
From: A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]
Sent: Thur 1/23/2020 10:26:22 AM (UTC-05:00)
To: john.ziebuhr@viro.med.uni-giessen.de[john.ziebuhr@viro.med.uni-giessen.de]; Baric, Ralph S[rbaric@email.unc.edu]; Sbak1@luc.edu[Sbak1@luc.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; bneuman@tamut.edu[bneuman@tamut.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]; christian.drosten@charite.de[christian.drosten@charite.de]
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear All,

While you are considering this timely request from John, here is the correct name of this species:

Severe acute respiratory syndrome-related coronavirus

it may NOT be abbreviated (unlike virus name)!

Best,

Sasha

From: John Ziebuhr [john.ziebuhr@viro.med.uni-giessen.de]
Sent: Thursday, January 23, 2020 4:21 PM
To: rbaric@email.unc.edu; Sbak1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Benjamin Neuman; Perlman, Stanley; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; Gorbalenya, A.E. (MSTAT)
Subject: Virus name, decision of the Coronaviridae Study Group

Dear All,

I would like to get your view (as members of the *Coronaviridae* Study Group) on the naming of the coronavirus causing the ongoing outbreak in Wuhan. Things are moving fast, so it would be good to get an agreement on this as soon as possible, ideally also with key WHO people involved once we have reached an agreement in the SG (similar to what we did with MERS in 2013, JVI paper).

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Regarding the phylogenetic position of the virus, it is clear that the virus is part of an existing species called *SARS-related coronavirus*. All other viruses/isolates in that species (irrespective of whether they were isolated from humans, bats or other animals) have "SARS" in their names (SARS-CoV XYZ, SARSr-CoV XYZ etc.). Thus, it would be more than justified to (also) have a reference to SARS in the name of this "new" virus.

My suggestion would be: hSARS-CoV 2019 (Human SARS coronavirus 2019).

Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back". The disease caused by the "new" virus may be very different from that caused by SARS-CoV. And it will be difficult to get the message across to the general public that closely related (even nearly identical) viruses may cause very different outcomes of disease (see vaccine strains etc.).

To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019).

Please let me know your views and get back to me as soon as possible.

Best regards,

John

Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen

Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: Leo Poon[lmpoon@hku.hk]
Sent: Thur 1/23/2020 10:38:51 AM (UTC-05:00)
To: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Baric, Ralph S[rbaric@email.unc.edu]; Sbak1@luc.edu[Sbak1@luc.edu]; Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Benjamin Neuman[bneuman@tamut.edu]; Perlman, Stanley[stanley-perlman@uiowa.edu]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]; Drosten, Christian[christian.drosten@charite.de]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Dear colleagues,

I agree this virus is technically a SL-CoV. But I am for the 2nd option, purely from the public health point of view. We don't want the public have any confusion between SARS and this new respiratory disease. This might create some misunderstands and miscommunications, which might end up with a even greater problem.

Cheers,

Leo

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: 23 January 2020 23:21
To: rbaric@email.unc.edu; Sbak1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Benjamin Neuman; Perlman, Stanley; lmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl
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E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: Benjamin Neuman[bneuman@tamut.edu]
Sent: Thur 1/23/2020 10:58:17 AM (UTC-05:00)
To: Perlman, Stanley[stanley-perlman@uiowa.edu]; Leo Poon[lmpoon@hku.hk]
Cc: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Baric, Ralph S[rbaric@email.unc.edu]; Sbak1@luc.edu[Sbak1@luc.edu]; Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]; Drosten, Christian[christian.drosten@charite.de]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]
Subject: Re: Virus name, decision of the Coronaviridae Study Group

I like WURS - it says "SARS-like, but not quite the same as SARS" succinctly - and, for what it is worth, I could see regular people, the news, etc, picking this up.

I think with a virus as talked-about as this, it makes sense to consider service to the wider audience outside the ICTV, if there is a way to do that that follows the rules and makes sense.

A good point also about trying to keep a lid on runaway fears by (correctly, in taxonomic terms) referencing SARS.

Benjamin Neuman
Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: Perlman, Stanley <stanley-perlman@uiowa.edu>
Sent: Thursday, January 23, 2020 9:51 AM
To: Leo Poon
Cc: Benjamin Neuman; John Ziebuhr; rbaric@email.unc.edu; Sbak1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; lmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl
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Stanley

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712

University of Iowa
Iowa City, IA 52242

On Jan 23, 2020, at 9:45 AM, Leo Poon <llmpoon@hku.hk> wrote:

Ben,

WHO doesn't want a virus named after a location any more.

Cheers,

Leo

From: Benjamin Neuman <bneuman@tamut.edu>

Sent: 23 January 2020 23:39

To: John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Perlman, Stanley; llmpoon@hku.hk; isola@cnb.csic.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl

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I think there might be push-back from the pathology side of our field on calling it a strain of SARS if the receptor is different, as appears to be the case from the divergent spike RBD.

I can live with either of those names proposed, if there is consensus.

What do you think of Human coronavirus-Wuhan 2019 (HCoV-Wuhan 2019), in the model of 229E, OC43, NL63 and HKU1?

Or perhaps abbreviate to HCoV-WU19?

Benjamin Neuman
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Fax: +49-641-9941209
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From: Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]
Sent: Thur 1/23/2020 11:12:15 AM (UTC-05:00)
To: Drosten, Christian[christian.drosten@charite.de]; Perlman, Stanley[stanley-perlman@uiowa.edu]
Cc: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Baric, Ralph S[rbaric@email.unc.edu]; Sbak1@luc.edu[Sbak1@luc.edu]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Benjamin Neuman[bneuman@tamut.edu]; llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]
Subject: RE: [ext] Virus name, decision of the Coronaviridae Study Group

I appreciate Stanley's point but there is no escaping from the fact that it belongs to the species sars related coronavirus. At present it is perceived by the public as something between SARS and MERS brought to us by snakes. Just adding 2019 to it may turn out to be confusing in the long run (should there be one) in case of separate subsequent introductions in coming years. Would it be an option to use numbers with location and year of isolation as per flu plus perhaps isolate identifier? (For example SARS CoV-2 Wuhan, 2019.

Best, Raoul

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: "Drosten, Christian" <christian.drosten@charite.de>
Date: 1/23/20 16:59 (GMT+01:00)
To: "Perlman, Stanley" <stanley-perlman@uiowa.edu>
Cc: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>, rbaric@email.unc.edu, Sbak1@luc.edu, "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>, b.haagmans@erasmusmc.nl, Benjamin Neuman <bneuman@tamut.edu>, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, A.E.Gorbalenya@lumc.nl
Subject: Re: [ext] Virus name, decision of the Coronaviridae Study Group

I have no good answer to this. John's suggestion of "Human SARS-CoV 2019" just tells what it is: another type of SARS-CoV. Like types of Enteroviruses species C, they can be more or less pathogenic depending on what type (=virus) they actually are. This includes the possibility of variable pathogenicity. I guess we have to explain this to the public outside taxonomy.

Christian

--

Professor Christian Drosten

Director, Institute of Virology

Scientific Director, Charité Global Health

Charité - Universitätsmedizin Berlin

Campus Charité Mitte

Chariteplatz 1

D-10117 Berlin

Germany

E-Mail: christian.drosten@charite.de

<https://virologie-ccm.charite.de/>

<https://globalhealth.charite.de/>

Von: "Perlman, Stanley" <stanley-perlman@uiowa.edu>

Datum: Donnerstag, 23. Januar 2020 um 16:53

An: Christian Drosten <christian.drosten@charite.de>

Cc: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>, "rbaric@email.unc.edu" <rbaric@email.unc.edu>, "Sbaker1@luc.edu" <Sbaker1@luc.edu>, "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, Benjamin Neuman <bneuman@tamut.edu>, "llmpoon@hkucc.hku.hk" <llmpoon@hkucc.hku.hk>, "isola@cnb.csic.es" <isola@cnb.csic.es>, "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>

Betreff: Re: [ext] Virus name, decision of the Coronaviridae Study Group

Christian,

This may be the correct nomenclature, but there is already widespread fear about this virus. If we decide to use this nomenclature in the long term, I wonder if there is something that we can do in the short term that would not contribute to this fear.

Stanley

Stanley Perlman, MD, Ph.D.

Professor

Depts of Microbiology and Immunology, and Pediatrics

BSB 3-712

University of Iowa

Iowa City, IA 52242

On Jan 23, 2020, at 9:48 AM, Drosten, Christian <christian.drosten@charite.de> wrote:

Dear All,

I favor some name that includes SARS-CoV. Everything else is not purely systematically motivated (note that any emergence of SARS-CoV is a PHEIC by definition and does not need specific decision by the emergency committee: https://en.wikipedia.org/wiki/Public_Health_Emergency_of_International_Concern. I guess that's why "SARS-CoV" per se is not popular these days. We don't have to call it "SARS-CoV" but I firmly believe we should point at the fact that it is a species member.

The species is *Severe acute respiratory syndrome-related coronavirus*

To the species belongs the SARS-CoV (a strain) as well as several bat-associated viruses usually abbreviated SARSr-CoV followed by some specific designation. A name such as "Human SARSr-CoV 2019" (the "r" borrowed from "related" as in the taxonomic species designation) is honest and at the same time discriminative enough. For my taste John's suggestion of Human SARS-CoV 2019 is even better because it is simple less subject to debate (I can already imagine the gossiping about the "r"). In any case my suggestion is to not drop the "SARS" engram from the strain designation. My concept as a more clinically – rooted virologist is that of a new serotype of SARS-CoV. This idea becomes even more real when considering the likely use of ACE2, suggesting technical serotype discrimination via antibodies interfering with receptor binding. Just like in enteroviruses, influenza, etc.

Christian

--

Professor Christian Drosten

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Campus Charité Mitte

Chariteplatz 1

D-10117 Berlin

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E-Mail: christian.drosten@charite.de

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Von: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Datum: Donnerstag, 23. Januar 2020 um 16:21

An: "rbaric@email.unc.edu" <rbaric@email.unc.edu>, "Sbaker1@luc.edu" <Sbaker1@luc.edu>, "[R.J. de \(Raoul\)](mailto:R.J.deGroot@uu.nl)" <R.J.deGroot@uu.nl>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, Benjamin Neuman <bneuman@tamut.edu>, "Perlman, Stanley" <stanley-perlman@uiowa.edu>, "llmpoon@hkucc.hku.hk" <llmpoon@hkucc.hku.hk>, "isola@cnb.csic.es" <isola@cnb.csic.es>, Christian Drosten <christian.drosten@charite.de>, "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>

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The numericals would be consistent with HIV, where we also have 1 and 2. With respect to the public, while it could add to fear in some it would be informative and correct and add to understanding to indicate that both viruses are separate spillovers of essentially the same virus species lurking in wide variation in bats. The analogy with flu A is evident.

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: "Perlman, Stanley" <stanley-perlman@uiowa.edu>
Date: 1/23/20 17:12 (GMT+01:00)
To: A.E.Gorbalenya@lumc.nl
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Subject: Re: Virus name, decision of the Coronaviridae Study Group

I am in communication with WHO and could ask unless Christian or Leo would like to.
Stanley

Stanley Perlman, MD, Ph.D.
Professor
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BSB 3-712
University of Iowa
Iowa City, IA 52242

On Jan 23, 2020, at 10:09 AM, A.E.Gorbalenya@lumc.nl wrote:

Dear All,

I assume that there are people on the CSG, who are involved with the WHO on this issue (Christian, Leo?). Could they enlighten about the WHO position and whether the WHO will be comfortable with the CSG deciding on this matter within a timeframe it finds reasonable?

Best,

Sasha

From: Perlman, Stanley [stanley-perlman@uiowa.edu]
Sent: Thursday, January 23, 2020 4:51 PM
To: Leo Poon
Cc: Benjamin Neuman; John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; lmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; Gorbalenya, A.E. (MSTAT)
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I would like to get your view (as members of the *Coronaviridae* Study Group) on the naming of the coronavirus causing the ongoing outbreak in Wuhan. Things are moving fast, so it would be good to get an agreement on this as soon as possible, ideally also with key WHO people involved once we have reached an agreement in the SG (similar to what we did with MERS in 2013, JVI paper).

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My suggestion would be: hSARS-CoV 2019 (Human SARS coronavirus 2019).

Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back". The disease caused by the "new" virus may be very different from that caused by SARS-CoV. And it will be difficult to get the message across to the general public that closely related (even nearly identical) viruses may cause very different outcomes of disease (see vaccine strains etc.).

To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019).

Please let me know your views and get back to me as soon as possible.

Best regards,

John

—

Prof. Dr. John Ziebuhr

Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]
Sent: Thur 1/23/2020 11:20:27 AM (UTC-05:00)
To: A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]
Cc: llmpoon@hku.hk[llmpoon@hku.hk]; bneuman@tamut.edu[bneuman@tamut.edu]; john.ziebuhr@viro.med.uni-giessen.de[john.ziebuhr@viro.med.uni-giessen.de]; Baric, Ralph S[rbaric@email.unc.edu]; Sbakel1@luc.edu[Sbakel1@luc.edu]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]; christian.drosten@charite.de[christian.drosten@charite.de]
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Totally agree. Best, Raoul

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: A.E.Gorbalenya@lumc.nl
Date: 1/23/20 17:19 (GMT+01:00)
To: stanley-perlman@uiowa.edu
Cc: llmpoon@hku.hk, bneuman@tamut.edu, john.ziebuhr@viro.med.uni-giessen.de, rbaric@email.unc.edu, Sbakel1@luc.edu, "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>, b.haagmans@erasmusmc.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Would it be in the best interest to convey that it is the CSG should be in charge, in consultation with other bodies, e.g. WHO, re virus naming.

Best,

Sasha

From: Perlman, Stanley [stanley-perlman@uiowa.edu]
Sent: Thursday, January 23, 2020 5:12 PM
To: Gorbalenya, A.E. (MSTAT)
Cc: Leo Poon; Benjamin Neuman; john.ziebuhr@viro.med.uni-giessen.de; Baric, Ralph; Baker, Susan; Groot, R.J. de (Raoul); B.L. Haagmans; llmpoon@hkucc.hku.hk; Isabel Sola; Drosten, Christian
Subject: Re: Virus name, decision of the Coronaviridae Study Group

I am in communication with WHO and could ask unless Christian or Leo would like to.
Stanley

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

On Jan 23, 2020, at 10:09 AM, A.E.Gorbalenya@lumc.nl wrote:

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Sent: Thursday, January 23, 2020 4:51 PM

To: Leo Poon

Cc: Benjamin Neuman; John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; Gorbalenya, A.E. (MSTAT)

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Professor

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BSB 3-712

University of Iowa

Iowa City, IA 52242

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WHO doesn't want a virus named after a location any more.

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Leo

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Sent: 23 January 2020 23:39

To: John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Perlman, Stanley; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl

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What do you think of Human coronavirus-Wuhan 2019 (HCoV-Wuhan 2019), in the model of 229E, OC43, NL63 and HKU1?

Or perhaps abbreviate to HCoV-WU19?

Benjamin Neuman
Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020 9:21 AM

To: rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Benjamin Neuman; Perlman, Stanley; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl

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John

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Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: Baker, Susan[Sbaker1@luc.edu]
Sent: Thur 1/23/2020 12:01:25 PM (UTC-05:00)
To: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Baric, Ralph S[rbaric@email.unc.edu]; Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Benjamin Neuman[bneuman@tamut.edu]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Ilmpoon@hkucc.hku.hk[Ilmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]; Drosten, Christian[christian.drosten@charite.de]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Hi All,

John- Thanks so much for starting this discussion. Many issues to consider, particularly the concept that there may be several closely related strains or isolates that emerge from this outbreak. I am open to several possibilities

SARSr-CoV 2019 may be appropriate, with additional details provided in the Genbank listing (location the virus was isolated from, full date of isolation, etc). The detailed extension of the name would be helpful for scientists, but not widely used for communicating with the public.

Whatever we decide to use as a starting point for the virus, we may also want to provide suggestions for the designation of the strains/isolates. How do groups decide on specific names for isolates (ie SARS-CoV-Urbani, SARS-CoV-Tor2, etc)? If the CDC is able to isolate virus from the case in USA, what will be the recommendation for the name of that isolate? (This assumes that the sequence may be different from the isolates already documented in Genbank).

Susan

Stanley – I really like WURS, but as Leo mentioned, the WHO is moving away from naming viruses by location.

Susan Baker, PhD
Professor of Microbiology & Immunology
Loyola University Stritch School of Medicine
2160 South First Ave, Bldg 115, Rm 232
Maywood, IL 60153
Ph:
Email: sbaker1@luc.edu

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, January 23, 2020 9:22 AM
To: rbaric@email.unc.edu; Baker, Susan <Sbaker1@luc.edu>; Groot, R.J. de (Raoul) <R.J.deGroot@uu.nl>; b.haagmans@erasmusmc.nl; Benjamin Neuman <bneuman@tamut.edu>; Perlman, Stanley <stanley-perlman@uiowa.edu>; Ilmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian <christian.drosten@charite.de>; A.E.Gorbalenya@lumc.nl
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Best regards,

John

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From: Perlman, Stanley[stanley-perlman@uiowa.edu]
Sent: Thur 1/23/2020 12:22:56 PM (UTC-05:00)
To: B.L. Haagmans[b.haagmans@erasmusmc.nl]
Cc: Drosten, Christian[christian.drosten@charite.de]; John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; Perlman, Stanley[stanley-perlman@uiowa.edu]; Ilmpoon@hku.hk[Ilmpoon@hku.hk]; bneuman@tamut.edu[bneuman@tamut.edu]; Sbaker1@luc.edu[Sbaker1@luc.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; Ilmpoon@hkucc.hku.hk[Ilmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]
Subject: Re: [ext] Re: Virus name, decision of the Coronaviridae Study Group

Bart,
Great.

