Review report Corman-Drosten et al. Eurosurveillance 2020

November 27, 2020

This extensive review report has been officially submitted to Eurosurveillance editorial board on 27th November 2020 via their submission-portal, enclosed to this review report is a retraction request letter, signed by all the main & co-authors. First and last listed names are the first and second main authors. All names in between are co-authors.

External peer review of the RTPCR test to detect SARS-CoV-2 reveals 10 major scientific flaws at the molecular and methodological level: consequences for false positive results.

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ABSTRACT

In the publication entitled “Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR” (Eurosurveillance 25(8) 2020) the authors present a diagnostic workflow and RT-qPCR protocol for detection and diagnostics of 2019-nCoV (now known as SARS-CoV-2), which they claim to be validated, as well as being a robust diagnostic methodology for use in public-health laboratory settings.

In light of all the consequences resulting from this very publication for societies worldwide, a group of independent researchers performed a point-by-point review of the aforesaid publication in which 1) all components of the presented test design were cross checked, 2) the RT-qPCR protocol-recommendations were assessed w.r.t. good laboratory practice, and 3) parameters examined against relevant scientific literature covering the field.

The published RT-qPCR protocol for detection and diagnostics of 2019-nCoV and the manuscript suffer from numerous technical and scientific errors, including insufficient primer design, a problematic and insufficient RT-qPCR protocol, and the absence of an accurate test validation. Neither the presented test nor the manuscript itself fulfils the requirements for an acceptable scientific publication. Further, serious conflicts of interest of the authors are not mentioned. Finally, the very short timescale between submission and acceptance of the publication (24 hours) signifies that a systematic peer review process was either not performed here, or of problematic poor quality. We provide compelling evidence of several scientific inadequacies, errors and flaws.

Considering the scientific and methodological blemishes presented here, we are confident that the editorial board of Eurosurveillance has no other choice but to retract the publication.

CONCISE REVIEW REPORT

This paper will show numerous serious flaws in the Corman-Drosten paper, the significance of which has led to worldwide misdiagnosis of infections attributed to SARS-CoV-2 and associated with the disease COVID-19. We are confronted with stringent lockdowns which have destroyed many people's lives and livelihoods, limited access to education and these imposed restrictions by governments around the world are a direct attack on people's basic rights and their personal freedoms, resulting in collateral damage for entire economies on a global scale.

There are ten fatal problems with the Corman-Drosten paper which we will outline and explain in greater detail in the following sections.

The first and major issue is that the novel Coronavirus SARS-CoV-2 (in the publication named 2019-nCoV and in February 2020 named SARS-CoV-2 by an international consortium of virus experts) is based on in silico (theoretical) sequences, supplied by a laboratory in China [1], because at the time neither control material of infectious ("live") or inactivated SARS-CoV-2 nor isolated genomic RNA of the virus was available to the authors. To date no validation has been performed by the authorship based on isolated SARS-CoV-2 viruses or full length RNA thereof. According to Corman et al.:

> ***"We aimed to develop and deploy robust diagnostic methodology for use in public health laboratory settings without having virus material available." [1]***

The focus here should be placed upon the two stated aims: a) *development* and b) *deployment of a diagnostic test for use in public health laboratory settings*. These aims are not achievable without having any actual virus material available (e.g. for

determining the infectious viral load). In any case, only a protocol with maximal accuracy can be the mandatory and primary goal in any scenario-outcome of this magnitude. Critical viral load determination is mandatory information, and it is in Christian Drosten's group responsibility to perform these experiments and provide the crucial data.

Nevertheless these in silico sequences were used to develop a RT-PCR test methodology to identify the aforesaid virus. This model was based on the assumption that the novel virus is very similar to SARS-CoV from 2003 as both are beta-coronaviruses.

The PCR test was therefore designed using the genomic sequence of SARS-CoV as a control material for the Sarbeco component; we know this from our personal email-communication with [2] one of the co-authors of the Corman-Drosten paper. This method to model SARS-CoV-2 was described in the Corman-Drosten paper as follows:

> ***"the establishment and validation of a diagnostic workflow for 2019-nCoV screening and specific confirmation, designed in absence of available virus isolates or original patient specimens. Design and validation were enabled by the close genetic relatedness to the 2003 SARS-CoV, and aided by the use of synthetic nucleic acid technology."***

The Reverse Transcription-Polymerase Chain Reaction (RT-PCR) is an important biomolecular technology to rapidly detect rare RNA fragments, which are known in advance. In the first step, RNA molecules present in the sample are reverse

transcribed to yield cDNA. The cDNA is then amplified in the polymerase chain reaction using a specific primer pair and a thermostable DNA polymerase enzyme. The technology is highly sensitive and its detection limit is theoretically 1 molecule of cDNA. The specificity of the PCR is highly influenced by biomolecular design errors.

What is important when designing an RT-PCR Test and the quantitative RT-qPCR test described in the Corman-Drosten publication?

1. The primers and probes:

a) the concentration of primers and probes must be of optimal range (100-200 nM)
b) must be specific to the target-gene you want to amplify
c) must have an optimal percentage of GC content relative to the total nitrogenous bases (minimum 40%, maximum 60%)
d) for virus diagnostics at least 3 primer pairs must detect 3 viral genes (preferably as far apart as possible in the viral genome)

2. The temperature at which all reactions take place:

a) DNA melting temperature (>92°)
b) DNA amplification temperature (TaqPol specific)
c) Tm; the annealing temperature (the temperature at which the primers and probes reach the target binding/detachment, not to exceed 2°C per primer pair). Tm heavily depends on GC content of the primers

3. The number of amplification cycles (less than 35; preferably 25-30 cycles);

In case of virus detection, >35 cycles only detects signals which do not correlate with

infectious virus as determined by isolation in cell culture [reviewed in 2]; if someone is tested by PCR as positive when a threshold of 35 cycles or higher is used (as is the case in most laboratories in Europe & the US), the probability that said person is actually infected is less than 3%, the probability that said result is a false positive is 97% [reviewed in 3]

4. Molecular biological validations; amplified PCR products must be validated either by running the products in a gel with a DNA ruler, or by direct DNA sequencing

5. Positive and negative controls should be specified to confirm/refute specific virus detection

6. There should be a Standard Operational Procedure (SOP) available

SOP unequivocally specifies the above parameters, so that all laboratories are able to set up the exact same test conditions. To have a validated universal SOP is essential, because it enables the comparison of data within and between countries.

MINOR CONCERNS WITH THE CORMAN-DROSTEN PAPER

1. In Table 1 of the Corman-Drosten paper, different abbreviations are stated – "nM" is specified, "nm" isn't. Further in regards to correct nomenclature, nm means "nanometer" therefore nm should read nM here.

2. It is the general consensus to write genetic sequences always in the 5'-3' direction, including the reverse primers. It is highly unusual to do alignment with reverse complementary writing of the primer sequence as the authors did in figure 2 of the Corman-Drosten paper. Here, in addition, a wobble base is marked as "y" without description of the bases the Y stands for.

3. Two misleading pitfalls in the Corman-Drosten paper are that their Table 1 does not include Tm-values (annealing-temperature values), neither does it show GC-

values (number of G and C in the sequences as %-value of total bases).

MAJOR CONCERNS WITH THE CORMAN-DROSTEN PAPER

A) BACKGROUND

The authors introduce the background for their scientific work as: "The ongoing outbreak of the recently emerged novel coronavirus (2019-nCoV) poses a challenge for public health laboratories as virus isolates are unavailable while there is growing evidence that the outbreak is more widespread than initially thought, and international spread through travelers does already occur".

According to BBC News [4] and Google Statistics [5] there were 6 deaths world-wide on January 21st 2020 – the day when the manuscript was submitted. Why did the authors assume a challenge for public health laboratories while there was no substantial evidence at that time to indicate that the outbreak was more widespread than initially thought?

As an aim the authors declared to develop and deploy robust diagnostic methodology for use in public health laboratory settings without having virus material available. Further, they acknowledge that "The present study demonstrates the enormous response capacity achieved through coordination of academic and public laboratories in national and European research networks."

B) METHODS AND RESULTS

1. Primer & Probe Design

1a) Erroneous primer concentrations

Reliable and accurate PCR-test protocols are normally designed using between 100 nM and 200 nM per primer [7]. In the Corman-Drosten paper, we observe unusually

high and varying primer concentrations for several primers (table 1). For the RdRp_SARSr-F and RdRp_SARSr-R primer pairs, 600 nM and 800 nM are described, respectively. Similarly, for the N_Sarbeco_F and N_Sarbeco_R primer set, they advise 600 nM and 800 nM, respectively [1].

It should be clear that these concentrations are far too high to be optimal for specific amplifications of target genes. **There exists no specified reason to use these extremely high concentrations of primers in this protocol. Rather, these concentrations lead to increased unspecific binding and PCR product amplification.**

Table1: Primers and probes (adapted from Corman-Drosten paper; erroneous primer concentrations are highlighted)

Assay/use	Oligonucleotide	Sequence[a]	Concentration[b]
RdRP gene	RdRp_SARSr-F	GTGARATGGTCATGTGTGGCGG	Use 600 nM per reaction
	RdRp_SARSr-P2	FAM-CAGGTGGAACCTCATCAGGAGATGC-BBQ	Specific for 2019-nCoV, will not detect SARS-CoV. Use 100 nM per reaction and mix with P1
	RdRP_SARSr-P1	FAM-CCAGGTGGWACRTCATCMGGTGATGC-BBQ	Pan Sarbeco-Probe will detect 2019-nCoV, SARS-CoV and bat-SARS-related CoVs. Use 100 nM per reaction and mix with P2
	RdRp_SARSr-R	CARATGTTAAASACACTATTAGCATA	Use 800 nM per reaction
E gene	E_Sarbeco_F	ACAGGTACGTTAATAGTTAATAGCGT	Use 400 nm per reaction
	E_Sarbeco_P1	FAM-ACACTAGCCATCCTTACTGCGCTTCG-BBQ	Use 200 nm per reaction
	E_Sarbeco_R	ATATTGCAGCAGTACGCACACA	Use 400 nm per reaction
N gene	N_Sarbeco_F	CACATTGGCACCCGCAATC	Use 600 nm per reaction
	N_Sarbeco_P	FAM-ACTTCCTCAAGGAACAACATTGCCA-BBQ	Use 200 nm per reaction
	N_Sarbeco_R	GAGGAACGAGAAGAGGCTTG	Use 800 nm per reaction

[a] W is A/T; R is G/A; M is A/C; S is G/C. FAM: 6-carboxyfluorescein; BBQ: blackberry quencher.

[b] Optimised concentrations are given in nanomol per litre (nM) based on the final reaction mix, e.g. 1.5 µL of a 10 µM primer stock solution per 25 µL total reaction volume yields a final concentration of 600 nM as indicated in the table.

1b) Unspecified ("Wobbly") primer and probe sequences

To obtain reproducible and comparable results, it is essential to distinctively define the primer pairs. In the Corman-Drosten paper we observed six unspecified positions, indicated by the letters R, W, M and S (Table 2). The letter W means that at this position there can be either an A or a T; R signifies there can be either a G or an

A; M indicates that the position may either be an A or a C; the letter S indicates there can be either a G or a C on this position.

This high number of variants not only is unusual, but it also is highly confusing for laboratories. These six unspecified positions could easily result in the design of several different alternative primer sequences which do not relate to SARS-CoV-2 (2 distinct RdRp_SARSr_F primers + 8 distinct RdRp_SARS_P1 probes + 4 distinct RdRp_SARSr_R). **The design variations will inevitably lead to results that are not even SARS CoV-2 related. Therefore, the confusing unspecific description in the Corman-Drosten paper is not suitable as a Standard Operational Protocol. These unspecified positions should have been designed unequivocally.**

These wobbly sequences have already created a source of concern in the field and resulted in a Letter to the Editor authored by Pillonel et al. [8] regarding blatant errors in the described sequences. These errors are self-evident in the Corman et al. supplement as well.

Table 2: Primers and probes (adapted from Corman-Drosten paper; unspecified ("Wobbly") nucleotides in the primers are highlighted)

Assay/use	Oligonucleotide	Sequence[a]	Concentration[b]
RdRP gene	RdRp_SARSr-F	GTGARATGGTCATGTGTGGCGG	Use 600 nM per reaction
	RdRp_SARSr-P2	FAM-CAGGTGGAACCTCATCAGGAGATGC-BBQ	Specific for 2019-nCoV, will not detect SARS-CoV. Use 100 nM per reaction and mix with P1
	RdRP_SARSr-P1	FAM-CCAGGTGGWACRTCATCMGGTGATGC-BBQ	Pan Sarbeco-Probe will detect 2019-nCoV, SARS-CoV and bat-SARS-related CoVs. Use 100 nM per reaction and mix with P2
	RdRp_SARSr-R	CARATGTTAAASACACTATTAGCATA	Use 800 nM per reaction
E gene	E_Sarbeco_F	ACAGGTACGTTAATAGTTAATAGCGT	Use 400 nm per reaction
	E_Sarbeco_P1	FAM-ACACTAGCCATCCTTACTGCGCTTCG-BBQ	Use 200 nm per reaction
	E_Sarbeco_R	ATATTGCAGCAGTACGCACACA	Use 400 nm per reaction
N gene	N_Sarbeco_F	CACATTGGCACCCGCAATC	Use 600 nm per reaction
	N_Sarbeco_P	FAM-ACTTCCTCAAGGAACAACATTGCCA-BBQ	Use 200 nm per reaction
	N_Sarbeco_R	GAGGAACGAGAAGAGGCTTG	Use 800 nm per reaction

W is A/T; R is G/A; M is A/C; S is G/C. FAM: 6-carboxyfluorescein; BBQ: blackberry quencher.

[b] Optimised concentrations are given in nanomol per litre (nM) based on the final reaction mix, e.g. 1.5 µL of a 10 µM primer stock solution per 25 µL total reaction volume yields a final concentration of 600 nM as indicated in the table.

The WHO-protocol (Figure 1), which directly derives from the Corman-Drosten paper, concludes that in order to confirm the presence of SARS-CoV-2, two control genes (the E-and the RdRp-genes) must be identified in the assay. It should be noted, that the RdPd-gene has one uncertain position ("wobbly") in the forward-primer (R=G/A), two uncertain positions in the reverse-primer (R=G/A; S=G/C) and it has three uncertain positions in the RdRp-probe (W=A/T; R=G/A; M=A/C). So, two different forward primers, four different reverse primers, and eight distinct probes can be synthesized for the RdPd-gene. Together, there are 64 possible combinations of primers and probes!

The Corman-Drosten paper further identifies a third gene which, according to the WHO protocol, was not further validated and deemed unnecessary:

> ***"Of note, the N gene assay also performed well but was not subjected to intensive further validation because it was slightly less sensitive."***

This was an unfortunate omission as it would be best to use all three gene PCRs as confirmatory assays, and this would have resulted in an almost sufficient virus RNA detection diagnostic tool protocol. Three confirmatory assay-steps would at least minimize-out errors & uncertainties at every fold-step in regards to "Wobbly"-spots. (Nonetheless, the protocol would still fall short of any "good laboratory practice", when factoring in all the other design-errors).

As it stands, the N gene assay is regrettably neither proposed in the WHO-recommendation (Figure 1) as a mandatory and crucial third confirmatory step, nor is it emphasized in the Corman-Drosten paper as important optional reassurance "for a routine workflow" (Table 2).

Consequently, in nearly all test procedures worldwide, merely 2 primer

matches were used instead of all three. This oversight renders the entire test-protocol useless with regards to delivering accurate test-results of real significance in an ongoing pandemic.

Figure 1: The N-Gene confirmatory-assay is neither emphasized as necessary third step in the official WHO Drosten-Corman protocol-recommendation below [8] nor is it required as a crucial step for higher test-accuracy in the Eurosurveillance publication.

Background
We used known SARS- and SARS-related coronaviruses (bat viruses from our own studies as well as literature sources) to generate a non-redundant alignment (excerpts shown in Annex). We designed candidate diagnostic RT-PCR assays before release of the first sequence of 2019-nCoV. Upon sequence release, the following assays were selected based on their matching to 2019-nCoV as per inspection of the sequence alignment and initial evaluation (Figures 1 and 2).

All assays can use SARS-CoV genomic RNA as positive control. Synthetic control RNA for 2019-nCoV E gene assay is available via EVAg. Synthetic control for 2019-nCoV RdRp is expected to be available via EVAg from Jan 21st onward.

First line screening assay: E gene assay
Confirmatory assay: RdRp gene assay

1c) Erroneous GC-content (discussed in 2c, together with annealing temperature (Tm))

1d) Detection of viral genes

RT-PCR is not recommended for primary diagnostics of infection. This is why the RT-PCR Test used in clinical routine for detection of COVID-19 is not indicated for COVID-19 diagnosis on a regulatory basis.

> ***"Clinicians need to recognize the enhanced accuracy and speed of the molecular diagnostic***

> ***techniques for the diagnosis of infections, but also to understand their limitations. Laboratory results should always be interpreted in the context of the clinical presentation of the patient, and appropriate site, quality, and timing of specimen collection are required for reliable test results". [9]***

However, it may be used to help the physician's differential diagnosis when he or she has to discriminate between different infections of the lung (Flu, Covid-19 and SARS have very similar symptoms). For a confirmative diagnosis of a specific virus, at least 3 specific primer pairs must be applied to detect 3 virus-specific genes. Preferably, these target genes should be located with the greatest distance possible in the viral genome (opposite ends included).

Although the Corman-Drosten paper describes 3 primers, these primers only cover roughly half of the virus' genome. This is another factor that decreases specificity for detection of intact COVID-19 virus RNA and increases the quote of false positive test results.

Therefore, even if we obtain three positive signals (i.e. the three primer pairs give 3 different amplification products) in a sample, this does not prove the presence of a virus. **A better primer design would have terminal primers on both ends of the viral genome. This is because the whole viral genome would be covered and three positive signals can better discriminate between a complete (and thus potentially infectious) virus and fragmented viral genomes (without infectious potency).** In order to infer anything of significance about the infectivity of the virus, the Orf1 gene, which encodes the essential replicase enzyme of SARS-

CoV viruses, should have been included as a target (Figure 2). The positioning of the targets in the region of the viral genome that is most heavily and variably transcribed is another weakness of the protocol.

Kim et al. demonstrate a highly variable 3' expression of subgenomic RNA in Sars-CoV-2 [23]. These RNAs are actively monitored as signatures for asymptomatic and non-infectious patients [10]. It is highly questionable to screen a population of asymptomatic people with qPCR primers that have 6 base pairs primer-dimer on the 3 prime end of a primer (Figure 3).
Apparently the WHO recommends these primers. We tested all the wobble derivatives from the Corman-Drosten paper with Thermofisher's primer dimer web tool [11]. The RdRp forward primer has 6bp 3prime homology with Sarbeco E Reverse. At high primer concentrations this is enough to create inaccuracies.

Of note: There is a perfect match of one of the N primers to a clinical pathogen (Pantoea), found in immuno-compromised patients. The reverse primer hits Pantoea as well but not in the same region (Figure 3).

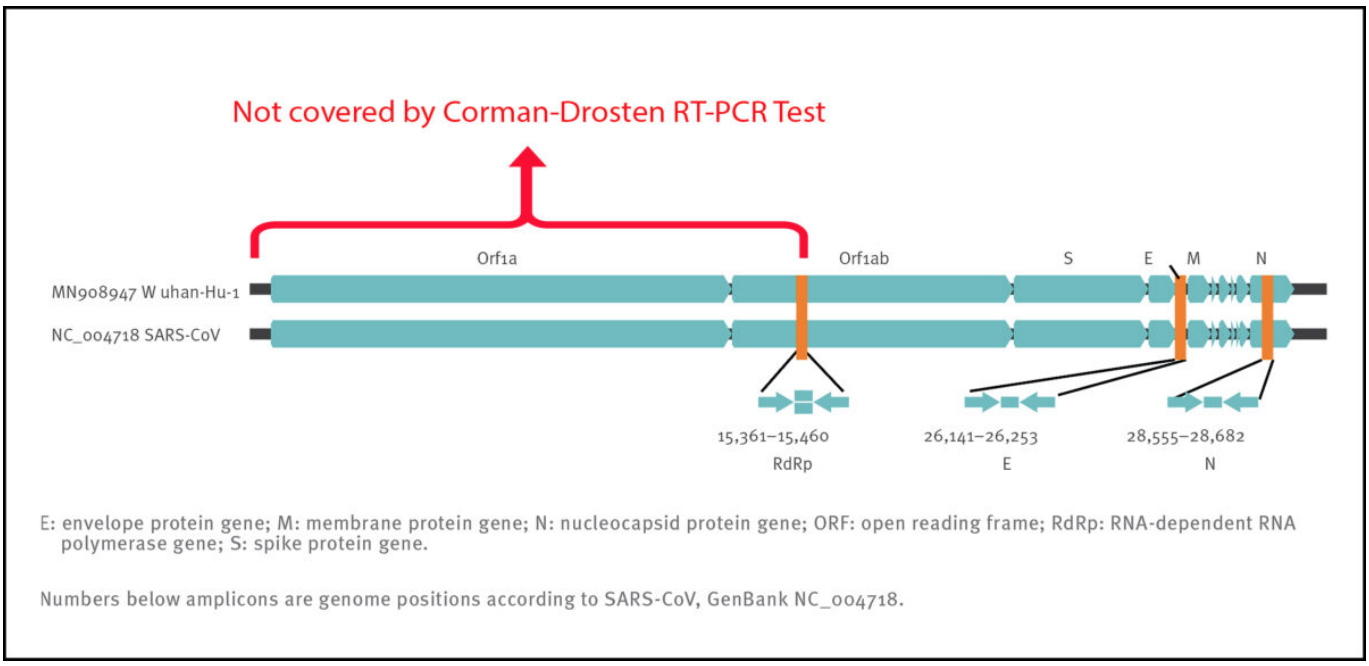
These are severe design errors, since the test cannot discriminate between the whole virus and viral fragments. The test cannot be used as a diagnostic for SARS-viruses.

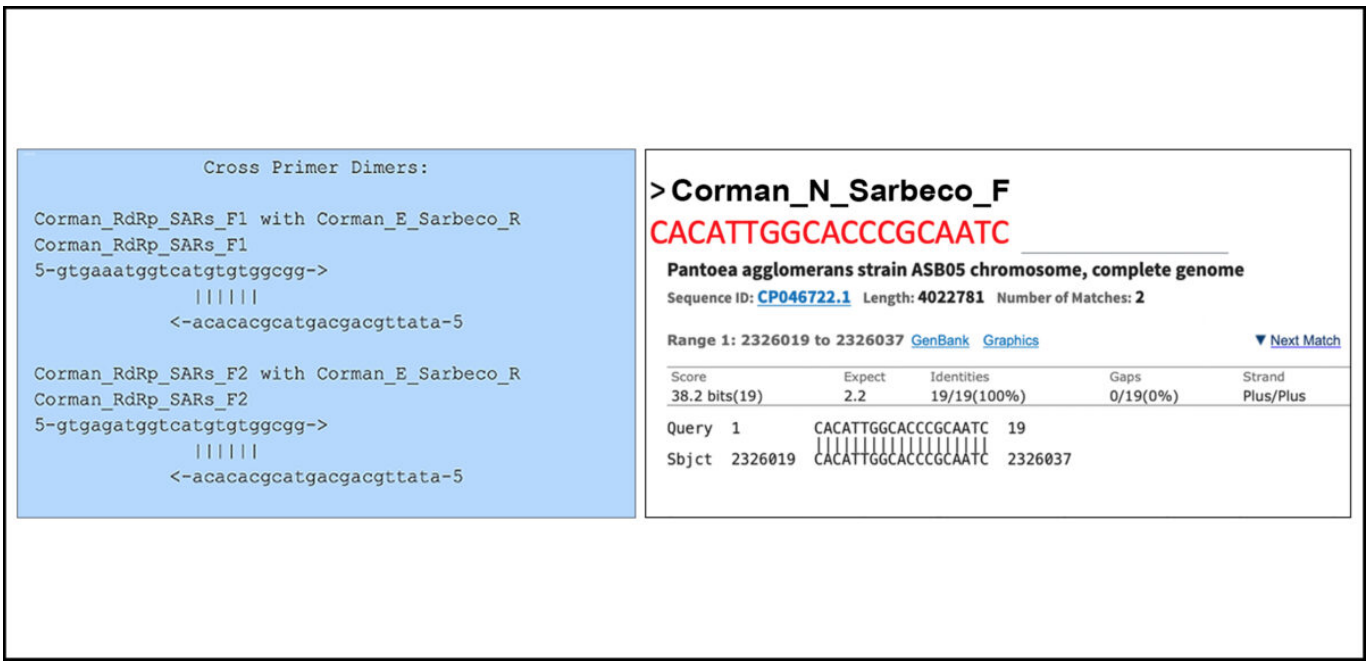
Figure 2: Relative positions of amplicon targets on the SARS coronavirus and the 2019 novel coronavirus genome. ORF: open reading frame; RdRp: RNA-dependent RNA polymerase. Numbers below amplicon are genome positions according to SARS-CoV, NC_004718 [1];

Figure 3: A test with Thermofischer's primer dimer web tool reveals that the RdRp forward primer has a 6bp 3`prime homology with Sarbeco E Reverse (left box). Another test reveals that there is a perfect match for one of the N-primers to a clinical pathogen (Pantoea) found in immuno-compromised patients (right box).

