

# COVID-19: first long-term care facility outbreak in the Netherlands following cross-border introduction from Germany, March 2020

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## Research Article

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# Abstract

**Background:** The Dutch province of Limburg borders the German district of Heinsberg, which had a large cluster of COVID-19 cases linked to local carnival activities in February, before any cases were reported in the Netherlands. However, Heinsberg was not included as an area reporting local or community transmission per the national case definition at the time. In early March, two residents from a long-term care facility (LTCF) in Sittard, a Dutch town located in close vicinity to the district of Heinsberg, started experiencing respiratory symptoms and were admitted to the regional hospital at which they were tested for COVID-19. Introduction of the virus could have occurred following the carnival activities in the surrounding area by LTCF visitors or health care workers.

**Methods:** Surveys and semi-structured oral interviews were conducted with all present residents by health care workers during regular points of care for information on new or unusual signs and symptoms of disease. Both throat and nasopharyngeal swabs were taken from residents suspect of COVID-19 for the detection of SARS-CoV-2 by Real-time Polymerase Chain Reaction and whole genome sequencing was performed using a SARS-CoV-2 specific amplicon-based Nanopore sequencing approach. Additionally, twelve random residents were sampled for possible asymptomatic infections.

**Results:** Since the start of the outbreak, nineteen (19%) residents tested positive for COVID-19. Eleven samples were sequenced, along with three random samples from COVID-19 patients hospitalized in the regional hospital at the time of the LTCF outbreak.

**Conclusions:** All samples were linked to COVID-19 cases from the cross-border region of Heinsberg, Germany. Symptoms were reported only in about two third of the cases, and tended to be generally mild. We therefore recommend low-level screening of HCWs and residents following a confirmed COVID-19 case, even in the absence of symptoms. Since the LTCF residents who tested positive did not meet the criteria for suspect cases of COVID-19 at the time, this highlights the importance of cooperation among cross-border partners in order to establish a coordinated implementation of infection control measures in the region on top of national guidelines to limit the spread of infectious diseases such as COVID-19.

## Background

Rapid global spread of the novel coronavirus SARS-CoV-2 has led to an increasing number of cases of coronavirus disease 2019 (COVID-19) in the Netherlands. Since the first case of COVID-19 in the Netherlands was reported on February 27, 2020 [1], COVID-19 has spread within the general population, with major clusters in the provinces of Brabant and Limburg [2-4]. In the beginning of the outbreak, most cases were identified in returning travellers, mainly from northern Italy. Containment efforts included testing of suspected cases, contact tracing, isolation of cases and quarantine of contacts, as well as medical monitoring of exposed individuals. Suspected cases in that stage of the pandemic were defined by symptoms of fever, with cough or dyspnoea, together with an epidemiological link, i.e. contact with a laboratory-confirmed case, or prior visit to a COVID-19 endemic area [3, 5]. On February 26<sup>th</sup>, in addition to

the previous case definition, diagnostic testing for COVID-19 for all hospitalized patients with unexplained pneumonia was introduced. These tests were performed in dedicated and certified labs in the Netherlands.

The Dutch province of Limburg borders the German district of Heinsberg in the federal state of North Rhine-Westphalia which had a large cluster of COVID-19 cases linked to local carnival activities, even before the first cases were reported in the Netherlands [6]. An immunocompromised man had attended several densely-packed carnival celebrations in the town of Gangelt (in the Heinsberg region) on February 15<sup>th</sup> 2020 [6]. He developed progressive respiratory symptoms shortly after, and was eventually hospitalized on February 24<sup>th</sup> in deteriorating condition, testing positive for COVID-19 on February 25<sup>th</sup> [7]. The outbreak in Heinsberg was likely fuelled by large crowds of carnival revellers (superspreading event) being exposed to this immunocompromised, supposedly super-spreading patient [8].