Stanley

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

On Jan 23, 2020, at 11:22 AM, B.L. Haagmans <b.haagmans@erasmusmc.nl> wrote:

To me that is also clear and straight forward....
I will contact Maria van Kerkove at WHO on their position or whom to contact
Bart

Van: Drosten, Christian <christian.drosten@charite.de>
Verzonden: donderdag 23 januari 2020 18:06
Aan: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>; Baric, Ralph S <rbaric@email.unc.edu>
CC: A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; Ilmpoon@hku.hk; bneuman@tamut.edu; Sbaker1@luc.edu; R.J.deGroot@uu.nl; B.L. Haagmans <b.haagmans@erasmusmc.nl>; Ilmpoon@hkucc.hku.hk; isola@cnb.csic.es
Onderwerp: Re: [ext] Re: Virus name, decision of the Coronaviridae Study Group

I fully support SARS-CoV-2.

Christian
--

Professor Christian Drosten
Director, Institute of Virology
Scientific Director, Charité Global Health

Charité - Universitätsmedizin Berlin
Campus Charité Mitte

Chariteplatz 1
D-10117 Berlin
Germany

E-Mail: christian.drosten@charite.de
<https://virologie-ccm.charite.de/>
<https://globalhealth.charite.de/>

Von: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Datum: Donnerstag, 23. Januar 2020 um 18:01
An: "Baric, Ralph S" <rbaric@email.unc.edu>
Cc: "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>, "stanley-perlman@uiowa.edu" <stanley-perlman@uiowa.edu>, "llmpoon@hku.hk" <llmpoon@hku.hk>, "bneuman@tamut.edu" <bneuman@tamut.edu>, "Sbaker1@luc.edu" <Sbaker1@luc.edu>, "R.J.deGroot@uu.nl" <R.J.deGroot@uu.nl>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, "llmpoon@hkucc.hku.hk" <llmpoon@hkucc.hku.hk>, "isola@cnb.csic.es" <isola@cnb.csic.es>, Christian Drosten <christian.drosten@charite.de>
Betreff: [ext] Re: Virus name, decision of the Coronaviridae Study Group

Many thanks for all your input. It seems we are approaching a consensus in terms of keeping "SARS" in the virus name. To keep the name simple, I would like to come back to Raoul's suggestion: SARS-CoV-2. This would correctly reflect the phylogenetic relationship of the virus and perhaps, in the short term, not contribute too much to fear in the public (because health authorities may keep saying that this virus differs from SARS-CoV).

Best,
John

Am 23.01.2020 um 17:49 schrieb Baric, Ralph S <rbaric@email.unc.edu>:

Dear All, Dr. Shi has a biorix paper showing the new SARS-like CoV uses hACE2 as a receptor for entry. Seems to me there is no escaping the fact that it is a kissing cousin to SARS-CoV. Given the fact that several other SARS-like CoV are circulating in bats that also use ACE2 receptors and grow in primary human cells, I don't think it is appropriate to uncouple the relationship with SARS-CoV-both for long-term planning, public health priorities and desire to alleviate public concern. The fact is that a range of SARS-like bCoV that vary between 1-25% are likely positioned to emerge at sometime in the future. Moreover, it is impossible at this point to alleviate public concern after 20 million people in two cities have been placed under quarantine. Consequently, I favor a name that reflects the biological origins of the virus-as it will prove critical for long-term global health planning for repeat events in the future. I like Human SARSr-CoV 2019" or hSARS-CoV 2019 (Human SARS coronavirus 2019) or even SARS-like HCoV 2019.

I also believe that the CSG should be in charge, in consultation with other bodies, e.g. WHO, re virus naming.
Ralph

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>
Sent: Thursday, January 23, 2020 11:09 AM

To: stanley-perlman@uiowa.edu; llmpoon@hku.hk
Cc: bneuman@tamut.edu; john.ziebuhr@viro.med.uni-giessen.de; Baric, Ralph S
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Schubertstrasse 81 (BFS)
35392 Giessen
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Tel.
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]
Sent: Thur 1/23/2020 12:51:47 PM (UTC-05:00)
To: john.ziebuhr@viro.med.uni-giessen.de[john.ziebuhr@viro.med.uni-giessen.de];
bneuman@tamut.edu[bneuman@tamut.edu]
Cc: Baric, Ralph S[rbaric@email.unc.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu];
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b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl];
llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es];
christian.drosten@charite.de[christian.drosten@charite.de]
Subject: RE: Virus name, decision of the Coronaviridae Study Group

... and I would also add that the extension could also include host, where from a particular virus was isolated, e.g. human, thus resolving a controversial issue whether this virus must be called human or not.

From: John Ziebuhr [john.ziebuhr@viro.med.uni-giessen.de]
Sent: Thursday, January 23, 2020 6:41 PM
To: Benjamin Neuman
Cc: Baric, Ralph S; Gorbalenya, A.E. (MSTAT); stanley-perlman@uiowa.edu; llmpoon@hku.hk; Sbaker1@luc.edu;
R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
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Ben,
I think it will be just a matter of time that, similar to what happened to HIV-1 (instead of HIV) in the past, people will start using the name SARS-CoV-1 if they want to refer to the virus from the 2003 epidemic. Re Susan's question: The relatively short name SARS-CoV-2 could easily be extended by sample/lab/sequence numbers. This would be much less practicable if we used long virus names, such as SARS-like HCoV 2019.
John

Am 23.01.2020 um 18:14 schrieb Benjamin Neuman <bneuman@tamut.edu>:

I can get behind SARS-CoV-2 as well - presumably naming a place and a date as in influenza would be OK for a particular isolate? And does it mean retrospectively constructing an informal umbrella or perhaps serogroup without formal taxonomic standing for the previous epidemic SARS as SARS-CoV-1? That seems like it would be a reasonable recommendation, if it is what the committee proposes.

Benjamin Neuman
Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020 11:01 AM

To: Baric, Ralph S

Cc: A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Benjamin Neuman; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

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Best,

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Am 23.01.2020 um 17:49 schrieb Baric, Ralph S <rbaric@email.unc.edu>:

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From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Sent: Thursday, January 23, 2020 11:09 AM

To: stanley-perlman@uiowa.edu; llmpoon@hku.hk

Cc: bneuman@tamut.edu; john.ziebuhr@viro.med.uni-giessen.de; Baric, Ralph S <rbaric@email.unc.edu>; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

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be comfortable with the CSG deciding on this matter within a timeframe it finds reasonable?

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Sent: Thursday, January 23, 2020 4:51 PM

To: Leo Poon

Cc: Benjamin Neuman; John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; lmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; Gorbalenya, A.E. (MSTAT)

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Stanley

Stanley Perlman, MD, Ph.D.

Professor

Depts of Microbiology and Immunology, and Pediatrics

BSB 3-712

University of Iowa

Iowa City, IA 52242

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Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back". The disease caused by the "new" virus may be very different from that caused by SARS-CoV. And it will be difficult to get the message across to the general public that closely

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To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019).

Please let me know your views and get back to me as soon as possible.

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Prof. Dr. John Ziebuhr
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Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
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Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

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Sent: Thur 1/23/2020 1:31:09 PM (UTC-05:00)
To: John Ziebuhr[John.Ziebuhr@viro.med.uni-giessen.de]
Cc: Benjamin Neuman[bneuman@tamut.edu]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; llmpoon@hku.hk[llmpoon@hku.hk]; Sbaker1@luc.edu[Sbaker1@luc.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]; christian.drosten@charite.de[christian.drosten@charite.de]
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Dear all,

I agree that the name SARS-CoV-2 is adequate in many aspects.

It reflects the phylogeny of the virus, as part of the severe acute respiratory syndrome-related coronavirus species. Therefore, in the long term, it would be a fair decision.

In addition, it would follow the WHO recommendation of not including geographic information.

However, in the short-term, I would favor a name that implies that this virus has some singularities as compared to SARS-CoV, not only the time when it emerged, but most likely some other properties to be characterized (pathogenicity...). According to this, WURS-CoV would be an option.

I accept that when naming a virus, the long-term perspective should prevail over the short-term considerations. However, do you think that the number 2 in SARS-CoV-2 might be replaced by a more significant extension? SARS-CoV-WU19 or SARS-CoV-Wuham?

Best regards

Isabel

Enviado desde mi iPhone

El 23 ene 2020, a las 18:41, John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de> escribió:

Ben,

I think it will be just a matter of time that, similar to what happened to HIV-1 (instead of HIV) in the past, people will start using the name SARS-CoV-1 if they want to refer to the virus from the 2003 epidemic.

Re Susan's question: The relatively short name SARS-CoV-2 could easily be extended by sample/lab/sequence numbers. This would be much less practicable if we used long virus names, such as SARS-like HCoV 2019.

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From: Baric, Ralph S[/O=EXCHANGELABS/OU=EXCHANGE ADMINISTRATIVE GROUP (FYDIBOHF23SPDLT)/CN=RECIPIENTS/CN=BB0D9CC80C184735A4E862C3BDD8A15D-RALPH S BAR]
Sent: Thur 1/23/2020 2:33:42 PM (UTC-05:00)
To: Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]; John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Baker, Susan[Sbaker1@luc.edu]
Cc: Benjamin Neuman[bneuman@tamut.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; llmpoon@hku.hk[llmpoon@hku.hk]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]; christian.drosten@charite.de[christian.drosten@charite.de]
Subject: RE: Virus name, decision of the Coronaviridae Study Group

I am okay with SARS-CoV-2. I see no need to rename SARS-CoV, SARS-CoV-1 as this is simply an unnecessary incremental change. Ralph

From: Groot, R.J. de (Raoul) <R.J.deGroot@uu.nl>
Sent: Thursday, January 23, 2020 1:51 PM
To: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>; Baker, Susan <Sbaker1@luc.edu>
Cc: Benjamin Neuman <bneuman@tamut.edu>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
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It may not be our formal remit, but the CSG could and should take a lead in issues like this. It is a representation of the groups active and deeply rooted in the field, and the body itself has a long tradition, also in matters outside taxonomy. Previously, the CSG has made recommendations on nomenclature for RNAs, proteins genes and the sort, and thus helped our field forward, so there is precedent. If anyone should guide the field, it is the CSG rather than outside entities like the WHO or individual authors, which would almost certainly create chaos. So, recommendation for SARS-CoV-2 with a second recommendation to use SARS-1 should be ok. Better not have Wuhan in the name. Although I do not see any problem with geographic names as they add relevant context on origin and history, and poetry (O'Nyong Nyong, Semliki Forest, West Nile, Ross River...), the WHO would not approve.

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Date: 1/23/20 19:29 (GMT+01:00)
To: "Baker, Susan" <Sbaker1@luc.edu>
Cc: Benjamin Neuman <bneuman@tamut.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, A.E.Gorbalenya@lumc.nl, stanley-perlman@uiowa.edu, llmpoon@hku.hk, "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>, b.haagmans@erasmusmc.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de
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Hi Susan,

No, this does not fall within the remit of the CSG (it is below the species level). Also, I think it would cause major confusion in the community if people started renaming PREVIOUSLY characterized isolates from different species that have been available in databases for many years.

John

Am 23.01.2020 um 19:02 schrieb Baker, Susan <Sbaker1@luc.edu>:

Hi John,

If we go with SARS-CoV-2 (which seems reasonable), should our study group report suggest that people use SARS-CoV-1 when they refer to the 2003 epidemic?

Susan

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Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

On Jan 23, 2020, at 9:45 AM, Leo Poon
<llmpoon@hku.hk> wrote:

Ben,

WHO doesn't want a virus named after a location any more.

Cheers,

Leo

From: Benjamin Neuman <bneuman@tamut.edu>

Sent: 23 January 2020 23:39

To: John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Perlman, Stanley; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl

Subject: Re: Virus name, decision of the Coronaviridae Study Group

The name Wuhan seems to be the most often used by the public, but I think Wuhan seafood market pneumonia virus, as posted on the original genome sequence, is a bit wordy. But presumably, it would be a bit stigmatizing to name-check Wuhan?

I think there might be push-back from the pathology side of our field on calling it a strain of SARS if the receptor is different, as appears to be the case from the divergent spike RBD.

I can live with either of those names proposed, if there is consensus.

What do you think of Human coronavirus-Wuhan 2019 (HCoV-Wuhan 2019), in the model of 229E, OC43, NL63 and HKU1?

Or perhaps abbreviate to HCoV-WU19?

Benjamin Neuman

Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020 9:21 AM

To: rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de

(Raoul); b.haagmans@erasmusmc.nl; Benjamin Neuman;
Perlman, Stanley; llmpoon@hkucc.hku.hk; isola@cnb.csic.es;
Drosten, Christian; A.E.Gorbalenya@lumc.nl
Subject: Virus name, decision of the Coronaviridae Study Group

Dear All,

I would like to get your view (as members of the *Coronaviridae* Study Group) on the naming of the coronavirus causing the ongoing outbreak in Wuhan. Things are moving fast, so it would be good to get an agreement on this as soon as possible, ideally also with key WHO people involved once we have reached an agreement in the SG (similar to what we did with MERS in 2013, JVI paper). Sasha and I are planning to put together a short paper in which we (and I hope all members of the Coronaviridae Study Group will join in) make a statement on the position of this virus within the existing taxonomy. Sasha is currently working on this.

Regarding the phylogenetic position of the virus, it is clear that the virus is part of an existing species called *SARS-related coronavirus*. All other viruses/isolates in that species (irrespective of whether they were isolated from humans, bats or other animals) have "SARS" in their names (SARS-CoV XYZ, SARSr-CoV XYZ etc.). Thus, it would be more than justified to (also) have a reference to SARS in the name of this "new" virus.

My suggestion would be: hSARS-CoV 2019 (Human SARS coronavirus 2019). Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back".

The disease caused by the "new" virus may be very different from that caused by SARS-CoV. And it will be difficult to get the message across to the general public that closely related (even nearly identical) viruses may cause very different outcomes of disease (see vaccine strains etc.).

To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019).

Please let me know your views and get back to me as soon as possible.

Best regards,

John

—
Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: Drosten, Christian[christian.drosten@charite.de]
Sent: Thur 1/23/2020 2:39:23 PM (UTC-05:00)
To: Baric, Ralph S[rbaric@email.unc.edu]
Cc: Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]; John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Baker, Susan[Sbaker1@luc.edu]; Benjamin Neuman[bneuman@tamut.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; llmpoon@hku.hk[llmpoon@hku.hk]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]
Subject: Re: [ext] RE: Virus name, decision of the Coronaviridae Study Group

I totally agree with Ralph. Naming it SARS-CoV-2 is the single necessary and simple move.
Christian

Prof C Drosten
Institute of Virology
Charite Campus Mitte
Berlin
iPhone

Am 23.01.2020 um 20:33 schrieb Baric, Ralph S <rbaric@email.unc.edu>:

I am okay with SARS-CoV-2. I see no need to rename SARS-CoV, SARS-CoV-1 as this is simply an unnecessary incremental change. Ralph

From: Groot, R.J. de (Raoul) <R.J.deGroot@uu.nl>
Sent: Thursday, January 23, 2020 1:51 PM
To: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>; Baker, Susan <Sbaker1@luc.edu>
Cc: Benjamin Neuman <bneuman@tamut.edu>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

It may not be our formal remit, but the CSG could and should take a lead in issues like this. It is a representation of the groups active and deeply rooted in the field, and the body itself has a long tradition, also in matters outside taxonomy. Previously, the CSG has made recommendations on nomenclature for RNAs, proteins genes and the sort, and thus helped our field forward, so there is precedent. If anyone should guide the field, it is the CSG rather than outside entities like the WHO or individual authors, which would almost certainly create chaos. So, recommendation for SARS-CoV-2 with a second recommendation to use SARS-1 should be ok. Better not have Wuhan in the name. Although I do not see any problem with geographic names as they add relevant context on origin and history, and poetry (O'Nyong Nyong, Semliki Forest, West Nile, Ross River...), the WHO would not approve.

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Date: 1/23/20 19:29 (GMT+01:00)
To: "Baker, Susan" <Sbaker1@luc.edu>
Cc: Benjamin Neuman <bneuman@tamut.edu>, "Baric, Ralph S" <rbaric@email.unc.edu>, A.E.Gorbalenya@lumc.nl, stanley-perlman@uiowa.edu, llmpoon@hku.hk, "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>, b.haagmans@erasmusmc.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Hi Susan,

No, this does not fall within the remit of the CSG (it is below the species level). Also, I think it would cause major confusion in the community if people started renaming PREVIOUSLY characterized isolates from different species that have been available in databases for many years.

John

Am 23.01.2020 um 19:02 schrieb Baker, Susan <Sbaker1@luc.edu>:

Hi John,

If we go with SARS-CoV-2 (which seems reasonable), should our study group report suggest that people use SARS-CoV-1 when they refer to the 2003 epidemic?

Susan

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, January 23, 2020 11:41 AM
To: Benjamin Neuman <bneuman@tamut.edu>
Cc: Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Baker, Susan <Sbaker1@luc.edu>; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Ben,

I think it will be just a matter of time that, similar to what happened to HIV-1 (instead of HIV) in the past, people will start using the name SARS-CoV-1 if they want to refer to the virus from the 2003 epidemic.

Re Susan's question: The relatively short name SARS-CoV-2 could easily be extended by sample/lab/sequence numbers. This would be much less practicable if we used long virus names, such as SARS-like HCoV 2019.

John

Am 23.01.2020 um 18:14 schrieb Benjamin Neuman
<bneuman@tamut.edu>:

I can get behind SARS-CoV-2 as well - presumably naming a place and a date as in influenza would be OK for a particular isolate? And does it mean retrospectively constructing an informal umbrella or perhaps serogroup without formal taxonomic standing for the previous epidemic SARS as SARS-CoV-1? That seems like it would be a reasonable recommendation, if it is what the committee proposes.

Benjamin Neuman

Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, January 23, 2020 11:01 AM
To: Baric, Ralph S
Cc: A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Benjamin Neuman; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks for all your input. It seems we are approaching a consensus in terms of keeping "SARS" in the virus name. To keep the name simple, I would like to come back to Raoul's suggestion: SARS-CoV-2. This would correctly reflect the phylogenetic relationship of the virus and perhaps, in the short term, not contribute too much to fear in the public (because health authorities may keep saying that this virus differs from SARS-CoV).