2. Reaction temperatures

2a) DNA melting temperature (>92°).





Adequately addressed in the Corman-Drosten paper.

2b) DNA amplification temperature.

Adequately addressed in the Corman-Drosten paper.

2c) Erroneous GC-contents and Tm

The annealing-temperature determines at which temperature the primer attaches/detaches from the target sequence. For an efficient and specific amplification, GC content of primers should meet a minimum of 40% and a maximum of 60% amplification. **As indicated in table 3, three of the primers described in the Corman-Drosten paper are not within the normal range for GC-content. Two primers (RdRp_SARSr_F and RdRp_SARSr_R) have unusual and very low GC-values of 28%-31% for all possible variants of wobble bases, whereas primer E_Sarbeco_F has a GC-value of 34.6% (Table 3 and second panel of Table 3).**

It should be noted that the GC-content largely determines the binding to its specific target due to its three hydrogen bonds in base pairing. Thus, the lower the GC-content of the primer, the lower its binding-capability to its specific target gene sequence (i.e. the gene to be detected). This means for a target-sequence to be recognized we have to choose a temperature which is as close as possible to the actual annealing-temperature (best practise-value) for the primer not to detach again, while at the same time specifically selecting the target sequence.

If the Tm-value is very low, as observed for all wobbly-variants of the RdRp reverse primers, the primers can bind non-specifically to several targets, decreasing specificity and increasing potential false positive results.

The annealing temperature (Tm) is a crucial factor for the determination of the specificity/accuracy of the qPCR procedure and essential for evaluating the accuracy of qPCR-protocols. Best-practice recommendation: Both primers (forward and reverse) should have an almost similar value, preferably the identical value.

We used the freely available primer design software Primer-BLAST [12, 25] to evaluable the best-practise values for all primers used in the Corman-Drosten paper (Table 3). We attempted to find a Tm-value of 60° C, while similarly seeking the highest possible GC%-value for all primers. A maximal Tm difference of 2° C within primer pairs was considered acceptable. Testing the primer pairs specified in the Corman-Drosten paper, we observed a difference of 10° C with respect to the

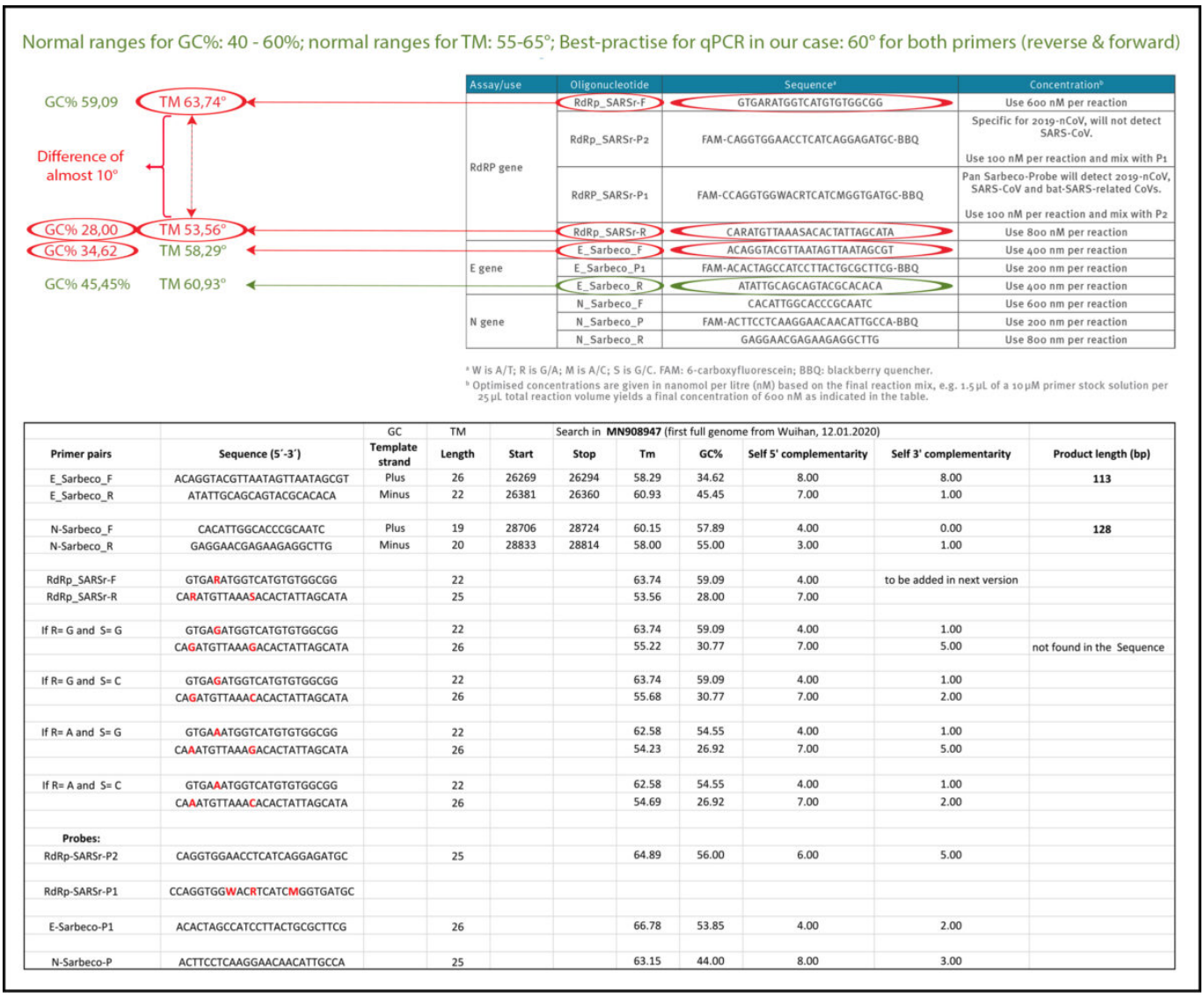
annealing temperature Tm for primer pair1 (RdRp_SARSr_F and RdRp_SARSr_R). **This is a very serious error and makes the protocol useless as a specific diagnostic tool.**

Additional testing demonstrated that only the primer pair designed to amplify the N-gene (N_Sarbeco_F and N_Sarbeco_R) reached the adequate standard to operate in a diagnostic test, since it has a sufficient GC-content and the Tm difference between the primers (N_Sarbeco_F and N_Sarbeco_R) is 1.85° C (below the crucial maximum of 2° C difference). Importantly, this is the gene which was neither tested in the virus samples (Table 2) nor emphasized as a confirmatory test. In addition to highly variable melting temperatures and degenerate sequences in these primers, there is another factor impacting specificity of the procedure: the dNTPs (0.4uM) are 2x higher than recommended for a highly specific amplification. There is additional magnesium sulphate added to the reaction as well. This procedure combined with a low annealing temperature can create non-specific amplifications. When additional magnesium is required for qPCR, specificity of the assay should be further scrutinized.

The design errors described here are so severe that it is highly unlikely that specific amplification of SARS-CoV-2 genetic material will occur using the protocol of the Corman-Drosten paper.

Table 3: GC-content of the primers and probes (adapted from Corman-Drosten paper; aberrations from optimized GC-contents are highlighted. Second Panel shows a table-listing of all Primer-BLAST best practices values for all primers and probes used in the Corman-Drosten paper by Prof. Dr. Ulrike Kämmerer & her team

3. The number of amplification cycles



Assay/use	Oligonucleotide	Sequence[a]	Concentration[b]
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	RdRp_SARSr-P2	FAM-CAGGTGGAACCTCATCAGGAGATGC-BBQ	Specific for 2019-nCoV, will not detect SARS-CoV. Use 100 nM per reaction and mix with P1
	RdRP_SARSr-P1	FAM-CCAGGTGGWACRTCATCMGGTGATGC-BBQ	Pan Sarbeco-Probe will detect 2019-nCoV, SARS-CoV and bat-SARS-related CoVs. Use 100 nM per reaction and mix with P2
	RdRp_SARSr-R	CARATGTTAAASACACTATTAGCATA	Use 800 nM per reaction
E gene	E_Sarbeco_F	ACAGGTACGTTAATAGTTAATAGCGT	Use 400 nm per reaction
	E_Sarbeco_P1	FAM-ACACTAGCCATCCTTACTGCGCTTCG-BBQ	Use 200 nm per reaction
	E_Sarbeco_R	ATATTGCAGCAGTACGCACACA	Use 400 nm per reaction
N gene	N_Sarbeco_F	CACATTGGCACCCGCAATC	Use 600 nm per reaction
	N_Sarbeco_P	FAM-ACTTCCTCAAGGAACAACATTGCCA-BBQ	Use 200 nm per reaction
	N_Sarbeco_R	GAGGAACGAGAAGAGGCTTG	Use 800 nm per reaction

[a] W is A/T; R is G/A; M is A/C; S is G/C. FAM: 6-carboxyfluorescein; BBQ: blackberry quencher.
[b] Optimised concentrations are given in nanomol per litre (nM) based on the final reaction mix, e.g. 1.5 µL of a 10 µM primer stock solution per 25 µL total reaction volume yields a final concentration of 600 nM as indicated in the table.

		GC	TM		Search in **MN908947** (first full genome from Wuihan, 12.01.2020)					
Primer pairs	**Sequence (5'-3')**	**Template strand**	**Length**	**Start**	**Stop**	**Tm**	**GC%**	**Self 5' complementarity**	**Self 3' complementarity**	**Product length (bp)**
E_Sarbeco_F	ACAGGTACGTTAATAGTTAATAGCGT	Plus	26	26269	26294	58.29	34.62	8.00	8.00	**113**
E_Sarbeco_R	ATATTGCAGCAGTACGCACACA	Minus	22	26381	26360	60.93	45.45	7.00	1.00	
N-Sarbeco_F	CACATTGGCACCCGCAATC	Plus	19	28706	28724	60.15	57.89	4.00	0.00	**128**
N-Sarbeco_R	GAGGAACGAGAAGAGGCTTG	Minus	20	28833	28814	58.00	55.00	3.00	1.00	
RdRp_SARSr-F	GTGARATGGTCATGTGTGGCGG		22			63.74	59.09	4.00	to be added in next version	
RdRp_SARSr-R	CARATGTTAAASACACTATTAGCATA		25			53.56	28.00	7.00		
If R= G and S= G	GTGAGATGGTCATGTGTGGCGG		22			63.74	59.09	4.00	1.00	
	CAGATGTTAAAGACACTATTAGCATA		26			55.22	30.77	7.00	5.00	not found in the Sequence
If R= G and S= C	GTGAGATGGTCATGTGTGGCGG		22			63.74	59.09	4.00	1.00	
	CAGATGTTAAACACACTATTAGCATA		26			55.68	30.77	7.00	2.00	
If R= A and S= G	GTGAAATGGTCATGTGTGGCGG		22			62.58	54.55	4.00	1.00	
	CAAATGTTAAAGACACTATTAGCATA		26			54.23	26.92	7.00	5.00	
If R= A and S= C	GTGAAATGGTCATGTGTGGCGG		22			62.58	54.55	4.00	1.00	
	CAAATGTTAAACACACTATTAGCATA		26			54.69	26.92	7.00	2.00	
Probes:										
RdRp-SARSr-P2	CAGGTGGAACCTCATCAGGAGATGC		25			64.89	56.00	6.00	5.00	
RdRp-SARSr-P1	CCAGGTGGWACRTCATCMGGTGATGC									
E-Sarbeco-P1	ACACTAGCCATCCTTACTGCGCTTCG		26			66.78	53.85	4.00	2.00	
N-Sarbeco-P	ACTTCCTCAAGGAACAACATTGCCA		25			63.15	44.00	8.00	3.00	

It should be noted that there is no mention anywhere in the Corman-Drosten paper of a test being positive or negative, or indeed what defines a positive or negative result. These types of virological diagnostic tests must be based on a SOP, including a validated and fixed number of PCR cycles (Ct value) after which a sample is deemed positive or negative. The maximum reasonably reliable Ct value is 30 cycles. Above a Ct of 35 cycles, rapidly increasing numbers of false positives must be expected .

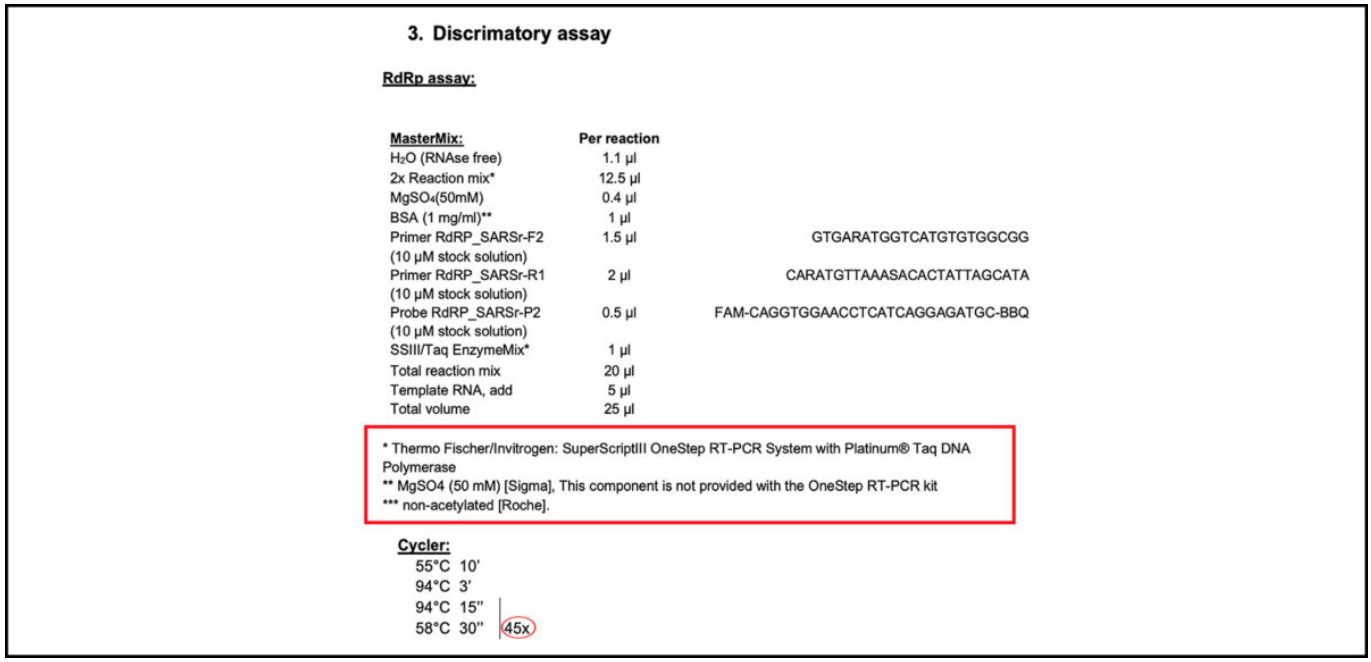
PCR data evaluated as positive after a Ct value of 35 cycles are completely unreliable.

Citing Jaafar et al. 2020 [3]: "At Ct = 35, the value we used to report a positive result for PCR, <3% of cultures are positive." **In other words, there was no successful virus isolation of SARS-CoV-2 at those high Ct values.**

Further, scientific studies show that only non-infectious (dead) viruses are detected with Ct values of 35 [22].

Between 30 and 35 there is a grey area, where a positive test cannot be established with certainty. This area should be excluded. Of course, one could perform 45 PCR cycles, as recommended in the Corman-Drosten WHO-protocol (Figure 4), but then you also have to define a reasonable Ct-value (which should not exceed 30). But an analytical result with a Ct value of 45 is scientifically and diagnostically absolutely meaningless (a reasonable Ct-value should not exceed 30). All this should be communicated very clearly. It is a significant mistake that the Corman-Drosten paper does not mention the maximum Ct value at which a sample can be unambiguously considered as a positive or a negative test-result. This important cycle threshold limit is also not specified in any follow-up submissions to date.

Figure 4: RT-PCR Kit recommendation in the official Corman-Drosten WHO-protocol [8]. Only a "Cycler"-value (cycles) is to be found without corresponding and scientifically reasonable Ct (Cutoff-value). This or any other cycles-value is nowhere to be found in the actual Corman-Drosten paper.



3. Discrimatory assay

RdRp assay:

MasterMix:	Per reaction	
H_2O (RNAse free)	1.1 µl	
2x Reaction mix*	12.5 µl	
$MgSO_4$(50mM)	0.4 µl	
BSA (1 mg/ml)**	1 µl	
Primer RdRP_SARSr-F2 (10 µM stock solution)	1.5 µl	GTGARATGGTCATGTGTGGCGG
Primer RdRP_SARSr-R1 (10 µM stock solution)	2 µl	CARATGTTAAASACACTATTAGCATA
Probe RdRP_SARSr-P2 (10 µM stock solution)	0.5 µl	FAM-CAGGTGGAACCTCATCAGGAGATGC-BBQ
SSIII/Taq EnzymeMix*	1 µl	
Total reaction mix	20 µl	
Template RNA, add	5 µl	
Total volume	25 µl	

* Thermo Fischer/Invitrogen: SuperScriptIII OneStep RT-PCR System with Platinum® Taq DNA Polymerase
** MgSO4 (50 mM) [Sigma], This component is not provided with the OneStep RT-PCR kit
*** non-acetylated [Roche].

Cycler:
55°C 10'
94°C 3'
94°C 15"
58°C 30" 45x

4. Biomolecular validations

To determine whether the amplified products are indeed SARS-CoV-2 genes, biomolecular validation of amplified PCR products is essential. For a diagnostic test, this validation is an absolute must.

Validation of PCR products should be performed by either running the PCR product in a 1% agarose-EtBr gel together with a size indicator (DNA ruler or DNA ladder) so that the size of the product can be estimated. The size must correspond to the calculated size of the amplification product. But it is even better to sequence the amplification product. The latter will give 100% certainty about the identity of the amplification product. Without molecular validation one can not be sure about the identity of the amplified PCR products. Considering the severe design errors described earlier, the amplified PCR products can be anything.

Also not mentioned in the Corman-Drosten paper is the case of small fragments of qPCR (around 100bp): It could be either 1,5% agarose gel or even an acrylamide gel.

The fact that these PCR products have not been validated at molecular level is another striking error of the protocol, making any test based upon it useless as a specific diagnostic tool to identify the SARS-CoV-2 virus.

5. Positive and negative controls to confirm/refute specific virus detection.

The unconfirmed assumption described in the Corman-Drosten paper is that SARS-CoV-2 is the only virus from the SARS-like beta-coronavirus group that currently causes infections in humans. The sequences on which their PCR method is based are in silico sequences, supplied by a laboratory in China [23], because at the time of development of the PCR test no control material of infectious (“live”) or inactivated SARS-CoV-2 was available to the authors. The PCR test was therefore designed using the sequence of the known SARS-CoV as a control material for the Sarbeco component (Dr. Meijer, co-author Corman-Drosten paper in an email exchange with Dr. Peter Borger) [2].

All individuals testing positive with the RT-PCR test, as described in the Corman-Drosten paper, are assumed to be positive for SARS-CoV-2 infections. There are three severe flaws in their assumption. First, a positive test for the RNA molecules described in the Corman-Drosten paper cannot be equated to "infection with a virus". A positive RT-PCR test merely indicates the presence of viral RNA molecules. As demonstrated under point 1d (above), **the Corman-Drosten test was not designed to detect the full-length virus, but only a fragment of the virus. We already concluded that this classifies the test as unsuitable as a diagnostic test**
for SARS-virus infections.

Secondly and of major relevance, the functionality of the published RT-PCR Test was not demonstrated with the use of a positive control (isolated SARS-CoV-2 RNA) which is an essential scientific gold standard.

Third, the Corman-Drosten paper states:

> ***"To show that the assays can detect other bat-associated SARS-related viruses, we used the E gene assay to test six bat-derived faecal samples available from Drexler et al. [...] und Muth et al. [...]. These virus-positive samples stemmed from European rhinolophid bats. Detection of these phylogenetic outliers within the SARS-related CoV clade suggests that all Asian viruses are likely to be detected. This would, theoretically, ensure broad sensitivity***

even in case of multiple independent acquisitions of variant viruses from an animal reservoir."

This statement demonstrates that the E gene used in RT-PCR test, as described in the Corman-Drosten paper, is not specific to SARS-CoV-2.

The E gene primers also detect a broad spectrum of other SARS viruses.
The genome of the coronavirus is the largest of all RNA viruses that infect humans and they all have a very similar molecular structure. Still, SARS-CoV1 and SARS-CoV-2 have two highly specific genetic fingerprints, which set them apart from the other coronaviruses. First, a unique fingerprint-sequence (KTFPPTEPKKDKKKK) is present in the N-protein of SARS-CoV and SARS-CoV-2 [13,14,15]. Second, both SARS-CoV1 and SARS-CoV2 do not contain the HE protein, whereas all other coronaviruses possess this gene [13, 14]. **So, in order to specifically detect a SARS-CoV1 and SARS-CoV-2 PCR product the above region in the N gene should have been chosen as the amplification target.** A reliable diagnostic test should focus on this specific region in the N gene as a confirmatory test. **The PCR for this N gene was not further validated nor recommended as a test gene by the Drosten-Corman paper, because of being "not so sensitive" with the SARS-CoV original probe [1].**

Furthermore, the absence of the HE gene in both SARS-CoV1 and SARS-CoV-2 makes this gene the ideal negative control to exclude other coronaviruses. The Corman-Drosten paper does not contain this negative control, nor does it contain any other negative controls. **The PCR test in the Corman-Drosten paper therefore contains neither a unique positive control nor a negative control to exclude the presence of other coronaviruses. This is another major design flaw which classifies the test as unsuitable for diagnosis.**

6. Standard Operational Procedure (SOP) is not available

There should be a Standard Operational Procedure (SOP) available, which unequivocally specifies the above parameters, so that all laboratories are able to set up the identical same test conditions. To have a validated universal SOP is essential, because it facilitates data comparison within and between countries. **It is very important to specify all primer parameters unequivocally. We note that this has not been done.** Further, the Ct value to indicate when a sample should be considered positive or negative is not specified. It is also not specified when a sample is considered infected with SARS-CoV viruses. As shown above, the test cannot discern between virus and virus fragments, so the Ct value indicating positivity is crucially important. This Ct value should have been specified in the Standard Operational Procedure (SOP) and put on-line so that all laboratories carrying out this test have exactly the same boundary conditions. It points to flawed science that such an SOP does not exist. The laboratories are thus free to conduct the test as they consider appropriate, resulting in an enormous amount of variation. Laboratories all over Europe are left with a multitude of questions; which primers to order? which nucleotides to fill in the undefined places? which Tm value to choose? How many PCR cycles to run? At what Ct value is the sample positive? And when is it negative? And how many genes to test? Should all genes be tested, or just the E and RpRd gene as shown in Table 2 of the Corman-Drosten paper? Should the N gene be tested as well? And what is their negative control? What is their positive control?

The protocol as described is unfortunately very vague and erroneous in its design that one can go in dozens of different directions. There does not appear to be any standardization nor an SOP, so it is not clear how this test can be implemented.

