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Making Waves: Collaboration in the time of SARS-CoV-2 - rapid development of an international co-operation and wastewater surveillance database to support public health decision-making

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Corresponding Author:	Lian Lundy, PhD Lulea Tekniska Universitet London, SWEDEN
First Author:	Lian Lundy, PhD
Order of Authors:	Lian Lundy, PhD
	Despo Fatta Kassinos
	Jaroslav Slobodnik
	Popi Karaolia
	Lubos Cirka
	Norbert Kreuzinger
	Sara Castiglioni
	Lubertus Bijlsma
	Valeria Dulio
	Genevieve Deviller
	Foon Yin Lai
	Manuela Barneo
	Jose Antonio Baz-Lomba
	Frederic Béen
	Marianna Cíchová
	Kelly Conde
	Adrian Covaci
	Erica Donner
	Andrej Ficek
	Francis Hassard
	Annelie Hedström
	Félix Hernandez
	Veronika Janská
	Kelly Hill
	Jan Hofman
	Pei-Ying Hong
	Barbara Kasprzyk-Hordern
	Stoimir Kolarević

	Jan Krahulec
	Dimitra Dimitra Lambropoulou
	Rosa de Llanos
	Tomáš Mackuľak
	Lorena Martinez-García
	Francisco Martínez
	Gertjan Medema
	Adrienn Micsinai
	Mette Myrmel
	Leonor Nozal
	Mohammed Nasser
	Harald Niederstaetter
	Herbert Oberacher
	Věra Očenášková
	Leslie Ogorzaly
	Beatriz Peinado
	Tarja Pitkänen
	Dimitrios Papadopoulos
	Margarita Poza Dominguez
	Soraya Rumbo-Feal
	Maria Blanca Sánchez
	Anna Székely
	Andrea Soltysova
	Juan Vallejo
	Alexander van Nuijs
	Maria Viklander
Abstract:	The presence of SARS-CoV-2 RNA in wastewater was first reported in March 2020. Over the subsequent months, the potential for wastewater surveillance to contribute to COVID-19 mitigation programmes has been the focus of intense national and international research activities, gaining the attention of policy makers and the public. As a new application of an established methodology, focused collaboration between public health practitioners and wastewater researchers is essential to developing a common understanding on how, when and where the outputs of this non-invasive community-level approach can deliver actionable outcomes for public health authorities. Within this context, the NORMAN/SCORE “SARS-CoV-2 in sewage” database provides a platform for rapid, open access data sharing, validated by the uploading of 137 data sets from nine countries to-date. Through offering direct access to underpinning meta-data sets (and describing its use in data interpretation), the NORMAN SCORE database is a resource for the development of recommendations on minimum data requirements for wastewater pathogen surveillance. It is also a tool to engage public health practitioners, providing an opportunity to build mutual understanding of the demand and supply for data and facilitate the translation of this promising research application into public health practice.
Suggested Reviewers:	Andrew Singer Centre for Ecology and Hydrology Oxford: UK Centre for Ecology & Hydrology acsi@ceh.ac.uk Head of the UK wastewater surveillance network

	Jean-Marie Mouchel Ecole des Ponts ParisTech mouchel@cereve.enpc.fr Published in the field
	Rolf Halden Arizona State University Rolf.Halden@asu.edu Leader researcher in the field
	David Allen London school of hygeine and tropical medicine David.Allen@lshtm.ac.uk Active researcher in the field

Making Waves: Collaboration in the time of SARS-CoV-2 - rapid development of an international co-operation and wastewater surveillance database to support public health decision-making

Lian Lundy[1], Despo Fatta Kassinos[2], Jaroslav Slobodnik[3], Popi Karaolia[2], Lubos Cirka[3,4], Norbert Kreuzinger[5], Sara Castiglioni[6], Lubertus Bijlsma[7], Valeria Dulio[8], Geneviève Deviller[9], Foon Yin Lai[10], Manuela Barneo[11], Jose Antonio Baz-Lomba[12], Frederic Béen[13], Marianna Cíchová[14], Kelly Conde[15], Adrian Covaci[16], Erica Donner[17], Andrej Ficek[18], Francis Hassard[19], Annelie Hedström[1], Félix Hernandez[7], Veronika Janská[14], Jan Hofman[20], Kelly Hill[21], Pei-Ying Hong[22], Barbara Kasprzyk-Hordern[23], Stoimir Kolarević[24], Jan Krahulec[18], Dimitra Lambropoulou[25,26], Rosa de Llanos[11], Tomáš Mackuľak[27], Lorena Martinez-García[28], Francisco Martínez[28], Gertjan Medema[13], Adrienn Micsinai[29], Leonor Nozal[28], Mette Myrmel[30], Mohammed Nasser[15], Harald Niederstaetter[31], Herbert Oberacher[31], Věra Očenášková[32], Leslie Ogorzaly[33], Beatriz Peinado[28], Tarja Pitkänen[34,35], Dimitrios Papadopoulos[25], Margarita Poza[15], Soraya Rumbo-Feal[15], Blanca Sánchez[28], Anna J. Székely[36], Andrea Soltysova[18,37], Juan Vallejo[15], Alexander van Nuijs [16], Maria Viklander[1]

