Supplement

eIntroduction. Camp outbreak background information

The Camp is a sleep-away summer camp that hosts multiple one-week sleep-away camp sessions throughout the summer. The camp utilizes youth staff members as counselors and program directors with a small number of senior staff residing at the camp. Starting on June 10, the camp held orientation for youth staff and trainees with most staff and trainees arriving on June 17. On June 20, trainees left camp as they were scheduled to return for subsequent camp sessions to serve as staff members. Staff remained at the camp for the start of the first camp session. On June 21, campers and additional senior staff arrived at the camp for the first camp session which was slated to end on June 27. On June 22, a teenage staff member developed chills and left the next day. The staff member was tested and reported a positive viral test result for SARS-CoV-2 to the camp on June 24. Parents of campers and staff were notified of the COVID19 case by camp officials on June 24 and the camp sent campers and staff members home between June 25 and July 1. On June 25, the Georgia Department of Public Health (DPH) was notified and initiated an investigation. DPH gave camp officials their quarantine and isolation guidelines to distribute to all campers and staff. Camp attendees who were symptomatic were advised to isolate and be tested. Those who were asymptomatic were advised to quarantine for 14 days and to get tested at day 10 of quarantine, or sooner if symptoms developed. Camp officials set up a voluntary drive through testing event for attendees after camp closed. DPH was supplied with a list of all attendees. DPH contact tracers attempted to call all attendees as all attendees were considered close contacts. More information about DPH's investigation can be found in an MMWR published in July 2020.¹

eMethods. Georgia camp outbreak: probabilistic reconstruction of transmission chains

Investigation of a cluster, supported by serial interval distribution of the disease, allows a probabilistic reconstruction of transmission chains and additional epidemiologic insight into transmissibility.

The analysis follows closely the method outlined by Wallinga and Teunis² to estimate case reproduction numbers, based on a serial interval distribution estimated by He et al.³ Any missing onset date was imputed using the distribution of time (within the data set) from symptom onset to test date for positive tests.

Following Wallinga and Teunis, if w(t) is the value of the serial interval distribution for a lag t between symptom onset dates, the probability that case i (symptom onset at t_i) was infected by case j (symptom onset at t_i) is

$$p_{ij} = \frac{w(t_i - t_j)}{\sum_{k \neq i} w(t_i - t_k)}.$$

The serial interval distribution used has support at negative values, making an unambiguous designation of an imported index case difficult. Here, those flagged as community onset cases in the dataset were considered imported cases.

A modified estimate of the transmission probabilities that explicitly demarcates an exposure window (i.e., period over which both infector and infectee are present at the gathering) follows. The notation here follows He *et al.* In terms of the infectivity profile versus time since onset, $\beta_c(t)$ and incubation period distribution, g(t), the weight (replacing $w(t_i - t_j)$ above) is

$$\omega(t_i - t_j) = \int_{t_1}^{t_2} \beta_c \left(t - t_j\right) g(t_i - t) dt$$

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where t_1 and t_2 are the beginning and end of the period when both the infector and infectee are at the gathering. The contribution to each of the transmission weights from presymptomatic transmission is

$$\omega_p(t_i - t_j) = \int_{t_1}^{\min(t_2, t_i)} \beta_c (t - t_j) g(t_i - t) dt$$

The random draw imputed estimates are based on five imputation runs. The intervals incorporate uncertainties within each run as well as those between runs.

Estimation of the instantaneous reproductive number, $R_t(t)$, closely follows the method outlined in Cori et al.⁴:

$$R_t(t) = \frac{I(t)}{\sum_{\tau=-\infty}^t w(t-\tau)I(\tau)}$$

Incident cases on a day were those with symptom onset (recorded or imputed) d days later, where d corresponds to the argument of the function g(t) at its maximum. The denominator, consequently, includes only those cases with incidence prior to t.

eResults. Camp description

A detailed interview with a senior staff member from the camp was conducted to assess mitigation measures adopted by the camp. The camp adopted all the components of the Georgia executive order⁵ and most of the components of CDC's "Suggestions for Youth and Summer Camps"⁶ to minimize the risk for SARS-CoV-2 introduction and transmission. Campers were required to supply a negative viral SARS-CoV-2 test result that was collected within 12 days prior to camp attendance. Face coverings were required for staff members but were not required for campers. The camp implemented daily symptom and temperature screening starting at arrival to camp. There was enhanced focus and messaging on respiratory and hand hygiene and on cleaning and disinfection, especially of shared equipment and spaces. Attendees were cohorted by single-sex cabin (≤ 26 persons) and paired with a cabin of the opposite sex when participating in camp activities and during meals; co-mingling between cabins was not allowed. Bunk beds were spaced 6 feet apart, and ultraviolet germicidal lights were used in the heating, ventilation, and air conditioning systems. Doors and windows were not opened for ventilation in indoor environments. Use of communal spaces was staggered between cohorts and physical distancing was required outside of cabin cohorts. Camp attendees engaged in a variety of indoor and outdoor activities. Full camp assemblies were held in a covered amphitheater and participants were socially distanced by cabin. Meals were served by masked staff members and cabins dined in socially distanced quadrants (4 cabin cohorts assigned to 4 corners of the dining hall).