7. Consequences of the errors described under 1-5: false positive results.

The RT-PCR test described in the Corman-Drosten paper contains so many molecular biological design errors (see 1-5) that it is not possible to obtain unambiguous

results. It is inevitable that this test will generate a tremendous number of so-called “false positives”. The definition of false positives is a negative sample, which initially scores positive, but which is negative after retesting with the same test. False positives are erroneous positive test-results, i.e. negative samples that test positive. And this is indeed what is found in the Corman-Drosten paper. On page 6 of the manuscript PDF the authors demonstrate, that even under well-controlled laboratory conditions, a considerable percentage of false positives is generated with this test:

> ***“In four individual test reactions, weak initial reactivity was seen however they were negative upon retesting with the same assay. These signals were not associated with any particular virus, and for each virus with which initial positive reactivity occurred, there were other samples that contained the same virus at a higher concentration but did not test positive. Given the results from the extensive technical qualification described above, it was concluded that this initial reactivity was not due to chemical instability of real-time PCR probes and most probably to handling issues caused by the rapid introduction of new diagnostic tests***

and controls during this evaluation study." [1]

The first sentence of this excerpt is clear evidence that the PCR test described in the Corman-Drosten paper generates false positives. Even under the well-controlled conditions of the state-of-the-art Charité-laboratory, 4 out of 310 primary-tests are false positives per definition. Four negative samples initially tested positive, then were negative upon retesting. This is the classical example of a false positive. In this case the authors do not identify them as false positives, which is intellectually dishonest.

Another telltale observation in the excerpt above is that the authors explain the false positives away as "handling issues caused by the rapid introduction of new diagnostic tests". Imagine the laboratories that have to introduce the test without all the necessary information normally described in an SOP.

8. The Corman-Drosten paper was not peer-reviewed

Before formal publication in a scholarly journal, scientific and medical articles are traditionally certified by "peer review." In this process, the journal's editors take advice from various experts ("referees") who have assessed the paper and may identify weaknesses in its assumptions, methods, and conclusions. Typically a journal will only publish an article once the editors are satisfied that the authors have addressed referees' concerns and that the data presented supports the conclusions drawn in the paper." This process is as well described for Eurosurveillance [16].

The Corman-Drosten paper was submitted to Eurosurveillance on January 21st 2020 and accepted for publication on January 22nd 2020. On January 23rd 2020 the paper was online. On January 13th 2020 version 1-0 of the protocol was published at the official WHO website [17], updated on January 17th 2020 as document version 2-1 [18], even before the Corman-Drosten paper was published on January 23rd at Eurosurveillance.

Normally, peer review is a time-consuming process since at least two experts from the field have to critically read and comment on the submitted paper. In our opinion, this paper was not peer-reviewed. Twenty-four hours are simply not enough to carry out a thorough peer review. Our conclusion is supported by the fact that a tremendous number of very serious design flaws were found by us, which make the PCR test completely unsuitable as a diagnostic tool to identify the SARS-CoV-2 virus. Any molecular biologist familiar with RT-PCR design would have easily observed the grave errors present in the Corman-Drosten paper before the actual review process. We asked Eurosurveillance on October 26th 2020 to send us a copy of the peer review report. To date, we have not received this report and in a letter dated November 18th 2020, the ECDC as host for Eurosurveillance declined to provide access without providing substantial scientific reasons for their decision. On the contrary, they write that "disclosure would undermine the purpose of scientific investigations." [24].

9. Authors as the editors

A final point is one of major concern. It turns out that two authors of the Corman-Drosten paper, Christian Drosten and Chantal Reusken, are also members of the editorial board of this journal [19]. Hence there is a severe conflict of interest which strengthens suspicions that the paper was not peer-reviewed. It has the appearance that the rapid publication was possible simply because the authors were also part of the editorial board at Eurosurveillance. This practice is categorized as compromising scientific integrity.

SUMMARY CATALOGUE OF ERRORS FOUND IN THE PAPER

The Corman-Drosten paper contains the following specific errors:

1. There exists no specified reason to use these extremely high concentrations of primers in this protocol. The described concentrations lead to increased nonspecific bindings and PCR product amplifications, making the test unsuitable as a specific

diagnostic tool to identify the SARS-CoV-2 virus.

2. Six unspecified wobbly positions will introduce an enormous variability in the real world laboratory implementations of this test; the confusing nonspecific description in the Corman-Drosten paper is not suitable as a Standard Operational Protocol making the test unsuitable as a specific diagnostic tool to identify the SARS-CoV-2 virus.

3. The test cannot discriminate between the whole virus and viral fragments. Therefore, the test cannot be used as a diagnostic for intact (infectious) viruses, making the test unsuitable as a specific diagnostic tool to identify the SARS-CoV-2 virus and make inferences about the presence of an infection.

4. A difference of 10° C with respect to the annealing temperature Tm for primer pair1 (RdRp_SARSr_F and RdRp_SARSr_R) also makes the test unsuitable as a specific diagnostic tool to identify the SARS-CoV-2 virus.

5. A severe error is the omission of a Ct value at which a sample is considered positive and negative. This Ct value is also not found in follow-up submissions making the test unsuitable as a specific diagnostic tool to identify the SARS-CoV-2 virus.

6. The PCR products have not been validated at the molecular level. This fact makes the protocol useless as a specific diagnostic tool to identify the SARS-CoV-2 virus.

7. The PCR test contains neither a unique positive control to evaluate its specificity for SARS-CoV-2 nor a negative control to exclude the presence of other coronaviruses, making the test unsuitable as a specific diagnostic tool to identify the SARS-CoV-2 virus.

8. The test design in the Corman-Drosten paper is so vague and flawed that one can go in dozens of different directions; nothing is standardized and there is no SOP. This highly questions the scientific validity of the test and makes it unsuitable as a specific diagnostic tool to identify the SARS-CoV-2 virus.

9. Most likely, the Corman-Drosten paper was not peer-reviewed making the test unsuitable as a specific diagnostic tool to identify the SARS-CoV-2 virus.

10. We find severe conflicts of interest for at least four authors, in addition to the fact that two of the authors of the Corman-Drosten paper (Christian Drosten and Chantal Reusken) are members of the editorial board of Eurosurveillance. A conflict of interest was added on July 29 2020 (Olfert Landt is CEO of TIB-Molbiol; Marco Kaiser is senior researcher at GenExpress and serves as scientific advisor for TIB-Molbiol), that was not declared in the original version (and still is missing in the PubMed version); TIB-Molbiol is the company which was "the first" to produce PCR kits (Light Mix) based on the protocol published in the Corman-Drosten manuscript, and according to their own words, they distributed these PCR-test kits before the publication was even submitted [20]; further, Victor Corman & Christian Drosten failed to mention their second affiliation: the commercial test laboratory "Labor Berlin". Both are responsible for the virus diagnostics there [21] and the company operates in the realm of real time PCR-testing.

In light of our re-examination of the test protocol to identify SARS-CoV-2 described in the Corman-Drosten paper we have identified concerning errors and inherent fallacies which render the SARS-CoV-2 PCR test useless.

CONCLUSION

The decision as to which test protocols are published and made widely available lies squarely in the hands of Eurosurveillance. A decision to recognise the errors apparent in the Corman-Drosten paper has the benefit to greatly minimise human cost and suffering going forward.

Is it not in the best interest of Eurosurveillance to retract this paper? Our conclusion is clear. In the face of all the tremendous PCR-protocol design flaws and errors described here, we conclude: There is not much of a choice left in the framework of scientific integrity and responsibility.

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Description RT-PCR RKI Germany, on page 10 of this link:
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BRM: Planned and conducted the research, conceptualising the figures and manuscript.

MY: Proofreading the analyses and research.

KMcK: Conducted the analyses and research, conceptualized the manuscript.

KS: Conducted the analyses and research.

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Addendum

Update 2.12.2020:

Author Contribution Dr. Michael Yeadon changed to:
Proofreading the analyses and research.

Author Affiliation Kevin Mckernan changed to:
Medicinal Genomics.

next »

Comments

1. **Sebe Vpgel** says:
   November 29, 2020 at 11:36 pm

   Thanks for your excellent work!

   Reply

1.  **robvdz** says:
   November 30, 2020 at 6:58 pm

   Beside all of this, I won't let somebody that is not medically schooled fidle around in my nose cavities for what ever reason.

   Reply

   1.  **Bayaba** says:
      December 1, 2020 at 1:44 am

      I won't let someone who is medically trained do that. That includes my own brother, who is an MD and who is the president and CEO of the family practice he runs.

      Reply

   2.  **Madaload** says:
      December 1, 2020 at 8:35 pm

      Unless, of course, the government makes testing mandatory. Slovakia already had a few rounds of full scale (all citizens) AG testing. It wasn't mandatory per se. But if you didn't get tested, you didn't get a certificate and had to self isolate for 10 days. If you didn't get tested in the second round, same thing with 14 days isolation and your employer wouldn't let you work without the cert. After serious protests, the government now says AG positive results will be validated by PCR tests and 3 rounds of this "non mandatory" testing by Christmas.

      Reply

      1.  **Lieveke** says:

December 2, 2020 at 11:30 pm

How sad ! Will be with Slovakia in mind…

Reply

1. **Chantal** says:
   December 3, 2020 at 5:46 pm

   Hey is that u Liev?

2. **Dr. med. dent. Klaus Wilhelm Rocholl** says:
   November 30, 2020 at 12:43 am

   Congratulation – and my deepest and most sincere admiration for your impressive work.
   I hope you maybe literally helped to save the world!

   Reply

   1. **Wim Sturm** says:
      November 30, 2020 at 5:25 pm

      Thank you for your great work!

      Facts outweigh fiction and open people's eyes to this ridiculous fictional reality that has been created in the world based on the Corman Drosten paper.

      Thank you again for distinguishing fiction from reality with you retraction paper.

      Reply

3. **J.** says:
November 30, 2020 at 12:50 am

Great job! Heroes of the universe!!!

Reply

4. **LIVIANA*** says:
November 30, 2020 at 2:26 am

Thank you
Dankuwel
Obrigado
Merci
Vielen dank
Und viel Erfolg

Reply

5. **DUC** says:
November 30, 2020 at 2:37 am

Thanks for publishing what I have been saying in essence all along (but sure not in such detail). Lets hope there are consequences which are in balance with the damage done to the world population.

M.sc., D.sc., former researcher in molecular genetics, HIV, immunology, among others 6 y at NIH(USA)

Reply

1. **Liam King** says:
December 1, 2020 at 11:33 pm

Glad to hear you've been saying this all along.

Where were you shouting about this when you couldn't be heard?

Let me know so I can warn others to stay clear of such ineffectual places (and I will of course point them here instead).

Reply

6. **D. Krüger** says:
November 30, 2020 at 3:05 am

Ein wundervoller Hoffnungsschimmer am Horizont der dem ganzen Irrsinn hoffentlich ein baldiges Ende setzt bevor noch mehr unnötiges Leid und Elend verursacht wird.

Herzlichen Dank, für Ihre wissenschaftliche Integrität die einigen Ihrer Kollegen offenbar abhanden gekommen ist !

Reply

7. **Hoijtink** says:
November 30, 2020 at 3:20 am

Good to see that at least some scientists still use common sense and brains. In my book you are heroes. Sadly it remains to be seen what politicians will do next, they have their own (hidden?) agenda.

Thank you all ….

Reply

8. **Solveig Warren** says:
November 30, 2020 at 4:26 am

Thank you for telling the truth in such a professional manner and using science appropriately! You are true heroes of our Universe! It is a tough job to to stand up for honesty with the Media having a one track mind!

Reply

9. **Marlee Ponich** says:
November 30, 2020 at 4:48 am

Much love and gratitude!

Reply

10. **Autoglas** says:
November 30, 2020 at 6:05 am

Thank you for all ... I hope the best

Reply

11. **Fred K.** says:
November 30, 2020 at 6:26 am

Many thanks for the extremely good and bitterly necessary work! I hope that this work can make a fundamental contribution to finally putting a stop to the madness. If the faulty paper is not voluntarily withdrawn by the authors, I very much hope that there is a way to force this through the courts with the help of dedicated lawyers. Thank you for your extraordinary commitment!

Reply

12. **Christoph Schmitz (Univ.Prof. Dr.med.)** says:
November 30, 2020 at 6:41 am

I cannot comment on PCR issues; this is not my field of expertise (I am a

neuroanatomist at LMU Munich/Germany with approximately 200 papers listed in PubMed). I would just like to comment on the “points of major concern” #8 and #9 outlined above:

#8: it is indeed feasible (and not unusual) to perform a scientifically sound peer-review of a manuscript within a few hours after having obtained the request by a journal, particularly if you are an expert in the field. The fact that the manuscript that is discussed here was accepted for publication one day after submission does not mean that it was not peer-reviewed.

#9: every serious academic journal has an internal policy that manuscripts submitted by a member (or members) of the editorial board are handled and reviewed by other members of the editorial board of the journal. The fact that Christian Drosten has served as corresponding author of the manuscript described here does not imply that “scientific integrity was compromised”. In particular, this fact may not support the “suspicions that the paper was not peer-reviewed”.

In summary, I warmly recommend to separate the “points of major concern” #8 and #9 outlined above from the other points of major concern in order to place this important discussion on a more objective footing.

Reply

1.  **Dr. Frank Potthast** says:
   November 30, 2020 at 2:31 pm

   In my opinion, you cannot separate the issues; if the editorial board has commmon sense, that this publication should be accepted for publication within a few hours, the scientific quality must be double-checked if you don´t want to risk accuses of wangle.
   The mistakes concerning good laboratory practice are so obvious, that I cannot believe, that it wouldn´t have been noticed by any of the experts.

Reply

2. **Maritta Mathis** says:
December 1, 2020 at 12:29 am

With all due respect, have you not actually recognized the dimensions and scope of this scandal, that you only criticize these two points, but are silent overall about the outrageously unscientific approach (where I live this is called fraud)?

Reply

1. **Christoph Schmitz** says:
December 1, 2020 at 7:04 am

Please read my comment again. I simply cannot comment on PCR issues; this is not my field of expertise (I have never worked with PRC). This must be done by others (which I highly welcome, no doubt). However, when reading all these comments here it looks that there are so many experts around that my non-expert opinion is really not necessary.

Reply

1. **PD Dr. Jörg Gerke** says:
December 7, 2020 at 10:48 am

Dear Dr. Schmitz,
I understand your points and find them reasonable. The scientific content should be discriminated from the “social” content. However, a review within 24 hours is very unusual at least in the field of my experience. Instead the publication of the reviews by the reviewer of the Journal should be recommended.

Reply

2.  **Evgeniy Gilenko** says:
December 1, 2020 at 5:39 pm

Think, the scope of the comment above is restricted to these two subtopics. Even though the practice of approval processes and publishing of scientific articles relies in my opinion mainly just on scientific integrity of reviewers, which I personally would like to trust, and the with regards to the massive impact of the study – direct or not – on the economies, societies etc., I simply would assume, that at the moment of submission and publication there were no evidence of pandemic outbreak of the SARS-COV-2 and therefore no self-evident need for deeper review of the study. Shortly saying, they probably didn't think the study would have any significant impact on anything. What I am asking myself instead, is why the first critical review appears only on 27th of November and was not conducted or initiated by the journal itself?

Reply

1.  **Ralph Nimmann** says:
December 2, 2020 at 9:07 pm

VERY good question "why the first critical review appears only on 27th of November and was not conducted or initiated by the journal itself?"
I added a summary of this peer review on https://healthtruth.info/weve-got-it-all-wrong-fighting-the-virus/#pcr

Reply

13. **Els van Veen** says:
November 30, 2020 at 6:42 am

Danke! Dankuwel! Thank you!

Ik ben een Nederlandse huisarts en hoop dat nu snel het krankzinnige testen (buiten de kliniek) kan worden gestaakt.
De lockdowns opgeheven.
De mondkapjes weggedaan.
De wetenschap in ere hersteld.
Het recht zal winnen van het onrecht en de leugen.

Reply

14. **Dipl.Psych. Hans-J. Steiner** says:
November 30, 2020 at 7:01 am

Interesting work, however – after all tthese hoax-reports and "scientific" looking statements of people all over the wolrd, which came finally out, not being cited corectly or just abused for never done citations or just the person was "virtual", there will be much work to immunize that work from "Faktencheckers" and other discreditions. That will be even the more relevant work to be done urgently to make this paper an evicent part of public, scientific and political discussion!

Reply

1. **Udo** says:
November 30, 2020 at 10:19 am

Dear Hans,

that is a very valid point. I wonder already since a long time about the "circular reasoning" in the so called "fact check", as generally speaking

they don't make sense or the find "one specialst" who will explain it (putting a few minutes of effort in it).

Reply

Bobby says:
November 30, 2020 at 2:47 pm

https://www.dailywire.com/news/candace-owens-challenges-fact-checker-and-wins

Reply

1. 

   Tatjana Z. says:
   December 3, 2020 at 6:13 pm

   Danke für die Antwort! Dann hoffe ich sehr, dass ihr auch gehört werdet!

   Reply

15. 

    Monika says:
    November 30, 2020 at 7:58 am

    Thank You All for the great work! God bless you!

    Reply

16. 

    Dr .Andreas Gloge says:
    November 30, 2020 at 8:22 am

    Man muß das Wahre immer wiederholen, weil auch der Irrtum um uns her immer wieder gepredigt wird, und zwar nicht von einzelnen, sondern von der Masse. In Zeitungen und Enzyklopädien, auf Schulen und Universitäten, überall

ist der Irrtum oben auf, und es ist ihm wohl und behaglich, im Gefühl der Majorität, die auf seiner Seite ist.

Johann Wolfgang von Goethe

Reply

1.  **Gertrud Adam** says:
   December 10, 2020 at 10:33 am

   Vielen Dank, kannte ich noch gar nicht. Autorenschaft überraschte mich, als ich sie drunter entdeckte.

   Reply

17.  **Brigid** says:
    November 30, 2020 at 9:13 am

    Thank you for this excellent piece of work which clarifies in detail and in a factual way what is felt by many. This is the proof. My hope is that this will enlighten those who need to know.

    Reply

18.  **ursula b.** says:
    November 30, 2020 at 9:54 am

    The more one tries to opress truth the brighter it shines throughout the universe.
    Thank you so much for your great work and dedication. With many small steps we will win the race 1nce and forever

    Reply

19. **STRNTVRVLND** says:
November 30, 2020 at 9:56 am

Let's hope this effort will put a end to the disproportionate mesures. Please make this understandable for all by also presenting this information on micro-level instead of moleculare.

May a revolution be upon us

Reply

20. **B Anderson** says:
November 30, 2020 at 10:01 am

So, if the test to confirm you have covid-19 is useless...what virus is the vaccine that is soon to be distributed going to prevent you from getting?

Reply

1. **Eva** says:
November 30, 2020 at 7:10 pm

You are right. And The Expert answers: "Good question, thank you. Next question, please..."

Reply

1. **human** says:
November 30, 2020 at 10:00 pm

Actually, we are no longer permitted to question anything.

Because once questions are allowed, the answers will inevitably indict extremely powerful individuals and organizations of crimes against

humanity.

Reply

2. **Angela** says:
December 8, 2020 at 10:38 pm

Exactly. This is the more pressing question. WHAT IS IN THE VACCINE?
Judging from their behaviour so far, I don't trust the intentions of authorities worldwide.
Next question: What else is to come?
Believe me, lockdown and other measures will look benign in comparison to what else they will unleash on us.

Reply

21. **Maria** says:
November 30, 2020 at 10:26 am

Thank you for doing this work and bringing real science to the table. Hoepfully this will end this epidemic of false positives which is causing so much human suffering. The cost of lockdowns: https://www.aier.org/article/cost-of-us-lockdowns-a-preliminary-report/

Reply

22. **Robert Michel** says:
November 30, 2020 at 10:32 am

Thank you,

If you have an hammer – every thing looks like a nail....
It becomes dangerious if political leader says "we will be only rescued,

when we would have that vacination" and Media is following narrowminded.

We are spending Billions just on test-positiv cases on a RTPCR-test of one Corona-Virus,
instead looking on infektion problems in general.

Where are the programs to prevent infected people will not become hostpital patients?

Why not use unspecific inflammation marker CRP test to prevent infections in hospitals
and nursing homes? Every worker could be tested on CRP strikings before his shift, just
one drop blood, <5€ test and 5 minutes. There are many infection beside of Corona aviodable,
when health (also of the workes from doctor to the cleaning stuff) and not the duty rosta
and financial proffit would roule (have higest priority).
Influnenca, Streptokken, Pneumokokken, MSRA... all other infectes spread by doctors are
dangerious for their patients. In case of a CRP strike, more diagnostic should follow
before first contact with patients.
Over 200 doctors and medical workes had died in Italy in spring, not because the virus
is so agressive, major reason has been the working condition, to countious to work even
with illness.

Such test could help to stop the need to work full time with mask.

Why not having just a study about this, that the medical and care busines could do more
than washing hands and wearing masks.

A Chinese guidline how to deal with corona cases from March 2020 recomended to do
CRP tests in early stages it was translated and recomended by an German association of
eye clinics: http://www.vsdar.de/corona/
From March to May did I request action by authorities in NRW and Germany nd try to make
this public with small demoes in front of the German health ministery in Bonn, and in
the center of Bonn – see: http://www.corona-demo.de

IMHO a CRP could help to distinguish between persons with inhalated Corona-Gen and being
infected, too. But officials in Germany (RKI) count death with several negativ PCR-test
to the Corona-Death-counter: https://heise.de/-4973792.

I'm just an civil engineer, but I learnd as helper in 1994 in Goma and Bukavu (Kongo)
during the colera epedime from experienced developing professionls that it is important
to have an open exchance about challanges, ressources, ideas, and experiances.

So thank you again for your review, what do you think about CRP tests?
Robert Michel, Germany

Reply

23. **Ruud van Wees** says:
November 30, 2020 at 10:34 am

Thanks so much, all of you, the real scientists annex freedom fighters.
So many branches of science these days seem corrupted and sent into deadend streets by scientists bowing for the mammon or other kinds of pressure.

I dearly hope this is the beginning of the end of this politicized corona nightmare. If not, then we know for sure there is another dark agenda behind it.

Reply

1. **Eric Vieira** says:
   December 6, 2020 at 10:42 am

   The dark agenda seems to be coordinated by the U.N. and WHO. Great Reset? Agenda 21? Agenda 2030? The virus outbreak in Wuhan was even negated by WHO for a while, allowing the virus to spread worldwide. That the more SAR-Cov2 virus-specific primers as negative/positive controls were not recommended tells a tale by itself.

   Reply

24. **jb** says:
November 30, 2020 at 11:06 am

Remember, this pandemic has started with hiding the truth that dr Li Wenliang told. Please keep in mind his last words in his poem: "...Goodbye, my dear ones.
Farewell, Wuhan, my hometown.
Hopefully, after the disaster,
You'll remember someone once
Tried to let you know the truth as soon as possible.
Hopefully, after the disaster,
You'll learn what it means to be righteous...."

Reply

1. **human** says:
   November 30, 2020 at 10:07 pm

   What is your evidence that Li Wenliang story is factual?

Since when does the Communist Party of China apologize to a citizen? They made an exception for Li Wenliang.

“Hopefully, after the disaster”

Is this the “plague” that the good doctor is talking about?

“Tried to let you know the truth as soon as possible.”

Dr. Li sounds like a fictional character out of PLA psyops units. His story was to sell the fiction of people dropping dead in Wuhan. (Remember those?) His warning about the “disaster” was fuel for the propaganda fire of the plague that is not a plague.

“You’ll learn what it means to be righteous....””

That sounds ominous. Is that an oblique reference to coming re-education camps for plague deniers?

Reply

1. **Vlrdngr** says:
   December 1, 2020 at 12:11 pm

   What if... He is talking about something else entirely, and the whole covid story was just a smokescreen or a cover up?

   Reply

25. **Rehabilitation** says:
November 30, 2020 at 11:16 am

I was suggested this blog by my cousin. I am not sure whether this post is written by him as nobody else know such detailed about my problem. You are amazing! Thanks!

Reply

26. **frank** says:
November 30, 2020 at 11:20 am

Why you removed the reply's from willem engel, who is talking about a fungus.

Reply

Bobby says:
November 30, 2020 at 12:34 pm

There was a Bug in the comment-system and some comments vanished (2 or 3), this problem has been fixed.

Reply

27. **Mario Wolf** says:
November 30, 2020 at 11:47 am

Excellent. Hopefully this clarification will have the necessary impact

Reply

28. **Guy Verstraeten** says:
November 30, 2020 at 11:58 am

Eindelijk , en nu hopen dat de onzin ophoudt. Please keep giving updates about the retraction itself ! Thank you so much.

Reply

1. **Eric Vieira** says:
December 6, 2020 at 10:48 am

I fully support this. It would be essential to also follow the careers of the authors of this retraction request paper, to see if they become victims of repressive measures...

Reply

Bobby says:
December 6, 2020 at 11:28 am

I see, that was my fault. Deleted prior argument of mine. I oversaw the ” ” “. Sorry for that.