Corresponding author: Lian Lundy L.Lundy@mdx.ac.uk

[1]DRIZZLE Centre of Excellence, Luleå University of Technology, VA-Teknik, 971 87 Luleå, Sweden; [2]Department of Civil and Environmental Engineering, NIREAS-International Water Research Center, University of Cyprus, Cyprus; [3]Environmental Institute, Okruzna 784/42, 97241 Kos, Slovakia; [4]Faculty of Chemical and Food Technology, Slovak University of Technology in Bratislava, Radlinskeho 9, 81237 Bratislava, Slovakia; [5]Technische Universität Wien; Institute for Water Quality and Resources Management, Karlsplatz 13/226-1; 1040 Vienna, Austria; [6]Istituto di Ricerche Farmacologiche Mario Negri IRCCS, Department of Environmental Sciences, Via Mario Negri 2, 20156, Milan, Italy; [7]Environmental and Public Health Analytical Chemistry, Research Institute for Pesticides and Water, University Jaume I, Castellón, Spain; [8]National Institute for Environment and Industrial Risks, Rue Jacques Taffanel, Parc Technologique ALATA, Verneuil-en-Halatte, 60550 France; [9]DERAC

consulting, 104 grande rue 44240 Sucé-sur-Erdre (Nantes), France; [10]Department of Aquatic Sciences and Assessment, Swedish University of Agricultural Sciences (SLU), SE-75007 Uppsala, Sweden; Unidad Predepartamental de Medicina (Facultad de Salud), Universitat Jaume I, 12071 Castellón, Spain; [12]Norwegian Institute for Water Research (NIVA), Gaustadalléen 21, NO-0349 Oslo, Norway; [13]KWR Water Research Institute, Groningenhaven 7, 3430 BB Nieuwegein, The Netherlands; [14]Water Research Institute, Nábrežie arm. gen. L. Svobodu 5, 812 49, Bratislava, Slovak Republic; **[15]**Microbiology Service, University Hospital-Biomedical Research Institute-University of A Coruña, Spain; [16]Toxicological Center, University of Antwerp Universiteitsplein 1, 2610 Wilrijk, Belgium; [17]Future Industries Institute (FII), University of South Australia, Building X, University Boulevard, Mawson Lakes, 5095, South Australia, Australia; Department of Molecular Biology, Faculty of Natural Sciences, Comenius University, Bratislava, Slovakia; [19]School of Water, Energy and Environment, Cranfield University, Cranfield, Bedfordshire MK43 0AL, UK; [20]University of Bath, Department of Chemical Engineering, Water Innovation and Research Centre, Claverton Down, Bath BA2 7AY, UK; [21]Water Research Australia Limited | Level 2, 250 Victoria Square / Tarntanyangga Adelaide SA 5000 | GPO Box 1751 Adelaide SA 5001, Australia; [22]Division of Biological and Environmental Science and Engineering, Water Desalination and Reuse Center, King Abdullah University of Science and Technology (KAUST), Thuwal 23955-6900, Saudi Arabia;[23]Department of Chemistry, University of Bath, Bath, UK; [24]University of Belgrade, Institute for Biological Research "Siniša Stanković", National Institute of Republic of Serbia, Department for Hydroecology and Water Protection, Bulevar despota Stefana 142, 11000 Belgrade, Serbia; [25]Laboratory of Environmental Pollution Control, Department of Chemistry, Aristotle University of Thessaloniki, GR–541 24 [26]Thessaloniki, Greece; Center for Interdisciplinary Research and Innovation (CIRI-AUTH), Balkan Center, Thessaloniki, GR-57001; [27]Institute of Chemical and Environmental Engineering, Faculty of Chemical and Food Technology, Slovak University of Technology, Radlinského 9, 812 37 Bratislava, Slovakia; [28]IMDEA Water Institute, Science and Technology Campus of the University of Alcalá, Avenida Punto Com 2, 28805, Alcalá de Henares, Spain; [29]WESSLING Hungary Kft. Budapest, Anonymus u. 6, 1045 Hungary;[30]Norwegian University of Life Sciences, Faculty of Veterinary Medicine, Virology Unit, P.O. Box 8146 Dep., N-0033 Oslo, Norway; [31]Institute of Legal Medicine and Core Facility Metabolomics, Medical University of Innsbruck, Muellerstrasse 44, A-6020 Innsbruck, Austria; [32]T. G. Masaryk Water Research Institute, p.r.i., Branch of Analysis and Assessment of Environmental Components, Podbabská 2582/30, 160 00

