2021中国国际食品安全与质量控制会议

CIFSQ Conference October 27 - 28, 2021 | Beijing, China

Dr Guerrino Macori

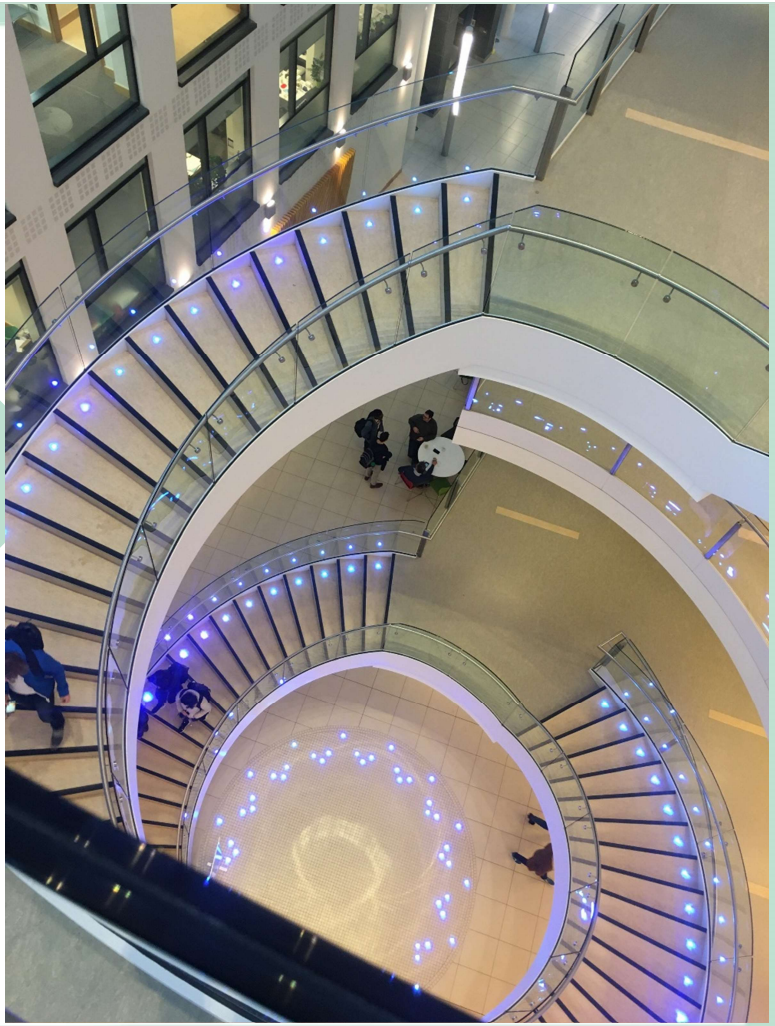
Investigating the Presence of SARS-CoV-2 in Selected Foods and Food Production Environments Using Harmonised RT-qPCR and WvGS Protocols

www.ucd.ie/cfs

Centre for Food Safety

UCD-Centre for Food Safety
School of Public Health,
Physiotherapy and Sports Science,
University College Dublin, Ireland

Centre for Food Safety



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Application of techniques for sequencing and WGS analysis

Professor Séamus Fanning

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protocols.io

- Standard operating procedures (SOPs)
- bacterial culture and extraction
- library preparation
- bioinformatics workflow
- genomic comparison of 22 isolates
- ***whole viral genome sequencing (WvGS) of SARS-CoV-2 and computational analysis***

Application of techniques for sequencing and WGS analysis

Professor Séamus Fanning

SARSfood

- Investigating the presence of SARS-CoV-2 in selected foods and food production environments using qPCR and WvGS

Prof. Seamus Fanning, Lauren Russell, Francisco Cores Rodriguez, Alexander Floss-Jones, Charlene Bennet, Siobhan McCarthy

World Health Organization

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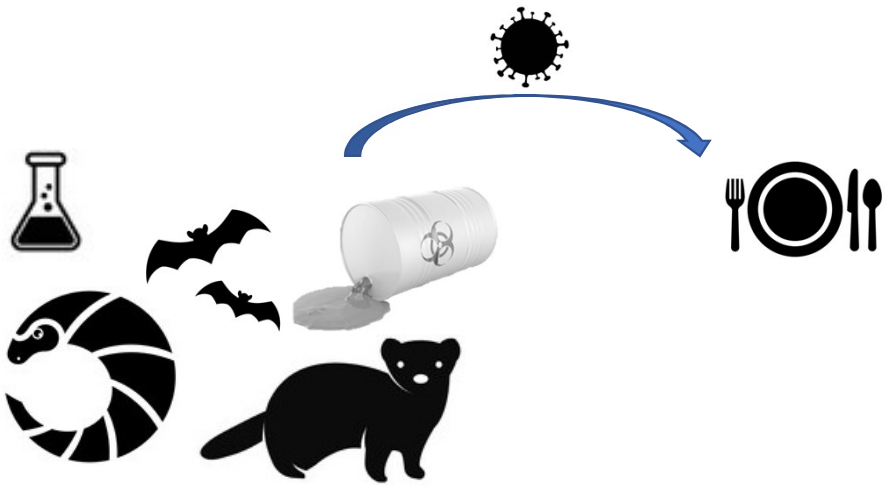
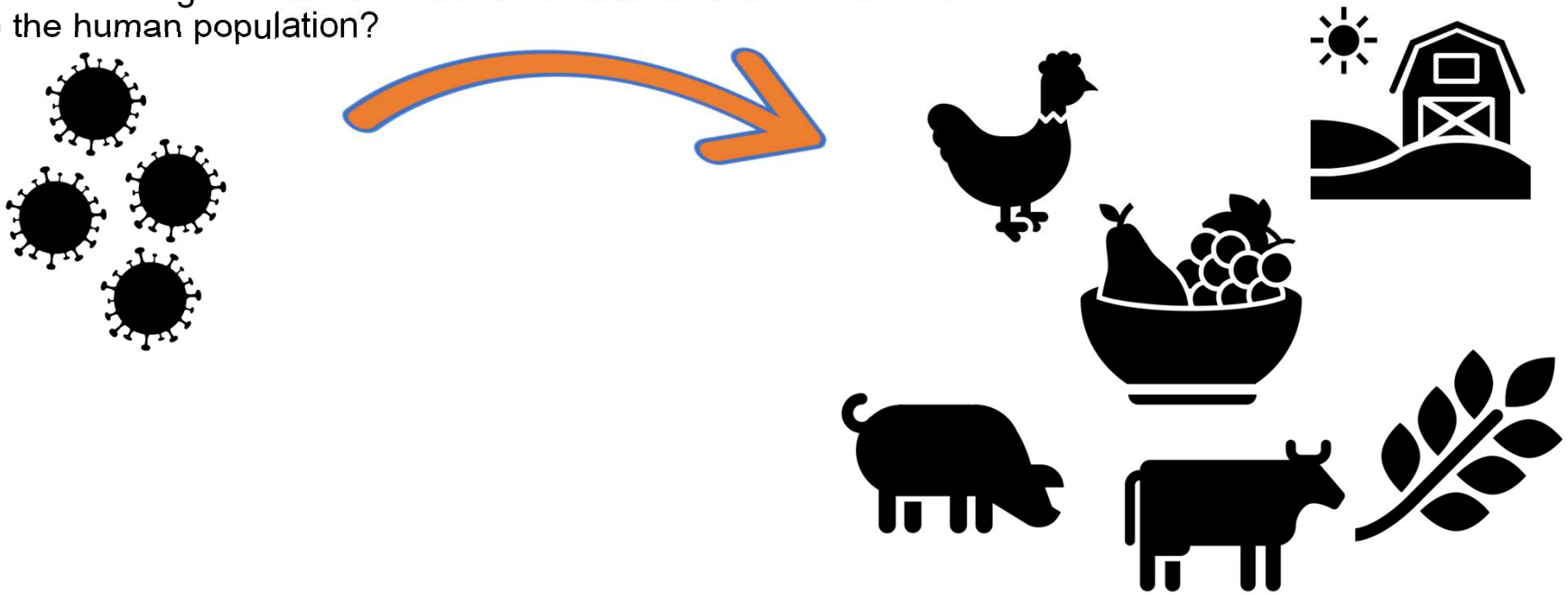
Possible source of virus SARS-CoV-2, animals may be natural hosts. Is it a zoonoses?



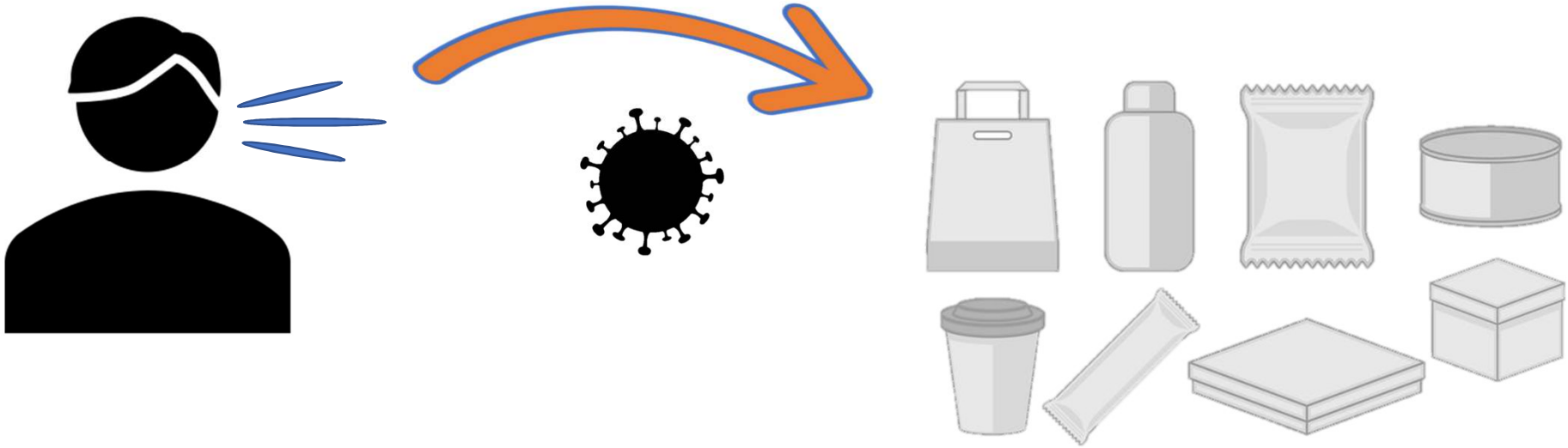
In particular, the role (if any) of **domesticated food-producing animals and the meat derived from them**

- necessitating the development of suitable diagnostic protocols; implementation of intervention measures along the food chain and recognising transmission routes.

- Could also be possible for SARS- CoV-2 a series of barrier jumps?
- Are food preparations and cooking habits considered a risk factors for the re-emergence of this virus in the human population?



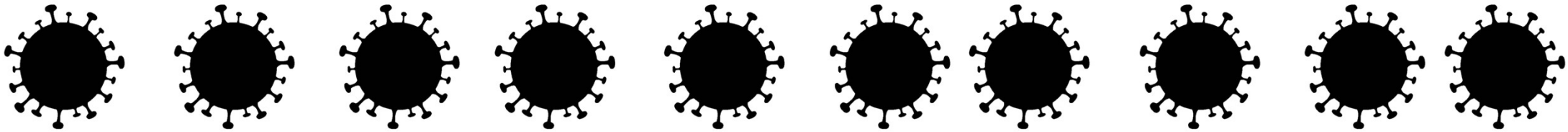
Of concern are **processed foods and food packaging**, wherein the SARS-CoV-2 could reach a susceptible consumer following cross-contamination from a previously infected individual (after bouts of coughing or sneezing).



Although there is no direct and credible evidence to state that COVID-19 is a food-borne disease, contact with food and food packaging surfaces remains a low risk in the context of the ongoing pandemic.

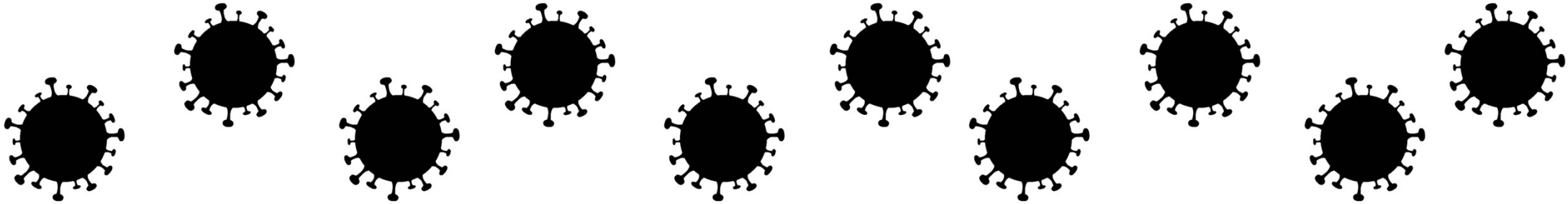
The **COVID-19 pandemic has presented several challenges to stakeholders along the food chain.** These must be overcome in order to ensure food safety and will involve the ability to reliably detect the virus in various food matrices and the built food production environment. As we move towards a post-pandemic era, public health surveillance will involve not only screening human populations, but also monitoring of foods; preparation surfaces and related environments, to assess risk and implement scientifically- based countermeasures.

Although, several **meat processing plants (MPPs)** in the US, Europe and elsewhere, suspended operations, when workers tested positive, though no food recalls were instituted

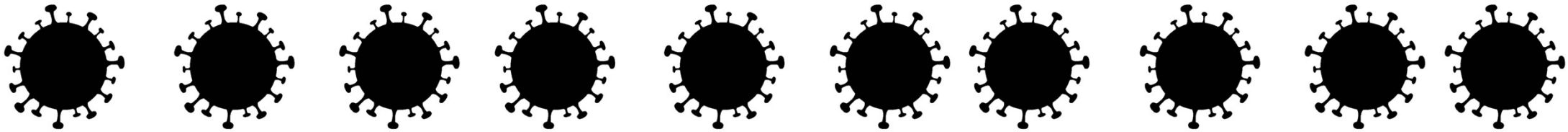


This project would set out to provide with evidence on the following:

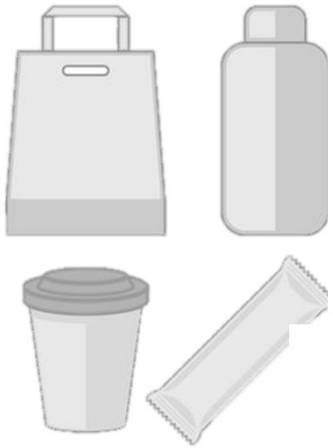
- describe the detection of SARS-CoV-2 in selected food matrices (raw meat; selected vegetables and fruits);
- describe the detection of SARS-CoV-2 in selected built food processing environments (FPP) to include sampling of various locations (including taps; door handles; refrigerator handles; smear samples from air conditioning units and other locations considered high-touch);
- determine the whole virus genome sequence (WvGS) of all viral strains recovered from selected food matrices and locations within the built food production environments;
- using WvGS make provide data describing a comparative genomic study to provide information on the potential relationships between these foods, ecological niches and those sequences deposited within GISAID

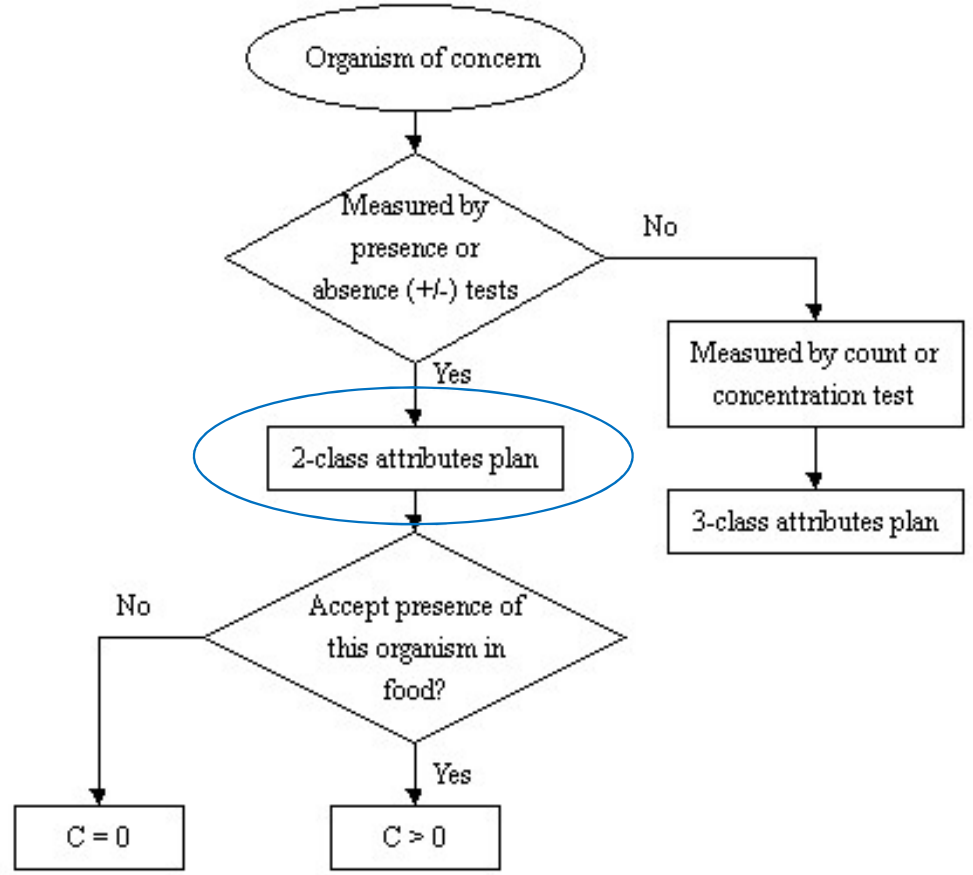


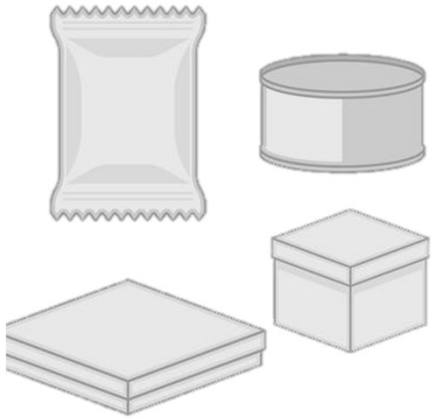
- Identification of SARS-CoV-2 RNA in selected food production environments and foods, by RT-qPCR
- Characterisation of qPCR positive samples by whole virus genome sequencing (WvGS) and comparative genome analysis of these viral strains with those globally available



Sampling plan: the model







Assuming that in this study is preferred a sampling plan with the highest confidence on the results, among the binomial staged sampling plans, is chosen the table with the confidence limit of **0.99 and 0.10** as the upper confidence level.

