

## COVID-19 in a remote First Nations community in Canada:

### An outbreak summary

Authors:

Courtney R. Smith, MPH<sup>1,2</sup>

Charmaine Enns, MD<sup>3</sup>

Dan Cutfeet, MD<sup>4</sup>

Shannon Alfred<sup>5</sup>

Nicole James, BScN<sup>4</sup>

Jennifer Lindbeck, MSc<sup>6</sup>

Shannon Russell, PhD<sup>7</sup>

### Affiliations

1. Population Health Assessment, Surveillance, and Epidemiology, Island Health, Victoria, BC, Canada
2. Canadian Field Epidemiology Program, Public Health Agency of Canada, Ottawa, Ontario, Canada
3. Department of Public Health & Preventive Medicine, Island Health, Courtenay, BC, Canada
4. 'Namgis Health Centre, Alert Bay, BC, Canada
5. 'Namgis First Nation, Alert Bay, BC, Canada
6. Communicable Disease Program, Island Health, Courtenay, BC, Canada
7. Public Health Laboratory, BC Centre for Disease Control, Vancouver, BC, Canada

### Corresponding author

Courtney R. Smith, [courtneyr.smith@canada.ca](mailto:courtneyr.smith@canada.ca)

### Contributor's statement

C.E., D.C., N.J., J.L led and/or contributed to outbreak response, including testing, case and contact management and implementation of public health measures. S.A. coordinated emergency response for the community. C.R.S analysed and interpreted all data and drafted the initial manuscript. S.R. conducted and interpreted the whole genome sequencing analysis. All authors contributed to the final manuscript, gave final approval for the version to be published, and agree to act as guarantor of the work.

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**Abstract**

Background: In April 2020, BC experienced its first outbreak of COVID-19 in a remote First Nations community. The outbreak was also one of the first of its kind in Canada.

Methods: After identification of the first eight cases, the community declared a state of emergency, and public health measures were introduced. Cases underwent investigation and contact tracing. Supports were provided to ensure successful isolation and quarantine for cases and contacts. Testing was recommended for all symptomatic individuals. Messaging to the community was circulated by trusted community members. Descriptive and social network analyses were conducted to describe the outbreak as it evolved. All case specimens underwent whole genome sequencing (WGS).

Results: Thirty cases were identified with a median age of 34 years. The majority identified as female (63%) and as First Nations (90%). The most common symptoms included chills, cough, diarrhea, headache, and fever. Five cases were hospitalized (17%) and one died (3%). Percent positivity was 18%. Transmission primarily occurred within social gatherings and households. Two weeks after control measures were initiated, no further cases were identified. All cases were considered genetically related by 2 single nucleotide polymorphisms (SNPs) or less, and belonged to the most dominant SARS-CoV-2 lineage identified in BC at the time.

Interpretation: This was the first outbreak of COVID-19 to be identified in a remote First Nations community within BC and one of the first to be identified in Canada. A community-wide and community-led response were essential to effective containment and prevented onward transmission of the virus.

## Introduction

The first case of coronavirus disease (COVID-19) arrived in Canada in late January 2020 from a traveller returning from Wuhan, China. By March, community transmission was occurring, and the pandemic took hold within Canada. As of December 18 2020, Canada has over 500,000 cases, and just under 14,000 deaths [1]. In the province of British Columbia (BC), there are over 45,000 cases and over 700 deaths [2]. The impact on the population has been significant, but the impact on vulnerable populations and communities has been even more pronounced. In April 2020, BC experienced its first outbreak of COVID-19 in a remote First Nations community. As the first outbreak of its kind in BC, and one of the first in Canada, the outbreak presented unique challenges and opportunities for public health response. The objective of this report will be to summarize the outbreak and the corresponding public health response, in order to inform action in similar communities in the coming months, and perhaps, years.

Cormorant Island is located off the northeast coast of Vancouver Island in BC, and is home to both a population on reserve (49% of the population) and off reserve (51% the population) [3]. The community consists of approximately 1,000 residents, and is accessible only by air and boat. On Saturday April 11, 2020 the first confirmed case of COVID-19 in a resident of Cormorant Island was reported. On April 14, intensive swabbing began for all symptomatic members of the community via a drive-through swabbing centre. By April 17, the case count had reached eight and a state of emergency was declared. By April 20, ferry travel was restricted to essential travel only and on April 21, a nightly curfew was established utilizing the local tsunami siren.

