
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]; Sbaker1@luc.edu[Sbaker1@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]; 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

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

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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.: +49-641-9941200
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]; 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]; 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; Sbaker1@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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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]; Sbaker1@luc.edu[Sbaker1@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]
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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
(903) 334 6654

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; Sbaker1@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
319-335-8549

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

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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 11:12:15 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]; Sbaker1@luc.edu[Sbaker1@luc.edu]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Benjamin Neuman[bneuman@tamut.edu]; Ilmpoon@hkucc.hku.hk[Ilmpoon@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, Sbaker1@luc.edu, "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>, b.haagmans@erasmusmc.nl, Benjamin Neuman <bneuman@tamut.edu>, Ilmpoon@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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D-10117 Berlin

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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>, "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>, "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
Cc: Leo Poon <lmpoon@hku.hk>, Benjamin Neuman <bneuman@tamut.edu>, john.ziebuhr@viro.med.uni-giessen.de, "Baric, Ralph" <rbaric@email.unc.edu>, "Baker, Susan" <Sbaker1@luc.edu>, "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>, "B.L. Haagmans" <b.haagmans@erasmusmc.nl>, lmpoon@hkucc.hku.hk, Isabel Sola <isola@cnb.csic.es>, "Drosten, Christian" <christian.drosten@charite.de>
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.
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BSB 3-712
University of Iowa
Iowa City, IA 52242
319-335-8549

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; llmpoon@hkucc.hku.hk; isola@cnb.csic.es; Drosten, Christian; Gorbalenya, A.E. (MSTAT)
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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
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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My suggestion would be: hSARS-CoV 2019 (Human SARS coronavirus 2019).

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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.

Best regards,
John

—

Prof. Dr. John Ziebuhr

Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.: +49-641-9941200
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: Ilmpoon@hku.hk[Ilmpoon@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]; Sbaker1@luc.edu[Sbaker1@luc.edu]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.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

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: Ilmpoon@hku.hk, bneuman@tamut.edu, john.ziebuhr@viro.med.uni-giessen.de, rbaric@email.unc.edu, Sbaker1@luc.edu, "Groot, R.J. de (Raoul)" <R.J.deGroot@uu.nl>, b.haagmans@erasmusmc.nl, Ilmpoon@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; Ilmpoon@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
319-335-8549

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

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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?

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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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Leo

From: Benjamin Neuman <bneuman@tamut.edu>

Sent: 23 January 2020 23:39

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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
(903) 334 6654

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35392 Giessen
Germany
Tel.: +49-641-9941200
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: 708-216-6910
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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Fax: +49-641-9941209
[E-mail: john.ziebuhr@viro.med.uni-giessen.de](mailto:john.ziebuhr@viro.med.uni-giessen.de)

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
319-335-8549

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 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
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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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Or perhaps abbreviate to HCoV-WU19?

Benjamin Neuman

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Tel.: +49-641-9941200
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]
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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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Benjamin Neuman
Professor and Chair of Biological Sciences
STEM 309D
Texas A&M University-Texarkana
Texarkana, TX 75503
(903) 334 6654

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

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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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Stanley

Stanley Perlman, MD, Ph.D.

Professor

Depts of Microbiology and Immunology, and Pediatrics

BSB 3-712

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Iowa City, IA 52242

319-335-8549

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

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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.

Best regards,

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Prof. Dr. John Ziebuhr
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Justus Liebig University Giessen
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35392 Giessen
Germany
Tel.: +49-641-9941200
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]; Ilmpoon@hku.hk[Ilmpoon@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]; Ilmpoon@hkucc.hku.hk[Ilmpoon@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:

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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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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; llimpoon@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
319-335-8549

On Jan 23, 2020, at 9:45 AM, Leo Poon
<llimpoon@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

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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
(903) 334 6654

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.: +49-641-9941200
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]; Ilmpoon@hku.hk[Ilmpoon@hku.hk]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.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

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; Ilmpoon@hku.hk; b.haagmans@erasmusmc.nl; Ilmpoon@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
(903) 334 6654

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
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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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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.: +49-641-9941200
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 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: (852) 3917 9943
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 <lmpoon@hku.hk>; 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

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; lmpoon@hku.hk; 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

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
(903) 334 6654

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
319-335-8549

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
(903) 334 6654

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.: +49-641-9941200
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]; 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

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: (852) 3917 9943
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.: 0641-9941200
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: (852) 3917 9943
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

perelman@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
(903) 334 6654

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
319-335-8549

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.c.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
(903) 334 6654

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@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.: +49-641-9941200
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: (852) 3917 9943
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 <llmpoon@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; 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.: 0641-9941200
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: (852) 3917 9943
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
(903) 334 6654

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-](mailto:stanley-perlman@uiowa.edu)

perlman@uiowa.edu; llmpoon@hku.hk

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

Ralph S

[<rbaric@email.unc.edu>](mailto:rbaric@email.unc.edu); lbaker1@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]

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
(903) 334 6654

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@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.: +49-641-9941200
Fax: +49-641-9941209
E-mail: [john.ziebuhr@viro.med.uni-
giessen.de](mailto: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]; 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]
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.

