The October Surprise in Wuhan

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OCTOBER SURPRISE IN WUHAN

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By

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This is the fourth part of a series of reports based on previously unpublished investigations into the origins of SARS-COV-2 by William Bostickson and Yvette Ghannam, which took place in 2020. This report also contains novel insights from ongoing joint investigations with Gilles Demaneuf from the DRASTIC collective in 2021, but it is worth noting that the majority of the content was analysed in 2020. We wish to thank all the independent researchers who have contributed to this investigation.

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1. INTRODUCTION

A steadily accumulating mass of evidence from a variety of sources suggests that SARS-CoV-2 or its progenitor emerged in Wuhan in the autumn months of 2019. Significantly, the SCMP published leaked information about 9 cases (4 male, 5 female) with onset dates in November 2019, including an alleged November 17th 2019 "Patient Zero" (SCMP 2020, March 13). However, China insists that SARS-COV-2 first appeared overseas, based on an alleged lack of confirmed pre December 2019 cases in China combined with reports of SARS-COV-2 in clinical samples and sewage in foreign countries earlier than December 2019 (China Military, 2021), illustrated in Figure 1 below:

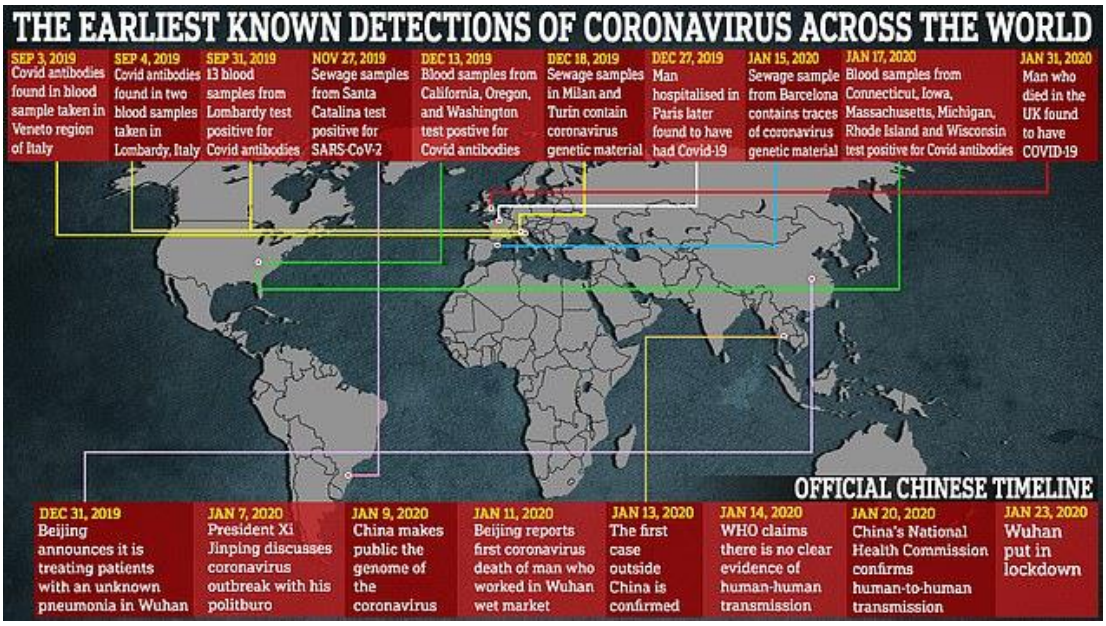


Figure 1. Official Chinese Timeline (Daily Mail, 2021)

According to China Military (2021):

"*As studies go deep, a growing body of evidence suggests the novel coronavirus was spreading globally months before the outbreak in China*".

Evidence for early cases (pre-December 2019) in China and elsewhere are analysed later in this report, but we will begin by looking at anecdotal evidence first:

2. INTERNATIONAL STUDENT INTERVIEW

An African International PhD Student at Wuhan University revealed an outbreak of unusual and severe Pneumonia cases between October and December in Wuhan (Arirang News, 2020).

Figure 2: Screenshot of International Student from Arirang News. (2020)

The interviewer asked him the following question:

QUESTION:

"*Prior to the city being put on lockdown did people in Wuhan suspect something odd was happening, and did you see people steadily getting sick?....Because at least to the outside world, this lockdown seemed to come out of the blue*"

ANSWER:

"*So basically somewhere in September there was outbreak of pneumonia, but we were told it is just one of those things because we are transitioning into the winter starting from November, so with that was just by the passing (sic), and then in November there was a major pneumonia outbreak, that is when people actually became aware that there was an outbreak of an epidemic in Wuhan, but then also the thing was concealed*"

3. UK STUDENT CLAIM

	
Connor Reed in China. News Sky (2020)	Connor Reed in China. Sky News (2020)

Figure Set 3: Connor Reed (sources under photographs)

Meanwhile, Connor Reed, a British Student who later died in Wales (Sky News, 2020), described his infection on November 25th 2019 while working at a school in Wuhan. He allegedly tested positive for Pneumonia in early December at Zhongnan Hospital, a tertiary care hospital affiliated with Wuhan University School of Medicine in Wuhan. He was allegedly informed by the hospital that he had positive results for Covid-19 on January 15th 2020 (Daily Mail, 2020a).

He recovered and returned to the UK, but later doctors concluded that he had suffered a COVID-19 infection. A diary of his illness is available (Daily Mail, 2020a) in which he described his COVID-19 symptoms as follows:

> "*That's where it scared me. I couldn't take a full breath and the breaths I did take, it sounded like I was breathing through a bag. It was very crackly, and I could only take half breaths. If I walked to the kitchen, I'd be breathing really shallow and really fast*" (Daily Mail, 2020a).

Sadly, at the early age of 25, Connor died in his room at Ffriddoedd Road, Bangor in October 2020 while studying at Bangor University (North Wales Chronicle, 2021). According to the UK Daily Post (2021) "*the provisional cause of death was given as respiratory failure due to bronchopneumonia caused by combined drug toxicity*" but was not being treated as suspicious (News Sky, 2020).

Research by the DRASTIC collective (Drastic Research, 2021) shows that Connor Reed lived in Building 1 of the Wufeng Jiayuan Phase II development (武丰佳园二期-1栋) in north Wuchang District. A video shows him walking out of east door of the building, through the gate (Figure 4) to nearby shops.

Figure 4: The Gate of Wufeng Jiayuan Phase II development. Source: Baidu Street Maps

Investigations reveal the Connor Reed may have worked at one of Shane English School's Wuhan locations on the 3rd Floor of Aoshan Century City, Heping Avenue, Qingshan District, Wuhan (武汉市青山区和平大道奥山世纪城3楼). His LinkedIn photo shows him standing in front of a Shane school poster and he lived only 3km away from a Shane School location. An ad for an English teacher manager posted for Shane School in 2018 matches the reference to him being a “manager”. A video shows him walking north on Sanyang Rd and down Jiefang Ave to a pharmacy at 1775 Jiefang Avenue.

Footage of Connor Reed shows him passing only 300m from the school on Sanyang Road on the way to a pharmacy. This was the school where another Welsh Teacher, Jamie Morris worked. Morris, who still lives and works in Wuhan, claimed he did not know Connor Reed, despite receiving a recommendation from Connor on his LinkedIn profile. He was diagnosed with pneumonia in December before testing for SARS-COV-2 was available.

He claims to have been sick for two weeks but never tested for Covid-19. He worked at Maron Carey Raycom Children's International School in Jianghan District (Figure 5 below):

Figure 5: Maron Carey Raycom Children's International School in Jianghan District.

Figure 6: Video still showing Connor Reed's walks around apartment and walk to pharmacy on Jiefang Ave 25 minutes away. Source: https://youtu.be/lR09P2hIL_k

4. WUHAN MILITARY GAMES – SICK ATHLETE CLAIMS

Figure 7: Wuhan 7th CISM Military World Games Mascot. Source: GK Today (2019).

The 7th International CSIM Military Military World Games commenced in Wuhan on October 18, 2019. It hosted over 9,000 military athletes from over 100 Nations, with 25 of these countries being represented by 100 plus athletes each (China Daily, 2019). The competitions took place in a variety of venues (Archive, 2019), as can be seen with the aid of a small magnifying glass in Figures 8 and 9 below:

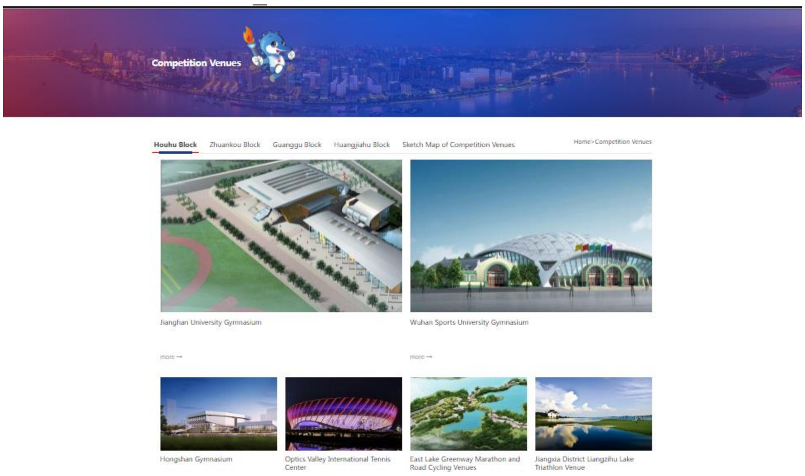


Figure 8: Competition Venues - 7th CISM Military World Games. (2019). Source: Archive (2019).

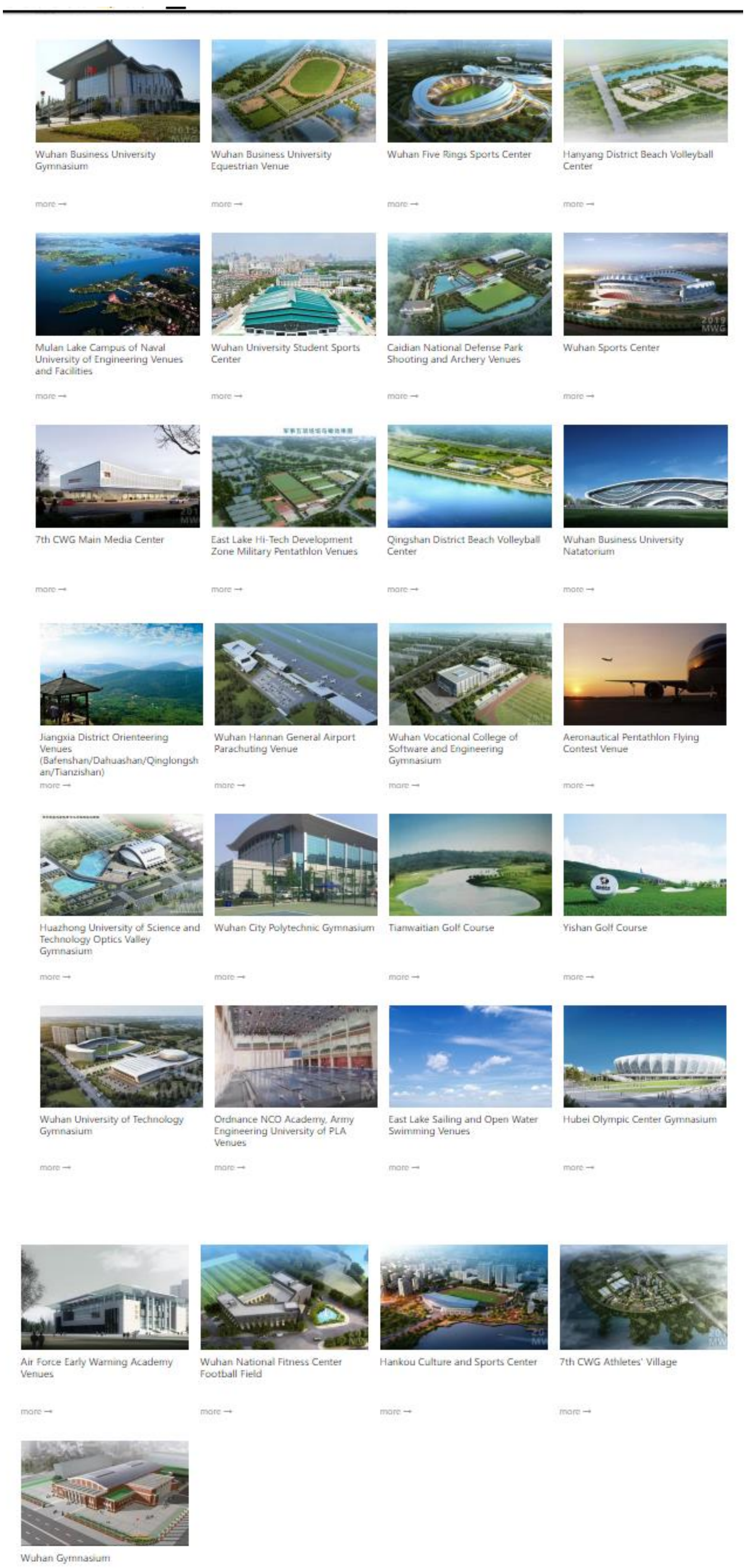


Figure 9: Competition Venues - 7th CISM Military World Games. (2019). Source: Archive (2019).

There is ample evidence that some of the participating athletes became infected with a respiratory virus with similar symptoms to COVID-19. This was confirmed during media inteviews with returning athletes (Inside the Games, 2020; Financial Post, 2021). This anecdotal evidence from the interviews is supported by subsequent news reports from many different countries of Military Athletes experiencing COVID-19 like symptoms in October and November 2019, during or immediately after the Wuhan Military Games. To complicate matters, generally speaking the Ministries of Defence of NATO countries declined to provide SARS-CoV-2 antibody tests for returning military athletes who complained of Covid-19 like symptoms (Revel News, 2021).

Following the World Military Games in Wuhan in October 2019, some of the Spanish military athletes displayed Covid-19 like symptoms (Kouimtsidis, 2020). Requests were made to have them tested for SARS-COV-2 (Kouimtsidis, 2020). However, the Spanish Minister of Defence, Margarita Robles, claimed in May 2020 that it was too late to test them and none had shown coronavirus symptoms (La Vanguardia, 2020). After a public uproar and questions in the Spanish Parliament, the Minister of Defence agreed to have IgM and IgG tests carried out on some of the 138 athletes who had demanded them (Niusdiario, 2020).

Surprisingly**,** 6 out of the 138 Spanish military athletes who travelled to Wuhan Games did in fact test positive for coronavirus antibodies (EFE, 2020; Web24, 2020a). Similar cases were described in the Italian media, for example, Repubblica.it (2020 and Football Italia (2020); in Sweden (The Local Sweden, 2020), the USA (Squitieri, 2020) and Norway (Covid19.No, 2020).

Cases involving well known athletes from different nations were discussed in news reports by Mishra, A. (2020, Web24 (2020, Sharpe, J. (2020), Inside the Games. (2020) and Dilkoff (2020). Gibert (2020), Hamid (2020), Vilar & Besnard (2020) discuss early cases in France from December 2019, while France Info (2021), RMC SPORT (2020), France TV Sport (2020), Oriol (2020), L’Equipe (2020, Grumberg (2020) published information on several military athletes who insisted that they had experienced a COVID-19 like illness while in Wuhan.

Nedelec & Guyader (2020) examined the French MOD's reactions and refusal to test the athletes, while Opoczynski (2020), Merchet (2020), Pérès & Ricotta (2020) published detailed interviews and accounts of alleged coronavirus like symptoms amongst the returning French military athletes and discussions they had on social media regarding their experiences.

Winter (2021), in her recent analysis of the impact of returning athletes from the World Military Games held in Wuhan in October 2019 on the subsequent spread of Covid-19, demonstrates that there is indeed some correlation indicated by curve fit and regression analysis:

> "*There is a correlation between the number of individuals who travelled to the event and the number of COVID-19 cases in the country to which they returned*"

And:

> "*This study shows a mathematical model to predict the number of COVID-19 cases in a country as a result of each infected individual travelling to that country*"

Figure 10 shows the number of athletes mapped against the number of cases of COVID-19 in that country.

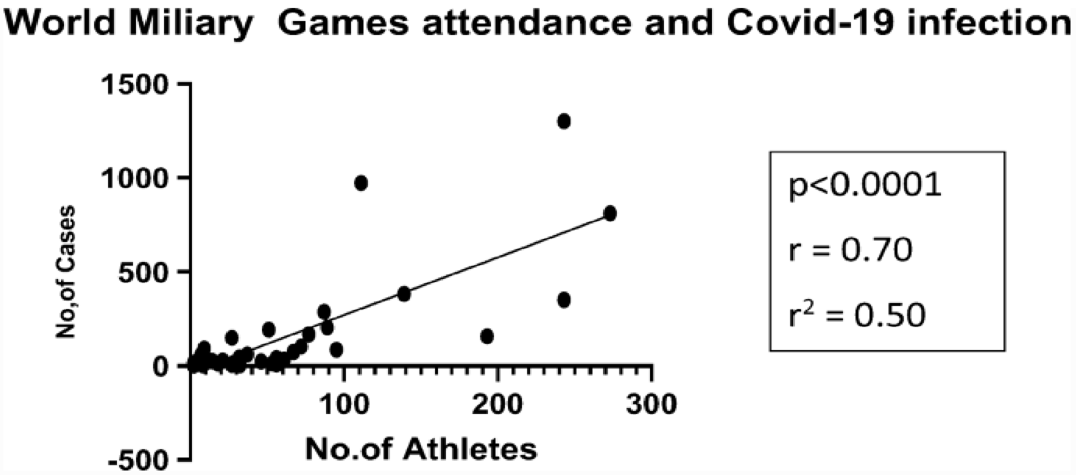


Figure 10: Graphical plot of the number of athletes on the *x*-axis with the number of infected cases per country (in thousands) for the period October 18, 2019, to October 18, 2020. (Winter, 2021)

However, certain flaws in this analysis render it of little value. For example, the cut-off date for listing cases, as after January 2020, the movement of infected people was of course significantly more important than the initial movement of athletes. Moreover, an R^2 less than 0.6 is considered relatively weak. The authors hope that further more rigorous analysis of these patterns can be investigated in the future.

Taken together, the above reports and analysis suggest that the October 2019 7th CISM Military World Games held in Wuhan may have been a vector for spreading SARS-CoV-2 or its progenitor virus. This could have occurred in October at any of the 35 venues and facilities, 33 stadiums or athletes' village located in 4 areas,_Houhu, WEDZ, Optics Valley, and Huangjiahu (Hubei, 2019).

Considering previously identified biosafety issues (Bostickson & Ghannam, 2021c) and documented cases of experiments involving chimeric bat coronaviruses and humanized mice at Wuhan University's IMA ABSL3 (Taiwan News, 2021, Jan 11, Sept 27; The Intercept, 2021, September 10, September 7), one possible venue would have been the Zall Stadium (Figure 11), a venue built in the west of the Wuhan University Campus, which welcomed badminton athletes worldwide and over 8000 spectators every day.

Figure 11: Zall Badminton Stadium at Wuhan University. Source: Wuhan University (2019).

The Games were staffed by over 200,000 eager volunteers, helping out at more than thirty venues like Zall Badminton Stadium (Figure 11). Some interviews with volunteers can be found in a news article by Wuhan University (2019):

> "*During this period, energetic and youthful students in green-and-white uniforms could be seen in various venues scattered in the city. "Smart Shuishan", what we call the volunteer group formed by more than* ***50 thousand university or college students****, became beautiful scenery in every corner of the venues and provided services to athletes, referees and spectators*" (Wuhan University, 2019).

A total of 1037 Wuhan University Students acted as volunteers as hostesses (Figure 13), helping with interpreting, guiding visitors or as English announcers. One of them was Shen Yuxi, an interpreter at the Zall Stadium for Lieutenant Colonel Marc C. De Wagter (Figure 12), Badminton Official CISM Representative and CISM Treasurer General (Wuhan University, 2019).

Figure 12: Shen Yuxi and Lieutenant Colonel Marc C. De Wagter. Wuhan University (2019).

Figure 13: Hostesses at the medal presentation ceremony Source: Wuhan University (2019).

Zhu Tong, a guide at the torch relay ceremony (Figure 14) and a Wuhan University postgraduate student explains his activity:

> "*I felt extremely lucky to join the volunteer team of the Games in my first year of postgraduate study. I had no chance to serve at the stadiums during the competitions because the recruitment process had ended before I came to Wuhan University, but I was fortunate enough to get the opportunity to be a volunteer at the torch relay ceremony on October 16th*" (Wuhan University, 2019).

Figure 14: 7th CISM Military World Games Torch Relay. 16/10 2019. Ministry of Defense (2019).

Researchers at GOP-Foreign Affairs (2021) speculated that, despite knowledge of an outbreak, the decision was made to allow the 2019 Military World Games to continue in order to prevent "national embarrassment". As a result of this decision:

- *"No spectators were allowed to attend the game"* GOP – Foreign Affairs (2021).
- "*International athletes and some of the 236,000 volunteers were infected*" GOP – Foreign Affairs (2021).
- "*Dozens of athletes fell ill with Covid-19 like symptoms*" GOP – Foreign Affairs (2021).
- "*A great number of athletes and volunteers become infected, but were asymptomatic*"
- "*The athletes returned to their home countries in late October, carrying SARS-CoV-2 across the world*" (GOP – Foreign Affairs, 2021).

5. SATELLITE DATA ON HOSPITAL TRAFFIC & SEARCH TERM QUERIES

According to interpretation of Satellite Data, some Wuhan hospitals were overwhelmed with patient visits from mid-September to October 2019, which also coincided with an alleged increase in search queries on the Chinese internet search engine, Baidu, for possible "coronavirus" like symptoms (cough, diarrhoea). As can be seen in Figure 15, the search term queries reached their peak in the last two months of 2019.

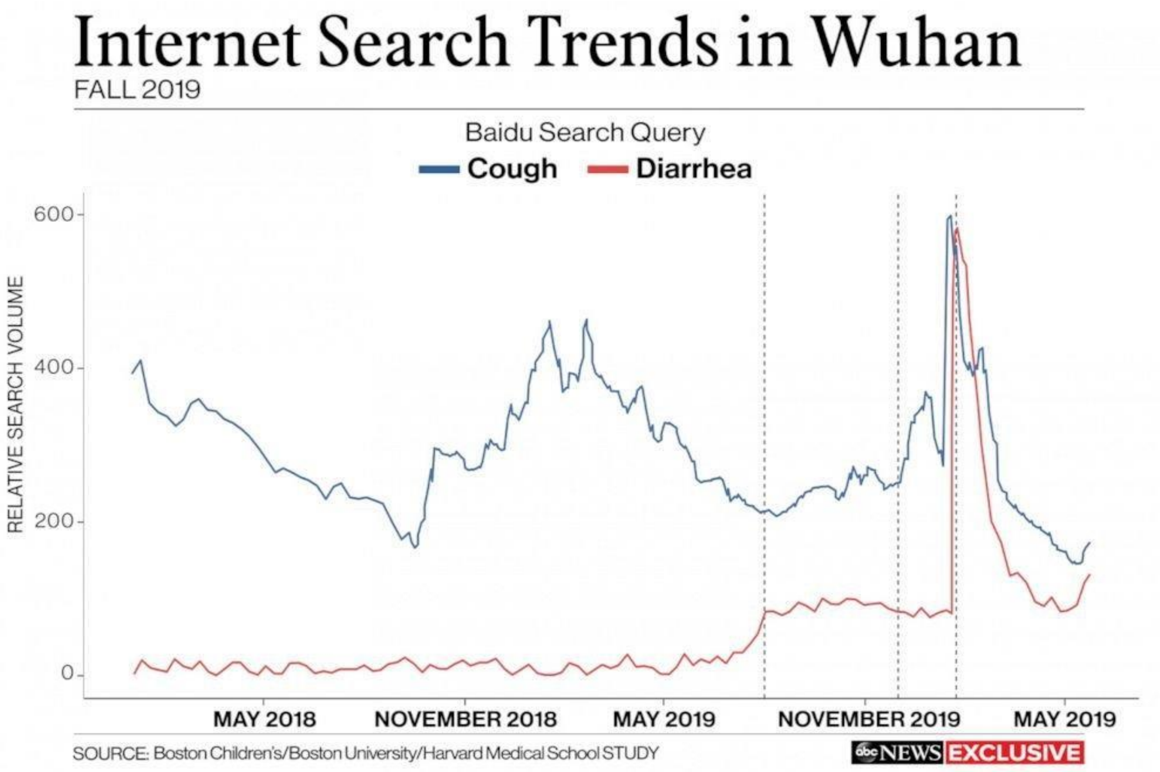


Figure 15: Baidu Search Queries. Source: ABC News (2020.)

Data from satellite image based traffic analysis (Nsoesie et al., 2020).at Wuhan Hospitals revealed that there may have been a distinct surge in hospital visits and consultations in Autumn 2019 at 6 hospitals (ABC News, 2020b; Seidler, 2020):

- Hubei Women and Children's Hospital
- Wuhan Central Hospital
- Wuhan Tianyou Hospital
- Wuhan Tongji Medical University
- Wuhan Union Hospital
- Zhongnan (Central South) Hospital of Wuhan University

The locations of the six hospitals listed above that allegedly experienced pattern of increased traffic in the autumn of 2019 can be visulaised in a map published in a recent addendum by GOP-Foreign Affairs (2021). This map (Figure 16) reveals that the 6 hospitals are clustered around the Wuhan Institute of Virology HQ in its old complex in Xiaohongshan, Wuchang District (BSL2 and BSL3 Labs). Note that the hospitals (blue icons) are all located within a 10 kilomtre radius of the WIV Headquarters (red icon).

Figure 16: 6 Hospitals and WIV Xiaohongshan Headquarters. Source: GOP-Foreign Affairs (2021).

This raises certain significant questions regarding the earliest official cases, for example, the so-called "*PLA Hospital Cases*" discussed by Quay (2020) in "*First COVID-19 Genomic Patient Cluster was at PLA Hospital in Wuhan, China*". Quay discovered that COVID-19 patient record holders (International bio specimen data repositories) were created by PLA scientists on December 10th 2019 at the General Hospital of Central Theater Command of People's Liberation Army at 627 Wulon Road, Wuchang District, Wuhan (Quay, 2020). The exact location of this PLA hospital and its close proximity to the WIV HQ in Xiaohongshan, Wuchang District can be seen in Figure 17 below:

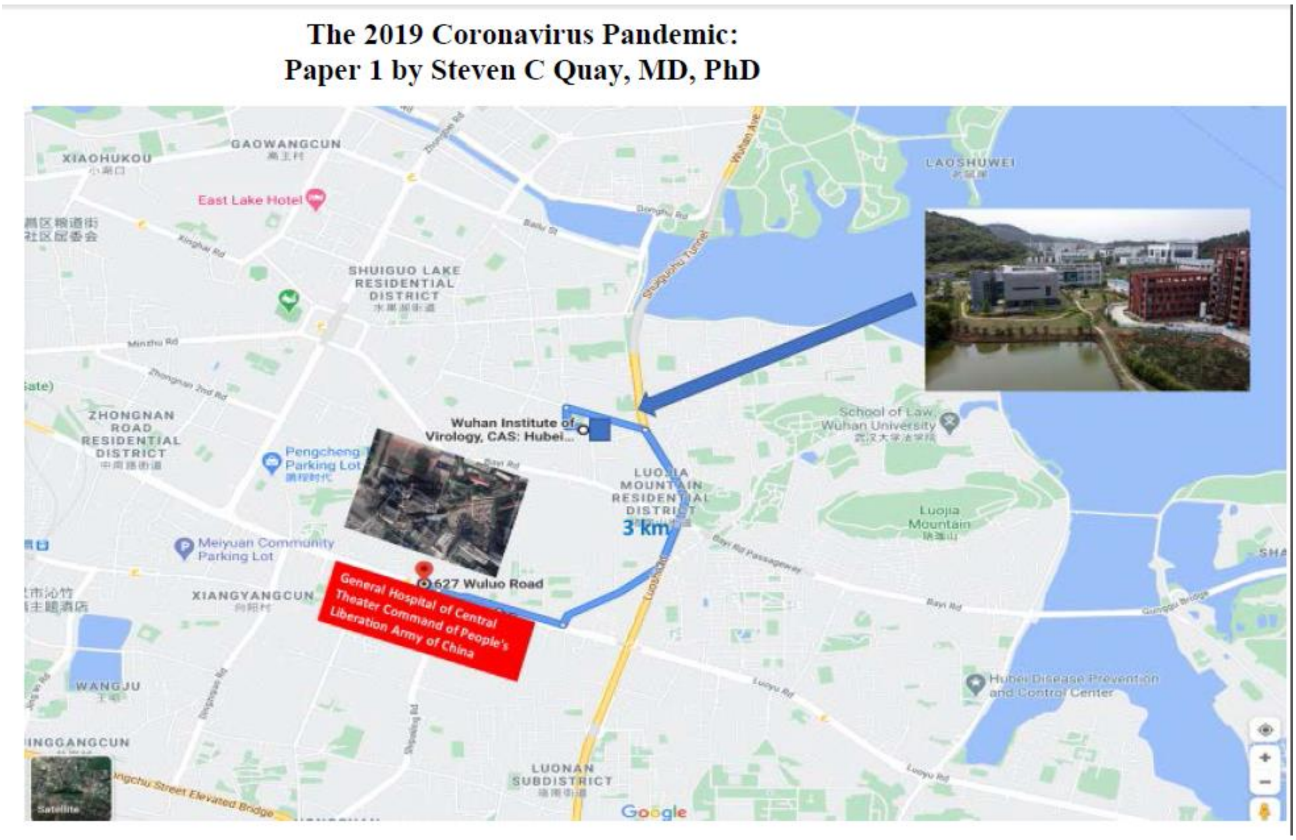
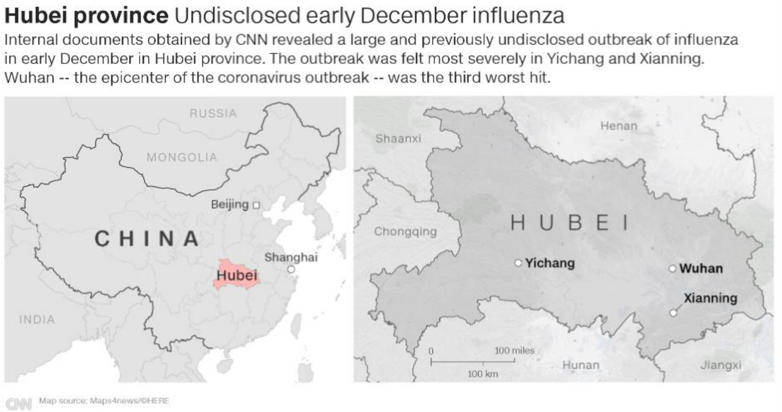


Figure 17: General Hospital of Central Theater Command of People's Liberation Army at 627 Wulon Road, Wuchang District, Wuhan (Quay, 2020).