Prague 6, Czech Republic; [33]Luxembourg Institute of Science and Technology (LIST), Environmental Research & Innovation department, 41 rue du Brill L-4422 Belvaux, Luxembourg; [34]Finnish Institute for Health and Welfare, Expert Microbiology Unit, Neulaniementie 4, FI-70701 Kuopio, Finland; [35]University of Helsinki, Faculty of Veterinary Medicine, Dept. Food Hygiene and Environmental Health, Agnes Sjöbergin katu 2, FI-00014 Helsingin yliopisto, Finland; [36]Evolutionary Biology Centre, Limnology, Uppsala University, Norbyvägen 18 D, SE-752 36 Uppsala, Sweden; [37]Institute for Clinical and Translational Research, Biomedical Research Center, Slovak Academy of Sciences, Dubravska Cesta 9, 84505 Bratislava, Slovakia.

Abstract

The presence of SARS-CoV-2 RNA in wastewater was first reported in March 2020. Over the subsequent months, the potential for wastewater surveillance to contribute to COVID-19 mitigation programmes has been the focus of intense national and international research activities, gaining the attention of policy makers and the public. As a new application of an established methodology, focused collaboration between public health practitioners and wastewater researchers is essential to developing a common understanding on how, when and where the outputs of this non-invasive community-level approach can deliver actionable outcomes for public health authorities. Within this context, the NORMAN/SCORE "SARS-CoV-2 in sewage" database provides a platform for rapid, open access data sharing, validated by the uploading of 137 data sets from nine countries to-date. Through offering direct access to underpinning meta-data sets (and describing its use in data interpretation), the NORMAN SCORE database is a resource for the development of recommendations on minimum data requirements for wastewater pathogen surveillance. It is also a tool to engage public health practitioners, providing an opportunity to build mutual understanding of the demand and supply for data and facilitate the translation of this promising research application into public health practice.

1. Introduction

Research continues apace into many aspects of the use of wastewater surveillance for the detection of SARS-CoV-2 and how data generated can be utilised within local public health decision-making. Also known as sewage or environmental surveillance, the approach has an established literature in terms of monitoring the occurrence and concentration of chemicals arriving at a wastewater treatment plant (WWTP) (Choi et al., 2018). Determined chemical concentrations such as illicit (González-Mariño et al., 2020; Ort et al., 2014) and licit drugs including tobacco, caffeine and alcohol (Castiglioni et al., 2015; Gracia-Lor et al., 2017; Ryu et al., 2016) are used to provide quantitative longitudinal data sets on the use at a catchment level. It is also possible to evaluate the rates of exposure to environmental or food contaminants using the same approach (Rousis et al., 2017; Lopardo et al., 2019). Furthermore, wastewater surveillance can be used to evidence changes overtime in relation to the implementation of new policy initiatives. The practical utility of chemical wastewater surveillance data sets is demonstrated by its use within local and national monitoring and public health programmes (EMCDDA, 2020; Riva et al. 2020; Lai et al., 2018). Prior to 2020, the use of wastewater surveillance for monitoring pathogens was gaining ground only slowly. Most notably, enterovirus wastewater surveillance systems have been established in several locations (Sedmak et al., 2003; Majumdar et al., 2018), with wastewater surveillance identified as playing a key role in polio eradication schemes in Israel, India and Egypt (WHO, 2020; Ashgar et al., 2014; Holm-Hansson et al., 2017). The first SARS-CoV-2 wastewater surveillance studies were undertaken in the Netherlands, with viral RNA material detected in wastewater treatment influent samples in seven Dutch cities and the international airport (Medema et al., 2020a). This landmark study included data on the detection of viral fragments in wastewater in one city prior to the detection of any clinical cases. This potential to provide an early warning on the presence of the virus within a community is a proof-of-concept and an evidence base that could be used by public health teams as a trigger to intensify clinical testing, facilitating the identification and isolation of positive cases (Thompson et al., 2020; POST, 2020). Hence, the use of wastewater surveillance for SARS-CoV-2 as a tool to address