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: +49 641 9941200

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.: 0641-9941200
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: (852) 3917 9943
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

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

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.Gorbal-enya@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.csi.c.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 constr
ucting 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
(903) 334 6654

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
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
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.
Gorbaleny
a@lumc.nl
<A.E.Gorb
aleny@lu
mc.nl>

Sent: Thur
sday,
January
23, 2020
11:09 AM

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

Cc: bneum
an@tamu
t.edu; joh
n.ziebuhr
@viro.me
d.uni-
giessen.de
; Baric,

Ralph S
rbalic@e-mail.unc.edu; Sbaker1@luc.edu; R.J.deGroot@uu.nl; b.haagmans@erasmusmc.nl; Ilmpoon@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@cnb.
csic.es](mailto:isola@cnbcsic.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
Microbiol
ogy and
Immunol
ogy, and
Pediatric
s
BSB 3-
712
Universit
y of
Iowa
Iowa
City, IA
52242
319-335-
8549

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@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
(903) 334 6654

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.: +49-641-9941200
Fax: +49-641-9941209
E-mail: john.ziebuhr@viro.med.uni-giessen.de

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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. +34-915854526

From: Drosten, Christian[christian.drosten@charite.de]
Sent: Fri 1/24/2020 7:16:18 AM (UTC-05:00)
To: 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[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]
Subject: 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
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: 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: 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
(903) 334 6654

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.: 0641-9941200
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: (852) 3917 9943
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
(903) 334 6654

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 \(Raoul\)](mailto:Groot, R.J. de (Raoul)); b.haagmans@e

rasmusmc.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
319-335-8549

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: Ben
jamin
Neuman
<bneuman@tamut.edu>

Sent: 23
January
2020
23:39

To: John
Ziebuhr; [rbaric@em
ail.unc.edu](mailto:rbaric@em
ail.unc.edu);
Sbaker1@luc.edu;
Groot, R.J.
de
(Raoul); [b.haagmans@erasmus
mc.nl](mailto:b.haagmans@erasmus
mc.nl);
Perlman,
Stanley; [llmpoon@h
kucc.hku.hk](mailto:llmpoon@h
kucc.hku.hk);
isola@cnb.csic.es;
Drosten,
Christian;
[A.E.Gorbal
enya@lumc.nl](mailto:A.E.Gorbal
enya@lumc.nl)
Subject: R
e: 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
consensu
s.

What do
you think
of Huma
n
coronavir
us-
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
(903) 334
6654

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;](mailto: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.: +49-641-
9941200
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

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
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: 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

319-335-8549

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

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: 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 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[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]
Subject: virus name

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

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

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

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

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

With many thanks and kind regards,

John Ziebuhr

—
Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
Germany
Tel.: +49-641-9941200
Fax: +49-641-9941209
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: 郭德银[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[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]
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: +49 641 9941200

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

Dear Dr. John and CSG members,

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

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

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

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

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

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

Thank you very much for your help!

Sincerely yours,

Deyin Guo, on behalf of the group:

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

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

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

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

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

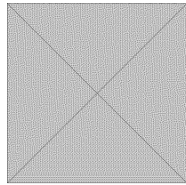
I very much hope that I was able to convince you that the CSG's decision on this particular virus name was made with the very best intentions and based purely on SCIENTIFIC judgement. Personally, I feel reassured by the positive response I have been receiving over the past few days from other colleagues, ICTV, NCBI and other

players and believe that the CSG has made a decision that will facilitate future communication among virologists studying these viruses. As part of these efforts, the CSG also suggested a naming convention to be used for specific SARS-CoV-2 isolates (and other coronavirus isolates).

With many thanks and kind regards,

John Ziebuhr

Prof. Dr. John Ziebuhr
Institute of Medical Virology
Justus Liebig University Giessen
Schubertstrasse 81 (BFS)
35392 Giessen
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Tel.: +49-641-9941200
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From: William Dowling[william.dowling@cepi.net]
Sent: Mon 2/24/2020 2:17:52 PM (UTC-05:00)
To: cheryl@gisaid.org[cheryl@gisaid.org]; peter@gisaid.org[peter@gisaid.org]; Carolyn Clark[carolyn.clark@cepi.net]; Florence, Clint (NIH/NIAID) [E[clint.florence@nih.gov]; larry.wolfraim@nih.gov[larry.wolfraim@nih.gov]; Raul Gomez Roman[raul.gomezroman@cepi.net]; Miles.Carroll@phe.gov.uk[Miles.Carroll@phe.gov.uk]; barney.graham@nih.gov[barney.graham@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][Connie.schmaljohn@nih.gov]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; Baric, Ralph S[rbaric@email.unc.edu]; HENAO RESTREPO, Ana Maria[henaorestrepa@who.int]; GSELL, Pierre[gsellp@who.int]; COSTA, Alejandro Javier[costaa@who.int]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; vincent.munster@nih.gov[vincent.munster@nih.gov]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Vasan, Vasan (H&B, Geelong AAHL)[Vasan.Vasan@csiro.au]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; jokim@ivi.int[jokim@ivi.int]; mksong@ivi.int[mksong@ivi.int]; Volker.gerds@usask.ca[Volker.gerds@usask.ca]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; leejooyeon@korea.kr[leejooyeon@korea.kr]; limhy0919@korea.kr[limhy0919@korea.kr]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; christian.brechot[christian.brechot@pasteur.fr]; Kayvon Modjarrad[kmodjarrad@eidresearch.org]; Amy C. Shurtleff[amy.c.shurtleff@cepi.net]; erik.stemmy@nih.gov[erik.stemmy@nih.gov]; Julia.Tree@phe.gov.uk[Julia.Tree@phe.gov.uk]; Mark Page[Mark.Page@nibsc.org]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Thue, Tracey[tracey.thue@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; Napper, Scott[scott.napper@usask.ca]; Nicola Rose[Nicola.Rose@nibsc.org]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; sgerber@cdc.gov[sgerber@cdc.gov]; djernigan@cdc.gov[djernigan@cdc.gov]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; Carroll, Darin (CDC/DDID/NCIRD/OD)[zuz4@cdc.gov]; Watson, John (CDC/DDID/NCIRD/DVD)[acq4@cdc.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; gustavo.f.palacios.civ@mail.mil[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; REIRELAND@mail.dstl.gov.uk[REIRELAND@mail.dstl.gov.uk]; SPoehlmann@dpz.eu[SPoehlmann@dpz.eu]; mhoffmann@dpz.eu[mhoffmann@dpz.eu]; sylvie.van-der-werf@pasteur.fr[sylvie.van-der-werf@pasteur.fr]; Nelson Michelle[MNELSON@dstl.gov.uk]; Lever Steve[MSLEVER@dstl.gov.uk]; Prior Joann L[JLPRIOR@dstl.gov.uk]; Marston, Hilary (NIH/NIAID) [E][hilary.marston@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; mit666666@pitt.edu[mit666666@pitt.edu]; Mellors, John W[jwm1@pitt.edu]; tlying@fudan.edu.cn[tlying@fudan.edu.cn]; christian.drosten@charite.de[christian.drosten@charite.de]
Cc: Guthrie, Erica (CDC/DDID/NCIRD/ID)[ilj2@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]
Subject: RE: WHO Consultation regarding nCoV Reagents and Cross -Reactivity - change of date from 3 PM CET Tuesday 2/25 to 3 PM CET Thursday 2/27

