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**Sent:** Thur 2/13/2020 3:26:25 AM (UTC-05:00)  
**Subject:** virus name

[A unique and unified name is needed for the novel coronavirus from Wuhan SJ\\_clean.docx](#)

Dear Ralph,

We heard that the 2019-nCoV was renamed as SARS-CoV-2. We had a fierce discussion among Chinese virologists. We have some comments on this name, I'm wondering if the CoV study group would consider a revision.

I attached the comments from me and my Chinese colleague.

Best regards,  
Zhengli,

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**A unique and unified name is needed for the novel coronavirus identified from Wuhan**

An outbreak of unusual pneumonia of unknown cause in Wuhan, China was first reported in December, 2019. By 5 January, 2020, Chinese scientists had quickly identified the causative agent as a new type of coronavirus (CoV) belonging to the *Betacoronavirus* genus of the *Coronaviridae* family that also includes severe acute respiratory syndrome (SARS)-CoV and Middle East respiratory syndrome (MERS)-CoV (Zhu et al., 2020; Zhou et al., 2020; Wu et al., 2020; Chen et al., 2020). On 12 January 2020, the World Health Organization (WHO) temporarily named the virus as **2019 novel coronavirus (2019-nCoV)** (WHO webpage). On 30 January, WHO recommended naming the disease as “2019-nCoV acute respiratory disease” (WHO webpage). On 8 February 2020, the China National Health Commission (CNHC) announced naming the disease as “**Novel Coronavirus Pneumonia**” (NCP) (CNHC webpage). On 11 February 2020, WHO renamed the disease as “**coronavirus disease 2019**” (COVID-19) (WHO webpage). On 7 February 2020, the Coronavirus Study Group (CSG) of the International Committee on Virus Taxonomy (ICTV) posted a manuscript at bioRxiv and suggested designating the novel coronavirus as “**severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)**” based on the phylogenetic analysis of related coronaviruses (Gorbalenya et al., 2020).

By 11 February 2020, the new coronavirus had caused more than 40,000 confirmed infections and more than 1000 deaths, mostly in mainland China, in spite of efforts by the Chinese government and its people to contain spread of the virus in past weeks. It goes without saying that the effects of the epidemic on all the aspects of Chinese life are devastating and, possibly, irreversible. Consequently, appropriately naming the virus and disease becomes a matter of importance to the Chinese people, in general, and virologists, in specific, and the issue has been fervently discussed and debated

among scientists with outcomes so far, as noted above. We fully agree that the new virus and SARS-CoV belong to the same virus species by classification. However, the consensus opinion of Chinese virologists is that none of the currently proposed names reflects the uniqueness and characteristics of the novel virus and that more consideration is needed for naming the virus. Based on the following reasons, we propose giving a unique and unified name to the new virus.

1. All proposed names are either too generic, or too similar, to previously well-known viruses, or contain an Arabic number. This makes it hard to remember or recognize, leading to a tendency among the general population and scientists alike to use a shorthand term such as “Wuhan coronavirus” or “Wuhan pneumonia”. This has, in fact, been the case since it was named as 2019-nCoV. This practice would, however, stigmatize and insult the people in Wuhan, who are still suffering from the outbreak.

2. The new virus has clinical, virological and epidemiological manifestations different from those of previously known coronaviruses, including SARS-CoV. Therefore, the name of the virus should be unique and characteristic to its identity. Phylogenetic analysis does show that the new virus and SARS-CoV, as well as many SARS-like-CoVs from bats and some intermediate hosts, belong to the same virus species (SARSr-CoV) (Guan et al., 2005; Ge et al., 2013; Zhou et al., 2020; Gorbalenya et al., 2020). Nonetheless, it is not appropriate to designate this new virus as SARS-CoV-2. First, if this new virus is named as SARS-CoV-2, then the previously known SARS-CoV should be renamed as SARS-CoV-1. This will lead bibliographic problems for the previous publications, and it is unnecessary. Second, the name SARS-CoV-2 does not reveal any apparent difference from SARS-CoV, thus misleading many into believing that it is just one type of SARS-CoV. This would, for example, lead many into thinking that the CFR of 2019-nCoV will increase to 10%, as it did for SARS, but this would cause worldwide panic and have a disastrous effect on the international economy. It might also be thought that a "SARS-CoV-2" epidemic will plateau by summer- time and be gone like the SARS virus. This may not be the case and may have adverse

effects on the implementation of the outbreak control activities.