Reply

29. **Helga Smilga** says:
November 30, 2020 at 12:15 pm

Thanks to the Bravehearts within the world of science (honest and courageous) the hinges of this utter madness will slowly but surely begin to creak.

Reply

30. **Andre N.** says:
November 30, 2020 at 12:20 pm

Thank you for Work, this is a hope, for all People in the World.
For democracy, the rule of law and freedom.
Especially for the scientists who have made it their mission to work scientifically.
The truth always wins!

Reply

31. **Jos K.** says:

November 30, 2020 at 12:36 pm

Excellent work!

Reply

32. **Dorothee O'Sullivan Burchard** says:
November 30, 2020 at 12:57 pm

Thank you for this excellent work! It will help to rectify the erroneous claims and measures put in place that curtail the human rights of millions of people! Concerns remain as to whether politicians of governments across the globe take this on board. If not, people need to rise up and continue the peaceful fight for their liberties.

Reply

33. **Michiel de Jong** says:
November 30, 2020 at 1:55 pm

Thank you for what you have done for society! We are in debt to you all.

Reply

34. **Gerlinde Hörr** says:
November 30, 2020 at 2:08 pm

Herzlichen Dank für Ihre Mühen! Ein Lichtblick und Hoffnungsschimmer nach acht düsteren Monaten voller Irrsinn! Danke, danke – vielmals!

Reply

35. **Jack AVALONE** says:
November 30, 2020 at 4:17 pm

You all need to spread the #TRUTH on twitter.

#President #TRUMP will surely see it.

Reply

36. **Tanya Sutterfield** says:
November 30, 2020 at 4:33 pm

I am deeply grateful for the service, we are indebted to all involved. I pray this is received and used to change the devastating course we are currently on and cease the criminal actions being perpetrated on humanity.

Reply

37. **Already Provided** says:
November 30, 2020 at 4:45 pm

Great work. A small point:
I'm not quite sure about the first part of your definition of a false positive.

"The definition of false positives is a negative sample, which initially scores positive, but which is negative after retesting with the same test".

–followed by:

"False positives are erroneous positive test-results, i.e. negative samples that test positive."

I would say the second sentence is correct, but not the first sentence. "initially positive but then testing negative negative after retesting" is in my view a case of imprecision (random error) of the test near the limit of detection, not a false positive.

Check out Hedderich, M Sachs L, "Angewandte Statistik" 17th edition, section 4.5 p 186 "Der diagnostische Test", Table 4.6. According to that source, a false

positive occurs when:

A sample from a patient *who does not have the disease* gives a positive result in the test.[conditional probability would be P(T+|K-)]

Of course the critical point is defining what the “disease” is. If it is defined as a infectious state attributable to Sars-Cov-2 then you could argue that *all* results from this test are false positive.

Reply

Bobby says:
November 30, 2020 at 5:18 pm

Not cencored, I have answered you and it is visible. but I’m approving it again. We have talked about your semantics concern and we will implement it with your resource links / references in the revised version. The outcome is nevertheless the same.

Reply

1. 

E.M. Oneal says:
December 1, 2020 at 9:33 am

My profound apologies! I had in fact submitted the comment to the other thread on the “Retraction request letter”, not this one, and you had already accepted it there. Thank you for your prompt response.

Reply

Bobby says:
December 1, 2020 at 9:46 am

No problem at all, it’s not the best comments widget around, so it can get confusing, but it serves the cause.

Reply

Bobby says:
November 30, 2020 at 5:22 pm

We are aware of this semantic problem and it will be implemented in the upcoming revisions. The outcome is nevertheless the same.

Reply

1. 

   E.M. ONeal says:
   December 1, 2020 at 9:52 am

   Some remarks by Prof. Ulrike Kämmerer in an interview by the "Corona Ausschuss" meade it clear to me that there is another source of false positives that are not covered by the statistical definition.

   There are extraneous factors that introduce contamination during the lab test procedure "on the bench" (or before!). Possibilities are the operator sneezing or positive control mnaterial finding its way into the test, or cross- contamination from other samples.

   That could account for the same sample testing positive on a re-test and would also be a false positive. Although one would expect that such errors are excluded in an accredited lab.

   There are myriad other potential sources of extraneous false positives, starting with test kit production (contaminated swabs?), through the sample collection from the subject, lab procedures, data analysis and reporting.

   Reply

Bobby says:

December 1, 2020 at 9:57 am

Dr. Michael Yeadon is very dedicated to this topic complex of “industrial complex / mass testing by non-experts”. Thank you for your remarks.

Reply

38. **Tatjana Z.** says:
November 30, 2020 at 4:51 pm

Hallo,

danke für eure Arbeit. Ich freue mich immer, wenn Menschen sich auch kritisch mit dem aktuellen Corona-Thema befassen!

Allerdings ist mir eines nicht klar (bitte entschuldigt, wenn ich hier komplett falsch liege, weil ich fachfremd bin, aber ich musste es zumindest mal adressieren):

Der Hauptkritikpunkt ist doch nicht neu und wurde schon von Dr. Drosten in seinem Podcast vom 18.3. aufgegriffen(09:26 min):
https://www.ndr.de/nachrichten/info/16-Coronavirus-Update-Wir-brauchen-Abkuerzungen-bei-der-Impfstoffzulassung,podcastcoronavirus140.html

Natürlich schadet es nicht auf Kritikpunkte mehrfach hinzuweisen, aber bis jetzt hat dieser Hauptkritikpunkt zumindest nicht dazu geführt, dass die Veröffentlichung zurück gezogen wurde.

Schöne Grüße
Tatjana

Reply

Bobby says:

November 30, 2020 at 5:21 pm

Der Hauptkritikpunkt in unserem Review Report sind die nicht zulässigen und “anti-good-laboratory practise” RT-qPCR-Protokoll / Primer Design Unzulänglichkeiten, auf diese geht Drosten in seinem Podcast natürlich nicht ein. Überhaupt ist Selbstreferenzierung oft ein schlechtes wissenschaftliches Gegen-Argument.

Reply

39.  **Dave Spars** says:
November 30, 2020 at 5:03 pm

Thank you, giving me hope.

Reply

40.  **Stephen** says:
November 30, 2020 at 5:12 pm

I am horrified to read this appalling misunderstanding of molecular biology and how PCRs work. This is as bad as HIV denialism. If you don’t understand how primer concentrations work and how realtime PCR works and how much of the genome was amplified, please stay at home and let the rest of us get on with dealing with COVID.

Reply

1.  **Martin** says:
November 30, 2020 at 7:15 pm

Could you please clarify in detail what has been done wrong by the authors of the review?
Which points in the process of rtPCR did they not understand fully?

Thanks for your answer!

Reply

2. **Peter Looman** says:
November 30, 2020 at 10:44 pm

Dit is toch geen serieuze reactie. Ik weet zeker dat de schrijvers open staan als er inhoudelijk fouten aangetoond worden door andere deskundigen. De reactie van Stephen heeft op deze manier de waarde van een gemiddeld Twitterbericht (en die is in mijn mening zeer laag).

Reply

3. **Chrisje** says:
December 1, 2020 at 10:51 am

Even trolls are targeting scientists. What's new?

Reply

4. **roland brautigam** says:
December 1, 2020 at 12:05 pm

It's clowns like you. You have the arrogance to claim that Peter Borger and Kevin McKernan and Mike Yeates don't know how primer concentrations work without coming with a counter argument?

Reply

5. **John Weir** says:
December 2, 2020 at 9:11 am

Please do not try to initiate a slanging match.

No-one will bite.

Reply

6.  **Hanno** says:
December 2, 2020 at 10:01 pm

I Love your reply Stephen 🙂 Quackery never died, snakeoil was never short, times don't change, it all comes back in cycles...

Reply

7.  **ura soul** says:
December 3, 2020 at 3:16 pm

I am horrified to read this appalling interjection into a hotly contested topic which accuses people of being dangerously reckless with peoples lives without even inserting any verifiable claims or evidence.

Reply

8.  **Thomas Ellenberg** says:
December 3, 2020 at 7:12 pm

I'm more horrified by ad hominem spammers who can't formulate a valid counter argument.

Reply

41.  **Jabra** says:
November 30, 2020 at 5:12 pm

Thanks for your hard work! Hopefully it will be retracted.

Reply

42. **Dr. Jörg Haberstock** says:
November 30, 2020 at 6:50 pm

Tolle Arbeit, Danke! Wie ist es zu erklären, dass die ganze Welt nirgendwo aktualisierte PCR-Standards mit SOP zu Covid entwickelt hat, wieso greifen die Ringversuche zum Qualitätsmanagement nicht ? Wie kann das alles weltweit und über mehr als 9 Monate unbemerkt geblieben sein? Das macht mich ratlos. Danke für Euren Mut

Reply

1. **Arnold Achen** says:
December 1, 2020 at 10:25 am

Was Sie verlangen wird von den Behörden nicht gefördert, weil sie mit den Konzerninteressen verflochten sind, die eine Fortführung der inszenierten Pandemie forcieren:

https://www.corona-schadensersatzklage.de/corona-status-quo-erste-pcr-klage-ist-anhaengig-gemacht-worden/

Und warum sollen die Labors an mehr QC interessiert sein wenn sie aktuell durch die reine Massentestung ein Vermögen verdienen?

Reply

43. **Caro oh oh** says:
November 30, 2020 at 6:51 pm

So, yes, this qPCR is not the best designed one, but due to the circumstances (designed in January as a broad Sars-corovnavirus detection test), this can be understood. Yet, this does not mean that the test does not work. It has been validated a lot by a lot of labs and instances. Every lab has to do a

validation/verification of the used tests. Furthermore internal and external controls are taken into account. You can find more details in the paper (and other papers) and also in the news article: https://www.rd.nl/meer-rd/gezondheid/pcr-test-overleeft-stortvloed-aan-kritiek-1.1718351. Next to this, a whole plethora of real-time PCR tests are available on the market.

And yes, having viral RNA in your nose is not the same as being infectious. However, it shows that you have been in contact with the virus. Together with symptoms, this diagnostic test can confirm a diagnosis. Concerning asymptomatic cases, it might be of interest to consider the viral load. It is a valuable point that persons with a low detected viral RNA concentration might not be infectious (yet), or not very well swabbed if no human control gene is taken along.

I will summarize the other issues I have with this report, as discussing all of them would lead us too far.

1. High primer concentrations: Primer concentrations between100-900 nM are standard (depending on the assay and also the supermix). As the primers contain wobble bases, rather high concentrations make sense. Furthermore, dNTP concentrations are not off from standard conditions.
2. In general wobble bases rather have a negative effect on PCR efficiency (as the correct primer might be exhausted). Here, this seems not the case. On the other hand, it seems that the RdRp assay has a lower sensitivity ((Vogels et al. https://www.nature.com/articles/s41564-020-0761-6), possibly due to a mismatch with some Sars-Cov-2 genomes.
3. Good real-time PCR designs are set-up to detect short fragments (preferably under 150 bp) to obtain a good reaction efficiency. Furthermore, lots of viruses have been sequenced by now (take a look in the NCBI,GISAID,Nextstrain databases for example). The RdRp assay will be transcribed less then the ORF1a transcript, as a frameshift is necessary to transcribe RdRp. Hence, this could theoretically lead to a lower sensitivity of the RdRp assay.
4. The RdRp-assay indeed has not the best design. However, this is a

confirmatory assay and it has rather a lower sensitivity (see Voghels et al.). Yes, the E-gene assay might also detect Sars-CoV-1, but this virus is not really going around (and is also causing severe disease).
Off note, concerning melting temperatures, the theoretical Tm calculations should take into account the reaction conditions. Furthermore it is not required to mention Tms, nor GC contents in publications (as you can just copy the primer sequence into an oligo analyzer tool). It is way more useful to validate the annealing temperature in practice (with a gradient PCR for example).
Concerning the primer dimers: as a probe will only detect specific amplicons and not primer dimers, these probably have rather a negative effect on detection.
5. A Cycle Quantification (Cq) threshold is not a unit and is workflow specific. Every lab will have to do its own validation. A Cq value will be dependent on the swab, transport, RNA-extraction, reverse transcription, PCR assay (design, supermix, sample, instrument, plastics) and analysis. You can maybe correlate viral load and time since symptom onset with infectiousness, but not nationwide Cq values (as this will at least be lab dependent, this is not even taking intralab variation into account).
6. I cannot judge about the validation protocol, as probably not every step is described. Melting curves during optimization or sequencing of amplicons is indeed good practice. But again, this assay is a confirmatory assay and has been wet-lab validated. (Gels are IMO for scientists stuck in the nineties and are risks for amplicon contamination.)
7. The test has been validated on negative, positive and other viral controls (read the paper!).
8. The paper and protocol on the WHO website contain a quite well described protocol. Furthermore, each laboratory has to do a proper validation. Btw, it would be unsuitable (in terms of supply chain for example) that every lab is using exactly the same protocol. Reference standards would be useful (but I guess they will come).
9. Funny, as this report is also not peer reviewed, nor has a DOI, and hence, cannot be pubpeer reviewed.

Regardless of this paper, a diagnostic procedure in a lab does not require publication and peer review. It requires wet lab validation.

In conclusion, the design of the RdRp assay is for sure not the best (but there is a good explanation for this). This remains a confirmatory assay after screening with the E-gene assay (or in a multiplex nowadays). The Charite protocol has been extensively validated and remains a valid diagnostic tool.

Reply

Bobby says:
November 30, 2020 at 8:03 pm

Copypaste answers by Prof. Dr. Ulrike Kämmerer:

Quote: So, yes, this qPCR is not the best designed one, but due to the circumstances (designed in January as a broad Sars-corovnavirus detection test), this can be understood. Yet, this does not mean that the test does not work. It has been validated a lot by a lot of labs and instances.

Answer: No, not at the time of publication and supporting the WHO with the Workflow – especially with the knowledge that the Chinese had the PCR and the virus and all informations so far (see literature reference 6 in the report)

Quote: Every lab has to do a validation/verification of the used tests. Furthermore internal and external controls are taken into account.

Answer: No, the real positive control (RNA isolated from the new virus) was not used.

Quote: You can find more details in the paper (and other papers) and also in the news article: https://www.rd.nl/meer-rd/gezondheid/pcr-test-overleeft-stortvloed-aan-kritiek-1.1718351.
Next to this, a whole plethora of real-time PCR tests are available on the

market.

Answer: That's not the subject of the criticism of the specific publication.

Quote: And yes, having viral RNA in your nose is not the same as being infectious. However, it shows that you have been in contact with the virus. Together with symptoms (!!! Yes, but nobody tests symptomatic persons only), this diagnostic test can confirm a diagnosis. Concerning asymptomatic cases, it might be of interest to consider the viral load. It is a valuable point that persons with a low detected viral RNA concentration might not be infectious (yet), or not very well swabbed if no human control gene is taken along.

Answer: Yes, but nobody tests symptomatic persons only!

Quote: 1. High primer concentrations: Primer concentrations between100-900 nM are standard (depending on the assay and also the supermix). As the primers contain wobble bases, rather high concentrations make sense.

Answer: Maybe – but not in the case of the E- and N-Gene PCR without wobble bases.

Quote: 2. In general wobble bases rather have a negative effect on PCR efficiency (as the correct primer might be exhausted). Here, this seems not the case. On the other hand, it seems that the RdRp assay has a lower sensitivity ((Vogels et al. https://www.nature.com/articles/s41564-020-0761-6), possibly due to a mismatch with some Sars-Cov-2 genomes.

Answer: Yes, but why the mismatches – the genomes were available at the time of submitting the manuscript and the Vogels paper is from Jul 10 2020.

Quote: 3. Good real-time PCR designs are set-up to detect short fragments (preferably under 150 bp) to obtain a good reaction efficiency.

Answer: Correct.

Quote: Furthermore, lots of viruses have been sequenced by now (take a look in the NCBI,GISAID,Nextstrain databases for example). The RdRp assay will be transcribed less then the ORF1a transcript, as a frameshift is necessary to transcribe RdRp. Hence, this could theoretically lead to a lower sensitivity of the RdRp assay.

Answer: not of interest – its about the publication from January.

Quote: 4. The RdRp-assay indeed has not the best design. However, this is a confirmatory assay and it has rather a lower sensitivity (see Voghels et al.). Yes, the E-gene assay might also detect Sars-CoV-1, but this virus is not really going around (and is also causing severe disease.

Answer: Yes – but for an "novel" virus the detection system must be highly specific.

Quote: Off note, concerning melting temperatures, the theoretical Tm calculations should take into account the reaction conditions. Furthermore it is not required to mention Tms, nor GC contents in publications (as you can just copy the primer sequence into an oligo analyzer tool). It is way more useful to validate the annealing temperature in practice (with a gradient PCR for example).

Answer: 10 degree difference is a no-go and yes, everybody optimizes the PCR primers for GC and melting temperature before ordering them… so a rubbish argument.

Quote: Concerning the primer dimers: as a probe will only detect specific amplicons and not primer dimers, these probably have rather a negative effect on detection.

Answer: This is correct.

Quote: 5. A Cycle Quantification (Cq) threshold is not a unit and is workflow specific. Every lab will have to do it's own validation. A Cq value will be dependent on the swab, transport, RNA-extraction, reverse transcription, PCR assay (design, supermix, sample, instrument, plastics) and analysis. You can maybe correlate viral load and time since symptom onset with infectiousness, but not nationwide Cq values (as this will at least be lab dependent, this is not even taking intralab variation into account).

Answer: Well – they have "validated" their PCR so they should have shown their PCR data and CT values – and indeed every lab had to adapt the Test inhouse – but this point is missing in the publication – so not ok.

Quote: 6. I cannot judge about the validation protocol, as probably not every step is described. Melting curves during optimization or sequencing of amplicons is indeed good practice. But again, this assay is a confirmatory assay and has been wet-lab validated. (Gels are IMO for scientists stuck in the nineties and are risks for amplicon contamination.)

Answer: no – not wet-lab validated: no clear results for negative and positive controls are shown (including CT).

Reply

1. **roland brautigam** says:
   December 1, 2020 at 12:15 pm

   How about responses to quotes 7 to 9?

   Reply

1. **Randomer** says:

November 30, 2020 at 10:23 pm

Thank you for confirming the paper by stating three times that the design might not be the best one. Cheers.

Reply

2.  **theasdgamer** says:
December 1, 2020 at 2:44 am

"Together with symptoms, this diagnostic test can confirm a diagnosis."

Confirm a diagnosis for what purpose? Adding delays for testing decreases prognosis. Patients are often dilatory about testing and most patients max their viral load on day 3 post symptom onset and maybe contact their primary care physician on day 2 post symptom onset best case. If the doctor won't treat with an antiviral, who cares about any PCR test? A doctor will treat the symptoms of a URTI. If you do treat with an antiviral, you can't wait for the return of test results to begin treating. If the antiviral works, what purpose does the PCR test serve?

And I'm not a physician.

Reply

1.  **Lothar Lammfromm** says:
December 3, 2020 at 10:59 am

Yes, you are not a physician and you don't know anything about Covid-19-Science.

This sentence is pure rubbish:

"most patients max their viral load on day 3 post symptom onset"

No, usually (but this can vary) it is the day before (!) system onset.

Reply

1. **Lothar Lammfromm** says:
   December 3, 2020 at 2:06 pm

   symptom onset

   Reply

2. **ShowMeTheFacts** says:
   December 6, 2020 at 1:12 pm

   "...what purpose does the PCR test serve?"

   1) To maximize the Casedemic
   2) To use as junk science to justify totalitarian policy (businesses restrictions, community activities, sports, etc.)
   3) To use as junk science to quarantine non-infectious teachers, students, staff, etc.
   4)...
   5)...
   6)...

   Reply

44. **Dipl. Ing. (FH), M. Eng. Andreas Macher** says:
    November 30, 2020 at 7:24 pm

    Um dem nächsten Wahnsinn einer Pseudo-Epedemie vorzubeugen müssen unbedingt rechtzeitig vor den unsicheren Test wirklich sichere Tests für die wahrscheinlich virulenten Virusarten entwickelt werden. Damit nimmt man der Impfindustrie den Spielraum, den sie mit den falsch positiven Tests in dieser Epedemie hatten, für die Zukunft. Als nächstes Target zeichnet sich MERS ab.

Wenn dieses kompetente Team dafür sorgen würde, dass die relevanten Varianten von MERS wirklich sicher detektiert werden können, wird es nicht noch so eine Panikreaktion in der Bevölkerung geben, wie wir es mit SARS-CoV-2 erleben mussten.

Reply

1.  **Linda Weingärtner** says:
   November 30, 2020 at 9:03 pm

   Die Panikreaktion der Bevölkerung kam durch die Angstmache der Politik und der Medien zustande.
   Die kritischen Stimmen der Experten werden ja bis dato immer noch nicht gehört.

   Reply

2.  **Julian** says:
   December 4, 2020 at 3:40 pm

   Well, you don't have to worry about MERS.

   Because dr. Drosten himself said in a 2014 interview that PCR isn't suitable for detecting MERS.
   He admits the PCR technique is too sensitive, which leads to an explosion in case numbers and that the media tends to blow up these case numbers out of proportion.

   https://www.wiwo.de/technologie/forschung/virologe-drosten-im-gespraech-2014-die-who-kann-nur-empfehlungen-aussprechen/9903228-2.html

   Reply

45.  **Eva** says:
November 30, 2020 at 7:27 pm

Thank you so much for standing up and speaking out. Scientists like you could restore my faith in science.

Reply

46.  **Ordinary Doc** says:
November 30, 2020 at 8:20 pm

I do not understand the technicalities of pcr testing. I am however an experienced clinician and I understand what I see in my everyday practice. What you are saying seems absolutely correct. False positives++. Well done and good luck.

Reply

47.  **Danae** says:
December 1, 2020 at 10:12 am

God bless you all for this incredible work. It is time to cleanse our system from monetarism which is subverting science, medical reserach, press and politics. We cannot have independent, impartial science if it is “financed/bribed” by groups of have clear conflicts of interest. This paper is an important step to stopp the attack on civil liberties and stands between many people being injured by vaccination or even death or infertility. No vaccination is without risks, there are no studies ever being done on how different vaccinations interact with each other. Where there is risk there must be choice.
God bless you and protect you and my he help us all to stay for truth, love and peace.

Reply

1. **Eric Vieira** says:
December 6, 2020 at 11:14 am

What worries me is that no studies have been done wrt ADE (antibody induced enhancement). This effect has been observed with related SARS and MERS viruses in animal models. There are other corona viruses out there which were up to now not so lethal, but the situation could get to be much worse if ADE in vaccinated people occurs.

Reply

48. **Michael Wiedom** says:
December 1, 2020 at 11:12 am

Herzlichen Dank für diese hervorragende Arbeit. Bin gespannt, wie es jetzt weitergehen wird.

Reply

49. **Petra von Kopp** says:
December 1, 2020 at 11:40 am

Danke... Danke...

Reply

50. **OrAnd** says:
December 1, 2020 at 11:56 am

Thanks for your work, I do have a comprehension question regarding 3.: How can there be false positives at all by this PCR-test? In the text (3) and reference [2][3] I can see only points stating why there can be false negatives (not false positives). Am I missing something here?

Reply

1. **Kevin McKernan** says:
   December 2, 2020 at 6:12 pm

   We present evidence of promiscuous primers. These can create both False Negatives and False Positives. There are additional sources of FPs as the assay fails to discern infectious from non-infectious people and when used on asymptomatic people, the term ‘case’ must be infectious. This is exacerbated by the selection of a reduced number of assays and assays positioned on the 3′ region of the genome. Wolfel et al describes qPCR amplicons that do a better job discerning infectious from non-infectious people. Drosten is an author on this paper. This would have been a good time to withdraw the assays failing to discern the difference between infectious cases and non-infections false cases.

   Reply

51. **Ruud Brouwer** says:
    December 1, 2020 at 12:09 pm

    Will this report be peer reviewed? I really doubt it will make it through

    Reply

52. **RHB** says:
    December 1, 2020 at 12:29 pm

    Well done to all involved. Meticulous scrutiny with massive implications. Not my area of detailed expertise but, if I’m reading broadly right, could even bring down the leadership of the country I’m posting from.