The specific topic of tracing back the earliest Wuhan Covid-19 cases will be dealt with in more detail in an upcoming report (November 2021) by the authors and collaborators from the DRASTIC collective (Drastic Research, 2021).

6. HUBEI INFLUENZA OUTBREAK

Although it has been claimed (CNN, 2020) that accounts of sickness in Wuhan between October 2019 and November 2019 may have been due to a severe influenza outbreak in Hubei Province, the reported dates fail to support that hypothesis.



Hubei province Undisclosed early December influenza

Internal documents obtained by CNN revealed a large and previously undisclosed outbreak of influenza in early December in Hubei province. The outbreak was felt most severely in Yichang and Xianning. Wuhan -- the epicenter of the coronavirus outbreak -- was the third worst hit.

Figure 18: Hubei Influenza Outbreak in 2019. (CNN, 2020).

According to Hubei official internal documents leaked to CNN (2020) by a local whistle-blower, Hubei Province saw a "significant influenza outbreak" in early December 2019, with 20 times more cases than 2018 (Figure 18). The main findings are listed below:

1. "*Yichang, 320 kilometers west of Wuhan, was hit hardest by the influenza outbreak, with 6,135 cases, Xianning, with 2,148 cases. Wuhan with 2,032 new cases that week*" CNN (2020).
2. "*The spike, which **occurred in the week beginning December 2,** saw cases rise by approximately 2,059% compared to the same week the year before*" CNN (2020).
3. "*Testing carried out on influenza patients returned **a high number of unknown results***" CNN (2020).
4. "*The Wuhan CDC later conducted retrospective research into influenza cases dated as early as October 2019 in two Wuhan hospitals but claimed they were unable to detect samples of SARS-COV-2 dating back earlier than January 2020*" CNN (2020).
5. *The Chinese health authorities **failed to conduct similar studies in other Hubei cities**.*
6. "*The flu spike could have helped to unintentionally accelerate the coronavirus' early spread as people were seeking care in hospitals, increasing the chances of COVID infection there*" CNN (2020).

7. LEAKED WUHAN HOSPITAL DOCUMENTS

武汉市新冠肺炎样病例影像学特征筛查登记表

报告单位：武汉亚心总医院
报告时间：2020.02.21
专家小组签字：满宁
分管领导签字：金捷
联系人：曹常影
联系电话：1851452[redacted]

序号	姓名	发病日期	检查日期	主要临床表现	手机号	身份证号
1	吴[redacted]炎	2019.10.03	2019.10.4	嗽、咳痰、左侧肢体无	1311436[redacted]	4201141937080[redacted]
2	施[redacted]臣	2019.10.30	2019.10.31	咳嗽、胸闷、喘息	1393633[redacted]	2301021963021[redacted]
3	彭[redacted]秀	2019.10.24	2019.11.1	发热、咳嗽、咳痰	1307124[redacted]	4201011941021[redacted]
4	邹[redacted]兰	2019.10.10	2019.11.1	咳嗽	1507128[redacted]	4201051951032[redacted]
5	李[redacted]国	2019.10.19	2019.11.23	咳嗽、咳痰、胸闷	1309880[redacted]	4201011952091[redacted]
6	杨[redacted]阶	2019.12.15	2019.11.24	发热、畏寒	1355420[redacted]	4201051953010[redacted]
7	李[redacted]春	2019.12.01	2019.12.9	咳嗽	1337789[redacted]	4201051955061[redacted]
8	高[redacted]秀	2019.12.09	2019.12.1	呕血、心悸、头痛	1372024[redacted]	4201011941062[redacted]

Figure 19: Screenshot of leaked hospital documents. Source: (Fu, 2020)

Indeed, leaked hospital documents (NTDTV, 2020) from a purported Chinese Ministry Investigation in early February 2020 show details of October and November Covid-19 cases at 10 hospitals in Wuhan (Jian, 2020). According to the internal documents obtained by The Epoch Times, an anti-CCP newspaper (Jian, 2020), the Chinese government ordered Wuhan CDC to search hospital records for any early cases dating back to October 2019. Published images (Figure 19) of the leaked hospital records (Epoch Times, 2020) attest to early cases of Covid-19 in October 2019, although the Chinese Ministry Investigation has yet to confirm or publish the details of these alleged "*early cases*" (Knikkv387, 2020).

A letter and documents leaked to The Epoch Times (Fu, 2020) from February 18th 2020, revealed that a Chinese national investigation team "*wished to trace early cases of the disease. It asked local authorities for data from all Wuhan medical institutions over the period between Oct. 1 to Dec. 10, 2019*". The records obtained by this team actually showed more than "*40 suspected COVID-19 patients across eight hospitals*", including 9 deaths due to COVID-19-like conditions at three specific hospitals:

1. Five deaths between November and December 2019 at the Wuhan No. 6 Hospital.
2. Three deaths at The Wuhan Hospital of Traditional Chinese Medicine in October.
3. One death at Wuhan No. 8 Hospital (Fu, 2020).

According to an analysis by Dr. Lin Xiaoxu, a former US Army microbiology researcher and director of the Department of Virology at the Walter Reed Army Research Institute, the initial Wuhan outbreak began in October and November 2019, with some hospitals "reporting cases of new coronary pneumonia-like cases with imaging characteristics" (Epoch Times,2020).

Although the skeptical reader may question the source of these leaked documents, careful analysis reveals that they are genuine and ongoing investigations are taking place to identify and track these early cases. In fact, in another leaked document (SCMP, 2020), nine Covid-19 cases were identified in November 2019 (4 male and 5 female aged between 39 and 79). These cases were later confirmed retrospectively according to Chinese government sources, including a 55 year old man on 17th November, 2019, who the SCMP suggested may have been "patient zero" (SCMP, 2020), At the same time, it should be noted that the younger cases mentioned above were not hospitalised, which in turn implies a higher November case count including relatively more healthy people under 39 who had mild symptoms.

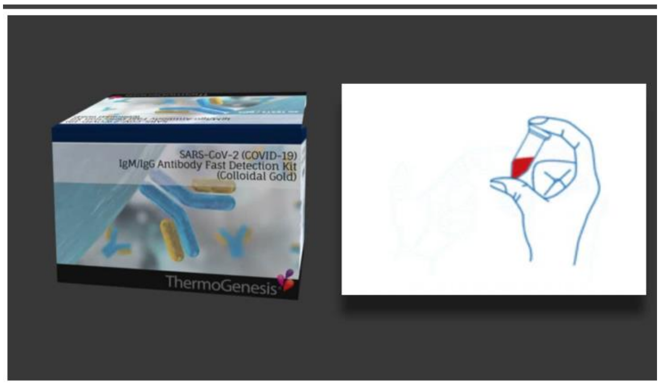
Finally, a now deleted 27th February 2020 article in the Chinese Health Times (2020) revealed the suspected case of "Patient Su" on 14th November 2019. Patient Su was treated at Rongjun Hospital in Wuhan and lived in the Kaile Guiyan community on Zhuodaoquan Street, about 600 metres from the medical centre. The Health Times article identifies the second patient in November as Mr. Wang, aged 62, who was treated at Hanyang hospital, on 21st November 2019, as subsequently reported in the UK Daily Mail (2021b).

8. THERMOGENESIS CLAIM

Figure 20: Thermogenesis HQ. Source: KTXL (2020)

Further anecdotal evidence from the US suggest that at least one company which developed testing kits (Figure 21) for SARS-COV-2 (Good Day Sacramento, 2020) initially became aware of the outbreak in November 2019. Paul Coelho (Figure 20), the CTO of a Sacramento company, Thermogenesis (Figure 22) claimed "*they knew about the outbreak back in November 2019*" (KTXL, 2020). Coelho insisted that ThermoGenesis had been working on developing:

> "*A rapid antibody test since November, when they first learned of the new coronavirus*" (KTXL, 2020) and "*Antibody testing is not new with us, so the rush was to get kits that would accurately and solely detect this virus*" (Mensch, 2020)



by: KTXL

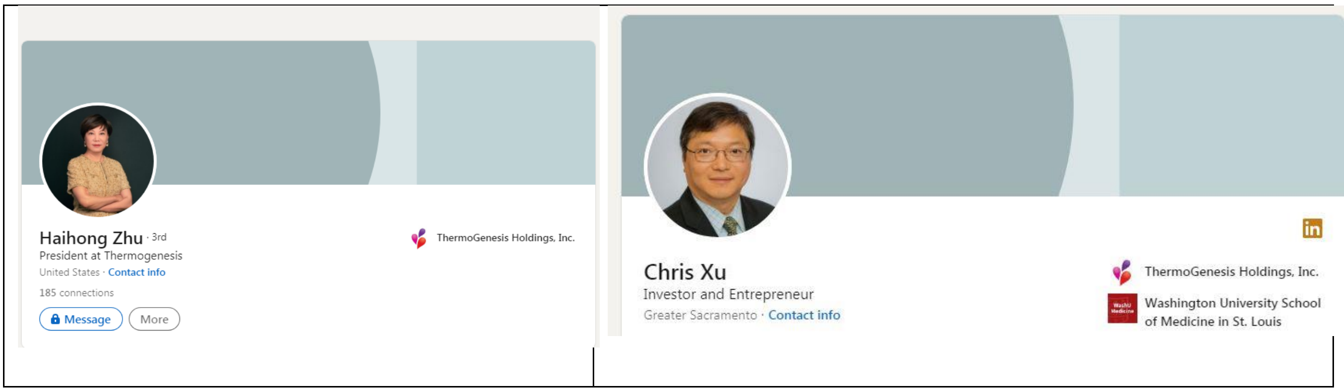
Posted: Apr 2, 2020 / 07:43 AM PDT / Updated: Apr 2, 2020 / 07:43 AM PDT

Figure 21: Thermogenesis Testing Kit for Covid-19. Source: KTXL (2020).

Figure 22: Video Screenshot of Phil Coehlo (ThermoGenesis). Source: KTXL (2020)

The full details of the Thermogeneseis Covid-19 test kit can be viewed here: https://thermogenesis.com/app/uploads/2020/05/ThermoGenesis-Rapid-PoC-COVID-19-Test.pdf and here: https://thermogenesis.com/covid-19-test-kit/ with an accompanying video: https://youtu.be/Ve3kEXqMI40

This raises the question of how and from whom did Thermogenesis learn of SARS-COV-2 in November 2019. Thermogenesis has many links to China, specifically via Haihong Zhu (LinkedIn. (2021a, Figure 23), who is President of Thermogenesis (2021). Secondly, via Chris Xu (LinkedIn, 2016, Figure 23), who is Chairman and CEO of ThermoGenesis. Chris Xu is also a Professor at the Institute of Molecular Medicine, Peking University (Thermogenesis, 2021).



Haihong Zhu · 3rd
President at Thermogenesis
United States · Contact info
185 connections
ThermoGenesis Holdings, Inc.

Chris Xu
Investor and Entrepreneur
Greater Sacramento · Contact info
ThermoGenesis Holdings, Inc.
Washington University School of Medicine in St. Louis

Figure 23: LinkedIn Profiles of Chris Xu and Haihong Zhu. LinkedIn (2016 and 2021a)

Figure 24: Haihong Zhu. Source: Thermogenesis (2021b)

"*Haihong Zhu, Chief Operating Officer, joined ThermoGenesis in 2004, with 20 years of technical and sales experience in stem cell research. She has contributed significantly to the establishment of **Thermogenesis' commercial presence in China**. Ms. Zhu graduated from the Shanghai University of Science & Technology with a Bachelor's in Biology and also studied statistics at Boston University*" (Thermogenesis. 2021b).

Figure 25: Chris Xu. **Source: Thermogenesis (2021b)**

"Dr. Xu has served on ThermoGenesis Holdings' board of directors since March 2016, and was appointed chairman and interim chief executive officer in November 2016 and CEO in August 2017. In 2009, Dr. Xu founded Boyalife Group, a global diversified life sciences holding company and is currently the principal shareholder of ThermoGenesis Holdings. Prior to founding Boyalife, Dr. Xu served as a project leader at Pfizer, as a director of research at two publicly-traded companies and as a vice president at Founder Group, a technology conglomerate with $20 billion annual revenue" (Thermogenesis. 2021b).

Figure 26: Paul Coelho. Source: Thermogenesis (2021b)

"*Mr. Coelho joined ThermoGenesis Holdings as chief technology officer from SynGen Inc. in July 2017, where he was CTO and co-founder. Mr. Coelho is an engineer and inventor who has been awarded more than 30 U.S. patents related to cell cryopreservation, cryogenic robotics, cell selection, blood protein harvesting, and surgical hemostasis. Prior to co-founding SynGen, Mr. Coelho founded and ran several companies including ThermoGenesis Holdings' device division, ThermoGenesis Corp., where he also served as chairman and chief executive officer. At ThermoGenesis Holdings, he led the development of many of the company's key products. Mr. Coelho has gathered detailed knowledge of the practices of the major public and private cord blood banks in 30 countries and has developed working relationships with many scientists, clinicians and directors associated with these cord blood banks. As CTO of ThermoGenesis Holdings, Mr. Coelho is leading the development of new products for the clinical and research fields*" (Thermogenesis. 2021b)

Thermogenesis is part of the BoyaLife Group which has 30 subsidiaries in The United States, China, South Korea and India, notably in Sacramento, Beijing and Tianjin (Figures 27 and 28).

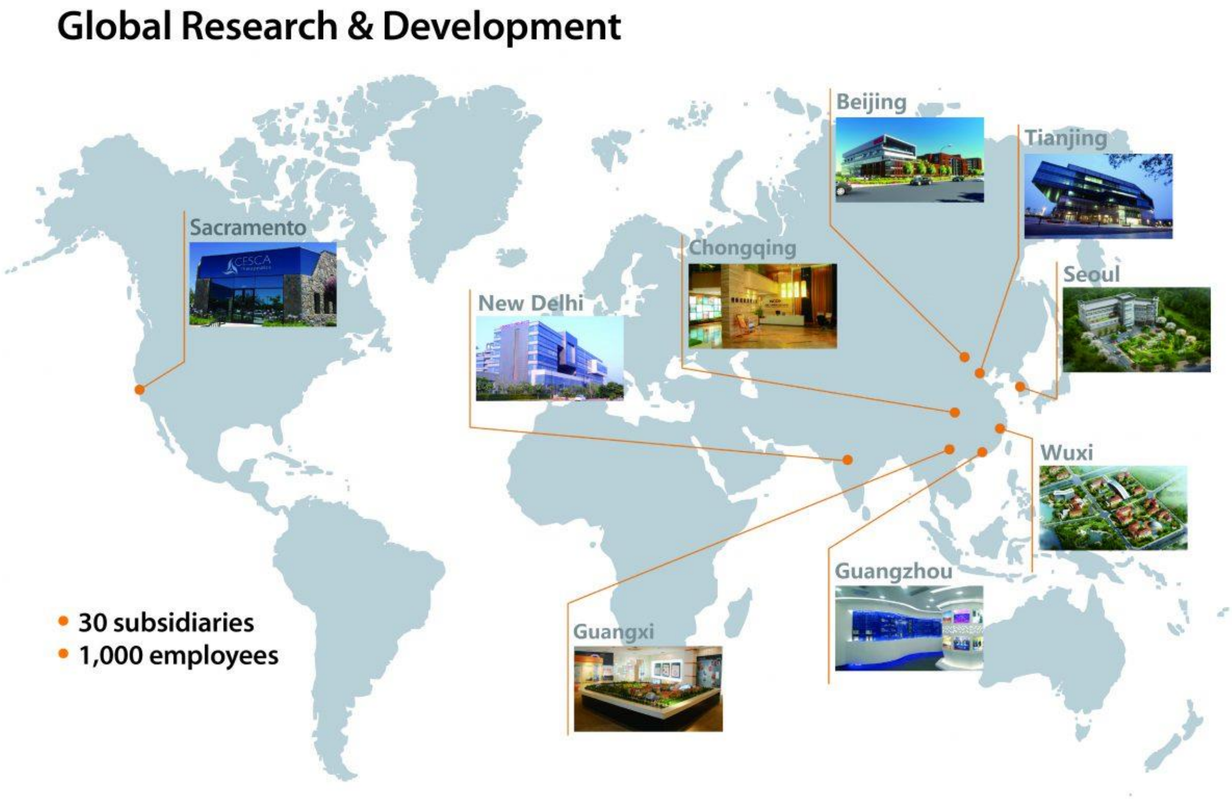


Figure 27: Boyalife subsidiaries and R & D. Source: Boya Life (2018)

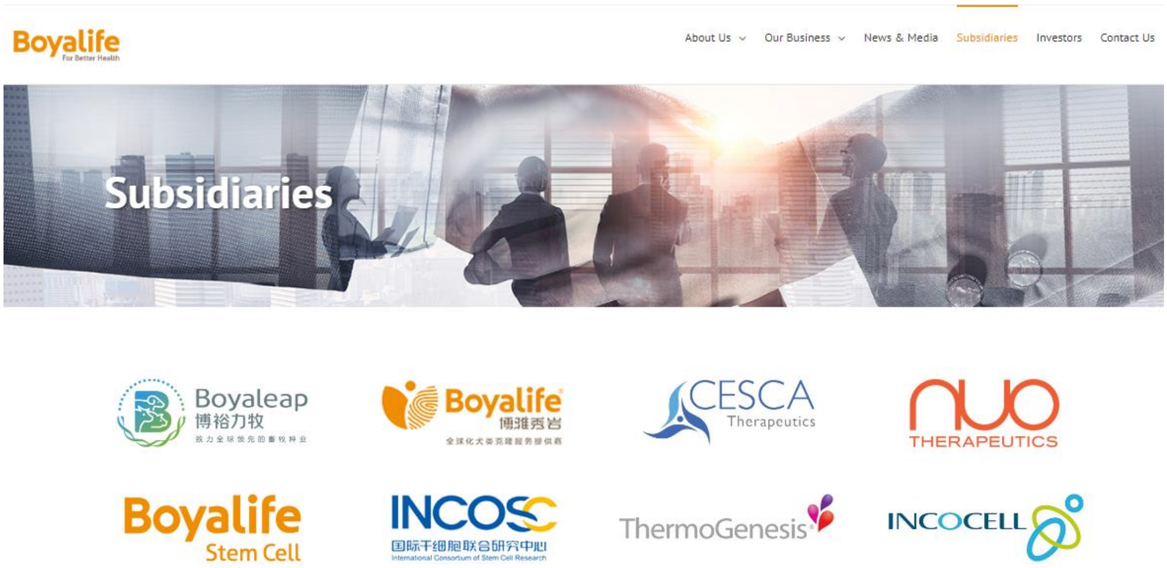


Figure 28: Boyalife Subsidiaries. Source: Boya Life (2018).

With reference to these subsidiaries and its international research networks, Chris Xu, CEO of Thermogenesis, claimed in an interview with the Sacramento Bee (2020):

- "*We are so advanced at this because we leveraged our unique global resources. When this epidemic started to surface in Asia***, we have several top universities in China where we collaborate & developed the science behind this & did screening***. So now we are probably at least four to six months ahead of any other comparable research institution here (in the US)* (The Sacramento Bee, 2020).
- "*We are taking a systematic approach to address several critical unmet needs in the fight against COVID-19.* ***By working closely with our global collaborators, we had a head start on this critical research***" (Thermogenesis, 2020b).

Regarding the biological therapy developed at ThermoGenesis **and its affiliate, ImmuneCyte,** Chris Xu made a series of interesting statements:

1. "*They began using their kit to screen for those individuals months ago,* ***long before COVID-19 began to infect a low number of U.S. citizens****"*

2. "ThermoGenesis and ImmuneCyte scientists ***got whole blood plasma from recently recovered individuals*** *and began identifying and isolating white blood cells"*

3. "They made a huge (DNA expression) library looking for which B cells or DNA from B cells can recognize the virus. ***So we screened millions of those candidates in the library****"*

*4. "They picked over 1,700 clones before finding 456 that seemed particularly effective at recognizing SARS-CoV-2. Then, they sequenced each of them, identifying 50 unique DNA sequences****. They then made 50 unique full-length human antibodies, each of which could be a single product****"*

5. "We're looking at whether there's an antibody that can block the virus from not only recognizing the cell, but also from entering the cell, so, out of that 50 we sequenced, 16 neutralizing antibodies were identified."

*6. "****ThermoGenesis and ImmuneCyte researchers and their collaborators produced four antibodies – all clones of a unique parent cell*** *– that showed the highest affinity to bind with the new coronavirus and block its entry into human cells, Xu said. The two companies hope to get the first monoclonal antibody treatment into the market*" The Sacramento Bee (2020).

Boyalife established ThermoGenesis in 2017 and a corporate timeline (Boyalife, 2018) reveals connections with the research centres in Tianjin and Peking University via Chris Xu (Boya Life, 2019).

2017- Boyalife establishes the ThermoGenesis Corp.
2015 - Boyalife Genomics opens a cloning facility in Tianjin for cattle breeding.
2014 - Boyalife Genomics clones the first Chinese Tibetan Mastiff.
2013 - Dr. Xiaochun "Chris" Xu wins 2013 China Economic Figure Award
2012 - PKU y & Boyalife jointly form PKU-Boyalife Institute
2012 - PKU acquires 40% position in Bejing Boyalife Stem Cell
2011- **Boyalife signs agreement with Institute of Molecular Medicine at Peking University** (Boyalife, 2018).

The Honorary Chairman at Boyalife since 2009 has been Dr. Zhihong Xu, who previously was the President of Peking University from 1999 to 2008, as well as vice president of the Chinese Academy of Sciences from 1992 to 2001 (Boya Life, 2018). His further roles include:

- Academician at the Chinese Academy of Sciences
- Professor of life sciences at Peking University
- Director of the Chinese Plant Physiology Society
- Professor emeritus at the University of Hong Kong
- Vice President of the China Society of Biological Engineering (Boya Life, 2018).

Thus, it is indeed possible that ThermoGenesis received information about the early outbreak in Wuhan via Chris Xu from Peking University's Institute of Molecular Medicine and the company **ImmuneCyte/IncoCell who allegedly supplied data and samples for the Covid-19 rapid tests (**Thermogenesis, 2020). In March 2018, the CEO of Cesca Therapeutics (a subsidiary of Boyalife), Chris Xu, announced that "*its device subsidiary, ThermoGenesis signed a license agreement* ***with IncoCell Tianjin,*** *a wholly-owned subsidiary of Boyalife Group*" (Contract Pharma, 2018), which covered Asian countries, including China:

.

> *"China is among the leading markets for CAR-T developers, and together with the U.S., represent the two countries with the highest number of ongoing CAR-T clinical trials "This agreement with IncoCell signifies our first CDMO collaboration, and is consistent with our goal of expanding beyond off-the-shelf cellular processing solutions into higher-value contract manufacturing and development services"* (Contract Pharma, 2018).

Two years later, in April 2020, we find that there was a joint venture between ThermoGenesis and ImmuneCyte, a company 19% owned by Thermogenesis (2020), to develop:

> "*Therapeutic treatment against Covid-19, based on Convalescent Plasma and polyclonal antibodies, as well a high-affinity monoclonal antibody drug candidates*" (Thermogenesis, 2020).

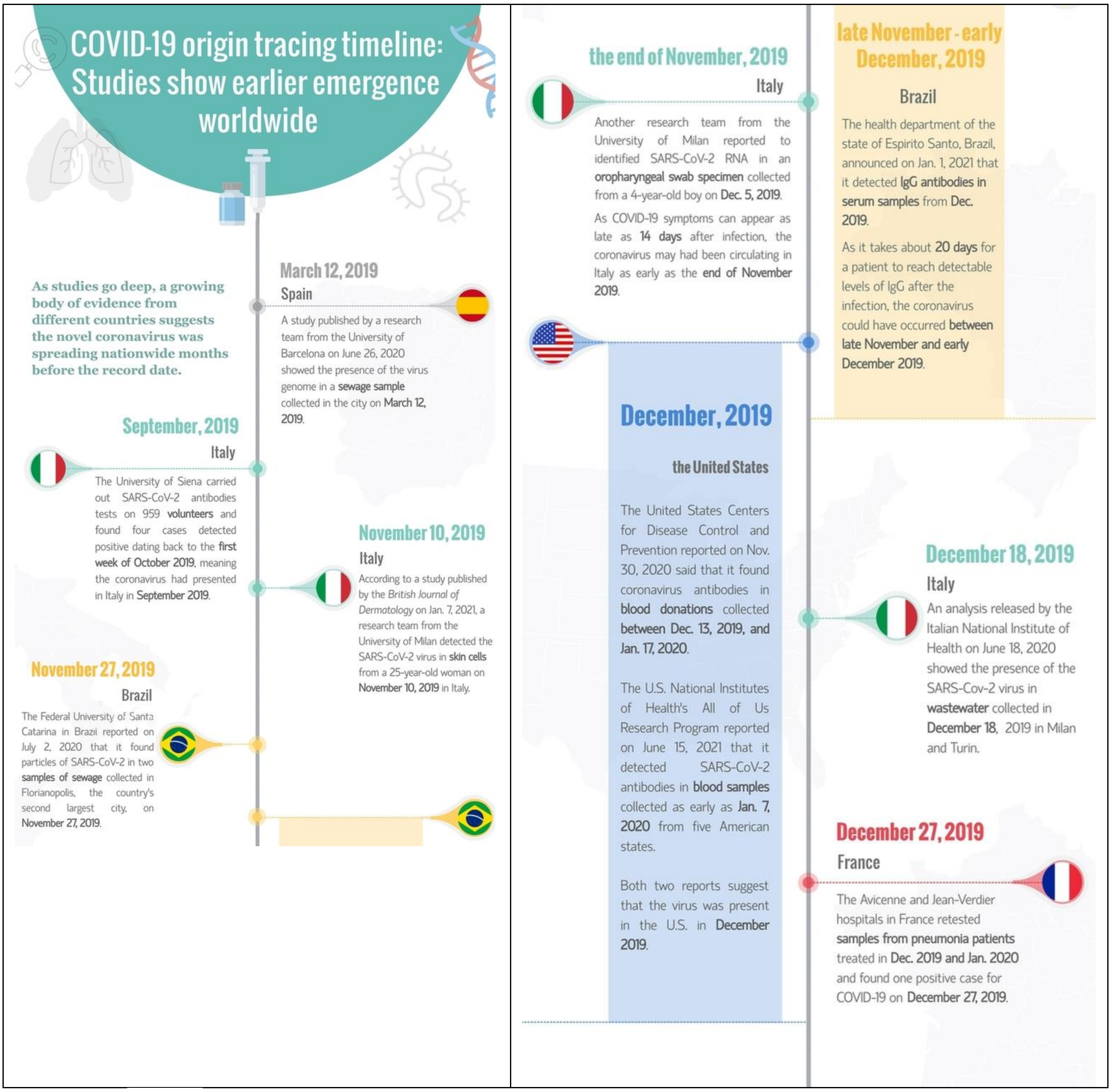
It is interesting to note two facts revealed in an online article by Thermogenesis in 2020:

> 1. "*ThermoGenesis is working towards developing strategies to identify and isolate* ***polyclonal antibodies from the blood of individuals who have recovered from the disease using convalescent whole blood or plasma,*** *which could then be used as a potential therapeutic treatment for patients with of COVID-19*" Thermogenesis (2020).
>
> 2. "*ImmuneCyte, has acquired from its collaborators worldwide intellectual property of four high-affinity monoclonal antibody drug candidates against COVID-19 virus. These high-affinity neutralizing monoclonal antibodies were also identified from convalescent whole blood from individuals who have recently recovered from COVID-19*" Thermogenesis (2020).

