H.Fuseli, l'incubo, 1782

The origin of COVID: Did people or nature open Pandora’s box? From the origin to variants

The origin of the pandemic remains uncertain: what scientific data is available, which gives clues to what happened ???
it is possible to evaluate the complex question of guilt if someone or something is to blame?

Let's talk about Spillover, let's talk about Laboratory

Massimo Ciccozzi. Full prof of epidemiology
Univ of biomedical campus

two main theories about its origin.

One is that it jumped naturally from wildlife to people.

The other is that the virus was studied in a laboratory, from which it escaped, due to human error

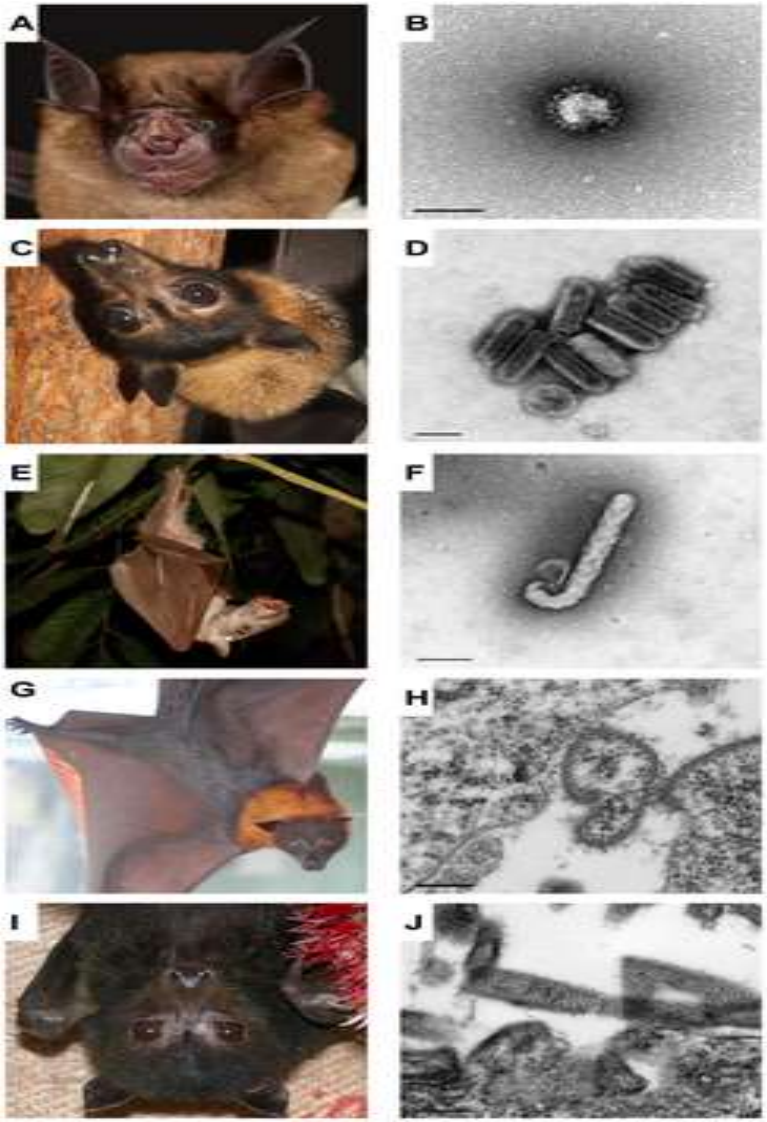
It is very important to know this for prevention if we want to avoid a second event of this type.

After the pandemic first broke out in December 2019, Chinese authorities reported that many cases had occurred in the wet market a place selling wild animals for meat - in Wuhan.

Natural o created in laboratory: the mistery of the origin

Coronaviruses have been detected in various members of the animal kingdom and, in multiple instances, they have been protagonists of zoonosis, sometimes resulting in very insidious human pathogens.

Bats and rodents are the most common gene source of most Alpha- and Beta- coronavirus, while birds are mostly of Gamma- and Delta-coronavirus. The majority of the currently known human coronaviruses and a large number of SARS-related coronaviruses have emerged from bats .
Indeed, bats are ideal “virus spreaders”, given their longevity, sociability, and ability to fly. **In this host, coronaviruses are well adapted, non-pathogenic but with a great genetic diversity and potential to infect humans.**



Bats are diverse, as are the viruses that infect them.

The Chinese horseshoe bat (**A**; *Rhinolophus sinicus*) is one of many *Rhinolophus* sp. that are a natural host of SARS-like coronaviruses (**B**; scale bar 100 nm).

The spectacled flying fox (**C**; *Pteropus conspicillatus*) along with other *Pteropus* sp. are reservoirs for the Australian Bat lyssavirus (**D**; scale bar 100 nm).

A number of African fruit bats including *Hypsignathus monstrosus* (**E**) have been found to host Ebola virus (**F**; Ebola Reston, scale bar 200 nm).

The Malayan flying fox (**G**; *Pteropus vampyrus*) is the natural host of Nipah virus (**H**; scale bar 200 nm).

All four pteropid Australian bat species including *Pteropus alecto* (**I**) have been found to carry Hendra virus (**J**; scale bar 200 nm).

Wynne JW, Wang LF (2013) Bats and Viruses: Friend or Foe?. PLOS Pathogens 9(10): e1003651. https://doi.org/10.1371/journal.ppat.1003651
https://journals.plos.org/plospathogens/article?id=10.1371/journal.ppat.1003651

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RESEARCH ARTICLE

JOURNAL OF MEDICAL VIROLOGY WILEY

The 2019-new coronavirus epidemic: Evidence for virus evolution

Domenico Benvenuto[1] | Marta Giovanetti[2] | Alessandra Ciccozzi[1] | Silvia Spoto[3] | Silvia Angeletti[4] | Massimo Ciccozzi[2]

PATHOGENS AND GLOBAL HEALTH
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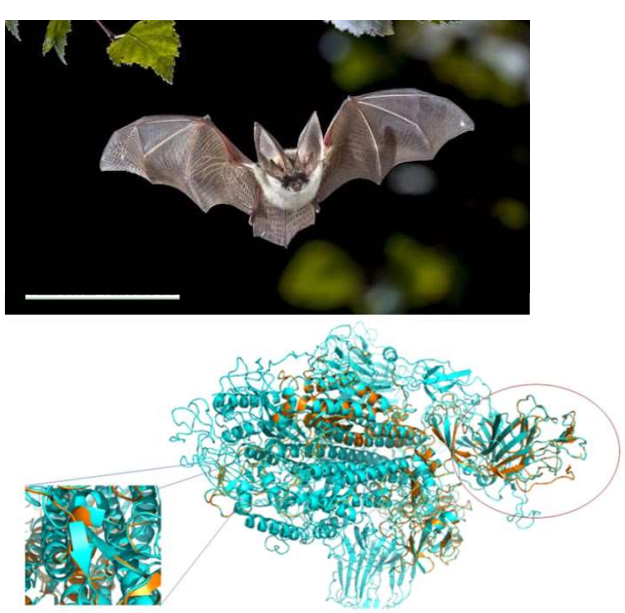
The global spread of 2019-nCoV: a molecular evolutionary analysis

