Limeng Yan wraps herself as holding the truths which are actually not originated from herself at all

Let's remember the real pioneers, heroes and whistleblowers

Author: Vincent Hung

COVID19, which has been the causal agent of the global pandemic since late 2019, displays several unnatural characteristics, including the Furin cleavage site and the unusual similarity to the Zhoushan bat virus ZC45/ZXC21. Besides, several lines of evidence have indicated RaTG13 is a possible manipulated fake virus, not as to mention the possible fake pangolin virus Pan-SL-CoV/GD. These important findings are all included in Limeng Yan's so called scientific reports (since September 14, 2020). However, when we take a deeper look at these findings in a chronological order, we found all of these compelling evidence and insightful findings were actually not first found, proposed or done by Limeng Yan at all. Limeng Yan's reports are more of reviews rather than scientific reports based on her own knowledge. Here I sorted up the timelines and recovered who were the first persons to find out these key evidence and results, who were the real heroes, pioneers and whistle blowers.

Is Limeng Yan the first person who found the intimate relationships between Zhoushan Bat virus and COVID19? Definitely not.

Let's first look at who is the first to expose the close evolutionary relationship between Zhoushan Bat virus ZC45/ZXC21 and COVID19. Yongzhen Zhang from Fudan University in Shanghai wrote up a paper entitled "A new coronavirus associated with human respiratory disease in China" and submitted it to *Nature* at January 7, 2020, which is the earliest traceable literature source[1] (Fig. 1). Yongzhen Zhang's paper first revealed the close evolutionary relationship between Zhoushan bat virus ZC45/ZXC21 and COVID19[1] (Fig 2). As it takes at least several days to finish writing a paper, Zhang's team might know this truth even earlier than January 7, 2020. According to Gene Bank's records, Yongzhen Zhang uploaded the first version of COVID19 genome sequence at January 5, 2020 (https://www.ncbi.nlm.nih.gov/nuccore/MN908947.1), which might be released to public (all over the world) around January 10, 2020. From then on, scientists and curious people all over the world could start to use the genome to conduct bioinformatic analysis. The simplest analysis was just putting the nucleotides sequence of COVID19 into a BLAST program in NCBI to search for the closest relatives. I am sure most of them would find ZC45/ZXC21 were the top two hits shown in the BLAST results, as what I did by myself (Fig 3). Also Shan Gao from Nankai University in China sorted up a time line showing that in early time of the pandemic, various people undertook different ways to warn the public about the pandemic (Fig 4):

12-30-2019: Jinsong Shi warned him through personal Wechat the possible explode of the virus.

(Please note: also at 12-30-2019, Dr. Wenliang Li warned the public through Wechat of a new SARS outbreak.)

12-31-2019: Shan Gao tried to make a warning about the pandemic in the famous Chinese website Zhihu (知乎) but failed due to censorship.

1-3-2020: Shan Gao successfully made a warning about the possible explode of the virus in the famous Chinese website Zhihu and got prepared for the successive research need.

(Please note: also at 1-3-2020, Dr. Wenliang Li was punished by the local police due to his warning to public through Wechat before this date.)

1-10-2020: The first COVID19 genome sequence was released by Chinese scientists.

1-13-2020: Shan Gao finished the bioinformatic analysis of the public available COVID19 genome sequence, got important findings, and started to prepare manuscript.

Based on the above-mentioned efforts by the pioneering Chinese whistle blowers, Limeng Yan neither was the first one to recover the Zhoushan bat virus's intimate relationship with COVID19, nor was she among the first ones to warn the Chinese folks and the world of the severity of the pandemic.