3. The new virus is still evolving, and it is still too early to predict the outcome of the current outbreak. However, it is already clear that the infection of the new virus has diverse symptoms, from asymptomatic infection to severe pneumonia and even death. It has less case-fatality rate and higher transmissibility than SARS-CoV, indicating its clear difference from SARS-CoV. Again, therefore, it is not appropriate to designate the new virus as SARS-CoV-2 before we know more properties of the virus.

4. In consideration of the above reasoning and in view of the contagiousness and transmissibility of the new virus, we suggest proposing a unique and easy-to-use name for it, such as “**Transmissible acute respiratory coronavirus (TARS-CoV)**” (Jiang and Shi, 2020). Another choice is “**Human acute respiratory coronavirus (HARS-CoV)**”. In this way, the new coronavirus and SARS-CoV, as well as related bat SARS-like coronaviruses, would, together, comprise the biological species of SARS-CoV, which complies with the conventions of the classification and nomenclature of ICTV.

#### **Proposers:**

Zhengli Shi, Wuhan Institute of Virology, Chinese Academy of Sciences

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Wenjie Tan, China Center for Disease Control and Prevention

Yuelong Shu, Sun Yat-sen University, School of Public Health (Shenzhen)

Deyin Guo, Sun Yat-sen University School of Medicine

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**To:** 郭德银[guodeyin@mail.sysu.edu.cn]  
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**Sent:** Sat 2/15/2020 7:55:22 AM (UTC-05:00)  
**Subject:** Re: virus name

Dear Dr. Deyin Guo, dear colleagues,  
I am sorry to learn that I was not able to get my point across, which is that the name SARS-CoV-2 links this virus to other viruses (called SARS-CoVs or SARSr-CoVs) in this species including the prototype virus of the species rather than to the disease that once inspired the naming of this prototype virus nearly 20 years ago. The suffix -2 is used as a unique identifier and indicates that SARS-CoV-2 is yet ANOTHER (but closely related) virus in this species. I'd like to thank you for your comments because they indicate that we may need to explain our line of reasoning even more clearly when it comes to publishing a more advanced version of our manuscript.

As you again link virus classification and naming to specific diseases (as was unfortunately done quite frequently in the pre-genomic era) rather than to sequence relationships of the respective virus with previously identified viruses, I would like to ask you whether your reasoning implies that researchers describing all the other viruses in that species were wrong when they named the viruses they discovered? To my knowledge, the vast majority of these viruses has not been shown to cause a human disease called SARS and yet, they were called SARS coronaviruses or SARS-related coronaviruses in virtually all cases. I think it is accepted in the field that these viruses are genetically closely related but also differ in specific phenotypic aspects from one another, which is reflected (at the level of naming) by attaching pre- and suffixes to the (SARS-containing) virus name. When introducing the name SARS-CoV-2, the CSG followed the tradition established mainly by Chinese researchers to name viruses in this particular species.

With kind regards,

John Ziebuhr

—  
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Am 15.02.2020 um 07:32 schrieb 郭德银 <guodeyin@mail.sysu.edu.cn>:

Dear Dr. John and CSG members,

Thank you very much for your prompt reply and for your willingness to listen to us, the representatives of Chinese virologists in coronavirus studies.

After discussing with many members of the Chinese Society for Virology of Chinese Society for Microbiology, and the Sub-Society for Medical Virology of Chinese Medical Association, we still believe that SARS-CoV-2 is not the most appropriate name for 2019-nCoV.

You claimed that the CSG does not intend to make any reference to a specific disease (for example a severe respiratory disease in humans) when introducing yet another virus name derived from the term "SARS".