On March 1<sup>st</sup> 2020, the first long-term care facility (LTCF) resident in Sittard, a Dutch town located in close vicinity to the district of Heinsberg, started experiencing moderate respiratory symptoms, but did not meet the national test criteria for COVID-19. Two LTCF residents were admitted on the 5<sup>th</sup> and the 6<sup>th</sup> of March to two different wards of the regional hospital with a suspected respiratory infection, and were tested for COVID-19. The Public Health Service South Limburg received first reports of two COVID-19 positively tested residents on March 7<sup>th</sup> 2020.

Introduction of the virus could have occurred following the carnival activities in the surrounding area by LTCF visitors or health care workers (HCWs). This assumption is fuelled by the fact that the border region of Sittard (The Netherlands) and Heinsberg (Germany) is typified for its cross-border travel. Therefore, these densely-packed carnival activities were most likely visited by HCWs, as well as citizens from both sides of the border.

In this report, we describe the first known COVID-19 outbreak in a Dutch LTCF, in which we performed whole genome sequencing on eleven SARS-CoV-2 viruses from the LTCF, along with a set of three SARS-CoV-2 samples from hospitalized patients in the regional hospital, and compared these to SARS-CoV-2 sequences from the Heinsberg region.

## Methods

We performed a cross-sectional epidemiological and laboratory investigation of an ongoing COVID-19 outbreak that occurred in a LTCF in South Limburg, the Netherlands, in early March 2020. Surveys were conducted with all present residents during regular points of care. On the day of survey, HCWs from the LTCF performed semi-structured oral interviews of all 99 present LTCF residents, divided over five different wards, to collect information on age, sex, new or unusual signs and symptoms of disease, complemented with comorbidity information from their patient records and taking their temperature (rectally) in the morning and the evening during regular moments of care. An increase in temperature from 37.5 to 38 degrees Celsius was categorized as subfebrile temperature, whereas 38.0 Celsius and above was classified as fever. Optimal collection of signs and symptoms was hampered by the fact that part of the residents had some stage of impaired cognition.

These data were shared with the Public Health Service South Limburg. No HCWs were tested, as HCWs who experienced any symptoms were instructed to stay at home. Twelve random samples of possible asymptomatic residents were taken from residents from all five wards to avoid possible selection bias. Any missing data was coded as missing and was not imputed. All descriptive analyses were done using IBM SPSS Statistics version 26 (IBM, Armonk, NY, USA).

## Case definition

Both international and national case definition for suspect cases at the time included a sudden onset of either cough, fever, shortness of breath with no other aetiology that fully explains the clinical presentation. Additionally, a suspect case must have met an epidemiological criterium of a history of travel or residence in a country/area reporting local or community transmission, or have had to be in close contact with a confirmed, or probable COVID-19 case [5]. Within Dutch hospitals, patients were also suspected of COVID-19 when they were diagnosed with a pneumonia with unknown cause irrespective of an epidemiological link. At this moment in time, Heinsberg was not included as one of these areas in the national case definition. Therefore, in Limburg, we included travel to or from Gangelt, (in the Heinsberg region) after intensive local contact (not being only buying fuel or food) as an adjusted regional case definition. Because of the cluster of two COVID-19 positively tested cases, we used a more sensitive case definition for COVID-19 suspected cases for the residents of the LTCF involved, i.e. any respiratory symptoms or fever, including subfebrility (defined as temperature between 37.5 en 38 degrees Celsius).

Suspect residents of the LTCF (n=10), according to this adjusted case definition for COVID-19, were sampled on March 8<sup>th</sup>, which resulted in six confirmed COVID-19 cases on March 9<sup>th</sup>. Subsequent screening of contacts in the same ward as the index patient and on other wards (n=14) revealed additional COVID-19 cases. Additionally, a random sample of twelve asymptomatic residents were tested on March 11<sup>th</sup>.