Domenico Benvenuto[a*], Marta Giovanetti[b*], Marco Salemi[c,d], Mattia Prosperi[c,d], Cecilia De Flora[a], Luiz Carlos Junior Alcantara[b], Silvia Angeletti[e*] and Massimo Ciccozzi[b*]

[a]Unit of Medical Statistics and Molecular Epidemiology, University Campus Bio-Medico of Rome, Italy; [b]Laboratório de Flavivírus, Instituto Oswaldo Cruz, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil; [c]Department of Epidemiology, University of Florida, Gainesville, FL, USA; [d]Emerging Pathogens Institute, University of Florida, Gainesville, FL, USA; [e]Unit of Clinical Laboratory Science, University Campus Bio-Medico of Rome, Italy



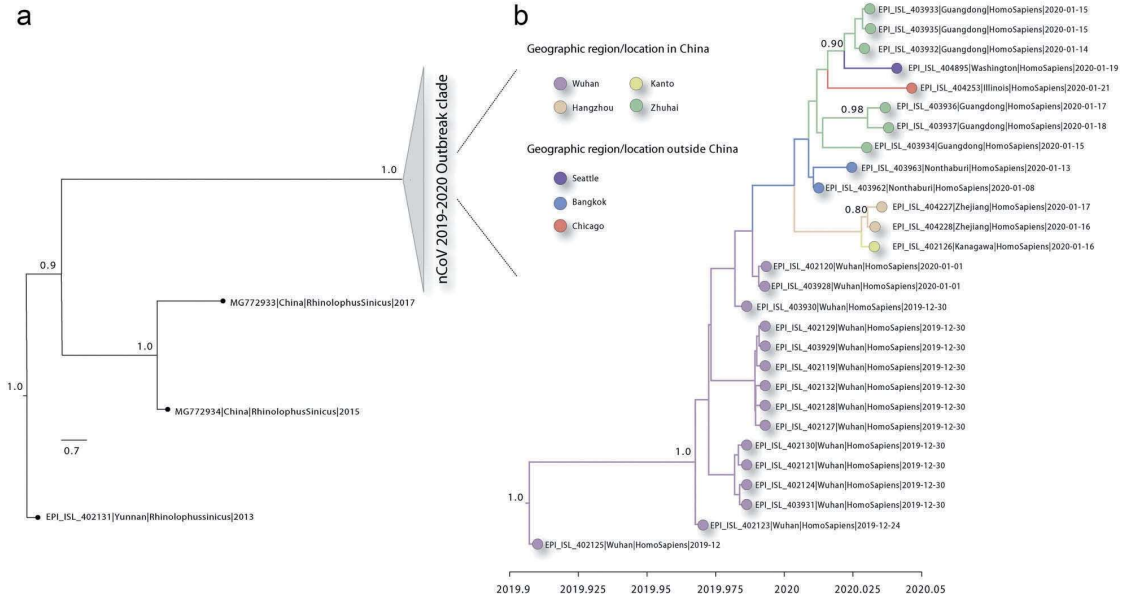


FIGURE 3 Cartoon model of the structural superposition between the homology model of the 2019-nCoV in blue and the spike glycoprotein of SARS coronavirus (PDB code 6acc.1) in orange. The red circle highlights the presence of a variable region on the 2019-nCoV at the beginning of the protein, whereas the blue square highlights the presence of two beta-sheets on the 2019-nCoV (401:KYR and 440:LND) that are not present on the SARS-CoV structure; SARS, severe acute respiratory syndrome

J Med Virol. 2020 Jun 3 : 10.1002/jmv.26104.
doi: 10.1002/jmv.26104 [Epub ahead of print]
PMCID: PMC7300971
PMID: 32492183

Evidence for mutations in SARS-CoV-2 Italian isolates potentially affecting virus transmission

Domenico Benvenuto, [1] Ayse Banu Demir, [2] Marta Giovanetti, [3] Martina Bianchi, [4] Silvia Angeletti, [5] Stefano Pascarella, [4] Roberto Cauda, [6], [7] Massimo Ciccozzi, [1] and Antonio Cassone [8]

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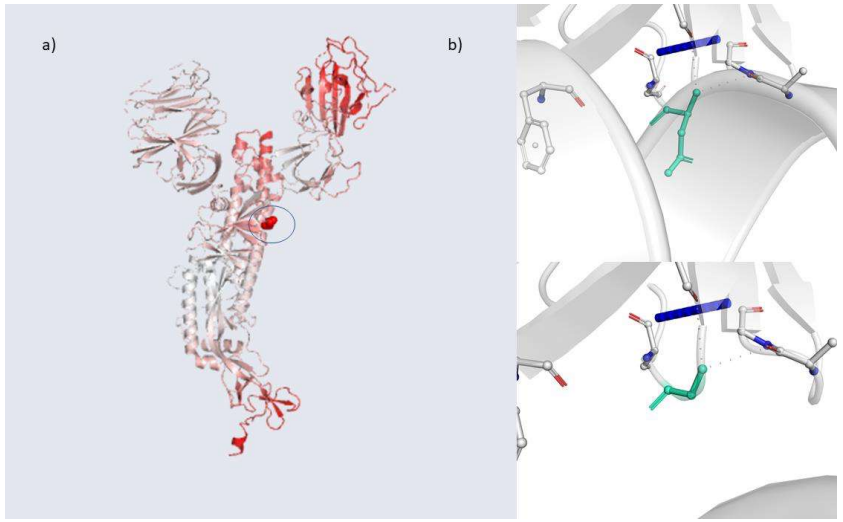


Figure 1, a) A model of spike glycoprotein monomer displaying the amino acids coloured according to the vibrational entropy change upon mutation, Red regions are those gaining in flexibility, The amino acidic mutation is blue circled; b) the top image shows the molecular interaction between the side chain of the wild-type amino acid and the side chains of the surrounding amino acid; the bottom image shows the molecular interaction between the side chain of the mutated amino acid and the side chains of the surrounding amino acid