    Substantiates gut feeling going right back to March, as per blog comments by “Ancient Briton,” “RHB” and “Aweson Walles” on Derek Lowe’s In the Pipeline

blog (dominated March onwards by virus postings):

https://blogs.sciencemag.org/pipeline/archives/2020/03/12/real-information-a-public-good#comment-313468

16 March, 2020 at 9:09 am

https://blogs.sciencemag.org/pipeline/archives/2020/11/18/vaccine-possibilities

19 November, 2020 at 6:49 am

https://blogs.sciencemag.org/pipeline/archives/2020/11/23/oxford-az-vaccine-efficacy-data#comment-333601

29 November, 2020 at 10:21 am

Reply

53.  **roland brautigam** says:
December 1, 2020 at 1:13 pm

Bobby have you seen the response from Marion Koopmans and Adam Meijer:
https://www.rd.nl/vandaag/binnenland/pcr-test-overleeft-stortvloed-aan-kritiek-1.1718351

She claims molecular validation was done.
She claims peer review was done
She claims they started working on the protocol from 12 January when China released the genetic code
She claims the guidelines for the PCR test were changed by RIVM on 25 September but that these should not change the outcome. I have a few statistics which prove the opposite.
Adam Meijer states that false positives could be 0,5-4%. 4% is catastrophic already.

Article is under “conspiracy theory” header…

Reply

Bobby says:
December 1, 2020 at 2:22 pm

Dr. Peter Borger will give an answer on this soon. I’ll notify you.

Reply

54. 

Joerg says:
December 1, 2020 at 3:21 pm

Hallo,
Danke fuer die Recherche, das Corman-Drosten et al.Paper war halt ein Schnellschuss.

Mich wuerde interessieren, ab wann (im Zeitverlauf, zB ab September2020?) es bessere Tests (weniger Kreuzreaktionen, weniger Falsch-Positive, 3Gen-Prinzip, spezifischer, Beachtung von Ct-Werten) in den Test-Laboratorien gibt? Gibt’s ein Labormediziner, der hier mit liest?

Ich kann mir nicht vorstellen, dass eine Vielzahl von Laboren immer noch die gewobelten RdRp-Primer verwendet? Oder?

LG Joerg

Reply

1. 

M. Hoffmann says:
December 1, 2020 at 4:08 pm

Bessere Tests für was? Für ein Virus das unter Umständen gar nicht existiert–laut Angaben des CDC gibt es kein messbares Isolat von sars-cov-2

weltweit– oder sich funkionell nicht von üblichen Coronaviren unterscheidet und auf jeden Fall denen gegenüber keine höhere Mortalität aufweist?

Was soll das klinische Korrelat zum “Test” sein? Welche therapeutischen Massnahmen sollen auf Grund von welchem Testergebnis eingeleitet werden und ergeben dies überhaupt einen Sinn, außer Unterdrückung?

Haben Sie in der Vergangenheit je einen Test für Grippe oder schwere Erkältung durchgemacht und was hat das gebracht?

Laut der Dokumentation zu Event 201 handelt es sich ohnehin um eine globale Simulation zur Bereicherung von “öffentlich-privaten Partnerschaften”.

Es ist die Jagd nach einem Phantom, das benutzt wird, schwere psychologische und wirtschaftliche Schäden anzurichten.

Reply

1. **Joerg** says:
   December 2, 2020 at 3:20 pm

   Vielen Dank, M. Hoffmann, dann wissen Sie also nicht, ob aktuelle RT-PCR-Tests noch auf dem hier kritisierten Paper beruhen bzw welche Verbesserungen hinsichtlich Spezifitaet, Genauigkeit inzwischen unternommen wurden, bzw Eingang in aktuelle RT-PCR-Kits gefunden haben?!
   Sonst jemand?

   Sie antworten dagegen auf Fragen, die ich nicht gestellt habe. Gerne aber meine Meinung dazu:
   a) “Virus das unter Umstaenden nicht existiert” “und auf jeden Fall denen gegenüber keine höhere Mortalität aufweist”
   Belege dazu? Sind erhoehte Mortalitaeten in anderen Laendern als in

D also alle gefaket? Wie erklaeren Sie erhoehte Mortalitaeten (zB auf http://www.euromomo.eu/graphs-and-maps) bei unseren Nachbarn?
b) “klinische Korrelat zum “Test” sein?”
Wie waere es mit dem Versuch, die Verbreitung etwas einzudaemmen, um Gesundheitssysteme/Intensivbetten nicht zu ueberlasten? Also keine klinische Konsequenz sondern eine epidemiologische?!
c) “Haben Sie in der Vergangenheit je einen Test für Grippe oder schwere Erkältung durchgemacht”
Nein, warum auch? Gibt’s denn solche? Bin nicht in der Risikogruppe 😉
d) “Laut der Dokumentation zu Event 201”
Sie meinen, http://www.weforum.org/great-reset/? Da haette ich viel zu tun, alle dubiosen Traeume, Stilblueten und Ideen im Internet zu verfolgen 😉
e) “Es ist die Jagd nach einem Phantom, das benutzt wird, schwere psychologische und wirtschaftliche Schäden anzurichten.”
Wissen Sie, dass manche Kommentare mehr ueber den Kommentator aussagen als ihnen Sinn und Zweck innewohnt?
Meinen Sie wirklich, alles geschieht aus boesartiger Taktik?
Meist reichen Angst, Unwissenheit, Inkompetenz, Unfaehigkeit aus, um fast alles “gut gemeinte” zu erklaeren … meine Erfahrung jedenfalls.
Sie kaempfen gegen Windmuehlen?!
LG Joerg

Reply

2. **Kane** says:
December 3, 2020 at 11:05 am

Ähmm.. Quelle [3] dieses Reports spricht eindeutig von Isolaten “1941 SARS-CoV-2 isolates could be obtained”
Also du stimmst diesem Report hier zu, aber dessen Quellen lehnst du

ab? Versteh ich das so richtig?

Reply

1. **Joerg** says:
   December 3, 2020 at 4:05 pm

   @Kane,
   ich weiss nicht, was du meinst? Wolltest du unter einem anderen Kommentar kommentieren?

   Quelle [3] finde ich interessant und verstehe sie genauso wie du? (also es wurden sehr wohl viele Covid19-Isolate untersucht sowohl per RT-PCR als auch in Subkultur).
   Bei RT-PCR gibt's halt eine gewisse Gefahr von Falschpositiven, auch gibt es einen laborspezifischen Effekt (Labore mit mehr / weniger Expertise?) aber es ist trotzdem die beste aller Nachweismethoden fuer epidemiologische Studien (Schnelligkeit, Durchsatz) und so zu tun, als wuerde da "Irgendwas" rumamplifiziert ist m.E. weiter weg von der Realitaet als 0,5-2%? Fehler.
   Alle machen Fehler, nix ist vollkommen in dieser Welt.
   Trotzdem ist es ein sinnvolles und berechtigtes Ansinnen fuer mehr Sensitivitaet und Spezifitaet beim Corona-Testen einzustehen! Ein erster Schritt waere viell. bei jedem Test auch den Ct-Wert mit zu liefern? und Getestete mit Ct >30 und ohne Symptome sollten berechtigterweise maulig werden!
   LG Joerg

   Reply

   1. **Joerg** says:
      December 3, 2020 at 4:10 pm

Ah, hab jetzt die Kommentarstruktur gecheckt, du antwortest auf M. Hoffmann.
Sorry, Joerg

2. **Kane** says:
December 4, 2020 at 5:28 am

Genau 😉
Ging mir nur um dieses “laut Angaben des CDC gibt es kein messbares Isolat von sars-cov-2 weltweit” von M. Hoffmann, was eine Aussage des CDC von Juli fehlinterpretiert.

2. **roland brautigam** says:
December 2, 2020 at 4:12 pm

Schnellschuss?? Glaube das dass nichgt ganz war ist:
https://pubmed.ncbi.nlm.nih.gov/23231891/

Aus 2012!

Reply

55. **Francine** says:
December 1, 2020 at 5:06 pm

Ik heb een vraag over paragraaf 3 op blz 6. Waarom is daar letterlijk de persoonlijke mening over de PCR test overgenomen van de twee rechters van het Hof van beroep in Lissabon inzake het onrechtmatig in quarantaine plaatsen van vier Duitse toeristen. De zaak waardoor Wybren van Haga meende te moeten melden in de Kamer dat de rechter in Portugal de PCR test naar de prullenbak heeft verwezen.
Deze ‘conclusie’ is te lezen onder punt 17 van het arrest. Zij hebben deze

aanname gemaakt na een foutief interpreteren van het onderzoek van Jafaar et al. Dit is dus geenszins de conclusie van de studie van Jafaar et al. Ook onder reviewed 3 maakt u een fout, het gaat hier niet primair om het aantal cycli (35) van de PCR waarboven besmetting < 3% is. Het gaat om het vermogen waarop besmette samples nog in staat zijn cellen in kweek te infecteren, dat was na 3 weken < 3% Dit om zicht te krijgen op duur van isolatie van covid-19 patiënten.
Morgen dient een zaak over de bemoeienis van beide rechters bij de Hoge Justitiële Raad van Portugal.
Volgens het SCM hebben de rechters hier hun bevoegdheden overschreden. Zij hadden geen opmerkingen moeten maken over de mate van betrouwbaarheid van de tests die momenteel worden gebruikt. Daarom zullen ze morgen op 2 december vragen moeten beantwoorden in een tuchtonderzoek door de Justitiële Raad, uitspraak door het Superior Council of Magistrature of de twee rechters juist gehandeld hebben.
Ik ben benieuwd of u hiervan op de hoogte bent en zal de uitspraak gevolgen voor de tekst op blz.6 paragraaf 3 hebben.

Reply

56. **Rich** says:
December 1, 2020 at 7:00 pm

These are theoretical weaknesses you may find in most scientific paper. As many of the reviewers are affiliated with biomedical institutions, why don't you just show experimentally the predicted consequences for false positives? When the assay is really that bad, this shouldn't be difficult!?

Reply

Bobby says:
December 1, 2020 at 7:58 pm

Sorry, this statement is completely irrelevant and refuted. Either you didn't read the review report or you forgot to pay attention.

Reply

1. **Rich** says:
   December 1, 2020 at 9:43 pm

   of course I did not spend too much time for this... but as it was already mentioned above a diagnostic test needs experimental validation, not whatever this is. Just show what you claim. It would be so easy to do this.

   Reply

   1. **Adam** says:
      December 2, 2020 at 7:20 pm

      “of course I did not spend too much time for this... “... so why did you leave a comment? Sometimes it is better to su. The authors did spend a lot of time to identirfy the weaknesses of this “study”. It seems we have here a Drosten Fan Boy? For you this is almost religious...

      Reply

      1. **Rich** says:
         December 3, 2020 at 8:36 am

         Yes, they spend a lot of time to selectively search for minor weaknesses and of course they did not do any wet lab experiments because as apparently they have experience with qPCR, they know that in the end none of this will have a great effect, that the PCR works and that there are no “consequences for false positives” or whatsoever.

2. **Kevin McKernan** says:
December 4, 2020 at 7:07 am

See my comment on the thread.
We don't need to perform any experiments as we have provided 4 manuscripts that have already documented this effect.

Reply

Bobby says:
December 1, 2020 at 7:55 pm

What a weak comment. That's like asking why are you "running a website and making sure that nothing illegal is posted"? Failed troll-attempt.

Reply

57. **Francine** says:
December 1, 2020 at 9:07 pm

Ik zie dat mijn commentaar is geweigerd, kunt u mij zeggen wat de reden is van het weigeren?

Reply

Bobby says:
December 1, 2020 at 9:16 pm

Sorry, oversaw your comment, have approved it now. We will come back to your point and notify you.

Reply

1. **Francine** says:
   December 1, 2020 at 9:37 pm

   Dankuwel

   Reply

58. **Francine** says:
    December 1, 2020 at 9:32 pm

    Sorry te snel gereageerd, ik wacht uw antwoord af

    Reply

59. **Carlyn Mildrum** says:
    December 2, 2020 at 2:29 am

    immaculate article

    Reply

60. **Bölecke** says:
    December 2, 2020 at 6:24 am

    Ich bin begeistert. Jetzt weiß ich warum die (unsere ?) Regierung nicht mit schlüssigen Erklärungen die Situation beschrieben hat.

    Reply

61. **Kim ten Napel** says:
    December 2, 2020 at 8:12 am

    Following this Corman/ Drosten retraction paper with interest and hope for a better world.

How this ONE PCR test can cause such panic and be used to control the people is remarkable,as this one PCR test has so much power why hasn't it been tested and retested by every country.
I applaud Peter Borger & Co for this admirable difficult investigation.

Reply

62. **John Weir** says:
December 2, 2020 at 9:04 am

Not a direct comment on the paper in question but the following is a statement by C. Whitty made in an interview with the BMJ.

"For the great majority of the infections I've dealt with—and I'm an infectious disease epidemiologist—you never get herd immunity. You don't get it for malaria, you don't get it for HIV, you don't get it for Ebola."

With particular reference to HIV , am I the only person to see this statement as utterly ridiculous ?

Expert comment if someone would be so kind.

Sorry this is somewhat off-topic.

Reply

63. **Dr. med. Karla Lehmann** says:
December 2, 2020 at 9:21 am

Herzlichen Dank für Ihre äußerst wertvolle und notwendige kritische Einschätzung dieses CormanDrosten-Papers. Ihre Arbeit hat mir die Zuversicht zurückgegeben, daß es noch Wissenschaftler gibt, die die Dinge hinterfragen und der Sache auf den Grund gehen.

Reply

64. **John Weir** says:
December 2, 2020 at 10:09 am

Possible correction required.

“To obtain reproducible and comparable results, it is essential to distinctively define the primer pairs. In the Corman-Drosten paper we observed six unspecified positions, indicated by the letters R, W, M and S (Table 2). ”

Should this be “Figure 2” instead of “Table 2” ?

Thanks

Reply

65. **Inhope** says:
December 2, 2020 at 10:38 am

Does any of you, the authors, SPEAK to humans you know?!
If you have any credibility around you, why haven’t you disseminated all this personally?
You know, word of mouth is very potent! The interlocutors would diffuse it further with something like this:
“I know this person. I trust them. I will act as they advise.” And so on.
I guess you are just tinkering with details.
Because if you knew that “viruses” are not real, you would have spoken long ago, and this report would have been unnecessary!
I am close to dying from old age. I have had time to acquire knowledge in more fields than anyone I heard of. Quantum Physics, Artificial Intelligence/Robotics, Electrodynamics, Philosophy of Science.
The last one mentioned provided the space where I, and others, could really take apart all the preposterous statements and outright lies of the “scientists”

all over.
They all go to the brainwashing centers called universities and get poisoned by older brainwashed “professors”. They have no chance of waking up later on because they never leave the fetid “educational” environment that raised them. One in a million does, but then they are afraid of losing their grants or professorships! So they continue in the complicity to murder and maim!
Have you heard of Thomas Kuhn?
Stefan Lanka?
One quit physics because of what I criticize, the other has been speaking for decades against his original domain: “virology”.
Get informed.
And get honest.

Reply

1. **roland brautigam** says:
   December 2, 2020 at 4:33 pm

   Understand your point well. However I believe that people like you (and me) who study or show a strong interest in QM especially on a level with neurology, quantum consciousness or nano-biology, our intellectual understanding is larger than 99,9999% of the general population. One in a million. It puts us in a position where sarcasm and anger in times like these are closer than enlightenment unfortunately. I have had doubts about the (people behind) the Drosten protocol from the beginning. There is just too much money involved. Hundreds of billions of dollars. Ab Oosterhaus for example was involved in the first studies in 2012. For me he is (one of) the Devil(s). I wish you lots of strength and especially happiness in your final years.

   Reply

66. **Peter Barnum** says:

December 2, 2020 at 11:44 am

I have two immediate questions:

1) The primer dimers you found are between one primer for the E gene assay and one for the RdRp assay. In real life testing, the two test are conducted in different wells, aren't they? So these two primers should never be in the same pot and therefore the potential dimers don't matter!?
2) Even if primer dimers form and are elongated by the polymerase, this would not lead to increased fluorescence, since a probe-based assay is used in contrast to intercalating dyes which would indeed just indicate any dsDNA being present.

Regards
Peter

Reply

Bobby says:
December 2, 2020 at 1:19 pm

We will be shortly in contact with you about your questions and remarks. Thank you very much.

Reply

1. 

   Peter Barnum says:
   December 2, 2020 at 8:45 pm

   I am looking forward to that!

   Reply

2. 

   Peter Barnum says:
   December 4, 2020 at 5:15 am

As long as you can answer other stuff and choose not to address my questions, I'm assuming that I am right and this is a blatant error in your report. So blatantly indeed that in combination with your ongoing unwillingness to discuss it, it makes me think that you knew this all along. This would mean that you knowingly pulished statements you knew were wrong, seriously questioning your scientific motivation!

Reply

Bobby says:
December 4, 2020 at 5:39 am

Kevin McKernan answered you. Your prior conclusions are irrelevant in this case.

Reply

1. 

   Peter Barnum says:
   December 4, 2020 at 5:47 am

   I have so far not been able to find that answer. Was that under a twitter post and would you be so kind to share it with me? I am no longer ablo to see his own post, since he blocked me.

   

   Bobby says:
   December 4, 2020 at 5:49 am

   https://cormandrostenreview.com/report/#comment-304

1. 

   Kevin McKernan says:
   December 4, 2020 at 4:29 am

Thank you for your comment.

We have evidence of labs reducing the number the amplicons in the test to cut costs from 3 amplicons to even a single amplicon used in Italy.

We are assuming a minority of people are multiplexing the test as well to cut costs but this is not material to our argument.

Even if you assume 100% singleplex utilization, there are multiple peer reviewed publications that demonstrate singleplex primer-dimers, false positives, and unreliable results. Are these dimers a result of inter-assay primer contamination with high concentration oligonucleotides? There are other (presumably unextendable) singleplex dimers with the RdRp probe as well.

The in-silico work is demonstrative of haste in design but should defer to wet performance seen in peer review journals which demonstrate unacceptable levels of promiscuous priming and false results that are not properly addressed in the Corman paper.

1)Muenchhoff et al writes

“A reduced sensitivity was noted for the original Charite’ RdRp gene confirmatory protocol, which may have impacted the confirmation of some COVID-10 cases in the early weeks of the pandemic. The protocol needs to be amended to improve the sensitivity of the RdRP reaction.”

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7315722/
Drosten is an author on this paper that declares the need to replace the primers that were reviewed in 24 hours.

You cant have it both ways. If they are promiscuous primers and known to be leading to false positives or false negatives in the literature, then the Author of such disinformation has an obligation to correct record when peer review was clearly compromised.

2)Etievant et al

“The E Charité and N2 US CDC assays were positive for all specimens, including negative samples and negative controls (water). These false-positive results were explored (details below), but the sensitivity of these assays was not further assessed.”

“No false-positive results were obtained on clinical samples that tested negative for SARS-CoV-2 and/or positive for other viruses than SARS-CoV-2, except for E Charité and N2 US CDC, which were positive for all specimens.

Sensitivity was first assessed using SARS-CoV-2 cell culture supernatants. Using both specific SARS-CoV-2 (S) and non-specific (NS; detecting SARS-CoV-2, SARS-CoV, and bat-SARS-related CoVs) RdRp Charité assays”

Notice the term “non-specific” Charite’ primers.

“Thus, the false-positive amplification obtained using E Charité might be derived from a contamination (amplicon size at 121 bp) but could also be associated with an aspecific amplification (amplicon size at 84 bp)”

https://www.mdpi.com/2077-0383/9/6/1871

This paper stops evaluating the Charite’ primer half way through the study due to performance issues.

3)Jung et al

“On the other hand, the RdRp_SARSr (Charité) set shows less effective amplification than the other two primer sets at all reaction temperatures including their recommended extension temperature (58 °C). Unexpected amplifications from NTC samples were observed with the RdRp_SARSr (Charité) set. The electrophoresis and melting curve analysis showed nonspecific amplification at lower positions (Lane 5, Figure S5b) and

temperatures (Figure S5a) than the result of specific amplification with the RdRP_SARSr (Charité) set."

Evidence of Non Template controls amplifying in multiple peer reviewed journals will directly result in quarantine of non-infectious people and create a chain reaction of legal liability.

4)Gand et al.
"Interestingly, for Assay_2_RdRp-P2, similar false-positive results as obtained in our in silico study were obtained in the wet lab by Chan and colleagues, who detected SARS-CoV when using the probe P2 targeting the RdRp gene that is considered strictly specific to SARS-CoV-2 [30]"

"The sensitivity of Assay_2_RdRp-P2 (Charité) was already demonstrated in the wet lab to be lower than that of other assays investigated in this study"

These four manuscripts all point to flaws in these primers.

Christian Drosten is an author on one of these manuscripts that concludes they must be replaced!

The error prone primers still exist on the WHO website with a link to Eurosurveillance.

The liability of these erroneous methods leads back to Eurosurveillance and once they have been informed of the issue, we are confident they will do the right thing and retract the paper. A failure to retract the paper absorbs the liability as opposed to placing that liability onto the source of the deception; the authors themselves.

Citations are contained in this thread.
https://t.co/2St1wmWLAH?amp=1

Reply

1. **Peter Barnum** says:
December 4, 2020 at 5:57 am

This is not an answer to my question, it's a repetition of his twitter thread, which is worthy of its own discussion. I asked why in your report there is a primer dimer reported between two unrelated primers. None of the above mentioned papers said anything about multiplexing, nor does the original Corman-Drosten paper. For all I know right now, this is purely your assumption! And you still should have mentioned that this primer dimer only becomes relevant in multiplex assays. At the very least your report shows the same lack of scientific rigour it criticises in the Drosten-Corman paper!

Reply

1. **Kevin McKernan** says:
December 4, 2020 at 6:15 am

There is an in-silica single-plex dimer on RdRp probe. This is reported in the peer reviewed literature as causing problems. Primer contamination happens and primer designs for population level screens take this into consideration, especially when the effort to do so is automated with 20 year old in-silico tools.

Reply

1. **Peter Barnum** says:
December 4, 2020 at 6:32 am

Yes, that is all correct and all I want is this to be stated in this cautionary manner. How do you get from this to, and I quote from your twitter, "We are quite clear, that they have no clue what their primers detect as the methods produce primer

dimers." Which of these primer dimers leads to the PCR just detecting anything? Most of them rather lead to lower sensitivity, as it is extensively described in literature...

2. **Peter Barnum** says:
December 4, 2020 at 6:54 am

And this is all still ignoring that even in the original paper they tested 297 clinical samples from patients infected with around 20 different viruses and all of them were negative. Assuming that they didn't blatantly made that up (which would of course be an unprecedented scandal), this also doesn't support the "It colcd detect anything" hypothesis....

Bobby says:
December 4, 2020 at 9:20 am

Quote is out of the CD-paper:
https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.3.2000045#html_fulltext

Using the E and RdRp gene assays, we tested a total of 297 clinical samples from patients with respiratory disease from the biobanks of five laboratories that provide diagnostic services (one in Germany, ... (Table 2). In total, this testing yielded no false positive outcomes.In four individual test reactions, weak initial reactivity was seen but they were negative upon retesting with the same assay. These signals were not associated with any particular virus, and for each virus with which initial positive reactivity occurred, there were other samples that contained the same virus at a higher concentration but did not test positive. Given the results

from the extensive technical qualification described above, it was concluded that this initial reactivity was not due to chemical instability of real-time PCR probes but most probably to handling issues caused by the rapid introduction of new diagnostic tests and controls during this evaluation study.

Notice here:

The one sentence states “no false positive outcome”. The next sentence states: “In four individual test reactions, weak initial reactivity was seen but they were negative upon retesting with the same assay”.

The first sentence becomes irrelevant and wrong, the second sentence states 4 (!) false positives out of 310.

In my opinion this is the kind of “cautionary manner” that led to the current situation worldwide, contradictions and the all-of-a-sudden-scientific acceptance of those, embedded in “cautionary manners”.

The truth here is:

Four in ‘n=310’ primary-tests => false positives = 1.3 %.

1) This is a direct alegre to the many reported cases of “false positives”, then “negatives”.

Further:

2) Christian Drosten publicly states that this is his “validation concerning cross-reactivity”, we tend to see this as a pseudo-validation:

https://twitter.com/c_drosten/status/1309755692232904704

This is no validation, there are 4 false positives, it's clearly stated in the text accompanied to table 2 of the CD-paper. Further, table 2 does not state a) which "validated clinical sample with known virus" caused the false positive, b) which gene assay.

2) The editors of Eurosurveillance further state in their communications: https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.21.2001035

Quote:

Our strategy during establishment was to use a synthetic target for the SARS-CoV-2 E gene assay, while validating amplification of a full virus genome RNA using the RdRp assay that is specific for both, SARS-CoV and SARS-CoV-2, with the latter not being available to us in the form of an isolate or clinical sample at the time. Based on experimental validation, it later turned out that the mismatched base pairs do not reduce RT-PCR sensitivity and are not to be seen as the reason for somewhat higher Ct values with the RdRp assay as compared to the E gene assay [3].