Best,
John

Am 23.01.2020 um 17:49 schrieb Baric, Ralph S
<rbaric@email.unc.edu>:

Dear All, Dr. Shi has a biorix paper showing the new SARS-like CoV uses hACE2 as a receptor for entry. Seems to me there is no escaping the fact that it is a kissing cousin to SARS-CoV.

Given the fact that several other SARS-like CoV are circulating in bats that also use ACE2 receptors and grow in primary human cells, I don't think it is appropriate to uncouple the relationship with SARS-CoV-both for long-term planning, public health priorities and desire to alleviate public concern. The fact is that a range of SARS-like bCoV that vary between 1-25% are likely positioned to emerge at sometime in the future. Moreover, it is impossible at this point to alleviate public concern after 20 million people in two cities have been placed under quarantine. Consequently, I favor a name that reflects the biological origins of the virus-as it will prove critical for long-term global health planning for repeat events in the future. I like Human SARS-CoV 2019" or hSARS-CoV 2019 (Human SARS coronavirus 2019) or even SARS-like HCoV 2019.

I also believe that the CSG should be in charge, in consultation with other bodies, e.g. WHO, re virus naming.

Ralph

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>
Sent: Thursday, January 23, 2020 11:09 AM
To: stanley-perlman@uiowa.edu; llmpoon@hku.hk
Cc: bneuman@tamut.edu; john.ziebuhr@viro.med.uni-giessen.de; Baric, Ralph S <rbaric@email.unc.edu>; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear All,

I assume that there are people on the CSG, who are involved with the WHO on this issue (Christian, Leo?). Could they enlighten about the WHO position and whether the WHO will be comfortable with the CSG deciding on this matter within a timeframe it finds reasonable?

Best,

Sasha

From: Perlman, Stanley [stanley-perlman@uiowa.edu]
Sent: Thursday, January 23, 2020 4:51 PM
To: Leo Poon
Cc: Benjamin Neuman; John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; Gorbalenya, A.E. (MSTAT)
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Leo,

I know that you are correct about the WHO recommendation, but I like Ben's idea. John's nomenclature is also fine with me. My children call the disease WURS (Wuhan respiratory syndrome), which has an easy name to remember, like SARS, MERS. This also shows what we talk about at the dinner table.

Stanley

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

On Jan 23, 2020, at 9:45 AM, Leo Poon
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Sent: Thursday, January 23, 2020 9:21 AM

To: rbaric@email.unc.edu; Sbaker1@luc.edu;

Groot, R.J. de

(Raoul); b.haagmans@erasmusmc.nl; Benjamin

Neuman; Perlman,

Stanley; llmpoon@hkucc.hku.hk; isola@cnb.csic.es

; Drosten, Christian; A.E.Gorbalenya@lumc.nl

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My suggestion would be: hSARS-CoV 2019 (Human SARS coronavirus 2019).

Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back". The **disease caused by the "new" virus may be very different from that caused by SARS-CoV**. And it will be difficult to get the message across to the general public that closely related (even nearly identical) viruses may cause very different outcomes of disease (see vaccine strains etc.). To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019). Please let me know your views and get back to me as soon as possible.
Best regards,
John

—
Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]
Sent: Fri 1/24/2020 2:06:26 AM (UTC-05:00)
To: Leo Poon[lmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu];
A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl];
b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; john.ziebuhr@viro.med.uni-
giessen.de[john.ziebuhr@viro.med.uni-giessen.de]
Cc: Sbaker1@luc.edu[Sbaker1@luc.edu]; bneuman@tamut.edu[bneuman@tamut.edu]; stanley-
perlman@uiowa.edu[stanley-perlman@uiowa.edu];
lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es];
christian.drosten@charite.de[christian.drosten@charite.de]
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear all,

Adding the year as an identifier may become awkward if the virus is not eradicated and becomes established.
SARS-CoV 2019/2026/Nieuwegein?

As for Sasha's point: if a third virus would turn up, it would still be a separate, independent introduction. This might be an occasion where biological context, i.e. cross species transmission, overrides phylogeny and the distinction would still be useful to the field.

Raoul

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: Leo Poon <lmpoon@hku.hk>
Date: 1/24/20 02:07 (GMT+01:00)
To: "Baric, Ralph S" <rbaric@email.unc.edu>, A.E.Gorbalenya@lumc.nl, b.haagmans@erasmusmc.nl,
john.ziebuhr@viro.med.uni-giessen.de
Cc: Sbaker1@luc.edu, bneuman@tamut.edu, stanley-perlman@uiowa.edu, "Groot, R.J. de (Raoul)"
<R.J.deGroot@uu.nl>, lmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear all,

Sounds we almost get a consensus after my night.

I will go for hSARS-CoV2019. This highlights the human component first, and this also makes it look different from SARS.

Cheers,

Leo

Leo Poon
Professor
School of Public Health
The University of Hong Kong

Hong Kong

Tel:

Fax: (852) 2855 9587

From: Baric, Ralph S <rbaric@email.unc.edu>

Sent: Friday, 24 January 2020 8:59 AM

To: A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl; john.ziebuhr@viro.med.uni-giessen.de

Cc: Sbak1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; Leo Poon <llmpoon@hku.hk>;

R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Good point. SARS-HCoV 2019 or hSARS-CoV 2019, then year of discovery distinguishes between introductions?

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Sent: Thursday, January 23, 2020 6:49 PM

To: b.haagmans@erasmusmc.nl; john.ziebuhr@viro.med.uni-giessen.de

Cc: Sbak1@luc.edu; bneuman@tamut.edu; Baric, Ralph S <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu;

llmpoon@hku.hk; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Thank you, Bart!

Dear All,

People may read digit '2' in the virus name as the indicator of phylogenetic lineage or the number associated with second Introduction of the species into human population, or both, and all of these readings are accurate.

Now, I'd like to consider a hypothetical scenario with a third Introduction of the species into human population.

If the new virus was phylogenetically distinct from the current two, using digit '3' in its name would be straightforward move. However, if this hypothetical virus was close to either of the current two viruses, using '3' in its name would be poorly compatible with the virus phylogeny, while using a digit of the virus cousin would be misleading in respect to the virus spillover #, if we want the virus name to convey this aspect (do we?).

The above scenario shows that additional consideration of the name convention may be warranted before we go public.

For instance, the above problem could be solved if virus name includes double digit with each digit separated by dot, with the pre-dot part labeling phylogeny and post-dot part labelling spillover #. For the current virus, the name would include '2.1' instead of '2'.

Just a thought.

Best,

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>

Date: 1/23/20 22:25 (GMT+01:00)

To: "Gorbalenya, A.E. (MSTAT)" <A.E.Gorbalenya@lumc.nl>, john.ziebuhr@viro.med.uni-giessen.de

Cc: Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, stanley-perlman@uiowa.edu, llmpoon@hku.hk, R.J.deGroot@uu.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

CET Geneva ...

Van: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Verzonden: Thursday, January 23, 2020 10:06:12 PM

Aan: john.ziebuhr@viro.med.uni-giessen.de <john.ziebuhr@viro.med.uni-giessen.de>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>

CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>

Onderwerp: RE: Virus name, decision of the Coronaviridae Study Group

Bart,

What's the time zone Maria in?

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Date: 1/23/20 21:57 (GMT+01:00)

To: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>

Cc: "Gorbalenya, A.E. (MSTAT)" <A.E.Gorbalenya@lumc.nl>, Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, stanley-perlman@uiowa.edu, llmpoon@hku.hk, R.J.deGroot@uu.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks, Bart. I will do this tomorrow morning (CET), hoping that we can all (Leo?) agree with the name SARS-CoV-2.

Best regards,

John

Von meinem iPhone gesendet

Am 23.01.2020 um 21:43 schrieb B.L. Haagmans <b.haagmans@erasmusmc.nl>:

I talked to Maria van Kerkhove at WHO (vankerkhovem@who.int) and she will act as contact person. They are apparently convening a group to work on this.
So probably best if John communicates the outcome of our discussion to WHO on behalf of the Coronaviridae Study Group .
Bart

Van: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Verzonden: Thursday, January 23, 2020 8:14:00 PM

Aan: Alexander Gorbalenya (A.E.Gorbalenya@lumc.nl) <A.E.Gorbalenya@lumc.nl>

CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>

Onderwerp: Re: Virus name, decision of the Coronaviridae Study Group

Thanks, Sasha, for this clarification in your first sentence. I referred in my email to PREVIOUSLY established virus names (genome sequences were deposited in databases years ago and have been used in many publications!). I agree with you that, for NEW isolates detected in whatever species, names should now contain a reference to SARS-CoV-1 and, preferably, also contain some reference to indicate the host species from which the respective virus was isolated. We could recommend this.

Best,
John

Am 23.01.2020 um 19:50 schrieb <A.E.Gorbalenya@lumc.nl>
<A.E.Gorbalenya@lumc.nl>:

Hello,

There could be a room for proceeding with the Susan's suggestion, if it is applied to new isolates; we could expect that epidemiological research on SARS-CoV-1 will continue.

Since this application - as well as the virus naming (!) - is outside of the CSG remit, as John reminded, our decisions may be called "recommendations".

Best,

Sasha

From: John Ziebuhr [john.ziebuhr@viro.med.uni-giessen.de]

Sent: Thursday, January 23, 2020 7:29 PM

To: Baker, Susan

Cc: Benjamin Neuman; Baric, Ralph S; Gorbalenya, A.E. (MSTAT); stanley-perlman@uiowa.edu; llmpoon@hku.hk; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Hi Susan,

No, this does not fall within the remit of the CSG (it is below the species level). Also, I think it would cause major confusion in the community if people started renaming PREVIOUSLY characterized isolates from different species that have been available in databases for many years.

John

Am 23.01.2020 um 19:02 schrieb Baker, Susan <Sbaker1@luc.edu>:

Hi John,

If we go with SARS-CoV-2 (which seems reasonable), should our study group report suggest that people use SARS-CoV-1 when they refer to the 2003 epidemic?

Susan

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020 11:41 AM

To: Benjamin Neuman <bneuman@tamut.edu>

Cc: Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Baker, Susan <Sbaker1@luc.edu>; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Ben,

I think it will be just a matter of time that, similar to what happened to HIV-1 (instead of HIV) in the past, people will start using the name SARS-CoV-1 if they want to refer to the virus from the 2003 epidemic.

Re Susan's question: The relatively short name SARS-CoV-2 could easily be extended by sample/lab/sequence numbers. This would be much less practicable if we used long virus names, such as SARS-like HCoV 2019.

John

Am 23.01.2020 um 18:14 schrieb Benjamin Neuman
<bneuman@tamut.edu>:

I can get behind SARS-CoV-2 as well - presumably naming a place and a date as in influenza would be OK for a particular isolate? And does it mean retrospectively constructing an informal umbrella or perhaps serogroup without formal taxonomic standing for the previous epidemic SARS as SARS-CoV-1? That seems like it would be a reasonable recommendation, if it is what the committee proposes.

Benjamin Neuman

Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, January 23, 2020 11:01 AM
To: Baric, Ralph S
Cc: A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Benjamin Neuman; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks for all your input. It seems we are approaching a consensus in terms of keeping "SARS" in the virus name. To keep the name simple, I would like to come back to Raoul's suggestion: SARS-CoV-2. This would correctly reflect the phylogenetic relationship of the virus and perhaps, in the short term, not contribute too much to fear in the public (because health authorities may keep saying that this virus differs from SARS-CoV).

Best,
John

Am 23.01.2020 um 17:49 schrieb Baric, Ralph
S <rbaric@email.unc.edu>:

Dear All, Dr. Shi has a biorix paper showing the new SARS-like CoV uses hACE2 as a receptor for entry. Seems to me there is no escaping the fact that it is a kissing cousin to SARS-CoV. Given the fact that several other SARS-like CoV are circulating in bats that also use ACE2 receptors and grow in primary human cells, I don't think it is appropriate to uncouple the relationship with SARS-CoV-both for long-term planning, public health priorities and desire to alleviate public concern. The fact is that a range of SARS-like bCoV that vary between 1-25% are likely positioned to emerge at sometime in the future. Moreover, it is impossible at this point to alleviate public concern after 20 million people in two cities have been placed under quarantine. Consequently, I favor a name that reflects the biological origins of the virus-as it will prove critical for long-term global health planning for repeat events in the future. I like Human SARSr-CoV 2019" or hSARS-CoV 2019 (Human SARS coronavirus 2019) or even SARS-like HCoV 2019.

I also believe that the CSG should be in charge, in consultation with other bodies, e.g. WHO, re virus naming.

Ralph

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>
Sent: Thursday, January 23, 2020 11:09 AM
To: stanley-perlman@uiowa.edu; llmpoon@hku.hk
Cc: bneuman@tamut.edu; john.ziebuhr@viro.med.uni-giessen.de; Baric, Ralph S <rbaric@email.unc.edu>; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drossten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear All,

I assume that there are people on the CSG, who are involved with the WHO on this issue (Christian, Leo?). Could they enlighten about the WHO position and whether the WHO will be comfortable with the CSG deciding on this matter within a timeframe it finds reasonable?

Best,

Sasha

From: Perlman, Stanley [stanley-perlman@uiowa.edu]
Sent: Thursday, January 23, 2020 4:51 PM
To: Leo Poon
Cc: Benjamin Neuman; John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; Gorbalenya, A.E. (MSTAT)
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Leo,

I know that you are correct about the WHO recommendation, but I like Ben's idea. John's nomenclature is also fine with me. My children call the disease WURS (Wuhan respiratory syndrome), which has an easy name to remember, like SARS, MERS. This also shows what we talk about at the dinner table.

Stanley

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

On Jan 23, 2020, at 9:45 AM, Leo Poon <llmpoon@hku.hk> wrote:

Ben,

WHO doesn't want a virus named after a location any more.

Cheers,

Leo

From: Benjamin Neuman
<bneuman@tamut.edu>
Sent: 23 January 2020 23:39

To: John
Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de
(Raoul); b.haagmans@erasmusmc.nl;
Perlman,
Stanley; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten,
Christian; A.E.Gorbalenya@lumc.nl
Subject: Re: Virus name, decision of
the Coronaviridae Study Group

The name Wuhan seems to be the most often used by the public, but I think Wuhan seafood market pneumonia virus, as posted on the original genome sequence, is a bit wordy. But presumably, it would be a bit stigmatizing to name-check Wuhan?

I think there might be push-back from the pathology side of our field on calling it a strain of SARS if the receptor is different, as appears to be the case from the divergent spike RBD.

I can live with either of those names proposed, if there is consensus.

What do you think of Human coronavirus-Wuhan 2019 (HCoV-Wuhan 2019), in the model of 229E, OC43, NL63 and HKU1?

Or perhaps abbreviate to HCoV-WU19?

Benjamin Neuman

Professor and Chair of Biological
Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr

<john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020
9:21 AM

To: rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Benjamin Neuman; Perlman, Stanley; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl
Subject: Virus name, decision of the Coronaviridae Study Group

Dear All,

I would like to get your view (as members of the *Coronaviridae* Study Group) on the naming of the coronavirus causing the ongoing outbreak in Wuhan. Things are moving fast, so it would be good to get an agreement on this as soon as possible, ideally also with key WHO people involved once we have reached an agreement in the SG (similar to what we did with MERS in 2013, JVI paper).

Sasha and I are planning to put together a short paper in which we (and I hope all members of the Coronaviridae Study Group will join in) make a statement on the position of this virus within the existing taxonomy.

Sasha is currently working on this.

Regarding the phylogenetic position of the virus, it is clear that the virus is part of an existing species called *SARS-related coronavirus*. All other viruses/isolates in that species (irrespective of whether they were isolated from humans, bats or other animals) have "SARS" in their names (SARS-CoV XYZ, SARSr-CoV XYZ etc.). Thus, it would be more than justified to (also) have a reference to SARS in the name of this "new" virus.

My suggestion would be: hSARS-CoV 2019 (Human SARS coronavirus 2019).

Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back".

The disease caused by the "new" virus may be very different from that caused by SARS-CoV. And it will be difficult to get the message across to the general public that closely related (even nearly identical) viruses may cause very different outcomes of disease (see vaccine strains etc.).

To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019).

Please let me know your views and get back to me as soon as possible.

Best regards,

John

—

Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]
Sent: Fri 1/24/2020 3:16:04 AM (UTC-05:00)
To: Leo Poon[lmpoon@hku.hk]; John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Sbak1@luc.edu[Sbak1@luc.edu]; bneuman@tamut.edu[bneuman@tamut.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]; christian.drosten@charite.de[christian.drosten@charite.de]
Subject: RE: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2 (with option for SARS-CoV2.x per Sasha's advice). Naming it '19' in the long term would raise the question what 1-18 might be and in case of recurring introductions it would be a counting system anyway.

Best, Raoul

From: Leo Poon <lmpoon@hku.hk>
Sent: vrijdag 24 januari 2020 08:36
To: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl; Sbak1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; Groot, R.J. de (Raoul) <R.J.deGroot@uu.nl>; lmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear John,

I vote for hSARS-CoV-2019.

Best,

Leo

Leo Poon
Professor
School of Public Health
The University of Hong Kong
Hong Kong
Tel:
Fax: (852) 2855 9587

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Friday, 24 January 2020 3:31 PM
To: Leo Poon <lmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl; Sbak1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; lmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Cc: John.Ziebuhr@viro.med.uni-giessen.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Dear All,

Many thanks for this very helpful discussion. I try to summarize the outcome of our discussion:

The new name should:

1. indicate the phylogeny of the virus (member of the species *Severe acute respiratory syndrome-related coronavirus*)
2. indicate the host
3. be distinct from SARS-CoV (2003)
4. be suitable to accommodate future introductions of this virus
5. not be overly long and thus remain practicable (to reduce the risk of people coming up with all sorts of abbreviations)

Based on these considerations and having read your comments and suggestions again, I would like to propose four options. The order reflects my own preference.

1. hSARS-CoV-19 (human SARS coronavirus 19)
2. hSARS-CoV-2019
3. hSARS-CoV-2

(4. hSARS-CoV-2.19)

The first two options use the year of the first isolation as a unique identifier. Future introductions would then keep that virus name but be extended with sequence identifiers, e.g. hSARS-CoV-19 XY12345 or an additional number (if needed).