Hello all

I am sorry to change the time after some have accepted this meeting, but it has been brought to my attention that there is a competing meeting involving many invitees of this call, and we wish to have as many on the call as possible. I am therefore moving this to Thursday, 2/27 at 3 PM CET . I will send the draft minutes from last meeting and updated tables in advance.

Bill

-----Original Appointment-----

From: William Dowling

Sent: Sunday, February 23, 2020 9:27 PM

To: William Dowling; cheryl@gisaid.org; peter@gisaid.org; Carolyn Clark; Florence, Clint (NIH/NIAID) [E; larry.wolfram@nih.gov; Raul Gomez Roman; Miles.Carroll@phe.gov.uk; barney.graham@nih.gov; Schmaljohn, Connie (NIH/NIAID) [E; Michael.holbrook@nih.gov; lisa.hensley@nih.gov; rbaric@email.unc.edu; HENAO RESTREPO, Ana Maria; GSELL, Pierre; COSTA, Alejandro Javier; RIVEROS BALTA, Alina Ximena; vincent.munster@nih.gov; daszak@ecohealthalliance.org; b.haagmans@erasmusmc.nl; Vasan, Vasan (H&B, Geelong AAHL; linfa.wang@duke-nus.edu.sg; jokim@ivi.int; mksong@ivi.int; Volker.gerds@usask.ca; Giada.Mattiuzzo@nibsc.org; zlshi@wh.iov.cn; Barbara.Schnierle@pei.de; leejooyeon@korea.kr; limhy0919@korea.kr; lad7@cdc.gov; christian.brechot@pasteur.fr; Kayvon Modjarrad; Amy C. Shurtleff; erik.stemmy@nih.gov; Julia.Tree@phe.gov.uk; Mark Page; Graham, Barney (NIH/VRC) [E; Falzarano, Darryl; Thue, Tracey; Hodgson, Paul; Napper, Scott; Nicola Rose; M.P.G. Koopmans; sgerber@cdc.gov; djernigan@cdc.gov; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); Carroll, Darin (CDC/DDID/NCEZID/OD); Watson, John (CDC/DDID/NCIRD/DVD); Lathey, Janet (NIH/NIAID) [E; Degrace, Marciela (NIH/NIAID) [E; SATHIYAMOORTHY, Vaseeharan; gustavo.f.palacios.civ@mail.mil; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); MFrieman@som.umaryland.edu; REIRELAND@mail.dstl.gov.uk; SPoehlmann@dpz.eu; mhoffmann@dpz.eu; sylvie.van-der-werf@pasteur.fr; Nelson Michelle; Lever Steve; Prior Joann L; Marston, Hilary (NIH/NIAID) [E; De wit, Emmie (NIH/NIAID) [E; mit666666@pitt.edu; Mellors, John W; tlying@fudan.edu.cn; christian.drosten@charite.de

Cc: Guthrie, Erica (CDC/DDID/NCIRD/ID); Thornburg, Natalie (CDC/DDID/NCIRD/DVD)

Subject: WHO Consultation regarding nCoV Reagents and Cross -Reactivity - 3 PM CET

When: Thursday, February 27, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).

Where: Skype Meeting

Hello all

I am sorry to change the time after some have accepted this meeting, but it has been brought to my attention that there is a competing meeting involving many invitees of this call, and we wish to have as many on the call as possible. I am therefore moving this to Thursday, 2/27 at 3 PM CET . I will send the draft minutes from last meeting and updated tables in advance.