Article

A new coronavirus associated with human respiratory disease in China

https://doi.org/10.1038/s41586-020-2008-3

Received: 7 January 2020

Accepted: 28 January 2020

Published online: 3 February 2020

Open access

Check for updates

Fan Wu[1,7], Su Zhao[2,7], Bin Yu[3,7], Yan-Mei Chen[1,7], Wen Wang[4,7], Zhi-Gang Song[1,7], Yi Hu[2,7], Zhao-Wu Tao[2], Jun-Hua Tian[3], Yuan-Yuan Pei[1], Ming-Li Yuan[2], Yu-Ling Zhang[1], Fa-Hui Dai[1], Yi Liu[1], Qi-Min Wang[1], Jiao-Jiao Zheng[1], Lin Xu[1], Edward C. Holmes[1,5] & Yong-Zhen Zhang[1,4,6] ✉

Emerging infectious diseases, such as severe acute respiratory syndrome (SARS) and Zika virus disease, present a major threat to public health[1–3]. Despite intense research efforts, how, when and where new diseases appear are still a source of considerable uncertainty. A severe respiratory disease was recently reported in Wuhan, Hubei

Fig. 1 Screen shot of Yongzhen Zhang's *Nature* paper showing the publishing records which indicate Yongzhen Zhang submitted the manuscript to *Nature* at January 7, 2020[1].

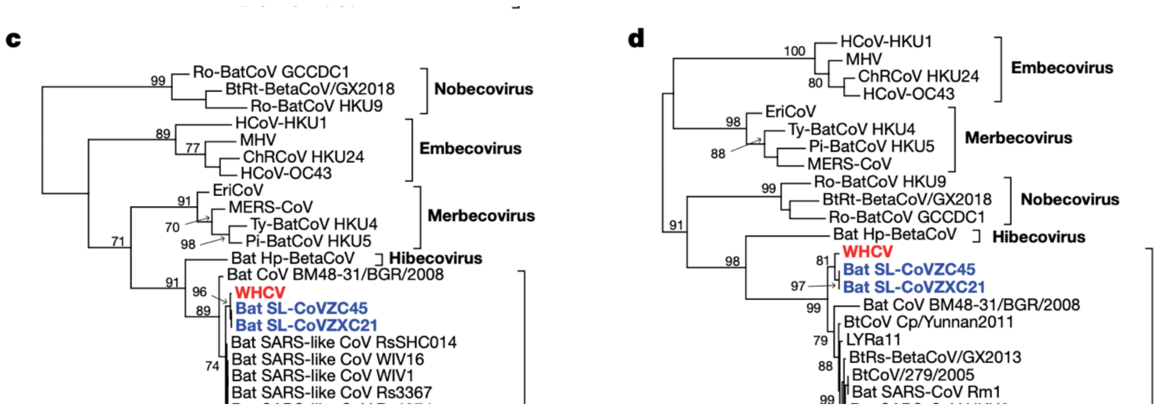
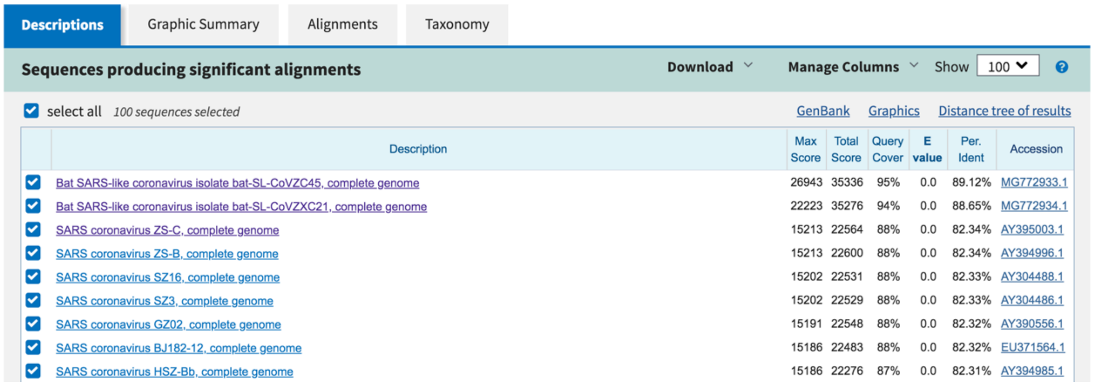


Fig. 2 Screen shot of Yongzhen Zhang's Nature paper showing phylogenetic trees which first revealed COVID19 was evolutionarily close to Zhoushan bat virus ZC45/ZXC21[1].