the COVID19 pandemic is a new application of an established method in a rapidly moving field.

SARS-CoV-2 wastewater surveillance studies to date have demonstrated the occurrence of its RNA genome in a range of compartments, primarily WWTP influents but it has also been reported in sludge and effluents as well as within receiving waters (Jones et al., 2020). In terms of infectivity potential of wastewater containing SARS-CoV-2 RNA, initial studies (Westhaus et al., 2021; Rimoldi et al., 2020; Bivins et al., 2020a) and expert opinion (WHO, 2020; Jones et al., 2020) indicate that detected RNA materials do not occur in the form of an infectious viral particle. Further studies also looked to establish a quantitative relationship between viral load and number of clinical cases reported within a catchment (Vallejo et al., 2020; Ahmed et al., 2020). However, variations in the load and duration of viral material shed in faeces by asymptomatic, pre-symptomatic and symptomatic cases, together with limited understanding of the fate of viral particles within sewer systems (which vary significantly in design and flow dynamics), and variations in analytical protocols and their associated extraction efficiencies, generates considerable uncertainty in terms of directly relating viral loads to numbers of cases. Hence, many open challenges exist within this research area and use of data by public health teams. Within the field, key research questions encompass the potential for viral materials to adsorb to biofilm and particles, degrade in the sewage system and optimising sample collection processes, including collection location and frequency (WHO, 2020). Moreover, the need to standardise and optimise analytical protocols has been clearly identified (Michael-Kordatou et al., 2020). In terms of interpreting data, key issues include data comparability between studies (e.g. use of a common marker for normalisation and how contextual data e.g. flow and other parameters are included in data interpretation), the identification of a SARS-CoV-2 RNA threshold value and the actions that exceeding a threshold value should trigger (Medema et al., 2020b). Variations in the amount of viral RNA excreted per person are a further unknown, and inherent levels of variability in shedding may make accurate predictions of prevalence impossible. However, the absence of an absolute

understanding of shedding rate behaviour does not preclude the use of this approach in public health contexts, where relative changes in signal (as opposed to its absolute value) can provide public health teams with valuable data.

2. The use of wastewater surveillance data within public health decision-making

Wastewater surveillance can be used to non-invasively screen 'hard to test' communities (i.e. where uptake of testing is low or challenging for resource reasons) at a sewer catchment level as a new public health tool to understand COVID-19 spread (CDC, 2020; POST, 2020). Detection of SARS-CoV-2 RNA fragments in wastewater is independent of clinical testing strategy bias (Thompson et al., 2020), can be used as an early warning of the need for further testing (e.g. reallocating/increasing local testing resources such as drive-through test facilities) or the implementation of wastewater surveillance upstream of the WWTP i.e. near-source tracking to identify location of cases (Hassard et al., 2020). For example, the detection of SARS-CoV-2 RNA concentrations can indicate the (re-)emergence of the virus in a catchment following a period of no clinical cases and an increase in viral RNA load can indicate the occurrence of new outbreaks, requiring the urgent tracing of infected individuals and their subsequent support to isolate (DEFRA, 2020). Likewise decreasing prevalence can indicate that infected individuals are 'known' and isolation/public health interventions are effective. Further, an increase in viral load over time against a trend of 'no-change' in daily positive case numbers could indicate that the clinical testing regime should be intensified (i.e. new cases are not being detected) (Thompson et al., 2020). Wastewater surveillance data sets can also be used to evidence the effect of alternative policy actions e.g. curfew vs local lockdown vs national lockdown at a community level, as well as track progress of vaccination campaigns.