## Test analysis

Both throat and nasopharyngeal swabs were taken from residents suspect of COVID-19 for the detection of SARS-CoV-2 by Real-time Polymerase Chain Reaction (RT-PCR) [9]. In addition to samples of residents who tested positive for COVID-19, samples from COVID-19 positive cases who were admitted at the Zuyderland Medical Center (i.e. the regional hospital) in the same time period, but unrelated to the LTCF, were also analysed to evaluate the relatedness of these strains with those from the LTCF and the German region of Heinsberg. Regarding the RT-PCR, RNA was extracted from the samples with the use of automated total nucleic acid extraction using the MP96 (Roche Diagnostics, Rotkreuz, Switzerland) per the manufacturer's instructions. In-house RT-PCR was performed using a Quantstudio 5 (Applied Biosystems,

MA, USA) based on the dual-target PCR published by Corman et al. [8] targeting the E-gene and RNA-dependent RNA polymerase (RdRp). For PCR, a 20 microliter PCR reaction was used, including 5 microliter Taqpath 1-step RT mastermix (Applied Biosystems), 100-800 nM of primers and probes and 10 microliter extracted RNA. Before extraction, all samples were spiked with murine cytomegalovirus (CMV) RNA, which was used as an extraction and amplification control. The Cycle Threshold (CT) values of symptomatic and asymptomatic residents were also determined.

## Whole genome sequencing

Whole genome sequencing was performed using a SARS-CoV-2 specific amplicon-based Nanopore sequencing approach [3]. Sequence reads were demultiplex using Porechop (<https://github.com/rrwick/Porechop>) after which a reference-based alignment was performed using minimap2 [10]. The consensus genome was determined using custom scripts as described by Oude Munnink et al. [3].

All available full-length SARS-CoV-2 genomes were retrieved from GISAID (supplementary) on the 17<sup>th</sup> of March 2020 and aligned with the Dutch SARS-CoV-2 sequences from this study using MUSCLE (Li, H. Minimap2: pairwise alignment for nucleotide sequences. *Bioinformatics* 34, 3094–3100 (2018)). Unfortunately, we could not incorporate a table to credit all contributing and submitting labs due to the huge number of people who have contributed. Sequences with >10% “Ns” were excluded. The alignment was manually checked for discrepancies after which IQ-TREE (Nguyen, L.T. et al. IQ-TREE a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. 2015) was used to perform a maximum likelihood phylogenetic analysis under the GTR+F+I+G4 model as best predicted model using the ultrafast bootstrap option with 1,000 replicates. Nucleic acid sequence data has been shared with the Global Initiative on Sharing All Influenza Data (GISAID) database.

## Results

Table 1 shows the resident characteristics of the 99 interviewed residents, as well as the test coverage per ward and the results.

*Table 1: Resident characteristics by ward level (1-5) from the LTCF (n=99).*

	Ward 1		Ward 2		Ward 3		Ward 4		Ward 5		Total	
	n/N <sup>a</sup>	%	n/N <sup>a</sup>	%	n/N <sup>a</sup>	%						
<b>Sex</b>												
Female	13/18	72	12/19	63	15/18	83	14/17	82	18/27	66	72/99	73
<b>Age in years (mean, standard deviation)</b>	83, 8.8		84, 7.5		84, 8.5		90, 4.1		87, 4.7 <sup>b</sup>		86, 7.1	
<b>Tested</b>												
Yes	5/18	28	4/19	21	14/18	78	6/17	35	17/27	63	46/99	47
Positive <sup>c</sup>	1/5	20	3/4	75	7/14	50	1/6	17	7/17	41	19/46	41
<b>Mortality</b>	0/18	0	1/19	5	1/18	6	0/17	0	3/27	11	5/99	5
a) <i>Unless stated otherwise.</i>												
b) <i>Age was known for 25 residents only</i>												
c) <i>Based on the number of residents who were tested.</i>												

The ages of the residents ranged from 64 to 97 years. Out of the 99 residents, 46 (47%) were tested for COVID-19 of whom nineteen (41%) tested positive. More tests were done on wards three and five, because COVID-19 was first detected here. Out of the twelve randomly tested asymptomatic residents, three (25%) tested positive for COVID-19.

At the moment of writing this manuscript, five (5%) residents have died. All deceased residents tested positive for COVID-19.