I believe the two-digit number should suffice to indicate the year (and reduce the length of the name by two or more syllables, depending on the language used).

I would prefer the year of discovery over a counting exercise of "introductions" (1st, 2nd, 3rd introduction). The counting would probably become a matter of debate in cases in which a virus is detected in just a single or very few individual(s).

I do not see a problem with year identifiers if a virus becomes established. The name would then still indicate the year in which it was discovered.

Can we have a vote on these options by later today, 6 pm (CET)?

Many thanks and best regards,

John

Prof. Dr. John Ziebuhr
Institut für Medizinische Virologie
Justus-Liebig-Universität Gießen
Schubertstraße 81 (BFS)
35392 Gießen
Tel.
Fax: 0641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

Am 24.01.2020 um 02:05 schrieb Leo Poon <llmpoon@hku.hk>:

Dear all,

Sounds we almost get a consensus after my night.

I will go for hSARS-CoV2019. This highlight the human component first, and this also makes it look different from SARS.

Cheers,

Leo

Leo Poon
Professor
School of Public Health
The University of Hong Kong
Hong Kong
Tel: .
Fax: (852) 2855 9587

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Friday, 24 January 2020 8:59 AM
To: A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl; john.ziebuhr@viro.med.uni-giessen.de
Cc: Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; Leo Poon <llmpoon@hku.hk>; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Good point. SARS-HCoV 2019 or hSARS-CoV 2019, then year of discovery distinguishes between introductions?

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>
Sent: Thursday, January 23, 2020 6:49 PM
To: b.haagmans@erasmusmc.nl; john.ziebuhr@viro.med.uni-giessen.de
Cc: Sbaker1@luc.edu; bneuman@tamut.edu; Baric, Ralph S <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu; llmpoon@hku.hk; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Thank you, Bart!

Dear All,

People may read digit '2' in the virus name as the indicator of phylogenetic lineage or the number associated with second Introduction of the species into human population, or both, and all of these readings are accurate.

Now, I'd like to consider a hypothetical scenario with a third Introduction of the species into human population.

If the new virus was phylogenetically distinct from the current two, using digit '3' in its name would be straightforward move. However, if this hypothetical virus was close to either of the

current two viruses, using '3' in its name would be poorly compatible with the virus phylogeny, while using a digit of the virus cousin would be misleading in respect to the virus spillover #, if we want the virus name to convey this aspect (do we?).

The above scenario shows that additional consideration of the name convention may be warranted before we go public.

For instance, the above problem could be solved if virus name includes double digit with each digit separated by dot, with the predot part labeling phylogeny and postdot part labelling spillover #. For the current virus, the name would include '2.1' instead of '2'.

Just a thought.

Best,

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>

Date: 1/23/20 22:25 (GMT+01:00)

To: "Gorbalenya, A.E. (MSTAT)" <A.E.Gorbalenya@lumc.nl>, john.ziebuhr@viro.med.uni-giessen.de

Cc: Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, stanley-perlman@uiowa.edu, llmpoon@hku.hk, R.J.deGroot@uu.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

CET Geneva ...

Van: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Verzonden: Thursday, January 23, 2020 10:06:12 PM

Aan: john.ziebuhr@viro.med.uni-giessen.de <john.ziebuhr@viro.med.uni-giessen.de>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>

CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>

Onderwerp: RE: Virus name, decision of the Coronaviridae Study Group

Bart,

What's the time zone Maria in?

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Date: 1/23/20 21:57 (GMT+01:00)

To: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>

Cc: "Gorbalenya, A.E. (MSTAT)"

<A.E.Gorbalenya@lumc.nl>, Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, stanley-perlman@uiowa.edu, llmpoon@hku.hk, R.J.deGroot@uu.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks, Bart. I will do this tomorrow morning (CET), hoping that we can all (Leo?) agree with the name SARS-CoV-2.

Best regards,
John

Von meinem iPhone gesendet

Am 23.01.2020 um 21:43 schrieb B.L. Haagmans <b.haagmans@erasmusmc.nl>:

I talked to Maria van Kerkhove at WHO (vankerkhovem@who.int) and she will act as contact person. They are apparently convening a group to work on this.

So probably best if John communicates the outcome of our discussion to WHO on behalf of the Coronaviridae Study Group .

Bart

Van: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Verzonden: Thursday, January 23, 2020 8:14:00 PM

Aan: Alexander Gorbalenya (A.E.Gorbalenya@lumc.nl) <A.E.Gorbalenya@lumc.nl>

CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>

Onderwerp: Re: Virus name, decision of the Coronaviridae Study Group

Thanks, Sasha, for this clarification in your first sentence. I referred in my email to PREVIOUSLY established virus names (genome sequences were deposited in databases years ago and have been used in many publications!). I agree with you that, for NEW isolates detected in whatever species, names should now contain a reference to SARS-CoV-1 and, preferably, also contain some reference to indicate the host species from which the respective virus was isolated. We could recommend this.

Best,
John

Am 23.01.2020 um 19:50 schrieb <A.E.Gorbalenya@lumc.nl>
<A.E.Gorbalenya@lumc.nl>:

Hello,

There could be a room for proceeding with the Susan's suggestion, if it is applied to new isolates; we could expect that epidemiological research on SARS-CoV-1 will continue.

Since this application - as well as the virus naming (!) - is outside of the CSG remit, as John reminded, our decisions may be called "recommendations".

Best,

Sasha

From: John Ziebuhr [john.ziebuhr@viro.med.uni-giessen.de]

Sent: Thursday, January 23, 2020 7:29 PM

To: Baker, Susan

Cc: Benjamin Neuman; Baric, Ralph S; Gorbalenya, A.E. (MSTAT); stanley-perlman@uiowa.edu; llmpoon@hku.hk; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Hi Susan,

No, this does not fall within the remit of the CSG (it is below the species level). Also, I think it would cause major confusion in the community if people started renaming PREVIOUSLY characterized isolates from different species that have been available in databases for many years.

John

Am 23.01.2020 um 19:02 schrieb Baker, Susan
<Sbaker1@luc.edu>:

Hi John,

If we go with SARS-CoV-2 (which seems reasonable), should our study group report suggest that people use SARS-CoV-1 when they refer to the 2003 epidemic?

Susan

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, January 23, 2020 11:41 AM
To: Benjamin Neuman <bneuman@tamut.edu>
Cc: Baric, Ralph S
<rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Baker, Susan
<Sbaker1@luc.edu>; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.dros-ten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Ben,

I think it will be just a matter of time that, similar to what happened to HIV-1 (instead of HIV) in the past, people will start using the name SARS-CoV-1 if they want to refer to the virus from the 2003 epidemic.

Re Susan's question: The relatively short name SARS-CoV-2 could easily be extended by sample/lab/sequence numbers. This would be much less practicable if we used long virus names, such as SARS-like HCoV 2019.

John

Am 23.01.2020 um 18:14 schrieb Benjamin Neuman <bneuman@tamut.edu>:

I can get behind SARS-CoV-2 as well - presumably naming a place and a date as in influenza would be OK for a particular isolate? And does it mean retrospectively constructing an informal umbrella or perhaps serogroup without formal taxonomic standing for the previous epidemic SARS as SARS-CoV-1? That seems like it would be a reasonable recommendation, if it is what the committee proposes.

Benjamin Neuman

Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020 11:01 AM

To: Baric, Ralph S

Cc: A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Benjamin Neuman; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks for all your input. It seems we are approaching a consensus in terms of keeping "SARS" in the virus name. To keep the name simple, I would like to come back to Raoul's suggestion: SARS-CoV-2. This would correctly reflect the phylogenetic relationship of the virus and perhaps, in the short term, not contribute too much to fear in the public (because health authorities may keep saying that this virus differs from SARS-CoV).

Best,
John

Am 23.01.2020 um 17:49 schrieb
Baric, Ralph S
<rbaric@email.unc.edu>:

Dear All, Dr. Shi has a biorix paper showing the new SARS-like CoV uses hACE2 as a receptor for entry. Seems to me there is no escaping the fact that it is a kissing cousin to SARS-CoV. Given the fact that several other SARS-like CoV are circulating in bats that also use ACE2 receptors and grow in primary human cells, I don't think it is appropriate to uncouple the relationship with SARS-CoV-both for long-term planning, public health priorities and desire to alleviate public concern. The fact is that a range of SARS-like bCoV that

vary between 1-25% are likely positioned to emerge at sometime in the future. Moreover, it is impossible at this point to alleviate public concern after 20 million people in two cities have been placed under quarantine. Consequently, I favor a name that reflects the biological origins of the virus-as it will prove critical for long-term global health planning for repeat events in the future. I like Human SARSr-CoV 2019" or hSARS-CoV 2019 (Human SARS coronavirus 2019) or even SARS-like HCoV 2019.

I also believe that the CSG should be in charge, in consultation with other bodies, e.g. WHO, re virus naming.
Ralph

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Sent: Thursday, January 23, 2020
11:09 AM

To: stanley-perlman@uiowa.edu; llmpoon@hku.hk

Cc: bneuman@tamut.edu; john.ziebuhr@viro.med.uni-giessen.de; Baric, Ralph S <rbaric@email.unc.edu>; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear All,

I assume that there are people on the CSG, who are involved with the WHO on this issue (Christian, Leo?). Could they enlighten about the WHO position and whether the WHO will be comfortable with the CSG deciding on this matter within a timeframe it finds reasonable?

Best,

Sasha

From: Perlman, Stanley [stanley-perlman@uiowa.edu]

Sent: Thursday, January 23, 2020
4:51 PM

To: Leo Poon

Cc: Benjamin Neuman; John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csi.c.es; Drosten, Christian; Gorbalenya, A.E. (MSTAT)

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Leo,

I know that you are correct about the WHO recommendation, but I like Ben's idea. John's nomenclature is also fine with me. My children call the disease WURS (Wuhan respiratory syndrome), which has an easy name to remember, like SARS, MERS. This also shows what we talk about at the dinner table.

Stanley

Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

On Jan 23, 2020, at 9:45 AM, Leo Poon <llmpoon@hku.hk> wrote:

Ben,

WHO doesn't want a virus named after a location any more.

Cheers,

Leo

From: Benjamin Neuman
<bneuman@tamut.edu>

Sent: 23 January 2020
23:39

To: John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Perlman, Stanley; llmpoon@hkuc.hku.hk; isola@cnb.csi.c.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl

Subject: Re: Virus name, decision of the Coronaviridae Study Group

The name Wuhan seems to be the most often used by the public, but I think Wuhan seafood market pneumonia virus, as posted on the original genome sequence, is a bit wordy. But presumably, it would be a bit stigmatizing to name-check Wuhan?

I think there might be push-back from the pathology side of our field on calling it a strain of SARS if the receptor is different, as appears to be the case from the divergent spike RBD.

I can live with either of those names

proposed, if there is consensus.

What do you think of Human coronavirus-Wuhan 2019 (HCoV-Wuhan 2019), in the model of 229E, OC43, NL63 and HKU1?

Or perhaps abbreviate to HCoV-WU19?

Benjamin Neuman

Professor and Chair of
Biological Sciences
STEM 309D
Texas A&M University-
Texarkana
Texarkana, TX 75503

From: John Ziebuhr
<john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, January 23, 2020 9:21 AM
To: rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Benjamin Neuman; Perlman, Stanley; limpoon@hkuc.hku.hk; isola@cnb.csi.csi.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl
Subject: Virus name, decision of the Coronaviridae Study Group

Dear All,
I would like to get your view (as members of the *Coronaviridae* Study Group) on the naming of the coronavirus causing the

ongoing outbreak in Wuhan. Things are moving fast, so it would be good to get an agreement on this as soon as possible, ideally also with key WHO people involved once we have reached an agreement in the SG (similar to what we did with MERS in 2013, JVI paper).

Sasha and I are planning to put together a short paper in which we (and I hope all members of the Coronaviridae Study Group will join in) make a statement on the position of this virus within the existing taxonomy. Sasha is currently working on this.

Regarding the phylogenetic position of the virus, it is clear that the virus is part of an existing species called *SARS-related coronavirus*. All other viruses/isolates in that species (irrespective of whether they were isolated from humans, bats or other animals) have "SARS" in their names (SARS-CoV XYZ, SARS-CoV XYZ etc.). Thus, it would be more than justified to (also) have a reference to SARS in the name of this "new" virus.

My suggestion would be:

hSARS-CoV 2019 (Human SARS coronavirus 2019).

Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back".

The disease caused by the "new" virus may be very different from that caused by SARS-

CoV. And it will be difficult to get the message across to the general public that closely related (even nearly identical) viruses may cause very different outcomes of disease (see vaccine strains etc.).

To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019).

Please let me know your
views and get back to me as
soon as possible.
Best regards,
John

—

Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: [john.ziebuhr@viro.med.uni-
giessen.de](mailto:john.ziebuhr@viro.med.uni-giessen.de)

From: Drosten, Christian[christian.drosten@charite.de]
Sent: Fri 1/24/2020 3:27:42 AM (UTC-05:00)
To: Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]; Leo Poon[lmpoon@hku.hk]; John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Sbaker1@luc.edu[Sbaker1@luc.edu]; bneuman@tamut.edu[bneuman@tamut.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]; isola@cnb.csic.es[isola@cnb.csic.es]
Subject: Re: [ext] RE: Virus name, decision of the Coronaviridae Study Group

My vote is hSARS-CoV-2

Christian

--

Professor Christian Drosten

Director, Institute of Virology
Scientific Director, Charité Global Health

Charité - Universitätsmedizin Berlin
Campus Charité Mitte

Chariteplatz 1
D-10117 Berlin
Germany

E-Mail: christian.drosten@charite.de
<https://virologie-ccm.charite.de/>
<https://globalhealth.charite.de/>

Von: "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>

Datum: Freitag, 24. Januar 2020 um 09:16

An: Leo Poon <lmpoon@hku.hk>, John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>, "Baric, Ralph S" <rbaric@email.unc.edu>, "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, "Sbaker1@luc.edu" <Sbaker1@luc.edu>, "bneuman@tamut.edu" <bneuman@tamut.edu>, "stanley-perlman@uiowa.edu" <stanley-perlman@uiowa.edu>, "lmpoon@hkucc.hku.hk" <lmpoon@hkucc.hku.hk>, "isola@cnb.csic.es" <isola@cnb.csic.es>, Christian Drosten <christian.drosten@charite.de>

Betreff: [ext] RE: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2 (with option for SARS-CoV2.x per Sasha's advice). Naming it '19' in the long term would raise the question what 1-18 might be and in case of recurring introductions it would be a counting system anyway.

Best, Raoul

From: Leo Poon <lmpoon@hku.hk>

Sent: vrijdag 24 januari 2020 08:36

To: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl; Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; Groot, R.J. de (Raoul) <R.J.deGroot@uu.nl>; lmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear John,

I vote for hSARS-CoV-2019.

Best,

Leo

Leo Poon
Professor
School of Public Health
The University of Hong Kong
Hong Kong
Tel: . . .
Fax: (852) 2855 9587

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Friday, 24 January 2020 3:31 PM
To: Leo Poon <lmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl; Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; lmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Cc: John.Ziebuhr@viro.med.uni-giessen.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Dear All,

Many thanks for this very helpful discussion. I try to summarize the outcome of our discussion:

The new name should:

1. indicate the phylogeny of the virus (member of the species *Severe acute respiratory syndrome-related coronavirus*)
2. indicate the host
3. be distinct from SARS-CoV (2003)
4. be suitable to accommodate future introductions of this virus
5. not be overly long and thus remain practicable (to reduce the risk of people coming up with all sorts of abbreviations)

Based on these considerations and having read your comments and suggestions again, I would like to propose four options. The order reflects my own preference.

1. hSARS-CoV-19 (human SARS coronavirus 19)
2. hSARS-CoV-2019
3. hSARS-CoV-2

(4. hSARS-CoV-2.19)

The first two options use the year of the first isolation as a unique identifier. Future introductions would then

keep that virus name but be extended with sequence identifiers, e.g. hSARS-CoV-19 XY12345 or an additional number (if needed).

I believe the two-digit number should suffice to indicate the year (and reduce the length of the name by two or more syllables, depending on the language used).

I would prefer the year of discovery over a counting exercise of "introductions" (1st, 2nd, 3rd introduction). The counting would probably become a matter of debate in cases in which a virus is detected in just a single or very few individual(s).

I do not see a problem with year identifiers if a virus becomes established. The name would then still indicate the year in which it was discovered.

Can we have a vote on these options by later today, 6 pm (CET)?

Many thanks and best regards,

John

—
Prof. Dr. John Ziebuhr
Institut für Medizinische Virologie
Justus-Liebig-Universität Gießen
Schubertstraße 81 (BFS)
35392 Gießen
Tel.
Fax: 0641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

Am 24.01.2020 um 02:05 schrieb Leo Poon <llmpoon@hku.hk>:

Dear all,

Sounds we almost get a consensus after my night.

I will go for hSARS-CoV2019. This highlight the human component first, and this also makes it look different from SARS.

Cheers,

Leo

Leo Poon
Professor
School of Public Health
The University of Hong Kong
Hong Kong
Tel: , ,
Fax: (852) 2855 9587

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Friday, 24 January 2020 8:59 AM

To: A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl; john.ziebuhr@viro.med.uni-giessen.de
Cc: Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; Leo Poon
<llmpoon@hku.hk>; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es;
christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Good point. SARS-HCoV 2019 or hSARS-CoV 2019, then year of discovery distinguishes between introductions?

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>
Sent: Thursday, January 23, 2020 6:49 PM
To: b.haagmans@erasmusmc.nl; john.ziebuhr@viro.med.uni-giessen.de
Cc: Sbaker1@luc.edu; bneuman@tamut.edu; Baric, Ralph S <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu; llmpoon@hku.hk; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es;
christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Thank you, Bart!

Dear All,

People may read digit '2' in the virus name as the indicator of phylogenetic lineage or the number associated with second Introduction of the species into human population, or both, and all of these readings are accurate.

Now, I'd like to consider a hypothetical scenario with a third Introduction of the species into human population.

