



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.



Short communication

Ad hoc laboratory-based surveillance of SARS-CoV-2 by real-time RT-PCR using minipools of RNA prepared from routine respiratory samples

Anna M. Eis-Hübinger^a, Mario Hönemann^b, Jürgen J. Wenzel^c, Annemarie Berger^d, Marek Widera^d, Barbara Schmidt^c, Souhaib Aldabbagh^a, Benjamin Marx^a, Hendrik Streeck^a, Sandra Ciesek^d, Uwe G. Liebert^b, Daniela Huzly^e, Hartmut Hengel^e, Marcus Panning^{e,*}

^a Institute of Virology, University of Bonn, Faculty of Medicine, Bonn, Germany

^b Institute of Virology, Medical Faculty, University of Leipzig, Leipzig, Germany

^c Institute of Clinical Microbiology and Hygiene, Regensburg University Hospital, Regensburg, Germany

^d Institute of Medical Virology, University Hospital, Goethe University Frankfurt am Main, Frankfurt, Germany

^e Institute of Virology, University Medical Center Freiburg, Faculty of Medicine, University of Freiburg, Freiburg, Germany

ARTICLE INFO

Keywords:

SARS-CoV-2

RT-PCR

Minipools

Surveillance

Laboratory

ABSTRACT

Background: A novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), emerged in China in late 2019 and subsequently caused a pandemic. Surveillance is important to better appreciate this evolving pandemic and to longitudinally monitor the effectiveness of public health measures.

Objectives: We aimed to provide a rapid, easy to establish and cost-effective laboratory-based surveillance tool for SARS-CoV-2. **Study design:** We used minipools of RNA prepared from nucleic acid extractions of routine respiratory samples. We technically validated the assay and distributed the protocol within an informal network of five German university laboratories.

Results: We tested a total of 70 minipools resembling 700 samples shortly before the upsurge of cases in Germany from 17.02.2020 to 10.03.2020. One minipool reacted positive and after resolution one individual sample tested SARS-CoV-2 positive. This sample was from a hospitalized patient not suspected of having contracted SARS-CoV-2.

Conclusions: Our approach of a laboratory-based surveillance for SARS-CoV-2 using minipools proved its concept is easily adaptable and resource-saving. It might assist not only public health laboratories in SARS-CoV-2 surveillance.

1. Background

As of 11 March 2020, WHO declared COVID-19 a pandemic [1]. Early case detection is crucial to contain the pandemic and symptom-based case definitions have been set up in many countries worldwide. However, there is evidence that transmission chains can be initiated by asymptomatic cases or only mildly diseased COVID-19 patients [2]. These cases will be missed by currently recommended symptom-based case definitions and may lead to unrecognized local spread, which has been seen in Italy, Iran and more recently in the US. To limit the pandemic an aggressive public health response has been set up in many countries worldwide. However, a resurgence of cases is anticipated whenever the strict public health isolation measures will be lifted. Therefore, one of the biggest challenges and unresolved issues for public health will be the surveillance and rapid identification of SARS-

CoV-2 in the time between epidemic peaks.

2. Objectives

To rapidly identify unrecognized cases in hospitals in an efficient, resource-saving and cost effective manner we propose an *ad hoc* laboratory-based surveillance approach for SARS-CoV-2. It is based upon minipool (MP) testing of nucleic acid preparations of respiratory samples submitted to laboratories for routine diagnostics.

3. Study design

The workflow comprises individual nucleic acid (NA) extraction of respiratory samples, pooling of extracted NA samples in batches of 10 and SARS-CoV-2 specific real-time RT-PCR. In a first step, we analyzed

* Corresponding author at: Institute of Virology, University Medical Centre Freiburg, Hermann-Herder-Str. 11, 79104, Freiburg, Germany.

E-mail address: marcus.panning@uniklinik-freiburg.de (M. Panning).

<https://doi.org/10.1016/j.jcv.2020.104381>

Received 9 April 2020; Accepted 19 April 2020

1386-6532/© 2020 Elsevier B.V. All rights reserved.