Notice here:

"Based on experimental validation, it later turned out that the mismatched base pairs do not reduce RT-PCR sensitivity ..."

Again we have this "cautionary manner": "The basic copies do not correspond to each other BUT that does NOT effect the sensitivity."... Trust us.

Nonsense! The supplementary data & material of this correspondance does not confirm that, which is provided

with this editor's / author's communication response.

3.  **Peter Barnum** says:
December 4, 2020 at 9:36 am

Once again, you are not addressing my main question: Which primer dimers do you think justify your claim that this PCR just detects anything? And you are interpreting "false positives" in "weak initial reactivity". I agree that this sentence woud justify questions, however it does not justify the claims you are making, i.e. that this PCR test is not suitable to detect SARS-CoV2.

And the fact that over the last months huge test numbers have resulted in extremely low numbers of positive tests (i.e. this Chinese study https://www.nature.com/articles/s41467-020-19802-w) counteracts your more general claim that this whole pandemic is only "present" due to false positive PCR tests. Even if this particular study gets retracted by the journal, this does not change anything about the situation regarding SARS-CoV2.

 **Bobby** says:
December 4, 2020 at 11:30 am

1) And you think the chinese study uses the Corman-Drosten protocol?

2) If so, could you back up this claim with references stating that they are using the CD-protcol?

3) We all know, that chinese laboratories are using much better protocols, f.e. Zhu's, which was not recommended by

the WHO, even though it was submitted to them in January 2020.

4) Drosten refutes himself here: https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.24.2001057

To quote Kevin Mckernan:

Muenchhoff et al. Same Journal

Conclusion:
RdRp needs to be pulled.

Drosten is an author. Same journal.

Can't have it both ways.

The WHO still points to old and faulty primers and the first review clearly missed the error. We expect this to be withdrawn soon!

Everything else is irrelevant concerning your supposedly-not-answered-question in regards to our review report on the CD-protocol, and also the referenced nature article (chinese study): We know that they are not using the CD-protocol, so it is irrelevant for our review report, which focuses on the Corman et al. publication and nothing else. This is a fallacity in itself.

5) We know that most of the western hemisphere uses 2 confirmatory assays. We know that China uses much better protocols (see point 3) than the CD-protocol. We know that Taiwan even uses 3 confirmatory assays – as everyone should (also compare the specific sections on this in our review

report). AND we know that Thailand uses two genes when arriving there, and when initially tested positive, then another 5 genes are used for confirmation to decide if the person is indeed positive or not, thus nearly no cases in Thailand.

So in summary I'd say, your question is heavily irrelevant in regards to our review report because it sets the scope outside the Corman-Drosten Protocol review (it's not so hard to stay on topic, our review report sets the framework).


Bobby says:
December 4, 2020 at 11:38 am

Addendum to your question: copypaste "Answer" by Prof. Dr. Ulrike Kämmerer:

https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.24.2001057

All labs have used ONE sample which was comprised of several extractions of RNA from ONE stool sample as positive control for SARS-CoV-2.

I wonder why they had not used the RNA of (well characterized?) SARS-CoV-2 isolates, like the one which is sold by the Charite (https://www.european-virus-archive.com/virus/human-2019-ncov-isolate). and labelled to be isolated from a Munich patient in Janary 29....

The article was submitted in May – so they should have access to not only this isolate but to many different isolates from all over the world as real positive controls. Further, no negative control and no

control samples with the RNA of other Coronaviruses were shown.

So its a publication on the detection of RNA from one Patient (and unusual: stool sample – why not from respiratory samples?) in different dilutions....

And not supporting anything about specificity but only sensitivity of the dilution series of this one specific sample.

2. **Peter Barnum** says:
December 4, 2020 at 6:09 am

Aand: Thanks for the pointer, must have overlooked that – my bad!

Reply

1. **Gertrud Adam** says:
December 10, 2020 at 11:06 am

Do you mean 11:30 or 11:38? (the pointer)?

Reply

67. **NN** says:
December 2, 2020 at 12:50 pm

This website here is nonsense. See here for the reasons why: https://twitter.com/BMauschen/status/1333468806203793411

Reply

Bobby says:
December 2, 2020 at 1:18 pm

We have answered Mäuschen extensively on her confusing thread, and also invited her to participate at the discussion directly here with all the authors. She didn't follow the invitation until yet. All her points are directly refuted and thoroughly debunked several times in her thread, it seems like she has no clue about the things she claims to have any kind of expertise. This thread is a PR think tank campaign by Christian Drosten & Co and we are quite disappointed that Christian Drosten & Victor Corman need paid shills (who don't know anything about the stuff that is written on their scripts) to address our 10 concerns, we would have expected more scientific integrity and backbone to be honest.

Reply

68.  **Tony** says:
December 2, 2020 at 2:37 pm

I would like to share some comments or questions:
1... nm means "nanometer" ....
This is a typo, no more and no less, and any lab technician will recognise it immediately.
2."First, a positive test for the RNA molecules described in the Corman-Drosten paper cannot be equated to "infection with a virus"
Where else would the RNA come from, if not through replication of the virus in the host. Could high RNA concentrations be caused by "contamination"?
3."...the Corman-Drosten test was not designed to detect the full-length virus, but only a fragment of the virus. We already concluded that this classifies the test as unsuitable as a diagnostic test..."
Detection of the full-length construct would be too costly, time demanding and therefore counterproductive. If you consider the PCR assay unsuitable for diagnosis, what about PCR-based liquid biopsies?
4."Secondly and of major relevance, the functionality of the published RT-PCR Test was not demonstrated with the use of a positive control (isolated SARS-

CoV-2 RNA) …"
The test does not work, because it was not originally validated with the isolated virus? Sounds weird to me.
5."The PCR test in the Corman-Drosten paper therefore contains neither a unique positive control nor a negative control to exclude the presence of other coronaviruses."
So far I remember, there were a lot of positive and negative controls included.(?)

6. "The first sentence of this excerpt is clear evidence that the PCR test described in the Corman-Drosten paper generates false positives"
„however they were negative upon retesting with the same assay". Positives will be retested anyway, even by amplification of another gene, isn't is?

Reply

69. **Stringer** says:
December 2, 2020 at 3:02 pm

Scenario:

1. SARS-Cov2 effectively does not exist except as a theoretical construction in a computer
2. It is part of the pandemic simulation called "Event 201" which aims at traumatizing and controlling the population and enabling public-private partnerships to plunder cash and resources on a massive scale
3. There is no preparation of the virus available in any lab worldwide in amounts sufficient to perform independent determinations of its identity, defined as a complete elucidation of the viral structure and characterization of its biological activity
4. There is no preparation of the virus available in any lab worldwide in amounts sufficient for use as a laboratory standard
5. No such virus has been isolated from any human dead or alive in sufficient quantities to perform a complete determination of identity (structure and

biological activity) in order to compare it with a standard
6. Therefore the current PCR test is “detecting” RNA fragments from common corona viruses that have been around for years
7. Even if the test is substantially improved, it will be chasing a phantom however many sequences may be simultanously targeted
8. There is no indication of the clinical utility of the PCR test except to tyrannize the population by enforcing quarantine and other punishment
9. The clinical utility of the PCR test for the tested persons is zero, otherwise such tests would have been in use for at least a decade to support diagnosis and therapy of influenza or heavy cold cases.

Factual and logical rebuttals are cordially invited.

Reply

1.  **Joerg** says:
   December 2, 2020 at 3:50 pm

   Yes it is a (your unreal) szenario!
   1) (non existence) Ask ill people or read cases, look to excess mortality charts (besides Germany)
   2) (conspiracy) Honestly, do you feel traumatized & controlled? Actually, we are far through the tunnel already. Fear, ignorance, incompetence, incapacity are enough to explain the most.
   3) (no big amounts of virus preps) Can’t comment on this one (no expert).
   4) (no lab standard available) Could be synthesized/PCR-amplified of infectious material?
   5) similar as 3) see 3)
   6) (common corona virus detected) Why then is there an excess mortality of positive tested patients?
   7) (there is no improved test) That’s what I’m asking. Why not? There are specific genes and discriminating sequences (stable enough/without mutation pressure) compared to common corona viruses?

8) (no clinical advantage) Yes. The tests are established to monitor the spreading, to shelter the healthcare system. Epidemiological reasons! (NOT clinical)
9) similar as 8) see 8)
Kind regards Joerg

Reply

1. **Dr Solomon** says:
   December 3, 2020 at 2:50 am

   There is no excess mortality in UK where I practice as a doctor.
   The numbers presented (59K) also include those thousands who were literally murdered in their care homes by Boris Johnson Govt as they were denied access to hospital.It also includes those who died months later from other causes and had tested positive (false positive) earlier.It also includes thousands of people who died in their homes due to heart attacks, strokes, infections and cancers because they were frightened to death by BBC propaganda and did not come to hospitals!
   So are you still surprised by slightly increased numbers of death this year ??
   Doctors think and Robots don't !
   Kind Regards

   Reply

   1. **Joerg** says:
      December 3, 2020 at 9:34 am

      Hello Dr. Solomon,

      please go to this site, they track the excess mortalities for Europe:
      http://www.euromomo.eu/graphs-and-maps
      Please, scroll down to the UK graph, there is a tremendous peak in

excess mortality in the calendar week 15 2020 (z-score 36).
Imagine, if you say “all these data (for other countries too) are a concerted fraud”, you better bring up proofs beside selective, specific, personal observations?
Why is the „fraud“ so naïve, leaving out countries as Germany (there is indeed no excess mortality) making a “conspiracy theory” more difficult?
Who should have ordered this fraud? How could it be concerted among different countries which are fighting each other on the level of EU policies?
The answer is: VERY, VERY PROBABLY THE GRAPHS PRESENTED ARE NOT WITHOUT MISTAKES BUT IN TOTAL THEY ARE THE BEST ESTIMATE OF THE TRUTH WE HAVE?!

Off course, one could and should earnestly discuss all the governmental actions according the “pandemic” (besides it is more or less severe).
But it is to easy to borrow “simple” answers for complex questions! This is typical human, but behold and think.

Thanks for your service as a doctor, much power and strength for your duty.
Joerg

Reply

1. **Thomas Ellenberg** says:
   December 3, 2020 at 9:16 pm

   “Please, scroll down to the UK graph, there is a tremendous peak in excess mortality in the calendar week 15 2020.”

   A virus is definitely not responsible for such a sharp peak. The cause was massive, experimental testing of potentially

lethal dosages of hydroxochloroquin which was initiated by the WHO. That's why you see this peak in multiple countries at the same time which, again, can't be caused by a virus. And you allready mentioned that it didn't happen in Germany. Well, it used reasonable dosages.
https://www.youtube.com/watch?v=0JcVglSdQ-c

2.  **Joerg** says:
December 4, 2020 at 10:56 am

@Thomas Ellenberg
That does not come temporally there!

Better check the facts and don't blindly believe what you pick up on the Internet.
https://www.nature.com/articles/s41419-020-2721-8

It was not until March 28 that hydroxychloroquine (HCQ) was briefly introduced by the U.S. Food and Drug Administration (FDA).
There were already many patients in the hospitals, do you really think that all of them had administered HCQ from 29th March (week 14) and in week 15 (peak) so many were dead? What about all the people who died in nursing homes or at home? Do you think they all received HCQ from their GPs as of 29 March?
If you have verifiable sources of it, give it to me.

Of course, it is true that many suboptimal treatments took place in March/Apr, but thanks to God, the mortality rate has decreased over time. A merit of the research, the doctors, the nursing staff.
As I said, it is easy to discuss whether many restrictions on

the part of politics are exaggerated.
Nevertheless, don't get involved in every witch-hunt! Please consider the scientifically verifiable facts, not just opinions on YouTube.

Kind regards Joerg

3.  **Thomas Ellenberg** says:
December 4, 2020 at 9:40 pm

"Better check the facts and don't blindly believe what you pick up on the Internet."

Better try to avoid irrelevant ad hominem spam and other fallacies.

"There were already many patients in the hospitals, do you really think that all of them had administered HCQ from 29th March (week 14) and in week 15 (peak) so many were dead?"

HCQ was the MAIN component of mal pratice. Using ventilators without medical necessety or using combos of immunosuppressive drugs were amongst many others. So what I'm saying is that malpractice was the reason for the sharpness of these peaks. And it happened simultaneously in multiple contries, especially in those with lots of deaths in Europe, but not in all which shows that this was man made. Even within Switzerland there was a difference between the mortality in the German, Italian or French speaking region and excess mortality was only found in the latter two. I highly doubt that a virus prefers killing French or Italian hosts.

I linked a Youtube video with Claus Koehnlein who also co-

authored this article:
https://www.rubikon.news/artikel/die-medikamenten-tragodie

4.  **Joerg** says:
December 5, 2020 at 7:13 pm

Hallo Herr Ellenberg,

vielen Dank fuer ihre Antwort.
Dass im Fruehjahr viele Behandlungsfehler vorkamen ist richtig. Dazu gab es ja Gott-Sei-Dank eine schnelle Lernkurve. Die Sterbestatistiken sind sehr heterogen, es gab keine einheitlichen Zaehlweisen in den Laendern, usw

Trotzdem bitte ich Sie die Charts bei Euromomo zu studieren:
– Es ist mE genauso ueber das Ziel hinausschiessend, die gesamte Datenlage zu verharmlosen.
– Wie erklaeren Sie laenderspezifische Uebersterblichkeitspeaks im Herbst (in A, B, F, I, SLO, CH)? Sind diese immer noch “unfaehig Patienten besser zu behandeln”? Sind da immernoch “Medikamenten-Tester” am Werk?

Glauben Sie mir, viele Massnahmen in D finde ich uebertrieben, mir waere selbstverantwortliches, freiheitliches Handeln lieber als Ge- und Verbote (zB wie in S, CH). Aber die dtsch. Mehrheit will es, die Politik setzt es um.

Thesen, weshalb es in manchen Laendern weniger schwere Covid19-Verlaeufe gibt, koennten sein: weniger Vorbelastungen? gutes Gesundheitssystem? bessere indiv.

Immunsysteme? genet. Disposition? vorherige Kontakte mit milden Corona-Viren? usw. Aber das hilft uns jetzt nicht. Bald haben wir es geschafft und dann entspannen sich alle hoffentlich wieder.

LG Joerg

2. **A. Berglund** says:
December 3, 2020 at 5:15 pm

1)You cannot prove that the “ill people” and “cases” are infected with “SARS-COv2”. The “diagnostic test” for RNA fragments is useless. It is a random number generator on the set (0,1).

2)”through the tunnel”–I’m sure the proprietors of hotels, restaurants, fitness and yoga studios and the travel industry who have lost up to 80% of their revenue compared to 2019, and the workers who have lost their jobs, will derive great comfort from those words. You must have a well-paid government job.

(6)and (8)the diagnostic test is useless for any purpose

Reply

70. **roland brautigam** says:
December 2, 2020 at 4:39 pm

Hi Bobby – assume you have seen that Eurosurveillance published this in 2012. Note that Ab Osterhaus is one of the authors. The devil himself!

https://www.eurosurveillance.org/content/10.2807/ese.17.49.20334-en

Reply

71. **tim** says:
December 2, 2020 at 5:15 pm

it's revolution time...

Reply

72. **Pierre Lutgen IFBV-Belgerb** says:
December 2, 2020 at 8:48 pm

The same questionable PCR testing is used to hide the inadequacies and failures of ACT (Coartem, Coarsucam, Artequick) malaria therapy

Reply

73.  **Rik Breuer** says:
December 2, 2020 at 8:51 pm

I would go one step further and question the validity of the "finding" of the virus itself.

I read the paper regarding the Chinese scientists in Wuhan taking a sample from "one" sick patient and "identifying" the new virus SARS-CoV-2. They didn't isolate the virus (that never happened anyway), they didn't fulfill Koch's postulates and without a Gold Standard they couldn't prove that this "virus" is causing an flu like illness which can't be clinical diagnosed.

I would say, this whole Covid19-pandemic is a scam from beginning to end.

I have looked up excess mortality in US and Germany. There is none.

Reply

1. **Kevin Corbett** says:

December 2, 2020 at 11:36 pm

I agree with you.

Reply

1. **Peter Looman** says:
   December 12, 2020 at 10:18 am

   I don't understand much of this all but try (serious) to understand bit by bit (if possible for me...). And have a question: I see complete genomes per example on the following page: https://www.ncbi.nlm.nih.gov/nuccore/MN988668. Why is this not conform the golden standard and why is it so important? Is it crucial or just the correct genome but not underwritten with the "golden" signture? More genomes you can find on https://mra.asm.org/content/9/11/e00169-20. I would really appriciate the answer, please understandable for me.

   Reply

74. **Terrence Joseph Bennett** says:
December 2, 2020 at 10:07 pm

Thank you for doing science!
Shame on those who prefer Crapitalism to truth

Reply

75. **heusenbeck** says:
December 3, 2020 at 2:21 am

Why is "A) BACKGROUND" a major concern with the corman drosten paper?

"According to BBC News [4] and Google Statistics [5] there were 6 deaths world-wide on January 21st 2020 – the day when the manuscript was submitted. Why did the authors assume a challenge for public health laboratories while there was no substantial evidence at that time to indicate that the outbreak was more widespread than initially thought?"

To quote Pieter Burger from another paper he released in april 2020:

"It was common knowledge that some strain of coronavirus-sooner or later-was going to cause a pandemic. It was known since the SARS-CoV-outbreak in 2003. In 2013 and 2015, the world was informed that a variant of SARS-CoV in bats was emerging as a threat for humans."
[https://www.researchgate.net/publication/341120750_A_SARS-like_Coronavirus_was_Expected_but_nothing_was_done_to_be_Prepared]

Like any virologist Drosten warned about the threat of emerging infectious diseases and as we know, he co-discovered SARS-CoV1, developed the first diagnostic test and contributed to research on MERS early on. So i dont know what the implification of your "major concern A)" is. Do you expect him or any scientist working in this field, with the necessary resources, to sit back and check google statistics till death rate is alarming?

Reply

76.  **Dr Solomon** says:
December 3, 2020 at 2:39 am

Dear team of Great Scientists,

Well done. You would be remembered in human history as those who chose to speak up against those who chose to sell their conscience to Pfizer, Astra-zeneca and Bill Gates.

I am a physician in UK and I see this fake and false positives on daily basis where literally hundreds of patients are being isolated and traumatized just because

their fake PCR test has detected some unknown bits of unknown RNA despite the fact that none of them would have any symptoms whatsoever !This madness in being practiced on daily basis across European hospitals under the name of Science(Fake Science)and worst of all, under the auspices of doctors who took oath of not harming their patients and defending them against the interests of the Mafia of Bill Gates and likes.

I understand these are unique and hard times in human history where the forces of big Pharma, Large banks and huge corporations are hell bent on enslaving us and taking away the very last bits of our independence and humanly existence as an extremely endangered specie.

The question is how can masses around the globe resist this mania ?

Wouldn't it be better if doctors and nurses around the globe came together under one umbrella with a view to give the common men their right to know the truth and help them fight back against these demons ?

I strongly believe it is the sole responsibility of health professionals around the globe to protect the people against this wave of sheer medical barbarianism , neo-slavery and worst fraud of human history. Nobody wants to be part of this new SS Medical Corps of Pfizer and others (Angels of Death) who are committing the most heinous crimes against humanity. What Bill Gates, Mafia of World Economic Forum and likes are suggesting looks very similar to what Hitler and his SS Medical Corps were doing seven decades ago !

I look forward to your thoughts on this. I bet Bill Gates will not be happy to hear this for he would prefer Robots to thinking doctors which is perhaps his next agenda!
Before we are all robotized in near future, it is time to wake up. A global Consortium of Doctors and Nurses backed by the people is the solution.

Together, We Can Make A DIFFERENCE!
IT IS NOW OR NEVER.....

Reply

77. **Busu** says:
December 3, 2020 at 6:16 am

Thank you for this important job!
What are your next steps? In Germany there are no reports about this study, I don't know are there to prevent this study.

Reply

78. **Franz** says:
December 3, 2020 at 7:28 am

Thanks for your huge effort giving a review on this paper. Would be great to get some more information about practical work of authors done on detection of SARS-CoV-2.

Reply

79. **Joerg** says:
December 3, 2020 at 9:11 am

Hello,

in the meanwhile I got answers from a molecular lab expert involved in Covid19 research & diagnostics:

Overall:
– One should rather honor that within days and largely based on alignments of SARS-like viruses such well-working PCR assays have been designed, one of which (E gene) is still the reliable backbone of diagnostics

Technically:
– Why discuss annealing temperatures when you can show experimentally that

these PCRs work?
– Why discuss wobble bases when the RdRP PCR is demonstrably specific and sensitive (statement from practice: we had more than once a false base in the primer, which made a specific PCR-assay better instead of worse)
– Why discuss the 'right' amount of primers? If the reverse RdRP primer is too weak (too short) and contains wobble bases, then it is only logical to use more of them [higher concentration]
-> PCR IS MUCH MORE EMPIRICAL THAN DESIGN THEORY!
Auf deutsch: "Entscheidend ist, was hinten rauskommt!"

Sensitivity & Specificity:
– In the January publication sensitivity (5 copies) and specificity (other cold pathogens do not make a signal) were determined experimentally.
– What is a diagnostic PCR? To find negative samples negative and find positive samples. These three PCR assays do this reliably.

Improvements since Jan:
– For RdRP an interaction with human DNA had been overlooked. The RdRP assay has different primers since March.

What has been researched since Jan?
– Well over 100,000 viruses have been sequenced since January and they are virtually all identical.
– The diagnostic regions were rarely affected by mutations (once Roche cobas and once CDC).

Conclusion:
– Without 'new' results (sequences) there are few needs for new assays [because the current ones work]

Kind regards Joerg

Reply

1. **Max** says:
December 3, 2020 at 9:50 am

same her – much fuzz about something that doesn't matter in practice. To the "reviewers":

.) you criticise that many of the steps of validation have been done with virtual data, but you never tried the assay on the bench. You have just gone through it "virtually". You had months of time to proof that the assay does not work (in the lab, on the bench!), but you did not even try to do it.

.) why is it important for you to discriminate between a virus fragment and whole virus? how should it get there if not via infection? There are no virus-pcr-detection systems, that detect the "whole virus", it's always a specific fragment you are searching for.

.) There are no Wobbly-positions in the 2019-nCoV specific primer.

.) there is no SOP and this could be improved, yes. but drosten gives information about sample preparation, primer-sequences, limits of detection and setup for PCR. Any routine lab can handle this information and setup their tests.

.) The cT value already has been corrected by drosten in an interview to a recommendation to cT ~30. But as this differs between labs, it should not be taken too precise, but validated by the labs. much more important are control samples, which are taken by serious labs anyway – positive virus sample, positive human DNA-sample, negative load,..

stay safe!

Reply

Bobby says:

December 3, 2020 at 11:01 am

REPLY FROM THE AUTHORS (DR. BORGER):"ANSWERS":

QUOTE:
.) you criticise that many of the steps of validation have been done with virtual data, but you never tried the assay on the bench. You have just gone through it "virtually". You had months of time to proof that the assay does not work (in the lab, on the bench!), but you did not even try to do it.

ANSWER:
We have now several labs worldwide, which report that the C-D test does not work in their labs and generates false positive results in different PCR machines. So this test cannot be sold as the golden standard.

QUOTE:
.) why is it important for you to discriminate between a virus fragment and whole virus? how should it get there if not via infection? There are no virus-pcr-detection systems, that detect the "whole virus", it's always a specific fragment you are searching for.

ANSWER:
Bad news for virus diagnostics. PCR virus diagnostics should only be to support differential diagnosis to exclude other virus diseases. It should never be used as a screening device, since virus-parts are inhaled all day long and trapped in the mucous of nose and lungs, exactly there were the samples are taken from.

QUOTE:
.) There are no Wobbly-positions in the 2019-nCoV specific primer.
.) there is no SOP and this could be improved, yes. but drosten gives information about sample preparation, primer-sequences, limits of

detection and setup for PCR. Any routine lab can handle this information and setup their tests.

ANSWER:
Bad science and even worse for diagnotics. There must be an online SOP, which must be used in all labs, germany-wide, world wide. And the SOP should be online update when required.

QUOTE:
.) The cT value already has been corrected by drosten in an interview to a recommendation to cT ~30. But as this differs between labs, it should not be taken too precise, but validated by the labs. much more important are control samples, which are taken by serious labs anyway – positive virus sample, positive human DNA-sample, negative load.