Sequences producing significant alignments

☑ select all *100 sequences selected*

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☑	Bat SARS-like coronavirus isolate bat-SL-CoVZC45, complete genome	26943	35336	95%	0.0	89.12%	MG772933.1
☑	Bat SARS-like coronavirus isolate bat-SL-CoVZXC21, complete genome	22223	35276	94%	0.0	88.65%	MG772934.1
☑	SARS coronavirus ZS-C, complete genome	15213	22564	88%	0.0	82.34%	AY395003.1
☑	SARS coronavirus ZS-B, complete genome	15213	22600	88%	0.0	82.34%	AY394996.1
☑	SARS coronavirus SZ16, complete genome	15202	22531	88%	0.0	82.33%	AY304488.1
☑	SARS coronavirus SZ3, complete genome	15202	22529	88%	0.0	82.33%	AY304486.1
☑	SARS coronavirus GZ02, complete genome	15191	22548	88%	0.0	82.32%	AY390556.1
☑	SARS coronavirus BJ182-12, complete genome	15186	22483	88%	0.0	82.32%	EU371564.1
☑	SARS coronavirus HSZ-Bb, complete genome	15186	22276	87%	0.0	82.31%	AY394985.1

Fig. 3 BLAST result using the COVID19 genome sequence as a bait in the middle of January, 2020 shows ZC45/ZXC21 as the top two hits.

2019年12月30日，接到施劲松微信，武汉发现冠状病毒，根据医院方面的信息，判定可能爆发；

2019年12月31日，武汉卫健委发布疫情通告，患病27人，重症7人，大约四分之一，确认爆发。

2019年12月31日，知乎发出预警，一直审核不过

2019年12月31日，知乎发出预警，一直审核不过

2020年1月3日，知乎发出预警成功，同时联系各位老师准备好数据，等待疫情爆发后随时跟进。

2020年1月10日，在国际压力下，中国公开基因组数据；

2020年1月13日，完成全部基因组分析，发现2个重大突变，开始写文章；

2020年1月21日，生物信息学期刊上线《武汉2019冠状病毒基因组的生物信息学分析》；

2020年1月21日，在researchgate网站公开论文《武汉2019冠状病毒S蛋白可能存在Furin蛋白酶切位点》；

(PDF) A furin cleavage site was discovered in the S protein of the Wuhan 2019 novel coronavirus

2020年1月21日，同时在知乎网站公开论文《武汉2019冠状病毒S蛋白可能存在Furin蛋白酶切位点》；

2020年1月27日，提交论文《武汉2019冠状病毒S蛋白可能存在Furin蛋白酶切位点》到中科院预印本，成功；

Fig. 4 Screen shot from Zhihu (https://www.zhihu.com/question/372527344). Time line sorted by Shan Gao showing multiple peoples used various ways including personal communications, posting warnings on the public media Zhihu, virus genome data analysis and research article writing to warn the public and the world the truths of COVID19.

Let's move on to the Furin cleavage site. Is Limeng Yan the first person who found it? The answer is definitely no. It is Shan Gao from Nankai University in China who found it first.

According to Shan Gao' records in Zhihu, he finished the COVID19 genome sequence analysis at January 13, 2020 and found two important mutational sites, one of which was the Furin cleavage site (Fig 4). Later at January 21, 2020 he posted his research article entitled "A furin cleavage site was discovered in the S protein of the Wuhan 2019 novel coronavirus" at research gate website and at the same time posted "武汉2019冠状病毒S蛋白可能存在Furin蛋白酶切位点" at the Zhihu website, which was later submitted to ChinaXiv as a preprint at January 27, 2020[2] (Fig. 4

and Fig. 5).