the impact of minipool (MP) testing in batches of 10 samples per pool. Nucleic acid was extracted from 200 µL respiratory specimen (pharyngeal swabs in viral transport medium, sputum, broncho-alveolar lavage fluid) using the MinElute Virus kit (Qiagen, Hilden, Germany) on the QIAcube system as recommended. Elution was done in a volume of 100 µL. For setting up MP, 5 µL of each individual NA preparation was combined in pools of 10 (dilution factor of 10). We retrieved 40 left-over NA preparations of respiratory samples from 2019 representing a variety of non-SARS-CoV-2 viruses from our local biobank in Freiburg and set up MP. We tested four MP using the same RT-PCR as for individual patient testing as described [3]. To exclude possible unspecific reactions of the MP procedure these MP were also tested using the SARS-CoV-2 specific real-time RT-PCR as described below. To determine the analytical sensitivity of the MP approach, we used *in vitro*-transcribed RNA standards for the E gene obtained by the European virus archive global (EVAg), <https://www.european-virus-archive.com>, and the SARS-CoV-2 E gene RT-PCR assay as described [4]. RT-PCR was done on an ABI 7500 instrument (Applied Biosystems, Weiterstadt, Germany). We spiked different *in vitro*-transcribed RNA concentrations in stored NA preparations of respiratory samples from 2019 and established MP. Replicate testing was done to determine the limit of detection (LOD) as described [4]. Finally, we used NA preparations from three actual SARS-CoV-2 cases in Freiburg (containing 4×10^4 copies/mL; 3.2×10^7 copies/mL; 1.6×10^7 copies/mL, respectively) and set up three MP each containing one SARS-CoV-2 positive NA preparation and retested these samples.

We distributed the workflow within an informal network of 5 German laboratories (Table 2). All sites are tertiary care centers with a total of 1.600 (site A), 1.300 (site B), 1.400 (site C), 840 beds (site D), and 1.500 (site E), respectively.

Ethical approval for this study was not required since all activities are according to legal provisions defined by the German Infection Protection Act (IfSG). All samples have been submitted for routine patient care and diagnostics and written informed consent has been obtained by each patient. All data used in the current study was anonymized prior to being obtained by the authors.

4. Results

We were able to detect all non-SARS-CoV-2 pathogens in MP which tested positive in individual RT-PCR (Table 1). No unspecific reactions were seen in these samples from 2019 using the SARS-CoV-2 RT-PCR. The LOD for the MP approach was 48 copies per reaction (95 % confidence interval: 33–184) (Fig. 1). Testing of MP spiked with SARS-CoV-2 RNA showed that except for the MP containing the lowest concentrated sample both other MP tested SARS-CoV-2 RNA positive.

We prospectively analyzed 42 MP comprising 420 samples using the SARS-CoV-2 E gene assay. We used all available NA samples which had been sent for routine diagnostics to the Institute of Virology in Freiburg excluding samples with a specific request for SARS-CoV-2 diagnostics from 17.02.2020 to 10.03.2020 (Fig. 2). One out of 42 MP tested positive. The MP was resolved and individual testing confirmed SARS-CoV-2 infection in one individual patient.

Invited laboratories of our informal network rapidly adopted the MP screening strategy and a total of 70 MP were tested from 17.02.2020 to 10.03.2020 (Fig. 2). At sites B to E all MP tested SARS-CoV-2 negative. Of note, site B provided another 4 MP artificially spiked with SARS-CoV-2 positive NA samples from actual cases to further validate the procedure. The Ct-values of SARS-CoV-2 RT-PCR in individual patient samples were 26, 26, 15, and 35, respectively. All artificially spiked MP tested SARS-CoV-2 positive and Ct-values were 29, 29, 18, and 38 indicating a dilution factor of 10 as expected.

5. Discussion

We report a diagnostic workflow for the laboratory-based

Table 1

Detection of respiratory viruses in samples using individual RT-PCR and in four minipools of 10 individual samples (A1 – A4), Freiburg, Germany, December 2019.

Patient sample	Pathogen	Ct-value (Individual patient analysis)	Minipool	Pathogen	Ct-value (Minipool analysis)
1	Influenza B virus	29	A1	Influenza B virus	25
2	negative			negative	
3	negative			negative	
4	negative			negative	
5	negative			negative	
6	negative			negative	
7	negative			negative	
8	negative			negative	
9	negative			negative	
10	negative			negative	
11	negative		A2	negative	
12	RSV ^a	25		RSV	29
13	negative			negative	
14	negative			negative	
15	Influenza A virus	33		Influenza A virus	34
16	negative			negative	
17	negative			negative	
18	negative			negative	
19	negative			negative	
20	negative			negative	
21	negative		A3	negative	
22	Rhinovirus, HMPV ^b	24, 25		Rhinovirus, HMPV	31, 30
23	negative			negative	
24	Adenovirus	25		Adenovirus	29
25	negative			negative	
26	negative			negative	
27	negative			negative	
28	RSV	32		RSV	35
29	Negative			negative	
30	negative			negative	
31	negative		A4	negative	
32	RSV	34		RSV	> 35
33	Influenza A virus	37		Influenza A virus	33
34	negative			negative	
35	Influenza A virus	32		Influenza A virus	29
36	negative			negative	
37	negative			negative	
38	negative			negative	
39	negative			negative	
40	HMPV	32		HMPV	34

^a RSV: respiratory syncytial virus.