ANSWERS:
When Ct is different Germanwide, worldwide, nothing can be compared. This is very bad science.

QUOTE:
stay safe!

ANSWER:
Stay free!

Reply

1. **Max** says:
   December 3, 2020 at 3:20 pm

   1) so you did not try to test the assay. just used "virtual data" and personal communication. why dont they have controls for false positive test – its no rocket science.

   2) yes, virus diagnostics should only be one part and this is what

drostens lab is saying. its not a corona-test, but a procedure they claim to be done! But no, there are no “dead” virus particles free floating, just happen to infect people. and no, even if you catch up one of these, they will not be tested positive! they need to reproduce 2-3 days until pcr-test will recognise them (thats wy pcr tests are false negative the first two days 😉

3) this can be enhanced, yes, but does not make the test itself bad. every trained lab-worker handling with pcr knows what to do, when getting drostens publication!

4.) well, this is fact with every PCR, and also every other (diagnostic) test. unless you use the exact same reagents (including LOTs) and the same equipment (and you can never do this in two different labs) you will have differences. Thats what trained lab-workers are here and you must not let beginners/student or simply untrained personnel do the diagnostics! even in the same lab you have to re-evaluate and re-validate your SOPs from time to time, also if you do not change anything. thats science. thats good science. relying on SOPs someone else made up with different reagents (included buffer solutions from different companies etc) is bad science.

Reply

1.  **Lorenzo** says:
December 5, 2020 at 6:17 pm

Max, how can a lab practically validate its results? You talk about control samples, I assume a _certain_ positive and a _certain_ negative, how can a lab acquire these? Regarding the samples I’m thinking about actual swabs material with a mix of human and multiple bacterial and viral genomes. I’ve read papers where water

with just individual viruses was used as a negative, it seems quite different from the real world situation.

Reply

Bobby says:
December 3, 2020 at 10:59 am

REPLY FROM THE AUTHORS (DR. BORGER): “ANSWERS”:

QUOTE:
Overall:
– One should rather honor that within days and largely based on alignments of SARS-like viruses such well-working PCR assays have been designed, one of which (E gene) is still the reliable backbone of diagnostics

ANSWER:
Indeed, but wouldn’t it be nice to know what it is detecting? It was not molecularly validated. It may detect any coronavirus and probably other viruses as well.

QUOTE:
Technically:
– Why discuss annealing temperatures when you can show experimentally that these PCRs work?
– Why discuss wobble bases when the RdRP PCR is demonstrably specific and sensitive (statement from practice: we had more than once a false base in the primer, which made a specific PCR-assay better instead of worse)
– Why discuss the ‘right’ amount of primers? If the reverse RdRP primer is too weak (too short) and contains wobble bases, then it is only logical to use more of them [higher concentration]
-> PCR IS MUCH MORE EMPIRICAL THAN DESIGN THEORY!
Auf deutsch: “Entscheidend ist, was hinten rauskommt!”

ANSWER:
We agree, but the Test is designed so sloppy, we simply don't know what positive results mean.

QUOTE:
Sensitivity & Specificity:
– In the January publication sensitivity (5 copies) and specificity (other cold pathogens do not make a signal) were determined experimentally.
– What is a diagnostic PCR? To find negative samples negative and find positive samples. These three PCR assays do this reliably.

ANSWER:
No, there is nothing in the test to exclude other viruses.

QUOTE:
Improvements since Jan:...

ANSWER:
Irrelevant for our external review report.

QUOTE:
What has been researched since Jan?
– Well over 100,000 viruses have been sequenced since January and they are virtually all identical.

ANSWER:
He means "puzzled together from 200 bp pieces" using a prespecified SARS-CoV-2 template.

QUOTE:
– The diagnostic regions were rarely affected by mutations (once Roche cobas and once CDC).

ANSWER:
There are now over 30'000 difference Sequences collected, including indels,

in glue: http://cov-glue.cvr.gla.ac.uk/#/home So, if 100,000 sequences have been collected, 1 in 3 is different.

QUOTE:
Conclusion:
– Without 'new' results (sequences) there are few needs for new assays [because the current ones work]

ANSWER:
We have now reports from all over the world that the PCR test does not work as described in the Corma-Drosten paper. Positive often even depends on the instruments used. This test should not be propagated as the golden standard, because it is not golden.

Reply

Bobby says:
December 3, 2020 at 11:11 am

REPLY BY THE AUTHORS (PROF.DR. KÄMMERER): "ANSWERS":

ma additional comments:

QUOTE:
– One should rather honor that within days and largely based on alignments of SARS-like viruses such well-working PCR assays have been designed, one of which (E gene) is still the reliable backbone of diagnostics

ANSWER (ADDITIONALLY TO DR.BORGER'S ANSWER):
There was NOR REAL nCoV2019 positive control in the test validation.

QUOTE:
Technically:
– Why discuss annealing temperatures when you can show experimentally that these PCRs work?

– Why discuss wobble bases when the RdRP PCR is demonstrably specific and sensitive (statement from practice: we had more than once a false base in the primer, which made a specific PCR-assay better instead of worse)

ANSWER:
This is not a good laboratory practice – normally you can create an PCR that is optimized for the gen target to be detected, especially in a case where sequences are available in the Genbank (or viruses GISAID). The Chinese CDC managed to fulfill ths aspect for both the primer pairs and probes for their very early PCR, so why did the authors of the cormandrosten PCR publication such a weak PCR compared to the Chinese scientists?

QUOTE:
Why discuss the 'right' amount of primers? If the reverse RdRP primer is too weak (too short) and contains wobble bases, then it is only logical to use more of them [higher concentration]

ANSWER:
There is no need to include wobble bases in a PCR when the correct gene sequence is known (se figure 2 in the Cormandrosten paper). One can easily select a primer pair that fits and can be used at low concentrations with the optimal melting temperature around 60°C by one of the many good database "Primer design" tools . In daily laboratory practice you create 2-3 different primer pairs for the same target, order them and then then you test them in the lab with correct positive and negative controls to figure out which pair works best. After further validation with "real" samples (tissue, swabs, cell culture, etc. you can publish it. Well, maybe this it common practice for "normal" labs
>>>> only, maybe not for TOP-virology labs....<<<<<

Reply

1.  **Kevin McKernan** says:

December 4, 2020 at 5:01 pm

Please see my comments addressing this for other questions proposed on this thread. There is no need for us to perform wet experiments when 4 peer reviewed articles are provided with wet evidence of false positives generated and a recommendation to eliminate the RdRp primers. One of the authors of a paper suggesting the RdRp assay be eliminated is published in Eurosurveillance with Drosten as an author (Muenchhoff et al). You can't have it both ways. 24 hour review had bad primers and the evidence comes from a paper with Drosten as a contributing author. It is his responsibility to remove the disinformation that he published before more false positives wreck peoples lives.

Reply

80. **wilhelm Lehberger** says:
December 3, 2020 at 1:34 pm

Es sollte selbstverständlich sein, dass im wissenschaftlichen Bereich und gemäß dem Anspruch einer demokratischen Gesellschaft Positionen ausgetauscht, geprüft und insbesondere im Falle derart gravierender Auswirkungen öffentlich erörtert werden können. Dies findet nicht statt und findet sich auch hier nur ansatzweise wieder.
Besorgte Nachfragen werden ignoriert und zu oft treten die übelsten menschlichen Eigenschaften zutage – denunzieren und diffamieren. Wenn also ein Ehepaar vor einer Reise Antigentests und in zeitlichem Abstand einen PCR-Schnelltest beim Hausarzt vornimmt, vorsorglich 3 Wochen private Kontakte ausschließt und der PCR-Test dann 1x negativ + 1x positiv ausfällt, dann ist das angesichts der hohen Infektionsgefahr nicht zu erklären. Das ist kein Einzelfall und nach dem Informationsstand nicht zu erklären. Es traten auch in der folgenden Quarantäne (die das Gesundheitsamt erst nach Ablauf und 4 Wochen nach dem Test anordnete) keine spezifischen Symptome auf. Was heißt das

nun? Wurde man nun infiziert oder nicht? Wenn ja, ist man dann “geheilt” oder “immun”? Bringt dazu ein erneuter Antigentest Erkenntnisse? War hingegen der Test falsch, bedeutet das ca.320 € für die Tests und 3.500 € Stornokosten (die Versicherungsbedingungen wurden zum 1.9. angepasst). Faktisch ist damit die Reisefreiheit auf unbestimmte Zeit aufgehoben, weil sie keinen “richtigen” PCR-Test innerhalb von 24 Std. nicht bekommen. Die “offizielle” Antwort wäre sicher, man solle ja nicht verreisen (gilt nicht für Pendler u. Geschäftsleute). Da muss man sich über Proteste nicht wundern und schon sind wir wieder (auch hier) bei Rechtsradikalen und Verschwörungstheoretikern. Da empfehle ich doch den Blick über den linken Zaun, da gibt es erhebliche Zweifel bis zum Protestaufruf. Und wenn Klaus Schwab und das Weltwirtschaftforum Verschwörungstheorien befördern (wie das in einem Kommentar anklang),zu dem u.a. Minister und Staatschefs anreisen, dann sollte das die Politik klarstellen. Dazu die alte JUSO-Frage: Wem nützt es? (Und wer zahlt es?)

Reply

1. **V. Scholz** says:
   December 3, 2020 at 4:16 pm

   Dieser Test ist ein Zufallszahlgenerator.

   RA Fuellmich redet nicht umsonst vom “vorsätzlichen sittenwidrigen Betrug”.

   Reply

   1. **Joerg** says:
      December 5, 2020 at 7:33 pm

      Hallo Herr Scholz,

      wenn es ein Zufallsgenerator waere, muesst die Anzahl der Positiven stets in einer Bandbreite zu der Anzahl der durchgefuehrten Tests

bleiben.

DAS WAR/IST ER ABER NICHT, im Mrz war er bei 9% Positive/Anzahl Test und jetzt im Herbst ebenfalls in D.
Das finden sie in allen Charts.
Erklaerung: Der qPCR-Test mag eine gewisse Fehlerrate (je nach Labor 0,x – 1,y%?) haben, aber er zeigt NICHT Zufall an und es werden auch mehr in's Krankenhaus eingeliefert, wenn die Rate Positiv-Getestet/Anzahl-Tests hoeher ist. Das koennen sie auch bei ordentlichen Datenaufarbeitungen deutlich erkennen:
https://www.querschuesse.de/corona-faktencheck/

Wut und Enttaeuschung ueber Einschraenkungen, WIE Entscheidungen getroffen wurden, ist verstaendlich, aber ein schlechter Ratgeber!

Positiv: in D stagnieren oder sinken die Infektionsraten OHNE, dass das Gesundheitssystem nur in die Naehe der Ueberlastung kam. Wir sind ziemlich sicher aus dem Groebsten raus!

Immer locker bleiben, oder verklagen? Joerg

Reply

81. **Oscar Drinnon** says:
December 3, 2020 at 4:33 pm

The use of bald-faced lies about an epidemic to conceal a political agenda was exemplified as early as 1968 in Stanely Kubrick's famous film "2001, A space odyssey".

The android-like bureaucrat "Dr. Heywood Floyd" informs moon base scientists that an epidemic is being used as a cover story for the news blackout after the discovery of the black monolith. He further informs them that they will have to

sign a written oath of secrecy:

'– https://www.youtube.com/watch?v=PdbhZBpqNPM –'

Reply

82. **Michael** says:
December 3, 2020 at 5:19 pm

Eurosurveillance has reacted:
https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.48.2012031

Let's hope science wins!

Reply

1. **Gyarmati** says:
December 3, 2020 at 6:50 pm

No way. They will reject the above paper and the retraction demand. The narrative cannot be threatened.

Reply

83.  **Frank Visser** says:
December 3, 2020 at 5:41 pm

This contradicts your story that the C/D PCR is defective, is completely aspecific and can't even work:

Comparative Performance of SARS-CoV-2 Detection Assays Using Seven Different Primer-Probe Sets and One Assay Kit

"We found that the most sensitive assays were those that used the E-gene

primer-probe set described by Corman et al. (V. M. Corman, O. Landt, M. Kaiser, R. Molenkamp, et al., Euro Surveill 25:2000045, 2020, https://doi.org/10.2807/1560-7917.ES.2020.25.3.2000045) and the N2 set developed by the CDC (Division of Viral Diseases, Centers for Disease Control and Prevention, 2020, https://www.cdc.gov/coronavirus/2019-ncov/downloads/rt-pcr-panel-primer-probes.pdf). All assays tested were found to be highly specific for SARS-CoV-2, with no cross-reactivity with other respiratory viruses observed in our analyses regardless of the primer-probe set or kit used."

Reply

Bobby says:
December 3, 2020 at 5:47 pm

We also have this editorial note, in my honest opinion, that doesn't sound plausible at all:
https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.21.2001035

Quote:
Our strategy during establishment was to use a synthetic target for the SARS-CoV-2 E gene assay, while validating amplification of a full virus genome RNA using the RdRp assay that is specific for both, SARS-CoV and SARS-CoV-2, with the latter not being available to us in the form of an isolate or clinical sample at the time. Based on experimental validation, it later turned out that the mismatched base pairs do not reduce RT-PCR sensitivity and are not to be seen as the reason for somewhat higher Ct values with the RdRp assay as compared to the E gene assay [3]

"More mismatches? No problem, test works, we assure you".

Reply

Bobby says:

December 3, 2020 at 5:59 pm

Sensitivity is not specifity. A lot of false positives increase sensitifity but decrease specificity.

Reply

84. **Ale vd sluis** says:
December 3, 2020 at 11:59 pm

nu maar weer hopen of niet, dat u uw inteletuaeel vermogen ten positive weet te aan te wenden. ik begrijp de frustratie maar denk echt dat er betere manieren zijn om uw gelijk aan t tonen als dat er al uberhaupt al toe doet.Kom op peter, waar blijft die toegevooegde waarde

Reply

1. **Robert** says:
December 4, 2020 at 8:11 pm

Heeft u bij Peter in het dorp gewoond? Aan uw Nederlands te lezen heeft u in ieder geval niet op dezelfde school gezeten. Mag ik u vragen wat u zelf vindt van de toegevoegde waarde van uw opmerkingen in een verder behoorlijk volwassen discussie?

Reply

1. **A. van der Sluis** says:
December 7, 2020 at 9:21 am

Op uw eerste vraag: ja. Uit mijn nederlands trekt u de verkeerde conclusie. Het antwoord op uw tweede vraag moet u misschien zoeken in het artikel in die Zeit; Shitstorms Steht den Wissenschaftlern bei! (Heeft u ongetwijfeld gelezen.) Het is welliswaar een epinierend artikel

en ik vermoed dat u het als niet relevant zult bestempelen?

Reply

85. **Emalsen** says:
December 4, 2020 at 12:22 am

No mention that the protocol in question was updated or of any further development in testing. Instead the authors, in comments above, made clear that their criticism aims solely at the original paper from nearly a year ago. In wich scale this specific protocol was or might still being used, the report unfortunately does not investigate. So any impact of misdiagnosis, even if they prove this old protocol eventually somehow guilty, stays unfounded. I wonder what they try to gain here?

Reply

Bobby says:
December 4, 2020 at 5:43 am

You are missing something substantial, and I suppose “on purpose”, the Eurosurveillance CD-paper has an Addendum, the Addendum shows the changes made:

Quote:

*Authors’ correction

The sentence As at 20 January 2020, 282 laboratory-confirmed human cases have been notified to WHO was originally published with a wrong date (As at 20 January 2019...). This mistake was corrected on 8 April 2020.

On 29 July 2020 the correct affiliation of Marco Kaiser was added and the remaining affiliations were renumbered.

** AddendumGo to section…

The Conflict of interest section was updated on 29 July 2020.

So your comment is a totally wrong & a weak lie – I suppose on purpose. Scroll down:
https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.48.2012031#html_fulltext

P.S.: Announced changes via Christian Drosten's podcast don't count. We want it in written official form.

Reply

1.  **Rob** says:
December 4, 2020 at 8:50 am

That's an issue that could be resolved by one short email from every test kit's manufacturer, if it's not already included in their literature. We already know the cyclic thresholds are way too high for all the tests, I suspect they probably contain many if not most or all of the issues raised here – easy enough to find out though.

Reply

86.  **Ale vd sluis** says:
December 4, 2020 at 1:12 am

peter , moast even dyn moderater bettere instrukties hjaan ,

Reply

87.  **Willy Schmid** says:
December 4, 2020 at 8:44 am

Please try to stop testing worldwide contacting the right persons/organisations who are ableto do this. By now, almost everybody knows that the PCR-test is not good at all. But in all countries, they continue to test, making more lockdowns. Now testing is even made with a quick test, which is less precise than the PCR-test according to the manufacturer Roche. Thanks.

Reply

88. **Y. Gielens** says:
December 4, 2020 at 9:01 am

I have not seen an analysis of the effects of variability in the sampling procedure, sample storage and sample extraction on the test results. (These are all steps prior to the test proper).

Examples of variables:
–Design and material of swabs. Are they fit for purpose? Have they been tested for contaminants that can cause false-positives? Is the production process controlled?

–Nature and amount of sample removed onto the swab from the oral or nasal cavity: (a) what matrix is actually sampled? Mucus? Water? Cell layers? (b) How much sample is removed, measured in microliters (fluid) or micrograms (solid)?

–What is the extraction variability from the matrix and from swab to swab?

–Effect of sampling site (oral or nasal). Is one targeted or both? Why?

–Stability of the molecular species to be anayzed (oligonicelotides?) in the sample after collection and during transport: temperature, mechanical stress?

–Efficiency of extraction from the sample matrix/swab of the molecular entities(oligonucleotides) to be analyzed ?

Have all of these factors been tested, for example by spike/recovery

experiments?

If two subjects “A” and “B” have the same amounts of RNA at the nasal/oral sampling sites, but subject “A” tests positive and subject “B” does not, the discrepancy could be due to variability in any of the above factors. Just one example: removing double the amount of sample material onto the swab from the nose and throat of A compared to B would suffice.

These are just technical points apart from the main issue of whether the molecules being analyzed have amy clinical relevance. But as long as (incredibly)such tests are still being performed, they have to be considered.

Reply

89.  **Ellis Mulder** says:
December 4, 2020 at 9:06 am

Thank you so much! Anyone should know this! I’m so proud of you all!

Reply

90.  **Y. Gielens** says:
December 4, 2020 at 9:11 am

A further question that I have not seen addressed:

The test apparently produces a binary yes/no output–“positive” or “negative”.

But what is the actual physical signal readout from the instrument? Subjective visual? Photometric? fluorimetric? Which wavelengths?

Such instrument signals are normally continuous variables. What criteria are used to convert them into the binary (“positive / negative”) readout and what are their statistical properties?

What data reduction techniques are used (standard curves?) Confidence

intervals?

Has an error analysis of the entire test procedure from sampling inn the subject to instrument readout and data analysis been performed–e.g. within and between-run imprecision, inaccuracy, variance components attributable to each step in the method?

I find the concept of a yes/no readout in clinical chemistry and clinical pharmacology rather fantastic –almost pseudo-science.

It's like if the doctor says: "Well, we did a thyroid workup on your blood and the result is positive. However, the cholesterol came out negative".

Reply

91. **Christl Meyer** says:
December 4, 2020 at 11:00 am

Thank you. It´s the same with testing for "HIV".
I am fighting since more than 20 years for truth.
https://www.academia.edu/11649973/GENE_OR_VIRUS_IN_HEALTH_AND_DISEASE_ITS_ALL_ABOUT_SELF_AND_NON-SELF

Reply

92. **Michael** says:
December 4, 2020 at 2:37 pm

"The E gene primers also detect a broad spectrum of other SARS viruses."

Sollte da nicht "corona viruses" stehen anstatt "SARS viruses"?

Passt auch besser zum Rest des Paragraphs

"Still, SARS-CoV1 and SARS-CoV-2 have two highly specific genetic fingerprints,

which set them apart from the other coronaviruses. First, a unique fingerprint-sequence (KTFPPTEPKKDKKKK) is present in the N-protein of SARS-CoV and SARS-CoV-2 [13,14,15]. Second, both SARS-CoV1 and SARS-CoV2 do not contain the HE protein, whereas all other coronaviruses possess this gene [13, 14].”

Reply

Bobby says:
December 4, 2020 at 2:44 pm

Da hast du Recht, vielen Dank für den Hinweis. Wird umgehend ausgebessert online und nachgereicht bei Eurosurveillance.

Reply

93. 

Jack Leenders says:
December 4, 2020 at 2:46 pm

Deep respect for your profound work, fingers crossed for the impact 👍👉

Reply

94. 

Geam Aston Martin V8 Convertible 1978 says:
December 4, 2020 at 3:33 pm

I constantly emailed this blog post page to all my contacts, because if like to read it after that my contacts will too. https://anunturi-parbrize.ro/index.php?cauta=geam+aston+martin

Reply

95. 

Hans Kleber says:
December 4, 2020 at 4:04 pm

debunked again
https://twitter.com/MarionKoopmans/status/1333002771738611712

this time from a Virologist.

Reply


Bobby says:
December 4, 2020 at 4:38 pm

Sorry to disappoint you:

1) this mini-"thread" was not a "debunk", it was more of an "epicleptic episode" in my very honest opinion.
2) it seems like Marion Koopmans either didn't read our review report or has any other kind of Attention Deficit Problem – non of our concern, here is an extensive response by Kevin Mckernan: https://threadreaderapp.com/thread/1333846936332464129.html
3) I personally can't take anyone serious who references the low-tier "virology down under" blog by Ian M. Mackay, the analogy therefor would be: To reference Alex Jones & Infowars and declare it as a valid resource for any scientific discussion.

Reply

96. 
Contra el Encierro says:
December 4, 2020 at 7:45 pm

Dear authors,

Thank you so much for you work and for your very good idea in making this live web site (with comments): this is what is needed and this is what they do not want: an open in-depth debate. You are at the highest point of your life. Congratulations.

We have just published a full translation of your report in Spanish: https://contraelencierro.blogspot.com/2020/12/review-report-corman-drosten-et-al.html

We will follow comments and news in your site very closely. Thanks again:

https://contraelencierro.blogspot.com

Courage!

Reply

Bobby says:
December 4, 2020 at 8:12 pm

Thank you very much, we have added it under the "spanish" sub section: https://cormandrostenreview.com/press-voices-social-media/

Reply

97. 

Georg Bauer says:
December 4, 2020 at 8:17 pm

If the percentage of false positive with 97% is correct the whole system of political efforts in Europe and the USA may collapse.

Reply

98. 

Meikel says:
December 4, 2020 at 9:11 pm

Liebes Team!

Vielen Dank für Ihre Arbeit!
Ich hoffe sehr, dass sie zu einem kritischen Blick auf die in meinen Augen

strategielose Testung bzgl. SARS-Cov2 führt.
Ich kann nicht beurteilen, ob der Corman-Drosten-Test gut oder schlecht ist. Vielleicht musste es ja wirklich schnell gehen, vielleicht auch nicht (es scheint eher Letzteres).
Prof. Kämmerer erwähnte in der Sitzung 28 (?) des Corona-Ausschuss, dass sinngemäß „ein Praktikant den Test so eben bestanden hätte“.
Natürlich ist es fatal, einen Test mit der Schulnote 4- (so nenne ich da jetzt mal) einzusetzen, um solch gravierende und in die Grundrechte eingreifende Massnahmen zu begründen.
Soweit ich mich über PCRs informieren konnte, weiß ich, dass „sie quasi jede noch so geringe Kleinigkeit finden könnten“, bei geringer Prävalenz mehr false-positiv generieren und zur DIAGNOSTIK nicht gedacht waren.
Trotzdem sind PCRs sicherlich sehr gut, wenn man weiß wann und wie man sie einsetzt und ebenso versteht, dass Ergebnis zu interpretieren.
Letzteres scheint mir Letzteres das derzeit das größte Problem zu sein.
Wie sollte es denn normalerweise in medizinischer Diagnostik laufen?
Der Patient geht zum Arzt, weil er „Probleme“/Symptome hat!
Der Arzt macht seine Anamnese und mögliche körperliche Untersuchungen.
Daraus entsteht eine Hypothese bzgl. der Diagnose, die womöglich noch durch technische Diagnoseverfahren (hier die PCR) unterstützt oder verworfen werden kann.
Kommt nun z.B. ein Pat. in eine Praxis und klagt über die typischen SARS-CoV2 Symptome, wäre der Arzt natürlich geneigt oder verpflichtet einen Test zur Abklärung einzusetzen.
Wählt er/sie nun die PCR, erhält er folgende mögliche Information ...
a) Test negativ, es folgt wohl die logische Erklärung „KEIN CORONA“, der Pat hat eine andere Erkältungserkrankung.
b) Test Ergebnis POSITIV
b.1) Der Arzt erhält zum Ergebnis POSITIV auch den CT Wert mit z.B. 40 ...
Das Problem beginnt ... das Gesundheitsamt verzeichnet den Patienten als CORONA-infiziert, der CT von 40 sagt aber eigentlich ... nicht mehr krank oder „nur mal was abbekommen“ ... die Infektiösität ist laut dieser Studie

(https://www.nature.com/articles/s41467-020-19802-w) quasi 0. Es folgt trotzdem QUARANTÄNE! K1 Personen desgleichen!
b.2) CT ist bei pos. Ergebnis <30 (ich bin nett und nehme den vom RKI empfohlenen Wert) … ja, hier darf man annehmen, das der Pat. wohl infiziert ist bzw. die Viruslast Massnahmen wie eine Quarantäne rechtfertigen würden.