Bill

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From: Kayvon Modjarrad[kmodjarrad@eidresearch.org]
Sent: Wed 2/26/2020 7:59:47 AM (UTC-05:00)
To: William Dowling[william.dowling@cepi.net]; cheryl@gisaid.org[cheryl@gisaid.org]; peter@gisaid.org[peter@gisaid.org]; Carolyn Clark[carolyn.clark@cepi.net]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; larry.wolfram@nih.gov[larry.wolfram@nih.gov]; Raul Gomez Roman[raul.gomezroman@cepi.net]; Miles.Carroll@phe.gov.uk[Miles.Carroll@phe.gov.uk]; barney.graham@nih.gov[barney.graham@nih.gov]; Schmaljohn, Connie (NIH/NIAID) [E][Connie.schmaljohn@nih.gov]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; Baric, Ralph S[rbaric@email.unc.edu]; HENAO RESTREPO, Ana Maria[henaorestrepa@who.int]; GSELL, Pierre[gsellp@who.int]; COSTA, Alejandro Javier[costaa@who.int]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; vincent.munster@nih.gov[vincent.munster@nih.gov]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Vasan, Vasan (H&B, Geelong AAHL)[Vasan.Vasan@csiro.au]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; jokim@ivi.int[jokim@ivi.int]; mksong@ivi.int[mksong@ivi.int]; Volker.gerds@usask.ca[Volker.gerds@usask.ca]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; leejooyeon@korea.kr[leejooyeon@korea.kr]; limhy0919@korea.kr[limhy0919@korea.kr]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; christian.brechot[christian.brechot@pasteur.fr]; Amy C. Shurtleff[amy.c.shurtleff@cepi.net]; erik.stemmy@nih.gov[erik.stemmy@nih.gov]; Julia.Tree@phe.gov.uk[Julia.Tree@phe.gov.uk]; Mark Page[Mark.Page@nibsc.org]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Thue, Tracey[tracey.thue@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; Napper, Scott[scott.napper@usask.ca]; Nicola Rose[Nicola.Rose@nibsc.org]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; sgerber@cdc.gov[sgerber@cdc.gov]; djernigan@cdc.gov[djernigan@cdc.gov]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; Carroll, Darin (CDC/DDID/NCEZID/OD)[zuz4@cdc.gov]; Watson, John (CDC/DDID/NCIRD/DVD)[acq4@cdc.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; gustavo.f.palacios.civ@mail.mil[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; REIRELAND@mail.dstl.gov.uk[REIRELAND@mail.dstl.gov.uk]; SPoehlmann@dpz.eu[SPoehlmann@dpz.eu]; mhoffmann@dpz.eu[mhoffmann@dpz.eu]; sylvie.van-der-werf@pasteur.fr[sylvie.van-der-werf@pasteur.fr]; Nelson Michelle[MNELSON@dstl.gov.uk]; Lever Steve[MSLEVER@dstl.gov.uk]; Prior Joann L[JLPRIOR@dstl.gov.uk]; Marston, Hilary (NIH/NIAID) [E][hilary.marston@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; mit666666@pitt.edu[mit666666@pitt.edu]; Mellors, John W[jwm1@pitt.edu]; tlying@fudan.edu.cn[tlying@fudan.edu.cn]; christian.drosten@charite.de[christian.drosten@charite.de]; David Vaughn[David.Vaughn@gatesfoundation.org]; Jacqueline Kirchner[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar[Karen.Makar@gatesfoundation.org]
Cc: Guthrie, Erica (CDC/DDID/NCIRD/ID)[ilj2@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Baric, Toni C[antoinette_baric@med.unc.edu]
Subject: Re: WHO Consultation regarding nCoV Reagents and Cross -Reactivity - Double invites for tomorrow?

My apologies all. When I accepted Bill's invitation, somehow an invitation was sent out from my email in error and then I paid the price of receiving all your acceptance emails. Per Bill, the invitation from me is erroneous.

Kayvon

From: William Dowling <william.dowling@cepi.net>

Sent: Wednesday, February 26, 2020 4:54 AM

To: cheryl@gisaid.org; peter@gisaid.org; Carolyn Clark; Florence, Clint (NIH/NIAID) [E; larry.wolfraim@nih.gov; Raul Gomez Roman; Miles.Carroll@phe.gov.uk; barney.graham@nih.gov; Schmaljohn, Connie (NIH/NIAID) [E]; Michael.holbrook@nih.gov; lisa.hensley@nih.gov; rbaric@email.unc.edu; HENAO RESTREPO, Ana Maria; GSELL, Pierre; COSTA, Alejandro Javier; RIVEROS BALTA, Alina Ximena; vincent.munster@nih.gov; daszak@ecohealthalliance.org; b.haagmans@erasmusmc.nl; Vasan, Vasan (H&B, Geelong AAHL; linfa.wang@duke-nus.edu.sg; jokim@ivi.int; mksong@ivi.int; Volker.gerdt@usask.ca; Giada.Mattiuzzo@nibsc.org; zlshi@wh.iov.cn; Barbara.Schnierle@pei.de; leejooyeon@korea.kr; limhy0919@korea.kr; Damon, Inger K. (CDC/OID/NCEZID); christian.brecht; Kayvon Modjarrad; Amy C. Shurtleff; erik.stemmy@nih.gov; Julia.Tree@phe.gov.uk; Mark Page; Graham, Barney (NIH/VRC) [E; Falzarano, Darryl; Thue, Tracey; Hodgson, Paul; Napper, Scott; Nicola Rose; M.P.G. Koopmans; sgerber@cdc.gov; djernigan@cdc.gov; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); Carroll, Darin (CDC/DDID/NCEZID/OD); Watson, John (CDC/DDID/NCIRD/DVD); Lathey, Janet (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; SATHIYAMOORTHY, Vaseeharan; gustavo.f.palacios.civ@mail.mil; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); MFrieman@som.umaryland.edu; REIRELAND@mail.dstl.gov.uk; SPOehlmann@dpz.eu; mhoffmann@dpz.eu; sylvie.van-der-werf@pasteur.fr; Nelson Michelle; Lever Steve; Prior Joann L; Marston, Hilary (NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; mit666666@pitt.edu; Mellors, John W; tlying@fudan.edu.cn; christian.drosten@charite.de; David Vaughn; Jacqueline Kirchner; Karen Makar