If the new virus was phylogenetically distinct from the current two, using digit '3' in its name would be straightforward move. However, if this hypothetical virus was close to either of the current two viruses, using '3' in its name would be poorly compatible with the virus phylogeny, while using a digit of the virus cousin would be misleading in respect to the virus spillover #, if we want the virus name to convey this aspect (do we?).

The above scenario shows that additional consideration of the name convention may be warranted before we go public.

For instance, the above problem could be solved if virus name includes double digit with each digit separated by dot, with the predot part labeling phylogeny and postdot part labelling spillover #. For the current virus, the name would include '2.1' instead of '2'.

Just a thought.

Best,

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>

Date: 1/23/20 22:25 (GMT+01:00)

To: "Gorbalenya, A.E. (MSTAT)" <A.E.Gorbalenya@lumc.nl>, john.ziebuhr@viro.med.uni-giessen.de

Cc: Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, stanley-perlman@uiowa.edu, llmpoon@hku.hk, R.J.deGroot@uu.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

CET Geneva ...

Van: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Verzonden: Thursday, January 23, 2020 10:06:12 PM

Aan: john.ziebuhr@viro.med.uni-giessen.de <john.ziebuhr@viro.med.uni-giessen.de>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>

CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>

Onderwerp: RE: Virus name, decision of the Coronaviridae Study Group

Bart,

What's the time zone Maria in?

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Date: 1/23/20 21:57 (GMT+01:00)

To: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>

Cc: "Gorbalenya, A.E. (MSTAT)"

<A.E.Gorbalenya@lumc.nl>, Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, stanley-

perlman@uiowa.edu, llmpoon@hku.hk, R.J.deGroot@uu.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks, Bart. I will do this tomorrow morning (CET), hoping that we can all (Leo?) agree with the name SARS-CoV-2.

Best regards,

John

Von meinem iPhone gesendet

Am 23.01.2020 um 21:43 schrieb B.L. Haagmans <b.haagmans@erasmusmc.nl>:

I talked to Maria van Kerkhove at WHO (vankerkhovem@who.int) and she will act as contact person. They are apparently convening a group to work on this.

So probably best if John communicates the outcome of our discussion to WHO on behalf of the Coronaviridae Study Group .

Bart

Van: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Verzonden: Thursday, January 23, 2020 8:14:00 PM

Aan: Alexander Gorbalenya (A.E.Gorbalenya@lumc.nl) <A.E.Gorbalenya@lumc.nl>

CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>

Onderwerp: Re: Virus name, decision of the Coronaviridae Study Group

Thanks, Sasha, for this clarification in your first sentence. I referred in my email to PREVIOUSLY established virus names (genome sequences were deposited in databases years ago and have been used in many publications!). I agree with you that, for NEW isolates detected in whatever species, names should now contain a reference to SARS-CoV-1 and, preferably, also contain some reference to indicate the host species from which the respective virus was isolated. We could recommend this.

Best,
John

Am 23.01.2020 um 19:50 schrieb <A.E.Gorbalenya@lumc.nl>
<A.E.Gorbalenya@lumc.nl>:

Hello,

There could be a room for proceeding with the Susan's suggestion, if it is applied to new isolates; we could expect that epidemiological research on SARS-CoV-1 will continue.

Since this application - as well as the virus naming (!) - is outside of the CSG remit, as John reminded, our decisions may be called "recommendations".

Best,

Sasha

From: John Ziebuhr [john.ziebuhr@viro.med.uni-giessen.de]
Sent: Thursday, January 23, 2020 7:29 PM
To: Baker, Susan
Cc: Benjamin Neuman; Baric, Ralph S; Gorbalenya, A.E. (MSTAT); stanley-perlman@uiowa.edu; llmpoon@hku.hk; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Hi Susan,

No, this does not fall within the remit of the CSG (it is below the species level). Also, I think it would cause major confusion in the community if people started renaming PREVIOUSLY characterized isolates from different species that have been available in databases for many years.

John

Am 23.01.2020 um 19:02 schrieb Baker, Susan
<Sbaker1@luc.edu>:

Hi John,
If we go with SARS-CoV-2 (which seems reasonable), should our study group report suggest that people use SARS-CoV-1 when they refer to the 2003 epidemic?
Susan

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, January 23, 2020 11:41 AM
To: Benjamin Neuman <bneuman@tamut.edu>
Cc: Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Baker, Susan <Sbaker1@luc.edu>; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Ben,

I think it will be just a matter of time that, similar to what happened to HIV-1 (instead of HIV) in the past, people will start using the name SARS-CoV-1 if they want to refer to the virus from the 2003 epidemic.

Re Susan's question: The relatively short name SARS-CoV-2 could easily be extended by sample/lab/sequence

numbers. This would be much less practicable if we used long virus names, such as SARS-like HCoV 2019.

John

Am 23.01.2020 um 18:14 schrieb Benjamin Neuman <bneuman@tamut.edu>:

I can get behind SARS-CoV-2 as well - presumably naming a place and a date as in influenza would be OK for a particular isolate? And does it mean retrospectively constructing an informal umbrella or perhaps serogroup without formal taxonomic standing for the previous epidemic SARS as SARS-CoV-1? That seems like it would be a reasonable recommendation, if it is what the committee proposes.

Benjamin Neuman

Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020 11:01 AM

To: Baric, Ralph S

Cc: A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Benjamin Neuman; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks for all your input. It seems we are approaching a consensus in terms of keeping "SARS" in the virus name. To keep the name simple, I would like to come back to Raoul's suggestion: SARS-CoV-2. This would correctly reflect the phylogenetic relationship of the virus and perhaps, in the short term, not contribute too much to fear in the public

(because health authorities may keep saying that this virus differs from SARS-CoV).

Best,
John

Am 23.01.2020 um 17:49 schrieb
Baric, Ralph S
<rbaric@email.unc.edu>:

Dear All, Dr. Shi has a biorix paper showing the new SARS-like CoV uses hACE2 as a receptor for entry. Seems to me there is no escaping the fact that it is a kissing cousin to SARS-CoV. Given the fact that several other SARS-like CoV are circulating in bats that also use ACE2 receptors and grow in primary human cells, I don't think it is appropriate to uncouple the relationship with SARS-CoV-both for long-term planning, public health priorities and desire to alleviate public concern. The fact is that a range of SARS-like bCoV that vary between 1-25% are likely positioned to emerge at sometime in the future. Moreover, it is impossible at this point to alleviate public concern after 20 million people in two cities have been placed under quarantine. Consequently, I favor a name that reflects the biological origins of the virus-as it will prove critical for long-term global health planning for repeat events in the future. I like Human SARSr-CoV 2019" or hSARS-CoV 2019 (Human SARS coronavirus 2019) or even SARS-like HCoV 2019.

I also believe that the CSG should be in charge, in consultation with other bodies, e.g. WHO, re virus naming.
Ralph

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Sent: Thursday, January 23, 2020

11:09 AM

To: stanley-perlman@uiowa.edu; llmpoon@hku.hk

Cc: bneuman@tamut.edu; john.ziebuhr@viro.med.uni-giessen.de; Baric, Ralph S <rbaric@email.unc.edu>; sbaker1@uc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear All,

I assume that there are people on the CSG, who are involved with the WHO on this issue (Christian, Leo?). Could they enlighten about the WHO position and whether the WHO will be comfortable with the CSG deciding on this matter within a timeframe it finds reasonable?

Best,

Sasha

From: Perlman, Stanley [stanley-perlman@uiowa.edu]

Subject: Re: Virus name, decision of the Coronaviridae Study Group

On Jan 23, 2020, at 9:45 AM, Leo Poon <llmpoon@hku.hk> wrote:

Ben,

WHO doesn't want a virus named after a location any more.

Cheers,

Leo

From: Benjamin Neuman
<bneuman@tamut.edu>

Sent: 23 January 2020
23:39

To: John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Perlman, Stanley; llmpoon@hkuc.hku.hk; isola@cnb.csi.c.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl

Subject: Re: Virus name, decision of the Coronaviridae Study Group

The name Wuhan seems to be the most often used by the public, but I think Wuhan seafood market pneumonia virus, as posted on the original genome sequence, is a bit wordy. But presumably, it would be a bit stigmatizing to name-check Wuhan?

I think there might be push-back from the pathology side of our field on calling it a strain of SARS if the receptor is different, as appears to be the case from the divergent spike RBD.

I can live with either of those names proposed, if there is consensus.

What do you think
of Human
coronavirus-
Wuhan 2019 (HCoV-
Wuhan 2019), in the
model of 229E, OC43,
NL63 and HKU1?

Or perhaps
abbreviate to HCoV-
WU19?

Benjamin Neuman

Professor and Chair of
Biological Sciences
STEM 309D
Texas A&M University-
Texarkana
Texarkana, TX 75503

From: John Ziebuhr
<john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January
23, 2020 9:21 AM

To: rbaric@email.unc.edu;
Sbaker1@luc.edu;

Groot, R.J. de
(Raoul); b.haagmans@erasmusmc.nl; Benjamin
Neuman; Perlman,

Stanley; lmpoon@hkuc.hku.hk; isola@cnb.csi.c.es; Drosten,

Christian; A.E.Gorbalenya@lumc.nl

Subject: Virus name,
decision of the
Coronaviridae Study
Group

Dear All,
I would like to get your view
(as members of
the *Coronaviridae* Study
Group) on the naming of the
coronavirus causing the
ongoing outbreak in Wuhan.
Things are moving fast, so it
would be good to get an

agreement on this as soon as possible, ideally also with key WHO people involved once we have reached an agreement in the SG (similar to what we did with MERS in 2013, JVI paper).

Sasha and I are planning to put together a short paper in which we (and I hope all members of the Coronaviridae Study Group will join in) make a statement on the position of this virus within the existing taxonomy. Sasha is currently working on this.

Regarding the phylogenetic position of the virus, it is clear that the virus is part of an existing species called *SARS-related coronavirus*. All other viruses/isolates in that species (irrespective of whether they were isolated from humans, bats or other animals) have "SARS" in their names (SARS-CoV XYZ, SARSr-CoV XYZ etc.). Thus, it would be more than justified to (also) have a reference to SARS in the name of this "new" virus.

My suggestion would be:

hSARS-CoV 2019 (Human SARS coronavirus 2019).

Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back". The disease

caused by the "new" virus may be very different from that caused by SARS-

CoV. And it will be difficult to get the message across to the general public that closely related (even nearly identical) viruses may cause very different outcomes of disease (see vaccine strains etc.).

To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019).

Please let me know your views and get back to me as soon as possible.

Best regards,
John

—

Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: John Ziebuhr[John.Ziebuhr@viro.med.uni-giessen.de]
Sent: Fri 1/24/2020 7:10:13 AM (UTC-05:00)
To: Isabel Sola[isola@cnb.csic.es]; Leo Poon[lmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Sbak1@luc.edu[Sbak1@luc.edu]; bneuman@tamut.edu[bneuman@tamut.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]; christian.drosten@charite.de[christian.drosten@charite.de]
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Dear All,

I am very sorry but I want to revoke the voting because I feel we should have another round of discussion before we make final decisions. Particularly, I would like to use this unique opportunity to set up a proper naming system for coronaviruses that, currently, does not exist. We could make such recommendations in the manuscript that we plan to publish in the near future.

This naming convention should accommodate additional information on specific isolates (similar to what is being done in the Flu field). I am sure that there will be hundreds of SARS-CoV-2 sequences in the near future, so it would be helpful to propose a system that is suitable to accommodate all these isolates.

Most importantly, we should again remove the host reference in the **prefix** („h") from the virus name because it is too restrictive at this position. Instead, the virus name should remain "broad" enough to accommodate viruses isolated from different host species. This important additional information should rather go to the **suffix**, together with two or three other important pieces of information.

The suffix should then contain information on (i) the host, (ii) year, (iii) location (iv) sequence identifier.

If we can agree on SARS-CoV-2 as the virus name to be used, we could extend this for specific isolates to generate something like SARS-CoV-2_hu/2019/Wuhan_XYZ12345 to refer to specific isolates.

So let me invite you to another round of discussion....

Best regards,

John

Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstr. 81, BFS
35392 Giessen, Germany
Phone:

Am 24.01.2020 um 11:37 schrieb Isabel Sola <isola@cnb.csic.es>:

Dear all,

My preference is hSARS-CoV-2019 as the first option and as second option, hSARS-CoV-19.

Thank you to all of you for the fruitful discussion.

Isabel

El 24/1/20 a las 8:31, John Ziebuhr escribió:

Dear All,

Many thanks for this very helpful discussion. I try to summarize the outcome of our discussion:

The new name should:

1. indicate the phylogeny of the virus (member of the species *Severe acute respiratory syndrome-related coronavirus*)
2. indicate the host
3. be distinct from SARS-CoV (2003)
4. be suitable to accommodate future introductions of this virus
5. not be overly long and thus remain practicable (to reduce the risk of people coming up with all sorts of abbreviations)

Based on these considerations and having read your comments and suggestions again, I would like to propose four options. The order reflects my own preference.

1. hSARS-CoV-19 (human SARS coronavirus 19)
2. hSARS-CoV-2019
3. hSARS-CoV-2

(4. hSARS-CoV-2.19)

The first two options use the year of the first isolation as a unique identifier. Future introductions would then keep that virus name but be extended with sequence identifiers, e.g. hSARS-CoV-19 XY12345 or an additional number (if needed). I believe the two-digit number should suffice to indicate the year (and reduce the length of the name by two or more syllables, depending on the language used). I would prefer the year of discovery over a counting exercise of "introductions" (1st, 2nd, 3rd introduction). The counting would probably become a matter of debate in cases in which a virus is detected in just a single or very few individual(s).

I do not see a problem with year identifiers if a virus becomes established. The name would then still indicate the year in which it was discovered.

Can we have a vote on these options by later today, 6 pm (CET)?

Many thanks and best regards,

John

—
Prof. Dr. John Ziebuhr
Institut für Medizinische Virologie
Justus-Liebig-Universität Gießen
Schubertstraße 81 (BFS)
35392 Gießen
Tel.
Fax: 0641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

Am 24.01.2020 um 02:05 schrieb Leo Poon <llmpoon@hku.hk>:

Dear all,

Sounds we almost get a consensus after my night.

I will go for hSARS-CoV2019. This highlight the human component first, and this also makes it look different from SARS.

Cheers,

Leo

Leo Poon
Professor
School of Public Health
The University of Hong Kong
Hong Kong
Tel:
Fax: (852) 2855 9587

From: Baric, Ralph S <rbaric@email.unc.edu>
Sent: Friday, 24 January 2020 8:59 AM
To: A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl;
john.ziebuhr@viro.med.uni-giessen.de
Cc: Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu;
Leo Poon <llmpoon@hku.hk>; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk;
isola@cnb.csic.es; christian.drosten@charite.de
Subject: RE: Virus name, decision of the Coronaviridae Study Group

Good point. SARS-HCoV 2019 or hSARS-CoV 2019, then year of discovery distinguishes between introductions?

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>
Sent: Thursday, January 23, 2020 6:49 PM
To: b.haagmans@erasmusmc.nl; john.ziebuhr@viro.med.uni-giessen.de
Cc: Sbaker1@luc.edu; bneuman@tamut.edu; Baric, Ralph S <rbaric@email.unc.edu>;

perlman@uiowa.edu; llmpoon@hku.hk; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Thank you, Bart!

Dear All,

People may read digit '2' in the virus name as the indicator of phylogenetic lineage or the number associated with second Introduction of the species into human population, or both, and all of these readings are accurate.

Now, I'd like to consider a hypothetical scenario with a third Introduction of the species into human population.

If the new virus was phylogenetically distinct from the current two, using digit '3' in its name would be straightforward move. However, if this hypothetical virus was close to either of the current two viruses, using '3' in its name would be poorly compatible with the virus phylogeny, while using a digit of the virus cousin would be misleading in respect to the virus spillover #, if we want the virus name to convey this aspect (do we?).

The above scenario shows that additional consideration of the name convention may be warranted before we go public.

For instance, the above problem could be solved if virus name includes double digit with each digit separated by dot, with the predot part labeling phylogeny and postdot part labelling spillover #. For the current virus, the name would include '2.1' instead of '2'.

Just a thought.

Best,

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>

Date: 1/23/20 22:25 (GMT+01:00)

To: "Gorbalenya, A.E. (MSTAT)"

<A.E.Gorbalenya@lumc.nl>, john.ziebuhr@viro.med.uni-giessen.de

Cc: Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, [\[perlman@uiowa.edu\]\(mailto:perlman@uiowa.edu\), \[llmpoon@hku.hk\]\(mailto:llmpoon@hku.hk\), \[R.J.deGroot@uu.nl\]\(mailto:R.J.deGroot@uu.nl\),](mailto:stanley-</p></div><div data-bbox=)

hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

CET Geneva ...

Van: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Verzonden: Thursday, January 23, 2020 10:06:12 PM

Aan: john.ziebuhr@viro.med.uni-giessen.de <john.ziebuhr@viro.med.uni-giessen.de>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>

CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>

Onderwerp: RE: Virus name, decision of the Coronaviridae Study Group

Bart,

What's the time zone Maria in?

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Date: 1/23/20 21:57 (GMT+01:00)

To: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>

Cc: "Gorbalenya, A.E. (MSTAT)"

<A.E.Gorbalenya@lumc.nl>, Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, stanley-perlman@uiowa.edu, llmpoon@hku.hk, R.J.deGroot@uu.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de

llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks, Bart. I will do this tomorrow morning (CET), hoping that we can all (Leo?) agree with the name SARS-CoV-2.

Best regards,
John

Von meinem iPhone gesendet

Am 23.01.2020 um 21:43 schrieb B.L. Haagmans
<b.haagmans@erasmusmc.nl>:

I talked to Maria van Kerkhove at WHO (vankerkhovem@who.int) and she will act as contact person. They are apparently convening a group to work on this.

So probably best if John communicates the outcome of our discussion to WHO on behalf of the Coronaviridae Study Group .