Sampling plan: the model

Confidence Limit .99		0 out of:	1 out of:	2 out of:
A	.30 ucl*	15	22	27
B	.25 ucl	19	27	34
C	.20 ucl	24	34	43
D	.15 ucl	35	47	59
E	.10 ucl	51	73	90
F	.05 ucl	107	161	190

Using this approach, for each type of food is ideally preferred a **number of 51 samples**.

1. **Food samples**
   - Raw meat
   - Vegetables
   - Fruit
2. **Abiotic surfaces of high-touch locations**
   - Air conditioning units;
   - Taps;
   - Door handles;
   - Refrigeration handles
   - Others
3. **Sewage from selected food/meat processing plants**

Sala-Comorera et al., 2021

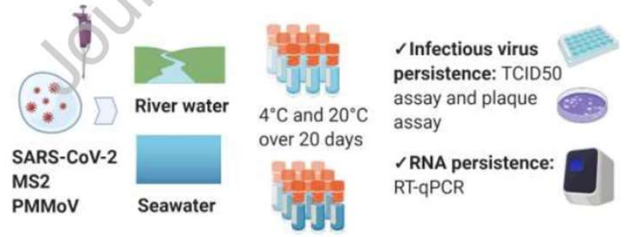
Decay of infectious SARS-CoV-2 and surrogates in aquatic environments

Laura Sala-Comorera[a], Liam J. Reynolds[a], Niamh A. Martin[a], John J. O'Sullivan[b], Wim G. Meijer[a]*, Nicola F. Fletcher[c].

a. UCD School of Biomolecular and Biomedical Science, UCD Earth Institute and UCD Conway Institute, University College Dublin, Dublin 4, Ireland
b. UCD School of Civil Engineering, UCD Dooge Centre for Water Resources Research and UCD Earth Institute, University College Dublin, Dublin 4, Ireland.
c. UCD School of Veterinary Medicine and UCD Conway Institute, University College Dublin, Belfield, Dublin 4, Ireland

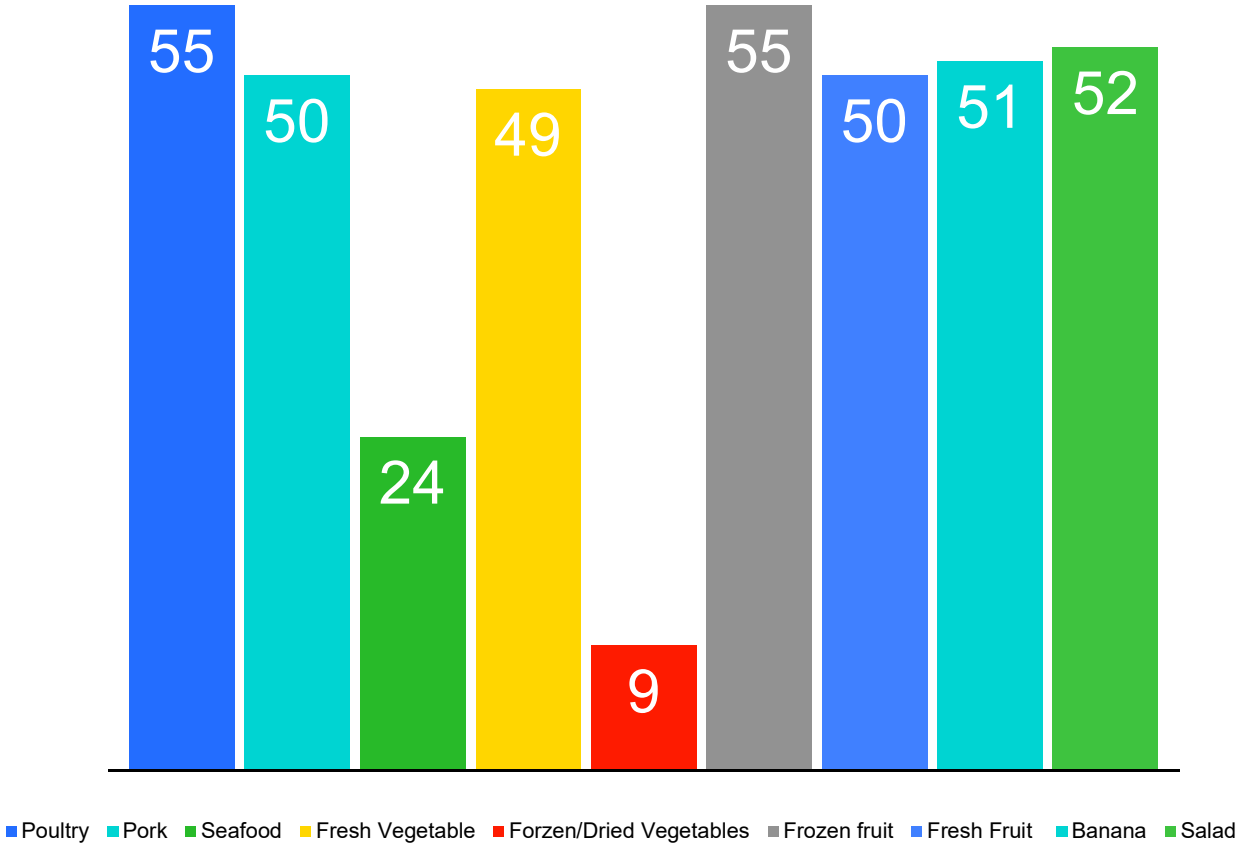
* Corresponding author: Wim G. Meijer, Tel: (+353) 17162778, Email: wim.meijer@ucd.ie

Graphical abstract



Highlights

- T_{90} of infectious SARS-CoV-2 at 4°C was 3.8 and 2.2 days in river and seawater

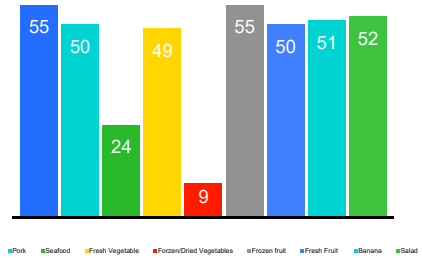


Samples:

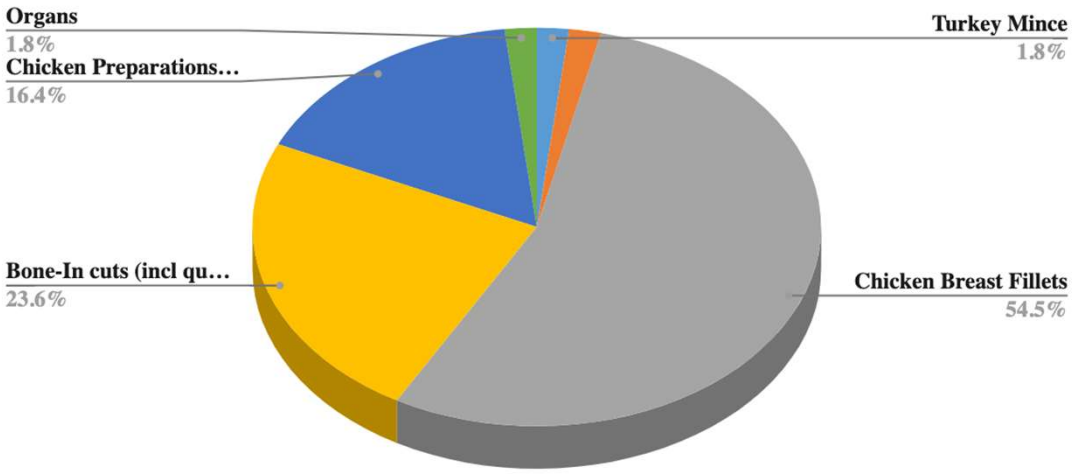
105 raw meat

101 fresh vegetables RTE

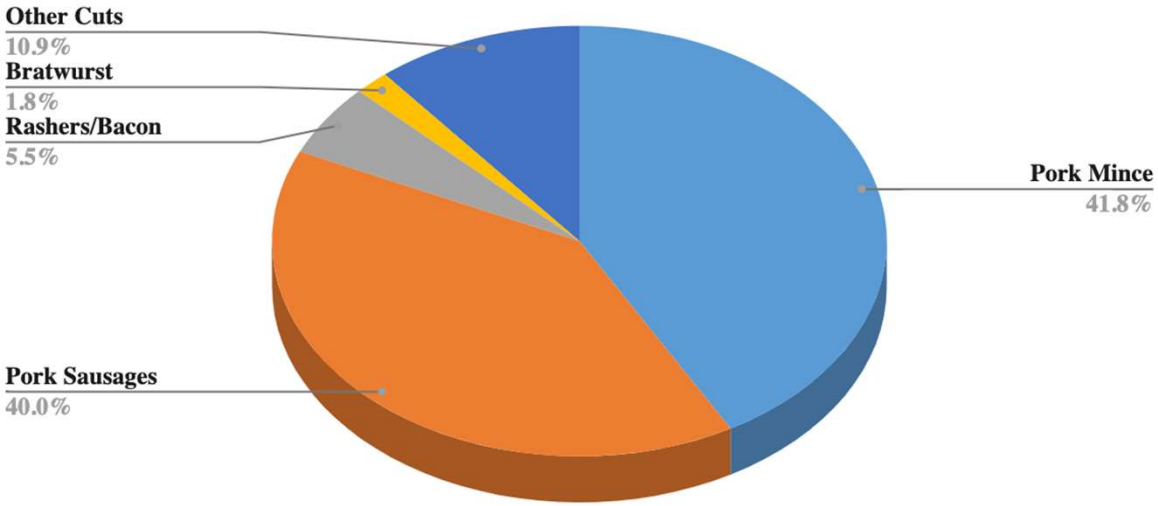
157 fruit RTE (fresh/frozen)



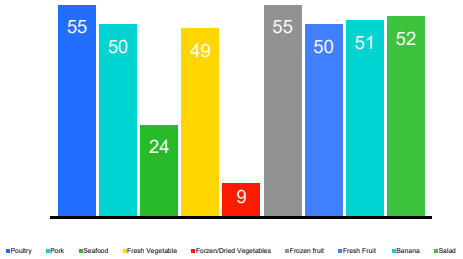
Poultry Sample Types - WHO Food SARS-COV-2

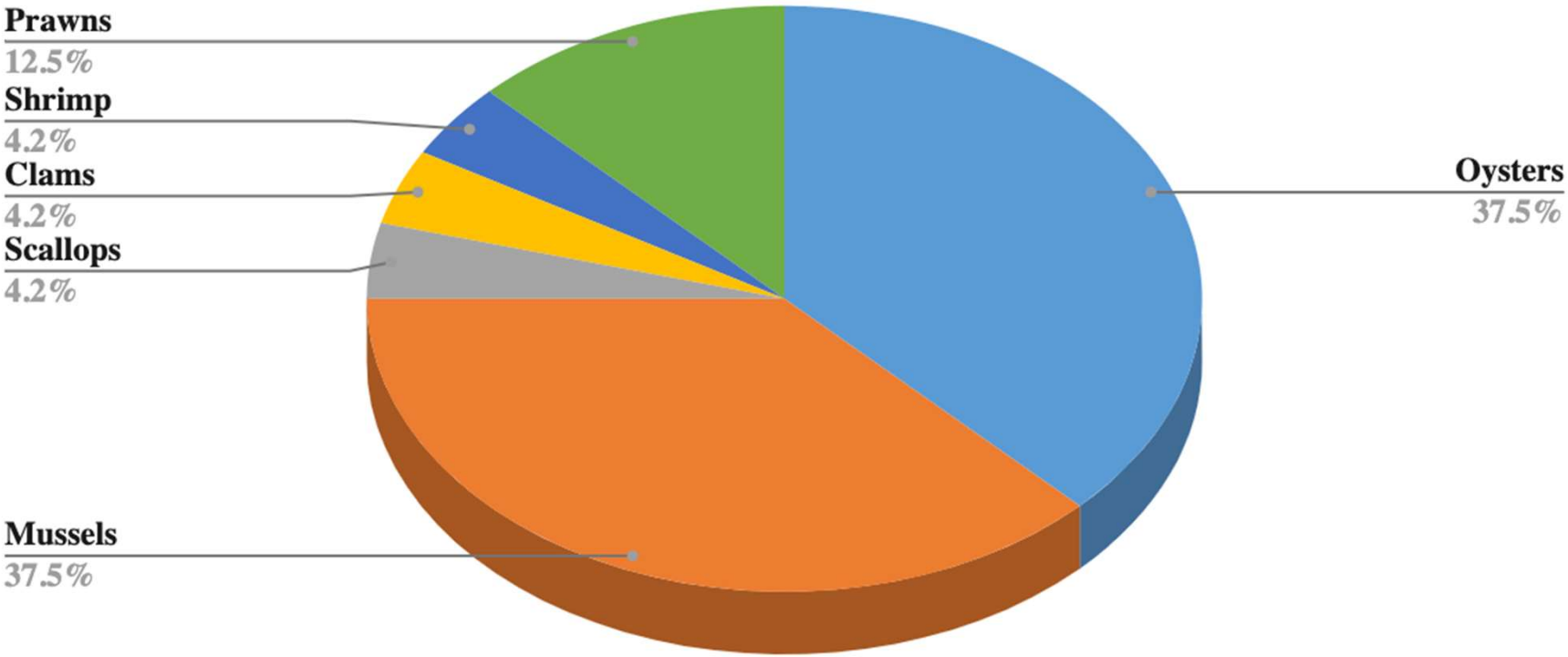


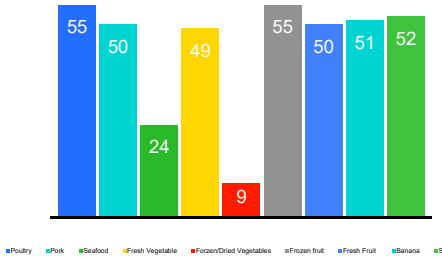
Pork Sample Types - WHO Food SARS-COV-2



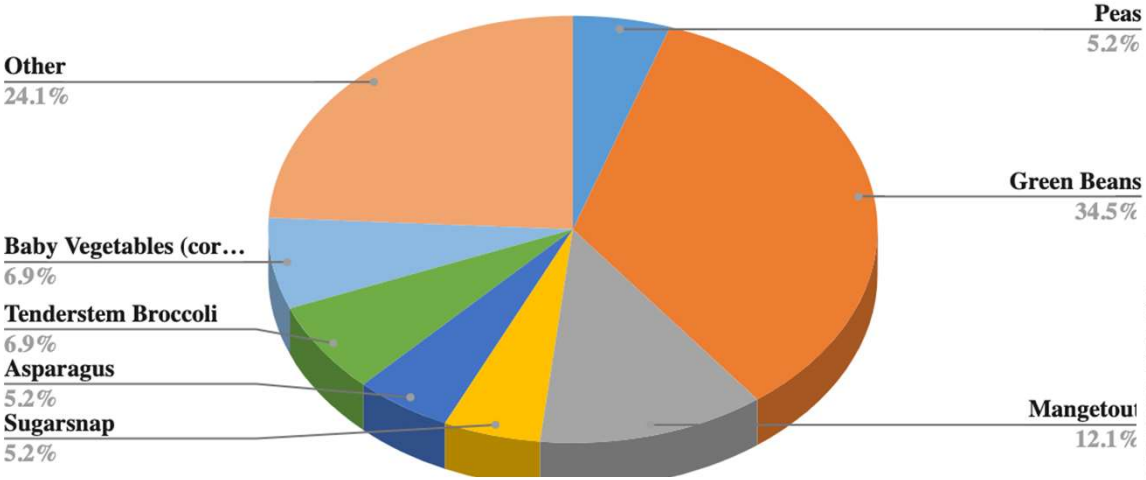
Seafood Sample Types - WHO Food SARS-COV-2