A.

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GQ153539      VNVFQTQAGCLIGAEHVNASYECDIPIGAGICASY--HTASV--LRSTGQKSIVAYTMSLGAENSIAYANNSIAIPT
GQ153540      VNVFQTQAGCLIGAEHVNASYECDIPIGAGICASY--HTASV--LRSTGQKSIVAYTMSLGAENSIAYANNSIAIPT
GQ153542      VNVFQTQAGCLIGAEHVNASYECDIPIGAGICASY--HTASV--LRSTGQKSIVAYTMSLGAENSIAYANNSIAIPT
JX993987      INVFQTQAGCLIGAEHVNASYECDIPIGAGICASY--HTASV--LRSTGQKSIVAYTMSLGAENSIAYANNSIAIPT
DQ071615      TNVFQTQAGCLIGAEHVNASYECDIPIGAGICASY--HTAST--LRSVGQKSIVAYTMSLGAENSIAYANNSIAIPT
DQ412043      VNVFQTQAGCLIGAEHVNASYECDIPIGAGICASY--HTASV--LRSTGQKSIVAYTMSLGAENSIAYANNSIAIPT
DQ412042      PYVFQTQAGCLIGAEHVNASYQCDIPIGAGICASY--HTASH--LRSTGQKSIVAYTMSLGAENSVAYANNSIAIPT
JX993988      VNVFQTQAGCLIGAEHVNASYECDIPIGAGICASY--HTASL--LRNTGQKSIVAYTMSLGAENSIAYANNSIAIPT
AY515512      NNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASY--HTVSS--LRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPT
AY572034      NNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASY--HTVSS--LRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPT
AY274119      NNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASY--HTVSL--LRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPT
MG772934      TSVFQTQAGCLIGAEHVNASYECDIPIGAGICASY--HTASI--LRSTGQKAIVAYTMSLGAENSIAYANNSIAIPT
MN908947      SNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPT
Secondary
Structure:    CCCCCCCCCEEECCCCCCCCCCCCCCCCCCEEECCCCCCCCCCCCCCCCCEEEEEECCCCCCCCCCCCCCCCEEEECCC
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B.

```
AY274119 AACAATGTATTCCAGACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATGTCGACACTTCTTATGAGTGCGACATTCCT
            ||||| || || || |  ||||||||| | ||||| ||||| |||||| |||  || |||||||| ||||| ||
MN908947 TCTAATGTTTTTCAAACACGTGCAGGCTGTTTAATAGGGGCTGAACATGTCAACAACTCATATGAGTGTGACATACCC

AY274119 ATTGGAGCTGGCATTTGTGCTAGTTACCATAC------AGTTTCTTTA------TTACGTAGTACTAGCCAAA-AATC
         ||||| || || || || |||||||| || ||         ||||           |||||||  |||| |   ||||
MN908947 ATTGGTGCAGGTATATGCGCTAGTTATCAGACTCAGACTAATTCTCCTCGGCGGGCACGTAGTG-TAGCTAGTCAATC

AY274119 TATTGTGGCTTATACTATGTCTTTAGGTGCTGATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTACT
          ||  | || || ||||||||  | ||||| || | |||| ||||||||||||||||| | ||||| ||||| ||
MN908947 CATCATTGCCTACACTATGTCACTTGGTGCAGAAAATTCAGTTGCTTACTCTAATAACTCTATTGCCATACCCACA
```

图 1. 2019 新型冠状病毒 S 蛋白可能存在 Furin 蛋白酶切位点

Fig1. A furin cleavage site was discovered in the S protein of the 2019 novel coronavirus

Fig. 5 Screen shot from Shan Gao's paper showing amino acids and nucleotides sequence alignment to demonstrate the existence of the Furin cleavage site[2].