Cc: Guthrie, Erica (CDC/DDID/NCIRD/ID); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Baric, Toni C

Subject: [EXTERNAL] WHO Consultation regarding nCoV Reagents and Cross -Reactivity - Double invites for tomorrow?

ATTENTION: This email originated from outside of the organization.
Do not open attachments or click on links unless you recognize the sender and
know the content is safe.

Hello all

Some of you may have gotten two invites for tomorrow , one for a half hour meeting at 2 PM CET from Kayvon Modjarrad and another for an hour meeting at 3 PM CET from me. I don't know how the 2 PM invite was generated, but please delete it. Our call is at 3 PM CET. Sorry for any confusion.

Bill

-----Original Appointment-----

From: William Dowling

Sent: Monday, February 24, 2020 3:27 AM

To: William Dowling; cheryl@gisaid.org; peter@gisaid.org; Carolyn Clark; Florence, Clint (NIH/NIAID) [E; larry.wolfraim@nih.gov; Raul Gomez Roman; Miles.Carroll@phe.gov.uk; barney.graham@nih.gov; Schmaljohn, Connie (NIH/NIAID) [E; Michael.holbrook@nih.gov; lisa.hensley@nih.gov; rbaric@email.unc.edu; HENAO RESTREPO, Ana Maria; GSELL, Pierre; COSTA, Alejandro Javier; RIVEROS BALTA, Alina Ximena; vincent.munster@nih.gov; daszak@ecohealthalliance.org; b.haagmans@erasmusmc.nl; Vasan, Vasan (H&B, Geelong AAHL; linfa.wang@duke-nus.edu.sg; jokim@ivi.int; mksong@ivi.int; Volker.gerdt@usask.ca; Giada.Mattiuzzo@nibsc.org; zlshi@wh.iov.cn; Barbara.Schnierle@pei.de; leejooyeon@korea.kr; limhy0919@korea.kr; lad7@cdc.gov; christian.brecht@pasteur.fr; Kayvon Modjarrad; Amy C. Shurtleff; erik.stemmy@nih.gov; Julia.Tree@phe.gov.uk; Mark Page; Graham, Barney (NIH/VRC) [E; Falzarano, Darryl; Thue, Tracey; Hodgson, Paul; Napper, Scott; Nicola Rose; M.P.G. Koopmans; sgerber@cdc.gov; djernigan@cdc.gov; Gerber, Susan I. (CDC/DDID/NCIRD/DVD); Carroll, Darin (CDC/DDID/NCEZID/OD); Watson, John (CDC/DDID/NCIRD/DVD); Lathey, Janet (NIH/NIAID) [E]; Degrace, Marciela (NIH/NIAID) [E]; SATHIYAMOORTHY, Vaseeharan; gustavo.f.palacios.civ@mail.mil; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD); MFrieman@som.umaryland.edu; REIRELAND@mail.dstl.gov.uk; SPOehlmann@dpz.eu; mhoffmann@dpz.eu; sylvie.van-der-werf@pasteur.fr; Nelson Michelle; Lever Steve; Prior Joann L; Marston, Hilary

(NIH/NIAID) [E]; De wit, Emmie (NIH/NIAID) [E]; mit666666@pitt.edu; Mellors, John W; tlying@fudan.edu.cn; christian.drosten@charite.de; David Vaughn; Jacqueline Kirchner; Karen Makar
Cc: Guthrie, Erica (CDC/DDID/NCIRD/ID); Thornburg, Natalie (CDC/DDID/NCIRD/DVD); Baric, Toni C
Subject: WHO Consultation regarding nCoV Reagents and Cross -Reactivity - 3 PM CET
When: Thursday, February 27, 2020 9:00 AM-10:00 AM (UTC-05:00) Eastern Time (US & Canada).
Where: Skype Meeting

Hello all

I am sorry to change the time after some have accepted this meeting, but it has been brought to my attention that there is a competing meeting involving many invitees of this call, and we wish to have as many on the call as possible. I am therefore moving this to Thursday, 2/27 at 3 PM CET . I will send the draft minutes from last meeting and updated tables in advance.