However, "SARS" is a disease name, and if the new virus is called SARS-CoV-2, it actually implies for SARS, especially for non-corona virologists and the public domain. In such sense, it is truly misleading. It is clear that there are significant differences in viral genome, transmissibility, and pathogenicity and pathogenesis of the diseases caused by 2019-nCoV and SARS-CoV. We are concerning about the name of a natural virus in one virus species, and we think that the natural virus should have its unique name to show some of its own properties. This is similar to the situation for Betacoronavirus 1, where the species includes several distinct natural viruses with their unique names, e.g. human OC43 and bovine coronavirus, and Alphacoronavirus, which includes distinct natural viruses like feline infectious peritonitis coronavirus, canine CoV and transmissible gastroenteritis coronavirus. It is not appropriate to use one disease-based virus' name (like SARS-CoV) to name all other natural viruses that belong to the same species but have very different properties.

To the best of our knowledge, none of the virologists from mainland of China attended the CSG's discussion on 2019-nCoV, and CSG had not consulted with virologists including the first discoverers of the virus and first describers of the disease from mainland of China before making the decision. It is our wish that the CSG can take our opinion into the consideration.

It appears to us (as from the News reports of Science and Nature) that the CSG and WHO did not consult with each other in naming the virus and the disease. It will be very confusing to use totally different or unrelated names for the virus and its disease. We hope that the CSG of ICTV, the WHO and the Chinese side can have a trilateral negotiation on the naming issues.

Because of these reasons, we still hope CSG being able to reconsider naming 2019-nCoV. Our suggestion is to name it as TARS-CoV, but not SARS-CoV-2.

Thank you very much for your help!

Sincerely yours,

Deyin Guo, on behalf of the group:

Zhengli Shi, Wuhan Institute of Virology, Chinese Academy of Sciences  
Shibo Jiang, Fudan University School of Medicine  
Wenjie Tan, China Center for Disease Control and Prevention  
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**Subject:** virus name

Dear Deyin, dear Zhengli, dear Shibo, dear colleagues,

Thank you very much for sharing your thoughts with me and other members of the CSG. Obviously, I (personally) cannot speak for other CSG members but would like to tell you and your colleagues that I am very grateful for your very thoughtful and balanced statement.

I am pleased that you agree with the study group's decision to assign this newly discovered coronavirus to the species *Severe acute respiratory syndrome-related coronavirus*. The scientific basis for the assignment and naming has been laid out in the paper we recently published in a manuscript submitted to the bioRxiv preprint server and, at this stage, I cannot add much to this. There is one key point, however, that I would like to stress again: In their decision on the virus name, the CSG did not intend to make any reference to a specific disease (for example a severe respiratory disease in humans) when introducing yet another virus name derived from the term "SARS". The universal use of "SARS(r)" in names of viruses in this species just serves to underline the close genetic relatedness of these viruses. A large proportion of viruses in this virus species have been identified in bats and other animals in China and a few other countries, and virtually all these viruses were named SARS or SARS-related coronaviruses – most of them not because of their association with a disease (called SARS) in humans but because of their close genetic relatedness with a previously described VIRUS (called SARS-CoV) and clearly NOT the DISEASE that this particular virus caused. This (and nothing else) was the reasoning behind the study group's decision to continue the naming tradition established by researchers studying animal and human viruses of this virus species.

In a slightly different context, I would like to point out that it is not within the remit of the CSG to decide on names for clinical manifestations, progression, transmissibility etc. of coronavirus-associated diseases. This lies within the responsibility of WHO. Obviously, Chinese clinicians involved in the clinical management of patients infected with SARS-CoV-2 would be in the best position to provide advise to WHO officials on that matter. On a more personal note (and outside my role as member of the ICTV and chair of the CSG), I feel that your suggestion to name the disease "Transmissible acute respiratory syndrome (TARS)" could be a very good starting point for discussions with WHO. In my opinion, the recently introduced disease name COVID-19 could be improved and I would encourage you to enter or renew discussions with WHO on this matter.

I very much hope that I was able to convince you that the CSG's decision on this particular virus name was made with the very best intentions and based purely on SCIENTIFIC judgement. Personally, I feel reassured by the positive response I have been receiving over the past few days from other colleagues, ICTV, NCBI and other players and believe that the CSG has made a decision that will facilitate future communication among virologists studying these viruses. As part of these efforts, the CSG also suggested a naming convention to be used for specific SARS-CoV-2 isolates (and other coronavirus isolates).

With many thanks and kind regards,

John Ziebuhr

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