Received: 2 February 2020 | Accepted: 3 February 2020
DOI: 10.1002/jmv.25699

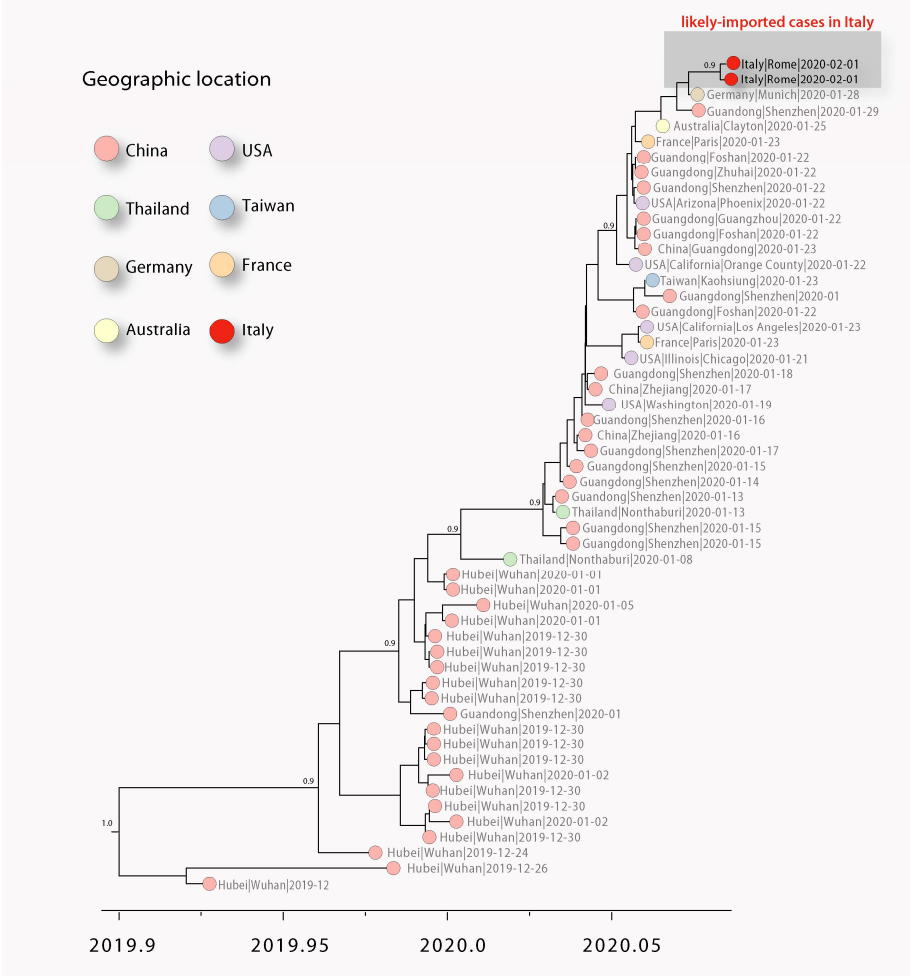
SHORT COMMUNICATION

JOURNAL OF MEDICAL VIROLOGY WILEY

The first two cases of 2019-nCoV in Italy: Where they come from?

Marta Giovanetti[1] | Domenico Benvenuto[2] | Silvia Angeletti[3] | Massimo Ciccozzi[2]

Chinese tourist were infected 19 January 2020 before their Arrival in Italy



Received: 11 March 2020 | Accepted: 16 March 2020

DOI: 10.1002/jmv.25773

SHORT COMMUNICATION

JOURNAL OF MEDICAL VIROLOGY WILEY

A doubt of multiple introduction of SARS-CoV-2 in Italy: A preliminary overview

Marta Giovanetti[1,2] | Silvia Angeletti[3] | Domenico Benvenuto[4] | Massimo Ciccozzi[4]

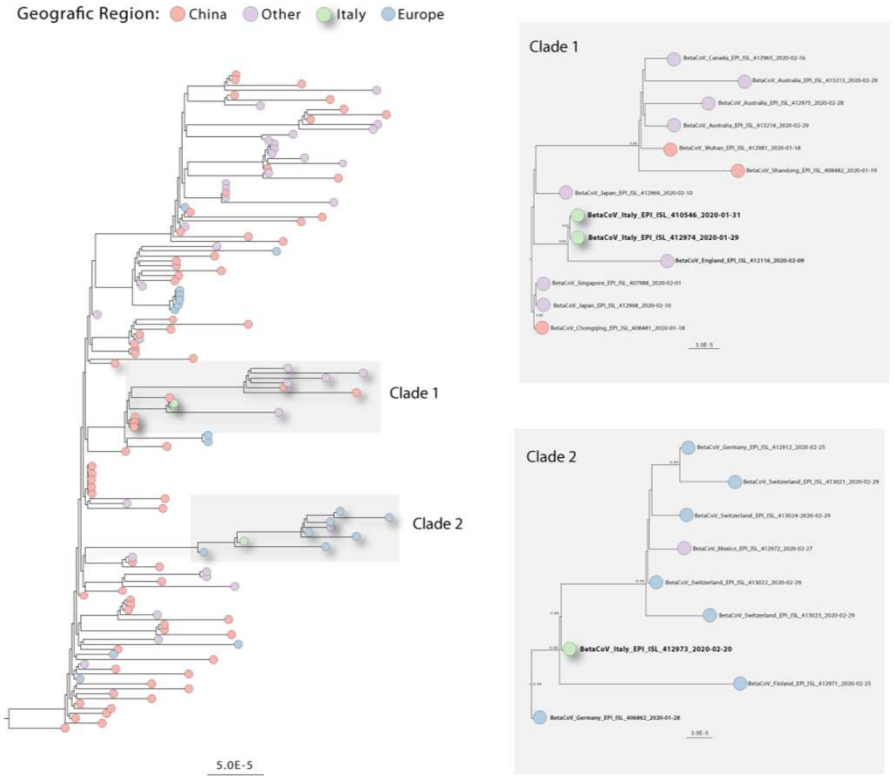


FIGURE 1 Maximum likelihood phylogeny, estimated from complete and near-complete coronavirus (CoV) genomes using genome data available in GISAID. Colors represent different locations (panels A and B represent expansions of the clades containing the Italian CoV isolates [green]) in clade 1 closely related with sequence from England, in clade B closely related with sequences from Germany

Received: 13 February 2020 | Accepted: 19 February 2020
DOI: 10.1002/jmv.25719

RESEARCH ARTICLE

JOURNAL OF MEDICAL VIROLOGY WILEY

COVID-2019: The role of the nsp2 and nsp3 in its pathogenesis

Silvia Angeletti[1] | Domenico Benvenuto[2] | Martina Bianchi[3] | Marta Giovanetti[4] | Stefano Pascarella[3] | Massimo Ciccozzi[2]

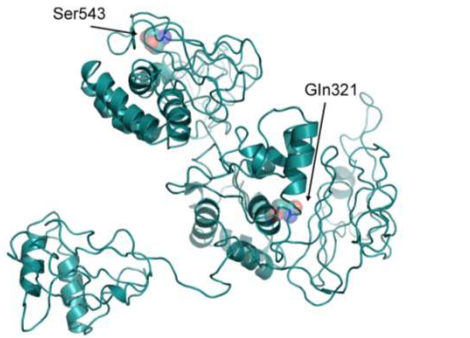


FIGURE 2 I-Tasser model of the COVID-2019 nsp2. Residues under positive selective pressure with a $P < .05$ are shown as sticks and transparent spheres and are marked by the corresponding labels. COVID-2019, novel Coronavirus; nsp2, non structural protein-2