To deliver these types of actionable outcomes i.e. to enable public health authorities to use wastewater surveillance data within their community level decision-making processes requires activities on several fronts. As well as addressing the wastewater surveillance methodological and analytical challenges identified earlier, data from wastewater needs to be collected

frequently and available rapidly in a format that is useful and useable by public health practitioners. Further collaboration between wastewater and public health practitioners is required to ensure that public health teams can access the type of data they require in a timeframe and format that integrates with current pandemic mitigation measures i.e. addressing public health data requirements needs to be front and centre of operationalising this new development in wastewater surveillance. The format and sampling strategies underpinning wastewater data sets may need to morph in terms of the locations and frequency of sample collection, quality assurance/quality control processes, scale at which data is generated and made available and the aspects of primary value from a public health perspective i.e. absolute values or trends analysis. Delivering this type of integrated data share 'dashboard' is already challenging under usual working conditions; working across disciplines during a pandemic when public health teams are at (or beyond) full capacity is extremely challenging. However, collaboration between public health and wastewater researchers – where public health practitioners take a lead role in determining dashboard development - is happening. For example, in Australia, the development of a SARS-CoV-2 wastewater surveillance dashboard was led by a collaboration between the Victorian state public health team and Water Research Australia. This has already matured from a research and development phase to an operational tool for day-to-day use with functional dashboards for both internal and external communications (Victoria State Government, 2020). Other countries with established monitoring programs include the Netherlands, Canada, Luxembourg, Italy, Finland, and Austria. In the UK, sharing of data between a government-led wastewater surveillance project and the national COVID-19 'track and trace' programme led to the identification of an increase in SARS-CoV-2 RNA in wastewater despite relatively low numbers of people taking clinical tests (DEFRA, 2020). This data was used to alert local health professionals to contact people in the area to warn of the increase in cases and encourage local populations to engage with clinical testing programmes.

The need for and benefits of collaboration among wastewater researchers has been recognised and several international and national collaborations rapidly established (e.g. Bivins et al., 2020b; WRF, 2020; WHO, 2020; JRC, 2020; Réseau Obépine, 2020; WRA, 2020; UCMERCED, 2020). These have focussed primarily on technical and analytical issues, facilitating opportunities for rapid discussion on a range of topics from recent publications to method development, predictive modelling and risk assessment. However, collaboration activities to-date have yet to address two key issues: firstly, the development of an open-access data platform to enable and facilitate the rapid sharing and critical evaluation of multiple wastewater meta-data sets to address technical issues (Bivins et al., 2020a). Secondly, engagement with public health authorities i.e. development of a critical mass of public health and wastewater researchers to collaboratively identify and deliver an operational SARS-CoV-2 wastewater surveillance public health system.

3. Open access data sharing to progress collaboration across disciplines

The NORMAN/SCORE SARS-COV-2 in sewage (SC2S) database is a platform, which can contribute to meeting both these needs. This open-access database is an output of the collaboration between two international networks: the NORMAN network (www.norman-network.net/) of research organisations supporting the validation and harmonisation of measurement methods and monitoring tools and SCORE (https://score-cost.eu) a network established to harmonise methodologies for measuring human biomarkers in wastewater to evaluate lifestyle, health and exposure at the community level. The database is located within the NORMAN Database System at https://www.norman-network.com/nds/ as the latest addition to its 13 database modules within the interlinked database system series for the collection and evaluation of data / information on emerging substances in the environment (Dulio et al., 2020). The SC2S database structure follows that of the NORMAN Antibiotic Resistance Bacteria/Genes database, enabling users to freely access data at a WWTP level as well us upload new data via a customised data collection template (DCT; downloadable from the website) which facilitates its automatic uploading to the system. On accessing the