This may well explain why Chris Xu, Chief Executive Officer of ThermoGenesis, claimed that:

> "*By working closely with our global collaborators, we had a head start on this critical research"* Thermogenesis (2020).

9. EARLY POSITIVE RESULTS IN ITALY, FRANCE, SPAIN, BRAZIL, US.



COVID-19 origin tracing timeline: Studies show earlier emergence worldwide

As studies go deep, a growing body of evidence from different countries suggests the novel coronavirus was spreading nationwide months before the record date.

March 12, 2019
Spain
A study published by a research team from the University of Barcelona on June 26, 2020 showed the presence of the virus genome in a **sewage sample** collected in the city on **March 12, 2019**.

September, 2019
Italy
The University of Siena carried out SARS-CoV-2 antibodies tests on 959 **volunteers** and found four cases detected positive dating back to the **first week of October 2019**, meaning the coronavirus had presented in Italy in **September 2019**.

November 10, 2019
Italy
According to a study published by the *British Journal of Dermatology* on Jan. 7, 2021, a research team from the University of Milan detected the SARS-CoV-2 virus in **skin cells** from a 25-year-old woman on **November 10, 2019** in Italy.

November 27, 2019
Brazil
The Federal University of Santa Catarina in Brazil reported on July 2, 2020 that it found particles of SARS-CoV-2 in two **samples of sewage** collected in Florianopolis, the country's second largest city, on **November 27, 2019**.

the end of November, 2019
Italy
Another research team from the University of Milan reported to identified SARS-CoV-2 RNA in an **oropharyngeal swab specimen** collected from a 4-year-old boy on **Dec. 5, 2019**.

As COVID-19 symptoms can appear as late as **14 days** after infection, the coronavirus may had been circulating in Italy as early as the **end of November 2019**.

late November - early December, 2019
Brazil
The health department of the state of Espirito Santo, Brazil, announced on Jan. 1, 2021 that it detected **IgG antibodies in serum samples** from **Dec. 2019**.

As it takes about **20 days** for a patient to reach detectable levels of IgG after the infection, the coronavirus could have occurred **between late November and early December 2019**.

December, 2019
the United States
The United States Centers for Disease Control and Prevention reported on Nov. 30, 2020 said that it found coronavirus antibodies in **blood donations** collected **between Dec. 13, 2019, and Jan. 17, 2020**.

The U.S. National Institutes of Health's All of Us Research Program reported on June 15, 2021 that it detected SARS-CoV-2 antibodies in **blood samples** collected as early as **Jan. 7, 2020** from five American states.

Both two reports suggest that the virus was present in the U.S. in **December 2019**.

December 18, 2019
Italy
An analysis released by the Italian National Institute of Health on June 18, 2020 showed the presence of the SARS-Cov-2 virus in **wastewater** collected in **December 18**, 2019 in Milan and Turin.

December 27, 2019
France
The Avicenne and Jean-Verdier hospitals in France retested **samples from pneumonia patients** treated in **Dec. 2019 and Jan. 2020** and found one positive case for COVID-19 on **December 27, 2019**.

Figure 29: COVID-19 origin tracing timeline: Studies of earlier emergence worldwide (China Military, 2021)

As mentioned in the Introduction to this report, China claims that there were no earlier cases than the official December 2019 ones, while there are several reports of earlier cases and positive samples from overseas (China Military, 2021; CGTN, 2021, Figure 29). We will now proceed to examine these claims in excruciating detail.

1. ITALY

In Italy, **the first two imported Covid-19 cases** were detected in Rome, two Chinese tourists who had travelled from Wuhan to Milan on 23rd of January 2020 before travelling to Rome via Parma in a hired car. They were then sent to the Spallanzani Hospital in Rome for treatment (Giovanetti et al., 2020). According to Giovanetti et al. (2020), their viral sequences "*clustered together and grouped with sequences isolated in Europe intermixing with viral strains from China*". These viral strains were dated back to the 18th and 19th of January, 2020 (Giovanetti et al., 2020).

Using Bayesian phylogenetic reconstruction, Giovanetti et al. (2020) estimated that the two tourists became infected before reaching Italy, and concluded that viral strains introduced into Europe were from China (Giovanetti et al., 2020). Finally, they also estimated the probable origin of 2019-nCoV to be Wuhan, dating back to the time of the most recent common ancestor of the human outbreak between 28th of September 2019 and 21st of December 2019 (Giovanetti et al., 2020).

According to the Italian News Agency, ANSA (2020) there was also "*a suspected case in the Veneto region, a minor from the Treviso area who recently got back from a trip to China*". However, no further updates on these putative cases have been reported as far as the authors are aware.

It was discovered that the first patient in North Italy met an asymptomatic traveller who had returned from China on the 21st of January 2020 (Thomas, 2020). Then on the 22nd January there were two deaths, resulting in closures of some public amenities in Lombardy and Veneto (Thomas, 2020).

Later, Massimo Galli, Head of Infectious Disease at Sacco Hospital in Milan, claimed that three different genetic sequences discovered in Lombardy implied that Covid-19 was actually spreading some weeks before Italy's first case:

> "*It is plausible that when Covid-19 landed in the country, it was still in incubation, and the infection developed in somebody with light or no symptoms at all*" (Thomas, 2020).

On 20 and 21 February 2020, **the first two locally acquired cases of COVID-19** were reported in Lombardy and Veneto, but were not linked to each other. According to Russo et al. (2020), the Veneto patient was 70 years old with no travel history to China and no contact tracing to anyone who had travelled to China:

> "*The case was admitted to a local hospital on 16 February with a severe respiratory insufficiency, tested positive for SARS-CoV-2 on 21 February and died on the same day*" (Russo et al., 2020)

Indeed, the Veneto Region suffered a disturbingly high rate of SARS-CoV-2 during the early days of the pandemic (Russo et al., 2020). As of September 2021, the total number of Covid-19 cases in Italy has reached more than 4.6 million, with Lombardy suffering the worst, at 881,000 cases (Statista, 2021).

The likely spread of SARS-COV-2 or its progenitor virus in late 2019 has also been proposed to explain the finding of recent positive serum antibody test results from Italy by Apolone et al. (2020) in "Unexpected detection of SARS-CoV-2 antibodies in the pre-pandemic period in Italy". They detected SARS-CoV-2 receptor-binding domain (RBD)–specific antibodies in blood samples of asymptomatic individuals enrolled in a prospective lung cancer screening trial in September 2019:

> "*SARS-CoV-2 RBD-specific antibodies were detected in 111 of 959 (11.6%) individuals, starting from September 2019 (14%)…in Lombardy*" (Apolone et al., 2020)

Although they claim that this study shows "*an unexpected very early circulation of SARS-CoV-2 among asymptomatic individuals in Italy several months before the first patient was identified*", it must be noted that they used an "*in-house designed RBD-based ELISA*" as their serologic assay. This was quite strongly criticized for using antibody detection instead of sequence-based detection which is considered the more reliable way to detect SARS-COV-2 in samples (Apolone et al., 2020).

The positive results include those from a young Milan boy in November 2019 (Salo, 2020), confirmed by Gianotti et al. (2021) in their paper "*COVID-19 related dermatosis in November 2019. Could this case be Italy's patient zero*?", which discussed the November 10th 2019 case of a 25 year old woman suffering from a sore throat and dermatosis on the arms (Figure 30):

> "*Subsequent immunohistochemical investigations for SARS-CoV-2 nucleocapsid antigens showed a cuticular staining of the glomerular part of the eccrine glands*"

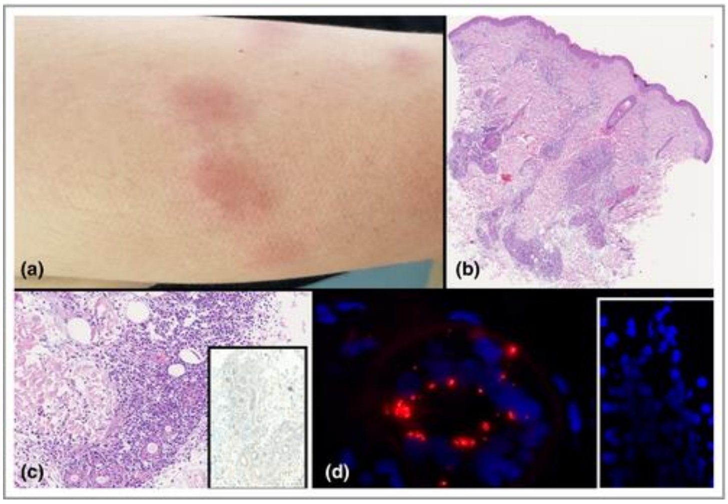


Figure 30: Immunohistochemical investigations for SARS-CoV-2 nucleocapsid antigens showed a cuticular staining of the glomerular part of the eccrine glands (Gianotti et al., 2021).

However, the authors confess that the sample was too degraded to provide sufficient RNA to sequence the virus (Sylvers, 2021):

"We *were not able to detect viral RNA with RT-PCR technology because the viral load was probably too low or degraded by RNA enzymes released after exogenous or cellular destruction*" (Gianotti et al., 2021).

In fact, the 25year old woman only tested positive for SARS-Cov-2 antibodies later in June 2020 (Sylvers, 2021), suggesting "*she had been exposed to an asymptomatic infection after her illness*".

On March the 30th, the WHO asked for further patient data to help clarify the suspected case. Unfortunately, the patient has not been located and neither the University of Milan nor the Policlinico hospitals have any of her details. To add to the confusion, Gianotti, who studied the case, died on the 27th of March (Sylvers, 2021). None of the researchers who co-authored the paper with Gianotti "*know the name, contact details or residence of the woman who yielded the skin sample*" (Sylver, 2021).

Amendola et al. (2021) also claimed that SARS-CoV-2 was circulating in Lombardy during the late summer of 2019, based on their study of samples collected from patients in at that time, including a throat swab from a child in Milan suspected of being infected with measles in early December 2019:

> "*The first positivity for SARS-CoV-2 RNA was found in a sample collected on September 12, 2019. Mutations typical of B.1 (PANGOLIN classification) strains, previously reported to have emerged in January 2020, had already been circulating in October 2019. Hence, we estimate SARS-CoV-2 progenitor of known human infections to have emerged in late June-late August 2019*" (Amendola et al., 2021).

However, it should be noted that they first did RT-PCR testing using US CDC procedures with negative results due to low viral load, and then they used specific primers for RdRp, Nsp3 and spike for subsequent tests, which may have involved contamination:

> "*All samples from positive patients only became positive after nested PCRs and none of the samples tested positive with the Real-Time PCR diagnostic protocol, indicative of low viral load at the detection limit*" (Amendola et al., 2021).

In a study supported by the European Virus Archive Global (EVA-GLOBAL) project, La Rosa et al. (2021) found that there was evidence from sewage analysis that SARS-CoV-2 was circulating in northern Italy since December 2019. They claim that:

> *"the first SARS-CoV-2 positive sewage samples were collected as early as 18 December 2019 ...Specifically, viral RNA first occurred in sewage samples collected on December 18th, in Milan (Lombardy) and Turin (Piedmont)"* La Rosa et al. (2021).

They point out that these positive sewage samples imply the existence of asymptomatic carriers, or of patients with covid-19 like symptoms who may have been diagnosed mistakenly as suffering from the flu in late 2019 (La Rosa et al., 2021). In view of the strong likelihood that SARS-COV-2 was already circulating in Wuhan and Hubei Province in late October and early November, these results merely reinforce our hypothesis. This is particularly the case with Northern Italian Regions such as Lombardy (Figure 31), which have a large Chinese illegal immigrant population, many of whom travelled from Wuhan to Italy during the period in question.

Figure 31: Regions of Italy Northern Italy Udine Lombardy Map. (PNGEGG, 2018)

The most famous city for legal and illegal Chinese immigration in Italy, Prato, has the second-largest Chinese population of any European city (New Yorker, 2018). According to the local authorities in Prato, up to 66 percent of the Chinese there are illegal immigrants (Fashion Network, 2014).

50,000 Chinese live and work in the area, with 5,000 workshops making "Made in Italy" clothes with cloth smuggled from China, "evading taxes and grossly violating health and labor regulations" (Fashion Network, 2014). As most of the workers are illegal immigrants, they do not have the requisite documentation necessary for accessing the "Servizio Sanitario Nazionale", leaving them without access to medical care. Conditions in these workshops (Figure 32) are described as "cramped" at best (Ho, 2020), and if workers became infected with SARS-COV-2, it would have been extremely difficult if not impossible to track and contacts trace them:

> "*If workers are forced to work in tight-knit closed quarters--sitting closer than the recommended 2 metres away from each other under current social distancing guidelines--just one infection can quickly balloon into a full-blown outbreak*" (Ho, 2020).

Figure 32: Chinese family living and working in a sweatshop in Prato (APA / Picturedesk) in Ho (2020).

Early on in the outbreak questions were asked about possible connections between these "underground" workshops and the "*incredibly rapid spread of the pandemic, particularly in the country's northern region*" during Italy's coronavirus crisis, for example by Ho (2020). However, to date, no direct link has yet been established between any of these workshops and Italy's Patient Zero. (Ho, 2020).

Interestingly, there was a claimed increase in illegal immigration in late 2019 to meet the increased demand stemming from the upcoming Milan Fashion Week scheduled to start on February 24th 2020, but cancelled as a result of the pandemic (Ho, 2020).

The city of Prato surprisingly saw relatively few cases of Covid-19 at the beginning of the outbreak in Italy (POLITICO, 2020), despite over 2,000 Chinese residents who returned from their Chinese New Year holidays in February 2020. According to Lorenzo Rocchi, a local politician:

> "*The idea of being in a city of so many Chinese with strong links to the home country made some people fearful. That turned out to be completely wrong — in the end **the virus arrived here from Lombardy***" (POLITICO, 2020).

So, rather than fueling the pandemic, it seemed that actions taken by the local Chinese community actually helped to "*protect Prato from the outbreak, through early adoption of strict isolation measures*" (POLITICO, 2020).

> "*Prato, where about 10 percent of residents are of Chinese origin, has seen just 479 cases of the coronavirus — fewer than any other province in the Tuscany region. Not a single member of the Chinese community there has tested positive for the virus, according to officials. In late January, weeks before Italy registered its first coronavirus case; many Prato Chinese went into self-isolation, closed businesses and kept children at home. Social pressure from the community ensured a scrupulous adherence to the*" (POLITICO, 2020).

Turning now to the situation in Lombardy where Italy's patient zero was traced to, Dr. Giuseppe Remuzzi of the Mario Negri Institute for Pharmacological Research in Milan reported that "*a strange pneumonia had been circulating in the northern Lombardy region as early as November 2019*" NPR (2020b). This was particularly the case at Codogno Hospital towards the end of December 2019, where patients were hospitalized with Covid-19 like symptoms but treated for influenza and pneumonia (Thomas, 2020). Remuzzi also claimed that several local Doctors witnessed:

> *"A very strange pneumonia, very severe, particularly in old people in December and even November" This means that the virus was circulating, at least in Lombardy and before we were aware of this outbreak occurring in China"* (NPR, 2020).

SCMP (2020b) also reported the case of a local resident in the village of Nebro, near Bergamo in Lombardy, who claimed that "*this thing has been around since the beginning of the year or even Christmas*". Indeed, a nursing home in Nebro saw "20 *anomalous deaths caused by pneumonia in January 2020*" (SCMP, 2020b).

Although cases such as these tend to reinforce the hypothesis that early cases of Covid-19 arose in Italy before the Wuhan outbreak, Remuzzi specifically chose to clarify his reports by stating that "**there remains little proof to support any theory that coronavirus originated outside of Wuhan"** (SCMP, 2020c). He further stated that:

- "*The key point in his NPR interview was not where the virus came from, but how far it had spread before it was discovered*". SCMP (2020c).
- "*A major question was how long the disease had been spreading in China before health authorities realised its severity"* (SCMP, 2020c).
- "*Taking into account the long incubation period, Remuzzi said he would not be surprised if some asymptomatic carriers had travelled around China or even abroad before December*" SCMP (2020c).

Remuzzi claimed that "*the unusual cases in November and December could mean that virus was already circulating in Lombardy, the country's worst*-hit *region, before people were aware of what was unfolding in Wuhan*" SCMP (2020c).

He pointed out that they could not be sure the patients had Covid-19 because they were unable to test for SARS-COV-2 at that time and X Rays were not taken (SCMP, 2020c). Remuzi also referred to some early cases in Lombardy which local doctors considered unusual as the patients had been vaccinated against influenza, namely:

- "*Two pneumonia cases in Scanzorosciate in northern Italy in December, where the patients developed high fever, a cough and had difficulty in breathing*" (SCMP, 2020c).
- "*10 patients who developed bilateral interstitial pneumonia in two other nearby towns, Fara Gera D'Adda and Crema, who had similar symptoms and who recovered within 15 days, with some receiving two or three courses of antibiotics"* (SCMP, 2020c).
- "*A patient diagnosed with bilateral interstitial pneumonia in Alzano Lombardo Hospital in Lombardy around the time*" (SCMP, 2020c).

Remuzzi's claims clearly point to the early introduction of SARS-COV-2 into the Lombardy region, well before the first patient was diagnosed with Covid-19 in Codogno (Lombardy) on February 20th 2020. This case was described by Dr. Annalisa Malara, an anesthesiologist in Codogno (Escardio, 2020) and in Reuters (2021):

> "*A previously healthy 38-year-old man, now known as Mattia or "patient one", had gone to the hospital with a high fever, cough and shortness of breath on Feb. 18, 2020. He refused to be admitted so was given antibiotics and went home. He returned that evening in worse shape and was put on oxygen. Two days later, Mattia's wife told doctors that a few weeks earlier he had gone to dinner with a colleague who had been in China*" (Reuters, 2021).

To conclude, early cases even dating back to November in Italy do not mean the outbreak originated in Italy. Neither do the published papers reviewed above make that claim, merely that "*it is possible that the earliest cases started in November or earlier, and then came over to Italy, most likely through international travel*" Medical News Today (2021).

2. FRANCE

Meanwhile, in France, it was reported by INSERM that:

> "*SARS-CoV-2 virus circulation and infection could have occurred as early as November 2019 in France*" (INSERM, 2021)

This claim was based on a paper publishes by INSERM researchers (Carrat et al., 2021). However, even the authors admit that:

> "*The critical issue is whether these findings might result from a lack of specificity of our serological methods. The proportion of ELISA-S positive reported may look overestimated given the time period the samples were collected"* (Carrat et al., 2021).

Another group of French researchers (Deslandes et al., 2020) reported an early December 2019 case in Paris:

"*A case of a patient hospitalised in December 2019 in an intensive care unit in a hospital in the north of Paris for hemoptysis with no aetiological diagnosis. RT-PCR was performed retrospectively on the stored respiratory sample and confirmed the diagnosis of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection*" (Deslandes et al., 2020)

However, the authors were unable to "*rule out false-negative results due to the sensitivity of RT-PCR and a technique of storage that may possibly impair the quality of samples*" (Deslandes et al., 2020). This singular case was gleefully reported by China Military (2021):

"*A retrospective analysis of samples taken from 24 patients treated in December 2019 and January 2020 with influenza-like symptoms at the Avicenne and Jean-Verdier hospitals in France found one patient positive for COVID-19 on December 27, 2019"* China Military (2021).

3. UNITED STATES

According to a recent document published by the Chinese Embassy in Germany "*U.S.: Virus found in blood samples in December 2019*" (De China Embassy, 2021):

"*A study published in June 2021 by the U.S. National Institutes of Health (NIH) was the latest and largest (in scale) one to suggest that the new coronavirus popped up in the U.S. in December 2019, weeks before cases were first recognized by health officials*" (De China Embassy ,2021)

This claim was also highlighted by China Military (2021):

"*A study published in the journal Clinical Infectious Diseases on June 15, 2021 showed evidence of coronavirus infections in five American states as early as December 2019 -- weeks before the first officially reported cases*" China Military (2021).

The first officially recorded Covid-19 infection in the United States was on January 20th, 2020, a Washington patient who had travelled from Wuhan, however, the US CDC only confirmed local community spread of the virus on February 26th 2020

However, it is correct that NIH researchers identified SARS-CoV-2 antibodies in 9 blood samples from a cohort of 24,000 people between January 2nd 2021 and March 18, 2021. As antibodies normally emerge two weeks after infection, this implies SARS-COV-2 infection in late December 2019. Similar SARS-COV-2 positive antibody results were detected by CDC researchers in 39 blood samples from California, Oregon and Washington dating back to mid-December 2019 (13th to 16th). A further 67 samples from Massachusetts, Michigan, Wisconsin, Iowa, Connecticut and Rhode Island collected between December 30th and January 17th had positive antibodies (WSJ, 2020).

This NIH study which showed new evidence of early SARS-CoV-2 infections in U.S. (NIH, 2021) was reported by NPR (2020) "*Coronavirus Was in U.S. Weeks Earlier than Previously Known, Study Says*", and by Reuters (2021):

- "*At least seven people in five U.S. states were infected with the novel coronavirus weeks before the states reported their first cases, pointing to the presence of the virus in the country as early as **December 2019***" Reuters (2021).
- "*The virus may have been present in Illinois as early as **December 24, 2019***" (Achenbach, 2021).

The first confirmed SAS-COV-2 sample was found in a January 7th sample from Illinois (Achenbach, 2021), as part of NIH's "All of Us" research program which collected samples from about 280,000 people. Althoff et al., (2020) analyzed blood samples from 24,000 people using two different antibody tests (NIH, 2021). Despite many claims that sick people in December 2019 and January 2020 appeared to have had covid-19 like symptoms, the fact that the NIH sampling program only found 9 positive samples from 24,000 suggests that this was not the case (Achenbach , 2021). There are however certain possible flaws in the NIH study which should be taken into account:

1. TRAVEL

- "*The researchers did not have travel information for any of the cases with positive results, which might have helped explain the test results*" Archive Ph (2021).
- "*We don't know that they didn't go to Wuhan. We don't know that they didn't interact with someone who came from Wuhan*" Achenbach (2021).
- "*With no travel histories of the sampled people, it is as yet impossible to determine if they were either infected in China or infected by other people who had been infected there*" (Achenbach, 2021).

2. NO MOLECULAR DIAGNOSTIC CONFIRMATION

> **"**Participants *were not confirmed to be infected with SARS-CoV-2 via molecular diagnostic tests or paired acute-convalescent serum specimens"* (Althoff et al., 2021)

3. CROSS REACTIVITY WITH OTHER CORONAVIRUSES.

It is common knowledge that "*nearly everyone over the age of five has had a common coronavirus infection and has antibodies against those viruses*" (Red Cross, 2020). Thus, it is certainly conceivable that preexisting, non-SARS coronavirus antibodies may have bound to the SARS-CoV-2 nucleocapsid and spike protein in these cases (Althoff et al., 2021). If so, cross reactivity cannot be completely ruled out.

4. TWO ANTIBODY TESTS

The researchers did their best to ensure valid results by carrying out two different IgG antibody tests in sequence, Abbott Architect SARS-CoV-2 IgG ELISA and the EUROIMMUN SARS-CoV-2 ELISA (IgG) platforms (NIH, 2021). IgG antibodies appear 14 days after initial infection. The researchers also examined 1,000 blood samples taken from 2018-19 during the winter influenza period and "found none that tested positive for antibodies to the coronavirus" (Archive Ph, 2021).

4. FALSE POSITIVES

Several scientists have suggested that some of the positive test results were actually false positives (Achenbach, 2021). For example, Michael Worobey, Professor of Evolutionary Biology at the University of Arizona, considers that the “the *earliest result from Illinois, when coronavirus cases were only beginning to spread in Wuhan, is the most likely candidate for a false positive*” (Achenbach, 2021). Scott Hensley, an immunologist at the University of Pennsylvania, pointed out that the possibility of a “methodological error” (Archive Ph, 2021):

“*It’s hard to know what a real signal is and what isn’t” due to the few positive samples detected*”

Although it seems that some of the nine samples may have been false positives, given the dual IGG antibody tests carried out, it is improbable that all nine of them would have been false. (Archive Ph, 2021).

5. FUTURE RESEARCH

To investigate early covid-19 positive cases in the US and elsewhere, it is imperative that other blood samples from the early months of the pandemic be inspected via multiple testing platforms (NIH, 2021). Althoff et al., (2020) claimed that they would “release more information following further analysis” (NIH, 2021), and that they would “contact the participants to ask about travel history” Archive Ph (2021). However, as far as the authors are aware, no updates have been published to date (Achenbach, 2021). Currently, as Dr., Althoff pointed out:

> “*The exact month at which it probably came into the U.S. is still unknown. It’s essentially a puzzle right now, and our study is just one piece of that puzzle*” Archive Ph (2021).
>
> Taken together, these findings show evidence of dispersed and isolated SARS-CoV-2 infections in December 2019 in the United States (Basavaraju et al., 2020), which would be expected if the initial outbreak in Wuhan began in October/early November 2019.

4. SPAIN

CGTN (2021) and China Military (2021) were excited to report perhaps the most controversial study on early evidence of SARS-COV-2, in Spanish sewage samples. The research published by a team from the University of Barcelona (UB, 2020) allegedly "*showed the presence of the virus genome in a sewage sample collected on March 12, 2019*". The researchers tested for three genes and said that a March 2019 sewage sample was positive for the SARS-COV-2 RdRp gene:

> "*They screened for two regions of this gene and both were only detected around the 39th cycle of amplification. PCR tests become less "specific" with increasing rounds of amplification. Scientists generally use 40 to 45 rounds of amplification*" (Crossan, 2020)

The leader of the sewage study, Albert Bosch, claimed that:

> "*The levels of SARS-CoV-2 were low but were positive*" (USA Today, 2020a)

Curiously enough, Albert Bosch was simultaneously trying to market a wastewater SARS_COV_2 monitoring kit at the time (La Vanguardia, 2020). This was developed by a group led by Cetaqua, the LABAQUA Lab & Albert Bosch, and was marketed as Agbar's (Barcelona H20) new test kit (La Vanguardia, 2020).

The authors of the study published a second research paper in 2021(Chavarria-Miró et al., 2021), stating that the earliest positive sewage sample was from **January the 15th 2020, not March 12th 2019.** This latest paper does not include any reference to the earlier preprint. Indeed, the March 12th findings by Chavarria-Miró et al. (2020) in "*Sentinel surveillance of SARS-CoV-2 in wastewater anticipates the occurrence of COVID-19 cases*" have been criticized for several serious flaws itemized below:

1. The test reaction may have been accidentally contaminated with SARS-CoV-2 positive samples which were present in the laboratory.
2. Other RNA or DNA in the sample matched the test target site enough to “show positive at the 39th cycle of amplification” (Crossan, 2020).
3. Such a significant and anomalous finding would need to be further tested and “replicated separately by independent laboratories” (Crossan, 2020). Dr. Villalbi (Spanish Society for Public Health and Sanitary Administration) pointed out that:

   "*When it’s just one result, you always want more data, more studies, more samples to confirm it and rule out a laboratory error or a methodological problem*" (USA Today, 2020a).

5. The March 2019 finding disagrees with epidemiological data about the virus, with no evidence of infections or respiratory disease cases in the local area at that time of sampling or thereafter (Crossan, 2020).

6. If SARS-COV-2 was discovered in a mere 800ml sewage sample from March 2019, logically it was also present in the local population at relatively high levels. However, it was not detected to be present again until 2020 during a 9 month period with no anti-Covid-19 controls in place (Crossan, 2020),

7. Why did this sample only show positive at the 39th replication when the exponential phase had finished, which “*would be considered below the limit of detection and LOQ indicating that the sample was contaminated*” (Chavarria-Miró et al., 2020).
8. In page 1 of the supplementary materials, the validation data showed improved sensitivity/LOD for the genes E, N1, and N2 than for IP2/IP4. However, logically if IP2/IP4 was detected in the March 12th, 2019 samples, then E, N1 and N2 should also have been detected. That was not the case and should not be deemed a positive result (Chavarria-Miró et al., 2020).