Bart

Van: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Verzonden: Thursday, January 23, 2020 8:14:00 PM

Aan: Alexander Gorbalenya (A.E.Gorbalenya@lumc.nl)
<A.E.Gorbalenya@lumc.nl>

CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>

Onderwerp: Re: Virus name, decision of the Coronaviridae Study Group

Thanks, Sasha, for this clarification in your first sentence. I referred in my email to PREVIOUSLY established virus names (genome sequences were deposited in databases years ago and have been used in many publications!). I agree with you that, for NEW isolates detected in whatever species, names should now contain a reference to SARS-CoV-1 and, preferably, also contain some reference to indicate the host species from which the respective virus was isolated. We could recommend this.

Best,
John

Am 23.01.2020 um 19:50 schrieb
<A.E.Gorbalenya@lumc.nl>
<A.E.Gorbalenya@lumc.nl>:

Hello,

There could be a room for proceeding with the Susan's suggestion, if it is applied to new isolates; we could expect that epidemiological research on

SARS-CoV-1 will continue.

Since this application - as well as the virus naming (!) - is outside of the CSG remit, as John reminded, our decisions may be called "recommendations".

Best,

Sasha

From: John Ziebuhr [john.ziebuhr@viro.med.uni-giessen.de]

Sent: Thursday, January 23, 2020 7:29 PM

To: Baker, Susan

Cc: Benjamin Neuman; Baric, Ralph S; Gorbalenya, A.E. (MSTAT); stanley-perlman@uiowa.edu; llmpoon@hku.hk; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Hi Susan,

No, this does not fall within the remit of the CSG (it is below the species level). Also, I think it would cause major confusion in the community if people started renaming PREVIOUSLY characterized isolates from different species that have been available in databases for many years.

John

Am 23.01.2020 um 19:02
schrieb Baker, Susan
<Sbaker1@luc.edu>:

Hi John,

If we go with SARS-CoV-2 (which seems reasonable), should our study group report suggest that people use SARS-CoV-1 when they refer to the 2003 epidemic?

Susan

From: John Ziebuhr

<john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020
11:41 AM

To: Benjamin Neuman
<bneuman@tamut.edu>

Cc: Baric, Ralph S
<rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Baker, Susan
<Sbaker1@luc.edu>; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Ben,

I think it will be just a matter of time that, similar to what happened to HIV-1 (instead of HIV) in the past, people will start using the name SARS-CoV-1 if they want to refer to the virus from the 2003 epidemic.

Re Susan's question: The relatively short name SARS-CoV-2 could easily be extended by sample/lab/sequence numbers. This would be much less practicable if we used long virus names, such as SARS-like HCoV 2019.

John

Am 23.01.2020 um
18:14 schrieb
Benjamin Neuman
<bneuman@tamut.edu>:

I can get behind SARS-CoV-2 as well - presumably naming a place and a date as in

influenza would be OK for a particular isolate? And does it mean retrospectively constructing an informal umbrella or perhaps serogroup without formal taxonomic standing for the previous epidemic SARS as SARS-CoV-1? That seems like it would be a reasonable recommendation, if it is what the committee proposes.

Benjamin Neuman

Professor and Chair of
Biological Sciences
STEM 309D
Texas A&M University-
Texarkana
Texarkana, TX 75503

From: John Ziebuhr
<john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, January 23, 2020 11:01 AM
To: Baric, Ralph S
Cc: A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk;
Benjamin Neuman; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: Re: Virus

name, decision of the
Coronaviridae Study
Group

Many thanks for all
your input. It seems
we are approaching a
consensus in terms of
keeping "SARS" in the
virus name. To keep
the name simple, I
would like to come
back to Raoul's
suggestion: SARS-CoV-
2. This would
correctly reflect the
phylogenetic
relationship of the
virus and perhaps, in
the short term, not
contribute too much
to fear in the public
(because health
authorities may keep
saying that this virus
differs from SARS-
CoV).

Best,
John

Am
23.01.20
20 um
17:49
schrieb
Baric,
Ralph S
<[rbaric@
email.unc
.edu](mailto:rbaric@email.unc.edu)>:

Dear All,
Dr. Shi has
a biorix
paper

showing
the new
SARS-like
CoV uses
hACE2 as
a receptor
for entry.
Seems to
me there
is no
escaping
the fact
that it is a
kissing
cousin to
SARS-CoV.
Given the
fact that
several
other
SARS-like
CoV are
circulating
in bats
that also
use ACE2
receptors
and grow
in primary
human
cells, I
don't
think it is
appropriat
e to
uncouple
the
relationshi
p with
SARS-CoV-
both for
long-term
planning,
public
health
priorities
and desire
to
alleviate
public
concern.
The fact is
that a

range of SARS-like bCoV that vary between 1-25% are likely positioned to emerge at sometime in the future. Moreover, it is impossible at this point to alleviate public concern after 20 million people in two cities have been placed under quarantine. Consequently, I favor a name that reflects the biological origins of the virus- as it will prove critical for long-term global health planning for repeat events in the future. I like Human SARSr-CoV

2019" or
hSARS-
CoV 2019
(Human
SARS
coronavir
us 2019)
or even
SARS-like
HCoV
2019.

I also
believe
that the
CSG
should be
in charge,
in
consultati
on with
other
bodies,
e.g. WHO,
re virus
naming.
Ralph

From: [A.E.
Gorbalenya@lumc.nl](mailto:A.E.Gorbalenya@lumc.nl)
<A.E.Gorbalenya@lumc.nl>

Sent: Thursday,
January
23, 2020
11:09 AM

To: [stanley-
perlman@
uiowa.edu](mailto:stanley-perlman@uiowa.edu)
; [llmpoon
@hku.hk](mailto:llmpoon@hku.hk)

Cc: [bneum
an@tamu
t.edu](mailto:bneuman@tamu.t.edu); [joh
n.ziebuhr
@viro.me
d.uni-
giessen.de](mailto:john.ziebuhr@viro.med.uni-giessen.de)
; Baric,

Ralph S
<rbaric@emil.unc.edu>; Sbaker1@luc.edu;
R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl;
llimpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear All,

I assume that there are people on the CSG, who are involved with the WHO on this issue (Christian, Leo?). Could they enlighten about the WHO position and whether the WHO will be comfortable with the CSG deciding on this matter

within a
timeframe
it finds
reasonable
?

Best,

Sasha

From: Per
Iman,
Stanley
[[stanley-
perlman@
uiowa.edu](mailto:stanley-perlman@uiowa.edu)
]

Sent: Thu
rday,
January
23, 2020
4:51 PM

To: Leo
Poon

Cc: Benja
min
Neuman;
John
Ziebuhr; [r
baric@em
ail.unc.edu](mailto:rbaric@email.unc.edu)
; [Sbaker1
@luc.edu](mailto:Sbaker1@luc.edu);
Groot, R.J.
de

(Raoul); [b.
haagmans
@erasmus
mc.nl](mailto:b.haagmans@erasmusmc.nl); [llm
poon@hku
cc.hku.hk](mailto:llmpoon@hkucc.hku.hk);
[isola@cncb.
csic.es](mailto:isola@cncb.csic.es);

Drosten,
Christian;
Gorbaleny
a, A.E.
(MSTAT)

Subject:
Re: Virus
name,
decision of
the
Coronaviri
dae Study
Group

Leo,

I know
that you
are
correct
about
the
WHO
recomm
endation
, but I
like
Ben's
idea.

John's
nomencl
ature is
also fine
with me.

My
children
call the
disease
WURS
(Wuhan
respirato
ry
syndrom
e), which
has an
easy
name to
rememb
er, like
SARS,
MERS.

This
also
shows
what we
talk
about at
the
dinner
table.

Stanley

Stanley
Perlman
, MD,

Ph.D.
Professor
r
Depts of
Microbiology and
Immunology, and
Pediatrics
s
BSB 3-
712
University of
Iowa
Iowa
City, IA
52242

On Jan 23, 2020, at 9:45 AM, Leo Poon
<lmpoon@hku.hk> wrote:

Ben,

WHO doesn't want a virus named after a location any
more.

Cheers,

Leo

From: Benjamin Neuman <bneuman@tamut.edu>
Sent: 23 January 2020 23:39
To: John
Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot,
R.J. de (Raoul); b.haagmans@erasmusmc.nl; Perlman,
Stanley; lmpoon@hkucc.hku.hk; isola@cnb.csic.es;
Drosten, Christian; A.E.Gorbalenya@lumc.nl
Subject: Re: Virus name, decision of the Coronaviridae
Study Group

The name Wuhan seems to be the most often used
by the public, but I think Wuhan seafood market
pneumonia virus, as posted on the original genome
sequence, is a bit wordy. But presumably, it would
be a bit stigmatizing to name-check Wuhan?

I think there might be push-back from the pathology side of our field on calling it a strain of SARS if the receptor is different, as appears to be the case from the divergent spike RBD.

I can live with either of those names proposed, if there is consensus.

What do you think of Human coronavirus-Wuhan 2019 (HCoV-Wuhan 2019), in the model of 229E, OC43, NL63 and HKU1?

Or perhaps abbreviate to HCoV-WU19?

Benjamin Neuman

Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020 9:21 AM

To: rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Benjamin Neuman; Perlman,

Stanley; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; A.E.Gorbalenya@lumc.nl

Subject: Virus name, decision of the Coronaviridae Study Group

Dear All,

I would like to get your view (as members of the *Coronaviridae* Study Group) on the naming of the coronavirus causing the ongoing outbreak in Wuhan. Things are moving fast, so it would be good to get an agreement on this as soon as possible, ideally also with key WHO people involved once we have reached an agreement in the SG (similar to what we did with MERS in 2013, JVI paper).

Sasha and I are planning to put together a short paper in which we (and I hope all members of the Coronaviridae Study Group will join in) make a statement on the position of this virus within the existing taxonomy. Sasha is currently working on this.

Regarding the phylogenetic position of the virus, it is clear that the virus is part of an existing species called *SARS-related coronavirus*. All other viruses/isolates in that species (irrespective of whether they were isolated from humans, bats or other animals) have "SARS" in their names (SARS-CoV XYZ, SARSr-CoV XYZ etc.). Thus, it would be more than justified to (also) have a reference to SARS in the name of this "new" virus.

My suggestion would be: hSARS-CoV 2019 (Human SARS coronavirus 2019).

Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back". The disease caused by the "new" virus may be very different from that caused by SARS-CoV. And it will be difficult to get the message across to the general public that closely related (even nearly identical) viruses may cause very different outcomes of disease (see vaccine strains etc.).

To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019).

Please let me know your views and get back to me as soon as possible.

Best regards,

John

—

Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

--

M^a Isabel Sola Gurpegui
Laboratorio Coronavirus
Departamento de Biología Molecular y Celular
Centro Nacional de Biotecnología, CNB-CSIC
Darwin, 3. Campus UAM-Cantoblanco
28049 Madrid
Tfno.

From: A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]
Sent: Fri 1/24/2020 7:24:20 AM (UTC-05:00)
To: John.Ziebuhr@viro.med.uni-giessen.de[John.Ziebuhr@viro.med.uni-giessen.de];
bneuman@tamut.edu[bneuman@tamut.edu]
Cc: Ilmpoon@hku.hk[Ilmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu];
b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl];
Sbaker1@luc.edu[Sbaker1@luc.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu];
R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; Ilmpoon@hkucc.hku.hk[Ilmpoon@hkucc.hku.hk];
isola@cnb.csic.es[isola@cnb.csic.es]; christian.drosten@charite.de[christian.drosten@charite.de]
Subject: RE: Virus name, decision of the Coronaviridae Study Group

...and **SARS-2** may be seen as a disease – rather than virus – definition...

From: John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>
Sent: vrijdag 24 januari 2020 13:22
To: Benjamin Neuman <bneuman@tamut.edu>
Cc: Leo Poon <Ilmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; Gorbalenya, A.E. (MSTAT) <A.E.Gorbalenya@lumc.nl>; b.haagmans@erasmusmc.nl; Sbaker1@luc.edu; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; Ilmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks, Ben. I agree with you. One thing is practicability, the other scientific correctness and usefulness for, say, epidemiological studies.

If we go for SARS-CoV-2, this is short (4 syllables) and distinctive enough and will probably be used. I am very pleased to see your suggestion in the second paragraph (which is essentially what I wanted to say...)

John

Am 24.01.2020 um 12:57 schrieb Benjamin Neuman <bneuman@tamut.edu>:

I think there is a balance to strike here between full information and usability.

My suggestion would be to try to say these names out loud.

Something like hSARS-CoV-2019 has twelve or thirteen syllables minimum, and it doesn't shorten gracefully to anything that would be distinct from SARS 2002.

In other words, you can name your kid Benjamin, but to everybody except his headstone, he is always just going to be Ben.

.....

Separately to the above, I prefer SARS-CoV-2 with an influenza-style host/place/month/year that is there for when you are writing things down and need precision, but would be dropped after the first time it appears in a paper.

A third outbreak is either phylogenetically closer to 1, 2 or different (3), but the details are built-in, and it can handle whatever weird new thing comes up.

The first part is for talking, the second part is for writing. It shortens to SARS-2 when you talk, and SARS-CoV-2 when you write.

I think people would actually use it. And SARS-2 is shorter to say than anything with Wuhan in the name, so the WHO and China feel OK about it.

Benjamin Neuman

Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Sent: Friday, January 24, 2020 1:31 AM

To: Leo Poon; Baric, Ralph S; A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl; Sbaker1@luc.edu; Benjamin Neuman; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Cc: John.Ziebuhr@viro.med.uni-giessen.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Dear All,

Many thanks for this very helpful discussion. I try to summarize the outcome of our discussion:

The new name should:

1. indicate the phylogeny of the virus (member of the species *Severe acute respiratory syndrome-related coronavirus*)
2. indicate the host
3. be distinct from SARS-CoV (2003)
4. be suitable to accomodate future introductions of this virus
5. not be overly long and thus remain practicable (to reduce the risk of people coming up with all sorts of abbreviations)

Based on these considerations and having read your comments and suggestions again, I would like to propose four options. The order reflects my own preference.

1. hSARS-CoV-19 (human SARS coronavirus 19)
2. hSARS-CoV-2019
3. hSARS-CoV-2

(4. hSARS-CoV-2.19)

The first two options use the year of the first isolation as a unique identifier. Future introductions would then keep that virus name but be extended with sequence identifiers, e.g. hSARS-CoV-19 XY12345 or an additional number (if needed).

I believe the two-digit number should suffice to indicate the year (and reduce the length of the name by two or more syllables, depending on the language used).

I would prefer the year of discovery over a counting exercise of "introductions" (1st, 2nd, 3rd introduction). The counting would probably become a matter of debate in cases in which a virus is detected in just a single or very few individual(s).

I do not see a problem with year identifiers if a virus becomes established. The name would then still indicate the year in which it was discovered.

Can we have a vote on these options by later today, 6 pm (CET)?

Many thanks and best regards,

John

—
Prof. Dr. John Ziebuhr
Institut für Medizinische Virologie
Justus-Liebig-Universität Gießen
Schubertstraße 81 (BFS)
35392 Gießen
Tel.: +49 641 9941209
Fax: 0641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

Am 24.01.2020 um 02:05 schrieb Leo Poon <lmpoon@hku.hk>:

Dear all,

Sounds we almost get a consensus after my night.

I will go for hSARS-CoV2019. This highlight the human component first, and this also makes it look different from SARS.

Cheers,

Leo

Leo Poon
Professor
School of Public Health
The University of Hong Kong
Hong Kong
Tel: +852 2855 9587
Fax: (852) 2855 9587

From: Baric, Ralph S <rbaric@email.unc.edu>

Sent: Friday, 24 January 2020 8:59 AM

To: A.E.Gorbalenya@lumc.nl; b.haagmans@erasmusmc.nl; john.ziebuhr@viro.med.uni-giessen.de

Cc: Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; Leo Poon <llmpoon@hku.hk>; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Good point. SARS-HCoV 2019 or hSARS-CoV 2019, then year of discovery distinguishes between introductions?

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Sent: Thursday, January 23, 2020 6:49 PM

To: b.haagmans@erasmusmc.nl; john.ziebuhr@viro.med.uni-giessen.de

Cc: Sbaker1@luc.edu; bneuman@tamut.edu; Baric, Ralph S <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu; llmpoon@hku.hk; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Thank you, Bart!

Dear All,

People may read digit '2' in the virus name as the indicator of phylogenetic lineage or the number associated with second Introduction of the species into human population, or both, and all of these readings are accurate.

Now, I'd like to consider a hypothetical scenario with a third Introduction of the species into human population.

If the new virus was phylogenetically distinct from the current two, using digit '3' in its name would be straightforward move. However, if this hypothetical virus was close to either of the current two viruses, using '3' in its name would be poorly compatible with the virus phylogeny, while using a digit of the virus cousin would be misleading in respect to the virus spillover #, if we want the virus name to convey this aspect (do we?).

The above scenario shows that additional consideration of the name convention may be warranted before we go public.

For instance, the above problem could be solved if virus name includes double digit with each digit separated by dot, with the predot part labeling phylogeny and postdot part labelling spillover #. For the current virus, the name would include '2.1' instead of '2'.

Just a thought.

Best,

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>
Date: 1/23/20 22:25 (GMT+01:00)
To: "Gorbalenya, A.E. (MSTAT)"
<A.E.Gorbalenya@lumc.nl>, john.ziebuhr@viro.med.uni-giessen.de
Cc: Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, stanley-perlman@uiowa.edu, llmpoon@hku.hk, R.J.deGroot@uu.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

CET Geneva ...

Van: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>
Verzonden: Thursday, January 23, 2020 10:06:12 PM
Aan: john.ziebuhr@viro.med.uni-giessen.de <john.ziebuhr@viro.med.uni-giessen.de>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>
CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>
Onderwerp: RE: Virus name, decision of the Coronaviridae Study Group

Bart,

What's the time zone Maria in?

Sasha

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Date: 1/23/20 21:57 (GMT+01:00)
To: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>
Cc: "Gorbalenya, A.E. (MSTAT)"
<A.E.Gorbalenya@lumc.nl>, Sbaker1@luc.edu, bneuman@tamut.edu, rbaric@email.unc.edu, stanley-perlman@uiowa.edu, llmpoon@hku.hk, R.J.deGroot@uu.nl, llmpoon@hkucc.hku.hk, isola@cnb.csic.es, christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks, Bart. I will do this tomorrow morning (CET), hoping that we can all (Leo?) agree with the name SARS-CoV-2.