227 database, users can search via country and/or WWTP or view the entire data set (both within
228 the database or it can be exported into MS Excel) without any restrictions. Data displayed in
229 the dashboard includes sampling date, gene copy (number of copies /mL and/or ng of
230 RNA/mL), cycle threshold (Ct), WWTP and country name, population served and the number
231 of people reported SARS-CoV-2 positive in the sewer catchment area on the day of sampling.
232 Table 1 identifies the requested reporting parameters and provides an overview of their role
233 in interpreting generated data sets. Finally, the full DCT containing all reported data on all
234 parameters can be downloaded for each dataset. In terms of engaging the attention of public
235 health authorities, as a first step it includes both wastewater and clinical case data. In addition,
236 and perhaps more importantly, it is a starting point for further discussions with public health
237 practitioners on what wastewater surveillance is, the types of longitudinal data sets it can
238 produce (together with process controls), and the potential of this non-invasive approach as a
239 tool to provide an early warning of new clusters as well as the impact of existing pandemic
240 mitigation measures.
241
242 To launch the database, invitations to participate were initially shared through both the
243 NORMAN and SCORE networks, with a request for members to disseminate further through
244 their own networks. To harmonise activities, participants were provided with a common
245 protocol covering sample collection, RNA extraction and analysis. The common protocol
246 (available at https://www.norman-network.com/nds/sars_cov_2/) adopts the Medema et al
247 (2020) methodology with an alternative simplified protocol for SARS-CoV-2 extraction from
248 wastewater via polyethylene glycol *(*PEG*)* precipitation (recognising that many
249 consumables/equipment currently in short supply). Submission of data using both methods is
250 welcomed, with space on the DCT to identify which approach was used and the genes
251 targeted. A further step was to establish a 'buddy system' for research groups who were able
252 to collect wastewater samples but whose laboratories were under lock-down and/or were not
253 familiar with RNA analysis. As such, the rapid sharing of a common protocol also had a
254 capacity building effect, enabling many groups to explore opportunities to undertake

wastewater surveillance for pathogens for the first time. Two scheduled sampling campaigns were held on June 1st 2020 and June 15th 2020, with data referring to further identified sampling campaigns now welcomed. To date the SC2S database contains 137 sets of data from nine different countries.

The impact of pandemic mitigation measures on working conditions impacted on the ability to both collect and manage samples e.g. reduced access to WWTPs and laboratories, and/or work force. As a result, 24 hour composite samples (either volume-weighted or time-weighted) were collected on several dates on or close to scheduled sampling dates (from 24th May 2020 – 16th June 2020) with grab and/or composite samples collected on further as local conditions permitted. Sample preparation date, date of analysis and storage conditions were identified, together with the method used for sample preparation, RNA extraction, analysis and the use of internal standards in the sample preparation phase (20% of samples) and the RNA extraction step (81% of samples). Reviewing the data set as a whole, a positive signal for SARS-CoV-2 was quantified in 33 of the 137 samples analysed. Genetic markers were reported for 132 of the samples; N1 gene in 114 samples, N2 gene in 3 samples, N3 in 4 samples, E gene in 9 samples with 6 samples referring to the genetic marker as 'N gene' only. Ct counts ranged from 34 - 41.9, with the number of gene copies/ml ranging from 0.04 – 148 gene copies/mL (median: 2.5 gene copies/mL). In terms of quality control, reported analysis included two to six replicates per sample with the use of a positive control reported in the analyses of 129 of the 137 samples. The analytical limit of detection was reported on 34 occasions (range: 0.5 - 266 gene copies/mL; median 3 gene copies/mL). However, no study reported their limit of quantification. In terms of clinical data, the number of positive cases reported in the local municipality (which may/may not reflect the sewer catchment) on the day of sampling was reported for 117 of the 137 samples analysed (range: 0 – 985; median = 54.5 cases).

4. Conclusions

The SC2S provides a snapshot of the occurrence of SARS-CoV-2 in wastewater at participating WWTPs and demonstrates the ad-hoc cooperation of the scientific community on data collection. However, more importantly, the NORMAN/SCORE initiative:

- demonstrates that the SC2S database is a workable multi-jurisdictional data-share platform with potential to facilitate development of an international dataset
- provides a tool to engage and inform discussions with public health practitioners on the potential role of wastewater surveillance as an additional approach to integrate within community public health strategies
- is open to all (contributors are warmly invited to submit data from any campaigns they are able to share, using the relevant sections on the DCT to document sample collection, storage and analytical details together with clinical case numbers)
- with continued use, this collection of wastewater meta-data will support a retrospective analysis of the impact of differing sewer/catchment/population variables on the use of wastewater surveillance as a tool in public health practice
- facilitated the collection of comparable data sets from an early phase of the pandemic; continued use will provides an opportunity to maximise operational insights gained during different phases of the pandemic and support development of robust best practice in wastewater surveillance.