Bill

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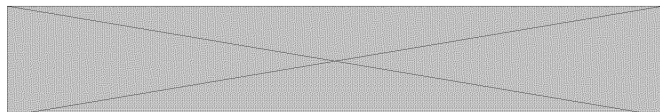
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From: A.E.Gorbalenya@lumc.nl[A.E.Gorbalenya@lumc.nl]
Sent: Wed 3/18/2020 6:08:53 AM (UTC-04:00)
To: john.ziebuhr@viro.med.uni-giessen.de[john.ziebuhr@viro.med.uni-giessen.de];
isola@cnb.csic.es[isola@cnb.csic.es]; llmpoon@hku.hk[llmpoon@hku.hk]; Baric, Ralph
S[rbaric@email.unc.edu]; 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: the CSG paper online at Nature Microbiology - THE name

Stat Roma pristina nomine, nomina nuda tenemus

From: Gorbalenya, A.E. (MSTAT)
Sent: Wednesday, March 18, 2020 10:48 AM
To: John Ziebuhr; Isabel Sola; Leo Poon; Baric, Ralph S; b.haagmans@erasmusmc.nl; Sbaker1@luc.edu; bneuman@tamut.edu;
stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; christian.drosten@charite.de
Subject: RE: the CSG paper online at Nature Microbiology - THE name

Dear All,

It is not custom for me to share a link to sources outside our professional realm, but at theses extraordinary times many things are being reconsidered. I hope you may find the link paper worth of your time

<https://qz.com/1820422/coronavirus-why-wont-who-use-the-name-sars-cov-2/>

Best,

Sasha

From: Gorbalenya, A.E. (MSTAT)
Sent: Monday, March 2, 2020 5:45 PM
To: John Ziebuhr; Isabel Sola; Leo Poon; Baric, Ralph S; b.haagmans@erasmusmc.nl; Sbaker1@luc.edu; bneuman@tamut.edu;
stanley-perlman@uiowa.edu; R.J.deGroot@uu.nl; llmpoon@hkucc.hku.hk; christian.drosten@charite.de; Gulyaeva, A. (MM);
Dmitry Samborskiy; Chris Lauber; Andrey Leontovich <aml@genebee.msu.su>; Sidorov, I. (MM)
Subject: the CSG paper online at Nature Microbiology

<https://rdcu.be/b2oZu>

From: William Dowling[william.dowling@cepi.net]
Sent: Wed 3/18/2020 10:17:07 AM (UTC-04:00)
To: cheryl@gisaid.org[cheryl@gisaid.org]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; Baric, Ralph S[rbaric@email.unc.edu]; HENAO RESTREPO, Ana Maria[henaorestrepa@who.int]; GSELL, Pierre[gsellp@who.int]; COSTA, Alejandro Javier[costaa@who.int]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; vincent.munster@nih.gov[vincent.munster@nih.gov]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Vasan, Vasan (H&B, Geelong AAHL)[Vasan.Vasan@csiro.au]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; jokim@ivi.int[jokim@ivi.int]; mksong@ivi.int[mksong@ivi.int]; Volker.gerds@usask.ca[Volker.gerds@usask.ca]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; leejooyeon@korea.kr[leejooyeon@korea.kr]; limhy0919@korea.kr[limhy0919@korea.kr]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; christian.brechot[christian.brechot@pasteur.fr]; Kayvon Modjarrad[kmodjarrad@eidresearch.org]; Amy C. Shurtleff[amy.c.shurtleff@cepi.net]; erik.stemmy@nih.gov[erik.stemmy@nih.gov]; Julia.Tree@phe.gov.uk[Julia.Tree@phe.gov.uk]; Mark Page[Mark.Page@nibsc.org]; Graham, Barney (NIH/VRC) [E[bgraham@mail.nih.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Thue, Tracey[tracey.thue@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; Napper, Scott[scott.napper@usask.ca]; Nicola Rose[Nicola.Rose@nibsc.org]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; sgerber@cdc.gov[sgerber@cdc.gov]; djernigan@cdc.gov[djernigan@cdc.gov]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; Carroll, Darin (CDC/DDID/NCEZID/OD)[zuz4@cdc.gov]; Watson, John (CDC/DDID/NCIRD/DVD)[acq4@cdc.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; gustavo.f.palacios.civ@mail.mil[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; REIRELAND@mail.dstl.gov.uk[REIRELAND@mail.dstl.gov.uk]; SPoehlmann@dpz.eu[SPoehlmann@dpz.eu]; mhoffmann@dpz.eu[mhoffmann@dpz.eu]; sylvie.van-der-werf@pasteur.fr[sylvie.van-der-werf@pasteur.fr]; Nelson Michelle[MNELSON@dstl.gov.uk]; Lever Steve[MSLEVER@dstl.gov.uk]; Prior Joann L[LJPRIOR@dstl.gov.uk]; Marston, Hilary (NIH/NIAID) [E][hilary.marston@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; mit666666@pitt.edu[mit666666@pitt.edu]; Mellors, John W[jwm1@pitt.edu]; tlying@fudan.edu.cn[tlying@fudan.edu.cn]; christian.drosten@charite.de[christian.drosten@charite.de]; David Vaughn[David.Vaughn@gatesfoundation.org]; Jacqueline Kirchner[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar[Karen.Makar@gatesfoundation.org]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]; perkinsm@who.int[perkinsm@who.int]; Guthrie, Erica (CDC/DDID/NCIRD/ID)[ilj2@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Baric, Toni C[antoinette_baric@med.unc.edu]; SALAMI, Kolawole[salamik@who.int]; Simon Funnell[Simon.Funnell@phe.gov.uk]; Cesar Munoz-fontela[munoz-fontela@bnitm.de]; Monalisa Chatterji[MONALISA.CHATTERJI@gatesfoundation.org]; Ashley.Smith1@hhs.gov[Ashley.Smith1@hhs.gov]; Karl.Erlandson@hhs.gov[Karl.Erlandson@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Lakshmi.Jayashankar@hhs.gov[Lakshmi.Jayashankar@hhs.gov]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Delgado Vazquez.Rafael[rafael.delgado@salud.madrid.org]; Morabito, Kaitlyn (NIH/VRC) [E][kaitlyn.dambach@nih.gov]
Cc: Cesar Munoz-fontela[munoz-fontela@bnitm.de]; COSTA, Alejandro Javier[costaa@who.int]
Subject: WHO International serological survey working group

Hello all

As mentioned on today's call, the WHO is standing up an International serological survey working group. If you are

interested in participating , please send an email to myself, Alejandro Costa (costaa@who.int) and Cesar Munoz-fontela (munoz-fontela@bnitm.de) .