It is noteworthy that a French group published "The spike glycoprotein of the new coronavirus 2019-nCoV contains a furin-like cleavage site absent in CoV of the same clade" at Feburary 20, 2020, exposing the same Furin site in COVID19. So Limeng Yan definitely was not the first one to discover the Furin cleavage site.

Let's move on to the unnatural RaTG13 and pangolin coronavirus (Pan-SL-CoV/GD). Is Limeng Yan the first one who found the unnatural characteristics of RaTG13 and pangolin virus? The answer is no.

As early as January 27, 2020, a group from Greece published "Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event", which proposed that it was not likely that COVID19 was naturally resulted from the recombination event between RaTG13 and other Bat SARS like viruses[3] (Fig 6).

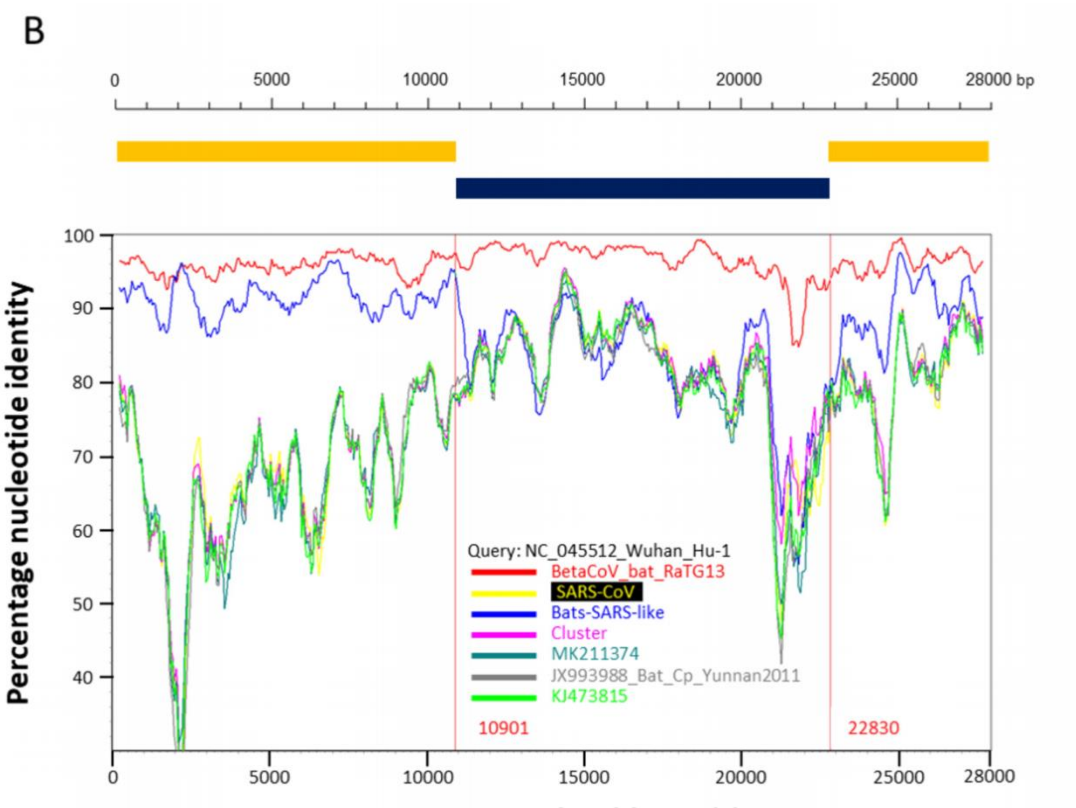


Fig. 6 Screenshot from “Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event” showing the Simplot of 2019-nCoV (NC_045512_Wuhan_Hu-1) against sequences of the listed viruses[3].

Another very compelling evidence which indicates RaTG13 is fake is the unnatural synonymous mutations/non-synonymous mutations statistical analysis results of the Spike encoding gene of RaTG13 when compared to that of COVID19[4] (Fig 7). This analysis was first published at May, 2020 and was done by the owner of the personal blog “Nerd Has Power”, who is also the second ranking coauthor of Limeng Yan’s reports.