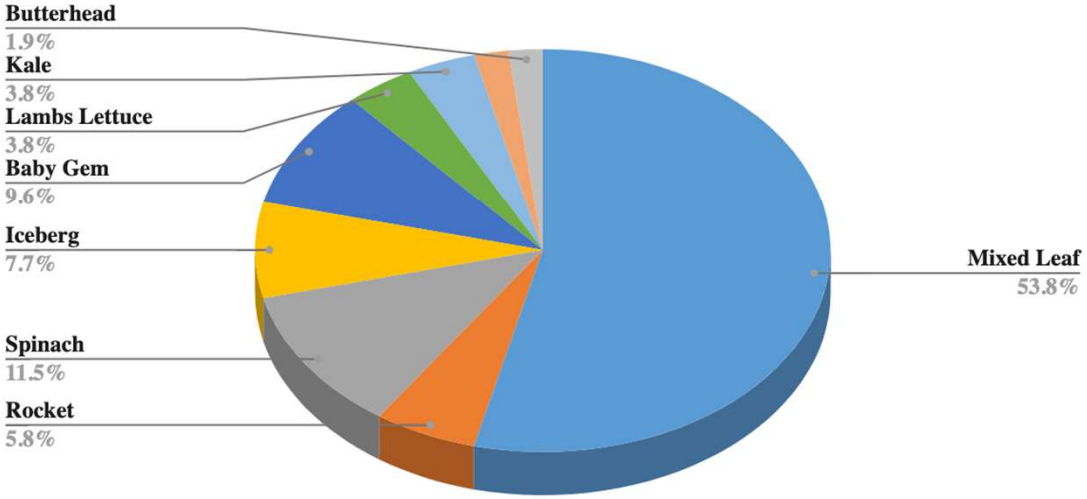




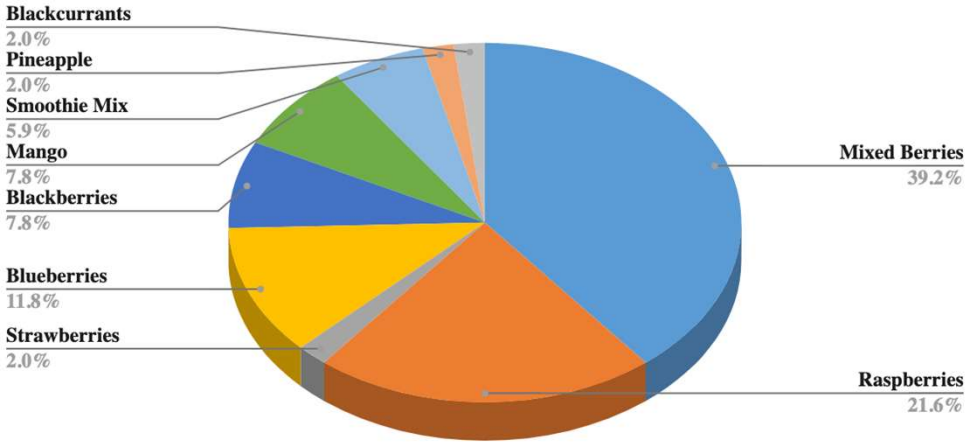
Vegetable Sample Types - WHO Food SARS-COV-2



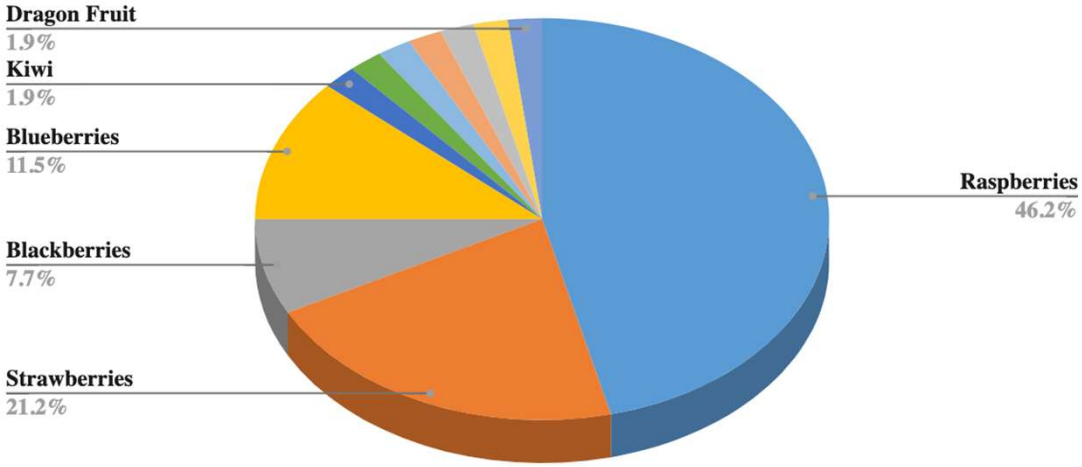
RTE Salad Sample Types - WHO Food SARS-COV-2



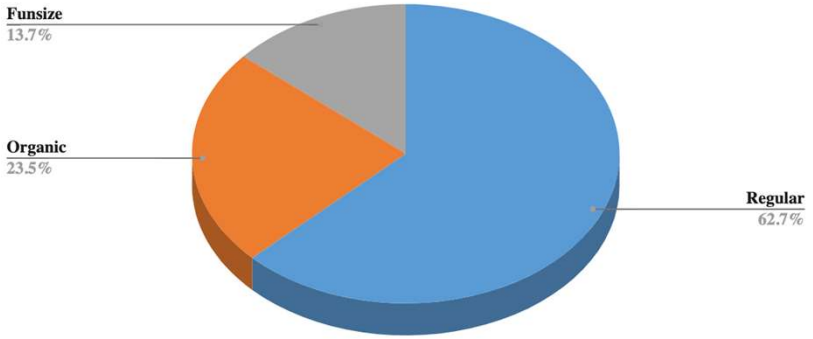
Frozen Fruit Sample Types - WHO Food SARS-COV-2

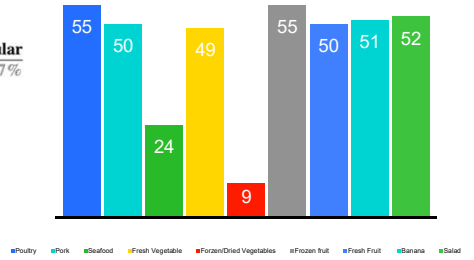


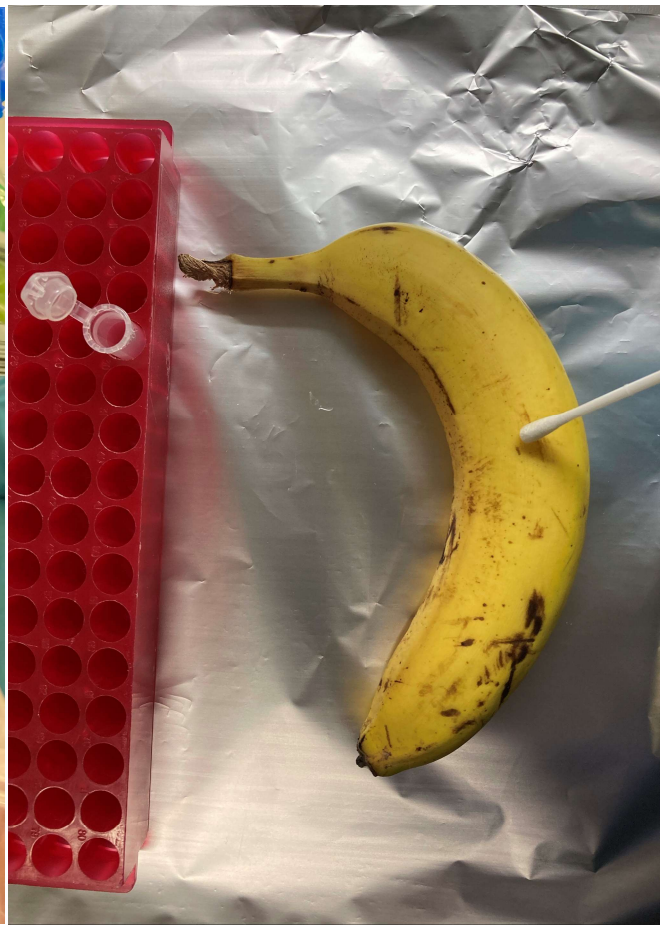
Fresh Fruit Sample Types - WHO Food SARS-COV-2



Banana Sample Types - WHO Food SARS-COV-2



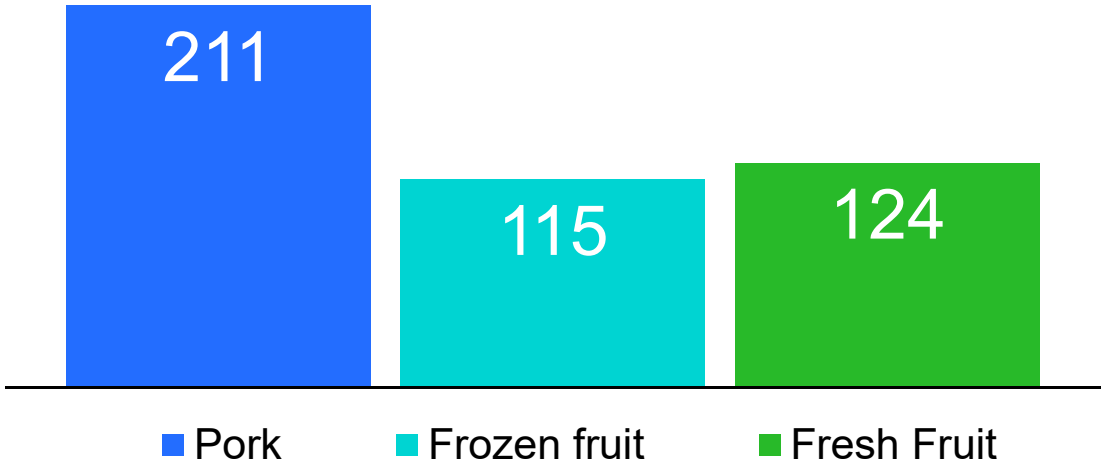




All the packaging were tested as surface swabs, including skin of bananas

367 samples

Retrospective study



Pork meat

- Small sausages: 74
- Large sausages: 63
- Fermented sausages: 45
- Pork liver: 29

Small Fruits

- Raspberry: 61
- Strawberry: 63
- Frozen Raspberry: 56
- Frozen Strawberry: 59

Abiotic surfaces of high-touch locations

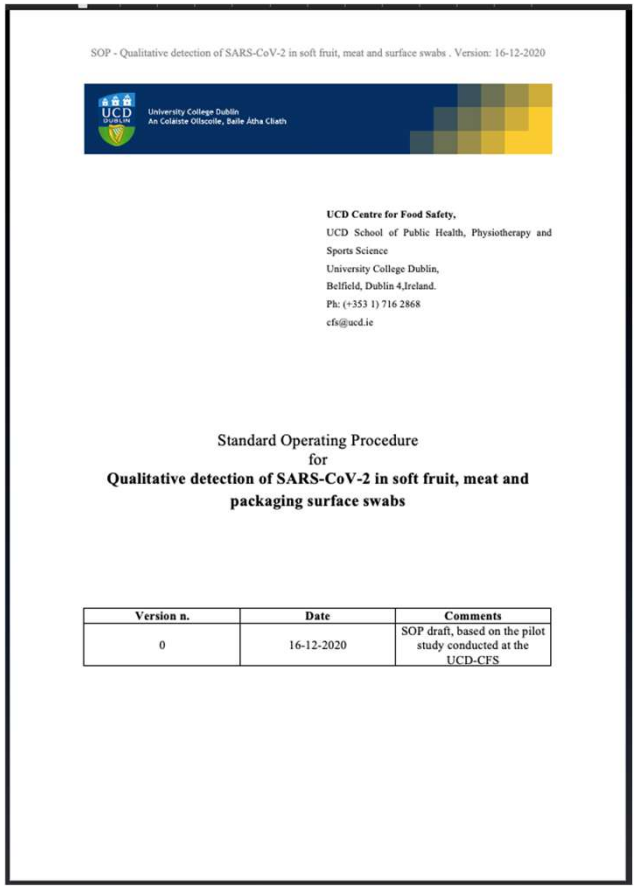
Wastewater samples

The samples were collected from a **line of untreated wastewater** (e.g., lift stations, interceptors, manholes) includes **waste from building use** (e.g., toilets, showers, sinks), which contains human faecal waste, as well as the waste of industrial use/rainwater.

Bangor University, 2020

Collection of the samples:

- **composite samples** are collected by **pooling multiple grab samples** at a specified frequency over a set time period – typically 8 hours for wastewater surveillance. You can collect composite samples of untreated wastewater manually (e.g., one sub-sample per 500 cubic meters of flow or 125 ml every 2 hours).
- **rapidly in one time (grab sample) reaching the point for the sampling**. However, grab samples may be less representative of community fecal contributions than composite samples. For untreated wastewater and sludge, grab samples represent a single moment in time and are highly influenced by daily fluctuations in wastewater flow and composition. If this is the case, we suggest taking the sample at the highest pick of usage in the working day.



SOP - Qualitative detection of SARS-CoV-2 in soft fruit, meat and surface swabs . Version: 16-12-2020

University College Dublin
An Coláiste Ollscoile, Baile Átha Cliath

UCD Centre for Food Safety,
UCD School of Public Health, Physiotherapy and Sports Science
University College Dublin,
Belfield, Dublin 4,Ireland.
Ph: (+353 1) 716 2868
cfs@ucd.ie

Standard Operating Procedure
for
Qualitative detection of SARS-CoV-2 in soft fruit, meat and packaging surface swabs

Version n.	Date	Comments
0	16-12-2020	SOP draft, based on the pilot study conducted at the UCD-CFS

- Remove the individually wrapped swab from the envelope and immerge immediately into sterile tubes containing 1-3 mL of VTM;
- Lightly tap the swab tip to the inside of the transport container to remove excess transport medium (liquid);
- Use swab to sample surface areas of interest (25 cm^2 is commonly used but a specified area is not required). Swab with moderate pressure while moving in at least two different directions and rotating the swab so that the entire swab surface area is used. Avoid letting the swab dry completely.
- Immediately after sampling, place the swab back into the transport container, cut the stick at the breakpoint, bending gently and screw the cap on tightly.

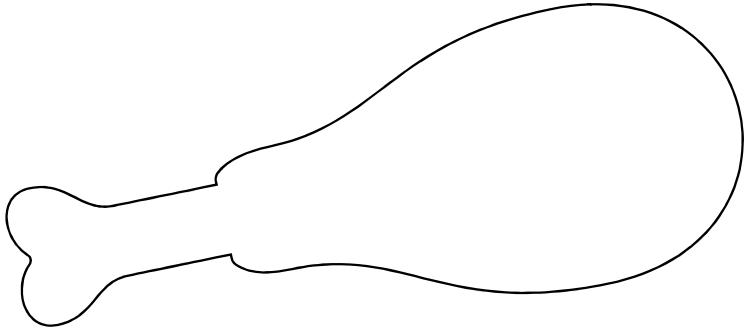
Date	Swab No.	Area	Location
15-Feb	1	Blank	Blank
15-Feb	2	Visitors entrance	Door inside
15-Feb	3	Whey SM office door	Door inside
15-Feb	4	Dairy Panel room door	Door outside
15-Feb	5	ED Room Door Handle	Door inside
15-Feb	6	Whey Lab door	Door inside
15-Feb	7	Liquid lab door	Door outside
15-Feb	8	Photocopier ED	Touch panel
15-Feb	9	Photocopier Admin	Touch panel
15-Feb	10	Driver fridge	Door outside
15-Feb	11	Driver freezer	Door outside
15-Feb	12	Foam Machine	Handle
15-Feb	13	Whey office air con unit	Unit on ceiling
15-Feb	14	Whey SM keyboard	Keyboard
15-Feb	15	Dairy SM office door handle	Inside handle
15-Feb	16	ED panelroom keybaord	Composite samples
15-Feb	17	Crystallisation keyboard	Keyboard
15-Feb	18	Chair Handle in Whey office	Peters chair
15-Feb	19	Elevator N3	Buttons
15-Feb	20	Control room phone ED	Composite samples
15-Feb	21	Casein Keyboard	Composite sample
15-Feb	22	Casein door handle	Door handle outside
15-Feb	23	Security hut	Antibiotic touch panel
15-Feb	24	Canteen	Composit sample of microwave handles
15-Feb	25	Bag off door handle	Door inside

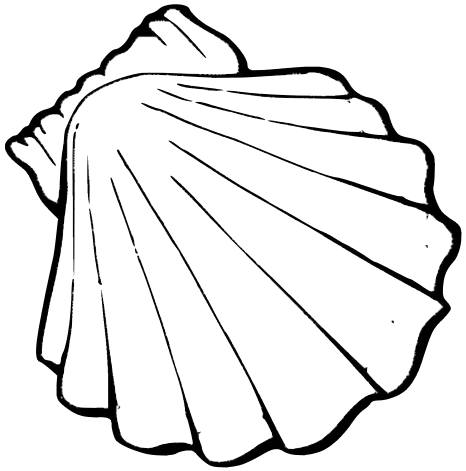
75 samples high touch swabs

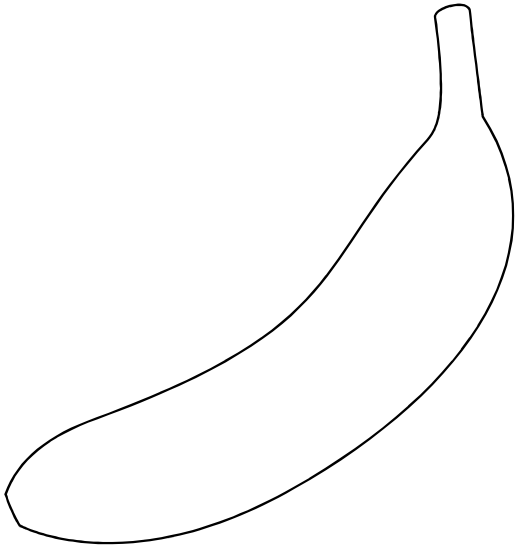
6 wastewater samples

Methods – Virus particles concentrations and RNA extraction

- Meat products
- Bivalve Molluscan Shellfish and Crustacean
- Fruits and vegetables

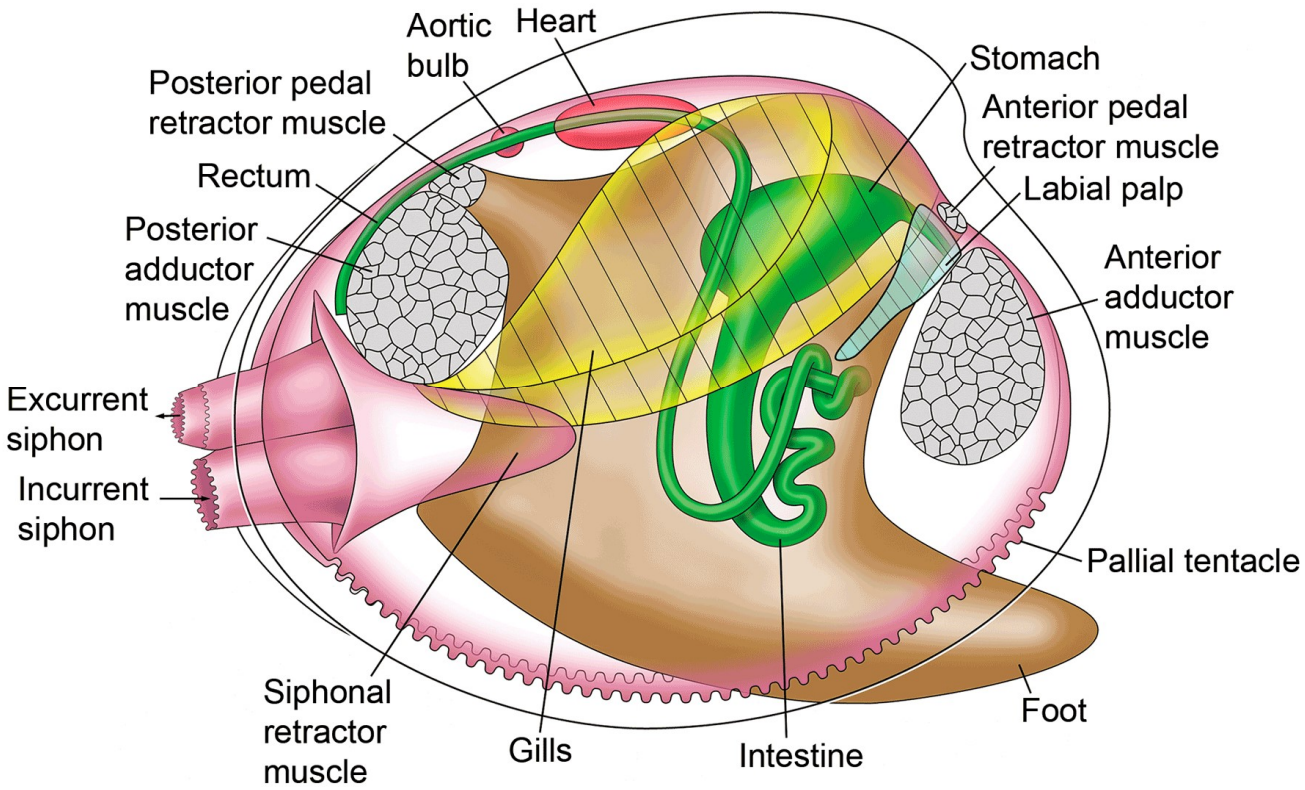






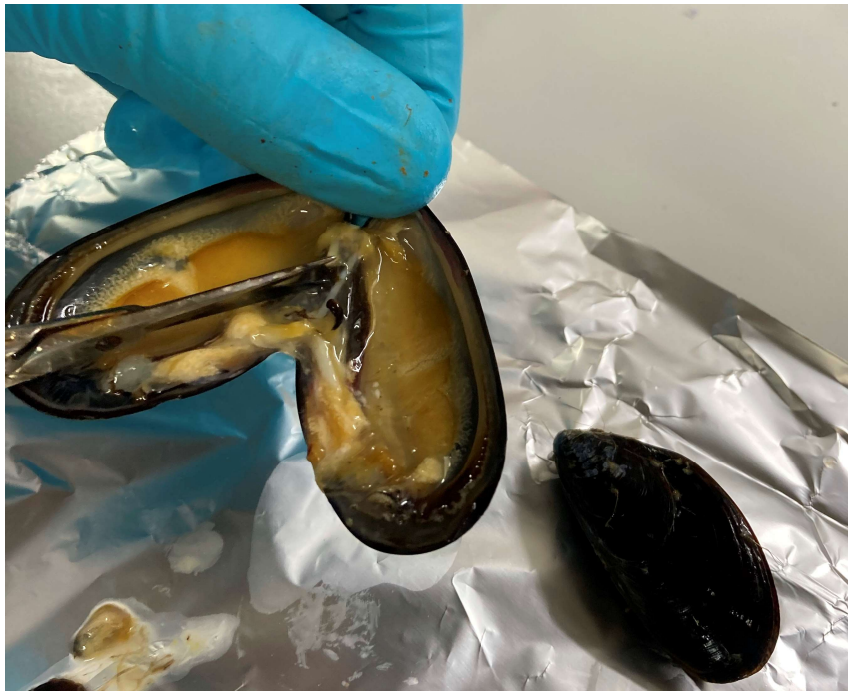
ISO 15216-1:2017 Horizontal method for determination of hepatitis A virus and norovirus using real-time RT-PCR
Meat products - validated SOP - UCD National Virus Reference Laboratory (Charlene Bennet)

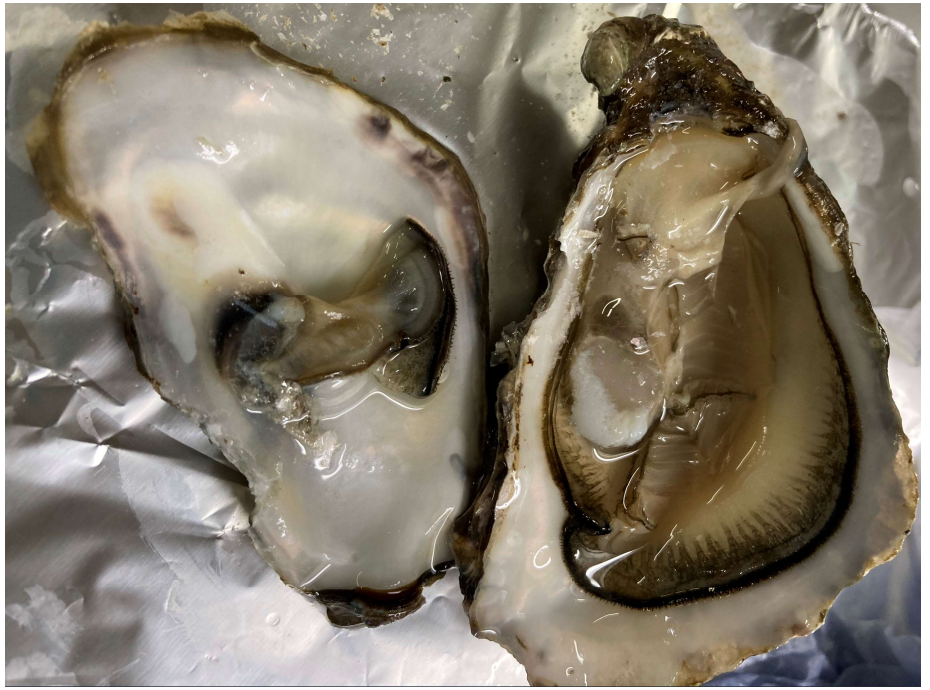
Methods – Virus particles concentrations and RNA extraction

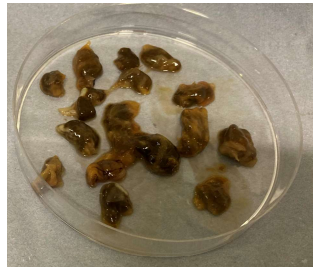


https://www.digitalatlasofancientlife.org/learn/mollusca/bivalvia/

Methods – Virus particles concentrations and RNA extraction

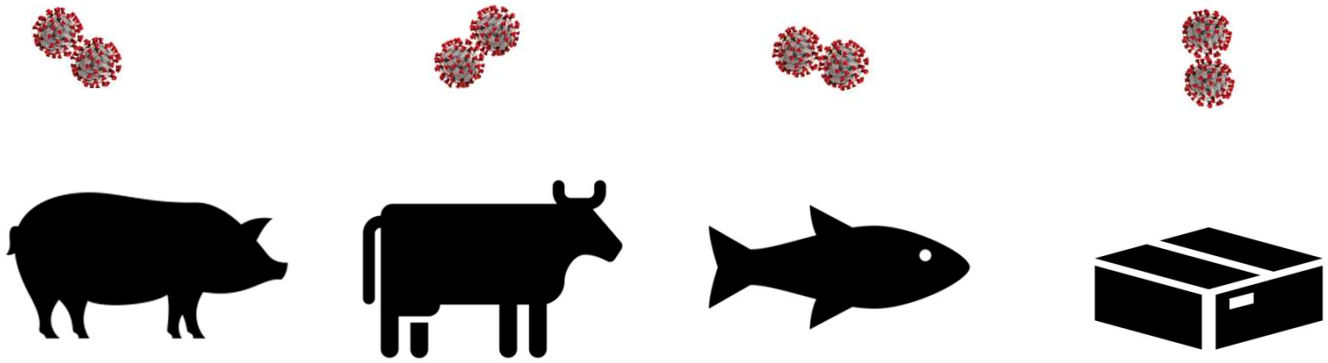






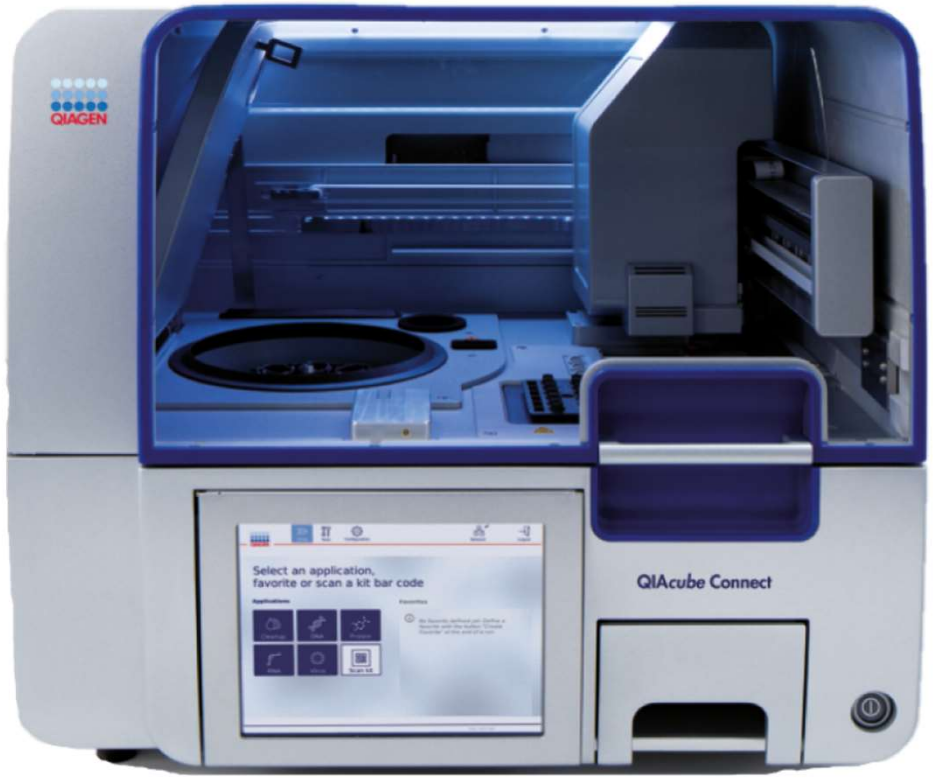
Experimental spiking of packaging, pork and meat (beef and salmon fillet)

Recovery of virus particles, cell cultures (counts)

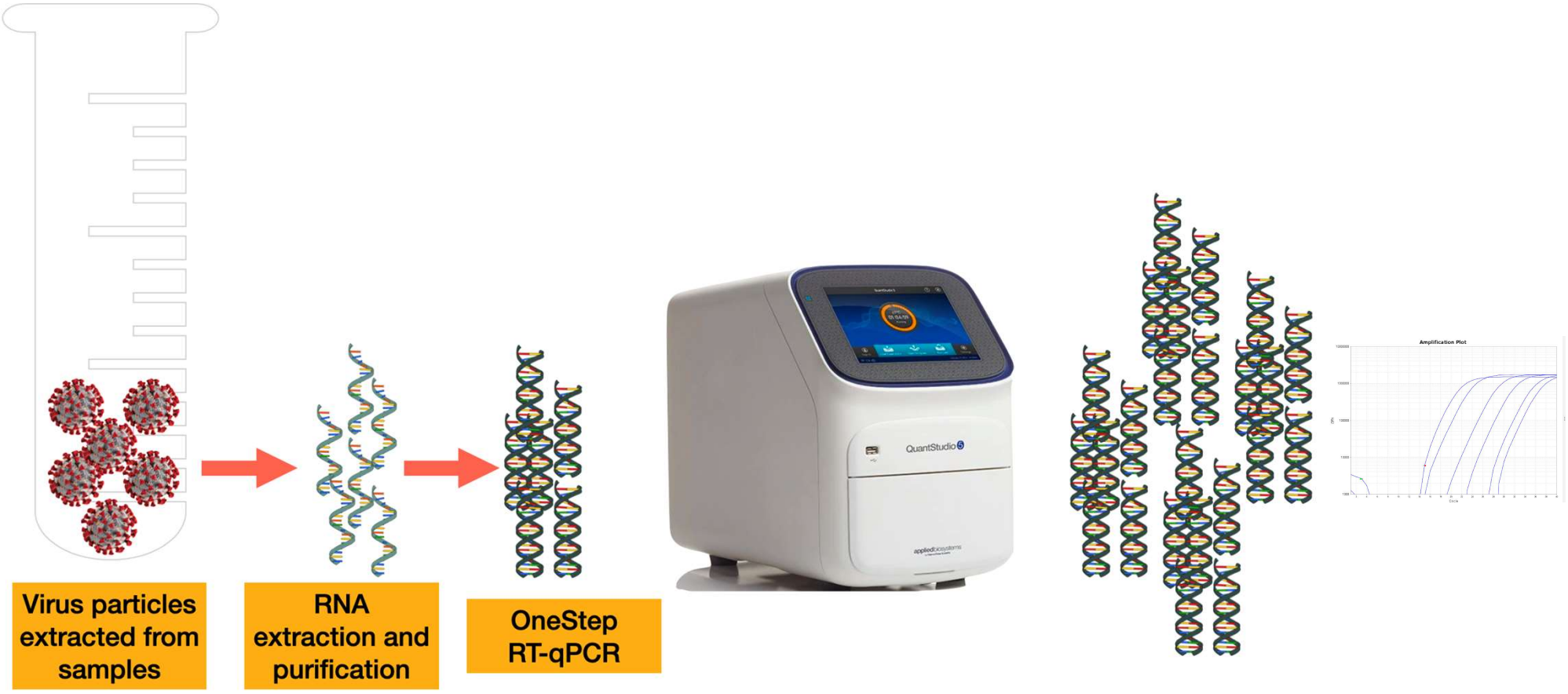


Methods – Virus particles concentrations and RNA extraction

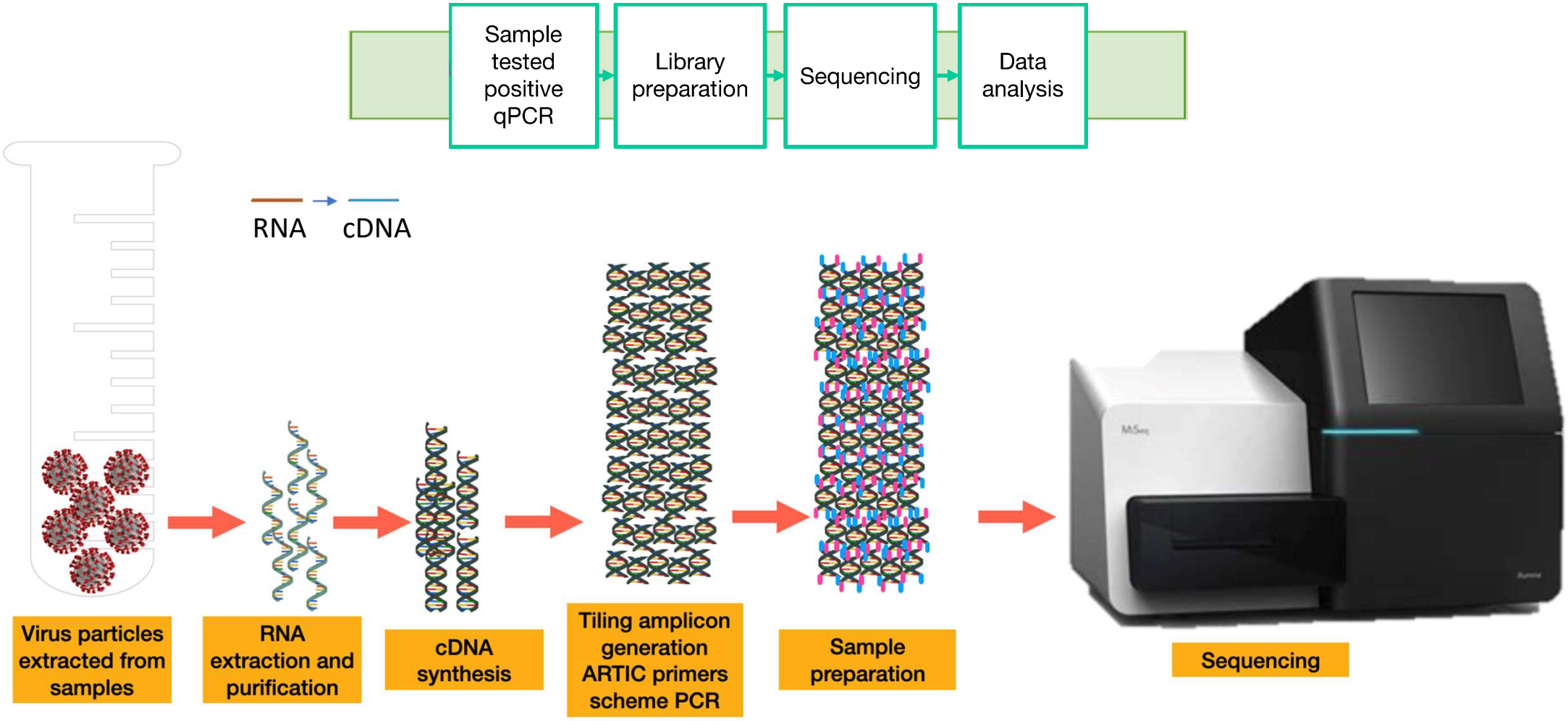
Automated purification of viral RNA using the QIAamp Viral RNA Mini Kit on QIAcube Connect



Methods – Reverse Transcriptase qPCR (RT-qPCR)



Methods – tiling amplicon sequencing



Implementation of a high-throughput Illumina MiSeq-based sequencing platform

PROTOCOL

Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples

Joshua Quick[1], Nathan D Grubaugh[2], Steven T Pullan[3], Ingra M Claro[4], Andrew D Smith[1], Karthik Gangavarapu[2], Glenn Oliveira[5], Refugio Robles-Sikisaka[2], Thomas F Rogers[2,6], Nathan A Beutler[2], Dennis R Burton[2], Lia Laura Lewis-Ximenez[7], Jaqueline Goes de Jesus[8], Marta Giovanetti[8,9], Sarah C Hill[10], Allison Black[11,12], Trevor Bedford[11], Miles W Carroll[3,13], Marcio Nunes[14], Luiz Carlos Alcantara Jr.[8], Ester C Sabino[4], Sally A Baylis[15], Nuno R Faria[10], Matthew Loose[16], Jared T Simpson[17], Oliver G Pybus[10], Kristian G Andersen[2,5] & Nicholas J Loman[1]

[1]Institute of Microbiology and Infection, School of Biosciences, University of Birmingham, Birmingham, UK. [2]The Scripps Research Institute, La Jolla, California, USA. [3]Public Health England, National Infection Service, Porton Down, Salisbury, UK. [4]Department of Infectious Disease and Institute of Tropical Medicine, University of Saõ Paulo, Saõ Paulo, Brazil. [5]Scripps Translational Science Institute, La Jolla, California, USA. [6]Massachusetts General Hospital, Boston, Massachusetts, USA. [7]Instituto Oswaldo Cruz, Fundação Oswaldo Cruz, Rio de Janeiro, Brazil. [8]Fundação Oswaldo Cruz (FIOCRUZ), Salvador, Brazil. [9]University of Rome, Tor Vergata, Italy. [10]Department of Zoology, University of Oxford, Oxford, UK. [11]Vaccine and Infectious Disease Division, Fred Hutchinson Cancer Research Center, Seattle, Washington, USA. [12]Department of Epidemiology, University of Washington, Seattle, Washington, USA. [13]University of Southampton, South General Hospital, Southampton, UK. [14]Instituto Evandro Chagas, Belem, Brazil. [15]Paul-Ehrlich-Institut, Langen, Germany. [16]DeepSeq, School of Life Sciences, University of Nottingham, Nottingham, UK. [17]OICR, Toronto, Canada. Correspondence should be addressed to N.J.L. (n.j.loman@bham.ac.uk).

Published online 24 May 2017; doi:10.1038/nprot.2017.066

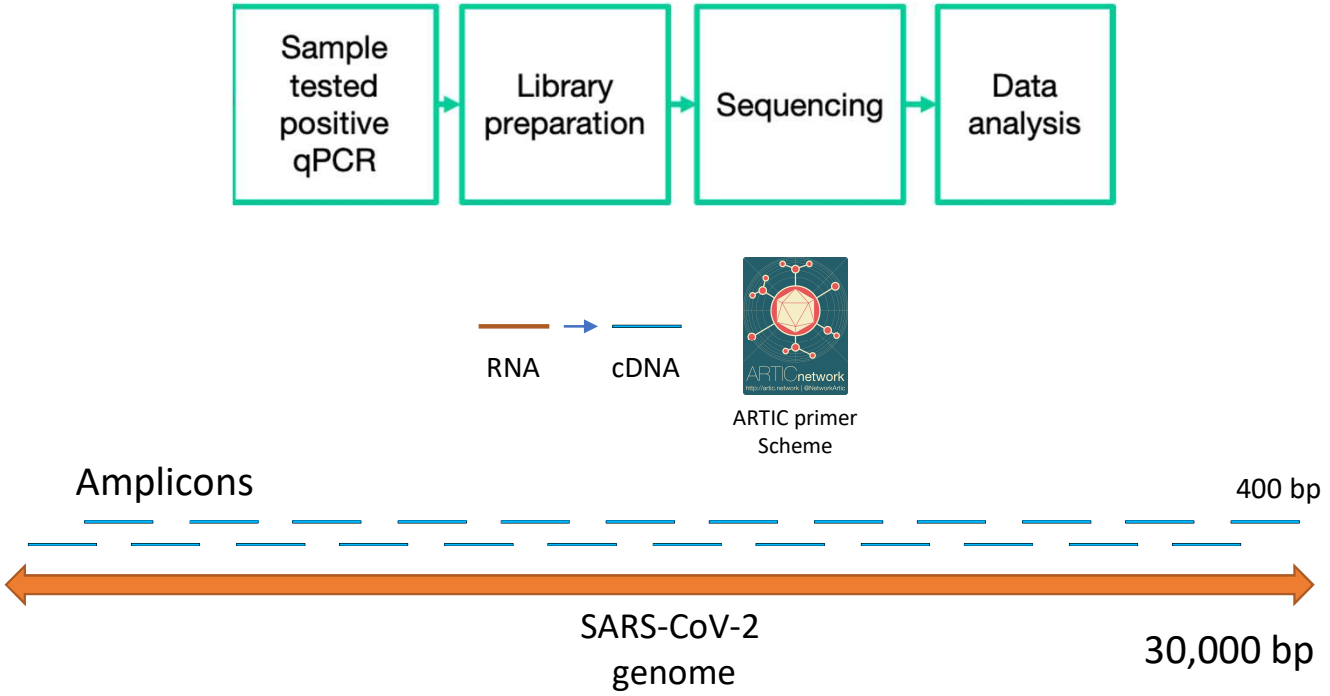
Genome sequencing has become a powerful tool for studying emerging infectious diseases; however, genome sequencing directly from clinical samples (i.e., without isolation and culture) remains challenging for viruses such as Zika, for which metagenomic sequencing methods may generate insufficient numbers of viral reads. Here we present a protocol for generating coding-sequence-complete genomes, comprising an online primer design tool, a novel multiplex PCR enrichment protocol, optimized library preparation methods for the portable MinION sequencer (Oxford Nanopore Technologies) and the Illumina range of instruments, and a bioinformatics pipeline for generating consensus sequences. The MinION protocol does not require an Internet connection for analysis, making it suitable for field applications with limited connectivity. Our method relies on multiplex PCR for targeted enrichment of viral genomes from samples containing as few as 50 genome copies per reaction. Viral consensus sequences can be achieved in 1–2 d by starting with clinical samples and following a simple laboratory workflow. This method has been successfully used by several groups studying Zika virus evolution and is facilitating an understanding of the spread of the virus in the Americas. The protocol can be used to sequence other viral genomes using the online Primal Scheme primer designer software. It is suitable for sequencing either RNA or DNA viruses in the field during outbreaks or as an inexpensive, convenient method for use in the lab.

INTRODUCTION

Genome sequencing of viruses has been used to study the spread of disease in outbreaks[1]. Real-time genomic surveillance is important in managing viral outbreaks, as it can provide insights into how viruses transmit, spread and evolve[1–4]. Such work depends on rapid sequencing of viral material directly from clinical samples—i.e., without the need to isolate the virus in pure culture. During the Ebola virus epidemic of 2013–2016, prospective viral genome sequencing was able to provide critical information on virus evolution and help inform epidemiological investigations[3–6]. Sequencing directly from clinical samples is faster, less laborious and more amenable to near-patient work than time-consuming culture-based methods. Metagenomics, the process of sequencing the total nucleic acid content in a sample (typically cDNA or DNA), has been successfully applied to both virus discovery and diagnostics[7–9]. Metagenomic approaches have seen rapid adoption over the past decade, fueled by relentless improvements in the yield of high-throughput sequencing instruments[5,10–12]. Whole-genome sequencing of Ebola virus directly from clinical samples without amplification was possible because of the extremely high virus copy numbers found in acute cases[13–15]. However, direct metagenomic sequencing from clinical samples poses challenges with regard to sensitivity: genome coverage may be low or absent when attempting to sequence viruses that are present at low abundance in a sample with high levels of host nucleic acid background.

Development of the protocol

During recent work on the Zika virus epidemic[16], we found that it was difficult to generate whole-genome sequences directly from clinical samples using metagenomic approaches (**Table 1**). These samples had cycle threshold (Ct) values between 33.9 and 35.9 (equivalent to 10–48 genome copies per microliter). Before sequencing, these samples were depleted of human rRNA and prepared for metagenomic sequencing on the Illumina MiSeq platform as previously described[2,17]. In these cases, sequences from Zika virus comprised <0.01% of the data set, resulting in incomplete coverage. Greater coverage and depth are critical for accurate genome reconstruction and subsequent phylogenetic inference. In addition, there are substantial sequencing, analysis and storage costs associated with generating large sequencing data sets; therefore, metagenomic approaches currently do not lend themselves to the cost-effective use of lower-throughput portable sequencing devices such as the Oxford Nanopore MinION.

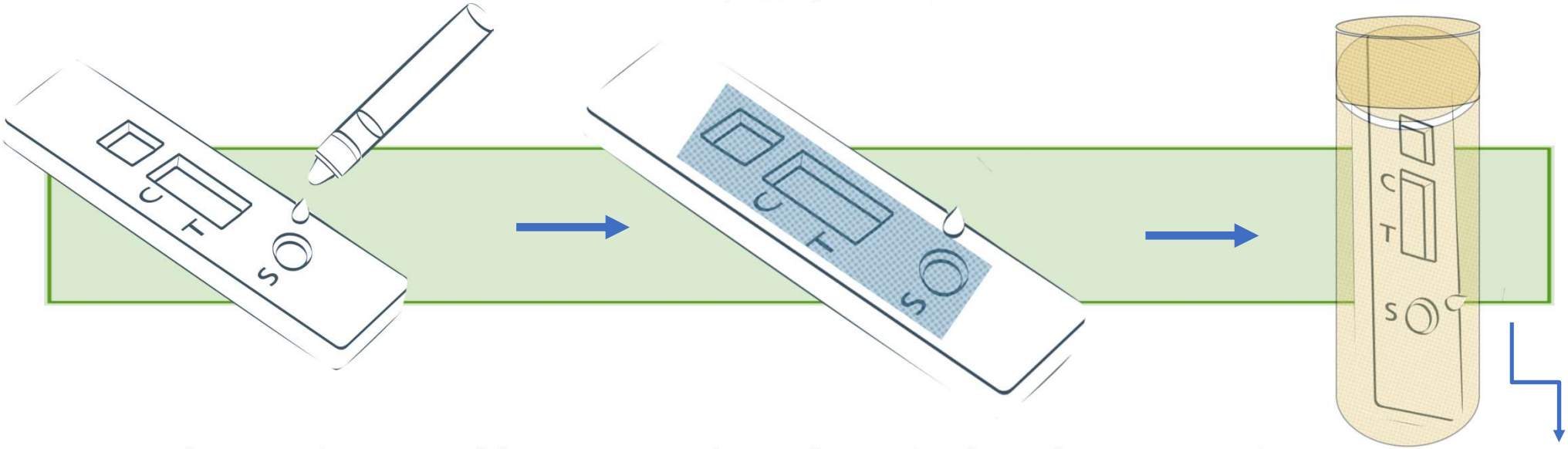


Methods – LFD

SFI-funded project:

Understanding and Preventing COVID-19 Outbreaks in Meat Processing Plants

https://upcom.ie/



Sequencing

Implemented a protocol for extracting the viral particles from the spent rapid tests

Extraction of high quality viral RNA

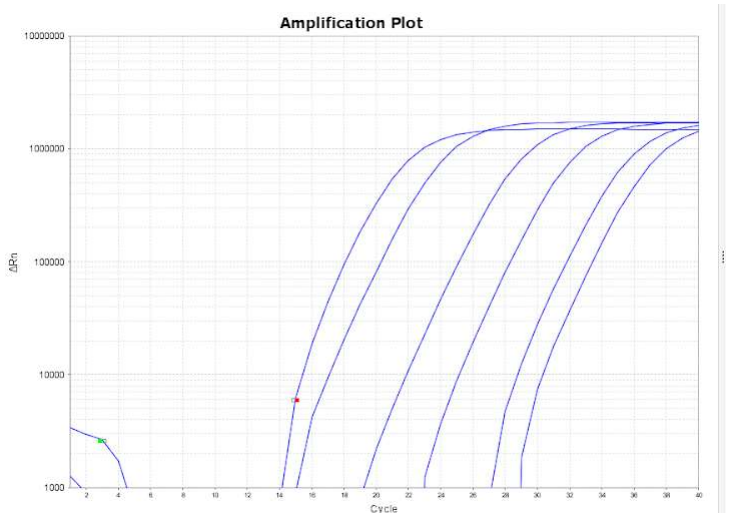
Direct Sequencing (not needed a second swabs from tested positive)

Detection of variants, tracing outbreaks, surveillance, *system for future outbreaks?*

Results – sampling and RT-qPCR

- 10 samples pooled
- Plasmidic DNA
- RNA positive samples
- Process control (MeV) lysis step.

1,261 samples in total



Results

The matrices were extracted and tested in ten units

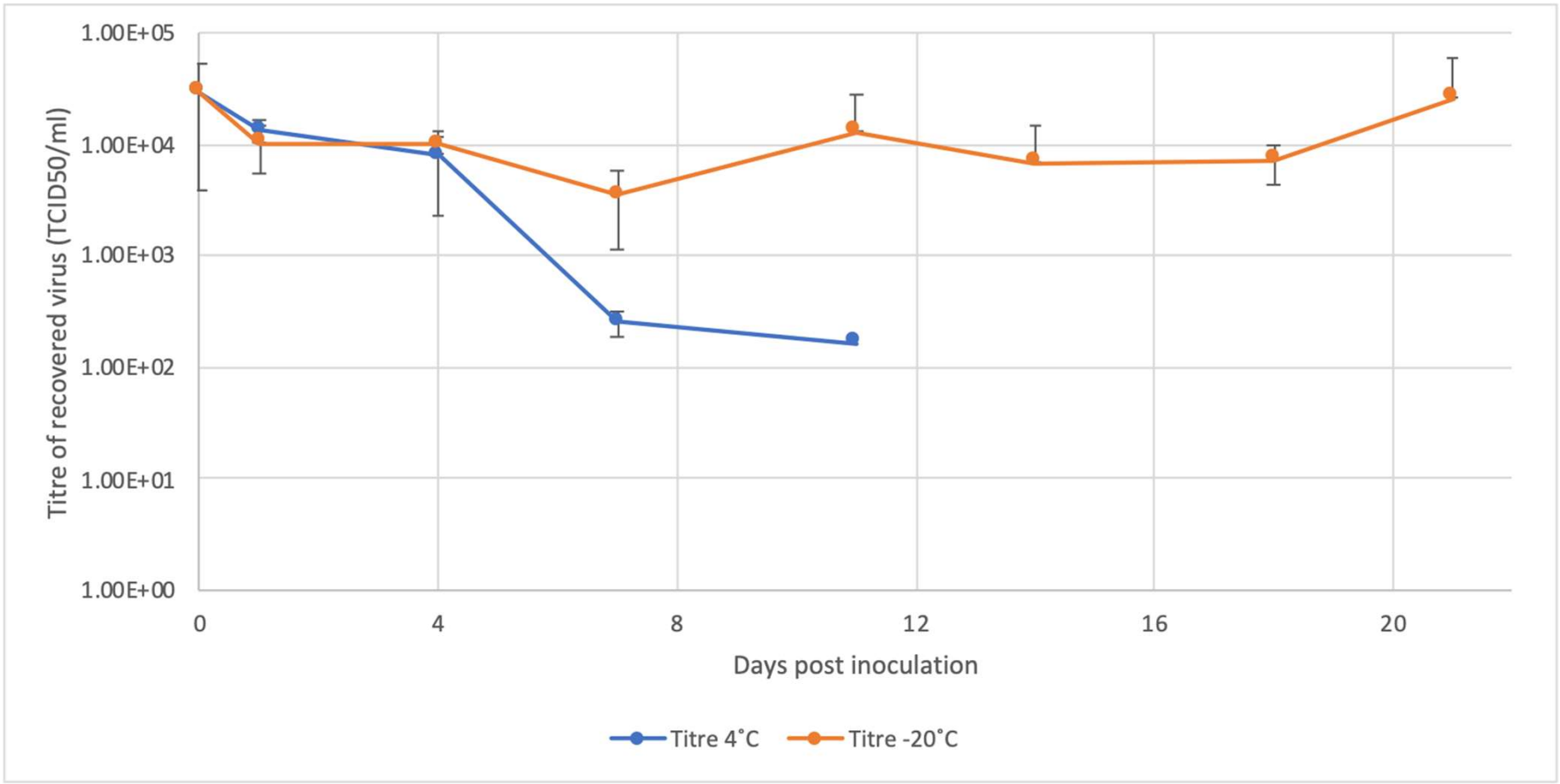
4 pools resulted very close to the limit of detection

Single samples repeated (40)

& Repeated the extraction from original samples

(31 swabs and 9 fresh vegetables)

All the samples resulted negative



Russell, 2021

Is there a risk from food or packaging?

Guidance from the World Health Organization (WHO) for businesses also states it is highly unlikely that people can contract COVID-19 from food or food packaging.

The risk of getting sick with COVID-19 from eating or handling food, including frozen food and produce and food packages, **is considered very low.** It is possible a person can get it by touching a surface or object, including food or packaging, that has the virus on it and then touching their mouth, nose, or possibly eyes, according to the Centers for Disease Control and Prevention.

Sampling plan: the model

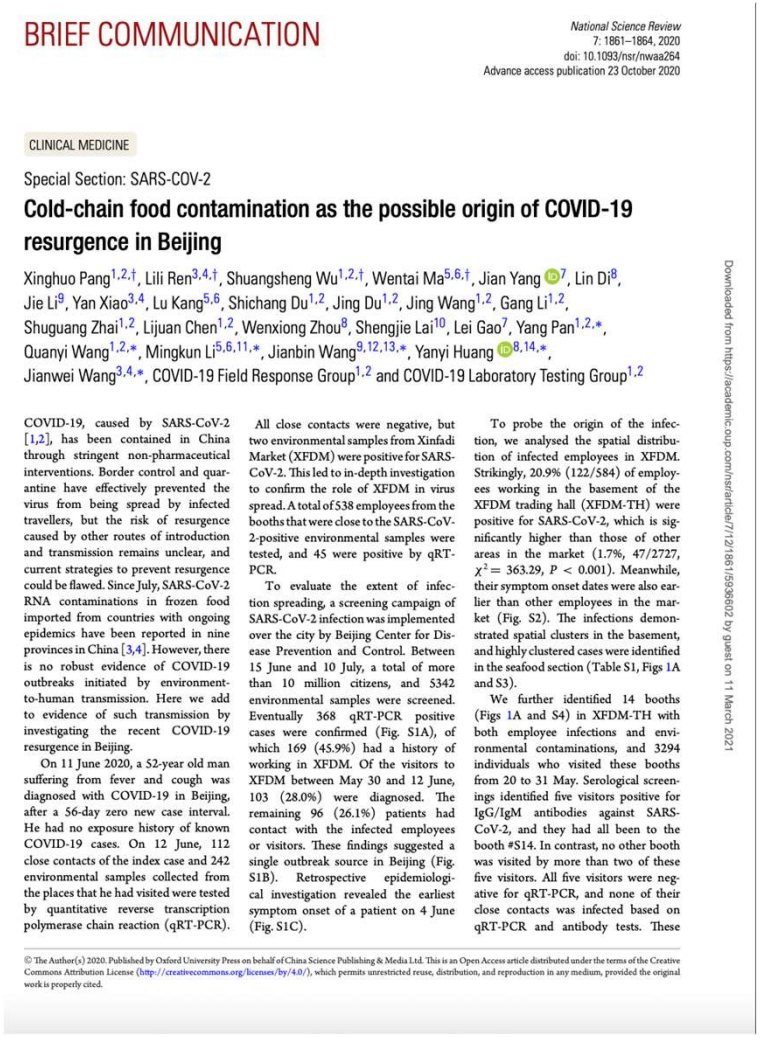
Time for the sampling 3 weeks - 21st January - 11th February

Is this enough?

SOPs

Sharing

Networking



BRIEF COMMUNICATION

National Science Review
7: 1861–1864, 2020
doi: 10.1093/nsr/nwaa264
Advance access publication 23 October 2020

CLINICAL MEDICINE

Special Section: SARS-COV-2

Cold-chain food contamination as the possible origin of COVID-19 resurgence in Beijing

Xinghuo Pang[1,2,†], Lili Ren[3,4,†], Shuangsheng Wu[1,2,†], Wentai Ma[5,6,†], Jian Yang[7], Lin Di[8], Jie Li[9], Yan Xiao[3,4], Lu Kang[5,6], Shichang Du[1,2], Jing Du[1,2], Jing Wang[1,2], Gang Li[1,2], Shuguang Zhai[1,2], Lijuan Chen[1,2], Wenxiong Zhou[8], Shengjie Lai[10], Lei Gao[7], Yang Pan[1,2,*], Quanyi Wang[1,2,*], Mingkun Li[5,6,11,*], Jianbin Wang[9,12,13,*], Yanyi Huang[8,14,*], Jianwei Wang[3,4,*], COVID-19 Field Response Group[1,2] and COVID-19 Laboratory Testing Group[1,2]

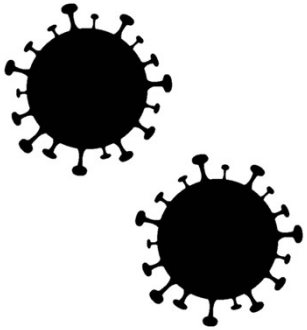
COVID-19, caused by SARS-CoV-2 [1,2], has been contained in China through stringent non-pharmaceutical interventions. Border control and quarantine have effectively prevented the virus from being spread by infected travellers, but the risk of resurgence caused by other routes of introduction and transmission remains unclear, and current strategies to prevent resurgence could be flawed. Since July, SARS-CoV-2 RNA contaminations in frozen food imported from countries with ongoing epidemics have been reported in nine provinces in China [3,4]. However, there is no robust evidence of COVID-19 outbreaks initiated by environment-to-human transmission. Here we add to evidence of such transmission by investigating the recent COVID-19 resurgence in Beijing.

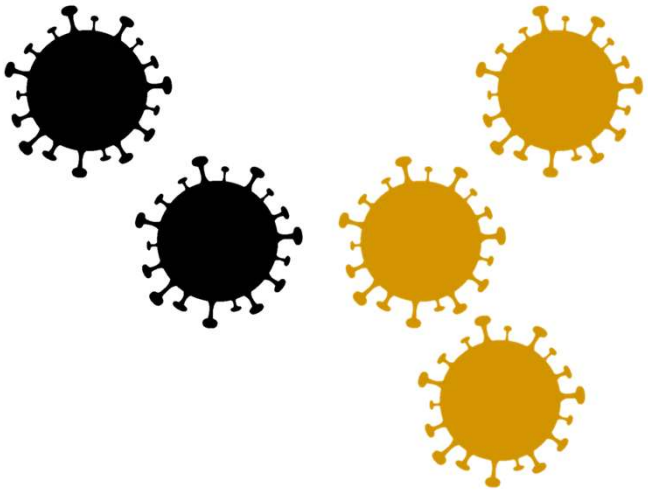
On 11 June 2020, a 52-year old man suffering from fever and cough was diagnosed with COVID-19 in Beijing, after a 56-day zero new case interval. He had no exposure history of known COVID-19 cases. On 12 June, 112 close contacts of the index case and 242 environmental samples collected from the places that he had visited were tested by quantitative reverse transcription polymerase chain reaction (qRT-PCR). All close contacts were negative, but two environmental samples from Xinfadi Market (XFDM) were positive for SARS-CoV-2. This led to in-depth investigation to confirm the role of XFDM in virus spread. A total of 538 employees from the booths that were close to the SARS-CoV-2-positive environmental samples were tested, and 45 were positive by qRT-PCR.

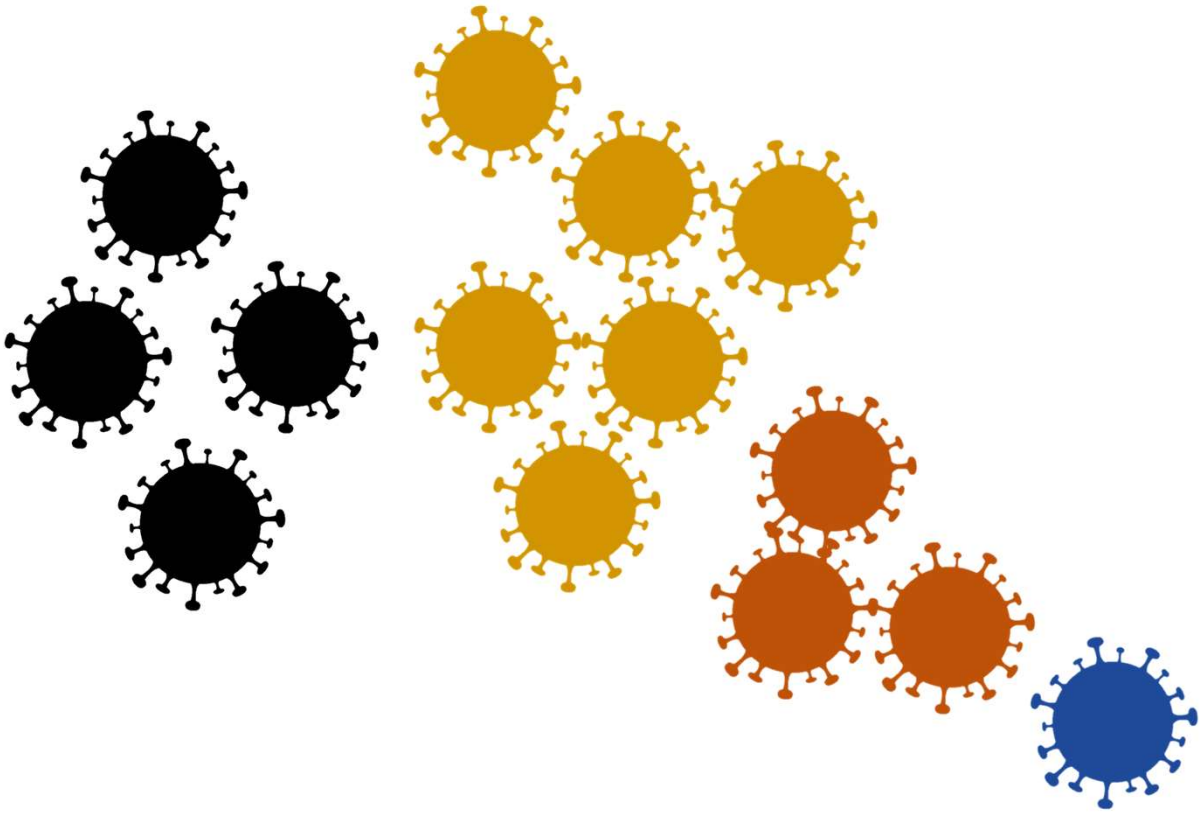
To evaluate the extent of infection spreading, a screening campaign of SARS-CoV-2 infection was implemented over the city by Beijing Center for Disease Prevention and Control. Between 15 June and 10 July, a total of more than 10 million citizens, and 5342 environmental samples were screened. Eventually 368 qRT-PCR positive cases were confirmed (Fig. S1A), of which 169 (45.9%) had a history of working in XFDM. Of the visitors to XFDM between May 30 and 12 June, 103 (28.0%) were diagnosed. The remaining 96 (26.1%) patients had contact with the infected employees or visitors. These findings suggested a single outbreak source in Beijing (Fig. S1B). Retrospective epidemiological investigation revealed the earliest symptom onset of a patient on 4 June (Fig. S1C).

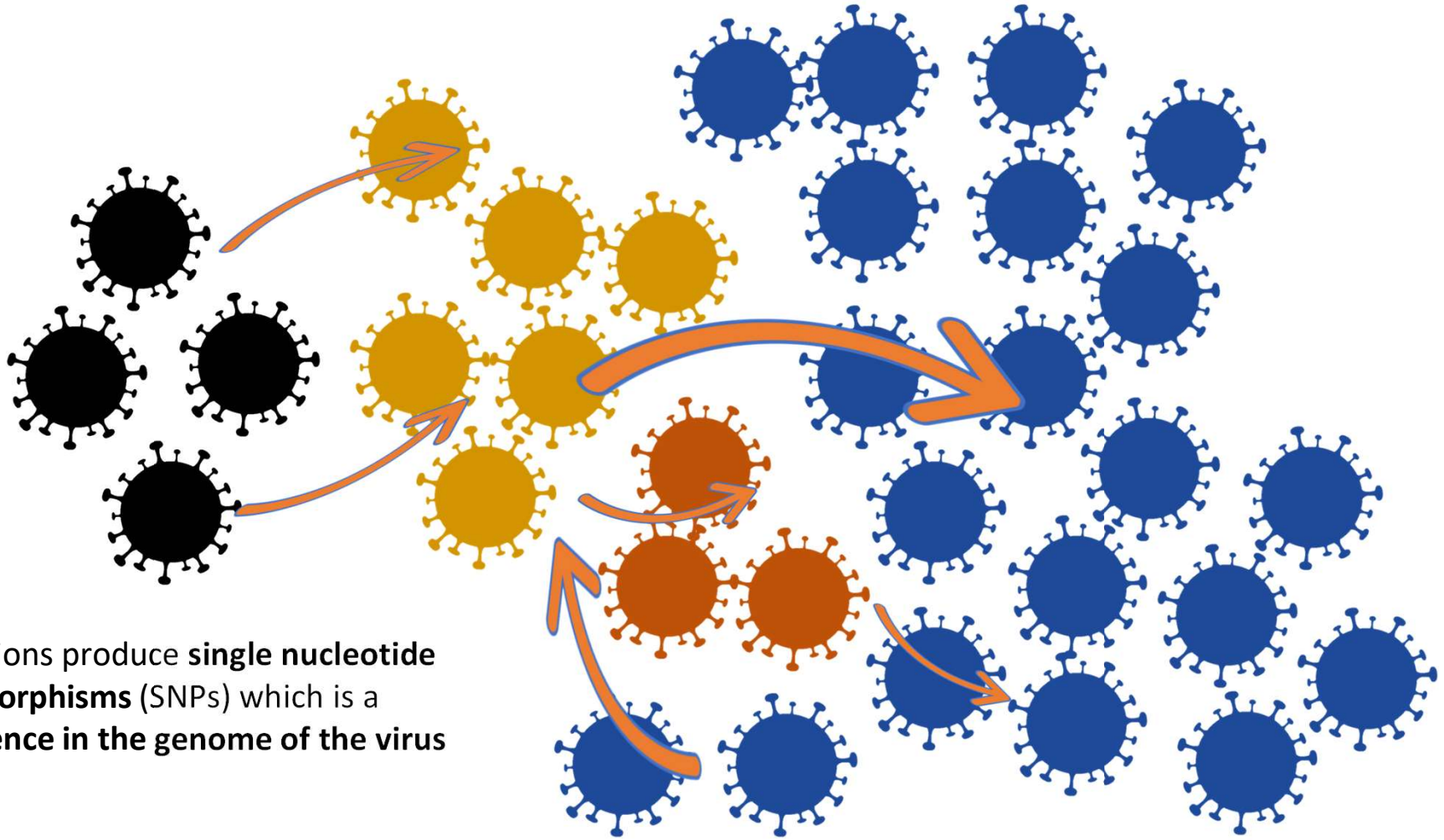
To probe the origin of the infection, we analysed the spatial distribution of infected employees in XFDM. Strikingly, 20.9% (122/584) of employees working in the basement of the XFDM trading hall (XFDM-TH) were positive for SARS-CoV-2, which is significantly higher than those of other areas in the market (1.7%, 47/2727, $\chi^2 = 363.29$, $P < 0.001$). Meanwhile, their symptom onset dates were also earlier than other employees in the market (Fig. S2). The infections demonstrated spatial clusters in the basement, and highly clustered cases were identified in the seafood section (Table S1, Figs 1A and S3).

We further identified 14 booths (Figs 1A and S4) in XFDM-TH with both employee infections and environmental contaminations, and 3294 individuals who visited these booths from 20 to 31 May. Serological screenings identified five visitors positive for IgG/IgM antibodies against SARS-CoV-2, and they had all been to the booth #S14. In contrast, no other booth was visited by more than two of these five visitors. All five visitors were negative for qRT-PCR, and none of their close contacts was infected based on qRT-PCR and antibody tests. These

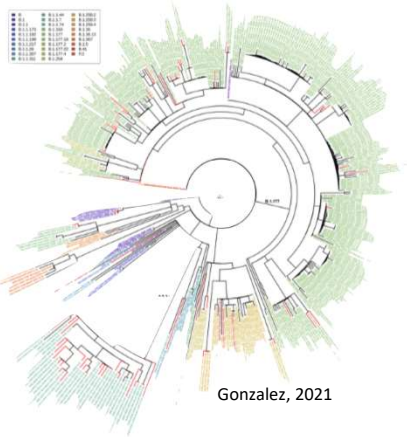




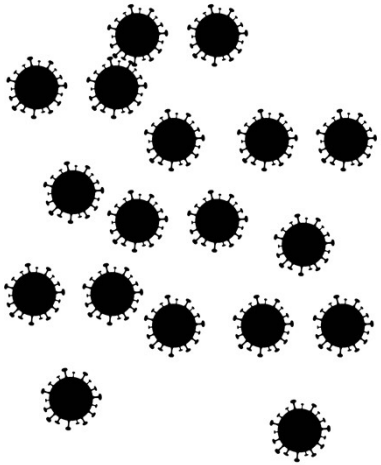


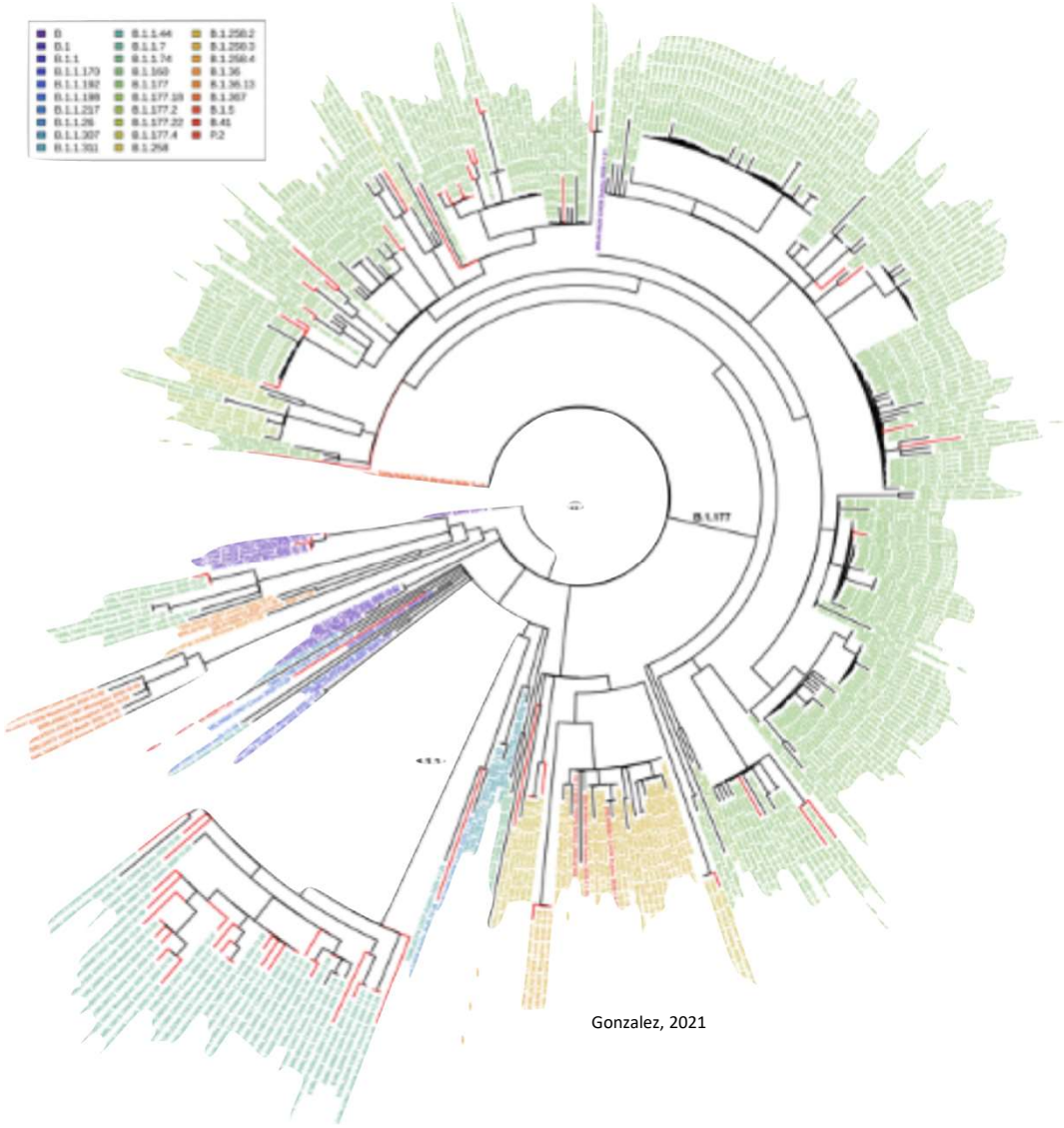


Mutations produce **single nucleotide polymorphisms** (SNPs) which is a **difference in the genome of the virus**