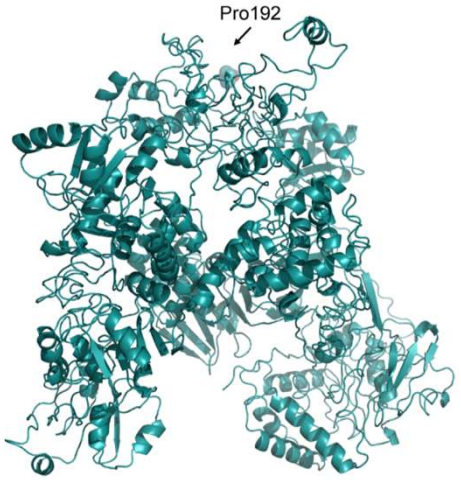


FIGURE 3 I-Tasser model of the COVID-2019 nsp3. The residue under positive selective pressure with a $P < .05$ is shown as sticks and transparent spheres and is marked by the corresponding label. COVID-2019, novel Coronavirus; nsp, non structural protein

Pachetti et al. J Transl Med (2020) 18:179
https://doi.org/10.1186/s12967-020-02344-6

Journal of Translational Medicine

RESEARCH Open Access

Emerging SARS-CoV-2 mutation hot spots include a novel RNA-dependent-RNA polymerase variant

Maria Pachetti[1,2†], Bruna Marini[4†], Francesca Benedetti[5], Fabiola Giudici[3], Elisabetta Mauro[4], Paola Storici[1], Claudio Masciovecchio[1], Silvia Angeletti[6], Massimo Ciccozzi[6], Robert C. Gallo[7,8], Davide Zella[5,9*] and Rudy Ippodrino[4*]

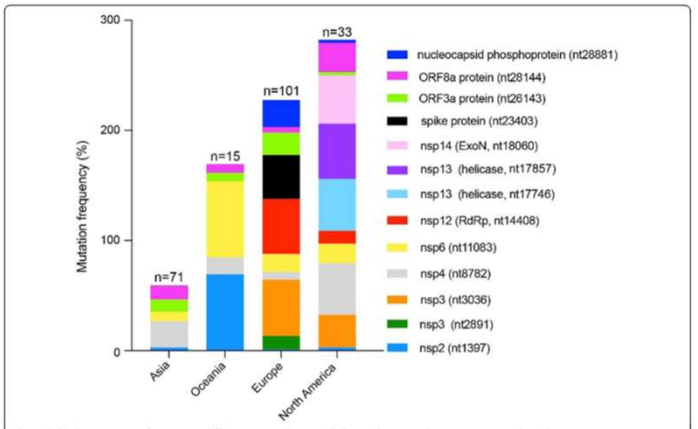


Fig. 1 SARS-CoV-2 mutation frequency in different geographic areas. Eight novel recurrent hotspots mutations (namely 1397, 2891, 14408, 17746, 17857, 18060, 23403 and 28881) and 5 hotspots already reported in literature (namely 3036, 8782, 11083, 28144 and 26143) were subdivided into 4 geographic areas: Asia (n = 71), Oceania (n = 15), Europe (n = 101), North America (n = 33). The mutation frequency was estimated for each of them, by normalizing the number of genomes carrying a given mutation in a geographic area, by the overall number of retrieved genomes per geographic area; the graph shows the cumulative mutation frequency of all given mutations present in each geographic area. Mutation locations in viral genes are reported in the legend as well as the proteins (i.e. non-structural protein, nsp) presenting these mutations. The figure shows that genomes from European and North American patients present an increase in mutation frequency compared to Asia. It is also possible to observe that Europe and North America show a differential pattern of mutations: mutation 14408 (red), 23403 (black), 28881 (electric blue) and 26143 (light green) are present mostly in Europe, whereas 18060 (pink), 17857 (purple) and 17746 (light blue) are present mostly in North America

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Evolutionary analysis of SARS-CoV-2: how mutation of Non-Structural Protein 6 (NSP6) could affect viral autophagy

Domenico Benvenuto[a,*], Silvia Angeletti[b], Marta Giovanetti[c], Martina Bianchi[d], Stefano Pascarella[d], Roberto Cauda[e,f], Massimo Ciccozzi[a], Antonio Cassone[g]

[a] Unit of Medical Statistics and Molecular Epidemiology, University Campus Bio-Medico of Rome, Via Álvaro del Portillo, 21, Rome 00128, Italy
[b] Unit of Clinical Laboratory Science, University Campus Bio-Medico of Rome, Via Álvaro del Portillo, 21, Rome 00128, Italy
[c] Laboratório de Flavivírus, Instituto Oswaldo Cruz, Fundação Oswaldo Cruz, Av. Brasil, 4365 - Manguinhos, Rio de Janeiro - RJ 21040-900, Brasil
[d] Department of Biochemical Sciences "A. Rossi Fanelli", University of Rome "La Sapienza", Viale Regina Elena, 332, Rome 00185, Italy
[e] UOC Malattie Infettive – Fondazione Policlinico Universitario "A.Gemelli" IRCCS, Largo Agostino Gemelli, 8, Rome 00168, Italy
[f] Department of Healthcare Surveillance and Bioethics, Catholic University of Sacred Heart, Largo Francesco Vito, 1, Rome 00168, Italy
[g] Center of genomics, genetics and biology, University of Siena, Petriccio e Belriguardo, 35, Siena 53100, Italy

Thus, its role would be to limit autophagosome expansion, directly or indirectly by starvation or chemical inhibition

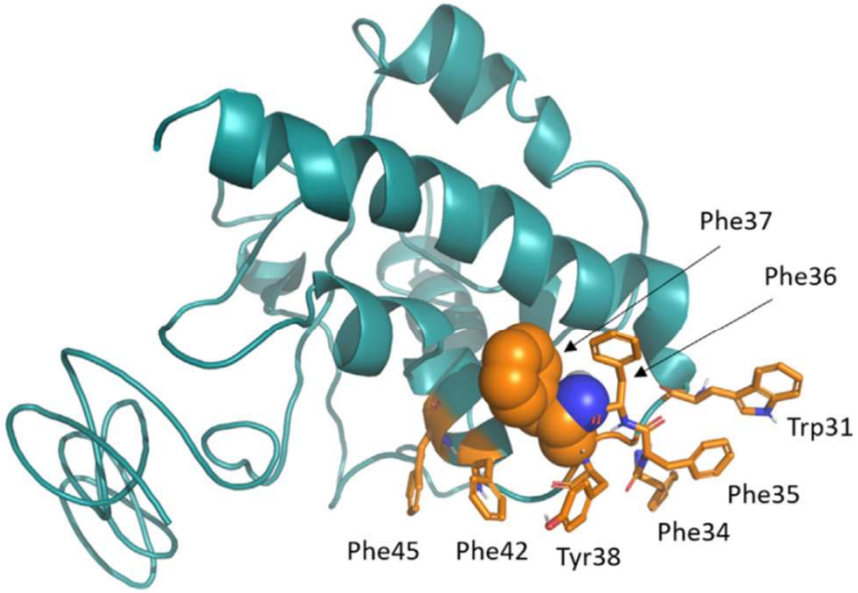


Fig. 1. I-TASSER model of NSP6. Residue under positive selective pressure with a $p < 0.05$ is shown as a sphere. Residues found in the structure proximity are shown in sticks. All residues are marked by the corresponding labels.

