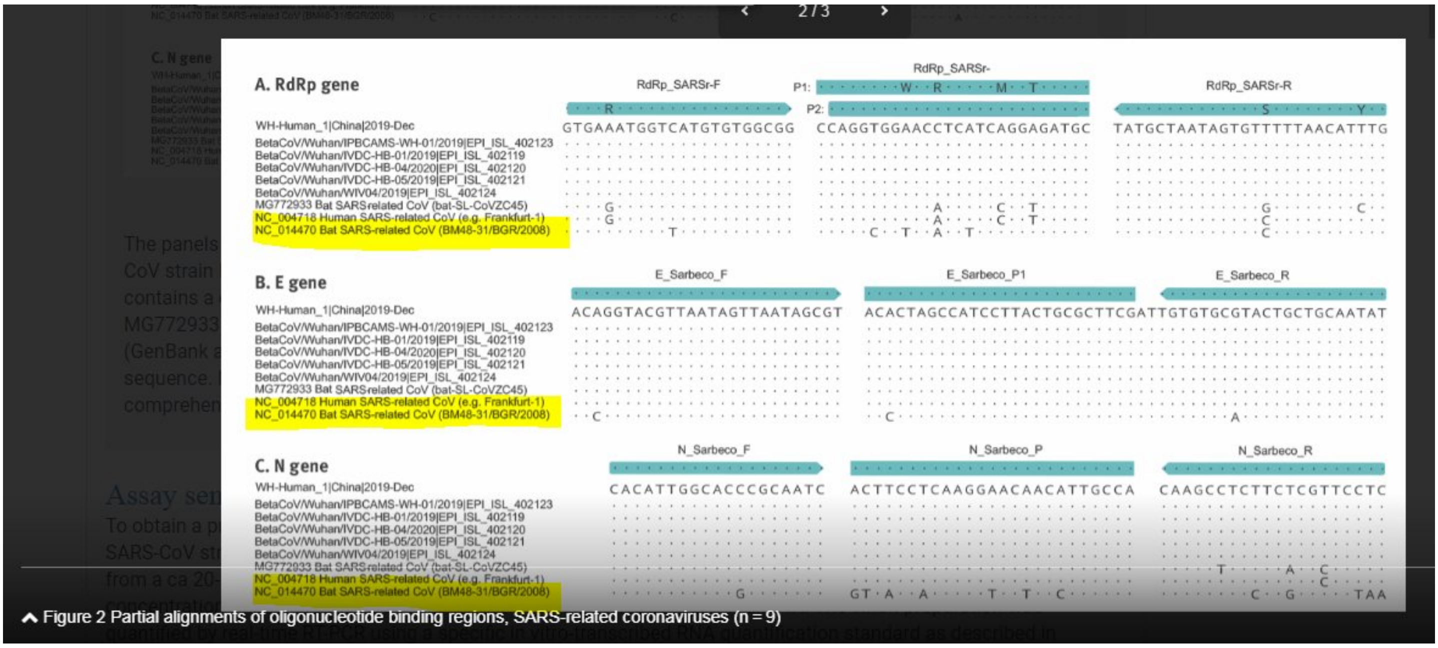


Figure 2 Partial alignments of oligonucleotide binding regions, SARS-related coronaviruses (n = 9)

@Daoyu15 @franciscodeasis @spectropan @ResearchGate @TheSeeker268 Despite claims by Abouelkhair MA. (2020) in "Non-SARS-CoV-2 genome sequences identified in clinical samples from COVID-19 infected patients" that these viral sequence traces are "Evidence for co-infections" https://t.co/xlLbkUDcNV
It is clear that this patient WAS NOT INFECTED...

@Daoyu15 @franciscodeasis @spectropan @ResearchGate @TheSeeker268 WITH A mysterious Bulgarian Bat Virus "BM48-31/BGR/2008". Instead it is yet more evidence of cross-contamination of Illumina sequence machines used by WIV as they were as far as we know the only institution in Wuhan to have experimented with this virus.
Correct me if I am wrong?