In the Author’s note and acknowledgement part, the blogger wrote that “The first addition is the analysis of synonymous/non-synonymous mutations of Spike-encoding gene of RaTG13. This was first identified and analyzed by Elannor D. Allens, who described this finding in a comment under my earlier article. Using the synonymous/nonsynonymous ratio between ZC45 and ZXC21 as an example of natural evolution was suggested by 冠军的亲爹.”[4] So, from this part we can conclude that the synonymous mutations and non-synonymous mutations analysis were actually done by three authors including the blogger Shu Kang, Elannor D. Allens and 冠军的亲爹. Obviously, this is not first proposed and done by Limeng Yan.

For the analysis of E protein mutation tolerance during the pandemic, the blogger wrote “The second addition is the analysis of recently observed mutations in the viral E proteins. This was first observed and analyzed by John F. Signus, who also posted his findings in a series of comments. The writing here owes greatly to their brilliance and insights."[4]

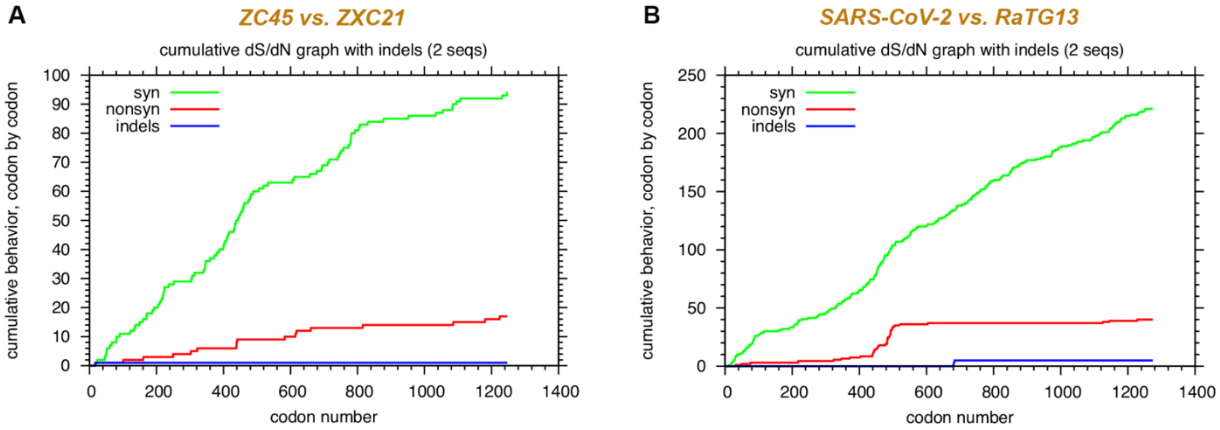
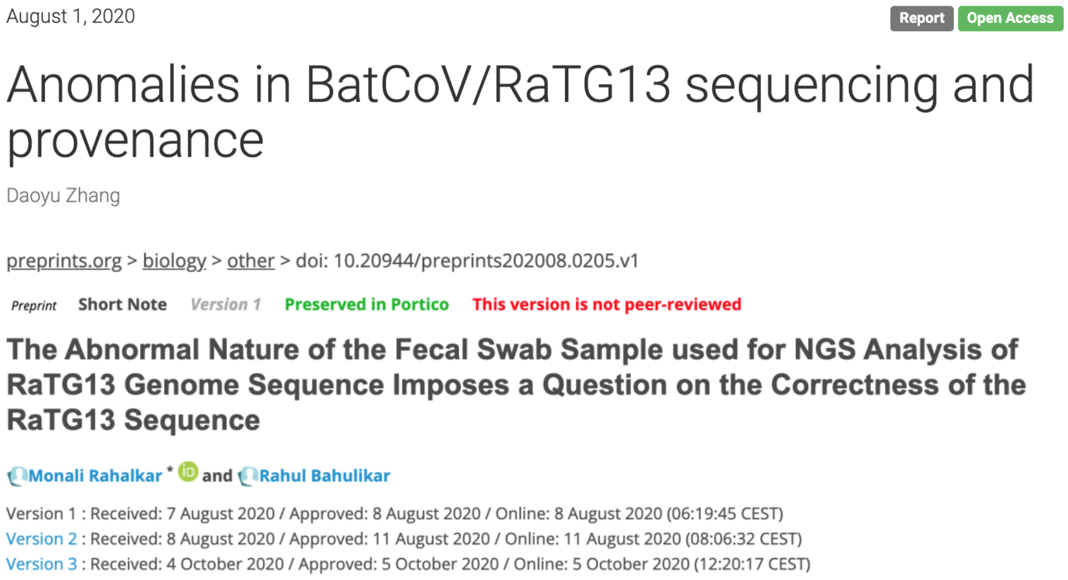