Jeder Test ist nur so gut, wie er im Gesamtkontext eingesetzt wird. Auch ein wesentlich besser „gebauter" PCR Test kann immer noch falsch eingesetzt werden, wenn die Fragen „Wann und wen teste ich?" und „Wie interpretiere ich das Ergebnis inkl. CT?" in Bezug auf die Anamnese des behandelnden Arztes nicht bedacht werden! Hier scheinen mir noch viel größere Fallstricke zu lauern.
Problematisch an dem Corman-Drosten-Test wäre für mich auch, sollte er wirklich so „schlecht" sein, dass er als GOLD-Standard definiert ist.
Jeder eigentlich „bessere" Test wird durch seine Abweichung zum GOLD-Standard somit als schlecht bewertet.
So hätte wohl auch der AntiGen-Test eine deutlich bessere Reputation, wenn er nicht mit den Positivraten des Drosten-PCR verglichen werden würde. Dazu z.B. auch jenen Diskussion (https://infekt.ch/2020/10/covid-19-antigen-test-schlechter-als-pcr-wirklich/)oder auch die Aussagen von Frau Prof. Kämmerer im Corona-Ausschuss.
Nochmals danke ich Ihnen allen für die Zeit und Mühen die Sie in dieses Paper gesteckt haben! Diese Arbeit ist einer der letzten Hoffnungsschimmer, die ich noch habe, dass sich „die Dinge" noch ändern könnten.

Reply

99. **steve gangloff** says:
December 4, 2020 at 10:20 pm

Can you provide a PDF of this document – please forward to my email below.
thanks

Reply

Bobby says:
December 5, 2020 at 5:45 am

You can get the PDF here: https://cormandrostenreview.com/downloads/

Reply

100. **Wolfgang E.** says:
December 5, 2020 at 5:09 am

Thank you for doing science!

Reply

101. **Emanuel E. Garcia, MD** says:
December 5, 2020 at 6:56 am

An exemplary scientific critique of the subject matter that deserves worldwide attention. It is abundantly clear to me that the so-called pandemic was driven by non-scientific agendas. Your analysis of the Corman-Drosten report, unlike most of what we get about COVID, represents real science. Thank you.

Reply

102. **五十嵐敬冶** says:
December 5, 2020 at 8:28 am

私も、このレポートが発表される以前に、ドロステンのRT-PCR法には「重大な欠陥」があると気付きました。
彼のプロトコルは2003年のSARSウィルス株のゲノムを参照して策定しています。
中国チームが採取したという検体のゲノムではありません。
「推測による検出方法」なのです。

それ故に、(一人でも多く「陽性者」を捕まえられるように。自説プロトコルが結果を示せるように。)必要以上にCt値(増幅サイクル数)が高く(45に)設定されているのです。

ModEdit: Translation:

Before this report was published, I also realized that Drosten's RT-PCR method had "serious flaws."
His protocol is based on the genome of the 2003 SARS virus strain.
It is not the genome of the sample collected by the Chinese team.
It is a "guessing detection method".
Therefore, the Ct value (amplification cycle number) is set higher (to 45) than necessary (so that as many "positive people" as possible can be caught. So that the self-explanatory protocol can show the result.).

Reply

103. **Charles** says:
December 5, 2020 at 11:01 am

Hi,

Thank you for the brave work you are doing, hopefully you can answer these questions i have ?

At Amphia Hospital and Bravis Hospital, total
nucleic acids were extracted for RT-PCR after an external
lysis step (1:1 with lysis binding buffer; Roche Diagnostics,
Almere, Netherlands), using MagnaPure96 (Roche) with
an input volume of 500 µL and output volume of 100 µL.

The extraction was internally controlled by addition of a
known concentration of phocine distemper virus (PDV) ??.

Is this a normal procedure that Koopmans et.al. use ?

And what are they selling at https://www.european-virus-archive.com/virus/human-2019-ncov-isolate if there is no Sars-Cov-2 isolate

https://www.european-virus-archive.com/evag-portal/evag-partners/rivm ?

Thank you and we keep monitoring them 😉

Charles..

Reply

1. **Robert** says:
   December 5, 2020 at 4:28 pm

   I have a hard time calling this an isolate, you?
   "Culture Medium: DMEM (Dulbecco's Modified Eagles Medium) (PAA, Cölbe, Germany) with 4.5 g/L Glucose (PAA) supplemented with 10% Foetal Bovine Serum (PAA), 1% Penicillin/Streptomycin 100 x concentrate (Penicillin 10000 U/mL, Streptomycin 10 mg/ mL) (PAA), 1% L-Glutamine 200 mM, 1% Sodium Pyruvate 100 mM (PAA), 1% MEM nonessential amino acids (NEAA) 100 x concentrate (PAA) – Subculture routine: Detachment with an EDTA/trypsin mixture (PAA)"

   Reply

   1. **Jan** says:
      December 8, 2020 at 3:42 pm

      Can you explain this for simple humans if possible ? 🙂

      Reply

104. **Charles** says:
     December 5, 2020 at 12:05 pm

Running on 45 cycles:

https://www.researchgate.net/publication/342651957_COVID-19_in_health-care_workers_in_three_hospitals_in_the_south_of_the_Netherlands_a_cross-sectional_study

At Amphia Hospital and Bravis Hospital:
Amplification was done in a 7500SDS (Thermofisher) with a cycling profile of 5 min at 50°C, 20 s at 95°C, 45 cycles of 3 s at 95°C, and 30 s at 58°C.

At Elisabeth-TweeSteden Hospital:

Amplification with Rotorgene (QIAgen) consisted of 5 min at 50°C and 15 min at 95°C followed by 45 cycles of 15 s at 95°C, 30 s at 60°C, and 15 s at 72°C.

Partly based on these data, SARS-CoV-2 was concluded to have already spread in the population in the province of North Brabant, which led to a change of policy, in which containment measures were complemented by targeted physical distance measures, starting in the south of the Netherlands initially and later comprising the whole country.

Reply

105. **RJ** says:
December 5, 2020 at 2:22 pm

Fix your zip file. The dcox and pdf files will not extract!

Reply

Bobby says:
December 5, 2020 at 2:51 pm

Thank you for pointing out and sorry for the inconvenience. The file names in the ZIP files were too long and it didn't matter on my Mac System. This has been fixed now here:

https://cormandrostenreview.com/downloads/

And also all supplementary hyperlinks have been fixed here in the reference list:

https://cormandrostenreview.com/report/

Reply

106. **оксана** says:
December 5, 2020 at 5:08 pm

огромная благодарность за проделанную работу!теперь все пазлы и сложились.

ModeEdit: Translation:

huge gratitude for the work done! now all the puzzles have come together.

Reply

107. **Su Obreen** says:
December 6, 2020 at 7:38 am

Finally! What 'VIRUSWAARHEID.NL' has already established from the start of the COVID19 gate is now being brought to light by other celebrities / prominent figures.

Reply

108. **jac** says:
December 6, 2020 at 10:23 am

Deep respect for your work.

Reply

109. **E** says:
December 6, 2020 at 10:47 am

FYI in this article the “friend” of P Borger claim that his (Marc Bonte UmcU) rapid test has 100% specificity.

Please stop this ongoining noncense!

https://www.medrxiv.org/content/10.1101/2020.10.16.20214189v1
https://www.medrxiv.org/content/10.1101/2020.10.16.20214189v1

Reply

1. **Joerg** says:
December 7, 2020 at 3:41 pm

Hello E.

What do you mean with your comment?

First: definitions:
“In medical diagnosis, test sensitivity is the ability of a test to correctly identify those with the disease (true positive rate),
whereas test SPECIFICITY is the ability of the test to correctly identify those without the disease (true negative rate)”

Second: So in your cited paper the authors state [as I understand] that in all

cases a negative antibody Covid19 Rapid assay was also in the RT-PCR test negative [95%CI: 99.7-100%].

What should be wrong with that? Or what exactly is “ongoing nonsense” in your opinion? I don’t get it?

Kind regards Joerg

Reply

2.  **Joerg** says:
December 7, 2020 at 4:12 pm

Sorry, I try to specify better:

There are four cases:
1) PCR + and AB + (ca. 90%) SENSITIVITY, true positive rate
2) PCR + and AB – (ca. 10%) false negatives related to AB-test
3) PCR – and AB – (100%) SPECIFICITY, true negative rate
4) PCR – and AB + (0%) false positives related to AB-test

Reply

110.  **ale** says:
December 6, 2020 at 1:23 pm

In the meantime it would b e unfair to all concerned to comment or discuss further untill we have looked at all the issues.(editorial note Eurosurvaillance.) Dr.Peter Borger”s opinion on that”?
And I guess you are expecting a second and about the same letter from ECDC in the very, very far future?.

Reply

Bobby says:
December 6, 2020 at 2:20 pm

Irrelevant, this was always thought as transparent and public extern review report. Otherwise it would have vanished unnoticed. Scientific additions / remarks are commented and that is an integral part of scientific discussions, that is the core reason why science has brought prosperity to mankind in the past, in the present and also in the future. Present time developments already indicate that future review processes will be more transparent and most probably hard to corrupt through decentralized technology & review process-procedures.

Further: Eurosurveillance had refused to make the review process transparent concerning the CD-paper, on two pages they explained why they can't reveal the review process protocol of the CD-paper, and none of the reasons given was in my honest opinion a valid one. In case of "fear" of revealing identities: They could have retracted names, and the rest of the necessary information could have been made available, but they refused to do so, which is a direct anti-thesis to common scientific discussions and transparent review processes. How would you check otherwise whether a review process was valid and clean if not by revealing the review process protocol and by inspecting the protocol for irregularities? Just by saying: "It was ok! Believe us!" ?

Further Note #2: The consequences of RT-qPCR-mass tests include the entire destroyment of whole economies, people's freedom is taken, death through restrictions, tragedies in elderly homes, ...

I think facing these consequences here, it is more than a valid step, to make the review report a) public and b) actively discuss it with the scientific community. It is in the interest of all involved, also Eurosurveillance.

We are far beyond the tipping point here to get lost in unrelevant

formalities. We are not revealing the next big thing in science here, we are discussing the flaws of currently approved publications & protocols.

If you want to educate yourself about the consequences of False Positives, head over to our guest article, with references given: https://cormandrostenreview.com/false-positives-consequences/

I have forwarded your remarks to Dr. Peter Borger, but I think I have answered it for him – he would give you most probably the same answer.

Another fact: Eurosurveillance has set-up a comments section now too at their journal portal, it's new. Is it in reaction to our approach to ensure more discussion and transparency?

Reply

1. **ale** says:
   December 7, 2020 at 1:22 pm

   Naar mijn eerlijke mening denk ik dat wel. net zoals ik denk dat de transparantie beneden peil is in dit gehele gebeuren.
   U had een bezwaar mogelijkheid tegen het besluit om niet te openbaren. Heeeft u deze gebruikt, zo, nee, waarom niet?

   Kunt u mij zeggen waarom mijn reply onder nr84 op Robert niet werd geplaatst? Dubbel naam/mail gebruik misschien?
   Als het geplaatst kan worden hoef ik daarover geen uitleg maar naar een inhoudelijk reactie ben ik erg benieuwd.
   Freonlike groet oan dr.Peter Borger.

   Reply

111. **Arturas Minajevas** says:
December 6, 2020 at 2:11 pm

Thanks alot from Lithuania!

Reply

112.  **Joerg** says:
December 6, 2020 at 3:43 pm

Hallo Bobby,
meine zwei Kommentare vom 05.12. wurden geloescht? Warum?
Falls es kein Versehen war, bitte auch alle anderen Kommentare von mir loeschen!
Vielen Dank im Voraus und alles Gute
Joerg

Reply

 **Bobby** says:
December 6, 2020 at 6:00 pm

Hi, entweder ist mir hier ein Versehen passiert oder es ist ein WordPress Template Fehler beim Comments Feld? Ich wurde gestern überschwemmt von spam bots, und es kann sein, dass mir da ein Fauxpas passiert ist und deine Comments dazwischengelandet sind beim Spam-Entfern-Vorgang. Kannst du deine gelöschten Kommentare nochmal rekonstruieren hier und mir vielleicht Comment Nummer sagen, dann setze ich sie dort als “Mod Edit” wieder ein.

Edit: Sie waren noch intakt im Spam Trash Can, wurden wieder hergestellt, sorry for that!.

Reply

1.  **Joerg** says:
December 7, 2020 at 3:13 pm

Danke, muss mehr Fragen und weniger Vermuten 😉

Tipps fuer die naechsten Beitraege/Blogs:
1) Eine Funktion fuer “neueste 10-20 Beitraege” in einer Spalte rechts oben oder ganz unten.

2) Da es ein moderierter Blog ist (Du und andere?), ist es legitim zwischen ARGUMENTEN und MEINUNGEN zu sortieren. Bei kontroversen Themen mischt sich das ja meistens stark und fuehrt zur Unuebersichtlichkeit bzw lenkt von urspruenglicher Intention Argumente zu einem Fachthema zu diskutieren ab (gibt’s auch als Troll-Angriffs-Strategie).
Es waere also moeglich ganz krude Aussagen (aber auch die vielen “prima, weiterso” Bekundungen auf eine “Plauderei-Version” zu diesem Blog-Post zu schieben (“Review report Corman-Drosten et al. Eurosurveillance 2020 Chitchat” und die Fachargumente hier zu lassen …
Aber macht sicher auch viel Arbeit … Hoffentlich lohnt es sich fuer Euch (die viele Arbeit).

LG Joerg

Reply

113. **Steffen Jurisch** says:
December 7, 2020 at 8:51 am

Dezember, 7., 2020 Danke für Ihre Arbeit. Leider interessiert diese die Psychoparhen von Politiker keinen Deut – sie machen weiter und drehen die faschistoide Diktaturschraube noch fester an und die Masse bejudelt es noch, weil sie dumm und zu faul ist, sich zu informieren.
Ich hoffe wirklich das der Spuk bald ein Ende hat und die Gerichte sämtliche Politiker und Mitläufer zur Verantwortung zieht…

Reply

114.  **Jo-Anne van Westing** says:
December 7, 2020 at 9:30 am

Goedemorgen, ik ben zooooo blij met alle artsen/wetenschappers die wat van zich laten horen. Ik merk in mijn eigen omgeving dat mensen moe van me worden als ik weer met iets nieuws kom dat aangeeft dat het allemaal niet klopt wat er nu gaande is. Mijn vreemde onderbuik gevoel startte met het uit de handel halen van het boek betreft vaccinaties.

Ik stuur dit beoordelingsrapport naar een paar huisartsen in mijn omgeving. Misschien kunnen meer mensen dat doen?

Ik vind het zo erg voor jongeren...
Ik hoop, ik hoop, ik hoop...

Reply

115.  **Daniel** says:
December 7, 2020 at 6:50 pm

I hope, I pray, I stand and I fight in heart and spirit for our children and for life!I pray that all doctors who are not compromised and scared step out and forward so together we can make an end to this horrid nightmare imposed to mankind by a select club of psychopaths. Together with the Notice of Liability I believe we can take back our freedom and lives!

Reply

116.  **Marrie** says:
December 7, 2020 at 8:32 pm

It's easier to fool the people than to convince them that they have been fooled.

Reply

117. **RALPH JACKSON** says:
December 8, 2020 at 6:20 pm

An excellent report. Our British Government should be taking to the War Tribunal for crimes against its citizens

Reply

118. **Dave** says:
December 8, 2020 at 10:18 pm

Thank you for your excellent work.

Here's an interesting post highlighting some of the problems with the CDC primers earlier this year:

https://tomeraltman.net/2020/03/03/technical-problems-COVID-primers.html

Reply

119. **Pjotr** says:
December 9, 2020 at 1:45 pm

This is a review of the paper and the therein described method, fine. But, for example in Germany, about 190 test laboratories are delivering PCR results. Do they all use the Corman test as it is described in the Corman paper? I don`t think so. I assume they took it as starting point and modified it. Therefore, it would be intersting to get the test methods from a number of laboratories and compare them,i.e., look at the primers, the cycle numbers and CT etc., they are using. The authors of the CormanDRostenReview should report the outcome of such a comparison of test methods. In addition, was cross laboratory validation done between certified laboratories? Does anyone have a report on this? A cross lab validation could be, e.g., lab A analyzed a large number of samples and sends

them to further laboratories B, C, D etc. for blinded analysis (not knowing the results of lab A). Labs B, C, D etc. send their results to lab A. Lab A compares the results, i.e., what is the %agreement on positive and negative PCR results between the labs. Any data available on such a comparison?

Reply

120. **Charles** says:
December 9, 2020 at 2:00 pm

En natuurlijk is geld weer de drijfveer achter de hele scam, !

https://www.ftm.nl/artikelen/vrijgevestigde-artsen-coronatesten

De laboratoria worden geleid door artsen-microbioloog.
Naar nu blijkt zijn de grote hoeveelheid coronatesten uiterst lucratief voor de artsen die vrijgevestigd zijn.
Deze geldstroom is tot op heden verborgen gebleven.

Bij welke ziekenhuizen en artsen de honderden miljoenen precies beland zijn, is een zorgvuldig bewaard geheim. De NVMM, het RIVM, het LCDK en de GGD'en weten precies hoeveel testen elk lab heeft verricht.

De labs zijn namelijk wettelijk verplicht dat te melden aan de GGD'en. Ook is er sinds 1 juni een IT-systeem (Coron-IT) waarbinnen de labs zulke data doorgeven aan de GGD en het LCDK. Bovendien houden de labs het RIVM op de hoogte met 'virologische dagstaten'.

Daardoor is eenvoudig te berekenen hoeveel omzet elk lab heeft gedraaid, en zou je schattingen kunnen maken van de extra inkomsten van de betrokken artsen. Maar al deze partijen weigeren transparant te zijn over de besteding van honderden miljoenen euro belastinggeld.

Zie ook https://www.ftm.nl/artikelen/kluytmans-belang-coronatesten

Let op:

de volgende lucratieve scam gaan ze draaien met deze nieuwe sneltesten:
In Nederland heeft het OMT [..] beoordeeld dat de Panbio COVID-19-Ag rapid test (Abbott), de SARS-CoV-2 Rapid Antigen Test (Roche), BD Veritor COVID test (Becton Dickinson), Sofia SARS Antigen FIA (Quidel) en Standard F-Covid-19 Ag (SD Biosensor) gebruikt kunnen worden bij mensen met klachten in teststraten.

KASSA!

Reply

121. **Ali** says:
December 9, 2020 at 9:34 pm

Your comment displays the very need for a Standard Operating Procedure (SOP) for all labs performing this diagnostic. Just one of the flaws found.

Reply

122. **Pjotr** says:
December 10, 2020 at 11:05 am

SOPs are written by the individual labs themselves, because SOPs must reflect the methods and processes of the lab. A scientific paper describes a method but does not provide an SOP

Reply

123. **Thomas** says:
December 10, 2020 at 11:43 am

Here a link to a study which strongly indicates that there was no (adequate) peer review:

http://www.aukema.org/2020/12/meta-data-analysis-at.html

It says:
To assess commonality in the review and acceptance process at eurosurveillance.org, the author collected and analysed meta-data for all 1,595 publications since 01-Jan-2015…
…Except for this one Research article (on 22-jan-2020)(the CormanDrosten Paper, Author's note), no other article has ever been reviewed and accepted within a single day since 2015."

Reply

124.  **Harold** says:
December 10, 2020 at 4:44 pm

Drosten on the PCR Test in 2014:

"Ja, aber die Methode ist so empfindlich, dass sie ein einzelnes Erbmolekül dieses Virus nachweisen kann. Wenn ein solcher Erreger zum Beispiel bei einer Krankenschwester mal eben einen Tag lang über die Nasenschleimhaut huscht, ohne dass sie erkrankt oder sonst irgend etwas davon bemerkt, dann ist sie plötzlich ein Mers-Fall. Wo zuvor Todkranke gemeldet wurden, sind nun plötzlich milde Fälle und Menschen, die eigentlich kerngesund sind, in der Meldestatistik enthalten. Auch so ließe sich die Explosion der Fallzahlen in Saudi-Arabien erklären. Dazu kommt, dass die Medien vor Ort die Sache unglaublich hoch gekocht haben."

https://amp2.wiwo.de/technologie/forschung/virologe-drosten-im-gespraech-2014-der-koerper-wirdstaendig-von-viren-angegriffen/9903228.html

Reply

125.  **Sam Laurey** says:
December 10, 2020 at 6:01 pm

Now as Mr. Drostens PCR test prooved as nonsense, what are the consequences now?
How to bring this wisdom down to practice? Soon?
Kind regards and thanks a lot
Or better late then never

/Sam Laurey

Reply

1. **Nathan** says:
December 11, 2020 at 7:17 am

That's what I'd like to know. Where to from here? Rather than just criticising a paper, are there any specific proposals for a better test, which can be clinically tested on symptomatic people and asymptomatic people who both test positive via PCR? Or is it a foregone conclusion the virus isn't a threat beyond other viruses humans have been living with?

Reply

126. **Nice** says:
December 11, 2020 at 12:06 am

I did not realise the Gates foundation had funded in March 2020, to the tune of $250,000 Drostens Charite University Berlin??? (Merkel's most trusted scientist)

https://www.gatesfoundation.org/How-We-Work/Quick-Links/Grants-Database/Grants/2020/03/INV-005971

Reply

127. **Nedas** says:
December 11, 2020 at 11:32 pm

Guys, you got me involved really, I am amazed at how far all can go and how long the flaws are not going wide public and rejected by mass media. Within hours managed to find interesting leads to information, one being legally binding by Portugal court decision (available in translation to EN see extract of the case
1783 / 20.7T8PDL.L1-3
Reporter: MARGARIDA RAMOS DE ALMEIDA
Descriptors: HABEAS CORPUS
INTEREST IN ACTING
SARS-COV-2
RT-PCR TESTS
DEPRIVATION OF
ILLEGAL DETENTION)
Your report being mentioned by Russia Today (not the best brand in the media business, but quite popular and pro-russian)
https://www.rt.com/op-ed/508383-fatal-flaws-covid-test/
Canadian media fresh news:
https://www.ottawabusinessdaily.ca/2020/12/08/evidence-emerges-that-covid-tests-are-faulty-fda-and-cdc-admit-as-much/

Reply

128.  **Nedas** says:
December 11, 2020 at 11:49 pm

Dear Team, thanks for such scrutiny job over the january paper. I am amazed at how silly? greedy? indiferent? lazy? the decision makers can be in order to let this flaw continue.

Hardly believe big media or politicians would make fast steps, but court decisions are binding :). This fresh court case from Portugal is important I think in further development of cases against illegal detainment and possible reviewal of tests applied. Group of German tourists won a case agains Portugese

autorities:
Judgment of the Lisbon Court of Appeal
Process:
1783 / 20.7T8PDL.L1-3
Reporter: MARGARIDA RAMOS DE ALMEIDA
Descriptors: HABEAS CORPUS
INTEREST IN ACTING
SARS-COV-2
RT-PCR TESTS
DEPRIVATION OF
ILLEGAL DETENTION

One of the reasons why they won:
.In view of the current scientific evidence, this test is, in itself, unable to determine, beyond reasonable doubt, that such positivity corresponds, in fact, to a person's infection with the SARS-CoV-2 virus, for several reasons. , of which we highlight two (to which the issue of the gold standard is added, which, due to its specificity, we will not even address):
For this reliability depend on the number of cycles that make up the test;
For this reliability depend on the amount of viral load present.

Reply

129.  **Dr R.A. Wilson** says:
December 12, 2020 at 10:07 am

Why not submitting a letter to the editor to stimulate debate?

Reply

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