## Methods

### *Case Definition*

A confirmed case of COVID-19 was defined as a person with laboratory confirmation of infection with SARS-CoV-2 performed at a community, hospital, or reference laboratory running a validated assay with detection of at least one specific gene target by a nucleic acid amplification test (NAAT) assay (e.g., real-time Polymerase Chain Reaction (PCR) or nucleic acid sequencing).

### *Case Finding*

From April 14 to May 9, a drive-through swabbing centre was utilized outside of the community hospital on-reserve to provide access to testing for the community. Testing was by appointment and was booked through a central call-in number that was widely circulated. Availability for testing continued after May 9 but at reduced operating hours. Testing was recommended for all individuals experiencing any COVID-19 related symptoms, including fever, chills, cough, shortness of breath, sore throat, odynophagia, rhinorrhea, nasal congestion, loss of sense of smell, headache, muscle aches, fatigue, or loss of appetite. Select testing was also provided at resident's homes for those unable to travel to the swabbing centre. Messaging about the availability and recommendation for testing was circulated by trusted community members, such as the senior community physician, the community nurse, and the Chief, through informal networks and via videos on the community Facebook page.

### *Laboratory Testing*

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3 All nasopharyngeal swabs were sent to the Island Health Laboratory in Victoria, BC for PCR testing for  
4 SARS-CoV-2. Specimens were also forwarded to the BC Centre for Disease Control (BCCDC) Public Health  
5 Laboratory (PHL) for whole-genome sequencing (WGS) to investigate the SARS-CoV-2 strain(s)  
6 circulating in the community relative to other cases in BC, as well as to understand the genetic  
7 relationships between cases and strains of the virus. Nucleic acids were extracted using a MagMAX  
8 instrument (ThermoFisher). WGS of SARS-CoV-2 was performed using the ARTIC protocol (version  
9 1.1.3) and the Oxford Nanopore Technologies' MinION sequencer. A detailed description of the  
10 amplification primers and the sequencing method have been described elsewhere [4]. High-quality  
11 sequences were assigned a SARS-CoV-2 lineage based on the Phylogenetic Assignment of Named Global  
12 Outbreak Lineages (Pangolin) tool, version 1.1.14 [5]. Phylogenetic analysis was performed using  
13 Nextstrain [6] (Augur version 10.0.0 and Auspice version 2.18.1).

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17 *Case Investigation and Monitoring*

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19 All confirmed cases underwent a case investigation conducted by a communicable disease nurse.  
20 Information gathered on cases included identifiers, demographic characteristics, risk factors, exposures,  
21 and symptoms. The case investigation also included contact tracing. Close contacts were defined as a  
22 person who provided direct care for the case, including healthcare workers, family members or other  
23 caregivers, or who had other similar close physical contact (e.g., intimate partner) without consistent  
24 and appropriate use of personal protective equipment (PPE); or lived with or otherwise had close face to  
25 face contact (within 2 metres) for more than 15 minutes (may be cumulative, i.e., multiple interactions);  
26 or had direct contact with infectious body fluids of a confirmed case (e.g., was coughed or sneezed on)  
27 while not wearing recommended PPE. The infectious period for contact tracing was defined as starting  
28 48 hours prior to symptom onset. For the small number of cases that could not define symptom onset or  
29 were asymptomatic, their infectious period was calculated based on the date of testing. In instances  
30 where contact tracing was challenging, the community health nurse (CHN) provided assistance. The CHN  
31 was also able to provide context for the complex social connections in the community that were not  
32 always captured through the case interview.

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36 Confirmed cases were asked to isolate from others for a period of 10 days following symptom onset.  
37 Close contacts were asked to quarantine for a period of 14 days from their last known exposure to a  
38 case. Monitoring occurred daily for both cases and contacts, and was available in online format with a  
39 symptom survey, or was conducted through a phone call or a home visit from the local CHN. Contacts  
40 that developed symptoms during their monitoring period were referred for testing. To support  
41 successful isolation and quarantine for cases and contacts, various resources were mobilized based on  
42 individual needs, including phones, credits for phone minutes, and tablets to facilitate daily monitoring,  
43 pulse oximetry for daily monitoring, alternative housing for those unable to adequately isolate or  
44 quarantine away from others, and a community managed alcohol program for those with dependencies.  
45 When necessary, arrangements were made to transfer cases to off-island hospitals for medical  
46 treatment. A low threshold for medical transfers off the Island was encouraged. Community cases were  
47 considered recovered if 10 days had passed since symptom onset with resolution of fever and  
48 improvement of symptoms.

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52 *Statistical Analysis*

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54 Excel and SAS [7] were used to summarize the epidemiological data collected during the case  
55 investigation and contact tracing process. Social network analysis was conducted in Pajek [8] to

understand transmission in the community, inform public health responses, and evaluate the completeness of contact tracing.

### *Ethics Approval*

Ethics approval was not required.

## **Results**

### *Epidemiological findings*

A total of 30 confirmed cases of COVID-19 were identified. Onset dates ranged from March 23 to April 28, 2020 (Figure 1). The median age was 34 years (range 15-77; Table 1). The majority of cases were female (63%), and identified as First Nations (90%). Seventeen percent (17%) of cases were hospitalized, and one case (3%) died as a result of their COVID-19 infection. The most predominant symptoms reported by cases included chills (80%), cough (70%), diarrhea (70%), headache (69%) and fever (57%).

**Table 1.** Demographic and clinical characteristics of confirmed COVID-19 cases (n=30).

Characteristic	n (%)
Age (years)	
Mean	38
Median	34
Range	15 - 77
Sex	
Female	19 (63%)
Male	11 (37%)
First Nations status	
First Nations	27 (90%)
Non First Nations	2 (7%)
Unknown status	1 (3%)
Hospitalization	
Ever hospitalized	5 (17%)
Never hospitalized	25 (83%)
Clinical outcome	
Recovered	29 (97%)
Deceased	1 (3%)
Symptoms	
Chills	24 (80%)
Cough	21 (70%)
Diarrhea	21 (70%)
Headache	20 (67%)
Fever	17 (57%)
Rhinorrhea	15 (50%)
Myalgia	13 (43%)
Shortness of breath/breathing difficulty	11 (37%)
Nausea	10 (33%)

Characteristic	n (%)
Weakness	10 (33%)
Arthralgia	8 (27%)
Pharyngitis	7 (23%)
Fatigue	7 (23%)
Conjunctivitis	6 (20%)
Irritability	4 (13%)
Hypotension	3 (10%)
Tachypnea	3 (10%)
Vomiting	3 (10%)
Confusion	2 (7%)
Nasal congestion	2 (7%)
Acute respiratory distress syndrome	0 (0%)

Transmission primarily occurred within two social gatherings, and several households (Figure 2). Several components of the social network analysis remained unconnected after completion of contact tracing, highlighting that while thorough, the scope of contact tracing was imperfect. Two weeks after the state of emergency was declared, there were no further cases identified.

The investigation did not determine how COVID-19 was introduced into the community. The index case did not report any travel off-island in the 14 days prior to their symptom onset, however, the index case did work within a setting where they may have had exposure to individuals with recent travel outside of the community. The state of emergency was declared over on May 9, 2020, and the cluster was declared over on May 26, 2020, 28 days (i.e. two incubation periods) after the last symptom onset of April 28, 2020.

*Laboratory findings*

At the time the outbreak was declared over, 16% of the population of Cormorant Island had been tested for COVID-19, with an overall test positivity of 18%. Twenty-one cases that underwent WGS generated high-quality sequence data, five cases generated partial sequence data and four cases failed. The Pangolin lineage designation for all cases in the Cormorant Island cluster was B.1, the most dominant SARS-CoV-2 lineage currently identified in COVID-19 cases from BC. All of the cases that were sequenced were considered genetically related by 2 single nucleotide polymorphisms (SNPs) or less (Figure 3). There were two clusters of cases that were considered genetically identical (one containing four cases, and the other containing twelve cases), and these clusters differed by a single SNP. The cluster of four identical Cormorant Island cases shown in Figure 3 is genetically identical to a large number of BC COVID-19 cases that occurred during the same time period. Some of these BC cases in this cluster have been epidemiologically linked back to the Pacific Dental Conference, a large super-spreading event in BC that occurred on March 5-7. The descendants of this cluster that were only detected on Cormorant island (including the cluster of twelve identical cases that had acquired one additional SNP) did not transmit any further in BC after the outbreak was declared over, based on over 3000 genomes that have been successfully sequenced by the BCCDC Public Health Laboratory as of October 2020. The SARS-CoV-2 sequences in the Cormorant Island cluster differed from the reference strain, MN908947.3 (Wuhan-Hu-1), by 6-8 SNPs.

**Interpretation**

Over the course of this outbreak, 30 confirmed cases were identified, comprising 3% of the community's population. At the time the outbreak was declared over, Cormorant Island had a cumulative incidence of 3,144 per 100,000 population. In comparison, at the same time point, BC had a cumulative incidence of 49.7 per 100,000 [9]. Even 7 months later, in the height of Canada's second wave in December 2020, Cormorant Island's cumulative incidence far surpasses that of BC (860 per 100,000), and Canada (1,310 per 100,000) [1]. In line with the findings for cumulative incidence, percent positivity also varied greatly between Cormorant Island (18%) and Canada overall (4%) [1]. The impact on this small community was disproportionate to that of the general population of BC and Canada.

Social network analysis of this cluster revealed several potential chains of transmission, including three small family clusters with 2-5 cases each, and two clusters with shared exposures at social gatherings that connected up to 18 of the 30 confirmed cases. The timing of these two social gatherings (April 9 and 12) suggest that they were major contributors to the outbreak peak in mid-April. The decrease in cases that occurred after the declaration of the state of emergency, and the absence of any new cases approximately two weeks after the state of emergency and control measures were implemented, indicates that these measures were successful in reducing transmission. WGS results also support this conclusion, as the specific sequence types observed in this outbreak did not transmit further in BC after the outbreak was declared over. The success in containing transmission is likely due in part to having trusted members of the community take the lead on communications. With information coming from individuals with longstanding relationships within the community, the measures were generally accepted and well-tolerated. This is even more significant given that this outbreak occurred at a time when similar measures were not in place elsewhere in the province.

The case fatality rate for Cormorant Island was similar when compared to Canada's case fatality in December 2020 (2.8%) [1]. The proportion of cases hospitalized, however, differs greatly. While Cormorant Island had a hospitalization rate of 17%, Canada's, as of December 2020, was only 8.4% [1]. The focus on symptomatic testing in this community, and the low threshold for medical transfers, may have inflated this value, but it's unlikely to explain the entire discrepancy. A similar trend of increased morbidity has been identified in Indigenous communities around the world during previous pandemics, where it was suggested that social and health inequities resulting from colonialism was a contributing factor [10]. This highlights the need to listen and respond to Indigenous communities as they define health, and to inform the collective actions needed to address inequities.

In addition to the health impacts of the COVID-19 outbreak on this First Nations community, it's important to highlight its cultural impact as well. In this community, like many other First Nations communities across Canada, potlatching, feasting, and other ceremonial practices play a vital role in cultural and spiritual well-being of its residents. Living without these gatherings takes a heavy toll, yet its long lasting impact may not always be evident in the midst of response. Consideration for these impacts should be high priority in any outbreak response, and efforts should be made to alleviate these impacts whenever possible.

### *Lessons learned*

This was the first cluster of COVID-19 to be identified in a remote First Nations community within BC and one of the first to be identified in Canada. A community-wide and community-led response were essential to effective containment. Several lessons learned can be brought forward in response to similar outbreaks. These lessons include: acknowledging the importance of a community-led response



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and that other providers/responders are partners *with* the community; having a consistent emergency coordinator within the community; implementing early and accessible testing; relying on trusted community members to deliver important messaging; building on and utilizing community health care capacity, including embedded health care providers; establishing clear and coordinated lines of communication with community leaders such as the Chief and council; providing supports to individuals to allow for successful isolation/quarantine, such as a community managed alcohol program and social support services; utilizing established relationships with providers from the regional health authority and First Nation Health Authority, and lastly, preparing to address various logistical challenges throughout the public health response, such as the availability of accommodations for isolation/quarantine (both within and outside the community), feasibility of moving cases to hospital and back into community, and securing proper technology and IT support to facilitate daily monitoring of cases and contacts in areas where internet and cell service may be unstable.

*Limitations*

There are several limitations to consider. First, since COVID-19 symptoms are non-specific, it is possible that symptom onset is inaccurate, impacting the epidemic curve, contact tracing, and the resulting social network analysis. Second, as this outbreak occurred early in the pandemic in Canada and BC, some symptoms were not asked about in the case investigation, such as loss of taste and smell. As such, we don't know the prevalence of these symptoms in the community. Third, contact tracing data was likely affected by recall bias and/or social desirability bias. The fact that there are several components of the social network analysis that remain unconnected signify that contact tracing did not capture all connections. Fourth, we were not able to identify a true index case for this outbreak; however, WGS results did indicate a potential connection to a super spreading event in Vancouver, BC. Lastly, some cases may have been missed, due to aforementioned limitations to contact tracing, but also due to the focus on symptomatic testing. For this reason, it's plausible that the cumulative incidence in this community was even higher than that reported here. Following this outbreak, community-wide antibody testing was offered for the purpose of measuring the extent, if any, of undetected spread. The results of this work are forthcoming.

*Conclusion*

This outbreak occurred at a time where First Nations communities in Canada were not yet significantly affected by the COVID-19 pandemic. The pandemic's second wave, however, has taken a significant toll on Indigenous communities. The description of this outbreak hopes to contribute to the knowledge base for COVID-19 response in First Nations communities, and provide important lessons learned to bring forward to similar outbreaks across the country.



**Data Sharing Statement**

As per the OCAP principles (First Nations principles of ownership, control, access, and possession) any sharing of the data with others requires consultation and approval of the Senior Administrator of 'Namgis First Nation. Please contact [courtneyr.smith@canada.ca](mailto:courtneyr.smith@canada.ca) to facilitate any requests.