## Symptoms

Out of the nineteen residents who tested positive for COVID-19, sixteen (84%) reported any signs and symptoms of disease. Out of these sixteen symptomatic residents, we were unable to fully evaluate the symptoms of three (19%) residents, as they were hospitalized and passed away before the interviews took place. The most common signs and symptoms in the remaining thirteen positive residents were fever (54%), subfebrile temperature (47%), and cough (39%). Other, less frequently reported symptoms, were fatigue (15%), malaise (15%), vomiting (8%), loss of appetite (8%), nausea (8%), and dizziness (8%). A

heatmap of these reported symptoms within symptomatic COVID-19 positively tested residents is shown below (table 2).

Additionally, another eighteen residents reported an increase in temperature, with seven reporting fever and eleven reporting subfebrility, but tested negative for COVID-19.

Table 2. A heatmap of reported symptoms from symptomatic COVID-19 positive residents, March 2020 (n=16).

Symptomatic resident	Coughing	Fatigue	Vomiting	Lack of Appetite	Subfebrile	Fever	Nausea	Dizziness	Malaise
+ <sup>a, b</sup>									
+ <sup>b</sup>						■			
0 <sup>a, b</sup>									
0 <sup>a, b</sup>									
+ <sup>a</sup>						■			
0 <sup>a</sup>					■				
+ <sup>0</sup>						■			
+ <sup>0</sup>	■	■	■	■					
+ <sup>0</sup>						■			
+ <sup>0</sup>					■				
+ <sup>0</sup>	■					■	■	■	
+ <sup>0</sup>	■				■				
+ <sup>0</sup>	■				■				
0 <sup>a</sup>	■	■				■			■
+ <sup>0</sup>				■	■				■
+ <sup>0</sup>				■	■				
Total	5	2	1	1	6	7	1	1	2

a. Resident was hospitalized.

b. Resident has died.

Present symptoms are depicted with a black cell. Fever is defined as a temperature of 38.0 degrees Celsius or higher, whereas subfebrile temperature is defined as a temperature below 38.0 degrees Celsius. Three

*residents were hospitalized before an interview could be conducted, and are depicted with grey cells. Out of the five residents who tested positive for COVID-19 and passed away, four reported any symptoms of disease.*

## **CT values**

The CT values of positively tested symptomatic residents (N=16) and asymptomatic residents (N=3) are shown in Figure 1. CT values ranged from 19 up to 35; median CT values were 33 and 29 for asymptomatic and symptomatic residents respectively. Symptomatic residents appeared to have a slightly higher load (lower CT value) compared to asymptomatic residents.

## **Genome sequencing**

Complete genome sequencing of the SARS-CoV-2 virus from eleven residents from the LTCF in South Limburg was performed. In addition, three random samples from the regional hospital were sequenced. All accession numbers for the sequences are shown in table 3.

*Table 3. Sequencing names and accession numbers, March 2020 (n=14).*

Name	Accession number	Location	Collection date	Data source
Limburg_7	EPI_ISL_415464	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_13	EPI_ISL_461001	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_14	EPI_ISL_461002	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_15	EPI_ISL_461003	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_66	EPI_ISL_461051	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_67	EPI_ISL_461052	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_68	EPI_ISL_461053	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_69	EPI_ISL_461054	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_70	EPI_ISL_461055	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_71	EPI_ISL_461056	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_72	EPI_ISL_461057	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_73	EPI_ISL_461058	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_74	EPI_ISL_461059	Europe / Netherlands / Limburg	March 2020	GISAID
Limburg_75	EPI_ISL_461060	Europe / Netherlands / Limburg	March 2020	GISAID

Figure 2 shows the part of the phylogenetic tree in which the sequence of the LTCF residents and the hospitalized patients are located. This figure shows that the sequences from the LTCF residents in Sittard and the hospitalized patients are part of the same cluster, pointing towards potential transmission within the nursing home. The sequences also cluster with sequences found in Heinsberg. The full phylogenetic tree can be found in the supplementary (additional file 1). The accession numbers are shown in table 3.