The origin of the Omicron variant have been a subject of controversy

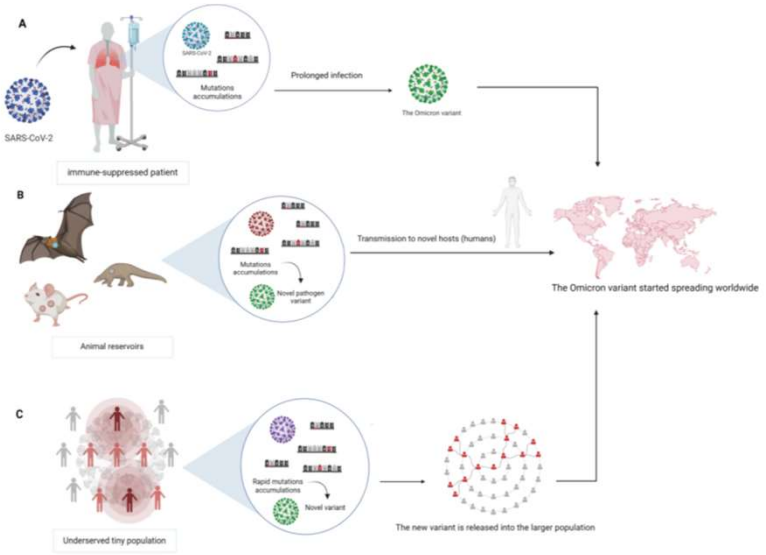
The three most likely scenarios for how the Omicron variant appeared.

A: Omicron could have developed and significantly mutated in an immune-suppressed patient with prolonged viral infections.

The idea was

B: The Omicron variant might have evolved in non-human reservoirs, such as animal source, and as of late spread from it to humans.

C: **The virus might began circulating and changing** in underserved places with **a tiny population**, where it had the opportunity to mutate rapidly, it could **then have been released into the larger population**, where it could have **spread to different groups.**



Early in the COVID-19 pandemic, Andersen and other scientists were consulted by the NIH and NIAID about the possibility of a lab leak.
Andersen, in an email to Anthony Fauci in January 2020, told Fauci, the government's top infectious disease expert, that some features of the virus made him wonder whether it had been engineered, and noted that he and his colleagues were planning to investigate further by analyzing the virus's genome.

Andersen and his colleagues initially suspected that **the virus could have escaped from a laboratory in Wuhan**, China, **after additional analyses and an accumulation of this scientific evidence, Andersen and his co-authors concluded that the hypothesis was unfounded.**

In a **2022** paper, Andersen concluded that animals sold in a market in Wuhan, China, were most likely to be the source of the virus

correspondence Nature Medicine

The proximal origin of SARS-CoV-2 To the Editor —

Since the first reports of novel pneumonia (COVID-19) in Wuhan, Hubei province, China1,2, there has been considerable discussion on the origin of the causative virus, SARS-CoV-23 (also referred to as HCoV-19)4. Infections with SARS-CoV-2 are now widespread, and as of 11 March 2020, 121,564 cases have been confirmed in more than 110 countries, with 4,373 deaths. SARS-CoV-2 is the seventh coronavirus known to infect humans; SARS-CoV, MERSCoV and SARS-CoV-2 can cause severe disease, whereas HKU1, NL63, OC43 and 229E are associated with mild symptoms6. Here we review what can be deduced about the origin of SARS-CoV-2 from comparative analysis of genomic data. We offer a perspective on the notable features of the SARS-CoV-2 genome and discuss scenarios by which they could have arisen. **Our analyses clearly show that SARS-CoV-2 is not a laboratory construct or a purposefully manipulated virus.**

Kristian G. Andersen1,2 ✉, Andrew Rambaut 3, W. Ian Lipkin Edward C. Holmes 4 5 and Robert F. Garry 1Department of Immunology and Microbiology,

A recent article published in Nature Medicine explains, thanks to a careful comparative analysis of the available genomic data, that SARS-CoV-2 cannot be a laboratory construct or a specially modified virus, and shows the probable scenarios from which it evolved.

The study of the structural and biochemical characteristics of the genome of this virus seems to suggest that: (i) it is optimized to bind to the human ACE2 receptor; and (ii) its surface protein "spike" has a functional polybasic cutting site (furin) at the junction between the two S1 – S2 subunits.

The receptor-binding domain (RBD) of the spike protein is the most variable part of the coronavirus genome. Six amino acids of RBD have been shown to be critical for binding to the ACE2 receptor and in determining the host spectrum of SARS-CoV-like viruses. Five of these residues appear to be different between SARS-CoV and SARS-CoV-2.

SARS-CoV-2 appears to have an RBD that binds with high affinity to ACE2 from humans, ferrets, cats, and other species with high receptor homology, even though computational analyses suggest a non-ideal spike-ACE2 interaction in the presence of an RBD other than that of SARS-CoV.

The high affinity binding of the SARS-CoV-2 spike protein to the human ACE2 receptor therefore appears to be the result of natural selection of the virus on a human or human-like receptor which has generated an alternative high affinity binding solution. This is clear evidence that SARS-CoV-2 is not the product of intentional manipulation.

The second feature of SARS-CoV-2 is a polybasic cleavage site (RRAR) at the junction of S1 and S2, which allows for effective cleavage by furin and other proteases and has a role in determining viral infectivity and the host spectrum of the virus.

Furthermore, a main proline is inserted into this site, the sequence is then PRRA; it is hypothesized that this insertion leads to the addition of O-glycans flanking the cleavage site.

The function of O-glycans is unclear, but they could create a “mucin-like domain” that protects key epitopes or residues on the spike protein.
In fact, numerous viruses use mucin-like domains as glycan shields involved in immune evasion.

In light of their analysis, the Authors consider it unlikely that SARS-CoV-2 emerged from the laboratory manipulation of a SARS-CoV-like coronavirus.
In fact, genomic data irrefutably show that the virus does not derive from any previously used viral structure.

The researchers propose, instead, two possible scenarios that can explain the origin of SARS-CoV-2: (i) natural selection in an animal host prior to zoonotic transfer; and (ii) natural selection in humans following zoonotic transfer.

https://www.nature.com/articles/s41591-020-0820-9

Fonte: Andersen, K.G., Rambaut, A., Lipkin, W.I. et al. The proximal origin of SARS-CoV-2. Nature Medicine, 2020.