9. The possibility of false positives cannot be ruled out, especially given that some of the PCR primers and probes used by the team may have bound to DNA in other human coronavirus genomes found in sewage (Covid Portugene, 2019). It is considered more prudent to use “SARS-COV-2 oligonucleotides with a high divergence to other strains” (Covid Portugene, 2019).
10. It could be due to contamination, so it is essential to fully sequence the amplicons to identify what lineages if any are present (Chavarria-Miró et al., 2020).
11. The study only detected IP2/IP4 resembling SARS-CoV-2, not SARS-COV-2 itself, nor the E and N1/N2 of SARS-COV-2 (Chavarria-Miró et al., 2020).
12. The qRT-PCR fluctuations observed even in the 2020 samples from different sewers are too high to trust the RT-PCRs reliability.
13. A more robust approach would have been to use metagenomics to sequence the sewage samples rather than doing a clearly less reliable RT-PCR assay (Chavarria-Miró et al., 2020).
14. The authors of the study have now published a second research paper stating surprisingly that the earliest positive sewage sample is actually from January the 15th 2020. This latest paper does not include any reference to the earlier preprint published on MedrXiv (Chavarria-Miró et al., 2021).

5. BRAZIL

Again, Chinese Media were excited to point out that:

"*The Federal University of Santa Catarina in Brazil reported on July 2, 2020 that it found particles of SARS-CoV-2 in two samples of sewage collected in Florianopolis, the country's second largest city, on November 27, 2019*" (China Military, 2021).

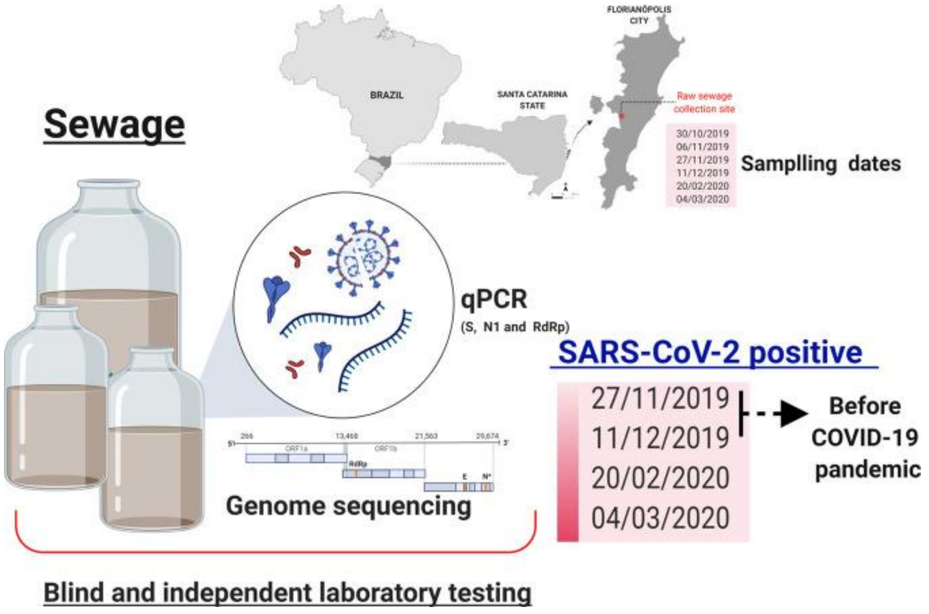


Figure 33: Sewage Testing in Santa Catarina. (Fongaro et al., 2021)

Indeed, Fongaro et al., (2021) did discover SARS-CoV-2 RNA in sewage samples from 27th November 2019, 3 months before the first case in Brazil and the Santa Catarina Region on March 20th 2020 (Figure 33). They were unable to confirm any early cases from patient clinical samples (Fongaro et al., 2021), although Stringari et al. (2021) did subsequently identify SARS-COV-2 positive patient samples in the State of Espirito Santo dating back to December the 18th, 2019.

Figure 34: Sampling Dates for Santa Catarina State, Brazil. (Fongaro et al., 2021)

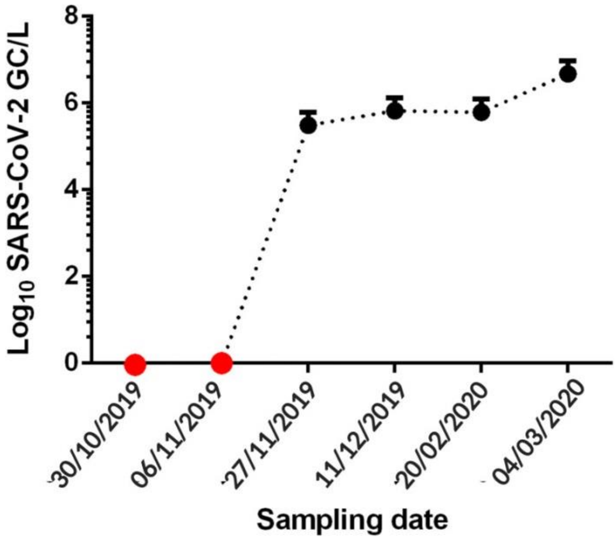


Figure 35: Sampling Data showing November Positive Sample (Fongaro et al., 2021)

> "*All samples were reported to be positive from the virus, beginning from* ***November 27, 2019****, to March 4, 2020. The viral load, overall, was 5.83 log10 copies L-1, which is similar to the viral loads in sewage studies in France and Spain, as well as the USA, during active infection*" (News Medical, 2020, Figures 34 and 35 above).

Another Brazilian study in Espirito Santo State detected IgG antibodies to SARS-COV-2 in 16 blood samples dating back from December 1st, 2019 to February 2020 (Stringari et al., 2021). Exposure to SARS-COV-2 in this area was thus likely prior to the first official Covid-19 case in March 4th 2020. This was yet another result of interest to the Chinese media:

“The health department stated that it takes about 20 days for a patient to reach detectable levels of IgG after infection, so it could have occurred between late November and early December 2019”.China Military (2021).

This was an interesting study which focused on IgG antibodies to SARS-COV-2 in blood samples taken from 7,370 patients suspected of having Dengue and Chikungunya, but not Covid-19, between December 1st 2019 and June 30th 2020 (Stringari et al., 2021).

“*Covert cases of SARS-CoV-2 were detected in 210 out of the 7,370 serum samples tested. The* ***earliest undiagnosed missed case of COVID-19 dated back to a sample collected on December 18, 2019****, also positive for Dengue Virus*” (Stringari et al., 2021).

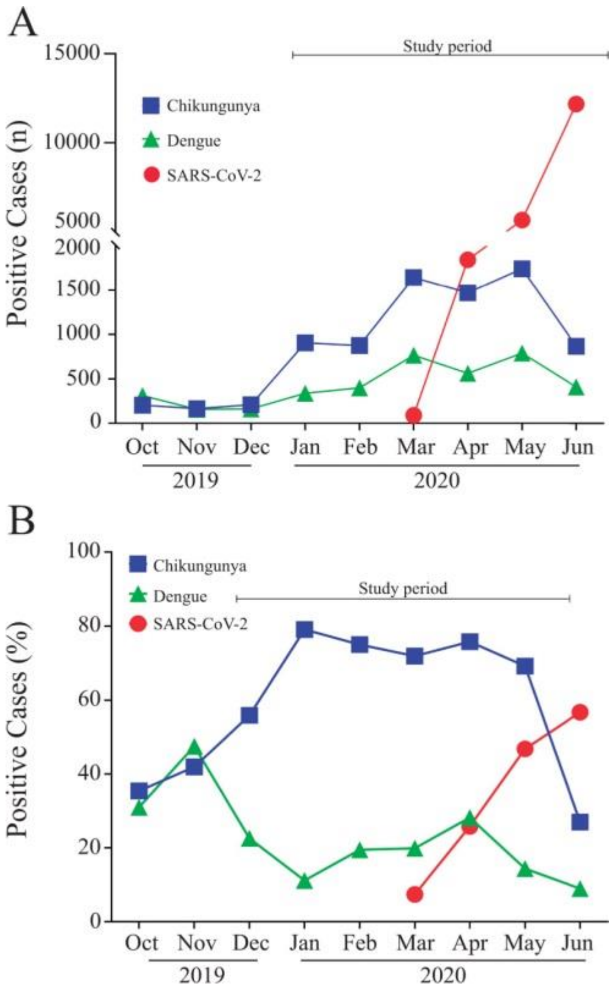


Figure 36: Cases of Severe Acute Respiratory Syndrome Coronavirus 2 in regions endemic for Dengue and Chikungunya viruses (Stringari et al., 2021).

The researchers made sure that the results were not caused by antigenic cross-reactivity with circulating human coronaviruses, by testing the 16 positive samples with "*Snibe CLIA Diagnostic—Maglumi2000 Plus 2019-nCov IgM and IgG assays*" (Stringari, 2021). This further test detected IgG and IgM antibodies to SARS-COV-2 in 8 of the 16 samples (Stringari, 2021).

> "*Differences observed here, regarding Abbott's CMIA and Snibe's CLIA results, may be justified by the fact that anti-N IgG response is known to appear earlier than the response targeting the S protein* " (Stringari et al., 2021)

The researchers also ensured that the SARS-CoV-2 positive results were not caused by "*cross-reactivity with Dengue antibodies*" (Stringari et al., 2021). They examined pre-pandemic samples from 42 Dengue fever patients in Espírito Santo a decade ago. 2 samples were taken, one during the acute phase of the disease and the other during the convalescent phase.

None of these 84 samples showed IgG antibodies to SARS-COV-2, which helps to rule out any claims that SARS-COV-2 positive samples detected in 2019/2020 were the result of false-positive reactions (Stringari et al., 2021). The study identified IgG antibodies for SARS-COV-2 as well as Dengue IgM in one blood sample taken **on December 18th** from a 60-year-old female patient from Vitória, who had Dengue Fever symptoms on December 9th 2019 (Stringari et al., 2021).

The distribution of the 210 positive cases of SARS-CoV-2 in Espírito Santo can be seen in the map below (Figure 37), where the red and black pins show sample collection dates (Stringari et al., 2021).

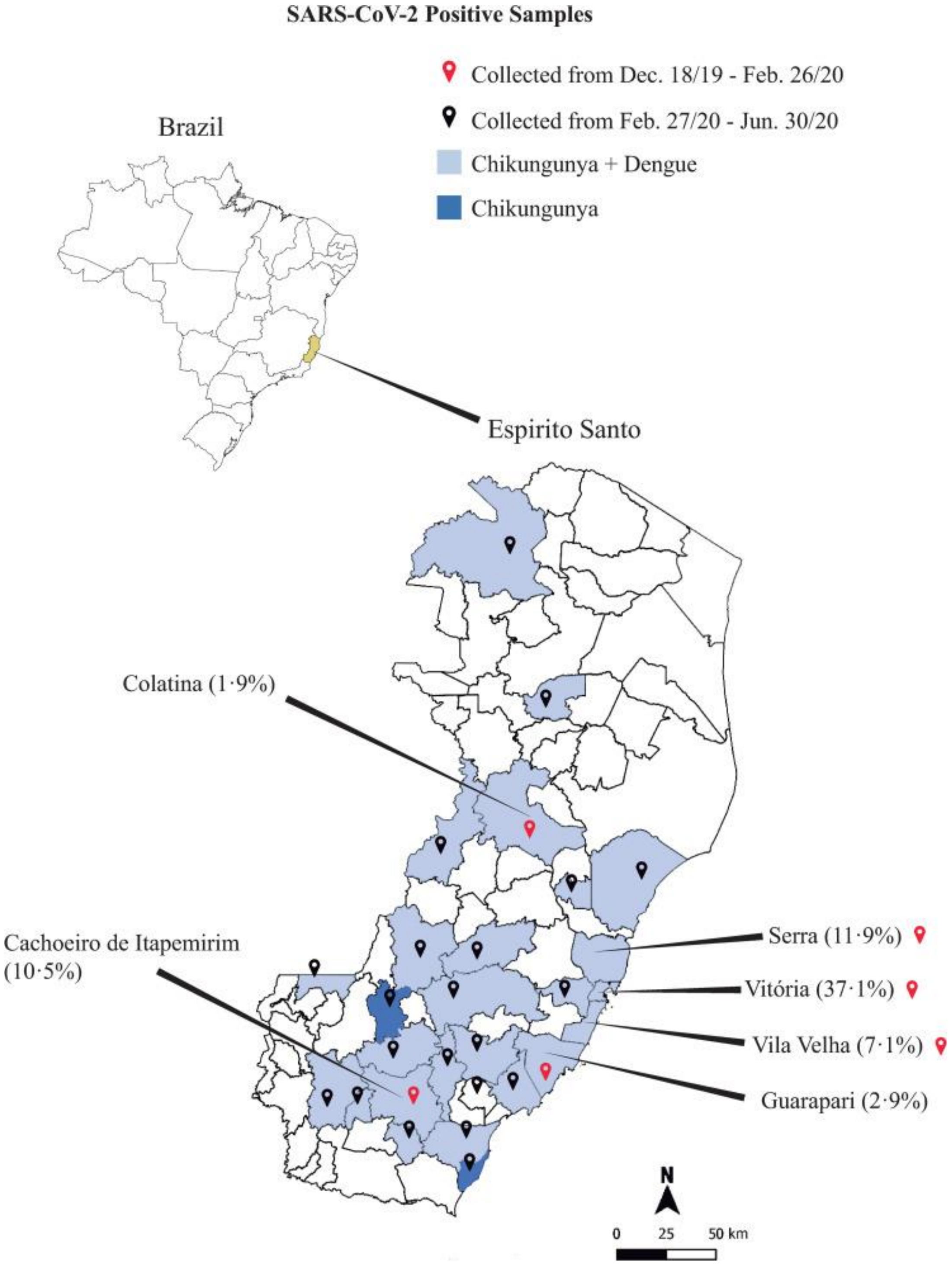
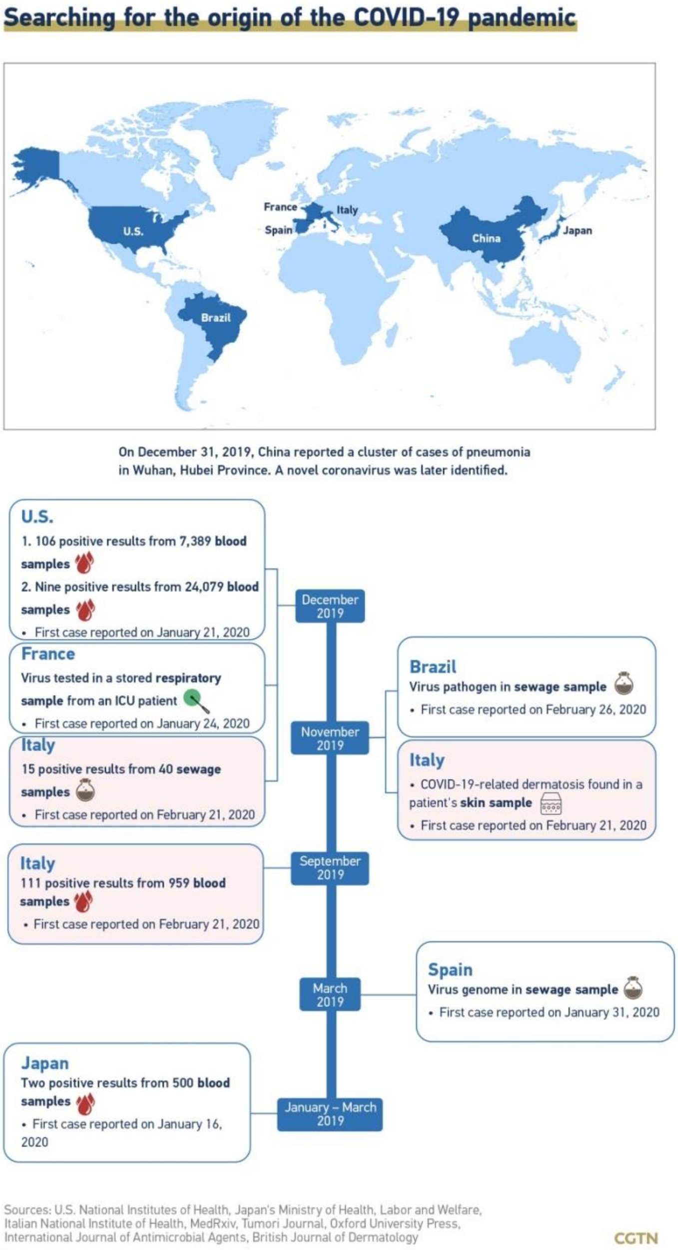


Figure 37: Distribution of the 210 positive cases of SARS-CoV-2 in Espírito Santo (Stringari et al, 2021)

This review of the evidence for early covid-19 incidence overseas in 2019 contradicts the agenda driven interpretation summarized in an infographic recently published by CGTN (2021), Figure 38 below:



On December 31, 2019, China reported a cluster of cases of pneumonia in Wuhan, Hubei Province. A novel coronavirus was later identified.

U.S.
1. 106 positive results from 7,389 **blood samples**
2. Nine positive results from 24,079 **blood samples**
- First case reported on January 21, 2020

France
Virus tested in a stored **respiratory sample** from an ICU patient
- First case reported on January 24, 2020

Italy
15 positive results from 40 **sewage samples**
- First case reported on February 21, 2020

Brazil
Virus pathogen in **sewage sample**
- First case reported on February 26, 2020

Italy
- COVID-19-related dermatosis found in a patient's **skin sample**
- First case reported on February 21, 2020

Italy
111 positive results from 959 **blood samples**
- First case reported on February 21, 2020

Spain
Virus genome in **sewage sample**
- First case reported on January 31, 2020

Japan
Two positive results from 500 **blood samples**
- First case reported on January 16, 2020

Sources: U.S. National Institutes of Health, Japan's Ministry of Health, Labor and Welfare, Italian National Institute of Health, MedRxiv, Tumori Journal, Oxford University Press, International Journal of Antimicrobial Agents, British Journal of Dermatology

Figure 38: Evidence of SARS-COV-2 in blood samples and sewage overseas. CGTN (2021).

Thus, despite recent claims in Chinese media (CGTN, 2021) and by Chinese researchers in the Lancet, "*SARS-CoV-2's origin should be investigated worldwide for pandemic prevention*" (Wu et al., 2021), these recent studies fail to undermine the argument that the outbreak occurred first in Wuhan in the autumn of 2019. In fact, none of the 2019 dates identified outside China (except the controversial and faulty Barcelona Study) are early enough to discount an October Surprise in Wuhan.

10. US INTELLIGENCE WARNING – NOVEMBER 2019

Figure 39: NCMI. Source Clemente (2013)

Claims of alleged US Intelligence warnings to Israel & NATO Allies about a possible pandemic outbreak in Wuhan in November 2019 were published in several news outlets in the USA and Israel. The reports quoted anonymous National Center for Medical Intelligence (NCMI) analysts as concluding that "it could be a cataclysmic event" (Margolin & Meek, 2020). Although the Pentagon issued a carefully worded denial of the claims published by ABC (Margolin & Meek, 2020), the information was confirmed by reports in the Israeli media (i24 NEWS, 2020). According to the Times of Israel (2020), the White House was "not interested in the intelligence", but as a courtesy to its allies, it was passed onto NATO and the IDF and eventually Israel's Health Ministry, but "nothing was done" (Times of Israel, 2020).

The subsequent Pentagon partial denial was that "no intelligence product had been produced in November" (Margolin & Meek, 2020), which only means that an assessment report was not produced, but does not preclude a situation report being produced, based on US consular analysis, communications intercepts and satellite photos. Indeed, a situation report merely describes the pieces of intelligence gathered but does not assess them.

Perhaps the naïve reader is unaware of the nature and scope of the National Center for Medical Intelligence (NCMI) and its history. Originally called the Armed Forces Medical Intelligence Center (AFMI), in 1963 the Defence Intelligence Agency (DIA) "absorbed" medical intelligence and Congress permanently transferred the AFMI to DIA in 1992 (DIA, 2019).

> "*this updates the designation of the Armed Forces Medical Intelligence Center as the National Center for Medical Intelligence (NCMI) for the conduct of medical intelligence within the DoD*" (KFF, 2012).
>
> "*it is DoD Policy that NCMI is the DoD lead activity for the production of medical intelligence and will prepare and coordinate integrated, all-source intelligence for the DoD on foreign health threats and other medical issues to protect U.S. interests worldwide*" KFF (2012).
>
> In July 2008, the DIA Director, U.S. Army LTG Michael Maples stated that:
>
> "*The National Center for Medical Intelligence is the critical link between Department of Defence force protection and broader homeland health protection…It demonstrates the vital contribution that medical intelligence makes to public health security*" DIA (2019).

The National Center for Medical Intelligence (NCMI), located at 39°26'40.0"N 77°24'47.3"W (810 Schreider St, Fort Detrick, MD 21702, USA) (Google Maps, 2011), is overseen by the Defence Intelligence Agency (DIA) with a "*mission to monitor, track and assess a full range of global health events that could negatively impact the health of US military and civilian populations*" (Reddit, 2020).

The NCMI produces "*all-source medical intelligence assessments and forecasts on foreign military and civilian health care capabilities and trends, worldwide infectious disease risks, global environmental health risks, and militarily significant issues*" KFF (2012).

Figure 40: NCMI Fort Detrick. Satellite View. Source: Reddit (2020).

Figure 41: Entrance to NCMI. Fort Detrick, Source: Reddit (2020).

NCMI works with the US CDC, the Department of Homeland Security (DHS) and other federal agencies to analyse biological events that may threaten national security (Clemente, 2013.). As we can observe from the DOD's organizational charts (Figures 42 and 43 below), NCMI reports to the DIA which reports to USD (Intelligence) and to the Secretary of Defense KFF (2012).

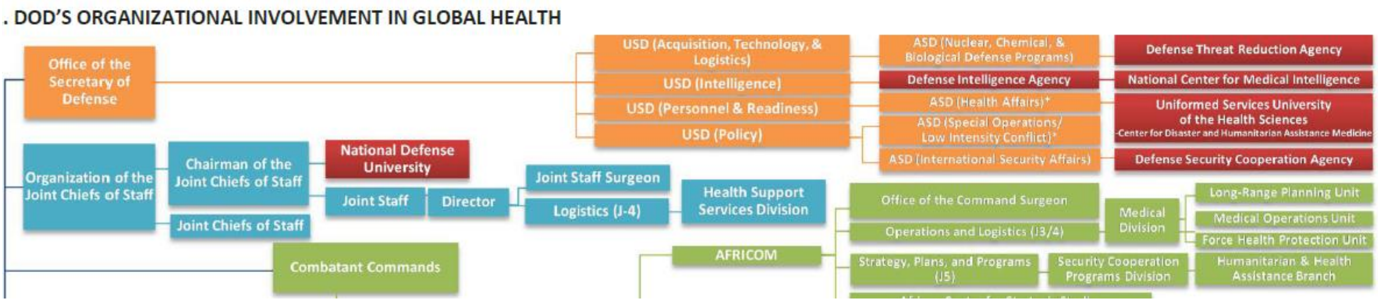


Figure 42: DOD's Organisational chain of command for NCMI. Source: KFF (2012).

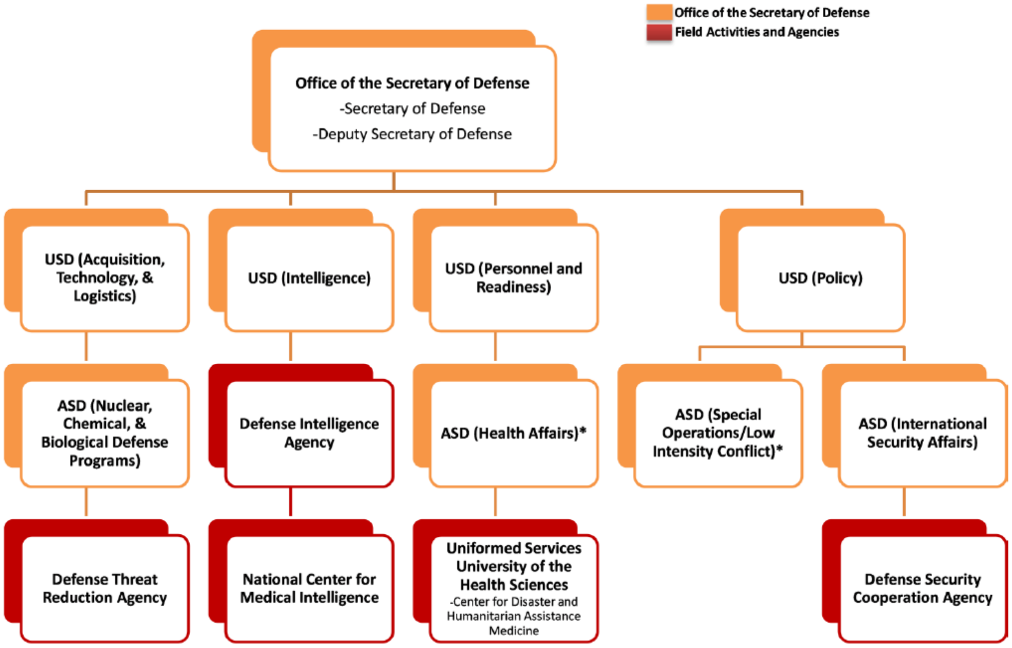


Figure 43: NCMI reports to DIA to USD (Intelligence) to Secretary of Defence. Source: KFF (2012).

To summarise, The NCMI is part of the Defence Intelligence Agency (DIA), based at the US Army Medical Institute of Infectious Diseases (USAMRIID) at Fort Detrick, Maryland, which:

> "*Tracks potential health and related threats to US military personnel overseas*" (NBC NEWS, 2020).

According to Riechmann (2020), the medical intelligence unit has:

> "*At least 100 epidemiologists, virologists, chemical engineers, toxicologists, biologists and military medical experts — all schooled in intelligence tradecraft*"

Although NCMI mainly uses open source material, the medical intelligence team also has "access to classified intelligence collected by the 17 U.S. spy agencies" (Riechmann, 2020):

- Signals intelligence and intercepts of communications collected by the NSA.
- Information that CIA officers pick up in the field overseas.
- National Geospatial-Intelligence Agency can share satellite imagery and terrain maps

> "*Former officials and outside experts say the NCMI calls upon all sources of intelligence — from communications intercepts to satellite imagery to human source reporting — to seek answers that elude public health authorities, including whether foreign governments are lying about the extent and nature of the disease in their countries*" NBC NEWS (2020a).

The "Infectious Disease Division" then provides intelligence reports to the US Military, White House, Department of State, Homeland Security, DHSS and other domestic customers and foreign partners. In the 2021 unclassified public report of the IC investigation ordered by President Biden (ODNI, 2021), one "*IC element*" was "*moderately confident*" that:

> *"the first human infection with SARS-CoV-2 most likely was the result of a laboratory-associated incident, probably involving experimentation, animal handling, or sampling by the Wuhan Institute of Virology"* (ODNI, 2021).

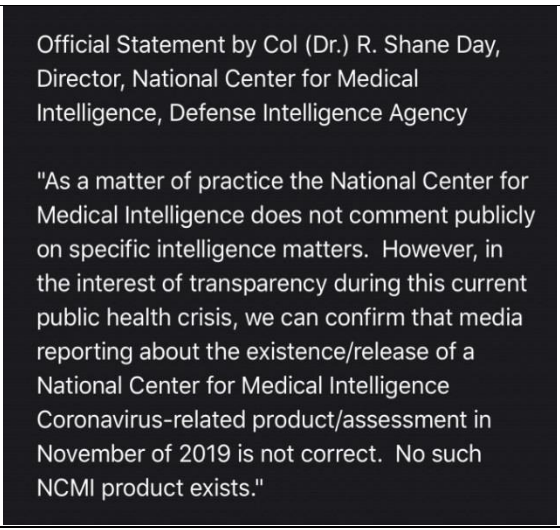
Demaneuf (2021b) suggests that the NCMI was the agency "*most positive about a research related accident being responsible for the Covid-19 outbreak*". However, it is more likely that the FBI was the agency in question (New York Times, 2021a).

The report was based on analysis of electronic intercepts and satellite images which gave rise to serious concerns about a possible outbreak that would "*pose a serious threat to U.S. forces in Asia -- forces that depend on the NCMI's work*" (Margolin & Meek, 2020). According to a US Defense official:

> *"The intelligence came in the form of communications intercepts and overhead images showing increased activity at health facilities, which was distributed to some federal public health officials in the form of a "situation report" in late November, but there was no assessment that a lethal global outbreak was brewing at that time*" NBC NEWS (2020b)

This lack of a formal intelligence assessment report in November 2019, allowed the NCMI Director, Colonel Shane Day (Figure 44 and 45), to deny its very existence:

> "*We can confirm that media reporting about the existence/release of a National Center for Medical Intelligence Coronavirus-related product/assessment in November of 2019 is not correct. No such NCMI product exists"* (Daily Mail, 2020).