Thanks
Bill

William Dowling, PhD (seconded to WHO)

Non-Clinical Vaccine Development Leader



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Sent: Tue 3/24/2020 4:57:31 PM (UTC-04:00)

To: cheryl@gisaid.org[cheryl@gisaid.org]; Michael.holbrook@nih.gov[Michael.holbrook@nih.gov]; lisa.hensley@nih.gov[lisa.hensley@nih.gov]; Baric, Ralph S[rbaric@email.unc.edu]; HENAO RESTREPO, Ana Maria[henaorestrepa@who.int]; GSELL, Pierre[gsellp@who.int]; COSTA, Alejandro Javier[costaa@who.int]; RIVEROS BALTA, Alina Ximena[lauriex@who.int]; vincent.munster@nih.gov[vincent.munster@nih.gov]; daszak@ecohealthalliance.org[daszak@ecohealthalliance.org]; b.haagmans@erasmusmc.nl[b.haagmans@erasmusmc.nl]; Vasan, Vasan (H&B, Geelong AAHL)[Vasan.Vasan@csiro.au]; linfa.wang@duke-nus.edu.sg[linfa.wang@duke-nus.edu.sg]; jokim@ivi.int[jokim@ivi.int]; mksong@ivi.int[mksong@ivi.int]; Volker.gerds@usask.ca[Volker.gerds@usask.ca]; Giada.Mattiuzzo@nibsc.org[Giada.Mattiuzzo@nibsc.org]; zlshi@wh.iov.cn[zlshi@wh.iov.cn]; Barbara.Schnierle@pei.de[Barbara.Schnierle@pei.de]; leejooyeon@korea.kr[leejooyeon@korea.kr]; limhy0919@korea.kr[limhy0919@korea.kr]; Damon, Inger K. (CDC/OID/NCEZID)[iad7@cdc.gov]; christian.brechot[christian.brechot@pasteur.fr]; Kayvon Modjarrad[kmodjarrad@eidresearch.org]; Amy C. Shurtleff[amy.c.shurtleff@cepi.net]; erik.stemmy@nih.gov[erik.stemmy@nih.gov]; Julia.Tree@phe.gov.uk[Julia.Tree@phe.gov.uk]; Mark Page[Mark.Page@nibsc.org]; Graham, Barney (NIH/VRC) [E][bgraham@mail.nih.gov]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Thue, Tracey[tracey.thue@usask.ca]; Hodgson, Paul[paul.hodgson@usask.ca]; Napper, Scott[scott.napper@usask.ca]; Nicola Rose[Nicola.Rose@nibsc.org]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; sgerber@cdc.gov[sgerber@cdc.gov]; djernigan@cdc.gov[djernigan@cdc.gov]; Gerber, Susan I. (CDC/DDID/NCIRD/DVD)[bhx1@cdc.gov]; Carroll, Darin (CDC/DDID/NCEZID/OD)[zuz4@cdc.gov]; Watson, John (CDC/DDID/NCIRD/DVD)[acq4@cdc.gov]; Lathey, Janet (NIH/NIAID) [E][janet.lathey@nih.gov]; Degrace, Marciela (NIH/NIAID) [E][marciela.degrace@nih.gov]; SATHIYAMOORTHY, Vaseeharan[moorthyv@who.int]; gustavo.f.palacios.civ@mail.mil[gustavo.f.palacios.civ@mail.mil]; Pallansch, Mark A. (CDC/DDID/NCIRD/DVD)[map1@cdc.gov]; MFrieman@som.umaryland.edu[MFrieman@som.umaryland.edu]; REIRELAND@mail.dstl.gov.uk[REIRELAND@mail.dstl.gov.uk]; SPoehlmann@dpz.eu[SPoehlmann@dpz.eu]; mhoffmann@dpz.eu[mhoffmann@dpz.eu]; sylvie.van-der-werf@pasteur.fr[sylvie.van-der-werf@pasteur.fr]; Nelson Michelle[MNELSON@dstl.gov.uk]; Lever Steve[MSLEVER@dstl.gov.uk]; Prior Joann L[LJPRIOR@dstl.gov.uk]; Marston, Hilary (NIH/NIAID) [E][hilary.marston@nih.gov]; De wit, Emmie (NIH/NIAID) [E][emmie.dewit@nih.gov]; mit666666@pitt.edu[mit666666@pitt.edu]; Mellors, John W[jwm1@pitt.edu]; tlying@fudan.edu.cn[tlying@fudan.edu.cn]; christian.drosten@charite.de[christian.drosten@charite.de]; David Vaughn[David.Vaughn@gatesfoundation.org]; Jacqueline Kirchner[Jacqueline.Kirchner@gatesfoundation.org]; Karen Makar[Karen.Makar@gatesfoundation.org]; florian.krammer@mssm.edu[florian.krammer@mssm.edu]; perkinsm@who.int[perkinsm@who.int]; Guthrie, Erica (CDC/DDID/NCIRD/ID)[ilj2@cdc.gov]; Thornburg, Natalie (CDC/DDID/NCIRD/DVD)[nax3@cdc.gov]; Baric, Toni C[antoinette_baric@med.unc.edu]; SALAMI, Kolawole[salamik@who.int]; Simon Funnell[Simon.Funnell@phe.gov.uk]; Cesar Munoz-fontela[munoz-fontela@bnitm.de]; Monalisa Chatterji[MONALISA.CHATTERJI@gatesfoundation.org]; Ashley.Smith1@hhs.gov[Ashley.Smith1@hhs.gov]; Karl.Erlandson@hhs.gov[Karl.Erlandson@hhs.gov]; Kovacs, Gerald (OS/ASPR/BARDA) (CTR)[Gerald.Kovacs@hhs.gov]; Little, James (OS/ASPR/BARDA)[James.Little@hhs.gov]; Lakshmi.Jayashankar@hhs.gov[Lakshmi.Jayashankar@hhs.gov]; wilsonp@uchicago.edu[wilsonp@uchicago.edu]; Florence, Clint (NIH/NIAID) [E][clint.florence@nih.gov]; Delgado Vazquez.Rafael[rafael.delgado@salud.madrid.org]; Morabito, Kaitlyn (NIH/VRC) [E][kaitlyn.dambach@nih.gov]; Corbett, Kizzmekia (NIH/VRC) [E][kizzmekia.corbett@nih.gov]; N.M.A. Okba[n.okba@erasmusmc.nl]