Enhancing viruses to better study them is a scientifically accepted practice,

several clues and gaps leave open the hypothesis of origin in the laboratory.

the origin of the SARS-CoV-2 virus, with two predominant hypotheses: the natural one and that of escape from the laboratory. The latter hypothesis points to Gain-of-Function (GoF), or gain-of-function, studies involving genetic manipulation of organisms, often viruses. These **studies are aimed at evaluating the effects of increased pathogenicity, transmissibility, ability to evade the immune system or changes in host range or tropism**.

The controversial role of GoF studies

Proponents of GoF studies point to its potential to understand how a virus gains the ability to overcome the species barrier or become more lethal. These studies could allow scientists to anticipate future pandemic threats and develop vaccines and therapies.

For example, GoF studies of influenza viruses have allowed the identification of key mutations associated with increased transmissibility in mammals, providing valuable information for the development of proactive vaccines. Likewise, they could contribute to the development of targeted therapeutic countermeasures, anticipating the mechanisms by which a pathogen could evolve resistance to existing drugs.

ethical and biosafety concerns regarding the risk of accidentally or intentionally releasing enhanced pathogens, with potentially catastrophic consequences for global public health.

The debate over GoF studies has intensified in recent years as a result of the COVID-19 pandemic and discussions about the possible origins of the SARS-CoV-2 virus.

The concerns relate in particular to risks related to potential accidents due to human error or unforeseen events, which cannot be completely excluded,

The origin of the COVID-19 pandemic: a debate that is still open

GoF studies are closely linked to the debate over the origin of the COVID-19 pandemic. On March 17, 2020, the journal Nature Medicine published the article "The proximal origin of SARS-CoV-2".

The authors, evaluating the genome sequence of SARS-CoV-2, concluded that the hypothesis of laboratory origin (that is, that the virus had escaped from the laboratory or that it had been manipulated intentionally) was not a plausible scenario, leaning towards a natural origin.

This paper played an influential, indeed, central role in communicating the narrative that science had established that SARS-CoV-2 had infected people through natural spillover. Since its publication, it has been consulted online more than five million times and widely cited in the media.

In 2022, a bipartisan Commission on the COVID-19 pandemic was established, tasked with examining whether government officials had unfairly and perhaps biasedly tipped the scales toward natural origin theory and whether scientific integrity had been ignored in favor of political expediency, perhaps to hide or belittle the government's relationship with the Wuhan Institute of Virology or to avoid blaming China for any complicity in triggering the pandemic.

On February 6, 2023, Biosafety, a non-governmental organization, launched a petition asking the journal Nature to withdraw the article “The proximal origin of SARS-CoV-2“, which was deemed a product of fraud and scientific misconduct. Another petition followed to prohibit GoF research on potential pandemic pathogens, reduce the number of high-level biocontainment laboratories, and strengthen biosecurity and biohazard management for pathogen research, in order to prevent future pandemics.

The clues supporting laboratory origin

The laboratory escape theory is now supported by solid evidence. Most recent documents obtained from US. Right to Know demonstrate that American scientists planned to work with the Wuhan Institute of Virology to design novel coronaviruses with the characteristics of SARS-CoV-2 the year before the outbreak of the pandemic.

This was under the DEFUSE grant proposal for conducting engineering experiments on coronaviruses, inter alia led by Peter Daszak, president of EcoHealth Alliance

– an international non-profit dedicated to the One Health approach to preventing pandemics– but also a lead member of the mission team that WHO sent to China to investigate the origin of SARS-CoV-2.

The laboratory origin hypothesis, at first thought to be heresy and largely ostracized, is currently recognized as a credible hypothesis.

In summary, as Richard Ebright, a US molecular biologist, documents in his oral testimony filed during the US Senate hearing, **multiple lines of evidence provide the evidence to support his assessment of the laboratory origin of SARS-CoV-2. In particular, studies on the insertion of a furin cleavage site into the human Spike protein and the fact that SARS-CoV-2 is the only one among the more than 800 SARS viruses known to possess such a site.** Mathematically, this, in itself, implies that the probability of finding a natural SARS virus with a furin cleavage site is less than 1 in 800. This constitutes an extremely strong case – a "smoking gun" – in favour of laboratory origin.

In November 2021, WHO established the SAGO (Scientific Advisory Group for the Origins of Novel Pathogens), a group of 27 international scientists with the objectives of investigating the origins of SARS-CoV-2 and other emerging pathogens, defining a framework for such investigations, and evaluating available scientific evidence. SAGO released its first findings and recommendations on June 9, 2022. In a more recent report, dated June 27, 2025 and titled "Independent assessment of the origins of SARS-CoV-2", previous assessments are examined based on scientific publications, intelligence reports, presentations and expert discussions.

four main hypotheses examined are:

Natural zoonotic origin: The virus passed from animals to humans, either directly or via an intermediate host.

Laboratory accident: The virus has infected humans following exposure during field research or due to a violation of biosafety procedures.

Introduction via cold chain: The virus arrived in animal markets via frozen products and infected humans.

Deliberate laboratory manipulation: The virus was created in the laboratory and subsequently leaked

Excluding hypothesis 3, which is not supported by solid evidence, the report focuses on the others. Regarding hypothesis 2 of a laboratory accident, SAGO complains about the cooperation of the Chinese Government which did not provide WHO or SAGO with information crucial for a full assessment.

In conclusion, although zoonotic origin is the hypothesis most accredited by current scientific data, the precise origins of SARS-CoV-2 remain undetermined pending further scientific information and data.

Significant data gaps remain that prevent SAGO from establishing with certainty how SARS-CoV-2 initially entered the human population.

Science

PERSPECTIVES

Cite as: S. Lytras *et al.*, *Science* 10.1126/science.abh0117 (2021).

The animal origin of SARS-CoV-2

Spyros Lytras[1], Wei Xia[2], Joseph Hughes[1], Xiaowei Jiang[3], David L. Robertson[1]

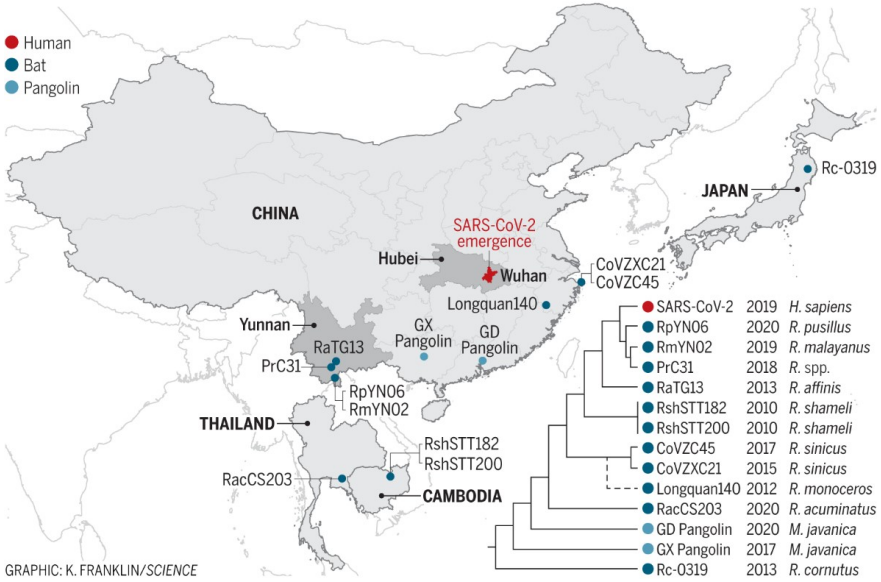
[1]Medical Research Council–University of Glasgow Centre for Virus Research, Glasgow, UK. [2]National School of Agricultural Institution and Development, South China Agricultural University, Guangzhou, China. [3]Department of Biological Sciences, Xi'an Jiaotong–Liverpool University, Suzhou, China.