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Highlights

- open access SARS-CoV-2 in sewage meta data base (137 datasets from nine countries)
- a tool to engage and inform discussions with public health practitioners
- continued use can enable analysis of catchment variables on wastewater surveillance
- commencing early in the pandemic provides an opportunity to inform best practice

Table 1. Overview of parameters recorded and their role in facilitating data analysis, interpretation and comparison

Type of data	**Parameters**	**Role in data interpretation**
Sampler information	Name, contact details	Auditability
Sampling site	WWTP name and country; longitude/latitude; altitude (m)	Identify sewer shed location; consider climatic influences
	Design capacity (PE); population served (PE); catchment size (m^2)	Consider drainage network size and WWTP loads/dynamics; calculate population density and population-normalised virus loads
SARS-CoV-2 clinical prevalence data	No. of people SARS-CoV-2 positive on sampling date	Relationship between viral load and clinical cases on day of sampling
	No. of people recovered from SARS-CoV-2 on sampling date	Relationship between viral load and all clinical cases to-date
	No. of people SARS-CoV-2 positive 2 weeks prior to sampling date	Longitudinal trends in clinical case numbers; consider shedding from active cases versus post-infection shedding
	No. of people recovered from SARS-CoV-2 2 weeks prior to sample date	
Sample matrix	Influent wastewater	Confirmation of sample type
Sampling date	Start and finish: hour; day; month; year	Seasonality
Sampling procedure	Composite (time- or flow-weighted with intervals reported) or grab sample	Understanding of sampling errors/bias
Inflow characteristics	Flow (total m^3; minimum/maximum m^3/h);	Consider drainage network and WWTP dynamics; calculate mass loads
	COD [mg/L]; TSS [mg/L]; Total N / NH4-N [mg N/L]	Consider effects of wastewater composition on RNA yield and occurrence of groundwater infiltration
	Rain (dry weather/number of days since last rain event	Occurrence of dilution due to rainfall
Sample preparation	Date of analysis; storage temperature (°C)	Potential for degradation of RNA
	Internal standard used (if so which)	Process quality control / quality assurance
	Method used for sample preparation	Potential differences in extraction efficiencies
	Volume of sample [mL]	Understanding of RNA copies per a certain wastewater volume
	Number of replicates	Quality control / quality assurance
RNA extraction	Date of and method used for RNA extraction	Quality control / quality assurance
	Genetic markers (N1, N2, N3 etc.)	Differences in sensitivity using qPCR analysis
	Internal standard used (if so which)	Quality control / quality assurance in understanding RNA extraction efficiency
	RNA [µL; ng / µL]	Quantitative identification of virus in wastewater
	Number of replicates	Quality control / quality assurance
Analytical method	Technique e.g. Conventional PCR / Real-time PCR / Illumina Myseq / Whole genome sequencing / LAMP-PCR / non-targeted analysis.	Quality control / quality assurance
	Limit of detection (number of copies/mL of sample)	The lowest level of virus that can be determined as present
	Limit of quantification (number of copies/mL of sample)	The lowest level of virus that can be quantified at a good confidence
	Uncertainty of the quantification (%RSD)	Potential variations in qPCR measurement
	Extraction efficiency	Understanding of performance of selected extraction methods
	Concentration of RNA in which analysis performed ([µL; ng/µL)	Quantitative information of virus measured in wastewater extracts
	Positive control used (if so which)	Process quality control / quality assurance; indication of method performance
	Number of replicates	Quality control / quality assurance
RNA concentration / abundance	Cycle threshold (Ct #)	Quality control / quality assurance
	Gene copy [number/mL of sample or number/ng of RNA)	Trend and spatial evaluations of virus levels within and across catchments. Calculations considering concentrations, wastewater flow and population served by a WWTP.

Key: WWTP = wastewater treatment plant

DRIZZLE Centre of Excellence
Luleå University of Technology
VA-Teknik
971 87 Luleå
Sweden

23 December 2020

Professor Stefan Wuertz
Editor: Water Research Making Waves

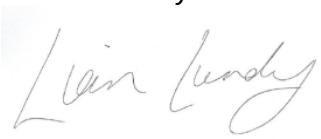
Dear Professor Wuertz

Further to our email discussions, I would like to submit the accompanying manuscript entitled ‘Making Waves: Collaboration in the time of SARS-CoV-2 - rapid development of an international co-operation and wastewater surveillance database to support public health decision-making’ for consideration for publication as a Water Research Making Waves research communication.

As an inclusive, multi-national initiative, I have invited all those who contributed to developing the concept, database and submitted data to be a co-author. All co-authors have reviewed the manuscript and provided comments.

Please let me know if you require any further information.

Yours faithfully



Professor Lian Lundy
Professor of Environmental Science

Declaration of interests

☒ The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

☐The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: