New Results

25 comments

Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin

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doi: https://doi.org/10.1101/2020.01.22.914952

Now published in *Nature* doi: 10.1038/s41586-020-2012-7

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Abstract

Since the SARS outbreak 18 years ago, a large number of severe acute respiratory syndrome related coronaviruses (SARSr-CoV) have been discovered in their natural reservoir host, bats. Previous studies indicated that some of those bat SARSr-CoVs have the potential to infect humans. Here we report the identification and characterization of a novel coronavirus (nCoV-2019) which caused an epidemic of acute respiratory syndrome in humans, in Wuhan, China. The epidemic, started from December 12th, 2019, has caused 198 laboratory confirmed infections with three fatal cases by January 20th, 2020. Full-length genome sequences were obtained from five patients at the early stage of the outbreak. They are almost identical to each other and share 79.5% sequence identify to SARS-CoV. Furthermore, it was found that nCoV-2019 is 96% identical at the whole genome level to a bat coronavirus. The pairwise protein sequence analysis of seven conserved non-structural proteins show that this virus belongs to the species of SARSr-CoV. The nCoV-2019 virus was then isolated from the bronchoalveolar lavage fluid of a critically ill patient, which can be neutralized by sera from several patients. Importantly, we have confirmed that this novel CoV uses the same cell entry receptor, ACE2, as SARS-CoV.

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Alpha6

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Jacob Marley • a month ago

Has the number of deaths overall, and from "pneumonia disease" in Wuhan (or elsewhere) per head of population increased since 12 December 2019, compared to the same period in previous years?

If not, how can COVID-19 be a new factor, or a relevant factor at all?

If so, how does this paper show that COVID-19 is the cause of disease or death when it states:

"we could no longer detect virus-positive samples in oral swabs, anal swabs and blood samples taken from these patients during the second sampling"

and

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* The Clinical Trials and Epidemiology subject categories are now closed to new submissions following the completion of bioRxiv's clinical research pilot project and launch of the dedicated health sciences server medRxiv (submit.medrxiv.org). New papers that report results of Clinical Trials must now be submitted to medRxiv. Most new Epidemiology papers also should be submitted to medRxiv, but if a paper contains no health-related information, authors may choose to submit it to another bioRxiv subject category (e.g., Genetics or Microbiology).

The paper states:

"we tested samples from 5 of the 7 virus-positive patients around 20 days after disease onset for the presence of viral antibodies (Extended Data Tables 1, 2). All patient samples —but not samples from healthy individuals—were strongly positive for viral IgG"

- but antibodies as referred to only indicate that blood proteins (antibodies) were produced in response to and counteracting a specific antigen, i.e. that the body has counteracted the antigen - a result that consequently does not indicate serious disease or death.

and

The cited "Clear cytopathogenic effects were observed in cells after incubation for three days" does not specify what these cell-damaging effects were, whether they were serious or irreversible or permanent.

Doesn't the presence of antibodies suggest they weren't?

Don't most symptoms of all mild illnesses, such as the common cold, create some degree of temporary cytopathogenic (cell-damaging) effects?

and

With regard to "qPCR analysis showed that the viral load increased" isn't there a problem here that PCR can not show 'viral load' i.e. actual amounts of a virus, because PCR artificially amplifies or multiplies the viral particle/s it finds, but cannot determine the total amount of viruses ('viral load') per sample?

Isn't it the case that PCR tests can detect genetic sequences that are from viruses, or theorised to be so, but not viruses themselves?

and

This study does not state that it has established the cause of the relevant acute respiratory syndrome in China and elsewhere, only that there is 'evidence of an association' between the disease and COVID-19, and that it is 'likely' to be the cause:
"The study provides a detailed report on 2019-nCoV, the likely aetiological agent responsible for the ongoing epidemic of acute respiratory syndrome in China and other countries. Virus-specific nucleotide-positive and viral-protein seroconversion was observed in all patients tested and provides evidence of an association between the disease and the presence of this virus."

and

The paper plainly states that "The association between 2019-nCoV and the disease has not been verified by animal experiments to fulfil the Koch's postulates to establish a causative relationship between a microorganism and a disease."

and

"We do not yet know the transmission routine of this virus among hosts."

and

The paper also remarkably states that:

"No statistical methods were used to predetermine sample size.
The experiments were not randomized and the investigators were not blinded to allocation during experiments and outcome assessment."

(!)

Isn't this paper the basis upon which all concern and activity about COVID-19 is based?

Science, anyone?

1 ^ | v • Reply • Share ›

PHIL D • a month ago

How can it be ensured when and where these folks collected these samples and from what sources?

1 ^ | v • Reply • Share ›

Aaron • 2 months ago
The article is now peer reviewed and published - why not update?
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2 | • Reply • Share ›

jean-claude perez • 2 months ago
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Jubin Rodriguez • 2 months ago
Quick questions: a) How many million PE reads were generated in total per sample and what percentage of these raw reads were represented by human DNA? b) What is the virus database that the authors used in their analysis? In case its an in-house database, I'm curious to know if it is based on sequence info available on NCBI and how it was built? c) I'm also curious to know if the authors tried any of the metaviromics tools out there (as opposed to read-mapping against a database of known viruses) so as to detect this novel corona virus? My guess is that most metaviromics tools (for e.g., FastViromeExplorer, virMine) may miss this virus.
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jean-claude perez • 3 months ago • edited
Please find here an updated release including 2 releases of wuhan coronavirus génome.

Using the following theoretical numerical approach of génomes data (pdf), I proove évidence of long range numerical standing waves structuring DNA genomics séquences:

https://www.google.com/url?...

THEN,
I briefly analyzed the standing waves of 7 SARS genomes ranging between 2003 and Wuhan 2020:
There is an evolution increasingly directed towards Fibonacci waves, as follows:

Fibonacci Wave Genomes:
Sars2003. No. 5
Sars2004. No. 5
Sars2004b. No. 5
Sars2015. 5 8. 13
Sars2017. 5 8. 13
Wuhan2020old 5 8 13 21
Wuhan 2020. 5 8. 13. 21
Where 5 8 13 21 are Fibonacci numbers numerical standing waves.
That is a formal proof of an évolution increasing global structure of SARS whole genomes, probably linked with génome intégrity and coherence and, probably pathogeneciity.
3 | • Reply • Share ›

Yen Shu Chen • 3 months ago
The authors did not share (no GenBank/GISAID accession number are provided) the genome sequence of the critical bat-CoV that represents a close relative to human 2019-nCoV.
No way to access/reproduce/further use their result. Do scientific journals accept such practice?
2 | 3 • Reply • Share ›

Xiang Chen ↗ Yen Shu Chen • 3 months ago
Read the full text. They have deposited it to GISAID.
| • Reply • Share ›

Prof.Fan ↗ Yen Shu Chen • 3 months ago
This is not a journal, this is a preprint. Also it is not an obligation to publish the sequence before patenting in the biology community.
| 7 • Reply • Share ›

lycophidion Prof.Fan • 3 months ago

Nevertheless, given the widely reported crisis of reproduceability in current biological research, and the disruptive and life threatening nature of this outbreak, it is incumbent on the researchers to share that data.

1 | • Reply • Share ›

Dirk Jochmans • 3 months ago

Great paper, a lot of info on the nCoV and the first patients. Thanks!

3 | 1 • Reply • Share ›