^b HMPV :human metapneumovirus.

Table 2

Number of minipools tested for SARS-CoV-2 RNA at five different sites, Germany, February – March 2020.

Laboratory site	Minipools tested (n =)	Individual samples (n =)	SARS-CoV-2 RT-PCR positive patients (n =)
A (Freiburg)	42	420	1
B (Bonn)	6	100	0
C (Leipzig)	9	90	0
D (Regensburg)	8	80	0
E (Frankfurt)	5	70	0
Total	70	700	0

surveillance of SARS-CoV-2 in a rapid and cost effective manner. Shortly after the identification of SARS-CoV-2 specific real-time RT-PCR protocols were set up and have been distributed worldwide [4,5]. The availability of rapid and reliable diagnostics for early case detection is

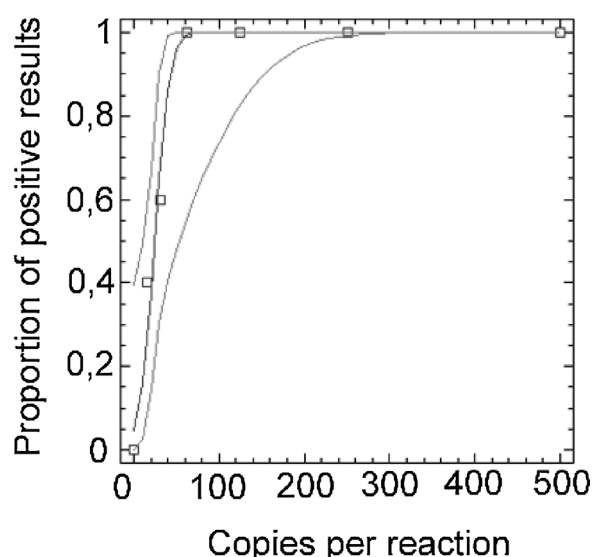


Fig. 1. Probit analysis of SARS-CoV-2 RNA detection rate (y axes) in relation to viral RNA concentration at different copy numbers per reaction (x axes).

instrumental in an outbreak scenario [6]. From a public health perspective an easy to establish and cost effective laboratory-based screening strategy may assist in rapid case detection, surveillance and ultimately in a better understanding of this epidemic [7]. Technically, this can be done in parallel using samples from routine diagnostics which are subsequently tested for SARS-CoV-2 RNA [8]. However, with the circulation of influenza cases across Europe merging with the upsurge of SARS-CoV-2 many laboratories may lack the capacity and resources to perform additional single patient sample testing for SARS-CoV-2. In addition, a shortage of PCR reagents has become an issue of concern as huge numbers of additional SARS-CoV-2 molecular tests are performed globally in a relatively short period of time. To minimize work load, resources and costs a pooling approach of nucleic acid extractions might be considered. We used the assay described by Corman et al. and were able to demonstrate an almost exactly 10-fold higher LOD which is due to MP related dilution factor of 10 [4]. Data from China showed SARS-CoV-2 RNA concentrations in the range of $1,5 \times 10^4$ to $1,5 \times 10^7$ copies per milliliter giving rise to the notion that the MP procedure will be sensitive enough for most clinical samples [9]. Another study of only mildly diseased patients showed an average of $3,4 \times 10^5$ copies per swab. However, at the moment there is a lack of comprehensive information on viral RNA concentrations in mildly diseased or asymptomatic cases. Critically, we were not able to detect one low concentrated samples diluted into a MP, which was close to the LOD of the pooling procedure.

Networks are paramount for an efficient response to emerging infections and we aimed to provide an easy to implement workflow [4,10]. We set up an informal network and were able to test a total of 70 MP covering different geographic regions of Germany. In perspective, this approach can be set up rather easily e. g. by public health

laboratories, can be done on a daily basis and at reduced costs compared to individual patient testing. It could allow for longitudinally monitoring the effectiveness of contact reduction measures at the population level and early detection of epidemic waves.

In light of an evolving SARS-CoV-2 epidemic and the possibility of unrecognized spread within the population we propose a rapid and straightforward screening strategy for SARS-CoV-2. This approach proved its principle and might assist public health laboratories in Europe and elsewhere to rapidly detect SARS-CoV-2 cases which might otherwise remain undetected.

Ethical considerations

All samples have been submitted for routine patient care and diagnostics. Ethical approval for this study was not required since all activities are according to legal provisions defined by the German Infection Protection Act (IfSG). Written informed consent has been obtained by each patient. All data used in the current study was anonymized prior to being obtained by the authors.

Funding

None.