Fig 7. Screen shot from "Nerd has Power" blog (https://nerdhaspower.weebly.com/ratg13-is-fake.html) showing the synonymous mutations and non-synonymous mutation analysis in two groups: ZC45/ZXC21 and SARS-COV-2 (COVID19)/RaTG13.

Another very convincing evidence are combined efforts from Daoyu Zhang[5] (published at Augst 1, 2020) and Monali C. Rahalkar & Rahul A. Bahulikar[6] (published at Augst 7, 2020) (Fig 8). Through the metagenomics analysis (basically analyzing the species distribution or origins of the sequencing reads) of the next generation sequencing results of RaTG13, they found only less than 1% reads came from bacteria, which was not usual, as a fecal sample should generate at least 60-70% or higher percentage of bacterial reads[5,6].



August 1, 2020

Anomalies in BatCoV/RaTG13 sequencing and provenance

Daoyu Zhang

preprints.org > biology > other > doi: 10.20944/preprints202008.0205.v1

Preprint Short Note Version 1 Preserved in Portico This version is not peer-reviewed

The Abnormal Nature of the Fecal Swab Sample used for NGS Analysis of RaTG13 Genome Sequence Imposes a Question on the Correctness of the RaTG13 Sequence

Monali Rahalkar * and Rahul Bahulikar

Version 1 : Received: 7 August 2020 / Approved: 8 August 2020 / Online: 8 August 2020 (06:19:45 CEST)
Version 2 : Received: 8 August 2020 / Approved: 11 August 2020 / Online: 11 August 2020 (08:06:32 CEST)
Version 3 : Received: 4 October 2020 / Approved: 5 October 2020 / Online: 5 October 2020 (12:20:17 CEST)

Fig. 8 Screen shots of the headings of Daoyu's and Monali C. Rahalkar & Rahul A. Bahulikar's paper[5,6].

By applying the same metagenomic analysis (basically analyzing the species distribution or origins of the sequencing reads) of the pangolin virus' NGS results, at June 8, 2020, Daoyu found that the pangolin samples may be heavily contaminated by human samples[7], as when they found there were reads from pangolin coronavirus in the pangolin samples, they could also detect reads from human, if there were no human reads, they could not detect reads from pangolin coronavirus (Fig 9). Part 2 of Limeng Yan's second reports is largely based on this pioneer paper.

June 8, 2020

Report Open Access

The Pan-SL-CoV/GD sequences may be from contamination.

Daoyu Zhang

Fig. 9 Screen shots of the headings of Daoyu's paper[7].

So from the time line sorting shown above, obviously Limeng Yan was not the first and also has done nothing with revealing truth of the fake RaTG13 and pangolin virus.

The last thing is the unusual switching/insertion of SARS Spike Receptor Binding Motif (RBM) into COVID19. Has Limeng Yan found this result? The answer is no.