Best regards,
John

Von meinem iPhone gesendet

Am 23.01.2020 um 21:43 schrieb B.L. Haagmans
<b.haagmans@erasmusmc.nl>:

I talked to Maria van Kerkhove at WHO (vankerkhovem@who.int) and she will act as contact person. They are apparently convening a group to work on this.

So probably best if John communicates the outcome of our discussion to WHO on behalf of the Coronaviridae Study Group .

Bart

Van: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Verzonden: Thursday, January 23, 2020 8:14:00 PM

Aan: Alexander Gorbalenya (A.E.Gorbalenya@lumc.nl)
<A.E.Gorbalenya@lumc.nl>

CC: Sbaker1@luc.edu <Sbaker1@luc.edu>; bneuman@tamut.edu <bneuman@tamut.edu>; rbaric@email.unc.edu <rbaric@email.unc.edu>; stanley-perlman@uiowa.edu <stanley-perlman@uiowa.edu>; llmpoon@hku.hk <llmpoon@hku.hk>; R.J.deGroot@uu.nl <R.J.deGroot@uu.nl>; b.haagmans@erasmusmc.nl <b.haagmans@erasmusmc.nl>; llmpoon@hkucc.hku.hk <llmpoon@hkucc.hku.hk>; isola@cnb.csic.es <isola@cnb.csic.es>; christian.drosten@charite.de <christian.drosten@charite.de>

Onderwerp: Re: Virus name, decision of the Coronaviridae Study Group

Thanks, Sasha, for this clarification in your first sentence. I referred in my email to PREVIOUSLY established virus names (genome sequences were deposited in databases years ago and have been used in many publications!). I agree with you that, for NEW isolates detected in whatever species, names should now contain a reference to SARS-CoV-1 and, preferably, also contain some reference to indicate the host species from which the respective virus was isolated. We could recommend this.

Best,
John

Am 23.01.2020 um 19:50 schrieb
<A.E.Gorbalenya@lumc.nl> <A.E.Gorbalenya@lumc.nl>:

Hello,

There could be a room for proceeding with the Susan's suggestion, if it is applied to new isolates; we could expect that epidemiological research on SARS-CoV-1 will continue.

Since this application - as well as the virus naming (!) - is outside of the CSG remit, as John reminded, our decisions may be called "recommendations".

Best,

Sasha

From: John Ziebuhr [john.ziebuhr@viro.med.uni-giessen.de]
Sent: Thursday, January 23, 2020 7:29 PM
To: Baker, Susan
Cc: Benjamin Neuman; Baric, Ralph S; Gorbalenya, A.E. (MSTAT); stanley-perlman@uiowa.edu; llmpoon@hku.hk; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de
Subject: Re: Virus name, decision of the Coronaviridae Study Group

Hi Susan,

No, this does not fall within the remit of the CSG (it is below the species level). Also, I think it would cause major confusion in the community if people started renaming PREVIOUSLY characterized isolates from different species that have been available in databases for many years.

John

Am 23.01.2020 um 19:02 schrieb Baker, Susan
<Sbaker1@luc.edu>:

Hi John,

If we go with SARS-CoV-2 (which seems reasonable), should our study group report suggest that people use SARS-CoV-1 when they refer to the 2003 epidemic?

Susan

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, January 23, 2020 11:41 AM
To: Benjamin Neuman <bneuman@tamut.edu>
Cc: Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Baker, Susan <Sbaker1@luc.edu>; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es

@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the
Coronaviridae Study Group

Ben,

I think it will be just a matter of time that, similar to what happened to HIV-1 (instead of HIV) in the past, people will start using the name SARS-CoV-1 if they want to refer to the virus from the 2003 epidemic.

Re Susan's question: The relatively short name SARS-CoV-2 could easily be extended by sample/lab/sequence numbers. This would be much less practicable if we used long virus names, such as SARS-like HCoV 2019.

John

Am 23.01.2020 um 18:14 schrieb
Benjamin Neuman
<bneuman@tamut.edu>:

I can get behind SARS-CoV-2 as well - presumably naming a place and a date as in influenza would be OK for a particular isolate? And does it mean retrospectively constructing an informal umbrella or perhaps serogroup without formal taxonomic standing for the previous epidemic SARS as SARS-CoV-1? That seems like it would be a reasonable recommendation, if it is what the committee proposes.

Benjamin Neuman

Professor and Chair of Biological
Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr

<john.ziebuhr@viro.med.uni-giessen.de>

Sent: Thursday, January 23, 2020
11:01 AM

To: Baric, Ralph S

Cc: A.E.Gorbalenya@lumc.nl; stanley-perlman@uiowa.edu; llmpoon@hku.hk; Benjamin

Neuman; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; christian.drosten@charite.de

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Many thanks for all your input. It seems we are approaching a consensus in terms of keeping "SARS" in the virus name. To keep the name simple, I would like to come back to Raoul's suggestion: SARS-CoV-2. This would correctly reflect the phylogenetic relationship of the virus and perhaps, in the short term, not contribute too much to fear in the public (because health authorities may keep saying that this virus differs from SARS-CoV).

Best,
John

Am 23.01.2020 um
17:49 schrieb Baric,
Ralph S
<rbaric@email.unc.edu
u>:

Dear All, Dr. Shi has a biorix paper showing the new SARS-like CoV uses hACE2 as a receptor for entry. Seems to me there is no escaping the fact that it is a kissing cousin

to SARS-CoV. Given the fact that several other SARS-like CoV are circulating in bats that also use ACE2 receptors and grow in primary human cells, I don't think it is appropriate to uncouple the relationship with SARS-CoV-both for long-term planning, public health priorities and desire to alleviate public concern. The fact is that a range of SARS-like bCoV that vary between 1-25% are likely positioned to emerge at sometime in the future. Moreover, it is impossible at this point to alleviate public concern after 20 million people in two cities have been placed under quarantine.

Consequently, I favor a name that reflects the biological origins of the virus-as it will prove critical for long-term global health planning for repeat events in the future. I like Human SARSr-CoV 2019" or hSARS-CoV 2019 (Human SARS coronavirus 2019) or even SARS-like HCoV 2019.

I also believe that the CSG should be in charge, in consultation with other bodies, e.g. WHO, re virus naming.
Ralph

From: A.E.Gorbalenya@lumc.nl <A.E.Gorbalenya@lumc.nl>

Sent: Thursday, January

23, 2020 11:09 AM

To: stanley-perlman@uiowa.edu; llmpoon@hku.hk

Cc: bneuman@tamut.edu; john.ziebuhr@viro.med.uni-giessen.de;

Baric, Ralph S

rbaric@email.unc.edu
>; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl;
llmpoon@hkucc.hku.hk
; isola@cnb.csic.es; christian.drosten@charite.de

Subject: RE: Virus name, decision of the Coronaviridae Study Group

Dear All,

I assume that there are people on the CSG, who are involved with the WHO on this issue (Christian, Leo?). Could they enlighten about the WHO position and whether the WHO will be comfortable with the CSG deciding on this matter within a timeframe it finds reasonable?

Best,

Sasha

From: Perlman, Stanley
[stanley-perlman@uiowa.edu]

Sent: Thursday, January 23, 2020 4:51 PM

To: Leo Poon

Cc: Benjamin Neuman; John

Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; [Groot, R.J. de \(Raoul\); b.haagmans@e](mailto:Groot, R.J. de (Raoul); b.haagmans@e)

rasmusmc.nl; lmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; Gorbalenya, A.E. (MSTAT)

Subject: Re: Virus name, decision of the Coronaviridae Study Group

Leo,

I know that you are correct about the WHO recommendation, but I like Ben's idea. John's nomenclature is also fine with me. My children call the disease WURS (Wuhan respiratory syndrome), which has an easy name to remember, like SARS, MERS. This also shows what we talk about at the dinner table.

Stanley

Stanley Perlman, MD,
Ph.D.
Professor
Depts of
Microbiology and
Immunology, and
Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

On Jan
23, 2020,
at 9:45
AM, Leo
Poon
<lmpoon@hku.hk>
> wrote:

Ben,

WHO
doesn't
want a
virus
named
after a
location
any
more.

Cheers,

Leo

From: Benjamin Neuman <bneuman@tamut.edu>

Sent: 23 January 2020 23:39

To: John Ziebuhr; rbaric@email.unc.edu; Sbaker1@luc.edu; Groot, R.J. de (Raoul); b.haagmans@erasmusmc.nl; Perlman, Stanley; ljmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; A.E.Gorbalenya@erasmusmc.nl

Subject: Re: Virus

name,
decision
of the
Coronaviri
dae Study
Group

The
name
Wuhan
seems to
be the
most
often
used by
the
public,
but I
think
Wuhan
seafood
market
pneumon
ia virus,
as posted
on the
original
genome
sequence
, is a bit
wordy.
But
presuma
bly, it
would be
a bit
stigmatizi
ng to
name-
check
Wuhan?

I think
there
might be
push-
back
from the
patholog

y side of
our
field on
calling it
a strain
of SARS if
the
receptor
is
different,
as
appears
to be the
case
from the
divergent
spike
RBD.

I can live
with
either of
those
names
proposed
, if there
is
consensus.

What do
you think
of Human
coronavirus-
Wuhan 2
019
(HCoV-
Wuhan
2019), in
the
model of
229E,
OC43,
NL63 and
HKU1?

Or

perhaps
abbreviat
e
to HCoV-
WU19?

Benjamin
Neuman

Professor
and Chair
of
Biological
Sciences
STEM
309D
Texas
A&M
University-
Texarkana
Texarkana
, TX 75503

From: Joh
n Ziebuhr
<[john.ziebuhr@viro.
med.uni-
giessen.de](mailto:john.ziebuhr@viro.med.uni-giessen.de)
>

Sent: Thur
sday,
January
23, 2020
9:21 AM

To: [rbaric
@email.u
nc.edu](mailto:rbaric@email.unc.edu); [Sb
aker1@lu
c.edu](mailto:Sbaker1@luc.edu);
Groot, R.J.
de
(Raoul); [b.
haagmans
@erasmus
mc.nl](mailto:b.haagmans@erasmusmc.nl);
Benjamin
Neuman;
Perlman,
Stanley;

kucc.hku.hk;
isola@cnb.csic.es;
Drosten,
Christian;
A.E.Gorbalenya@lumc.nl

Subject: Virus name,
decision of the
Coronaviridae Study
Group

Dear All,
I would like to get your view (as members of the *Coronaviridae* Study Group) on the naming of the coronavirus causing the ongoing outbreak in Wuhan. Things are moving fast, so it would be good to get an agreement on this as soon as possible, ideally also with key WHO people involved once we have reached an agreement in the SG (similar to what we did with MERS in 2013, JVI paper). Sasha and I are planning to put together a short paper in which we (and I hope all members

of the
Coronavirida
e Study
Group will
join in) make
a statement
on the
position of
this virus
within the
existing
taxonomy.
Sasha is
currently
working on
this.
Regarding
the
phylogenetic
position of
the virus, it
is clear that
the virus is
part of an
existing
species
called *SARS-
related
coronavirus*.
All other
viruses/isola
tes in that
species
(irrespective
of whether
they were
isolated
from
humans,
bats or other
animals)
have "SARS"
in their
names (SARS-
CoV XYZ,
SARSr-CoV
XYZ etc.).
Thus, it
would be
more than
justified to
(also) have a
reference to
SARS in the
name of this
"new" virus.
My
suggestion
would be:
hSARS-CoV
2019
(Human
SARS
coronavirus
2019).

Having said this, I am fully aware that there will be major concerns from health authorities which do not want to give the impression that "SARS is back".

The disease caused by the "new" virus may be very different from that caused by SARS-

CoV. And it will be difficult to get the message across to the general public that closely related (even nearly identical) viruses may cause very different outcomes of disease (see vaccine strains etc.).

To address this latter concern, we may call the virus: RS-CoV 2019 (Respiratory syndrome coronavirus 2019).

Please let me know your views and get back to me as soon as possible.

Best regards,
John

—
Prof. Dr. John
Ziebuhr
Institute of
Medical
Virology
Justus Liebig
University
Giessen
Schubertstrass
e 81 (BFS)
35392 Giessen
Germany
Tel.:

Fax: +49-641-
9941209

E-
[mail: john.ziebuhr@viro.med.
uni-giessen.de](mailto:john.ziebuhr@viro.med.uni-giessen.de)

From: Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]
Sent: Fri 1/24/2020 9:24:59 AM (UTC-05:00)
To: Baric, Ralph S[rbaric@email.unc.edu]; B.L. Haagmans[b.haagmans@erasmusmc.nl]; 'Drosten, Christian'[christian.drosten@charite.de]; John Ziebuhr[John.Ziebuhr@viro.med.uni-giessen.de]; Isabel Sola[isola@cnb.csic.es]; Leo Poon[lmpoon@hku.hk]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; Sbaker1@luc.edu[Sbaker1@luc.edu]; bneuman@tamut.edu[bneuman@tamut.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]
Subject: RE: [ext] Re: Virus name, decision of the Coronaviridae Study Group

Me too (except perhaps hu instead of human?)

Raoul

Sent from my Samsung Galaxy smartphone.

----- Original message -----

From: "Baric, Ralph S" <rbaric@email.unc.edu>
Date: 1/24/20 15:14 (GMT+01:00)
To: "B.L. Haagmans" <b.haagmans@erasmusmc.nl>, "'Drosten, Christian'" <christian.drosten@charite.de>, John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>, Isabel Sola <isola@cnb.csic.es>, Leo Poon <lmpoon@hku.hk>, A.E.Gorbalenya@lumc.nl, Sbaker1@luc.edu, bneuman@tamut.edu, stanley-perlman@uiowa.edu, "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>, lmpoon@hkucc.hku.hk
Subject: RE: [ext] Re: Virus name, decision of the Coronaviridae Study Group

I could be happy with this as well.

From: B.L. Haagmans <b.haagmans@erasmusmc.nl>
Sent: Friday, January 24, 2020 8:26 AM
To: 'Drosten, Christian' <christian.drosten@charite.de>; John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>; Isabel Sola <isola@cnb.csic.es>; Leo Poon <lmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; lmpoon@hkucc.hku.hk
Subject: RE: [ext] Re: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2/Human/2019/Wuhan_XYZ12345 would perfectly make sense to me.
Bart

Van: Drosten, Christian <christian.drosten@charite.de>
Verzonden: vrijdag 24 januari 2020 13:16
Aan: John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>; Isabel Sola <isola@cnb.csic.es>; Leo Poon <lmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; B.L. Haagmans <b.haagmans@erasmusmc.nl>; Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; lmpoon@hkucc.hku.hk
Onderwerp: Re: [ext] Re: Virus name, decision of the Coronaviridae Study Group

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Christian

--

Professor Christian Drosten

Director, Institute of Virology
Scientific Director, Charité Global Health

Charité - Universitätsmedizin Berlin
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Chariteplatz 1
D-10117 Berlin
Germany

E-Mail: christian.drosten@charite.de
<https://virologie-ccm.charite.de/>
<https://globalhealth.charite.de/>

Von: John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>

Datum: Freitag, 24. Januar 2020 um 13:10

An: Isabel Sola <isola@cnb.csic.es>, Leo Poon <lmpoon@hku.hk>, "Baric, Ralph S" <rbaric@email.unc.edu>, "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, "Sbaker1@luc.edu" <Sbaker1@luc.edu>, "bneuman@tamut.edu" <bneuman@tamut.edu>, "stanley-perlman@uiowa.edu" <stanley-perlman@uiowa.edu>, "R.J.deGroot@uu.nl" <R.J.deGroot@uu.nl>, "lmpoon@hkucc.hku.hk" <lmpoon@hkucc.hku.hk>, Christian Drosten <christian.drosten@charite.de>

Betreff: [ext] Re: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2_hu/2019/Wuhan_XYZ12345

From: Perlman, Stanley[stanley-perlman@uiowa.edu]
Sent: Fri 1/24/2020 10:57:24 AM (UTC-05:00)
To: John Ziebuhr[John.Ziebuhr@viro.med.uni-giessen.de]
Cc: B.L. Haagmans[b.haagmans@erasmusmc.nl]; Baker, Susan[Sbaker1@luc.edu]; Drosten, Christian[christian.drosten@charite.de]; Isabel Sola[isola@cnb.csic.es]; Leo Poon[lmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; bneuman@tamut.edu[bneuman@tamut.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]
Subject: Re: [ext] Re: Virus name, decision of the Coronaviridae Study Group

I am fine with this as well. Either Human or Hu is ok with me.

Stanley Perlman, MD, Ph.D.