	Official Statement by Col (Dr.) R. Shane Day, Director, National Center for Medical Intelligence, Defense Intelligence Agency "As a matter of practice the National Center for Medical Intelligence does not comment publicly on specific intelligence matters. However, in the interest of transparency during this current public health crisis, we can confirm that media reporting about the existence/release of a National Center for Medical Intelligence Coronavirus-related product/assessment in November of 2019 is not correct. No such NCMI product exists."
Figure 44: Colonel Shane Day, Director NCMI. Source: Daily Mail (2020).	**Figure 45**: Statement by Colonel Shane Day Source: (Twitter, 2021)

However, according to unnamed NCMI officials, although there was no formal assessment in November, there was intelligence that became a formal assessment in December 2019 which was eventually included in an intelligence briefing to President Trump in January 2020 (NBC NEWS, 2020b). This is further supported by claims published in the Times of Israel (2021), that:

> “*The US intelligence community became aware of the emerging disease in Wuhan in the second week of that month and drew up a classified document. Information on the disease outbreak was not in the public domain at that stage — and was known only apparently to the Chinese government*” (Times of Israel, 2021).
>
> “*The Americans also decided to update two allies with the classified document: NATO and Israel, specifically the IDF. The network said Israeli military officials later in November discussed the possibility of the spread of the virus to the region and how it would affect Israel and neighboring countries”* (Times of Israel, 2021).

It thus seems clear that this November 2019 situation report eventually became a formal intelligence assessment in December 2019 after checking, interpretation and validation**,** which then would have been sent to the usual suspects: US CDC, US Military, White House, Department of State, Homeland Security, and “*foreign friends*” (NATO, IDF, UK MOD, etc.).

> “*From that warning in November, the sources described repeated briefings through December for policy-makers and decision-makers across the federal government as well as the National Security Council at the White House. All of that culminated with a detailed explanation of the problem that appeared in the President's Daily Brief of intelligence matters in early January*” (Margolin & Meek, 2020).
>
> "*The timeline of the intel side of this may be further back than we're discussing, but this was definitely being briefed beginning at the end of November as something the military needed to take a posture on"(*Margolin & Meek, 2020).

In fact and presumably based on the NCMI findings, the recent unclassified IC report (ODNI, 2021) states that it is likely that SARS-CoV-2 “*emerged and infected humans through an initial small-scale exposure that occurred no later than November 2019 with the first known cluster of COVID-19 cases arising in Wuhan, China in December 2019*” (ODNI, 2021).

11. ALLEGED SICK RESEARCHERS AT WIV LABORATORIES

According to a fact sheet published by the United States Department of State (2021b) some researchers at the Wuhan Institute of Virology became sick in "Autumn 2019":

> "*The U.S. government has reason to believe that several researchers inside the WIV became sick in autumn 2019, before the first identified case of the outbreak, with symptoms consistent with both COVID-19 and common seasonal illnesses*" United States Department of State (2021b).

Since the fact sheet was published, more detailed evidence has come to light, firstly, according to an interview originally broadcast on Sky News Australia. (2021b) and later reported by WSJ (2021):

- ***Three researchers*** *from the Wuhan Institute of Virology (BSL3-coronavirus research lab (Hudson, 2021) "became sick enough in* ***November 2019*** *that they sought* ***hospital care***"
- The intelligence "was **provided by an international partner**"
- "It was **vetted** by U.S. intelligence agencies"
- "The information that we had coming from the various sources was of **exquisite quality**. It was **very precise**. What it didn't tell you was exactly **why they got sick**" (Sky News Australia, 2021b; WSJ (2021).

The claims were later confirmed by one of the WHO team members who visited Wuhan in 2020, Marion Koopmans, who admitted on NBC News that "*some WIV staff did fall sick in the autumn of 2019*". She also suggested that they likely suffered from a "*regular, seasonal sickness*" (WSJ, 2021).

> "*There were occasional illnesses because that's normal. There was nothing that stood out…maybe one or two. It's certainly not a big, big thing*" (*WSJ, 2021).*

This of course, directly contradicts claims by the Yuan Zhiming, Director of the Wuhan National Biosafety Laboratory that there were no sick researchers at that time (Global Times, 2021). He was interviewed by the Global Times (2021) in May 2021 and claimed: "*I've read it, it's a complete lie*" and more specifically:

"*Those claims are groundless. The lab has not been aware of this situation [sick researchers in autumn 2019], and I don't even know where such information came from*"

Further details of the sick researchers were revealed by David Asher, the former head of the US State Department task force on the origins of Covid-19, during a Hudson (2021) Institute seminar:

"*I'm very doubtful that* ***three people*** *in highly protected circumstances in* ***a level three laboratory working on coronaviruses*** *would all get sick with influenza that put them in the hospital or in severe conditions all in the same week, and it didn't have anything to do with the coronavirus. That's hard to believe"* Hudson (2021).

Later, David Asher went on to tell the UK's Mail on Sunday (Birrell, 2021a) that:

"*According to credible' information from a well-connected* ***foreign government****, the* ***wife of one researcher died later that month***"" (Birrell, 2021a)

"*The three scientists are believed to have become ill with the mysterious respiratory condition in the* ***second week of November, 2019***" (Birrell, 2021a)

A slightly confusing note was introduced in a recent televised interview with John Ratcliffe, who, when asked directly about the date the WIV researchers became sick, calmly stated that it was in October 2019, not November 2019, as asserted by David Asher (Sky News Australia, 2021c) However, whether October or November, as pointed out by Bunyan (2021), this concords with all the other evidence showing that SARS-COV-2 or its progenitor virus was infecting people in Wuhan, symptomatically or asymptomatically, well before "*China first reported it to the world , either as a result of the often-mild disease going undetected, or the result of a cover-up*" (Bunyan, 2021).

12. SCIENTISTS WHO CLAIMED EARLY KNOWLEDGE ABOUT THE OUTBREAK IN WUHAN

1. LAWRENCE GOSTIN

Figure 46: Lawrence Gostin. Source: The Australian (2021).

Lawrence Gostin is the Professor of Global Health Law, at Georgetown University in Washington DC, who severely criticized the decision by Chinese authorities to deny access to investigators to Wuhan for a year:

> "*I think it was unconscionable for China to delay for a full year before allowing the WHO to visit Wuhan….Delaying it for a year was completely inexcusable because it meant that we probably will never truly know the origins of the virus…It's almost like investigating the scene of the crime a year later after the crime scene has been scrubbed*" (The Australian, 2021).

Professor Lawrence Gostin claimed that he first heard about the novel coronavirus from a friend in Wuhan In **mid-December 2019**:

> "*I just heard from a friend in Wuhan that there is a novel coronavirus, and it looks very serious," Gostin remembered saying. "He just said, 'Pass the biscuits.' " Few people grasped the potentially catastrophic implications of an outbreak in China. Gostin would spend the next weeks imploring international bodies to take this new threat seriously*" (LA Times, 2020).

2. PROFESSOR IAN LIPKIN

Figure 47: Professor Ian Lipkin. Source: BBC (2021).

In an article in the Financial Times in April 2020 (Manson, 2020), Professor Lipkin from Columbia University claimed that he had heard about the outbreak in Wuhan in **mid-December** from his Chinese contacts. Later Lipkin specified in a Spike Lee HBO documentary that he found out on **December 15th** (Birrell, 2021b). In the interview, Spike Lee asks Lipkin, who repeats the date. “*This is a big deal, no? December 15th?*” (Figure 48). Lipkin confirmed the date once again:

> “*That’s when I hear about this [new outbreak],* ***on December 15th***”

Figure 48: Screenshot from Spike Lee Interview with Professor Lipkin. Source: Twitter (2021a)

Professor Lipkin also confirmed this mid-December knowledge of an outbreak in Wuhan in an interview with Vincent Racaniello ("This Week in Virology" TWiV) on March 28th, 2020; at the timestamp pf 17:00 minutes (Microbe TV, 2020). He clearly says:

"I first heard about this on the 15th of December"

In the podcast he further revealed that the source of this information was no other than his long term collaborator in Guangzhou, Professor Lu Jiahai.

Later in a BBC interview, Professor Lipkin mentioned a telephone call on New Year's Eve with Dr. George Gao Fu (Figure 49), the Director of China's CDC who told Lipkin that he had identified the virus as a novel coronavirus which was not highly transmissible. Lipkin expressed his surprise:

> *"This didn't really resonate with me because I'd heard that many, many people had been infected"* BBC (2021).

Figure 49: George Gao Fu (CCDC) Source: BBC (2021).

3. PROFESSOR NICHOLAS A. CHRISTAKIS

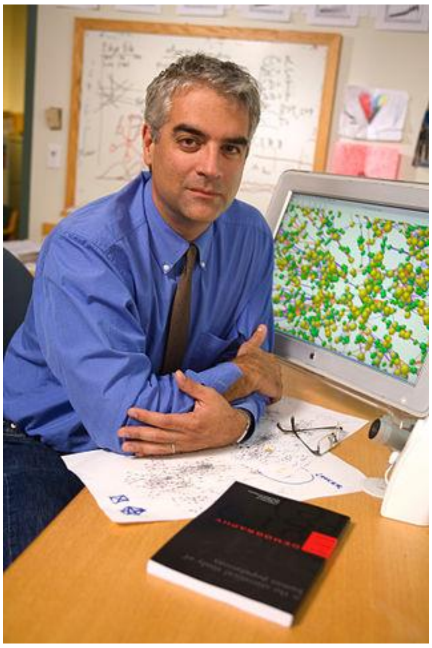


Figure 50: Nicholas Christakis. Source: Wikipedia (2021a)

On September 14th, obsessive internet sleuths observed with curiosity that Professor Nicholas Christakis, from Yale University, tweeted the following intriguing comment:

> "*There were American doctors visiting the Wuhan hospital, by chance, in mid-December, and they were aware of an outbreak of uncharacterized pneumonia at the time. This is known in **certain communities***" Twitter (2021b).

The ambiguous reference to "certain communities" will be discussed a little later in this report.

4. RUSSELL WESTERGARD (US DEPUTY CONSULAR CHIEF IN WUHAN)

Figure 51: Deputy US Consul General in Wuhan, Russell Westergard. Source: State Magazine (2020).

Natasha Loder (2021) recently claimed that a particularly "*vicious influenza outbreak*" described by the Deputy US Consul General in Wuhan, Russell Westergard, may have led to the closure of public schools in Wuhan in mid-December 2019. She also claimed that "*the spike of cases started in the week beginning December 2nd 2019, and saw cases rise by about 2,059% compared to the same week the year before*".

Loder's claims are based on an April 2020 article in State Magazine (2020) in which Russell Westergard stated that, by the middle of October of 2019, Wuhan was witnessing "*an unusually vicious flu season*" which continued into November 2019:

"*By **mid-October 2019**, the dedicated team at the U.S. Consulate General in Wuhan knew that the city had been struck by what was thought to be an **unusually vicious flu season**. The **disease worsened in November**"* (State Magazine, 2020).

> *"When city officials began to **close public schools in mid-December** to control the spread of the disease, **the team passed the word to Embassy Beijing** and continued monitoring"* (State Magazine, 2020).

5. PROFESSOR RON FOUCHIER

Figure 52: Professor Ron Fouchier. Source: Wikimedia Commons (2011)

A well-known Dutch Professor of Molecular Virology, Ron Fouchier, claimed that he discussed the outbreak in the **first week of December** with his colleague Marion Koopmans, a member of the WHO inquiry team (Birrell, 2021). In an April 2020 interview with the Dutch newspaper "*Het Algemeen Dagblad*" (AD NL 2020), he was asked when he first heard of the Wuhan outbreak, responding as follows:

> *"'I was on holiday when there was a commotion in infectious disease community in December. There were rumors that people had got sick and that it had to do with an animal market….**In the course of December it became clear that it was a coronavirus that could be transmitted via the airways**"* AD NL (2020).

Earlier Professor Fouchier had precisely confirmed this early December knowledge of the Wuhan Outbreak during an interview broadcast on VPRO's Tegenlicht (NPOSTART, 2020; YouTube, 2020). The journalist asked him where he was when he first heard about the outbreak, to which he replied laconically:

> "*We hear those things really early. And this was **just after Sinterklaas** that there were outbreaks of an unknown disease in Wuhan*" (NPOSTART, 2020; VPRO, 2020)

 it has english translation; he says he knew early december about wuhan Ron Fouchier virologist Erasmus MC We hear these things early on, so it was the first week of December. Virologists on the coronavirus outbreak | VPRO Documentary (eng subs) What do virologists know about the coronavirus? Was covid-19 a surprise, and could the coronavirus outbreak be prevented? In a ... youtube.com	 it has english translation; he says he knew early december about wuhan We were told about an outbreak of an unknown disease in Wuhan. Virologists on the coronavirus outbreak | VPRO Documentary (eng subs) What do virologists know about the coronavirus? Was covid-19 a surprise, and could the coronavirus outbreak be prevented? In a ... youtube.com
Figure 53: (NPOSTART, 2020; YouTube, 2020)	**Figure 54:** (NPOSTART, 2020; YouTube, 2020)

However, Professor Fouchier later claimed that he had been confused about the exact dates of his discussion with Marion Koopmans:

> "*I am sorry about this confusion. It must have been late December, not early. My mistake. I seem to remember discussing with Prof. Koopmans some unofficial news reports in China about illness associated with a food market in Wuhan"*(Birrell, 2021).

This apparent retraction of his initial claim is all the more startling because Professor Fouchier clearly referred to Sinterklaas (5th December) during his interview with VPRO (2020). It should be noted that "Sinterklaas", a Dutch Christmas holiday, is celebrated on the Eve of Saint Nicholas every year on the 5th of December (Wikipedia, 2021b).

To conclude, Professor Fouchier confirmed his early December knowledge to both VPRO Tegenlicht (March 22, 2020) and Het Algemeen Dagblad (April 5, 2020). It is indeed rather strange that Fouchier subsequently retracted his claim on the basis of his "inaccurate memory" (Birrell, 2021), something that has led to accusations of duplicity (Loder, 2021, Comments section)

6. CHINESE DISSIDENT WEI JINGSHENG

Figure 55: Wei Jingsheng Interview. Source: Coë & Parsons (2021).

Wei Jingsheng, a Chinese dissident living in the United States, claimed recently (Markson, 2021a) that he had first heard of a novel virus at the time of the World Military Games in Wuhan in October 2019 and warned US intelligence agencies, politicians (possibly former Secretary of State Mike Pompeo a) and a political activist, Dimon Liu of a coronavirus outbreak in November 2019:

"*I felt they were not as heavily concerned as I was so I tried my best to provide more detailed information. So I kept repeating myself in an effort to try to persuade them*" (Markson, 2021a).

Wei Jingsheng also claimed that the Wuhan World Military Games in October 2019 "*could have acted as the virus' first super spreader event*" (Markson, 2021a; Daily Mail, 2021a) and that he first became aware of the novel coronavirus from his network of contacts in Beijing:

"*Mr. Jingsheng said he was aware of what was happening through Beijing Communist Party insiders who shared their fears about the situation and described the central government cover-up*" (Markson, 2021b; Daily Mail, 2021a).

"*I talked to Dimon and some other American politicians in the House of the danger of this situation…There were officials from the White House at that time as well. In November 2019…We could have known in November of 2019, that there was a disaster occurring inside Wuhan — inside their most important biological facilities related to coronavirus research"* (Markson, 2021).

7. DIMON LIU (IPAC)

Figure 56: Dimon Liu. Source: IPAC GLOBAL (2020).

Dimon Liu, a member of the Inter-Parliamentary Alliance on China (IPAC GLOBAL, 2020), confirmed Wei's claim and that specifically he had mentioned the novel coronavirus over dinner on November 22nd, 2019 with her husband, Robert Suettinger, serving as a witness:

> "*I couldn't quite believe what he was saying…at that time, I had thought that the coronavirus could not be worse than SARS..Okay, there was an outbreak, but the authorities and the advance of medical sciences would be able to contain the spread of it*" (Markson, 2021).

She claims that despite the best of intentions, she failed to inform the former deputy national security adviser, Matt Pottinger, directly about Wei's claims. Instead she invited Pottinger to dinner with Wei, so he could tell Pottinger himself (Markson, 2021b):

> "*I didn't send it (the memo) to him because so many things were so incredulous…I wrote it, but I didn't send it because I decided it was better that Wei talks directly to Matt Pottinger*" (Markson, 2021a).

13. “CERTAIN COMMUNITIES”

Regarding the question of early knowledge amongst the so-called “*certain communities*” mentioned by Professor Nicholas Christakis, it is interesting to note that a certain Dr. Michael Callahan, a renowned expert in biowarfare and bioterrorism, was in Nanjing in December 2019 and would have been one of the first to be aware of any outbreaks as they emerged, given his close links to Doctors in Nanjing and Wuhan.

> “*in very early January 2020, the same Nanjing doctors, working with colleagues at Central Hospital of Wuhan, would share the first evidence that the novel coronavirus was spreading from person to person*” (Callahan, 2021).

Figure 57: Dr. Michael Callahan. Source: (Callahan, 2021)

Dr. Callahan is a Director at the Vaccine and Immunotherapy Center at Massachusetts General Hospital, and was the former head of DARPA’s Prophecy Project.

Interestingly, he has been *“deployed to nine international outbreaks including Marburg, Ebola and SARS-1” (Callahan, 2021),* but there was no need to deploy him to the SARS-COV-2 outbreak in China in 2019, as he was already coincidentally there.

Prior to his work with DARPA, he contributed to biological terrorism working groups at the National Academies of Sciences, the Department of Defense, and the Department of Homeland Security (Diego, 2020; IRP FAS, 2005). This work was listed during a 2005 US Congressional hearing on “*Engineering Bio-Terror Agents: Lessons from the Offensive U.S. and Russian Biological Weapons Programs*” (IRP FAS, 2005).

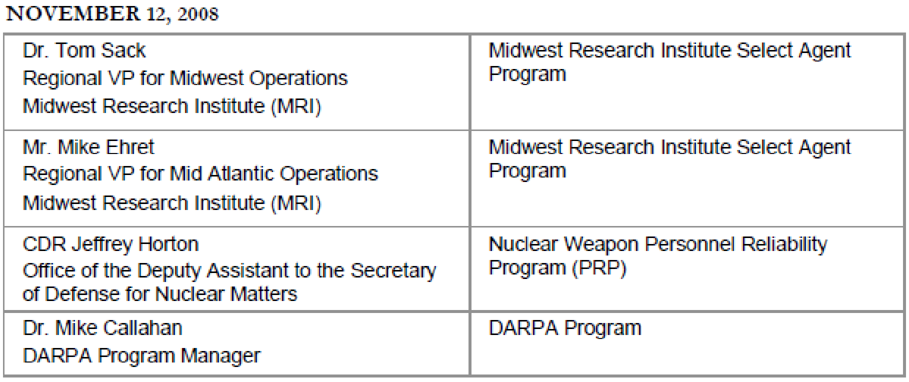
- “*I am a staff physician in the Division of Infectious Diseases at Massachusetts General Hospital in Boston, Massachusetts, and the* ***Director of Biological Threat Defense*** *at the Center for Integration of Medicine and Innovative Technology (CIMIT). CIMIT is a multi-institution, non-profit research organization funded by the U.S. Government to identify near-term solutions for critical military and civilian medical problems. Since January 2002*” (IRP FAS, 2005).
- “*I have also worked with the U.S. Department of State, in particular with the Bio-Industry Initiative (BII), a program which uses the U.S. biotechnology market and academic collaborations to redirect former Soviet biological weapons scientists to peaceful, sustainable medical research*” (IRP FAS, 2005).
- **“*Since the October 2001 anthrax attack, I have worked with biological terrorism working groups from the National Academy of Science, the Department of Defense and the Department of Homeland Security.*** *My focus areas are risk analysis of small scale biological weapon production, and consequence management following mass-casualty infections and poisonings*” (IRP FAS, 2005).

Dr. Callahan has a very extensive and interesting biography (NCBI, 2021), which is worth perusing with attention:

1. Michael Callahan is Diplomat of Mass Casualty Care & Tropical Medicine & Hygiene (UK).
2. His biodefense clinical research is focused on **vaccine defeat, immune evade** and multidrug-resistant organisms, and on best practices for highly dangerous pathogen infections in Africa where he prospectively enrolls cutaneous anthrax in Nigeria; and monkey pox, Ebola and Marburg in the Democratic Republic of the Congo and Angola (NCBI, 2021).
3. In 2002, he was appointed clinical director for Cooperative Threat Reduction programs at six former Soviet Union (ex) Biological Weapons Institutes (VECTOR, State Research Center for Applied Microbiology, Kirov, Bersk, RCMDT, Highly Pure & RIHOP), which included redirecting of unanticipated dual use and gain-of-function programs (NCBI, 2021). He was in charge of gain-of-function programs for viral pathogens at these facilities (NCBI, 2021).
4. Dr. Callahan is president of United Therapeutics (UTHR) Division of Cell Therapeutics, and maintains faculty appointments at Massachusetts General Hospital/Harvard Medical School and King Chulalongkom Medical University in Bangkok. (NCBI, 2021).
5. Dr. Callahan continues to advise on infectious disease and biosafety to the Academies, the NSC, BSEG, the Office of Net Assessment, NIAID, MITRE, ASM, Infectious Disease Society of America, and American Society of Tropical Medicine and Hygiene (NCBI, 2021).

From 2005 to 2012, Dr. Callahan headed the DARPA biodefense therapeutics portfolio (NCBI, 2021). While there he set up the DoD Accelerated Manufacture of Pharmaceuticals (AMP) Program (NCBI, 2021). Also while at DARPA, he launched “PROPHECY”, an international medical early alert network, which “*delivers 24/7 emergency consultation, reagents and therapeutics for catastrophic infectious disease outbreaks, SARS Hong Kong and **H7N9 Nanjing***” (NCBI, 2021).

Dr. Callahan was listed (Figure 58) in the Defense Science Board Task Force on Department of Defense Biological Safety and Security Program as DARPA Program Manager (FAS, 2009).

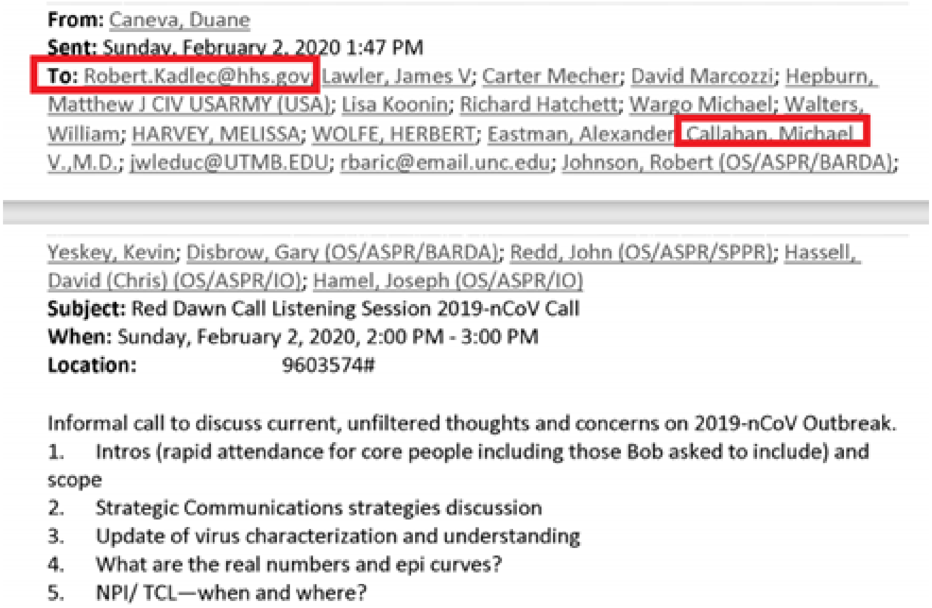


NOVEMBER 12, 2008

Dr. Tom Sack Regional VP for Midwest Operations Midwest Research Institute (MRI)	Midwest Research Institute Select Agent Program
Mr. Mike Ehret Regional VP for Mid Atlantic Operations Midwest Research Institute (MRI)	Midwest Research Institute Select Agent Program
CDR Jeffrey Horton Office of the Deputy Assistant to the Secretary of Defense for Nuclear Matters	Nuclear Weapon Personnel Reliability Program (PRP)
Dr. Mike Callahan DARPA Program Manager	DARPA Program

Figure 58: Dr. Callahan listed as DARPA MANAGER, Source: IRP FAS (2009)

In 2020, Callahan was "*recruited to be Special Adviser on COVID-19 to the Assistant Secretary of Preparedness and Response (ASPR), Robert Kadlec*" (Malone, 2020 in Diego, 2020). It is also worth noting that "United Therapeutics" (UNITHER, 2021), the company he directed, has been rumored to enjoy unorthodox State funding (Personal Communication with Author, 2021). Dr. Callahan's involvement with ASPR and Dr. Kadlec was evidenced in an email chain started by DHS chief medical officer, Dr. Duane C. Caneva, in January 2020. The email chain had the subject line "*Red Dawn Breaking*" (Figure 59a and 59b) and was obtained under a FOIA request by the New York Times (2020a) and reported on by USA Today (2020b).



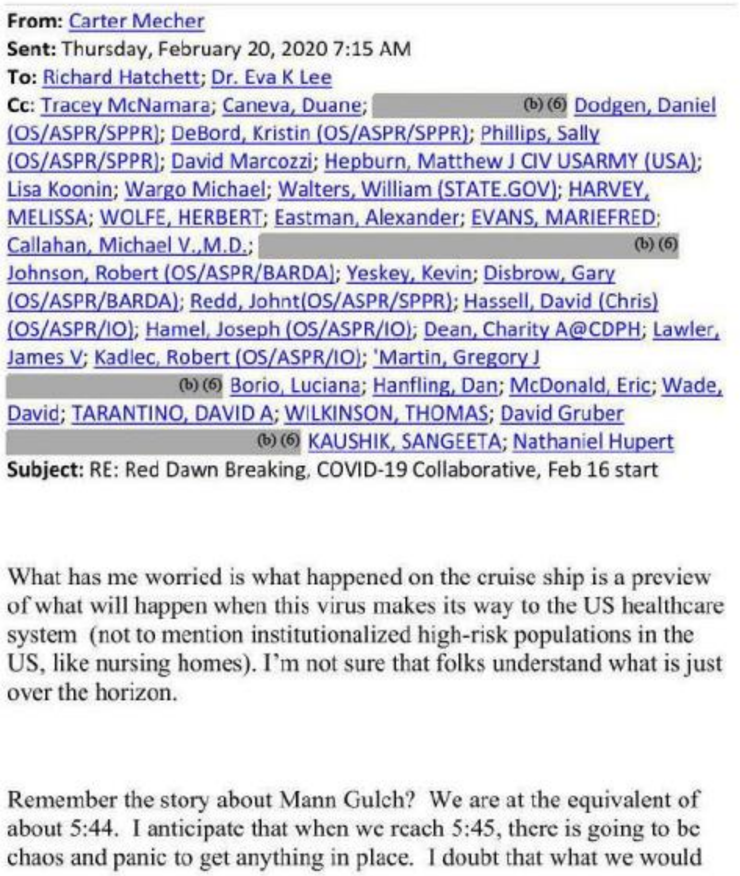
From: Caneva, Duane
Sent: Sunday, February 2, 2020 1:47 PM
To: Robert.Kadlec@hhs.gov; Lawler, James V; Carter Mecher; David Marcozzi; Hepburn, Matthew J CIV USARMY (USA); Lisa Koonin; Richard Hatchett; Wargo Michael; Walters, William; HARVEY, MELISSA; WOLFE, HERBERT; Eastman, Alexander; Callahan, Michael V.,M.D.; jwleduc@UTMB.EDU; rbaric@email.unc.edu; Johnson, Robert (OS/ASPR/BARDA);

Yeskey, Kevin; Disbrow, Gary (OS/ASPR/BARDA); Redd, John (OS/ASPR/SPPR); Hassell, David (Chris) (OS/ASPR/IO); Hamel, Joseph (OS/ASPR/IO)
Subject: Red Dawn Call Listening Session 2019-nCoV Call
When: Sunday, February 2, 2020, 2:00 PM - 3:00 PM
Location: 9603574#

Informal call to discuss current, unfiltered thoughts and concerns on 2019-nCoV Outbreak.