CRediT authorship contribution statement

Anna M. Eis-Hübinger: Investigation, Data curation, Writing - review & editing. **Mario Hönemann:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Jürgen J. Wenzel:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Annemarie Berger:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Marek Widera:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Barbara Schmidt:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Souhaib Aldabbagh:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Benjamin Marx:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Hendrik Streeck:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Sandra Ciesek:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Uwe G. Liebert:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Daniela Huzly:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Hartmut Hengel:** Investigation, Formal analysis, Methodology, Writing - review & editing. **Marcus Panning:** Conceptualization, Supervision, Writing - review & editing.

Declaration of Competing Interest

All authors have no conflict of interest to declare.

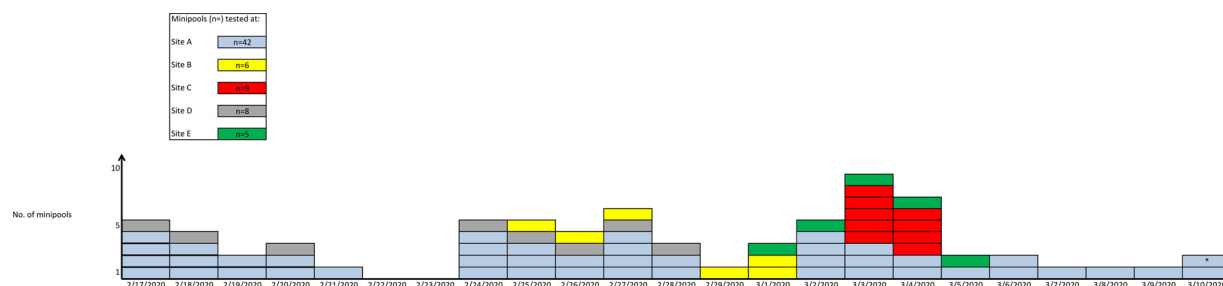


Fig. 2. Number of minipools tested by date at five sites in Germany, February-March 2020. The star indicates the first SARS-CoV-2 RNA positive minipool detected.

Acknowledgements

We are grateful to Claudia Ehret, Monika Häffner, Verena Schillinger and the team in Freiburg and the entire molecular diagnostic teams in Bonn, Frankfurt, Leipzig, and Regensburg for expert technical assistance.

References

- [1] World Health Organization, Director-General's Opening Remarks at the Media Briefing on COVID-19 - 11 March 2020, (2020).
- [2] R. Li, S. Pei, B. Chen, Y. Song, T. Zhang, W. Yang, et al., Substantial undocumented infection facilitates the rapid dissemination of novel coronavirus (SARS-CoV2), *Science* (2020), <https://doi.org/10.1126/science.abb3221>.
- [3] D. Huzly, K. Korn, S. Bierbaum, B. Eberle, V. Falcone, A. Knoll, et al., Influenza A virus drift variants reduced the detection sensitivity of a commercial multiplex nucleic acid amplification assay in the season 2014/15, *Arch. Virol.* 161 (9) (2016) 2417–2423.
- [4] V.M. Corman, O. Landt, M. Kaiser, R. Molenkamp, A. Meijer, D.K. Chu, et al., Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR, *Euro Surveill.* 25 (3) (2020).
- [5] C. Reusken, E.K. Broberg, B. Haagmans, A. Meijer, V.M. Corman, A. Papa, et al., Laboratory readiness and response for novel coronavirus (2019-nCoV) in expert laboratories in 30 EU/EEA countries, January 2020, *Euro Surveill.* 25 (6) (2020).
- [6] H.C. Johnson, C.M. Gossner, E. Colzani, J. Kinsman, L. Alexakis, J. Beauté, et al., Potential scenarios for the progression of a COVID-19 epidemic in the European Union and the European Economic Area, March 2020, *Euro Surveill.* 25 (9) (2020).
- [7] M. Lipsitch, D.L. Swerdlow, L. Finelli, Defining the epidemiology of Covid-19 – studies needed, *N. Engl. J. Med.* 382 (2020) 1194–1196.
- [8] L. Bordi, E. Nicastrì, L. Scorzolini, A. Di Caro, M.R. Capobianchi, C. Castilletti, et al., Differential diagnosis of illness in patients under investigation for the novel coronavirus (SARS-CoV-2), Italy, February 2020, *Euro Surveill.* 25 (8) (2020).
- [9] L. Zou, F. Ruan, M. Huang, L. Liang, H. Huang, Z. Hong, et al., SARS-CoV-2 viral load in upper respiratory specimens of infected patients, *N. Engl. J. Med.* 382 (2020) 1177–1179.
- [10] M. Panning, M. Eickmann, O. Landt, M. Monazahian, S. Olschlager, S. Baumgarte, et al., Detection of influenza A(H1N1)v virus by real-time RT-PCR, *Euro Surveill.* 14 (36) (2009).