**Funding Statement**

There was no funding received for this work

Confidential

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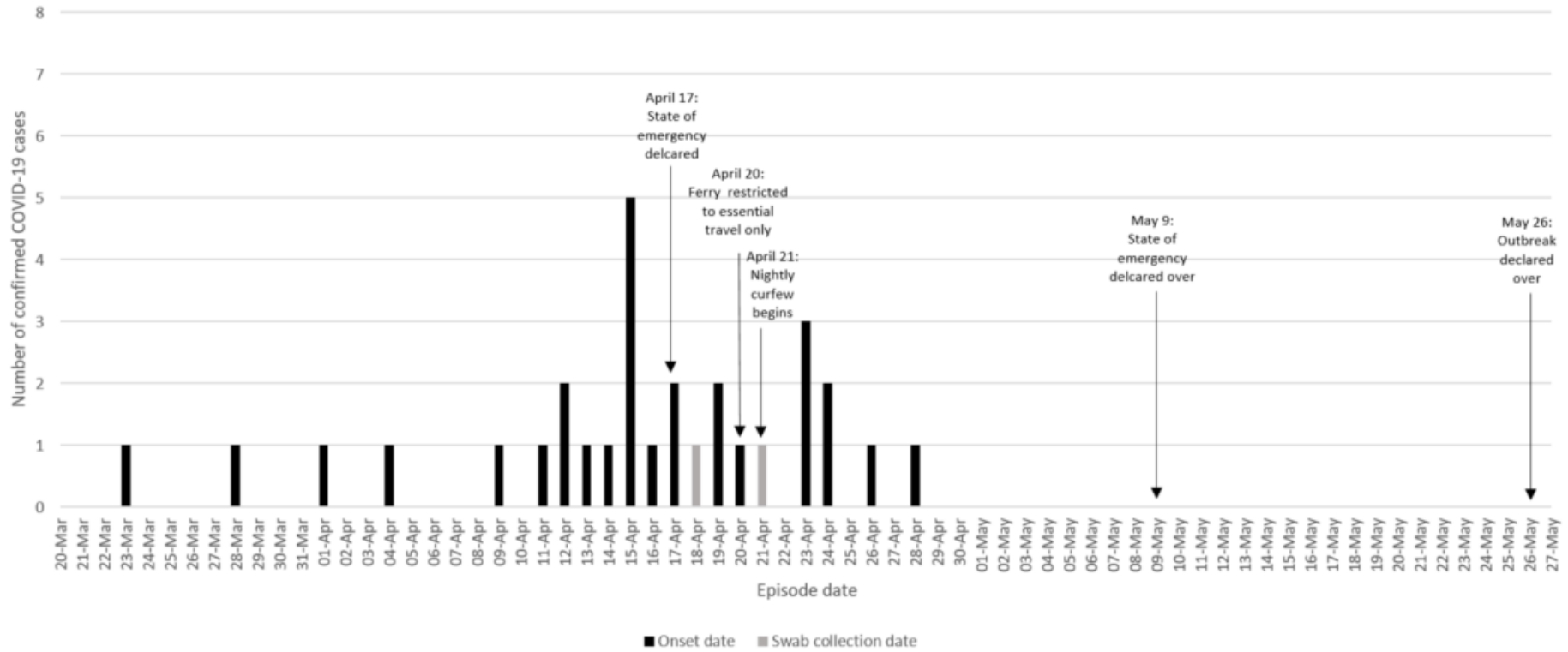
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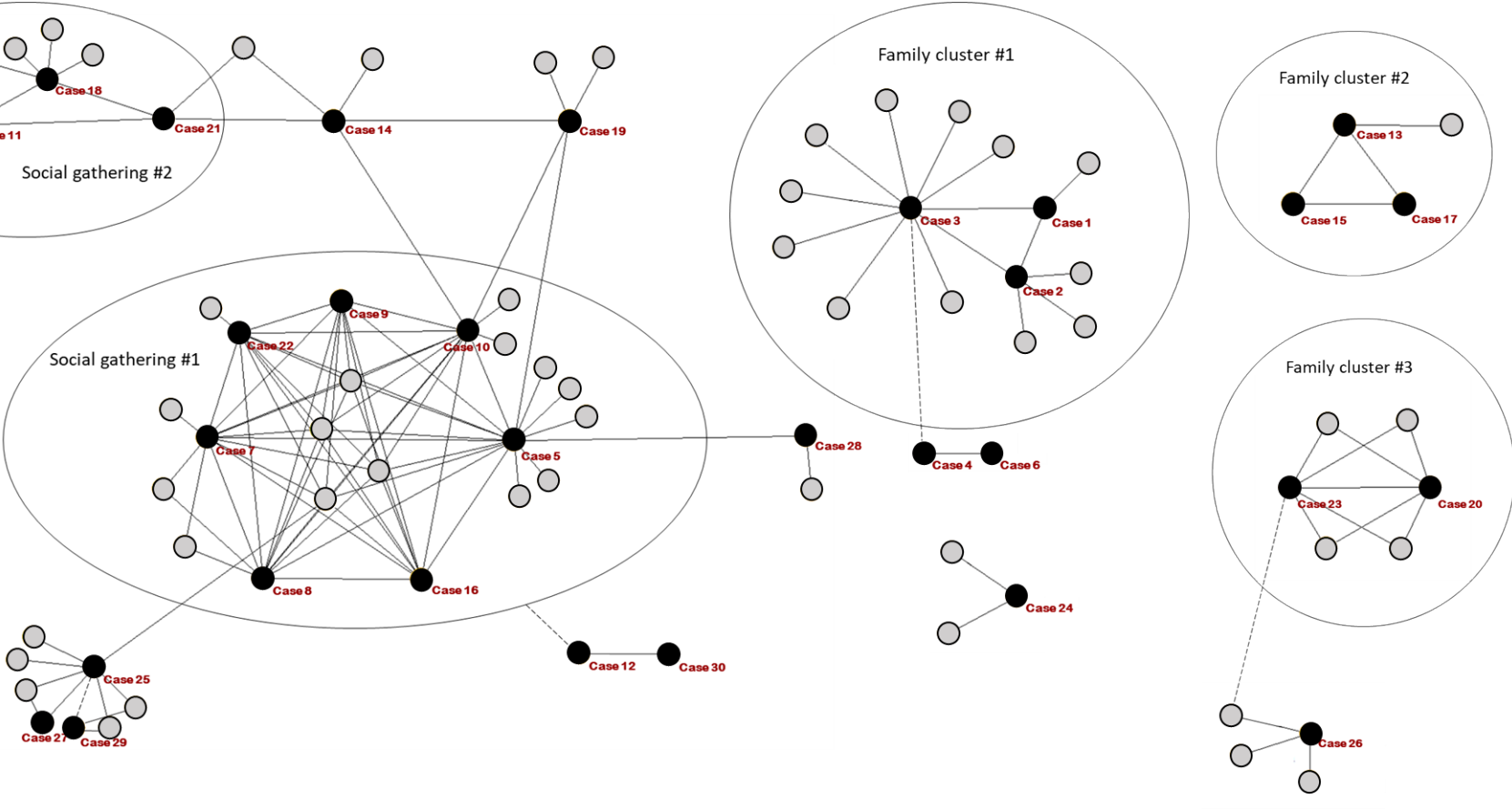
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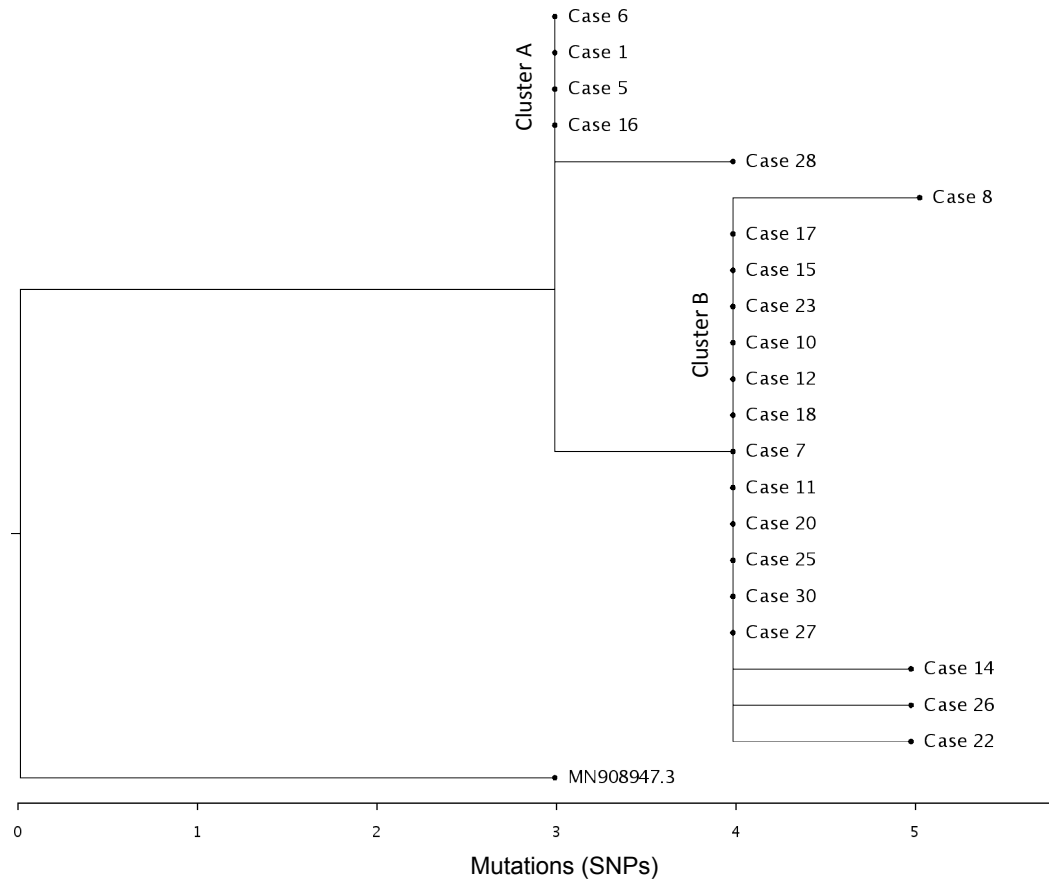
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Figure captions

**Figure 1.** Epidemic curve for confirmed COVID-19 cases, March to April 2020, by symptom onset or specimen collection date.

**Figure 2.** Social network analysis for confirmed COVID-19 cases and their contacts. Black indicates a confirmed case, grey indicates a close contact identified by contact tracing. A solid line indicates a known connection between individuals determined through contact tracing. A dotted line indicates a potential connection based on known relationships, but one that was not able to be confirmed via contact tracing.

**Figure 3.** Phylogenetic tree displaying the divergence between SARS-CoV-2 genomes for 21 confirmed COVID-19 cases that generated high quality sequence data, and the reference strain MN908947.3 (Wuhan-Hu-1). Scale bar represents the number of mutations, or single nucleotide polymorphisms (SNPs) detected in the SARS-CoV-2 genomes from the cases relative one another, as well as to MN908947.3. Sequences from cases displayed on each vertical line are considered identical.