Email: xiaowei.jiang@xjtlu.edu.cn; david.l.robertson@glasgow.ac.uk

Trading of animals susceptible to bat coronaviruses is the likely cause of the COVID-19 pandemic

Sarbecoviruses closely related to SARS-CoV-2

Coronaviruses that are evolutionarily closest to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) have been sampled in China, Cambodia, Japan, and Thailand (*5*). The phylogenetic tree, inferred from a genomic region minimized for recombination (*5*), shows sarbecoviruses closely related to SARS-CoV-2. Host species for each virus, horseshoe bat (*Rhinolophus*), human (*Homo sapiens*), and pangolin (*Manis javanica*) and the year of sample collection are shown in the key. Longquan140 is inferred from another genomic region (*5*) (dashed line). See supplementary table S1 for more details.



GRAPHIC: K. FRANKLIN/*SCIENCE*

The unresolved question on Covid-19 virus origin: the three cards game?

Alessandra Borsetti[1], Fabio Scarpa[2]*, Antonello Maruotti[3,4], Fabio Divino[5], Giancarlo Ceccarelli[6], Marta Giovanetti[7,8], Massimo Ciccozzi[9]

[1]National HIV/AIDS Research Center, Istituto Superiore di Sanità, 00162 Rome, Italy
[2]Department of Veterinary Medicine, University of Sassari, 07100 Sassari, Italy
[3]Department GEPLI, Libera Università Maria SS Assunta, Rome, Italy
[4]Department of Mathematics, University of Bergen, Bergen, Norway
[5]Laboratory of Biostatistics and Computational Epidemiology, Department of Biosciences, University of Molise, Campobasso, Italy
[6]Department of Public Health and Infectious Diseases, Policlinico Umberto I, Sapienza University of Rome, Italy
[7]Flavivirus Laboratory, Oswaldo Cruz Institute, Oswaldo Cruz Foundation, Rio de Janeiro 21040-360, Brazil
[8]Laboratório de Genética Celular e Molecular, ICB, Universidade Federal de Minas Gerais, Belo Horizonte, Minas Gerais, Brazi
[9]Department of Medicine Medical Statistics and Epidemiology Unit, Campus Bio-Medico University, Rome, Italy

The ongoing discussion about the real origin of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) feeds acrimonious debates. Where did SARS-CoV-2 come from? Was SARS-CoV-2 transmitted in the wild from an animal to a person before exploding in Wuhan or was it an engineered virus that escaped from research or a laboratory in Wuhan? Right now, we still don't know enough whether SARS-CoV-2 is human-made or not, and lab-leak theories remain essentially speculative. Many recent studies have pointed out several plausible scenarios. Anyhow, currently, even if suspicions by some about the possibility of lab-leak hypothesis still remain, the consensus view is that the pandemic probably started from a natural source and, to determine the real origin of the SARS-CoV-2 virus, further research is needed.

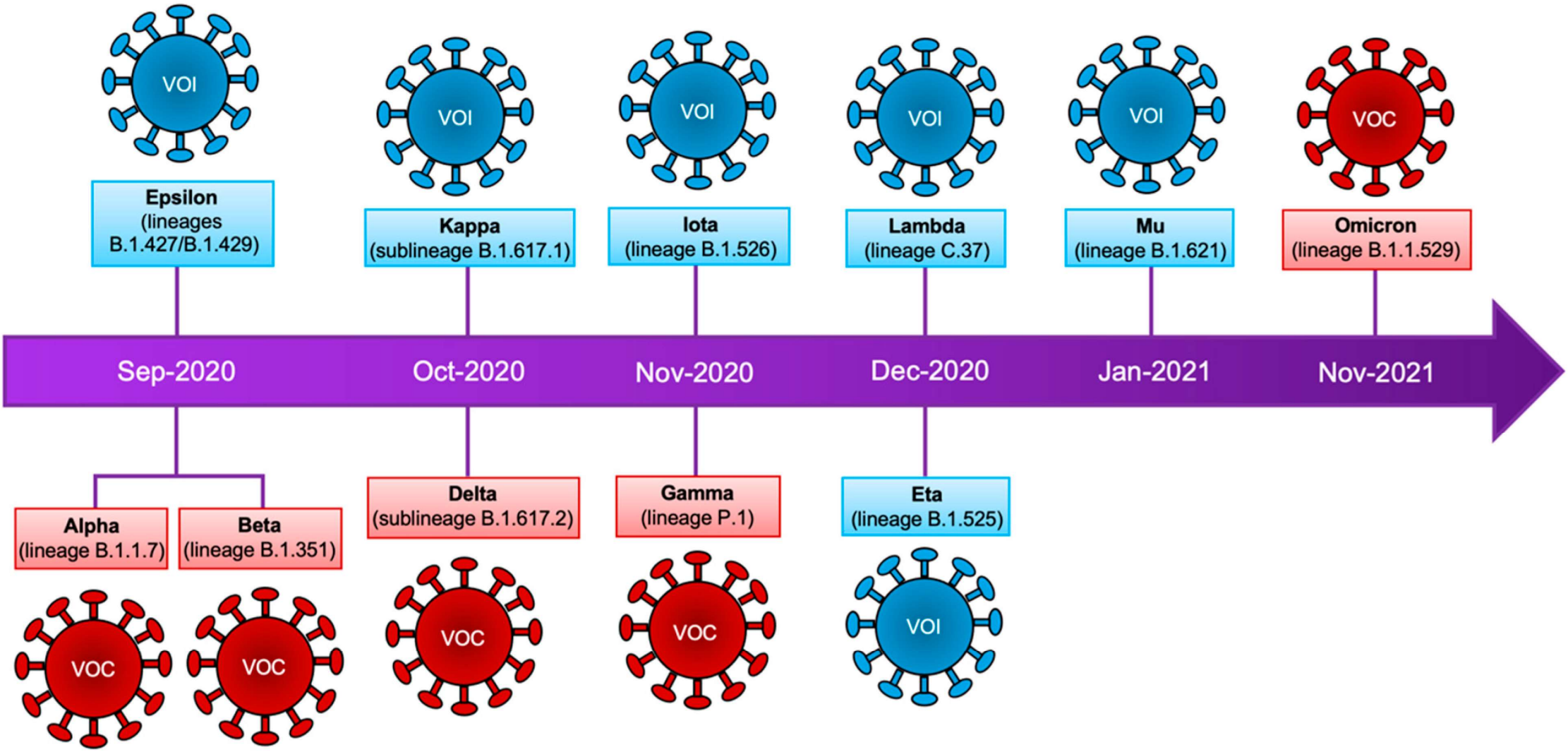
Many questions are open and need an answer..