# Outbreak control measures

As of March 8<sup>th</sup> 2020, additional infection control measures were implemented by the LTCF. In collaboration with the Public Health Service South Limburg, an outbreak management team was installed. Wards three and five, the wards on which the first residents tested positive for COVID-19, were isolated, meaning residents were not allowed to leave their rooms, and visitors were banned from entering these wards. Admission of new residents was temporarily halted throughout the LTCF. All suspect residents (residents with respiratory complaints with and without fever) and confirmed COVID-19 residents, as defined by the case definition as of March 2<sup>nd</sup> [5], as well as residents with (at least) subfebrility, were put into isolation, whilst all other residents were closely monitored by taking their temperature twice during regular moments of care in the morning and the evening, and checking for new or unusual signs and symptoms of disease, including coughing, subfebrility, and shortness of breath. Additionally, all planned group activities on all wards, such as group physical exercise and eating together in the dining room, were cancelled, and residents were served meals in their own rooms.

Visitors were still allowed to enter the other wards, but the number of visitors was limited to two per day. Upon entry, each visitor was required to report any signs and symptoms of disease and previous visits to areas with a high risk of transmission, including the Heinsberg region. In addition, visitors were told to keep a distance of at least 1.5 metres from the resident when visiting. Visitors reporting signs and symptoms of disease during the two weeks prior to their visit were not allowed to visit. However, when residents tested positive for COVID-19 on these remaining wards (wards one, two, and four) as well, a total visitor ban was also introduced for these wards.

HCWs worked in set teams and wore gowns, surgical mouth masks, and gloves when they expected to get in close contact (within 1.5 meters) with COVID-19 positive residents or their surroundings. Additionally, hand hygiene among HCWs was intensified. HCWs were regularly briefed with updates on a closed online portal, by team meetings with social distancing, and by newsletters shared via internal e-mail.

Since the implementation of these infection control measures, only one additional resident tested positive for COVID-19 on the 31<sup>st</sup> of March, and no more residents have been hospitalized or have died due to complications from COVID-19. As a result, this LTCF was among the first 37 of 139 LTCFs in our region to allow visitors again.

## Discussion

We aimed to provide sequencing data which could link the COVID-19 outbreak in the LTCF to the cluster in Heinsberg and surrounding districts in North Rhine-Westphalia. Complete genome sequencing of the SARS-COV-2 of the eleven LTCF residents from Dutch Limburg showed complete clustering with virus strains found in the neighbouring German region of Heinsberg. This is in line with the open-border region of Limburg and Heinsberg characterized by cross-border commuter activity in both directions. Given the mutual carnival festivities on both sides of the border, the initial outbreak of COVID-19 in Heinsberg was

accompanied by intensified cross-border movements. Though it has not been possible to identify the actual index case who introduced the SARS-CoV-2 virus into the LTCF, it seems plausible that the index was a (pre-)symptomatic carrier who picked up the virus through direct involvement in (carnival) activities across the border, or was a secondary contact, especially since pre-symptomatic cases and pre-symptomatic transmission have already been reported [11, 12] and spreading of the virus while being asymptomatic cannot be excluded. Most probably, this carrier would have been a visitor to the LTCF, or a HCW.

We observed a large number of cases among LTCF residents in a cross-sectional analysis following two hospitalized residents who tested positive for COVID-19. Many of the residents who tested positive did not meet the clinical criteria for suspect cases of COVID-19 at that time [5]. Symptoms were reported only in about two third of the cases, and tended to be generally mild. Furthermore, CT values of asymptomatic (and possible pre-symptomatic) residents seem to be somewhat higher compared to symptomatic residents. This suggests that asymptomatic and pre-symptomatic residents could have accelerated further spread of the virus within the LTCF. This shows that COVID-19 is difficult to recognize based on clinical signs and symptoms alone in this specific context. The definition for suspected cases at that moment in time turned out to be inappropriate for this LTCF population. In addition, even when the case definition for admitted cases was not completely met, a test for COVID-19 was immediately requested upon admission in the regional hospital, as the physicians in the region were uneasy with the diagnostic testing for SARS-CoV-2 for admitted patients with pneumonia only when these cases were unexplained, as in most cases of community acquired pneumonia a causal agent goes often undetected.

