



Nicola Bidoli

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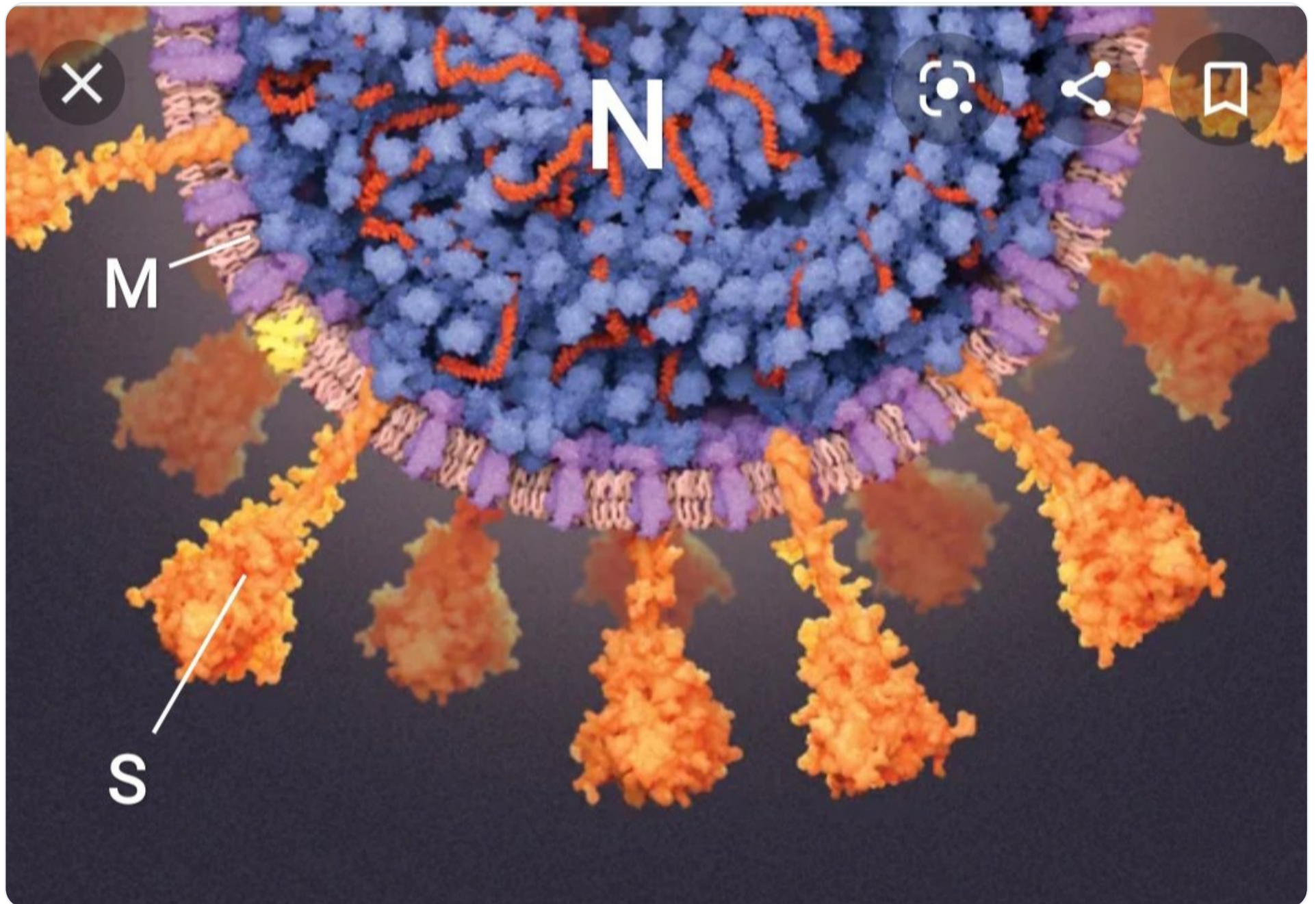
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IDENTIFICATION OF THE HIGHLY INFECTIVE GENOMIC COMPOSITION OF SARS COV 2 RNA:

1) SARS COV 2 is a particular chimeric "armored" virus, consisting of external protuberances of S (Spike) coated, externally, by glycans and, inside these protuberances, the TGEV



2) bacteria (E. Coli bacterium, of gastroenteritis) have been identified and HIV retroviruses.