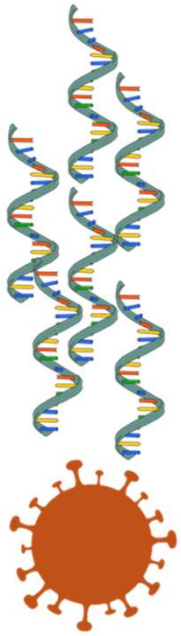


Gonzalez, 2021

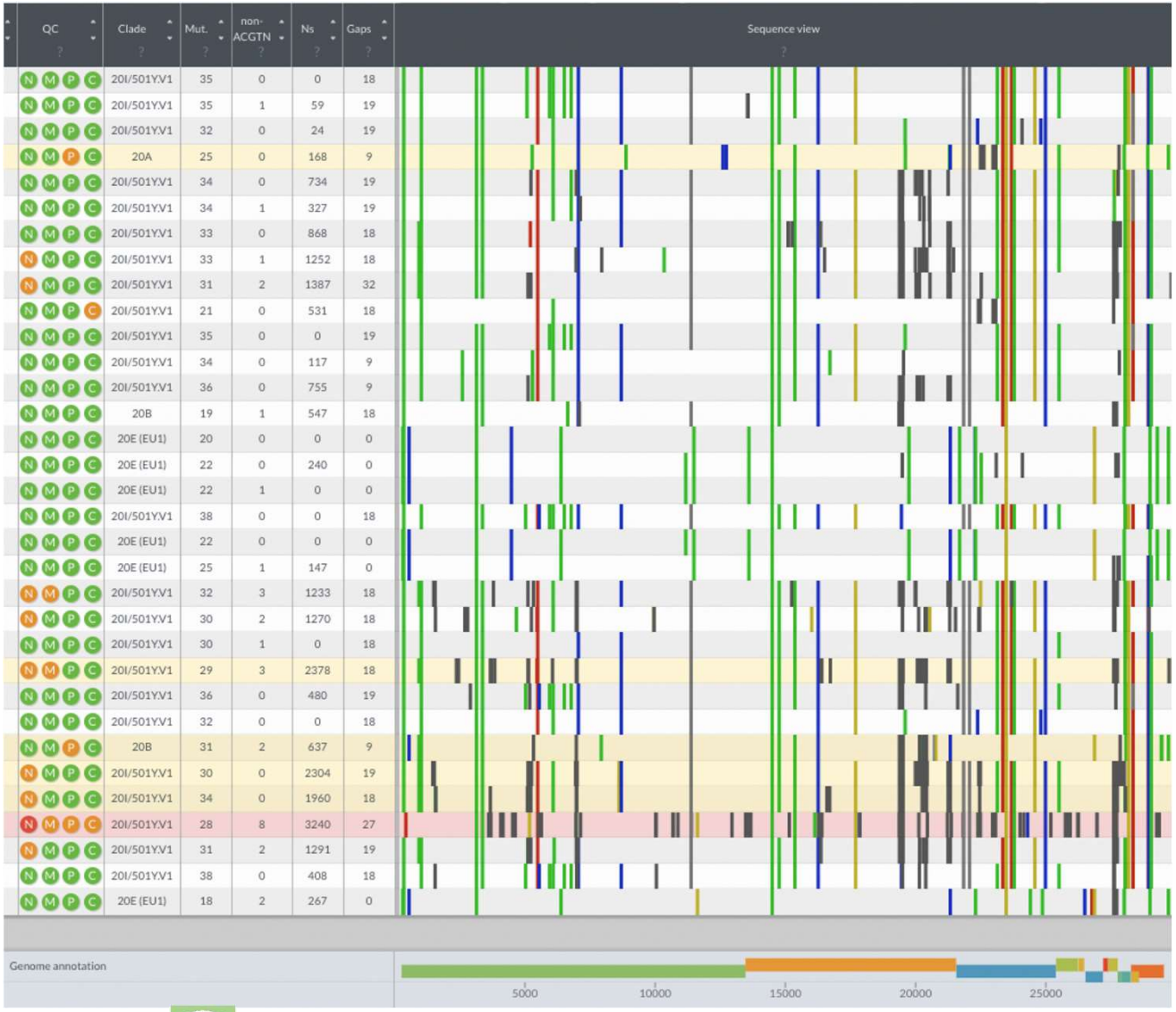




Gonzalez, 2021

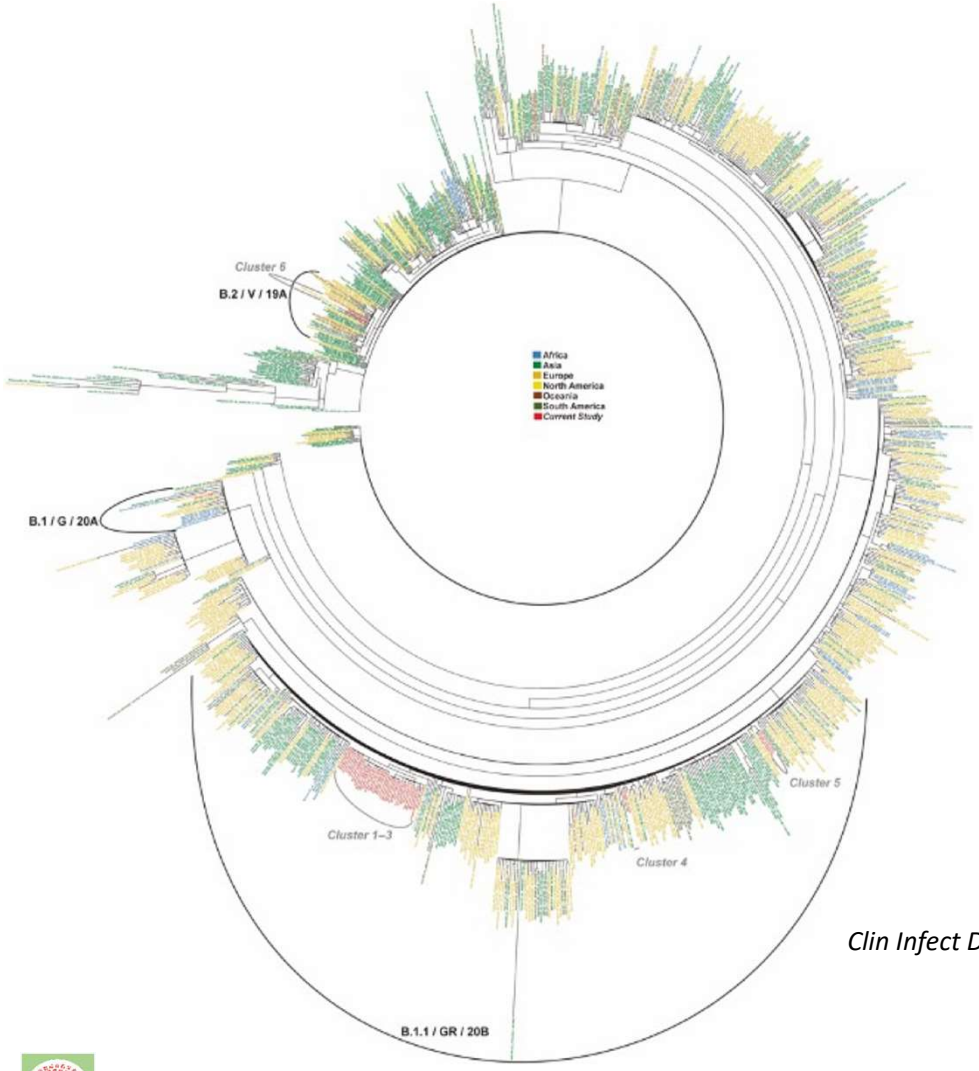


Viral RNA



COG-UK
PANGOLIN
NextStrain

GISAID



Clin Infect Dis, 72:11, 2021 https://doi.org/10.1093/cid/ciaa1433

COVID-19 “catastrophe” as one third of Ireland’s nursing homes test positive

There have been 155 outbreaks of COVID-19 in nursing homes across the country, according to the Health Service Executive (HSE).

Shane O'Brien @shamob96 Apr 16, 2020

COVID-19 has been diagnosed in almost one-third of Ireland's nursing homes as experts warn of a "catastrophe in the making."

There have been 155 outbreaks of COVID-19 in nursing homes across

August 6, 2021
5:17 PM IST
Last Updated 3 days ago

Europe

Seven residents of Belgian nursing home die after outbreak of B.1.621 lineage of COVID-19

2 minute read

Reuters

Los Angeles Times

CALIFORNIA

California names nursing homes with coronavirus outbreaks, number of cases

Emergency healthcare workers move a stretcher at the Gateway Care and Rehabilitation Center on April 9 in Hayward, Calif. (Ben Margot / Associated Press)

BY JACK DOLAN, ANITA CHABRIA, BRITTNY MEJIA

APRIL 18, 2020 UPDATED 5:14 PM PT

For the first time, California Department of Public Health officials have divulged the

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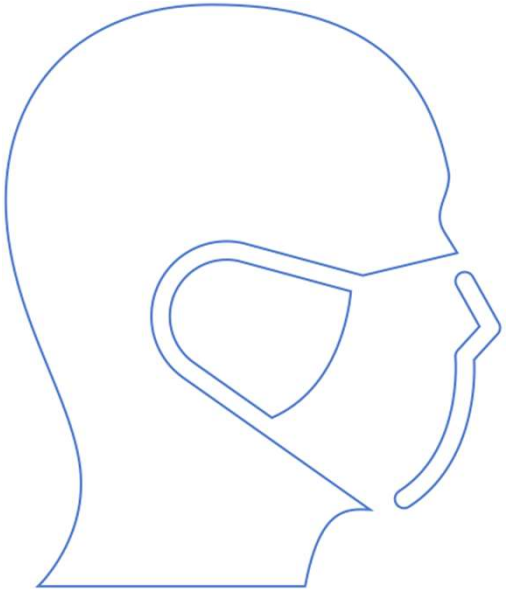
Irish News FactCheck Voices The Good Information Project Covid-19

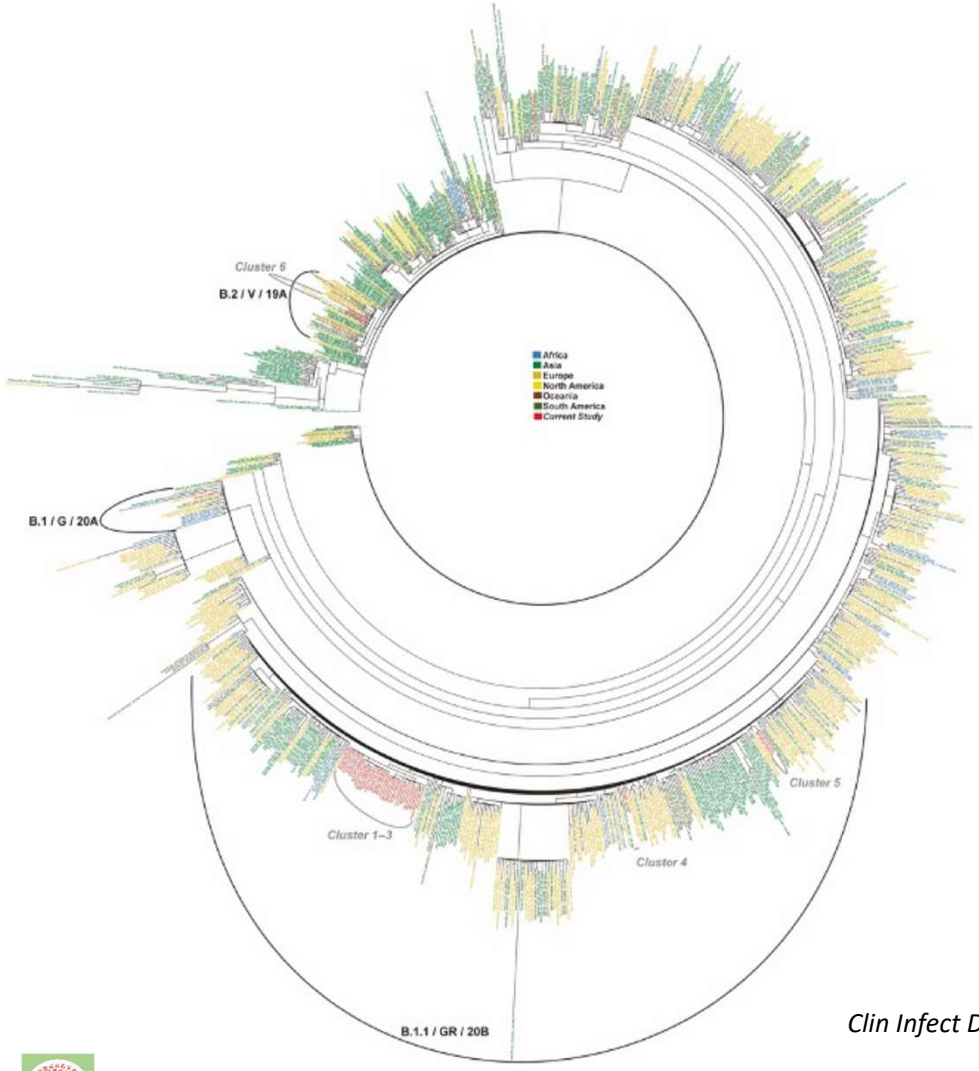
Report finds staffing and Covid training issues at Louth nursing home where over 20 patients died in April

A report from May – just a week after an outbreak at the nursing home – highlighted some areas of non-compliance at the centre.

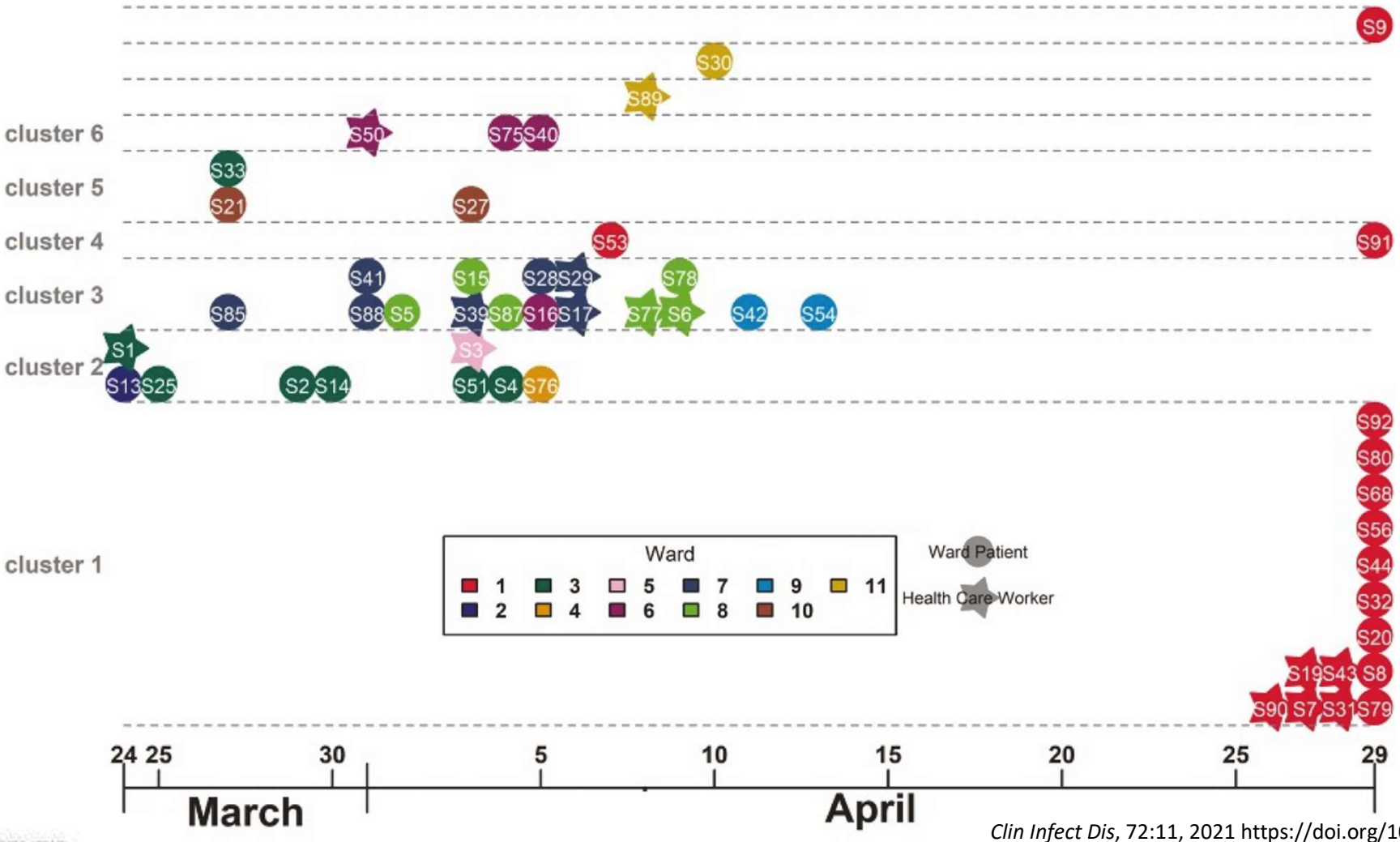
Oct 23rd 2020, 7:00 PM 18,402 Views 16 Comments Share 5 Tweet Email