Cc: dj56wood@gmail.com[dj56wood@gmail.com]; teresa.lambe@ndm.ox.ac.uk[teresa.lambe@ndm.ox.ac.uk]; brooke.bozick@nih.gov[brooke.bozick@nih.gov]; Luc Gagnon[Luc.Gagnon@nexelis.com]; Greg Kulnis[Greg.Kulnis@nexelis.com]

Subject: WHO Consultation on SARS-CoV -2 Reagents, Cross reactivity and immune Assays - Wed 2

PM CET

Hello all

We will have data presentations tomorrow followed by discussion and then updates, as time allows.

- Natalie Thornburg , CDC
- Barney Graham, NIAID
- Bart Haagmans , Erasmus
- Florian Krammer, Mount Sinai

Thanks

Bill

William Dowling, PhD

Non-Clinical Vaccine Development Leader



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From: Grant McFadden[grantmcf@asu.edu]
Sent: Wed 3/25/2020 3:03:17 PM (UTC-04:00)
To: Matthew Frieman[mfrieman@som.umaryland.edu]; Falzarano, Darryl[darryl.falzarano@usask.ca]; Menachery, Vineet[vimenach@UTMB.EDU]; M.P.G. Koopmans[m.koopmans@erasmusmc.nl]; Adolfo Garcia-Sastre[Adolfo.Garcia-Sastre@mssm.edu]; Baric, Ralph S[rbaric@email.unc.edu]; Stanley Perlman[stanley-perlman@uiowa.edu]
Cc: Erika Arch[earch@asu.edu]; Brenda Hogue[Brenda.Hogue@asu.edu]; Alexandra Lucas[arlucas5@asu.edu]; Ian Hogue[ihogue@asu.edu]; Julie Kurth[Julie.Kurth@asu.edu]; Dianne Price[Dianne.Price@asu.edu]; Kerri Robinson[Kerri.Robinson@asu.edu]; Stephen Munk[Stephen.Munk@asu.edu]; Oday Hana[Oday.Hana@asu.edu]; Neal Woodbury[NWoodbury@asu.edu]; Kenro Kusumi[Kenro.Kusumi@asu.edu]; Nancy Gonzales[nancy.gonzales@asu.edu]; Felicia Goodrum[fgoodrum@email.arizona.edu]; Paul Boehmer[boehmer@email.arizona.edu]; Steven Potts[sp@oncomyx.com]; Michael Wood[mw@oncomyx.com]; Leslie Sharp[leslie.sharp@oncomyx.com]
Subject: Friday Viroholics seminar series: the Zoom version

Matt, Darryl, Vineet, Marion, Adolfo, Ralph and Stan:

First, thank you all for tentatively agreeing to Zoom-speak in our Friday noon (PT) virology seminar series at ASU, that is now heavily focused on coronaviruses and treating respiratory virus diseases.

Second, I hope to have a tentative April-May speaker schedule for you by the end of this week, or early next week, but in the meantime, feel free to join us electronically for this Friday's Zoom seminar on coronavirus vaccines from Brenda Hogue ([https://asu.zoom.us/](https://asu.zoom.us/j/)):

Brenda G. Hogue, PhD
Professor
Biodesign Center for Immunotherapy, Vaccines and Virotherapy (B-CIVV)
School of Life Sciences
Arizona State University

"Virus-like Particles - a platform for coronavirus vaccines"

Friday, March 27, 2020
Noon - 1:00 PM (MST/same as PT now in Arizona)
Join via Zoom: <https://asu.zoom.us/j/>

Or Telephone:

Dial(for higher quality, dial a number based on your current location):

US: +1 669 900 6833 or +1 346 248 7799 or +1 646 876 9923 or +1 253 215 8782 or +1 301 715 8592 or +1

Meeting ID:

International numbers available: <https://asu.zoom.us/>

Or iPhone one-tap (US Toll): +16699006833,,244676617# or +13462487799.

We really appreciate your support!

Grant

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