1. Intros (rapid attendance for core people including those Bob asked to include) and scope
2. Strategic Communications strategies discussion
3. Update of virus characterization and understanding
4. What are the real numbers and epi curves?
5. NPI/ TCL—when and where?

Figure 59a: Email Chain including Robert Kadlec and Michael Callahan. Source: (New York Times, 2020a).



From: Carter Mecher
Sent: Thursday, February 20, 2020 7:15 AM
To: Richard Hatchett; Dr. Eva K Lee
Cc: Tracey McNamara; Caneva, Duane; [redacted] (b) (6) Dodgen, Daniel (OS/ASPR/SPPR); DeBord, Kristin (OS/ASPR/SPPR); Phillips, Sally (OS/ASPR/SPPR); David Marcozzi; Hepburn, Matthew J CIV USARMY (USA); Lisa Koonin; Wargo Michael; Walters, William (STATE.GOV); HARVEY, MELISSA; WOLFE, HERBERT; Eastman, Alexander; EVANS, MARIEFRED; Callahan, Michael V.,M.D.; [redacted] (b) (6) Johnson, Robert (OS/ASPR/BARDA); Yeskey, Kevin; Disbrow, Gary (OS/ASPR/BARDA); Redd, Johnt(OS/ASPR/SPPR); Hassell, David (Chris) (OS/ASPR/IO); Hamel, Joseph (OS/ASPR/IO); Dean, Charity A@CDPH; Lawler, James V; Kadlec, Robert (OS/ASPR/IO); 'Martin, Gregory J [redacted] (b) (6) Borio, Luciana; Hanfling, Dan; McDonald, Eric; Wade, David; TARANTINO, DAVID A; WILKINSON, THOMAS; David Gruber [redacted] (b) (6) KAUSHIK, SANGEETA; Nathaniel Hupert
Subject: RE: Red Dawn Breaking, COVID-19 Collaborative, Feb 16 start

What has me worried is what happened on the cruise ship is a preview of what will happen when this virus makes its way to the US healthcare system (not to mention institutionalized high-risk populations in the US, like nursing homes). I'm not sure that folks understand what is just over the horizon.

Remember the story about Mann Gulch? We are at the equivalent of about 5:44. I anticipate that when we reach 5:45, there is going to be chaos and panic to get anything in place. I doubt that what we would

Figure 59b: Email Chain including Robert Kadlec and Michael Callahan. Source: (New York Times, 2020a).

Dr. Robert Malone, a close colleague of Dr. Callahan, told AP (2021a) that:

"*He got a call on Jan. 4 from Michael Callahan, a fellow American doctor working in China, The doctor told Malone -- a molecular virologist who was chief medical officer of the Florida-based pharmaceutical company Alchem Laboratories -- about a new coronavirus-like disease outbreak in Wuhan, the provincial capital of China's Hubei province*".

According to AP News (2021a) "***Callahan was already in Wuhan working with Chinese infectious disease researchers in late 2019***" and that together with his colleagues (Chinese Doctors), he had "*analyzed the medical records of more than 6,000 hospitalized patients, 1,100 of whom had severe COVID-19 disease*" AP News (2021a). However, surprisingly, Dr. Callahan has refused to publish any of the analyzed data to support his claims (AP News, 2021a). Indeed, Dr. Robert Malone has directly challenged Callahan's claims:

> "*No one that I am aware of has or had ever seen the data from Wuhan that Michael (Callahan) alludes to. He had promised to show me those data, but never did"* AP News (2021a)

From the above, it is clear that Dr. Callahan was in Nanjing in late 2019 working on an "avian influenza project" and then travelled to Wuhan to work with local Doctors during the early stage of the Covid-19 outbreak. Interestingly, Dr. Callahan had accused China of hiding avian influenza samples in August 2018, which may have led him to be in Nanjing in 2019:

> "*Jeopardizing U.S. access to foreign pathogens and therapies to counter them undermines our nation's ability to protect against infections which can spread globally within days*" (New York Times, 2018).

This statement by Dr. Callahan was made after both the US government and researchers requested H7N9 samples under international agreements *"necessary for creating vaccines and preparing for future biological threats*" (Knowles, 2018) but failed to receive them "*for over a year*" (New York Times, 2018). In a press release on April 26th, 2020 Dr. Malone (2020) claimed that:

> *"With the advent of the outbreak of a novel coronavirus infection during December 2019, Dr. Callahan was granted a leave of absence by United Therapeutics' CEO Martine Rothblatt to travel to China to assist clinical colleagues in mass infection management of COVID 19 under his joint appointment*" (Malone, 2020 in Diego, 2020).

However, as he was already in China in 2029, why would he need a "leave of absence" to travel to China? As one of the US governments leading bioterrorism and biosafety experts, Dr. Michael Callahan's presence in Nanjing and Wuhan at the beginning of the Covid-19 outbreak has raised questions, albeit not in the mainstream US media. Regarding avian influenza, Dr. Callahan spoke in July 2005 at a House of Representatives Subcommittee on Prevention of Nuclear and Biological Attack "*Engineering Bio-Terror Agents: Lessons from the Offensive U.S. and Russian Biological Weapons Programs"* (IRP FAS, 2005):

> "*Yes. We find avian influenza disquieting in the extreme, and the reasons are basically that most of the work is already being done for the terrorists. Several of those countries have become more difficult to work with in recent history*" (China) (IRP FAS, 2005).

This was in response to a little "joke" by Dr. Brent:

> "***Dr. Callahan can run around the world picking clinical isolates out of disease outbreaks*** *and prioritize things that way. If I were, you know, doing things, I might do what I know. I might resynthesize SARS, put a toxin on it, infect myself, and cough on people*"(IRP FAS, 2005).

Although tangential to this report, some statements made at this 2005 hearing (IRP FAS, 2005) may interest even the most jaded reader:

> 1. "*Next generation biological weapons may also be engineered using negative selection techniques. In this case antigens to which the patient's immune response is directed are removed from the biological weapon. In worse case scenarios, the terrorist might eliminate the antigen on a bacteria, virus or toxin that was used as the basis for a government vaccine. If the patient was exposed to one of these antigen-negative biological weapons, they would be immunologically naive resulting in more severe infection and/or death. These types of agents are known as vaccine-evading biological weapons*" (IRP FAS, 2005).
>
> 2. "*One of the most disquieting publication in 2002 described a method for defeating vaccine-protected animals by inserting a gene which down-regulated the immune system resulting in overwhelming infection and death. Another publication describes a methodology which single-handedly solves two separate challenges facing a biological terrorist: how to move virulence genes from one agent to another and how to store a biological weapon without depending on freezers and liquid nitrogen (reference provided upon request)*" (IRP FAS, 2005).

3. *"One of the most ominous of engineering feats that could be used by biological weapon scientists is to induce host tropism into the agent, whereby the agent is altered to favour infection of a specific human genotype. This seemingly far-fetched concept is already demonstrated by certain tropical parasite infections that cause more significant infections and sequelae in certain ethnic groups*" (IRP FAS, 2005).

5. "*The efforts of the biological terrorist to produce a new threat agent can also be assisted by natural events. This scenario is best illustrated by the avian influenza in Southeast Asia. Since 1998, the pathogenicity of this bird virus has increased as has its ability to infect the upper respiratory systems of pigs and humans. The result is that infected patients are exposed to a novel, highly pathogenic respiratory virus to which their immune system is completely naive. The danger of this event is exacerbated by the fact that influenza, unlike anthrax, can be transmitted from person to person"* (IRP FAS, 2005).

Given the extent of Chinese State "*gag orders*" and documented threats against local doctors discussed later in this report (*COVER UP and GAG ORDERS, Section 17*), the authors recommend that **all US doctors in Wuhan in late 2019 and specifically Dr. Callahan and his colleagues, be interviewed by the security services and journalists regarding their early knowledge of the outbreak**. The authors also demand that Dr. Callahan publicly release the data from the alleged 6,000 "Famotidine" cases studies obtained in Wuhan at the beginning of the outbreak, as requested by Dr. Robert Malone (Malone, 2021).

14. EMERGENT BIOSOLUTIONS (EBS)

Figure 60: Emergent Biosolutions. Source: Jim Lo Scalzo (New York Times, 2021e).

In 2021, Dr. Callahan's United Therapeutics Company was acquired by Emergent Biosolutions (Pitchbook, 2021). Emergent Biosolutions enjoys intimate links to BARDA and Robert Kadlec via its Director Robert Kramer and Chairman, Fuad El-Hibri (Investors, 2021). The Washington Post (2021) recently exposed the rather sordid history of Emergent Biosolutions, culminating in a Congressional investigation (Mendez, 2021) into its federal vaccine contracts and a SEC hearing in May 2021 (Oversight House Gov, 2021). During that hearing held on May 19th, Robert Kramer admitted that:

> "*A $628 million contract allowed Emergent Biosolutions to collect $27 million per month from taxpayers regardless of manufacturing activity*" (Mendez, 2021)

Kramer was asked if EBS still got 27 million USD per month during those months when EBS was not manufacturing vaccines. He responded: "*I believe we were, yes*". He was then asked if EBS had ever supplied "usable" coronavirus vaccines in the US under the contract. He responded: "*None of the vaccine that we've manufactured has been made available to the U.S.*"

Figure 61: Fuad El-Hibri. Fuadelhibri (2012)

Figure 62: Robert Kadlec. Rubenstein (2018)

Although admittedly tangential to the October Surprise thesis presented in this report, the curious reader may be interested to know some of the dubious background listed by the Washington Post (2020) of this unique company which has now welcomed Dr. Callahan into its labyrinth, courtesy, it seems, of Dr. Robert Kadlec:

1. Emergent Biosolutions (EBS) is "*not only the highest-paid contractor responsible for maintaining the U.S. government's stockpile of emergency medical supplies, but also the only maker of multiple drugs the government deems crucial for the Strategic National Stockpile*"
2. EBS's "*advocacy for biodefense spending over more than a decade was aided by influential allies in Washington and tens of millions of dollars in lobbying campaigns"*
3. *EBS "pressed for the national stockpile and its $700 million budget to be moved under the control of Robert Kadlec, Trump's assistant HHS secretary for preparedness and response, or ASPR. The transfer took effect in 2018*"
4. Robert Kadlec worked as an "*aide to Senator Richard Burr in the Senate in 2005, helped draft legislation that created ASPR*" (Phe.Gov, 2021). "*Robert Kadlec consulted for EBS as a strategic adviser and started a biodefense consulting company with Emergent's founder (Fuad El-Hibri) in the year before starting work at BARDA"*.

5. Until 2015, Kadlec "*provided consulting services to Emergent through his company, RPK Consulting. Kadlec was confirmed to lead the office, which is within the Department of Health and Human Services, in 2017*" (Mendez, 2021).

6. When appointed to lead ASPR in 2017," *Kadlec was determined to shift the office's efforts toward those goals. He was convinced that biowarfare, not a natural pandemic, was the biggest threat facing the nation*"

7. Before the pandemic, "*ASPR paid EBS more than $894 million, more than double what it paid any other contractor*"

8. EBS's annual revenue increased from "$*235 million in 2009 to $1.1 billion a decade later, much of it in contracts for the stockpile that were awarded without competitive bidding*".

9. EBS "*gained control of at least seven medical treatments stockpiled by the federal government*"

10. EBS "*obtained 3 of those 7 stockpiled drugs when it bought the Canada's Cangene Corp in 2013. The same year, EBS acquired a smallpox vaccine, leading to a contract worth up to $2.8 billion that more than doubled the government's cost per dose. The next year, EBS acquired treatments for typhoid, cholera and opioid overdose*"

11. Since 2010, the US government has spent 50% of its yearly Strategic National Stockpile budget (250 million USD) on buying BioThrax from EBS:

> "*These purchases depleted funds needed to purchase vaccines and other supplies to respond to COVID-19 or other pandemics*" (New York Times, 2021b).

12, In 2017, EBS secured national stockpile contracts of $1 billion for BioThrax, a 100 million USD contract over 2 years from BARDA and a 911 million one from CDC for BioThrax vaccines until 2021 (Reed, 2107).

13. Two former EBS executives said the "*company wanted to gain control of as much of the biodefense industry as it could through consolidation*"

14. “*Emergent’s stock performed so well in 2020 that Mr. El-Hibri cashed in shares and options worth over $42 million, corporate filings show. Mr. Kramer took home a $1.2 million cash bonus and $2 million in stock awards*” (New York Times, 2021c).

15. Representative Jim Clyburn, the subcommittee’s chairman claimed that “*They all made millions in stock transactions while they seem to be hiding stuff from the public*” (New York Times, 2021c).

Figure 63: Emergent Bioslutions Locations. (Emergent Biosolutions, 2020)

The Washington Post (2020) published more historical background on Emergent Biosolutions’ former company, Bioport, as well as the BioThrax scandal involving EBS as the sole provider of a vaccine for anthrax poisoning. EBS allegedly charged the US government 5 times what it cost the company to produce BioThrax (Washington Post, 2020).

More in depth and aggressive research into EBS and Dr. Kadlec was published by Baden-Meyer (2020) and earlier by Webb (2020b) who recently stated that:

> “*Emergent Biosolutions is a hopelessly corrupt, criminal enterprise and should be shut down. Instead, it is set to manufacture your COVID-19 vaccine*” (Twitter, 2021c)

The authors highly recommend the following articles for interested researchers:

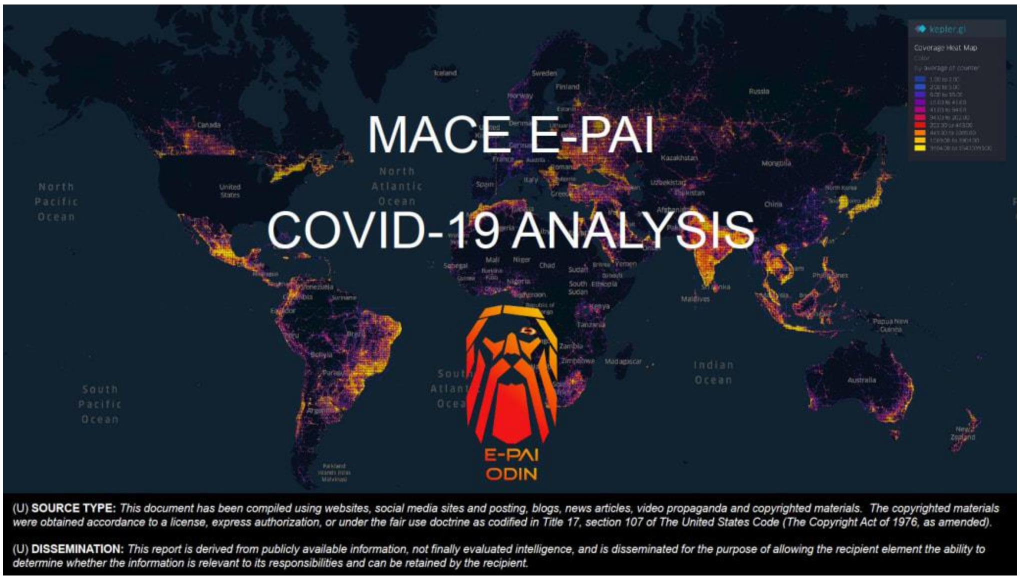
- EBS Covid 19 Vaccines (Diego, 2020).
- EBS's involvement in Covid-19 vaccines (Webb, 2020b) and EBS history (Webb, 2020f).
- Historical Background of EBS and Anthrax (Webb, 2020c).
- GOF work at UPMC (Webb, 2020d).
- Robert Kadlec (Webb, 2020e; Diego & Webb, 2020).

Figure 64: Robert Kadlec. Source: Webb (2020).

Finally, in April 2020, EBS shareholders asked Robbins LLP to sue the company, claiming that they were misled by EBS management (Business Wire, 2021). Schubert Jonckheer & Kolbe LLP (2021) is also currently investigating claims "*relating to possible false statements to investors and insider trading by officers and directors*". It appears that, at the same time as EBS was hard selling its ability to produce Johnson & Johnson and AstraZeneca COVID-19 vaccines, "*several high-level Emergent insiders sold more than $20 million of company stock at inflated prices*" (Schubert Jonckheer & Kolbe LLP, 2021). As we now know, the EBS Maryland vaccine manufacturing plant was characterized by a "*history of poor quality control which led to the cross contamination of 15 million doses of the J&J and AZ vaccines*" (Schubert Jonckheer & Kolbe LLP, 2021).

Although not directly relevant to the underlying thesis of this report, it is hoped that the curious reader will find the analysis of EBS and Dr. Callahan interesting, if not concerning, in its unstated implications.

15. WUHAN INSTITUTE OF VIROLOGY CELLPHONE DATA REPORT


MACE E-PAI

COVID-19 ANALYSIS

E-PAI
ODIN

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Figure 65: MACE E Pai report with Cell Phone claims. Source: (Document Cloud, 2020)

According to a report which analyzed Wuhan cell phone data posted by NBC News Investigations (2020), an October shutdown at the Wuhan Institute of Virology BSL3 or 4 Laboratories may have occurred, possibly due to a laboratory incident (Dilanian et al., 2020). Specifically, the report suggests that a "*dangerous event*" took place between October 6th and the 11th in the BSL3 and BSL4 areas of the new Wuhan Institute of Virology complex.

The report in question, "Mace E Pai covid-19 analysis redacted" (Document Cloud, 2020) has been subject to some subsequent criticism regarding its findings (Banco et al., 2020). For example, the authors claimed that an 18 day gap between October 6th and 24th 2019 in the normal usage of seven mobile devices at the WIV BSL4 laboratory was evidence of a lab leak. Critics suggested that this was due to the Chinese October holiday in 2019 (Banco et al., 2020). However, the National holiday period in 2019 lasted 7 days from 1st to the 7th of October 2019 (Tuesday to Monday), according to China Public Holidays (2019), Gov. Cn (2018) and China Briefing (2019).

More accurate cell phone analysis would of course help to prove or disprove some of the claims by the authors, as would access to the original data itself.

Despite some criticism of the report, it is important to understand where it fits into the intelligence gathering landscape. Firstly, it is not a formal assessment, it is one subcontracted data gathering report produced by the Sierra Nevada Corporation. Specifically:

- The report states to that it is part of a “MACE contract” and an “E-PAI ODIN” product (E-Public Available Information - Open Data Intelligence).
- The software used is likely 'Odin's Eye' (Novaindex, 2021; OEIS Denmark, 2020)
- The remit of the contractor is NOT to evaluate the information, but to provide the data which is then evaluated by the relevant government agencies. This is very clear in the disclaimer in the report itself:

> “*This report is derived from publicly available information, not finally evaluated intelligence, and is disseminated for the purpose of allowing the recipient element the ability to determine whether the information is relevant to its responsibilities and can be retained by the recipient*”

Sierra Nevada Corporation (SNC, 2021) is an aerospace and national security contractor with its HQ in Sparks, Nevada *(Comptroller Defense, 2012,* and has over 30 locations in the US, UK, Europe and Turkey. One of it sub-divisions is “*Information & Sensor Solutions (ISS)"* (SNC, 2018a):

> “*ISS is also home to nContext, offering analytical and engineering services that enable organizations to make data-driven decisions. SNC nContext provides these services to organizations focused in intelligence, risk analysis, marketing, and cyber. To foster public and private collaboration, and the reuse of technologies for the government, SNC nContext houses the Multi Agency Collaboration Environment (MACE). The MACE tackles specific problems related to Processing, Exploitation & Dissemination (PED), GEOINT, Systems Integration, and Software Development*” (SNC, 2018a).

Figure 66: Information & Sensor Solutions (ISS). Source: ISS (2017)

If anyone should be questioned by journalists about the MACE report, it would be the Corporate VP of ISS, Dave Klinger (SNC, 2018b):

> "*In the 15 years he has spent with the company, Klingler has led the engineering and business development efforts for sensors, processing and advanced missions systems to create industry leading solutions in the areas of SIGINT (Signal Intelligence), GEOINT (Geospatial Intelligence) and Information Systems*".

Figure 67: Dave Klingler. Corporate Vice President Information & Sensor Systems. (SNC, 2018b)

Sierra Nevada Corporation obtained grants from the Department of Defense to manage the Multi-Agency Collaboration Environment (MACE) which is based in Herndon, Virginia (Lensa , 2021; MACE, 2012) and shares information with DHS and DOD and other agencies. According to Gov Tribe (2014), Sierra Nevada received nearly 70 million USD in contracts for MACE since 2009. For example, it received a 2013 contract worth over 12 million USD for R & D in multi-agency collaboration environment (MACE) technology. While for 2012 -2014, it was awarded a $12.3m contract "*W911QX11D0005* Task Order 0002, Mace Technology Increment":

- "*Delivery Order W911QX11D0005-0002 was awarded to Sierra Nevada Corporation on Oct 12, 2012. The delivery order is funded by the Research Development and Engineering Command (DOD - Army - AMC). The potential value of the award is $12,503,363*" (Gov Tribe, 2013).
- "*Delivery Order W911QX11D0005-0003 was awarded to Sierra Nevada Corporation on Sep 30, 2013. The delivery order is funded by the Research Development and Engineering Command (DOD - Army - AMC). The potential value of the award is $12,222,723*" (Gov Tribe, 2021).

SNC's "MACE Fusion" website has now been deleted, but some idea of its ambit can be seen via screenshots from the Way Back Machine:

Mission

Protect the nation by leveraging the power of information to achieve cross agency interoperability, collaboration and shared awareness

Goals

- Achieve greater levels of situational awareness and enable more accurate and timely decision making across all U.S. government agencies
- Accelerate the interoperability, policy and security advancements needed to meet the future security and integration challenges that the United States will encounter

Approach

The MACE focuses on providing a neutral environment for the development of partnerships across government and industry. To do this, the MACE leverages:

- On Site Government Project Managers to Provide Dedicated Oversight and Feedback
- Best of Breed Industry Partnerships for Focused Interoperability Research and Development
- Flexible Contracting Framework to Reduce Cost and Accelerate Execution of Requirements
- Open Standards and Non-Proprietary Solutions to Enable Collaboration, Increase System Interoperability, and Reduce Cost
- Agile Commercial Development Model to Expedite Delivery Schedules

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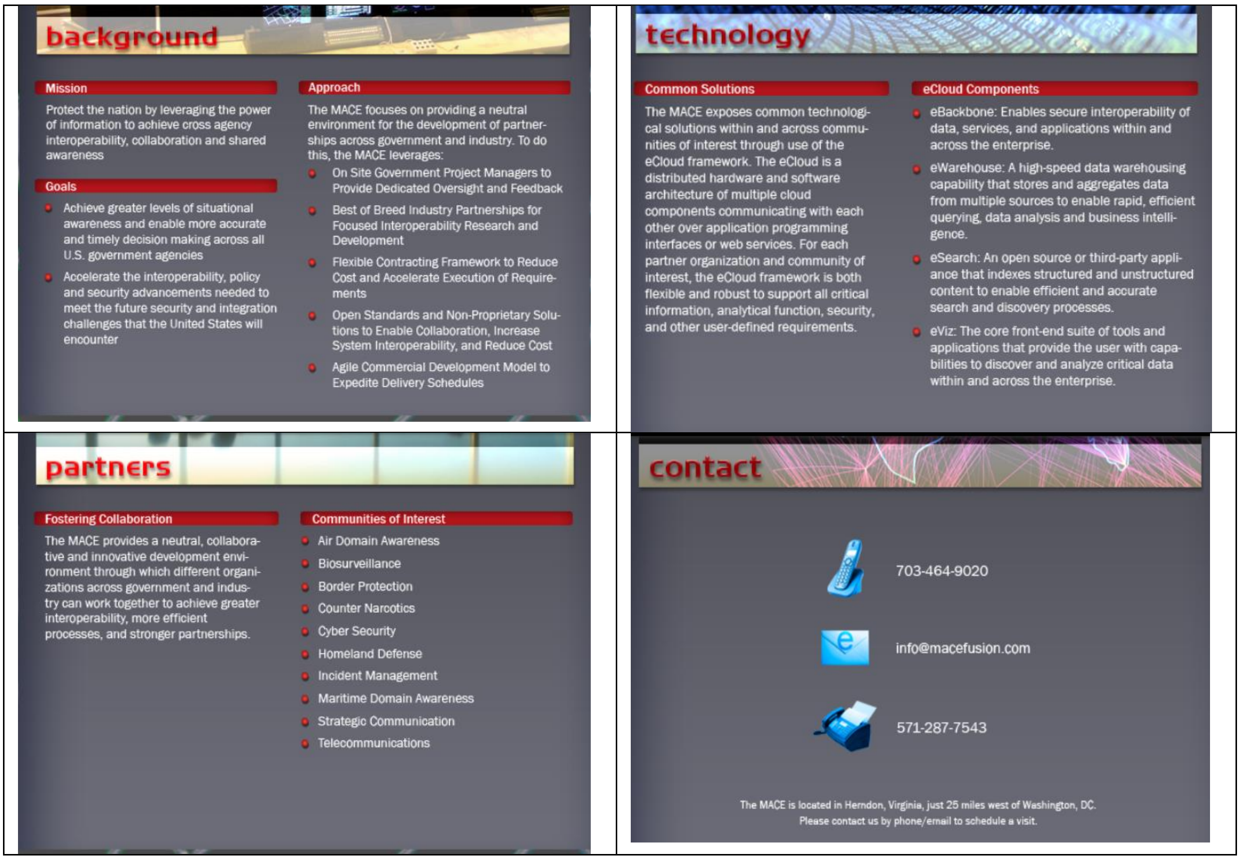
Figure 68: MACE FUSION website (deleted). Source: MACE. (2012).



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- Agile Commercial Development Model to Expedite Delivery Schedules

Common Solutions

The MACE exposes common technological solutions within and across communities of interest through use of the eCloud framework. The eCloud is a distributed hardware and software architecture of multiple cloud components communicating with each other over application programming interfaces or web services. For each partner organization and community of interest, the eCloud framework is both flexible and robust to support all critical information, analytical function, security, and other user-defined requirements.

eCloud Components

- eBackbone: Enables secure interoperability of data, services, and applications within and across the enterprise.
- eWarehouse: A high-speed data warehousing capability that stores and aggregates data from multiple sources to enable rapid, efficient querying, data analysis and business intelligence.
- eSearch: An open source or third-party appliance that indexes structured and unstructured content to enable efficient and accurate search and discovery processes.
- eViz: The core front-end suite of tools and applications that provide the user with capabilities to discover and analyze critical data within and across the enterprise.

Fostering Collaboration

The MACE provides a neutral, collaborative and innovative development environment through which different organizations across government and industry can work together to achieve greater interoperability, more efficient processes, and stronger partnerships.

Communities of Interest

- Air Domain Awareness
- Biosurveillance
- Border Protection
- Counter Narcotics
- Cyber Security
- Homeland Defense
- Incident Management
- Maritime Domain Awareness
- Strategic Communication
- Telecommunications

☎ 703-464-9020

info@macefusion.com

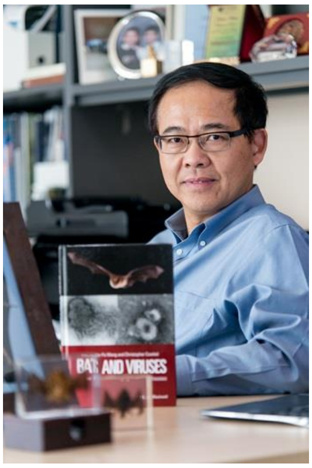
571-287-7543

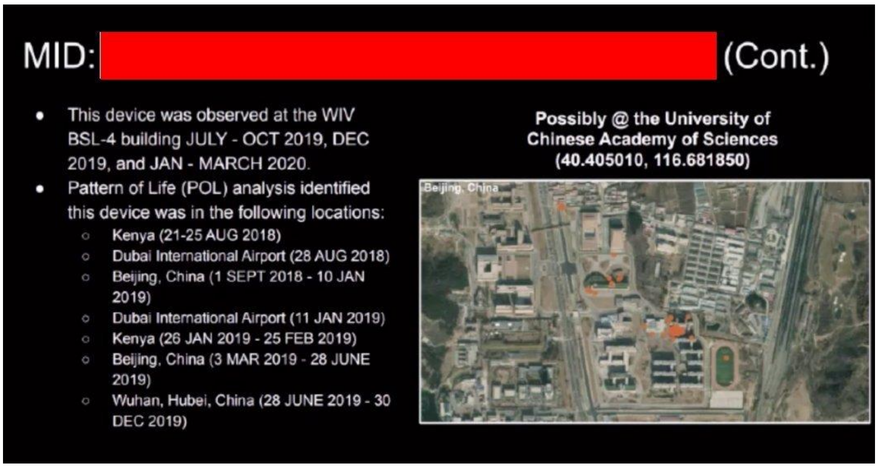
The MACE is located in Herndon, Virginia, just 25 miles west of Washington, DC.
Please contact us by phone/email to schedule a visit.