Professor

Depts of Microbiology and Immunology, and Pediatrics

BSB 3-712

University of Iowa

Iowa City, IA 52242

On Jan 24, 2020, at 8:35 AM, Baker, Susan <Sbaker1@luc.edu> wrote:

SARS-CoV-2/Human/2019/Wuhan_XYZ12345

Makes sense to me, and supports a consistent naming scheme. Thanks to all for the discussion.
Susan

From: B.L. Haagmans <b.haagmans@erasmusmc.nl>
Sent: Friday, January 24, 2020 7:26 AM
To: 'Drosten, Christian' <christian.drosten@charite.de>; John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>; Isabel Sola <isola@cnb.csic.es>; Leo Poon <lmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; Baker, Susan <Sbaker1@luc.edu>; bneuman@tamut.edu; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; lmpoon@hkucc.hku.hk
Subject: RE: [ext] Re: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2/Human/2019/Wuhan_XYZ12345 would perfectly make sense to me.
Bart

Van: Drosten, Christian <christian.drosten@charite.de>
Verzonden: vrijdag 24 januari 2020 13:16
Aan: John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>; Isabel Sola <isola@cnb.csic.es>; Leo Poon <lmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; B.L. Haagmans <b.haagmans@erasmusmc.nl>; Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; lmpoon@hkucc.hku.hk
Onderwerp: Re: [ext] Re: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2_hu/2019/Wuhan_XYZ12345 is good IMHO, but the "human" could as well go like with the influenza nomenclature: SARS-CoV-2/Human/2019/Wuhan_XYZ12345

Christian

--

Professor Christian Drosten

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D-10117 Berlin
Germany

E-Mail: christian.drosten@charite.de
<https://virologie-ccm.charite.de/>
<https://globalhealth.charite.de/>

Von: John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>

Datum: Freitag, 24. Januar 2020 um 13:10

An: Isabel Sola <isola@cnb.csic.es>, Leo Poon <lmpoon@hku.hk>, "Baric, Ralph S" <rbaric@email.unc.edu>, "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, "Sbaker1@luc.edu" <Sbaker1@luc.edu>, "bneuman@tamut.edu" <bneuman@tamut.edu>, "stanley-perlman@uiowa.edu" <stanley-perlman@uiowa.edu>, "R.J.deGroot@uu.nl" <R.J.deGroot@uu.nl>, "lmpoon@hkucc.hku.hk" <lmpoon@hkucc.hku.hk>, Christian Drosten <christian.drosten@charite.de>

Betreff: [ext] Re: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2_hu/2019/Wuhan_XYZ12345

From: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]
Sent: Fri 1/24/2020 1:12:29 PM (UTC-05:00)
To: Perlman, Stanley[stanley-perlman@uiowa.edu]; B.L. Haagmans[b.haagmans@erasmusmc.nl]; Baker, Susan[Sbaker1@luc.edu]; Drosten, Christian[christian.drosten@charite.de]; Isabel Sola[isola@cnb.csic.es]; Leo Poon[llmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; bneuman@tamut.edu[bneuman@tamut.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]
Subject: Re: [ext] Virus name, decision of the Coronaviridae Study Group

Dear All,

I think we reached an agreement, which is great! - I thank you all for these very constructive discussions.

The following decisions were made:

- 1) The name will be SARS-CoV-2 (SARS coronavirus 2).
- 2) A recommendation will be made that specific isolates should be named according to the following scheme: SARS-CoV-2/Human/2019/Wuhan_XYZ12345

I have contacted WHO this morning (indicating where the study group is going) but did not receive a reply yet. I can imagine that, in the current emergency state in China, WHO is not keen on going ahead with adopting a name that makes a reference to SARS. I must say that I fully understand this policy at this moment in time.

As for the CSG, it will now be important to put together a paper that firmly establishes the phylogeny of SARS-CoV-2 and puts this virus in context to previously described viruses in that particular species and lineage. Sasha is working on this. This manuscript will present the scientific basis for the decision of the CSG to introduce this particular virus name and it will also include biological implications of Sasha's analysis.

Many thanks again and best regards,

John

Am 24.01.2020 um 16:57 schrieb Perlman, Stanley <stanley-perlman@uiowa.edu>:

I am fine with this as well. Either Human or Hu is ok with me.
Stanley Perlman, MD, Ph.D.
Professor
Depts of Microbiology and Immunology, and Pediatrics
BSB 3-712
University of Iowa
Iowa City, IA 52242

On Jan 24, 2020, at 8:35 AM, Baker, Susan <Sbaker1@luc.edu> wrote:

SARS-CoV-2/Human/2019/Wuhan_XYZ12345

Makes sense to me, and supports a consistent naming scheme. Thanks to all for the discussion.

Susan

From: B.L. Haagmans <b.haagmans@erasmusmc.nl>

Sent: Friday, January 24, 2020 7:26 AM

To: 'Drosten, Christian' <christian.drosten@charite.de>; John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>; Isabel Sola <isola@cnb.csic.es>; Leo Poon <llmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; Baker, Susan <Sbaker1@luc.edu>; bneuman@tamut.edu; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk

Subject: RE: [ext] Re: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2/Human/2019/Wuhan_XYZ12345 would perfectly make sense to me.

Bart

Van: Drosten, Christian <christian.drosten@charite.de>

Verzonden: vrijdag 24 januari 2020 13:16

Aan: John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>; Isabel Sola <isola@cnb.csic.es>; Leo Poon <llmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; B.L. Haagmans <b.haagmans@erasmusmc.nl>; Sbaker1@luc.edu; bneuman@tamut.edu; stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk

Onderwerp: Re: [ext] Re: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2_hu/2019/Wuhan_XYZ12345 is good IMHO, but the "human" could as well go like with the influenza nomenclature: SARS-CoV-2/Human/2019/Wuhan_XYZ12345

Christian

--

Professor Christian Drosten

Director, Institute of Virology
Scientific Director, Charité Global Health

Charité - Universitätsmedizin Berlin
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Chariteplatz 1
D-10117 Berlin
Germany

E-Mail: christian.drosten@charite.de
<https://virologie-ccm.charite.de/>
<https://globalhealth.charite.de/>

Von: John Ziebuhr <John.Ziebuhr@viro.med.uni-giessen.de>

Datum: Freitag, 24. Januar 2020 um 13:10

An: Isabel Sola <isola@cnb.csic.es>, Leo Poon <llmpoon@hku.hk>, "Baric, Ralph S" <rbaric@email.unc.edu>, "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, "Sbaker1@luc.edu" <Sbaker1@luc.edu>, "bneuman@tamut.edu" <bneuman@tamut.edu>, "stanley-

perlman@uiowa.edu" <stanley-perlman@uiowa.edu>, "R.J.deGroot@uu.nl"
<R.J.deGroot@uu.nl>, "Ilmpoon@hkucc.hku.hk" <Ilmpoon@hkucc.hku.hk>,
Christian Drosten <christian.drosten@charite.de>

Betreff: [ext] Re: Virus name, decision of the Coronaviridae Study Group

SARS-CoV-2_hu/2019/Wuhan_XYZ12345

From: zlshi[zlshi@wh.iov.cn]
Sent: Thur 2/13/2020 3:26:25 AM (UTC-05:00)
To: Baric, Ralph S[rbaric@email.unc.edu]
Subject: virus name
Attachment: 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,

SHI Zhengli, Ph. D
Senior Scientist & Professor
Wuhan Institute of Virology, Chinese Academy of Sciences
44 Xiao Hong Shan
430071 Wuhan, Hubei
China
Tel & Fax:
Email: zlshi@wh.iov.cn

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 SARSr-CoV, which complies with the conventions of the classification and nomenclature of ICTV.

Proposers:

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

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

Deyin Guo, Sun Yat-sen University School of Medicine

References

1. Chen L., et al., RNA based mNGS approach identifies a novel human coronavirus from two individual pneumonia cases in 2019 Wuhan outbreak. *Emerg Microbes Infect.* 2020 Dec;9(1):313-319.
2. China National Health Commission, Official Announcement regarding the Name of Disease Caused by 2019-nCoV on 8 February 2020.

<http://www.nhc.gov.cn/xcs/zhengcwj/202002/18c1bb43965a4492907957875de02ae7.shtml>.

3. Ge XY, et al. (2013) Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. *Nature* 503:535-538.
4. Gorbalenya AE et al., Severe acute respiratory syndrome-related coronavirus – The species and its viruses, a statement of the Coronavirus Study Group. *BioRxiv* 2020.02.07.937862; doi: <https://doi.org/10.1101/2020.02.07.937862>
5. Guan Y, et al. Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China. *Science*. 2003; 302:276–8.
6. Jiang S, Shi Z. The first disease X is caused by a highly transmissible acute respiratory syndrome coronavirus (TARS-CoV). *Viol Sin*. 2020 Feb 9. doi: [10.1007/s12250-020-00206-5](https://doi.org/10.1007/s12250-020-00206-5).
7. World Health Organization. (2015). World Health Organization best practices for the naming of new human infectious diseases.
8. World Health Organization. (2020). Situation Report. <https://www.who.int/emergencies/diseases/novel-coronavirus-2019> on 30 January 2020.
9. World Health Organization. (2020). WHO Director-General's remarks at the media briefing on 2019-nCoV on 11 February 2020
10. Wu F, et al. A new coronavirus associated with human respiratory disease in China. *Nature*. 2020 Feb 3. doi: [10.1038/s41586-020-2008-3](https://doi.org/10.1038/s41586-020-2008-3). [Epub ahead of print]
11. Zhou P, et al., A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*. 2020 Feb 3. doi: [10.1038/s41586-020-2012-7](https://doi.org/10.1038/s41586-020-2012-7). [Epub ahead of print]
12. Zhu et al., (2020) A Novel Coronavirus from Patients with Pneumonia in China, 2019. *N Engl J Med*. 2020 Jan 24. doi: [10.1056/NEJMoa2001017](https://doi.org/10.1056/NEJMoa2001017). [Epub ahead of print]

From: Drosten, Christian[christian.drosten@charite.de]
Sent: Thur 2/13/2020 7:40:21 AM (UTC-05:00)
To: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Perlman, Stanley[stanley-perlman@uiowa.edu]; B.L. Haagmans[b.haagmans@erasmusmc.nl]; Baker, Susan[Sbaker1@luc.edu]; Isabel Sola[isola@cnb.csic.es]; Leo Poon[lmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; bneuman@tamut.edu[bneuman@tamut.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]
Subject: Re: [ext] Fwd: virus name

Dear John,

Bart and me joined a discussion in WHO while in the meeting yesterday. Your rendering of the situation is 100% correct. WHO entirely prioritizes on risk communication and inter-country sensitivities. Bart and I made the point that an acronym like COVID will inevitably be confused with a virus name because acronyms (HBV, CMV) are commonly associated with virus names. This whole discussion was to no avail. They will stick to COVID19 now that it is out, and will try to speak of "the virus that causes COVID19". We will have to live with this situation.

Christian

--

Professor Christian Drosten

Director, Institute of Virology
Scientific Director, Charité Global Health

Charité - Universitätsmedizin Berlin
Campus Charité Mitte

Chariteplatz 1
D-10117 Berlin
Germany

E-Mail: christian.drosten@charite.de
<https://virologie-ccm.charite.de/>
<https://globalhealth.charite.de/>

Von: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>

Datum: Donnerstag, 13. Februar 2020 um 13:20

An: "Perlman, Stanley" <stanley-perlman@uiowa.edu>, "B.L. Haagmans" <b.haagmans@erasmusmc.nl>, "Baker, Susan" <Sbaker1@luc.edu>, Isabel Sola <isola@cnb.csic.es>, Leo Poon <lmpoon@hku.hk>, "Baric, Ralph S" <rbaric@email.unc.edu>, "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>, "bneuman@tamut.edu" <bneuman@tamut.edu>, "R.J.deGroot@uu.nl" <R.J.deGroot@uu.nl>, "lmpoon@hkucc.hku.hk" <lmpoon@hkucc.hku.hk>, Christian Drosten <christian.drosten@charite.de>

Betreff: [ext] Fwd: virus name

Dear All,

I am swamped with emails from Chinese colleagues, including eminent scientists in the field. You might be experiencing similar things at the moment. As the vast majority of these emails (or statements) do not make reference to the SCIENTIFIC ESSENCE of our paper, I am more than reluctant to enter such discussions because I fear that I would end up in heated POLITICAL rather than scientific discussions. Also, I feel that, if we start compromising the scientific basis of our taxonomic assignment and naming of the virus, we will get lost in never-ending discussions that are not helpful at the end of the day and may even complicate things further.

In yesterday's discussions with WHO, CSG members including myself did their best to get across our central point that the name SARS-CoV-2 makes reference to a variety of (not just one) virus(es) isolated mainly from bats which all have been classified as belonging to an established virus species called *Severe acute respiratory syndrome-related coronavirus*. The virus name that the CSG decided upon makes reference to (the names of) genetically related viruses in that species (which all carry "SARS" in their names) rather than the disease (SARS) that few of these many viruses in that species caused in (some) humans in 2003. All this is laid out very clearly in our paper available at bioRxiv. And there is little to add...

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In short, it will be important that CSG members (when approached by the press) highlight that our decision is purely a SCIENTIFIC judgement. And this decision is unlikely to be changed.

Please let me know if you feel otherwise or want to have a discussion on this among study group members.

Many thanks and best regards,

John

—
Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.:
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: Benjamin Neuman[bneuman@tamut.edu]
Sent: Thur 2/13/2020 7:50:10 AM (UTC-05:00)
To: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Perlman, Stanley[stanley-perlman@uiowa.edu]; B.L. Haagmans[b.haagmans@erasmusmc.nl]; Baker, Susan[Sbaker1@luc.edu]; Isabel Sola[isola@cnb.csic.es]; Leo Poon[lmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]; Drosten, Christian[christian.drosten@charite.de]
Subject: Re: virus name

That really explains what the WHO has been doing - thanks.

I don't think changing the shared species name is a good option from a taxonomic or scientific perspective. And assuming the species stays, there really isn't much choice about what to call the virus.

I don't think the name needs to change. A better solution may be to keep talking to whoever will listen, and to eventually normalize the broader concept of what a SARS coronavirus is. You have explained it very well. It's going to be a slow process, but we will get there eventually.

Benjamin Neuman
Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: Thursday, February 13, 2020 6:14 AM
To: Perlman, Stanley; B.L. Haagmans; Baker, Susan; Isabel Sola; Leo Poon; Baric, Ralph S; A.E.Gorbalenya@lumc.nl; Benjamin Neuman; R.J.deGroot@uu.nl; lmpoon@hkucc.hku.hk; Drosten, Christian
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From: Groot, R.J. de (Raoul)[R.J.deGroot@uu.nl]
Sent: Thur 2/13/2020 7:53:41 AM (UTC-05:00)
To: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]; Perlman, Stanley[stanley-perlman@uiowa.edu]; B.L. Haagmans[b.haagmans@erasmusmc.nl]; Baker, Susan[Sbaker1@luc.edu]; Isabel Sola[isola@cnb.csic.es]; Leo Poon[lmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; bneuman@tamut.edu[bneuman@tamut.edu]; lmpoon@hkucc.hku.hk[lmpoon@hkucc.hku.hk]; Drosten, Christian[christian.drosten@charite.de]
Subject: RE: virus name

Dear all,

I fully concur. We should stick to our guns. As CSG and editors/reviewers of manuscripts, we are also in a position to ensure proper use of nomenclature in publications and we should do so. The issue will resolve itself. Politics and science mix poorly. You might be interested in the report by Martin Enserink in Science.

Kind regards, Raoul

From: John Ziebuhr <john.ziebuhr@viro.med.uni-giessen.de>
Sent: donderdag 13 februari 2020 13:14
To: Perlman, Stanley <stanley-perlman@uiowa.edu>; B.L. Haagmans <b.haagmans@erasmusmc.nl>; Baker, Susan <Sbaker1@luc.edu>; Isabel Sola <isola@cnb.csic.es>; Leo Poon <lmpoon@hku.hk>; Baric, Ralph S <rbaric@email.unc.edu>; A.E.Gorbalenya@lumc.nl; bneuman@tamut.edu; Groot, R.J. de (Raoul) <R.J.deGroot@uu.nl>; lmpoon@hkucc.hku.hk; Drosten, Christian <christian.drosten@charite.de>
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E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]
Sent: Fri 2/14/2020 9:26:34 AM (UTC-05:00)
To: guodeyin@mail.sysu.edu.cn[guodeyin@mail.sysu.edu.cn];
shibojiang@fudan.edu.cn[shibojiang@fudan.edu.cn]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]
Cc: Isabel Sola[isola@cnb.csic.es]; Leo Poon[llmpoon@hku.hk]; Baric, Ralph
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b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl];
Sbaker1@luc.edu[Sbaker1@luc.edu]; bneuman@tamut.edu[bneuman@tamut.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl];
llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk];
christian.drosten@charite.de[christian.drosten@charite.de]
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.

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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).

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E-mail: john.ziebuhr@viro.med.uni-giessen.de

From: John Ziebuhr[john.ziebuhr@viro.med.uni-giessen.de]
Sent: Sat 2/15/2020 7:55:22 AM (UTC-05:00)
To: 郭德銀[guodeyin@mail.sysu.edu.cn]
Cc: shibojiang@fudan.edu.cn[shibojiang@fudan.edu.cn]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Isabel Sola[isola@cnb.csic.es]; Leo Poon[llmpoon@hku.hk]; Baric, Ralph S[rbaric@email.unc.edu]; A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Sbaker1@luc.edu[Sbaker1@luc.edu]; bneuman@tamut.edu[bneuman@tamut.edu]; stanley-perlman@uiowa.edu[stanley-perlman@uiowa.edu]; R.J.deGroot@uu.nl[R.J.deGroot@uu.nl]; llmpoon@hkucc.hku.hk[llmpoon@hkucc.hku.hk]; christian.drosten@charite.de[christian.drosten@charite.de]
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

Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstr. 81, BFS
35392 Giessen, Germany
Phone:

Am 15.02.2020 um 07:32 schrieb 郭德銀 <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
Yuelong Shu, Sun Yat-sen University, School of Public Health (Shenzhen)
Deyin Guo, Sun Yat-sen University School of Medicine

-----Original Messages-----

From: "John Ziebuhr" <john.ziebuhr@viro.med.uni-giessen.de>

Sent Time:2020-02-14 22:26:34 (Friday)

To: guodeyin@mail.sysu.edu.cn, shibojiang@fudan.edu.cn, zlshi@wh.iov.cn

Cc: "Isabel Sola" <isola@cnb.csic.es>, "Leo Poon" <lmpoon@hku.hk>, "Baric, Ralph S" <rbaric@email.unc.edu>, "A.E.Gorbalenya@lumc.nl" <A.E.Gorbalenya@lumc.nl>, "b.haagmans@erasmusmc.nl" <b.haagmans@erasmusmc.nl>, "Sbaker1@luc.edu" <Sbaker1@luc.edu>, "bneuman@tamut.edu" <bneuman@tamut.edu>, "stanley-perlman@uiowa.edu" <stanley-perlman@uiowa.edu>, "R.J.deGroot@uu.nl" <R.J.deGroot@uu.nl>, "lmpoon@hkucc.hku.hk" <lmpoon@hkucc.hku.hk>, "christian.drosten@charite.de" <christian.drosten@charite.de>

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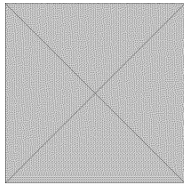
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