A recent study on COVID-19 within LTCFs by Arons et al. reports similar findings [13]. In a COVID-19 outbreak in a skilled nursing home in Washington, 48 out of 76 participating residents (63%) tested positive, of which 27 were asymptomatic at the time of testing, and 24 subsequently developed symptoms [13, 14]. Additionally, SARS-CoV-2 viral loads were similar between residents with (a)typical symptoms, pre-symptomatics, and asymptomatics [13], which differs from our findings. This difference might be explained as a result of the low number of asymptomatic residents tested in our LTCF. Arons et al. concluded that infection-control strategies focused solely on symptomatic residents were not sufficient to prevent transmission after SARS-CoV-2 virus introduction [13, 15]. Because COVID-19 sheds at high concentrations from the nasal cavity even before symptoms develop, Gandhi et al. urge for a mass testing policy in a LTCF setting, not limited to symptomatic residents, and to also include asymptomatic individuals [15]. Additionally, recent work on a large cohort of symptomatic HCWs showed general non-respiratory symptoms including muscle ache, ocular pain, general malaise, headache, extreme tiredness, and fever were most frequently reported, as opposed to respiratory symptoms such as cough and sneezing [16]. This illustrates the difficulty of screening for COVID-19 based on specific clinical signs. This is especially troublesome since identifying (a)symptomatic cases will help to minimise an outbreak and the overall impact of COVID-19 [17].

This outbreak showed that guidelines are not always sufficient or fully applicable in a specific region or in a specific setting. We have often collaborated with colleagues across the border, and even though we

wanted to do more with the cross-border information we had, we were limited in our options, because it would deviate from national guidelines and international agreements. For example, in this specific case we could not label Gangelt as a specific transmission area, although we were able to adjust the guideline to our own situation in practice.

We encountered several additional limitations in the investigating of the outbreak. Due to a large difference in (mild) types of symptoms, it was difficult to pinpoint the onset of disease for positively tested residents, which hampered us in presenting a trustworthy epicurve. Instead, we have given a detailed description of events surrounding the LTCF. Additionally, we were not able to acquire any follow-up data from the LTCF residents, which made it impossible to categorize any asymptomatic residents as pre-symptomatic residents. However, because the number of asymptomatic (and potentially pre-symptomatic) residents found was low (N=3), no decisive conclusions could have been made about the CT values concerning these groups. Lastly, although it is very likely that the introduction of the SARS-CoV-2 virus was caused by an asymptomatic or pre-symptomatic HCW or visitor, the transmission route into the LTCF could not be identified with certainty. In order to give more support to the likelihood that cross-border transmission took place, we sequenced eleven samples from positive residents, as well as three positive patients from the regional hospital, which showed a strong similarity between sequences from Limburg and Heinsberg.

In conclusion, the LTCF residents who tested positive did not meet the criteria for suspect cases of COVID-19. Whole genome sequencing can help to identify and resolve potential transmission clusters. Given the clustering sequences found between the LTCF residents and the Heinsberg samples, introduction of the SARS-CoV-2 virus by a pre-symptomatic visitor or HCW with direct or indirect cross-border contacts, seems highly likely. Based on our findings, we recommend low-level screening of HCWs and residents following a confirmed COVID-19 case, even in the absence of symptoms. Since the implementation of the aforementioned infection control measures, such as strict contact and droplet isolation, including visitor bans, only one more residents tested positive for COVID-19, affirming these measures are effective to curb similar outbreaks. Hospitals and public health institutions in border regions could benefit from more specific case-definitions taking into account the cross-border transmission risks. The cross-border nature of this outbreak underlines the importance of sharing information with cross-border partners in order to establish a coordinated implementation of infection control measures in the region on top of applicable national guidelines to limit the spread of infectious diseases.

## **Abbreviations**

COVID-19: Coronavirus disease 2019; LTCF: long-term care facility; HCWs: health care workers; RT-PCR: Real-time Polymerase Chain Reaction; RdRp: RNA-dependent RNA polymerase; CMV: murine cytomegalovirus; CT value: Cycle Threshold value; GISAID: Global Initiative on Sharing All Influenza Data.