VARIANTS ??????

THERAPY. ??

VACCINE. ?

ORIGIN. ???


VOI
Epsilon
(lineages
B.1.427/B.1.429)
VOI
Kappa
(sublineage B.1.617.1)
VOI
Iota
(lineage B.1.526)
VOI
Lambda
(lineage C.37)
VOI
Mu
(lineage B.1.621)
VOC
Omicron
(lineage B.1.1.529)
Sep-2020
Oct-2020
Nov-2020
Dec-2020
Jan-2021
Nov-2021
Alpha
(lineage B.1.1.7)
Beta
(lineage B.1.351)
Delta
(sublineage B.1.617.2)
Gamma
(lineage P.1)
Eta
(lineage B.1.525)
VOC
VOC
VOC
VOC
VOI

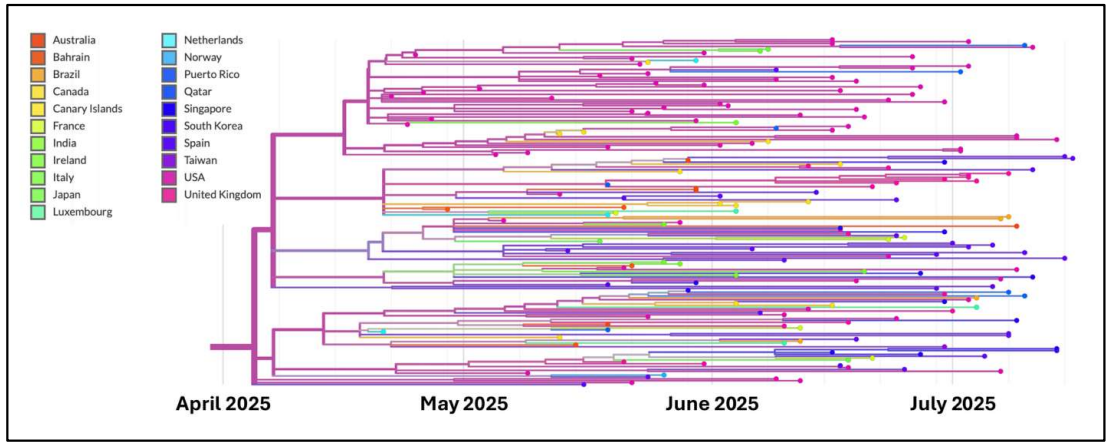
SARS-CoV-2 XFG: A Genomic Insight into the new recombinant

Authors: Francesco Branda1,, Massimo Ciccozzi1, Fabio Scarpa2*

Affiliation

1. Unit of Medical Statistics and Molecular Epidemiology, University Campus Bio-Medico of Rome, Rome, Italy.
2. Department of Biomedical Sciences, University of Sassari, Sassari, Italy

The latest SARS-CoV-2 recombinant is represented by the one labeled XFG (nicknamed *Stratus*), which has arisen through recombination between LF.7 and LP.8.1.2 [5]. SARS-CoV-2 XFG was detected for the first time on 27 January 2025 [6] and in 25 June 2025 it has been designed as VuM (Variant under Monitoring) [5]. Compared to the currently dominant SARS-CoV-2 variant NB.1.8.1, the XFG variant carries several additional mutations in the Spike protein, including: S31P, K182R, R190S, R346T, K444R, V445R, T478K, N487D, and T572I. In contrast, when compared to the JN.1 variant, XFG displays the following Spike mutations: T22N, S31P, K182R, R190S, R346T, K444R, V445R, F456L, N487D, Q493E, and T572I



Timeline of mRNA technology and key figures in vaccine development

Dr. Katalin Karikó began studying mRNA technology for humans at Temple, then UPenn

First iPhone

Facebook launches

SARS-CoV-1

MERS

SARS-CoV-2

Dr. Kizzmekia Corbett appointed to NIH Vaccine Research Center after years of working on viruses and vaccines

Dr. Graham and Dr. Corbett get genetic code for virus to create structure-based SARS-CoV-2 vaccine with Moderna

1990s

2000

2002

2005

2012

2013

2014

2017

2020

Dr. Barney Graham, head of Vanderbilt AIDS Vaccine Evalution Unit, recruited as one of founders of NIH Vaccine Research Center

First camera phone

Twitter launches

Dr. Karikó and Dr. Drew Weissman created successful synthetic mRNA delivery system

Dr. Graham and Dr. Jason McLellan solved way to modify RSV virus prefusion spike protein to allow for successful structure-based vaccine

Dr. Karikó joins BioNTech to oversee mRNA research

Dr. McLellan (UT Austin) and Dr. Andrew Ward (Scripps Research) figured out coronavirus prefusion spike structure

Dr. Graham partners with Moderna for mRNA MERS vaccine

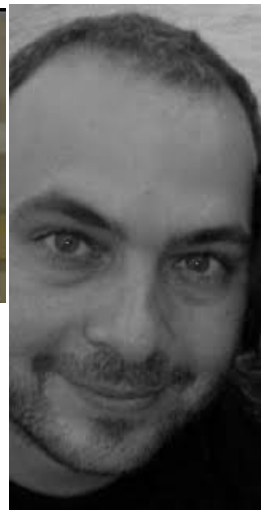
@ScrippsSHARCs https://cen.acs.org/pharmaceuticals/vaccines/tiny-tweak-behind-COVID-19/98/i38

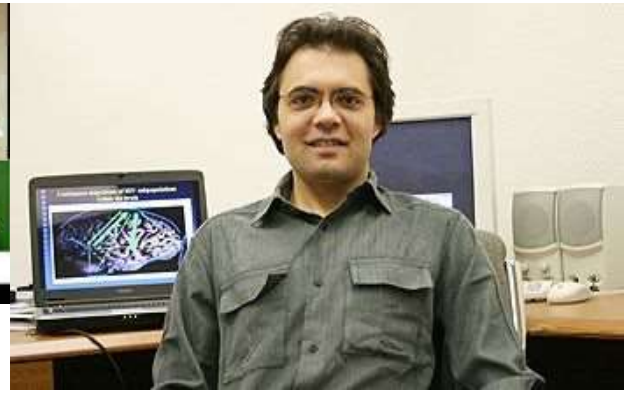
“Health is not everything, but without health everything is nothing”.

massimo

UP TO NOW

Completely conscious Ignorance is the prelude to any real progress in science
James Clerk Maxwell





147 papers
on Covid-19