Figure 69: MACE FUSION website (deleted). Source: Mace (2012)

Interestingly, the report identified two Singapore based devices via “Unique Device Identification” (Figures 70 and 71) inside the WIV new complex between 2019 & April 2020. It seems they belonged to:

1. Dr Linfa Wang, Chair of the Scientific Advisory Board, Centre for Emerging Infectious Diseases, Wuhan Institute of Virology (Wang, 2017).





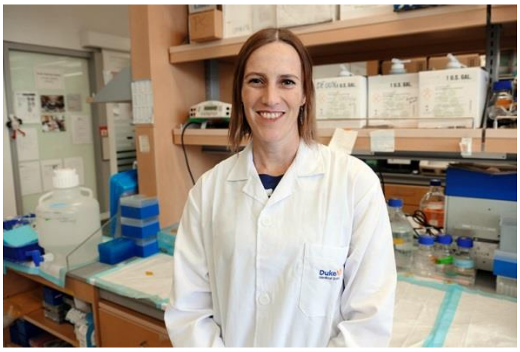
MID: [redacted] (Cont.)

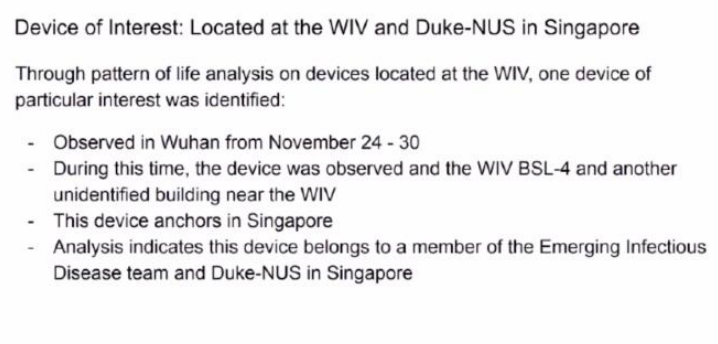
- This device was observed at the WIV BSL-4 building JULY - OCT 2019, DEC 2019, and JAN - MARCH 2020.
- Pattern of Life (POL) analysis identified this device was in the following locations:
  - Kenya (21-25 AUG 2018)
  - Dubai International Airport (28 AUG 2018)
  - Beijing, China (1 SEPT 2018 - 10 JAN 2019)
  - Dubai International Airport (11 JAN 2019)
  - Kenya (26 JAN 2019 - 25 FEB 2019)
  - Beijing, China (3 MAR 2019 - 28 JUNE 2019)
  - Wuhan, Hubei, China (28 JUNE 2019 - 30 DEC 2019)

Possibly @ the University of Chinese Academy of Sciences (40.405010, 116.681850)

Figure 70: Device of Interest. Source (Linfa Wang. Source: DocumentCloud. (2020) & Duke-NUS (2020)

2. Professor Danielle Anderson (Duke-NUS, Singapore)





Device of Interest: Located at the WIV and Duke-NUS in Singapore

Through pattern of life analysis on devices located at the WIV, one device of particular interest was identified:

- Observed in Wuhan from November 24 - 30
- During this time, the device was observed and the WIV BSL-4 and another unidentified building near the WIV
- This device anchors in Singapore
- Analysis indicates this device belongs to a member of the Emerging Infectious Disease team and Duke-NUS in Singapore

Figure 71: Device of Interest. Source (likely Professor Danielle Anderson) Source: DocumentCloud. (2020).

Both these Singapore based scientists enjoyed a close relationship with the WIV. Given their alleged presence during key periods in 2019 at WIV, it would be wise to ascertain details of their knowledge of any outbreak in Wuhan in the autumn of 2019.Thus, it is politely suggested yet again **that investigators interrogate the history of their digital devices**, as recommended by Bostickson & Ghannam (2021b).

16. THE WHO INVESTIGATION – SEROLOGICAL EVIDENCE

Figure 72: WHO convened Global study on COVID-19 origins Press Briefing. Source: China Today (2021)

Recently, both Chinese health officials and the WHO investigation team in Wuhan claimed that there was little serological evidence for the early spread of the virus prior to December in Wuhan (Hinshaw et al., 2021). However, the claim by the WHO team was based not on their own analysis of blood samples but rather submitted Chinese reports (Hinshaw et al., 2021).

Professor Dominic Dwyer, one of the WHO Team members who recently visited Wuhan, revealed that there were significant tensions over access to samples (Video.Twimg , 2021) and evidence of clear political pressure (Dye & Willan, 2021). Specifically, the local Chinese Scientists stated that they had carefully examined Wuhan hospital data of over 75,000 patients with respiratory illness during the months of October and November 2019.

However, they brazenly claimed they had identified less than one hundred cases which showed Covid-19 like signs and when the samples of these 100 patients were tested, the results were all conveniently negative (WHO, 2021).

> *"The Chinese scientists had identified 92 potential Covid-19 cases among some 76,000 people who fell sick between October and early December 2019"* WSJ (2021).

The WHO team members were then refused access to the raw data of the 76,000 cases which thus prevented them from clarifying why the Chinese health authorities decided to "*only test those 92 people for antibodies*" WSJ (2021). Furthermore, the WHO team was refused access to pre-December 2019 Wuhan blood samples and thus were unable to test them for SARS-COV-2 antibodies (WSJ, 2021).

Indeed, Chinese authorities refused to provide WHO investigators with "*raw, personalized data on early Covid-19 cases that could help them determine how and when the coronavirus first began to spread in China*" (Page & Hinshaw, 2021). When the WHO Team asked for early blood samples, they were informed that they "*couldn't conduct retrospective testing of samples in blood banks*" (Sherwell, 2021). Dr. Koopmans pointed out that the WHO team had:

> "*sought wastewater samples from China to check if the virus could be detected in sewage from late 2019, but were told those had been discarded, per standard policy, after a month*" (Brouwer, 2021).

The Chinese authorities also refused to provide physical samples from patients with respiratory diseases in hospitals form 2019, claiming that its hospitals didn't store such physical samples (Brouwer, 2021). Recent statements by WHO Team members now tend to support the hypothesis of early cases spreading in Wuhan before December 2019 (Brouwer, 2021; Mckay et al., 2021; Hinshaw et al., 2021):

> *"New evidence from China is affirming what epidemiologists have long suspected: The coronavirus likely began spreading unnoticed around the Wuhan area in November 2019, before it exploded in multiple different locations throughout the city in December"* (Mckay et al., 2021)

17. COVER UP and GAG ORDERS

The Chinese CDC (CCDC) leaked internal documents published by AP (Cheng et al., 2020), reveal that the Chinese authorities insisted all Covid-19 research & publications had to be centrally managed & coordinated like a propaganda "**game of chess**”. This was in order to “**prioritize the interests of the country**”, “**write papers on the land of the motherland**" and ensure no samples were provided to foreign researchers (Cheng, et al., 2020).

The gag orders seem to have been partly in reaction to three specific papers by Chinese researchers, the first published in the Lancet on January 24th 2020 “*Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China*” by Huang et al. (2020). This paper clearly showed some early Wuhan Covid-19 cases (December 1st and 10th 2019) with no connection to the Huanan seafood market (Figure 73):

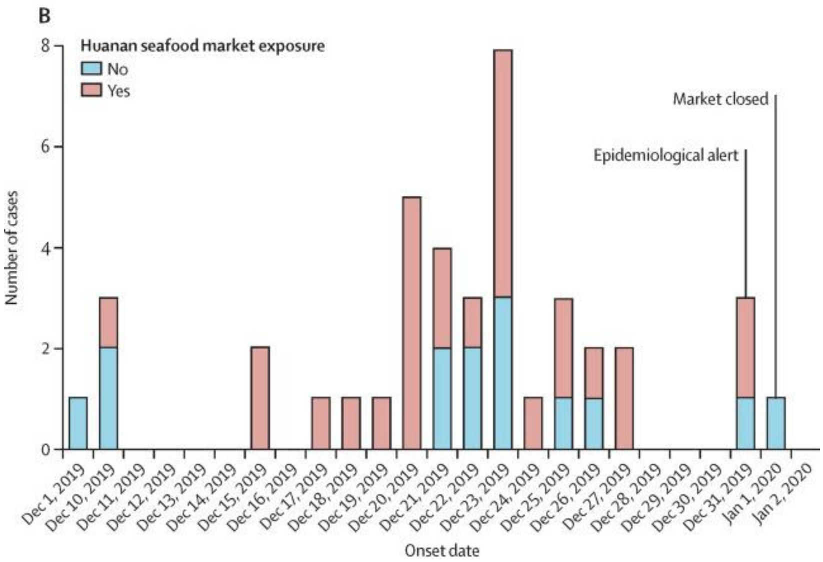


Figure 73: Date of illness onset of patients with lab-confirmed 2019-nCoV infection (Huang et al., 2020)

The second paper was “Decoding evolution and transmissions of novel pneumonia coronavirus using whole genomic data” by Yu et al. (2020). In this paper, published on the 21st of February 2020, the authors called for more transparency regarding early cases in Wuhan and concluded that the outbreak itself had started not in December, but rather in November.

The third paper "*The possible origins of 2019-nCoV coronavirus*" was a subsequently retracted and rather controversial pre-print published on February 6th 2020 by Xiao & Xiao (2020). The authors claimed that the novel coronavirus had leaked either from the WCDC laboratory at Machang Road near the Huanan seafood market or a WIV laboratory. The authors worked in Wuhan at the Huazhong University of Science and Technology and Tian You Hospital, Wuhan University of Science and Technology.

The three "gag order" documents (CCDC ones from February 24th 2020 and the State Regulations from March 3rd 2020), were published with original Chinese text and English translation here by the AP news agency (Document Cloud, 2021a & 2021b):

- State Regulations: https://documentcloud.org/documents/7340337-State-Research-regulations.html
- CCDC (1) https://documentcloud.org/documents/7340335-China-CDC-Sci-Tech.html
- CCDC (2) https://www.documentcloud.org/documents/7340336-China-CDC-Sup-Regs.html

The chilling effect of these "gag orders" is evidenced by the case of Professor Yu Chunhua from Wuhan University, who was interviewed by Guancha.Cn (2020). Tasked with managing a database of early patient data, he had discovered a number of earlier cases in November 2019:

> "*With the research of the database, Professor Yu Chunhua found more and more case data before December 8. There were 2 patient cases in November, and the onset time was November 14 and 21, 2019. Before December 8, there were also 5 or 6 cases. Among them, one patient who became ill at the end of November was hospitalized on December 2 & clinically diagnosed with pneumonia*" (Guancha.Cn, 2020).

The Guancha.cn interview occurred at the very same time as the infamous Chinese CDC Gag order mentioned previously. Coincidentally, Professor Yu Chunhua then called the journalist in order to claim that "*the dates had been entered incorrectly*" and that he wished to retract his statement (Birrell, 2021). Indeed, AP News (2020) reported that China failed to be transparent in the search for patient zero, specifically regarding "re-testing of old flu samples" which were stored in freezers in Wuhan and Hubei province.

Only 520 samples from 330,000 were used as data for publication by Chinese scientists (AP news, 2020). The AP News investigation also revealed that over 100 samples tested by Hubei CDC were not shared publicly, and that early samples were not tested, which according to a Chinese scientist involved in the work was:

> "*A very deliberate choice of the time period to study, because going too early could have been too sensitive*"

As the attentive reader will have guessed, this "very deliberate choice" was mainly due to the so-called gag order issued by the Chinese State and CCDC on February 24th 2020 (Document Cloud, 2021a and 2021b). One of these notices specifically ordered CDC staff not to "share any data, specimens or other information related to the coronavirus with outside institutions or individuals" (AP News, 2020). Then, on March 3rd, China's State Council ordered the central "management" of any publications relating to COVID-19 "under a special task force" in a document called "State Research Regulations" (Document Cloud, 2021c). According to the AP news investigation, a former CCDC Deputy Director confessed that:

> "*The regulations are very strict, and they don't make any sense…I think it's political, because people overseas could find things being said there that might contradict what China says, so it's all being controlled*" (AP News, 2020)

According to local sources in Wuhan who spoke to reporters from KYODO NEWS (2020**)**, Wuhan doctors were threatened and warned:

- "*They could be punished for espionage if they revealed what went on during the period*"
- "*They should not speak at all about the situation*"
- "*One doctor in Wuhan said that he was told by health authorities he would be punished by law if he revealed his experience, and if accused of espionage, the death penalty could be imposed*"
- "*Academic institutions in the city tried to keep records of the virus and treatment of the infection, but the plan was forced to be cancelled by authorities*" (KYODO NEWS, 2020).

18. CHINESE STRATEGY

Figure 74: "Fighting Covid-19 the Chinese Way". Source: China Daily (2019b).

From an analysis of the gag orders and behaviour of the Chinese authorities discussed in the previous section, a developing strategy can be deduced:

1. Do not release data on any new early cases.
2. Do not ever publish a case before December 20th 2019.
3. Remove early December cases (before the 8th December 2019).
4. Wait for retrospective sample testing to show early cases in foreign countries.
5. Point to the US, France, Italy, Spain, etc. as likely sources of SARS-COV-2.
6. Suggest SARS-COV-2 arrived in China via cold chain food transport from overseas.

Indeed, a year later, following an official request by the WHO for clarification about the total of 44 December 2019 cases reported on the 3rd of January 2020, the Chinese authorities claimed that there were only 41 confirmed cases in December (174 if the February 2021 semi-official WHO data release is included).

The Chinese authorities further insisted that there were zero official cases before December 2019, which is laughably absurd given the potential for retrospective testing and case reviews. As we have seen, the Chinese strategy involves denying the validity of any of the 200 plus early cases in 2019.

However, as Demaneuf (2020c) points out, it would have been to China's advantage to disclose the early cases IF they pointed to a foreign source of the virus. It would also have been to China's advantage to publish the earlier cases IF they pointed to a Huanan Seafood Market origin for SARS-COV-2.

Why? Because 14 out of the 41 official December 2019 cases were not linked to the seafood market, which in turn challenged the zoonotic origin hypothesis supported by China (Demaneuf, 2020c). Thus, the reason that the more than 150 early cases were covered up suggests that they were not connected to the seafood market, nor did they support a foreign cold chain import scenario (Demaneuf, 2020c), as proposed in the "WHO-convened Global Study of Origins of SARS-CoV-2: China Part" (WHO, 2021). See Figure 75:

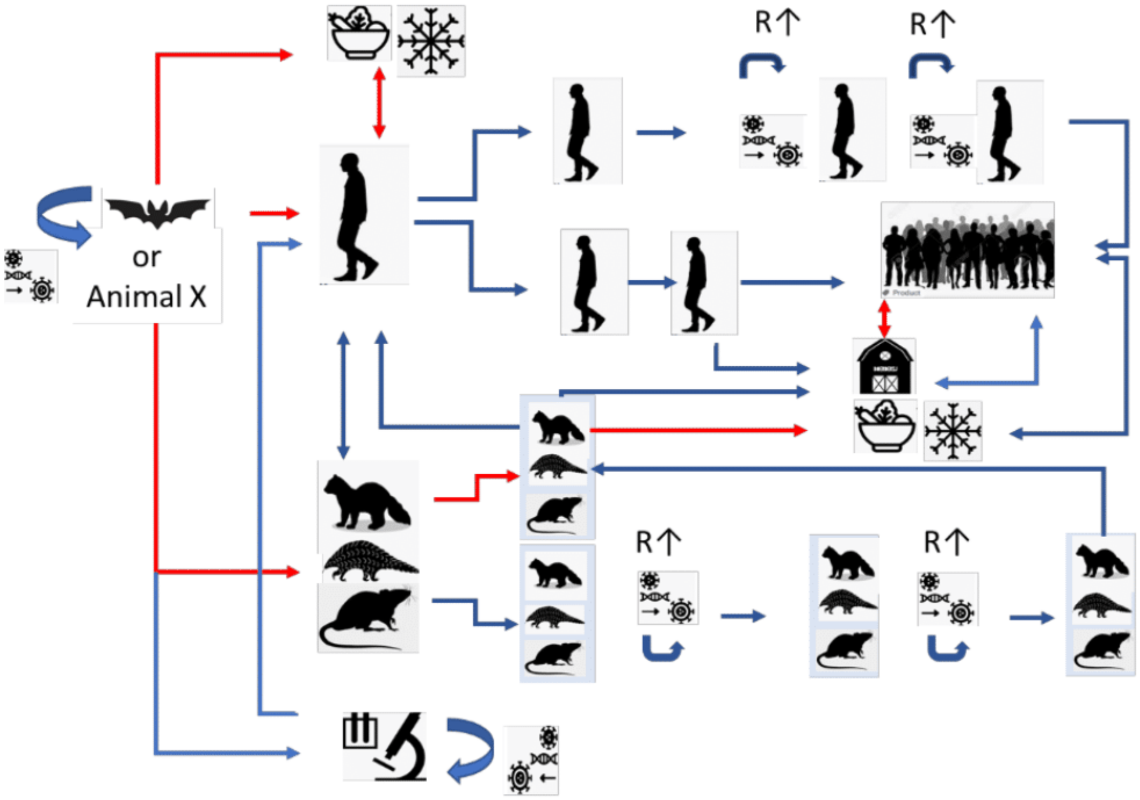


Figure 75: "Schema for the introduction of SARS-CoV-2 through the cold/food chain" from "WHO-convened Global Study of Origins of SARS-CoV-2: China Part" Source: The Bulletin (2021).

19. SARS-COV-2 PROGENITOR MUTATION ANALYSIS

Figure 76: Analysis of early mutations (Kumar et al., 2020b).

DIAGRAM KEY

“*Thick arrows mark the pathway of widespread variants and thin arrows show paths leading to other common mutations. The pie-chart sizes are proportional to variant frequencies in the 29KG data set, with pie-charts shown for variants with vf > 3% and pie color based on the world’s region where that mutation was first observed. A circle is used for all other variants, with the filled color corresponding to the earliest sampling region*” (Kumar et al., 2020b)

This is a brief introduction to the main findings from "An evolutionary portrait of the progenitor SARS-CoV-2 and its dominant offshoots in COVID-19 pandemic", by Kumar et al. (2020b) who show that the progenitor SARS-CoV-2 (proCoV2) can be dated back to **October to mid-November 2019**. Despite recent claims and speculation by Chinese scientists (Global Times, 2021; Shaikh, 2020; Shen et al,, 2020; Zhou & Shi, 2021), politicians (ABC News, 2020a; and media (Liu, 2020; Zhang, 2021), that SARS-COV-2 originated outside China, Kumar et al. (2020a) show from an analysis of early mutations (Figure 76), that this pro-CoV2 clearly "originated and evolved in China". In subsequent version of this paper, Kumar at al. (2021) concluded that:

> "*based on the assumption of a constant mutation rate, Kumar et al. estimated the time of the spillover event to be around **October or September 2019***" (Kumar et al.,2021)

Kumar et al. (2021) updated their previous work (Kumar et al., 2020b) in order to directly reconstruct the ancestral sequence and the mutational history of CoV-2 genomes, thus bypassing the difficulty of anchoring a phylogenetic tree, in order to estimate the tMRCA (time to most recent common ancestor). Their main findings were as follows:

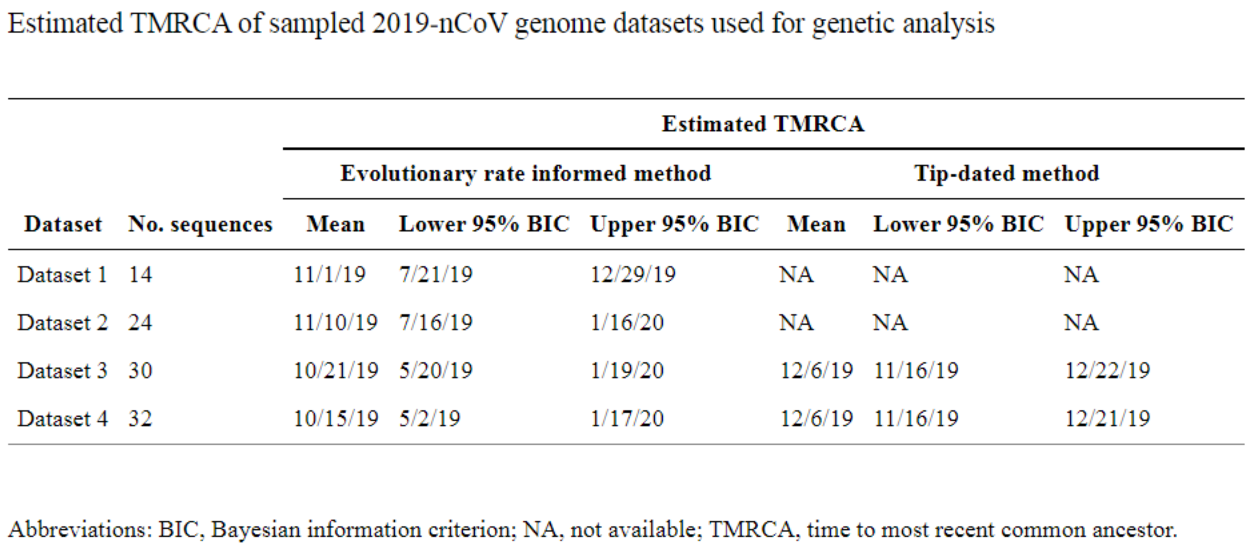
- **Wuhan-1 was not the direct ancestor** of all the early coronavirus infections globally.
- The progenitor of all genomes sequenced from human coronavirus infections **(proCoV2**) is **three bases different from the Wuhan-1 genome**.
- The tMRCA can be dated back to **late October to mid-November 2019**.
- The tMRCA is roughly one month older than the date for the MRCA of genomes presented by Pekar et al. (2021) because their analysis is restricted to the ancestry of the coronaviruses sampled from China only, which resulted in the exclusion of the "V lineage" from their analysis.
- The tIndex (first infection of a human) could have been as early as **September 2019,** based on approximately 1-month difference between MRCA and Index dates in #5 (Pekar et al., 2021).

- In effect **proCoV2 (the progenitor virus) was spreading worldwide months before the first reported cases of COVID-19 in China.**

Meanwhile, other evolutionary sequence analyses also point towards SARS-CoV-2 entering human hosts at some time in the autumn of 2019. For example, Hill & Rambaut (2020) give a time of origin of around **late November 2019**:

“*The date of the MRCA of the tree is consistent with a jump to humans from the second half of November to the first half of December*” (Hill & Rambaut, 2020),

Lu et al. (2020) in “*Genomic epidemiology of SARS-CoV-2 in Guangdong Province*”, estimated the TMRCA dates for 2019-nCoV from four smaller datasets as being **between 15th November and 13th December 2019** (Lu et al., 2020), illustrated in Table X below:



Estimated TMRCA of sampled 2019-nCoV genome datasets used for genetic analysis

		Estimated TMRCA					
		Evolutionary rate informed method			Tip-dated method		
Dataset	**No. sequences**	**Mean**	**Lower 95% BIC**	**Upper 95% BIC**	**Mean**	**Lower 95% BIC**	**Upper 95% BIC**
Dataset 1	14	11/1/19	7/21/19	12/29/19	NA	NA	NA
Dataset 2	24	11/10/19	7/16/19	1/16/20	NA	NA	NA
Dataset 3	30	10/21/19	5/20/19	1/19/20	12/6/19	11/16/19	12/22/19
Dataset 4	32	10/15/19	5/2/19	1/17/20	12/6/19	11/16/19	12/21/19

Abbreviations: BIC, Bayesian information criterion; NA, not available; TMRCA, time to most recent common ancestor.

Table 1: Estimated TMRCA for SAR-COV-2 datasets. Source: Li et al., (2020)

According to Volz et al. (2020), “Bayesian phylogenetic analysis points to a common ancestor of the analysed lineages of SARS-COV-2 as being between November 21st and December 20th, 2019 and the **TMRCA between 6th November and 13th December 2019** (Volz et al., 2020).

Duchene et al. (2020) calculated the time of origin to a mean of late November 2019 but with one dataset showing a **CI between late October and mid-December 2019**.

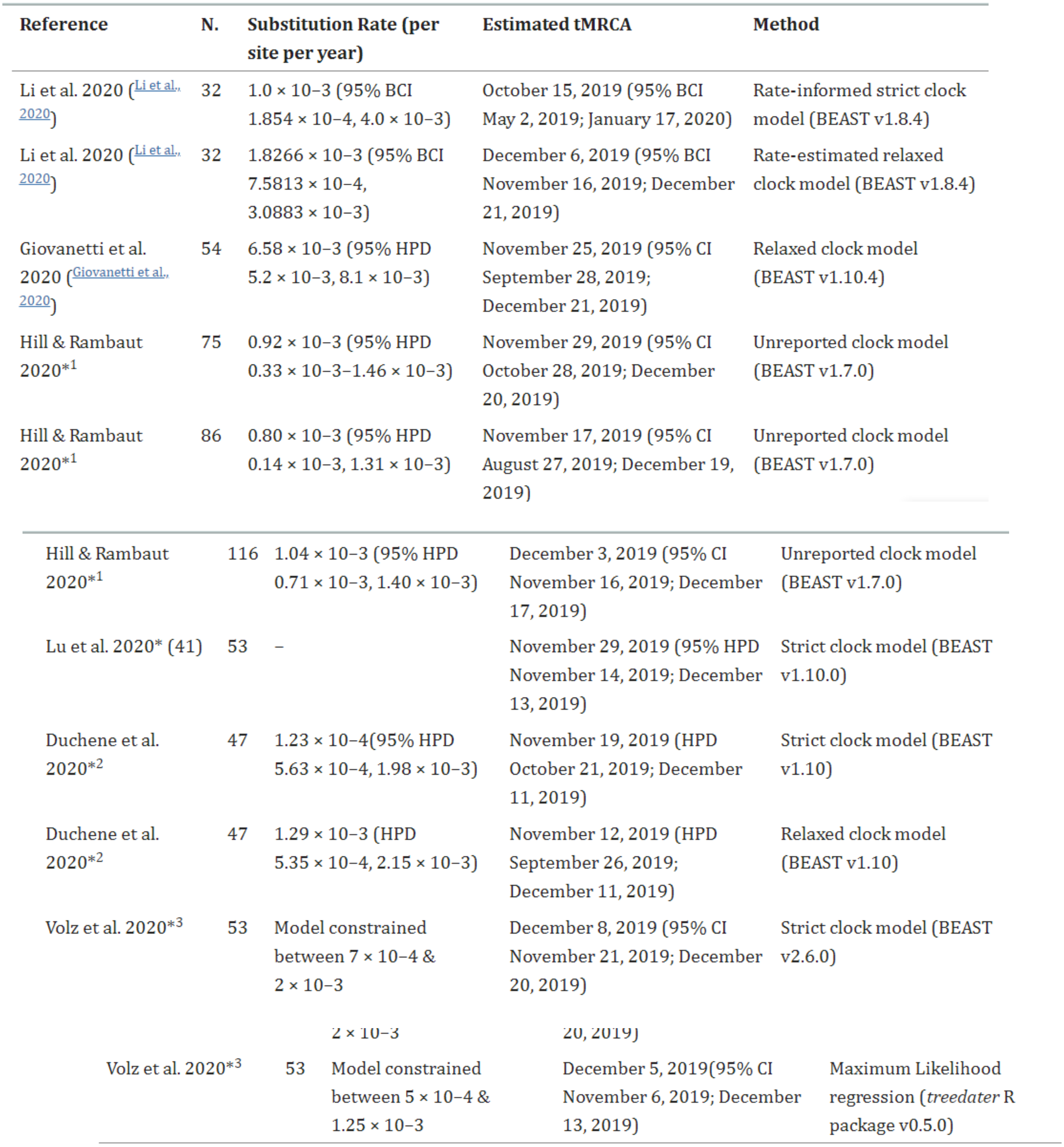
Roberts et al. (2021) point out that "*it is likely that SARS-CoV-2 spilled over into humans much earlier"* than the first recorded cases in December 2019. They claim that their research is in line with "*existing evidence*" and conclude that "*the first case of COVID-19 would have been sometime between early October and mid-November*" (Roberts et al., 2021).

Van Dorp et al. (2020) published an interesting analysis of over 7000 SARS-COV-2 genomes from different locations and estimated the time to most recent common ancestor (tMRCA) as being between "**6th October 2019 and 11th December 2019**" Alliance for Science (2020).

> "*We curated a dataset of 7666 public genome assemblies and analysed the emergence of genomic diversity over time. Our results are in line with previous estimates and point to all sequences sharing a common ancestor towards the end of 2019, supporting this as the period when SARS-CoV-2 jumped into its human host*"(Van Dorp et al.,2020).

> "*Results showed that all sequences shared a common ancestor towards the end of 2019 (**6 October 2019–11 December 2019**), indicating this as the period when SARS-CoV-2 jumped into the human population, and that the virus may have been transmitted between human hosts for quite some time before it was identified*" Van Dorp et al. (2020) .