## **Declarations**

## **Ethics approval and consent to participate**

All data were retrieved from regular infectious disease control activities and were de-identified. The study protocol was exempt from formal medical-ethical approval under prevailing laws in the Netherlands, as it concerns a retrospective observational study using anonymous data only (as stated by the National Central Committee for Human Studies: [www.ccmo.nl](http://www.ccmo.nl) and in the conduct of good behaviour in research).

## **Consent for publication**

Not applicable.

## **Availability of data and materials**

Nucleic acid sequence data has been shared with the Global Initiative on Sharing All Influenza Data (GISAID) database and can be accessed using the accession number as mentioned in table 3 of the article. The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

## **Competing interests**

The authors declare that they have no competing interests.

## **Funding**

This study has no funding support.

## **Authors' contributions**

MvH, CH and CdH designed the study. MvH, analysed the data and drafted the manuscript. PW, BOM, RS and EH participated in the analyses of the collected samples, including PCR and whole genome sequencing. VH and HtW were consulted on their cross-border expertise. All authors read, revised and approved the final manuscript.

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## Figures

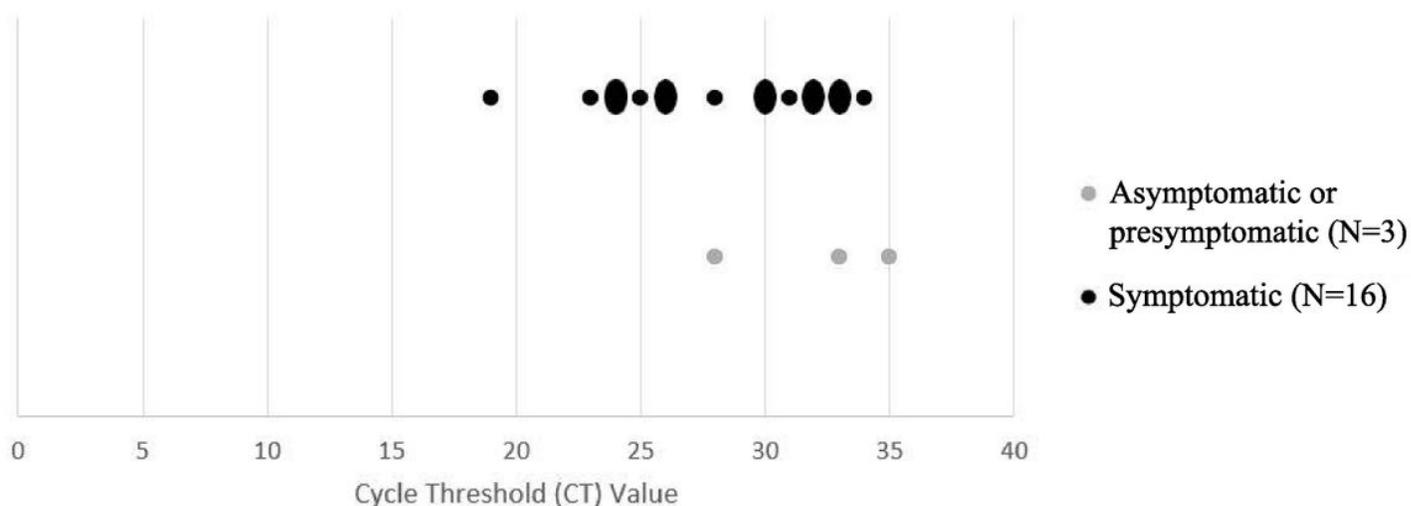
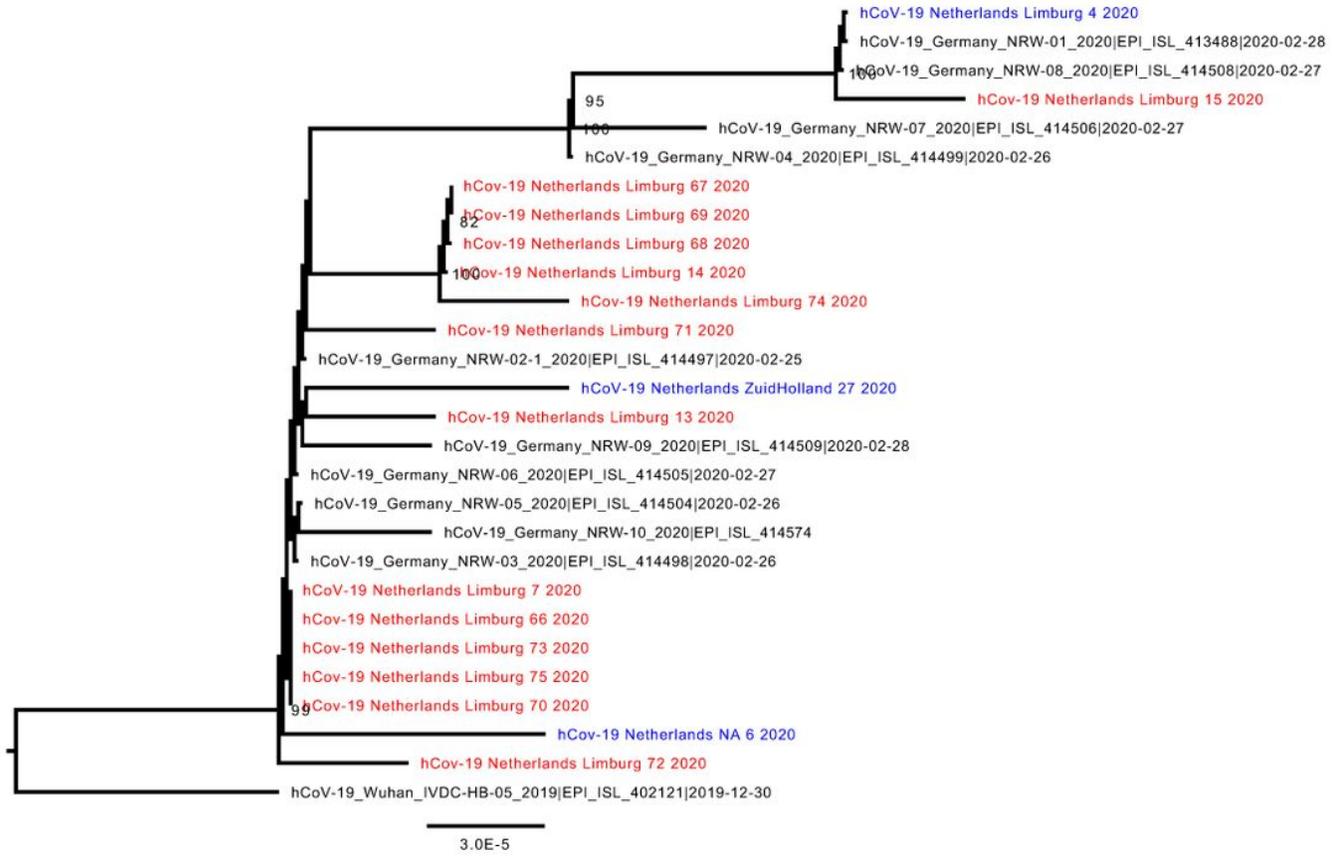


Figure 1

CT values of COVID-19 positive tested LTCF residents, March 2020 (n=19). Oval dots represent two residents with the same CT value.



**Figure 2**

Zoom in of the full phylogenetic tree on the Dutch LTCF residents from the LTCF in Sittard, the Netherlands, March 2020 (n=14). The scale bar represents the number of substitutions per site. Sequences from the Netherlands are depicted in blue, and specific sequences from this study in red. Samples 13, 14, and 15 depicted in red were samples acquired from hospitalized patients in the regional hospital around the same time of the LTCF outbreak. The remaining red samples were acquired from eleven COVID-19 positive LTCF residents.

## Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [FullphylogenetictreeLTCF.pdf](#)