AN INSPECTION REPORT at a Louth nursing home in which over



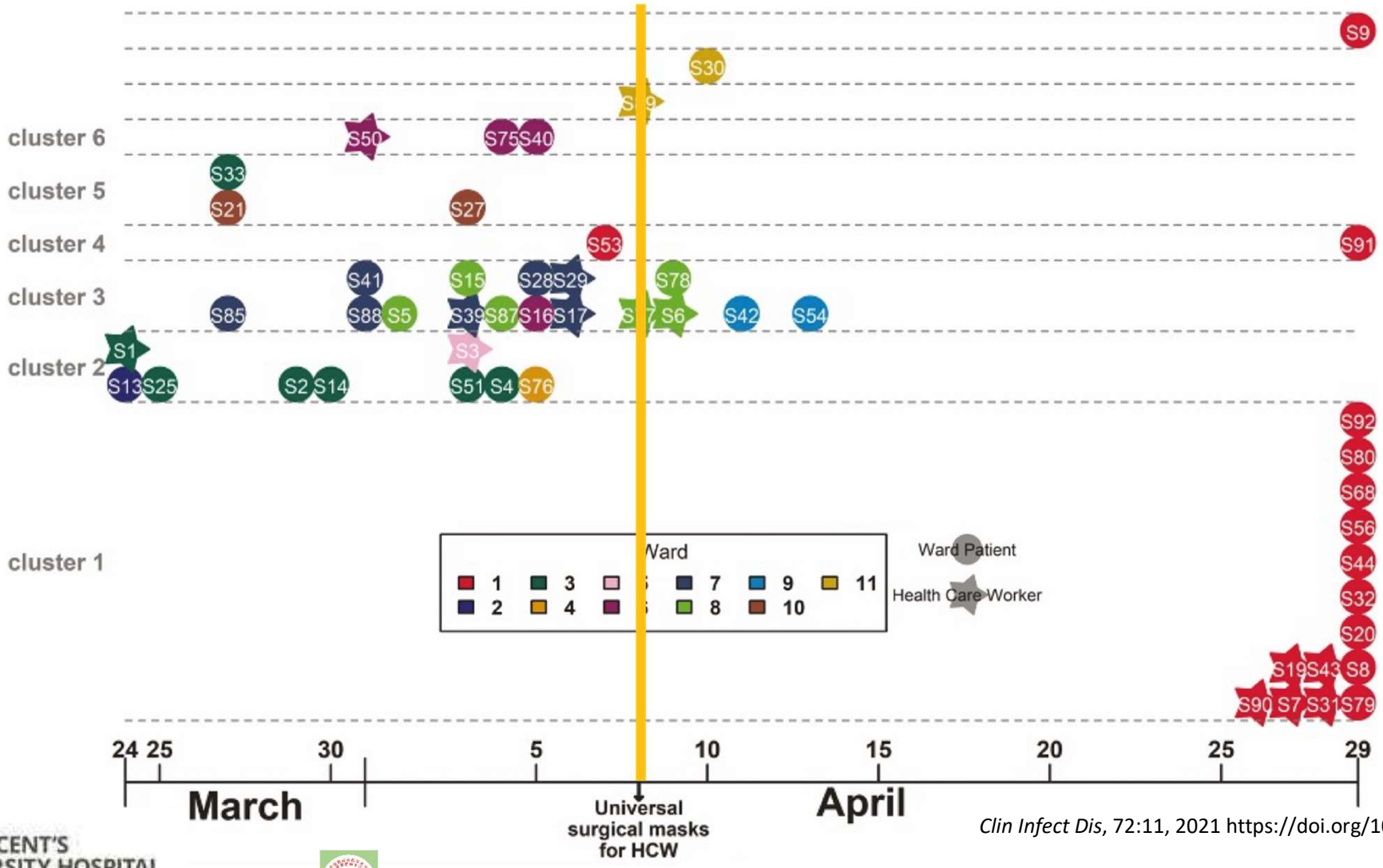


Clin Infect Dis, 72:11, 2021 https://doi.org/10.1093/cid/ciaa1433



Clin Infect Dis, 72:11, 2021 https://doi.org/10.1093/cid/ciaa1433

ST. VINCENT'S UNIVERSITY HOSPITAL
Elm Park



Sequencing
UCD-CFS

Clin Infect Dis, 72:11, 2021 https://doi.org/10.1093/cid/ciaa1433

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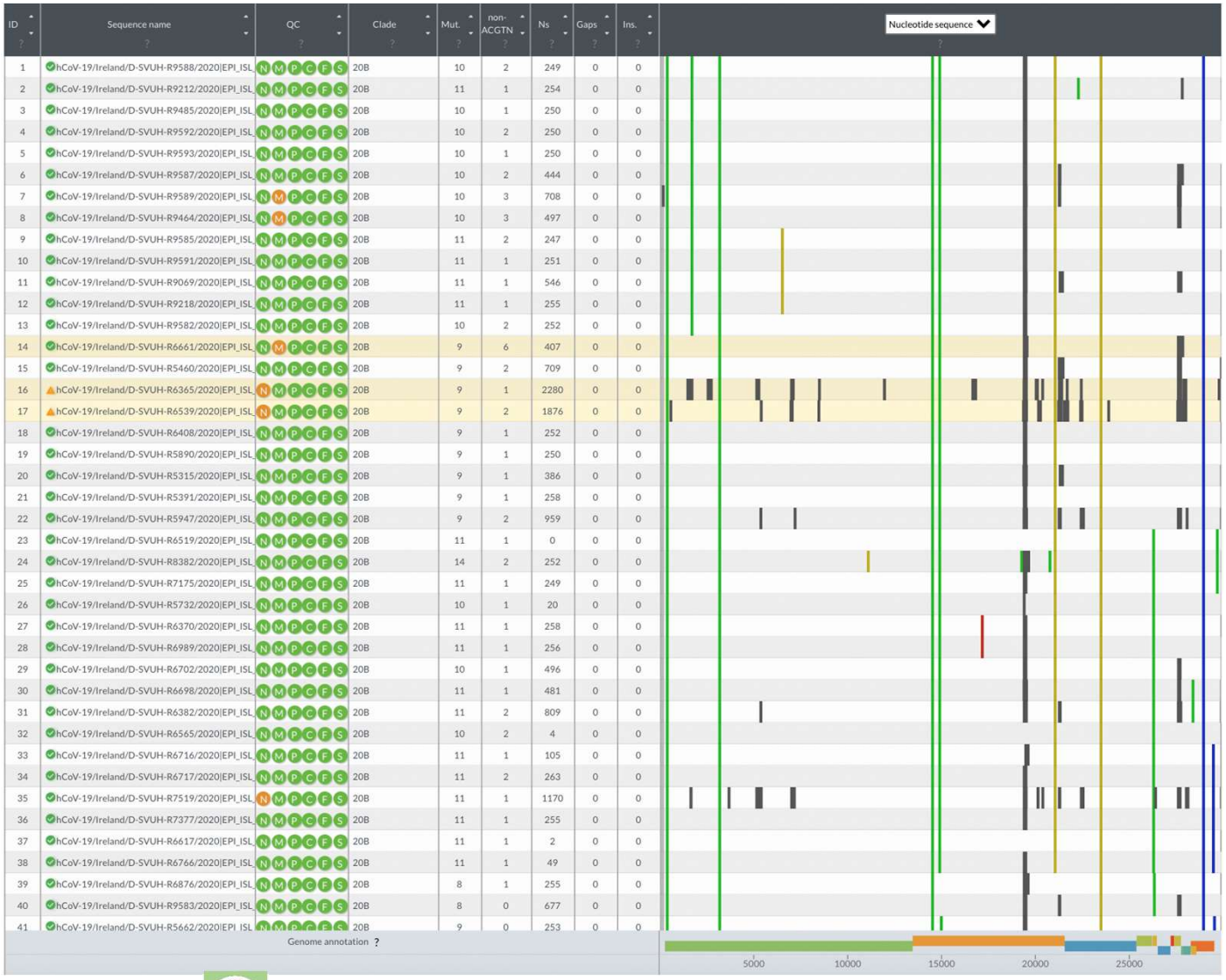
Elm Park

- Health care workers (HCW) - **close contacts**
- **Hospital-acquired (HA) COVID-19 cases** (patients admitted without symptoms of COVID-19 who had SARS-CoV-2 RNA detected at least 7 days after admission)
- Only **patients** that were **hospitalised for more than 14 days**

Clin Infect Dis, 72:11, 2021 https://doi.org/10.1093/cid/ciaa1433



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2	hCoV-19/Ireland/D-SVUH-R9212/2020|EPI_ISL	NMPCFS	20B	11	1	254	0	0
3	hCoV-19/Ireland/D-SVUH-R9485/2020|EPI_ISL	NMPCFS	20B	10	1	250	0	0
4	hCoV-19/Ireland/D-SVUH-R9592/2020|EPI_ISL	NMPCFS	20B	10	2	250	0	0
5	hCoV-19/Ireland/D-SVUH-R9593/2020|EPI_ISL	NMPCFS	20B	10	1	250	0	0
6	hCoV-19/Ireland/D-SVUH-R9587/2020|EPI_ISL	NMPCFS	20B	10	2	444	0	0
7	hCoV-19/Ireland/D-SVUH-R9589/2020|EPI_ISL	NMPCFS	20B	10	3	708	0	0
8	hCoV-19/Ireland/D-SVUH-R9464/2020|EPI_ISL	NMPCFS	20B	10	3	497	0	0
9	hCoV-19/Ireland/D-SVUH-R9585/2020|EPI_ISL	NMPCFS	20B	11	2	247	0	0
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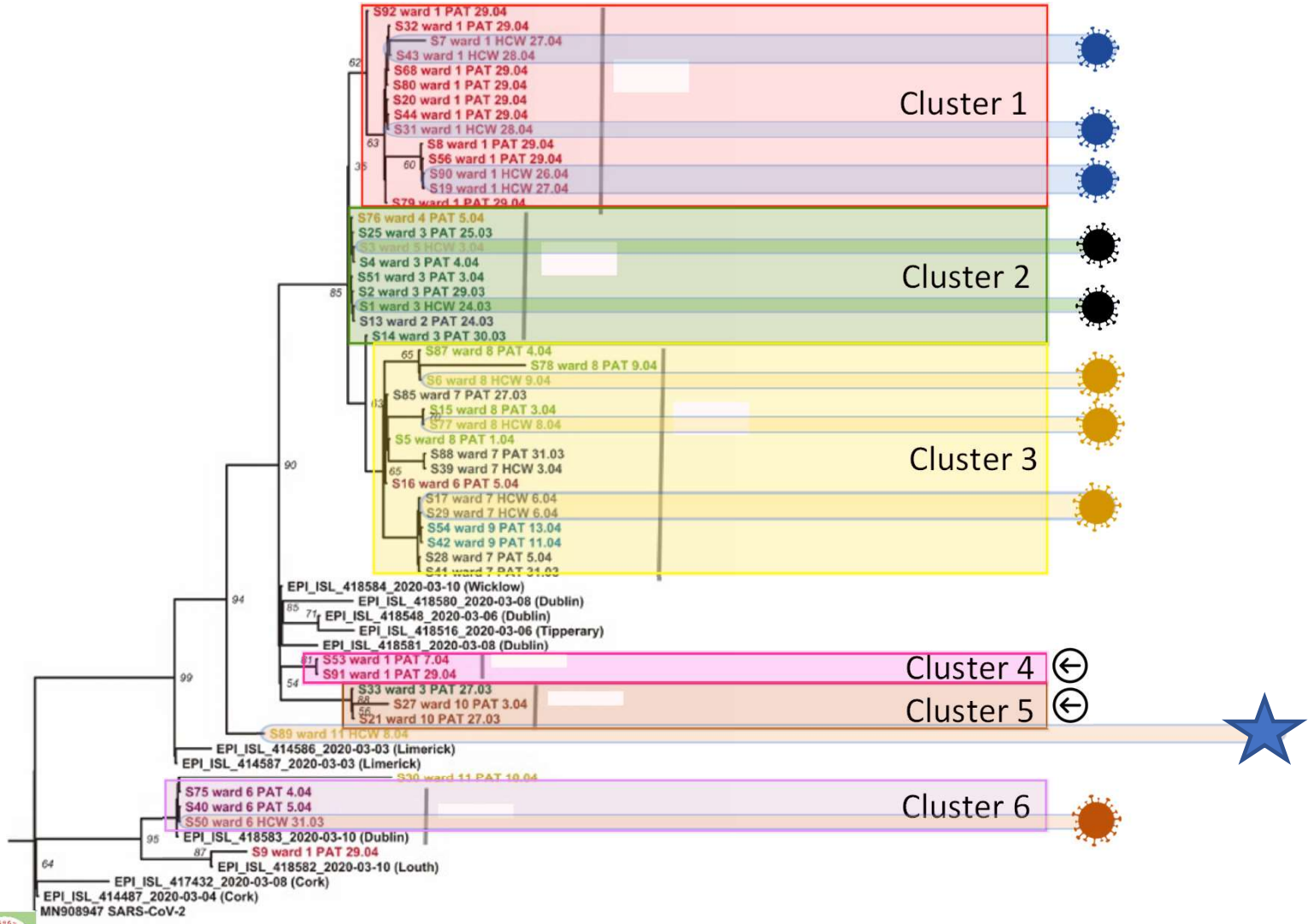
25	hCoV-19/Ireland/D-SVUH-R7175/2020|EPI_ISL	NMPCFS	20B	11	1	249	0	0
26	hCoV-19/Ireland/D-SVUH-R5732/2020|EPI_ISL	NMPCFS	20B	10	1	20	0	0
27	hCoV-19/Ireland/D-SVUH-R6370/2020|EPI_ISL	NMPCFS	20B	11	1	258	0	0
28	hCoV-19/Ireland/D-SVUH-R6989/2020|EPI_ISL	NMPCFS	20B	11	1	256	0	0
29	hCoV-19/Ireland/D-SVUH-R6702/2020|EPI_ISL	NMPCFS	20B	10	1	496	0	0
30	hCoV-19/Ireland/D-SVUH-R6698/2020|EPI_ISL	NMPCFS	20B	11	1	481	0	0
31	hCoV-19/Ireland/D-SVUH-R6382/2020|EPI_ISL	NMPCFS	20B	11	2	809	0	0
32	hCoV-19/Ireland/D-SVUH-R6565/2020|EPI_ISL	NMPCFS	20B	10	2	4	0	0
33	hCoV-19/Ireland/D-SVUH-R6716/2020|EPI_ISL	NMPCFS	20B	11	1	105	0	0
34	hCoV-19/Ireland/D-SVUH-R6717/2020|EPI_ISL	NMPCFS	20B	11	2	263	0	0
35	hCoV-19/Ireland/D-SVUH-R7519/2020|EPI_ISL	NMPCFS	20B	11	1	1170	0	0
36	hCoV-19/Ireland/D-SVUH-R7377/2020|EPI_ISL	NMPCFS	20B	11	1	255	0	0
37	hCoV-19/Ireland/D-SVUH-R6617/2020|EPI_ISL	NMPCFS	20B	11	1	2	0	0
38	hCoV-19/Ireland/D-SVUH-R6766/2020|EPI_ISL	NMPCFS	20B	11	1	49	0	0
39	hCoV-19/Ireland/D-SVUH-R6876/2020|EPI_ISL	NMPCFS	20B	8	1	255	0	0
40	hCoV-19/Ireland/D-SVUH-R9583/2020|EPI_ISL	NMPCFS	20B	8	0	677	0	0
41	hCoV-19/Ireland/D-SVUH-R5662/2020|EPI_ISL	NMPCFS	20B	9	0	253	0	0

Nucleotide sequence

Genome annotation

5000 10000 15000 20000 25000



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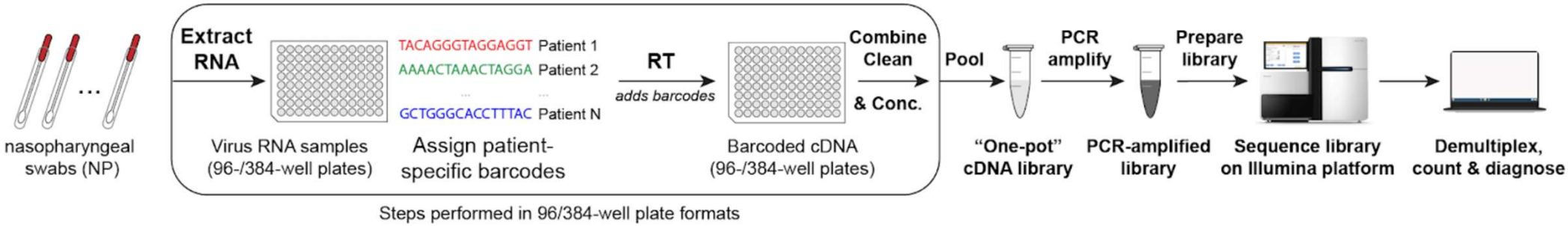
Massively parallel diagnostic assay (MPDA) platform

- Evaluation of the performances
- Release of a robust prototype



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- Antimicrobial Resistance genes
- Food-borne pathogens
- Sentinels programmes

Thanks to:

Prof. Seamus Fanning - Director Centre for Food Safety
Lauren Russell,
Francisco Cores Rodriguez,
Alexander Floss-Jones,
Charlene Bennet,
Siobhan McCarthy

Prof. Grace Mulcahy
Assistant Professor Gerald Barry
Dr Tristan Russell
Dr Leonardo Koolman
Prof. Alan Reilly
… and many others

Funding agency

SFI
World Health Organisation
UCD

…and keep in touch!

guerrino.macori@ucd.ie
@guerrino.macori