The outer membrane M has the TMPRSS2 protein which, associated with ACE2, allows the same protein S to enter the host cells.

This mechanism is well explained

3) by the process of fusion of the M membrane with the plasma membrane of the cell. (It is important to note that a TMPRSS2 inhibitor is BROMEXINE).

The inner nucleus N is instead composed of highly pathogenic viral genomes such as: MVH / HCV (Hepatitis C) an RNA virus

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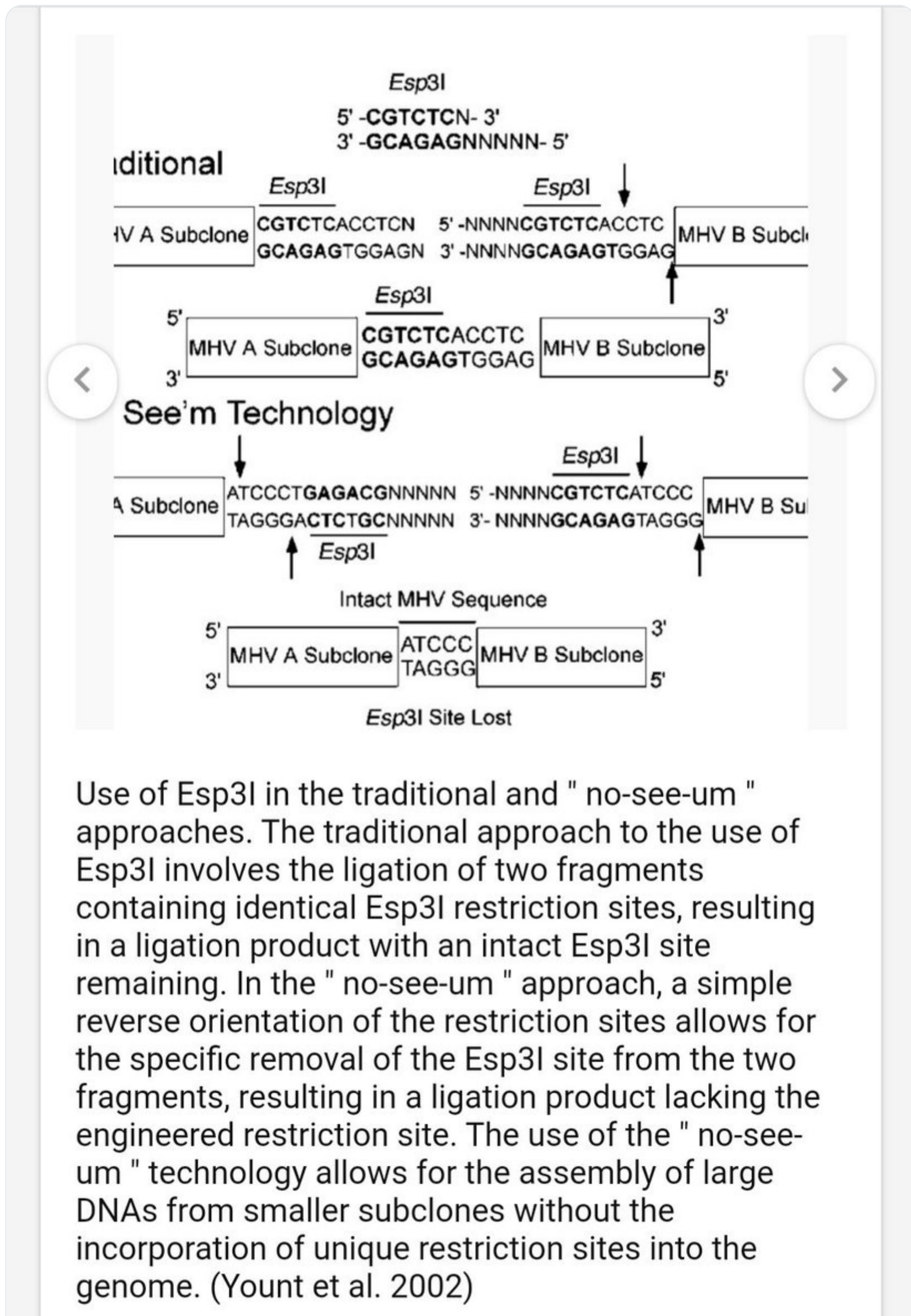
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4) belonging to the Flavivirus / Eie Yoelii family (malaria, such as ZIKA), and the viral sequences provided by the recombination of SARS with endogenous BaT CoV, such as: Marburg, Nipah, Hendra and Lyssavirus (rabies).

5)  SARS COV 2 CONSTRUCTION PROCESS:

 The fundamentals.

- The construction process of SARS COV 2 makes use of  "no-see-um" technology, developed by R. Baric, which allows the assembly of large DNAs, from smaller subclones, without the incorporation of



6) unique restriction sites in the genome. 📌

- Link:

researchgate.net/publication/81...

- This process consists of both serial passages in in-vitro cultures and the use of intermediate animals such as: humanized mice, ferrets, cats, hares, suckling pigs.

- This process was carried out in

7) the BSL2, BSL3, BSL4 Laboratories of the WIV / CAS of Whuan; where there have been several cases of environmental contamination and as many laboratory leaks caused by the use of laxive protocols.

- SARS (Acute Pulmonary Syndrome) + HCV (Hepatitis C) is

8) used to develop a first "armored virus" which is then recombined, in-vivo, with the "backbone" of some BaT CoV strains of bats which are natural carriers of highly infectious viral genomes.

- The consolidated infectious genome is then inoculated into

9) humanized, leukemic (HIV) mice to facilitate the passage of the virus into humanized T cells.

- An enhanced and advanced variant of SARS COV 2 is eventually transmitted, by airborne transmission, to ferrets (ORF8) in-vivo, in ACE2.

This enhanced version, obtained

10) using only the ORF8 protein, makes the SARS COV ORF8 virus extremely infectious, virulent and mutable.

📌📌📌 VIRAL ACTION OF SARS COV 2:

📌 The 3 strains:

1) TGEV / HIV

2) HCV / FLAVIVIRUS / ZIKA

3) MARBURG / NIPAH / HENDRA (BaT CoV)

were used to design different

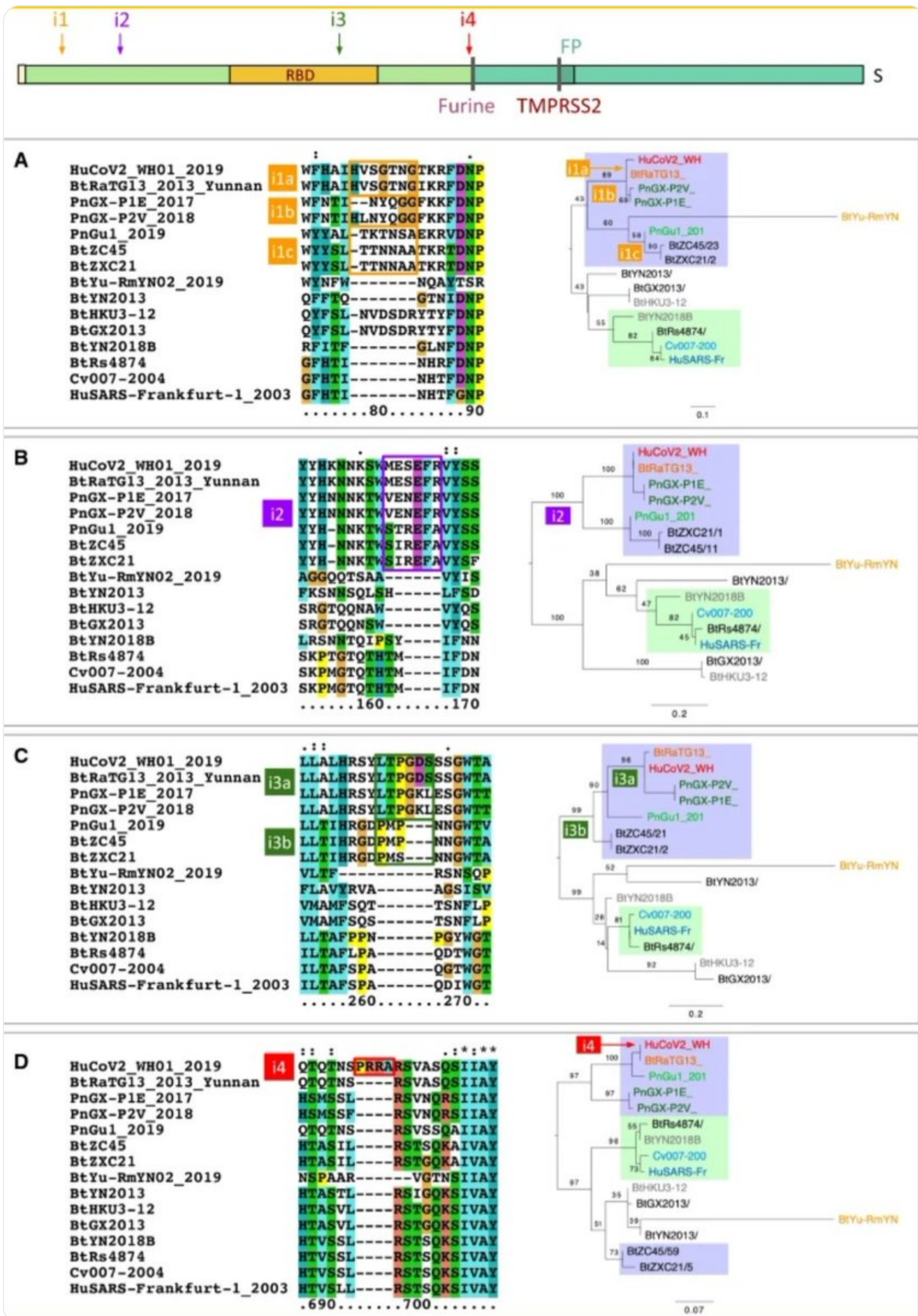
11) phases of aggression of the virus in the host ("clockwork effect").

📌 Phase 1) 4 HIV inserts (*) to create immunodeficiency of the host's immune system.

The HIV genome is surrounded by glycans (sugars) to deceive host cells and enter them (Perez / Montagnier).

📌 Phase 2) A first pathogenic action ZIKA (malaria) is then released which triggers the temperature increase in the host (Sorenson).

📌 Phase 3) takes advantage of the viral pathogens intrinsic characteristics of the BaT-CoV backbone used, for create, in the



13) host, a blood vessel constricting action, which causes a thrombin effect that coagulates the blood in the pulmonary alveoli of the host, leading to suffocation.

☞(*) Four insertions of short sequences were identified which are present in SARS-CoV-2 but

14) absent from some bats isolates and from SARS-CoV1.

In April 2020, Professor Luc Montagnier, the world's leading exponent for the study of HIV confirmed that these

15) out by humans.

This manipulation was carried out intentionally and, presumably, as part of a research aimed at developing vaccines against HIV.

Similar sequences between HIV and SARS-CoV-2 are short, around 30 nucleotides in a genome of 30,000, however bioinformatics

16) and molecular phylogeny approaches can provide interesting new information.

👉👉👉 ARCHIVE DOCUMENTATION VIRAL PATHOGENS UTILIZED FOR SARS COV 2:👉

👉 In MGC. AC Archive (China), is possible see an collection of pathogenic viruses used by PLA of CAS / WIV, of Whuan.👉

17) 👉 BAT SL COV ZC45

👉 BAT SL COV ZC21

👉 These three viruses are present in SARS COV 2, in addition to:

🔴 Bacterial group:

👉 TGEV (E. Coli / Gastroenteritis bacterium).

🔴 Retrovirus group:

👉 HIV1/HIV2, and SIV.

👉 MHV/HCV (Hepatitis C) FLAVIVIRUS (Malaria) EieYoelii / ZIKA.

18) 🔴 Pathogenic genomes:

👉 MARBURG

👉 NIPAH

👉 HENDRA.

👉 MGC. AC / CHN Archive: 👉

archive.is/Kof6L

19) End.

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


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


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9 Feb

🔗🔗🔗🔗 Lab Baric  "Our mouse adapted #SARSCoV2 strain, MA10, is now available from BEI Resources"   A Mouse-Adapted SARS-CoV-2 Induces Acute Lung Injury and Mortality in Standard Laboratory Mice. 
[cell.com/cell/fulltext/...](https://www.cell.com/cell/fulltext/...)



 Humanized C57BL / 6J mice, produced by Lab Baric and Jefferson Lab, are the most widely used strain.  It is commonly used to replicate human tests with highly pathogenic viruses.  Its resistance to tumors is known, and

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7 Feb

🔗🔗🔗🔗 The results of our 5-year SARSr-CoV surveillance in a cave inhabited by multiple species of horseshoe bats in Yunnan.  The Study reveal that the SARSr-CoVs circulating in this single location are highly diverse in the S, ORF3 and ORF8 gene!  1) A large number of




2) SARS-related coronaviruses (SARSr-CoV) have been detected in horseshoe bats since 2005 in different areas of China. However, these bat SARSr-CoVs show sequence

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4 Feb

 Construction of the SARS COV Chimera 2.  1) Between the Spike protein SARS COV 2 and human ACE 2 there is a occurre "mediator" = Spike RBD SARS COV 2.  In the silent cloning digest sites, of the genomic amino acid codon, the novel betacoronavirus, lineage B,






2) Spike RBD sequence is inserted. The seed particles plus

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2 Feb

   What happened in BSL 4, by Whuan, in spring 2018 and that Beijing does not want to admit.   Let's face it, working in a BSL4 is a continuous risk, for multiple reasons:

- 1) you can prick your fingers if you misuse a syringe; your suit will be contaminated and the virus can enter your circulatory system directly.

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
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1 Feb




@Geraldo22603187 @AlexandraJAlva4 @quay_dr @FLMIRONES  1)an RNA virus can never be extinguished, much less by a vaccine. There are too many variants that the virus can mutate, the coverage spectrum of a messenger mRNA vaccine is too targeted and therefore cannot include future variants. 2) An inactive vaccine may do better than an

@Geraldo22603187 @AlexandraJAlva4 @quay_dr @FLMIRONES mRNA vaccine, but its immunization is too

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31 Jan

 SARS COV 2 ORF8   A large number of SARS-related coronaviruses (SARSr-CoV) have been detected in horseshoe bats since 2005 in different areas of China. However, these bat SARSr-CoVs show sequence differences from SARS coronavirus (SARS-CoV) in different genes (S, ORF8, ORF3,

1) etc. and are considered unlikely to represent the direct progenitor of SARS-CoV. Herein, we report the findings of our 5-year surveillance of SARSr-CoVs in a cave inhabited by multiple species of horseshoe bats in Yunnan Province,

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