At March 15, 2020, this analysis was posted on Nerd Has Power (https://nerdhaspower.weebly.com/) by the owner of the personal blog who is also a coauthor of Limeng Yan's reports. He analyzed SARS-Spike/ACE2 protein complex 3D structure and performed multiple sequence analysis and found that the S1 part of Zhoushan Bat virus was exceptionally similar to that of COVID19 except the Receptor Binding Motif. Interestingly, the RBM region showed high similarity to SARS RBM except for a few amino acids mutations that were actually not essential for ACE2 binding (Fig 10). This was confirmed by his structural based analysis[8].

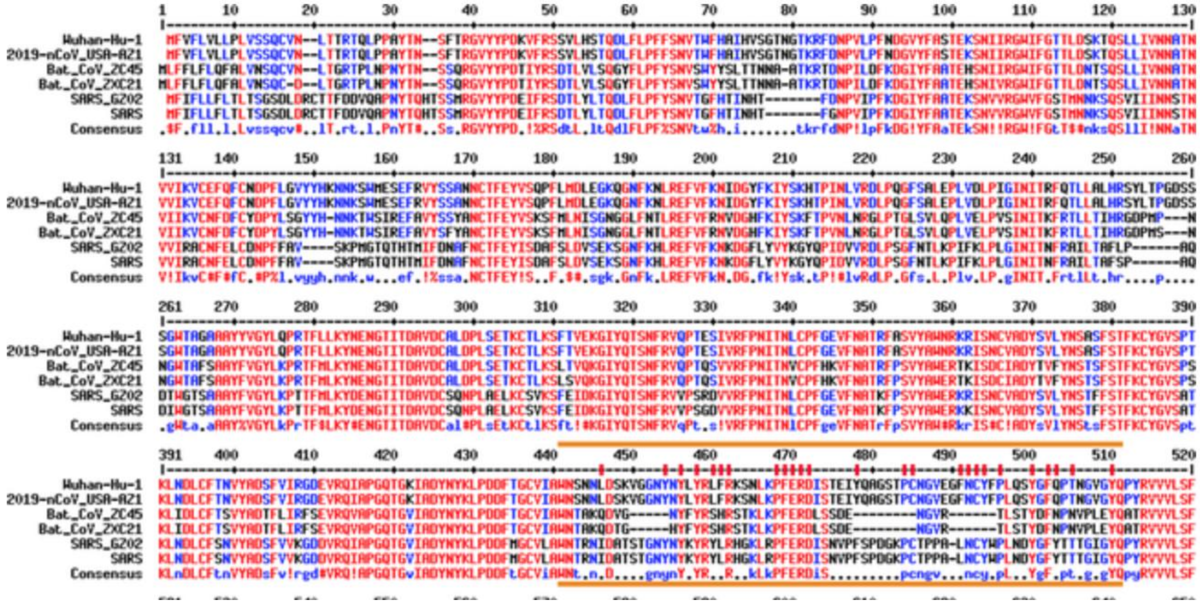


Fig 10. Screenshot from from Nerd has Power blog (https://nerdhaspower.weebly.com/) showing multiple sequence alignment of COVID19, SARS and ZX45/ZXC21[8].

Although Limeng Yan has boasted of herself holding the truths, from my timeline analysis in a chronological way to figure out who were the first contributors to tell the real truths, I can not find her.

Dr. Wenliang Li sacrificed his life warning the public of the outbreak of COVID, when he knew the truth.

Yongzhen Zhang and Shan Gao posted warning in website Zhihu and wrote scientific paper when they knew the truth.

A nurse in Heilongjiang Province wrote an Email to Fauci, when she knew the truth.

Limeng Yan wraps herself as holding the truths and brags about her “Yan reports”. But actually, those truths came from the rarely mentioned real pioneers and heroes as I show in this manuscript.

Let’s remember the real pioneers in this pandemic and don’t let others conceal or steal their contributions.

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