In their paper we can find a useful table listing different estimates of the tMRCA by researchers which generally point to October and November 2019 (Table 2).



Reference	N.	Substitution Rate (per site per year)	Estimated tMRCA	Method
Li et al. 2020 (Li et al., 2020)	32	1.0 × 10−3 (95% BCI 1.854 × 10−4, 4.0 × 10−3)	October 15, 2019 (95% BCI May 2, 2019; January 17, 2020)	Rate-informed strict clock model (BEAST v1.8.4)
Li et al. 2020 (Li et al., 2020)	32	1.8266 × 10−3 (95% BCI 7.5813 × 10−4, 3.0883 × 10−3)	December 6, 2019 (95% BCI November 16, 2019; December 21, 2019)	Rate-estimated relaxed clock model (BEAST v1.8.4)
Giovanetti et al. 2020 (Giovanetti et al., 2020)	54	6.58 × 10−3 (95% HPD 5.2 × 10−3, 8.1 × 10−3)	November 25, 2019 (95% CI September 28, 2019; December 21, 2019)	Relaxed clock model (BEAST v1.10.4)
Hill & Rambaut 2020*[1]	75	0.92 × 10−3 (95% HPD 0.33 × 10−3–1.46 × 10−3)	November 29, 2019 (95% CI October 28, 2019; December 20, 2019)	Unreported clock model (BEAST v1.7.0)
Hill & Rambaut 2020*[1]	86	0.80 × 10−3 (95% HPD 0.14 × 10−3, 1.31 × 10−3)	November 17, 2019 (95% CI August 27, 2019; December 19, 2019)	Unreported clock model (BEAST v1.7.0)
Hill & Rambaut 2020*[1]	116	1.04 × 10−3 (95% HPD 0.71 × 10−3, 1.40 × 10−3)	December 3, 2019 (95% CI November 16, 2019; December 17, 2019)	Unreported clock model (BEAST v1.7.0)
Lu et al. 2020* (41)	53	–	November 29, 2019 (95% HPD November 14, 2019; December 13, 2019)	Strict clock model (BEAST v1.10.0)
Duchene et al. 2020*[2]	47	1.23 × 10−4(95% HPD 5.63 × 10−4, 1.98 × 10−3)	November 19, 2019 (HPD October 21, 2019; December 11, 2019)	Strict clock model (BEAST v1.10)
Duchene et al. 2020*[2]	47	1.29 × 10−3 (HPD 5.35 × 10−4, 2.15 × 10−3)	November 12, 2019 (HPD September 26, 2019; December 11, 2019)	Relaxed clock model (BEAST v1.10)
Volz et al. 2020*[3]	53	Model constrained between 7 × 10−4 & 2 × 10−3	December 8, 2019 (95% CI November 21, 2019; December 20, 2019)	Strict clock model (BEAST v2.6.0)
Volz et al. 2020*[3]	53	Model constrained between 5 × 10−4 & 1.25 × 10−3	December 5, 2019(95% CI November 6, 2019; December 13, 2019)	Maximum Likelihood regression (*treedater* R package v0.5.0)

2 × 10−3 20, 2019)

Table 2: Estimates of SARS-CoV-2 time to most recent common ancestor (tMRCA). Van Dorp et al., (2021)

20. ANALYSIS OF THE VARIATION & EVOLUTION OF SARS-COV-2

Several attempts have been made to date the outbreak of SARS-COV-2 from an analysis of the genomes, with some key results, findings and dates listed below:

Zhou et al. (2020c) from Southern Medical University in Guangzhou (previously the PLA's First Military Medical University), **published** "*Analysis of the variation and evolution of the new coronavirus SARS-CoV-2*" on the 20th February 2020 (received on the 17th February). This was just two days before the February visit to Wuhan by the WHO team and a week before the CDC gag order on 27th February 2020, which was followed by the draconian State Council gag order on the 3rd of March 2020 (See Gag Orders Section). The main findings of this paper were that:

- Using a **tMRCA** (time to most recent common ancestor) estimate based on the evolutionary tree, the mean emergence date is around **10th November 2019** and the lower bound of the 95% C.I. for emergence of SARS-CoV-2 is: **23rd September 2019.**
- The tIndex (date of first human infection) can be expected to be around one month before tMRCA, which would give a **tIndex around 10th of October 2019**.

Another February 2020 paper by Yu et al. (2020) includes two authors form the Xishuangbanna Tropical Botanical Garden, (Mengla) which is a well-known bat sampling suite in Yunnan, not far from the Mojiang mine where RaTG13 and some of the closest known relatives of SARS-CoV-2 come from (Anon, 2020b; Bostickson & Ghannam, 2020c). This paper was first published on the 19th February 2020, with a revised version on the 21st February just before the previously mentioned gag orders. The main findings are:

- SARS-CoV-2 had already circulated widely among humans in Wuhan before December 2019, **probably beginning in mid to late November**, based on a haplotype analysis of 93 genomes from China and abroad.

- A likely **early expansion** (not the same as tMRCA) with an estimated date **of 8th December 2019**, with a lower bound to the 95% CI of **13th November 2019.**
- Genomic evidence did not support the Hua Nan market as the birthplace of SARS-CoV-2 and that instead the Hua Nan market boosted the virus circulation and spread it into the whole city in December 2019.
- Complains about the sequences for early cases not being published, which would greatly help understand the early evolution of the virus: ‘Because the currently available samples do not include the first identified infected patient and other patients from early December, the most common ancestral haplotype might be missed’(Yu et al, 2020).

In the “Who-Convened Global Study of Origins of Sars-Cov-2: China Part”, we can see on Page 7 that:

> “*Based on molecular sequence data, the results suggested that the outbreak may have started in the months before the middle of December 2019. The point estimates for the time to the most recent ancestor* **(tMRCA)** ***ranged from late September to early December, but most estimates were between mid-November and early December***” (WHO,2021)

It is important to note that the time to the most recent common ancestor (**tMRCA**) is different from the “**tIndex”** (the time of the index case) which has been estimated to be around 37 days prior to tMRCA. In a more recently published paper, “*Dating the Common Ancestor from an NCBI Tree of 83688 High-Quality and Full-Length SARS-CoV-2 Genomes*”, Xia (2021) points out that:

> “*All dating studies involving SARS-CoV-2 are problematic. Previous studies have dated the most recent common ancestor (MRCA) between SARS-CoV-2 and its close relatives from bats and pangolins. However, the evolutionary rate thus derived is expected to differ from the rate estimated from sequence divergence of SARS-CoV-2 lineages*” (Xia, 2021).

Based on a robustly "large phylogenetic tree with 86,582 high-quality full-length SARS-CoV-2 genomes", Xia (2021) concludes that the MRCA should be dated to the **16th of August 2019.** The author also points out that the NCBI tree shows "*ten SARS-CoV-2 genomes isolated from cats, collected over roughly the same time span as human COVID-19 infection*" and claims that the MRCA for these feline SARS-CoV-2 sequences can be dated to **30th of July 2019** (Xia, 2021).

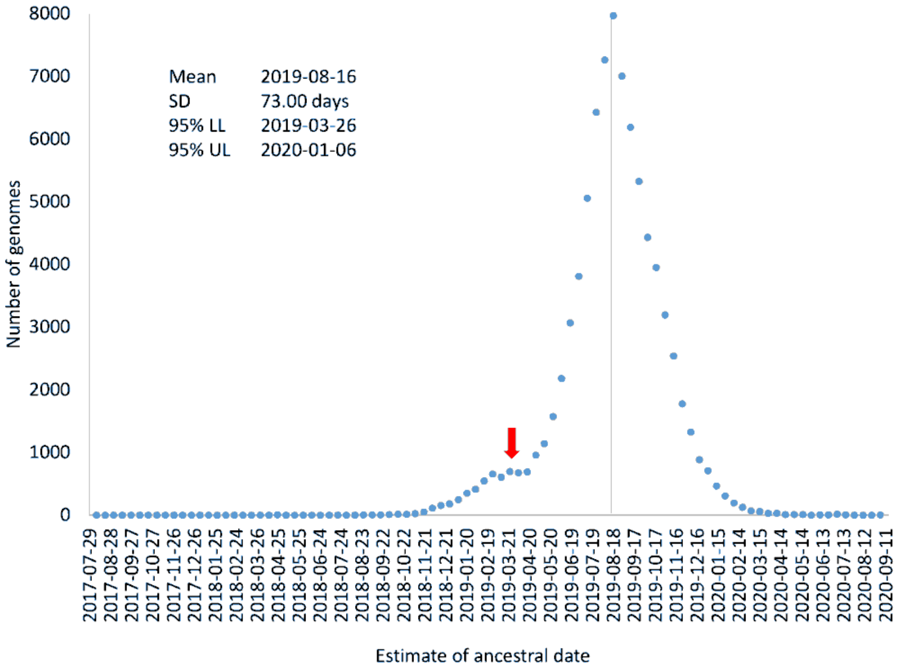


Figure 77: Frequency distribution for characterizing variation in T_A (the time for the origin of the common ancestor of the sampled SARS-CoV-2 genomes) (Xia, 2021)

Pekar et al. (2021), in "Timing *the SARS-CoV-2 index case in Hubei province",* revealed the following main findings:

- The first index case (tIndex) is from **mid-October to mid-November of 2019** based purely on Chinese sequences.
- It is highly probable that SARS-CoV-2 was circulating in Hubei province at low levels in **November 2019 and possibly as early as October 2019,** but not earlier.
- The inferred prevalence of this virus was too low to permit its discovery and characterization for weeks or months.

21. TOTAL NUMBER OF 2019 COVID-19 CASES IN WUHAN


China document leak shows flawed pandemic response
05:09

The Wuhan files

Leaked documents reveal China's mishandling of the early stages of Covid-19

Figure 78: The Wuhan Files - Case Numbers. Source: CNN (2020).

Turning now to the TOTAL number of 2019 Covid-19 CASES in Wuhan (suspected or confirmed), the following sources can help us shine a little light on the issue:

A. CDC Report of The 17th Feb 2020 (China CDC Weekly, 2020).

This was a CDC report entitled "*The Epidemiological Characteristics of an Outbreak of 2019 Novel Coronavirus Diseases (COVID-19) — China* "published on 17th February 2020. The report was based on accumulated data up to the 11th of February 20 20. It lists a total of 104 confirmed cases before 31st of December 2019, 25 of them being "*suspected cases*", and 37 being "*diagnosed cases*" (China CDC Weekly, 2020).

B. South China Morning Post (SCMP) leak of 14th March, 2020 (SCMP, 2020).

The SCMP "leak" of a retrospective review of cases came from Chinese government whistle-blowers. It showed a total of **266 confirmed cases** with onset **before 31st of December 2019**, and **381 as of 1st of January 2020**. The leaked documents also revealed a total of nine cases in November 2019 (SCMP, 2020).

C. CNN Leak of the 1st of December 2020 (CNN, 2020).

The CNN leak on the 1st of December 2020 involved 117 pages of leaked official documents from the Hubei Provincial Center for Disease Control and Prevention, validated for CNN by several experts and digital forensics.

> "*Metadata from the files seen by CNN contains the names of serving CDC officials as modifiers and authors. The metadata creation dates align with the content of the documents. Digital forensic analysis was also performed to test their computer code against their purported origins*" (CNN, 2020).

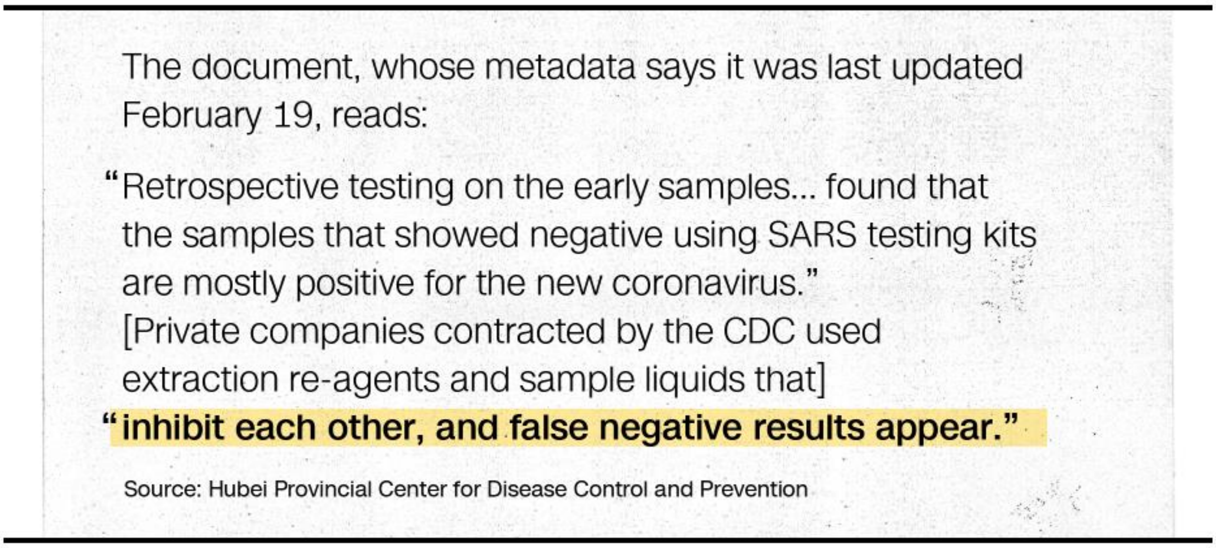
The leaked documents revealed **a total of 200 confirmed and clinically diagnosed cases in 2019**. Other findings include a flu outbreak in early December 2019 in Hubei Province and inadequate testing kits:

- "*Local health authorities in the province of Hubei, list a total of 5,918 newly detected cases on February 10, more* ***than double the official public number of confirmed cases***".
- **Testing was highly inaccurate,** resulting in only a 30% to 50% positive rate, among already confirmed cases.
- Hubei was dealing with a significant influenza outbreak. It caused cases to rise to 20 times the level recorded the previous year.
- The influenza "epidemic," was not only present in Wuhan in December, but was greatest in the neighboring cities of Yichang and Xianning.
- On February 10, when China reported 2,478 new confirmed cases nationwide, the documents show Hubei actually circulated a different total of 5,918 newly reported cases.

- **Many more 2019 coronavirus cases had been identified than previously claimed** (200 confirmed and clinically diagnosed cases):
  "In the bottom left hand column of the graph marked 2019 the number of "confirmed cases" and "clinically diagnosed" cases appears to reach ***around 200 altogether***" (CNN, 2020).

Another important revelation, confirmed by an AP investigation into CCDC corruption involving 3 initial testing kits, "*China testing blunders stemmed from secret deals with firms*" (AP NEWS, 2021b), is that testing was highly inaccurate:

- "*On January 10, one of the documents reveals how during an audit of testing facilities, officials reported that the SARS testing kits that were being used to diagnose the new virus were ineffective, regularly giving false negatives"* (AP NEWS, 2021b).
- *"It also indicated that poor levels of personal protective equipment meant that virus samples had to be made inactive before testing*" (AP NEWS, 2021b).



The document, whose metadata says it was last updated February 19, reads:

"Retrospective testing on the early samples... found that the samples that showed negative using SARS testing kits are mostly positive for the new coronavirus."
[Private companies contracted by the CDC used extraction re-agents and sample liquids that]
"**inhibit each other, and false negative results appear.**"

Source: Hubei Provincial Center for Disease Control and Prevention

Figure 79: Testing Kit. False Negatives. **(**CNN, 2020)

D. China-WHO Joint Study Group Visit (WHO, 2021).

The China-WHO joint study group visit in February 2021, reported 100 cases confirmed by tests and 74 clinically diagnosed cases with onset before the 31st of December 2019 (WHO, 2021). On Page 49 of the main report (WHO, 2021) and on Pages 144 to 146 of the Annexe, the Chinese side told the WHO that they had carried out a full search of "*all the fever patients, influenza-like illness patients, acute respiratory tract infection patients and unspecified pneumonia patients in all medical institutions in Wuhan (266 hospitals)*". They claimed that there were no suspected COVID-19 cases (WHO, 2021). This unusual claim surprised several members of the WHO team (McKay et al., 2021) and independent researchers (Demaneuf, 2020b). For example:

1. Dr. Marion Koopmans:

"*In examining 13 genetic sequences of the virus from December, Chinese authorities found similar sequences among those linked to the market, but slight differences in those of people without any link to it, according to the WHO investigators. The two sets likely began to diverge between mid-November and early December, but could possibly indicate infections as far back as September*" (McKay et al., 2021).

2. Professor Dominic Dwyer:

"*There must have been many, many more cases in December that people didn't know or recognize*"

3. Dr. Thea Fischer:

"(the virus) *has definitely circulated in the population before the first diagnosed serious cases, which were the "the tip of the iceberg*" (McKay et al., 2021).

Indeed, the WHO team "*considers those results inconclusive because the tests were done more than a year after any possible infection cleared*" (McKay et al., 2021).

22. ANOMALIES & MANIPULATION OF THE REPORTED CASE NUMBERS

Firstly, there are several issues with the case numbers given in the China-WHO joint study group report:

- The 100 confirmed cases for December 2019 contradict the official 104 confirmed cases published one year earlier.
- The total absence of any suspected Covid-19 cases across 266 hospitals in Wuhan **is not credible**, as it was obtained after reviewing a mere 92 possible cases between the 1st of October and 31st of December 2019 across these 266 hospitals.
- The WHO team was not allowed to review all the 92 cases and were only shown a few cases (Page & Hinshaw, 2021).
- As revealed in the SCMP (2020) leak, the numbers of cases show a bizarre jump on the 1st of January 2020, which is also reflected in contemporary CDC reports (News 39, 2020; China CDC, 2020).

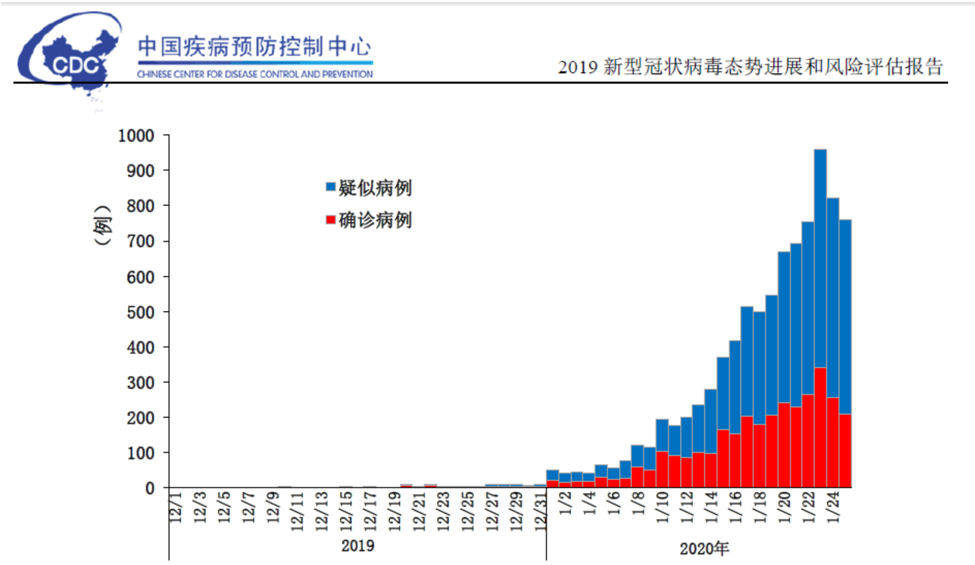
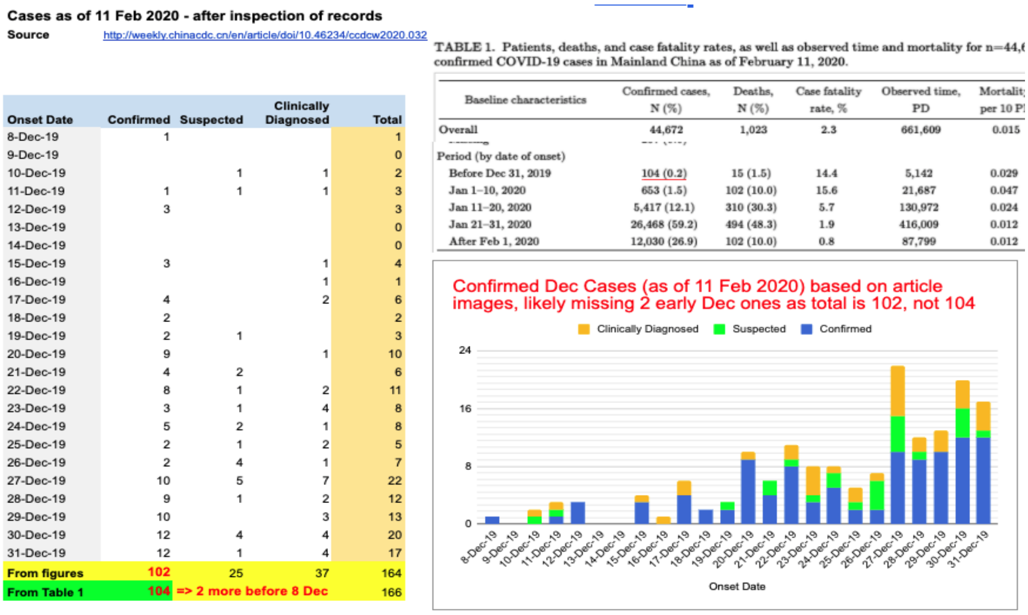


Figure 80: Bizarre clean jump in Covid-19 cases. Source: China CDC (2020)

If we discount this patently ridiculous clean jump in cases on January 1st 2020, we should instead take the average of the 266 cases before 31st December 2019 19 and the 381 cases from the January 1st 2020 to get a better estimate of the likely number of cases, around **320** confirmed cases with onset date in 2019.

As we have seen, there were likely 320 known confirmed cases for 2019 already identified by March 2020, as confirmed by the SCMP leak, which have been partially reflected in the Terms of Reference of the WHO report (WHO, 2021) with 124 cases confirmed in July 2020 but only disclosed in November) and the recent disclosure of 174 cases (100. confirmed + 74 diagnosed) (Demaneuf, 2020a; 2020b). There are many strange features in the reported cases numbers for 2019, for example the sudden clean jump of cases on January 1st 2020 (CDC, 2020). The CDC report of the 17th February 2020 shows two 2019 cases mysteriously missing from its graph (case number 104 in Table 1 and 102 in the graph). These two missing cases could be those from the 5th and the 7th of December 2019 from the January 26th 2020 CDC report (Demaneuf, 2020b).



Cases as of 11 Feb 2020 - after inspection of records
Source http://weekly.chinacdc.cn/en/article/doi/10.46234/ccdcw2020.032

Onset Date	Confirmed	Suspected	Clinically Diagnosed	Total
8-Dec-19	1			1
9-Dec-19				0
10-Dec-19		1	1	2
11-Dec-19	1	1	1	3
12-Dec-19	3			3
13-Dec-19				0
14-Dec-19				0
15-Dec-19	3		1	4
16-Dec-19			1	1
17-Dec-19	4		2	6
18-Dec-19	2			2
19-Dec-19	2	1		3
20-Dec-19	9		1	10
21-Dec-19	4	2		6
22-Dec-19	8	1	2	11
23-Dec-19	3	1	4	8
24-Dec-19	5	2	1	8
25-Dec-19	2	1	2	5
26-Dec-19	2	4	1	7
27-Dec-19	10	5	7	22
28-Dec-19	9	1	2	12
29-Dec-19	10		3	13
30-Dec-19	12	4	4	20
31-Dec-19	12	1	4	17
From figures	102	25	37	164
From Table 1	104	=> 2 more before 8 Dec		166

TABLE 1. Patients, deaths, and case fatality rates, as well as observed time and mortality for n=44,6
confirmed COVID-19 cases in Mainland China as of February 11, 2020.

Baseline characteristics	Confirmed cases, N (%)	Deaths, N (%)	Case fatality rate, %	Observed time, PD	Mortalit per 10 P
Overall	44,672	1,023	2.3	661,609	0.015
Period (by date of onset)					
Before Dec 31, 2019	104 (0.2)	15 (1.5)	14.4	5,142	0.029
Jan 1–10, 2020	653 (1.5)	102 (10.0)	15.6	21,687	0.047
Jan 11–20, 2020	5,417 (12.1)	310 (30.3)	5.7	130,972	0.024
Jan 21–31, 2020	26,468 (59.2)	494 (48.3)	1.9	416,009	0.012
After Feb 1, 2020	12,030 (26.9)	102 (10.0)	0.8	87,799	0.012

Figure 81: Confirmed Cases Discrepancies. Source: Demaneuf (2020b)

A total of 320 cases in 2019 would imply at least 2000 coronavirus cases in 2019 if we take into account asymptomatic and mild symptomatic cases. Even a conservative estimate of 250 confirmed cases for December 2019 would imply 1,600 plus cases in 2019. This analysis was confirmed by Dr. Embarek in an interview on February 15th 2021 (NZ Herald, 2021) who said that the WHO team was informed of 174 December 2019 cases from Wuhan and its environs, with 100 laboratory confirmed cases and 74 clinically diagnosed cases.

Based on those numbers, he assessed that: “*The larger number of cases could mean the virus hit more than* ***1000*** *people in Wuhan within the month*” (Demaneuf, 2020c; CNN, 2021b).

> "*We haven't done any modelling of that since. But we know ... in big ballpark figures ... out of the infected population, about 15 per cent end up severe cases, and the vast majority are mild cases*" (NZ Herald, 2020)

He also confirmed that the discovery of the 13 virus strains could also signal it had been circulating long before the first case was picked up, as suggested by Professor Edward Holmes in an interview with CNN (2021b):

> "*As there was already genetic diversity in SARS-CoV-2 sequences sampled from Wuhan in December 2019,* ***it is likely that the virus was circulating for longer than that month alone****,"*

In fact, the large number of cases in December 2019 logically implies Covid-19 cases in November and October 2019. To conclude, it is important to note that with cases identified in December 2019, it is of course more than probable that transmission of SARS-COV-2 or its progenitor virus would have occurred in November 2019. With alleged cases in November (SCMP, 2020), it is similarly possible that asymptomatic transmission would have been taking place in October 2019. For an extremely detailed discussion of the anomalies surrounding suspected early cases of Covid-19 in Wuhan, see Demaneuf (2020a).

To conclude, the cover up initiated by the Chinese authorities was formalized with the CDC “gag order” on the 25th February 2020 which was published the day after the WHO mission left China (Document Cloud, 2021a). This was followed by the State Council gag-order of the 3rd of March 2020 which was closely coordinated with their propaganda initiative (Document Cloud, 2021b) and resulted in centralized control of research. As a result of this vicious attack by the Chinese State on academic and scientific transparency, it is clear that many Covid-19 cases in 2019 were deliberately covered up. It is fair to conclude that the most accurate figures can be found in the SCMP leak of official documents (Demaneuf, 2020).

23. CONCLUSION

In conclusion, SARS-CoV-2 was quite likely spreading in Wuhan in October and most likely was already well spread by end of November 2019, on the basis of these facts and claims:

- Satellite data and traffic analysis of Wuhan Hospitals in autumn 2019.
- Social media search trend terms from the Baidu search engine.
- Reports of military athletes with Covid-19 like symptoms from multiple nations.
- Alleged Correlation between number of returning military athletes and covid-19 cases.
- Positive IgM and IgG antibody results from 6 Spanish military athletes.
- The alleged November warning by US intelligence to NATO and Israel.
- Claimed early knowledge by Thermogenesis in November 2019.
- Claimed early knowledge by Scientists, Diplomats and Dissidents.
- Anecdotal reports from an interview with an African PhD student in Wuhan.
- Leaked and documented hospital data from Wuhan hospitals.
- Positive sera antibody results from Italy dating back to November 2019.
- The 9 November 2019 cases reported by CCDC with claimed “patient zero” on Nov 17th.
- Serological evidence and the WHO Investigation.
- Chinese Cover Up and Gag Orders.
- Early Mutation Analysis of SARS-COV-2 and phylogenetic evidence.
- SARS-COV-2 progenitor mutation analysis.
- Case number anomalies and possible manipulations in the official numbers.
- How the number of December 2019 cases support a cryptic spread in November 2019.

In light of the above facts, an integral component of any proposed forensic investigation would be to identify the earliest infections during the outbreak. It is crucial to clarify via stored blood samples and wastewater samples if SARS-COV-2 or its progenitor virus were circulating in Wuhan and Hubei in the autumn of 2019. Furthermore, given the documented evidence of gag orders and threats against local Chinese doctors and scientists, any anecdotal accounts from foreign scientists, doctors, entrepreneurs or military athletes of an early outbreak before December 2019 need to be carefully investigated.

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