References

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	Whole-genome sequencing data available No. (col %)			
	Yes	Νο		
	(n = 22)	(n = 329)		
Case Status				
Community-associated case	2 (9)	10 (3)		
Camp-associated case	20 (91)	319 (97)		
Age, median (IQR)	12 (9–16)	15 (11–16)		
Sex				
Male	17 (77)	147 (45)		
Female	5 (23)	182 (55)		
Attendee Type				
Trainee	3 (14)	27 (8)		
Staff member	3 (14)	90 (27)		
Camper	16 (73)	212 (65)		
Residence				
Metro Atlanta	18 (82)	256 (78)		
Non-Metro Atlanta, Georgia	4 (18)	60 (18)		
Out-of-state	0	13 (4)		

eTable 1. Characteristics of Camp Attendees With and Without Whole-Genome Sequencing Data Available

	Interv		
	No. (
	Yes	No	
	(n = 450)	(n = 177)	p-value ^a
Age group			
6–10	67 (15)	29 (16)	0.12
11–14	155 (34)	42 (24)	
15–17	170 (38)	80 (45)	
18–21	51 (11)	24 (14)	
22–59	7 (2)	2 (1)	
Sex			
Male	203 (41)	73 (45)	0.38
Female	247 (59)	104 (55)	
Attendee Type			
Trainee	94 (21)	43 (24)	0.15
Staff Member	83 (18)	44 (25)	
Camper	273 (61)	90 (51)	
Residence			
Metro Atlanta	353 (78)	129 (73)	0.21
Non-Metro Atlanta, Georgia	81 (18)	37 (21)	
Out-of-state	16 (4)	11 (6)	

eTable 2. Characteristics of Camp Attendees Interviewed and Not Interviewed

^aChi-square test

		No. Cases ^a	Un	Unadjusted		Adjusted ^b
Characteristics	Total	-	RR	(95% CI)	RR	(95% CI)
All	404	234				
Age (years)						
6–10	63	38	1.0	(0.7–1.3)	1.1	(0.7–1.6)
11–14	140	92	1.1	(0.9–1.4)	1.1	(0.8–1.6)
15–17	157	78	0.9	(0.7–1.2)	1.2	(0.9–1.6)
18–21	44	26	1 [Reference]			
Sex						
Male	185	117	1 [Reference]			
Female	219	117	0.9	(0.7–1.1)		
Attendee type				`		
Trainee	87	16	1 (F	Reference]		
Staff member	68	55	3.5	(2.4–5.0)	4.5	(2.7–7.5)
Camper	249	163	2.8	(2.1–3.9)	3.8	(2.6–5.5)
Length of stay (days)						
≤ 4	148	56	1 [Reference]			
5–6	185	121	1.7	(1.5–2.0)	1.0	(0.8–1.3)
≥7	71	57	2.1	(1.7–2.5)	1.1	(0.7–1.5)
Stayed in cabin with a case upon arrival ^c						
Yes	100	67	1.1	(0.9–1.3)	1.1	(0.9–1.3)
No	304	167	1 [Reference]			
Contact with people outside cabin						
None/outdoor sports only	49	27	1 [F	Reference]		
Close contact ^d	153	87	1.0	(0.8–1.4)	1.0	(0.7–1.3)
Direct contact ^e	202	120	1.1	(0.8–1.4)	1.1	(0.8–1.5)
Exposures before attending camp				· · · · · ·		
Yes ^f	230	133	1.0	(0.9–1.2)		
No	174	101	1 [F	Reference]		
Exposures after attending camp						
Yes ^f	36	17	0.8	(0.6–1.1)		
No	368	217	1 (F	1 [Reference]		

eTable 3: Relative Risks (RR) of SARS-CoV-2 Infection by Characteristics of Camp Attendees Aged 6-21 Years

^aExcludes community-associated cases

^bMultivariable model includes all variables with a calculated adjusted RR.

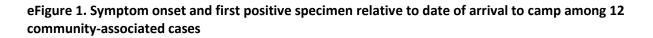
^cDefined as staying in a cabin with a community-associated case or a symptomatic camp-associated case on the day of arrival to camp.

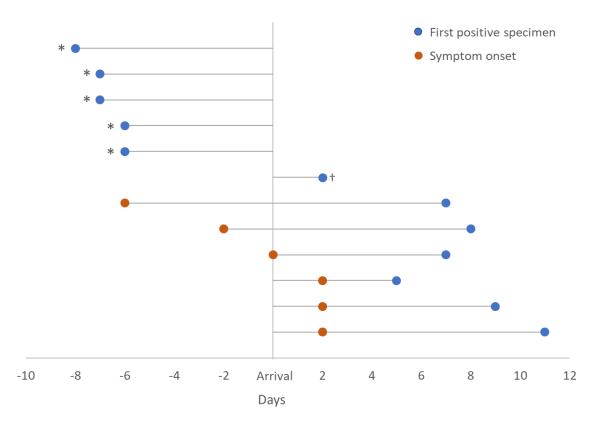
^dDefined as playing indoor sports or activities, traveling in vehicles, spending more than 15 minutes within 6 feet, having face-to-face contact within two feet, or spending any time within 6 feet while the other person was coughing or sneezing.

^eDefined as hugging or kissing the other person.

^fDefined as visiting, working, or volunteering in a healthcare setting, eating indoors at a restaurant, attending a gathering of any size with non-household members, using public transportation, attending

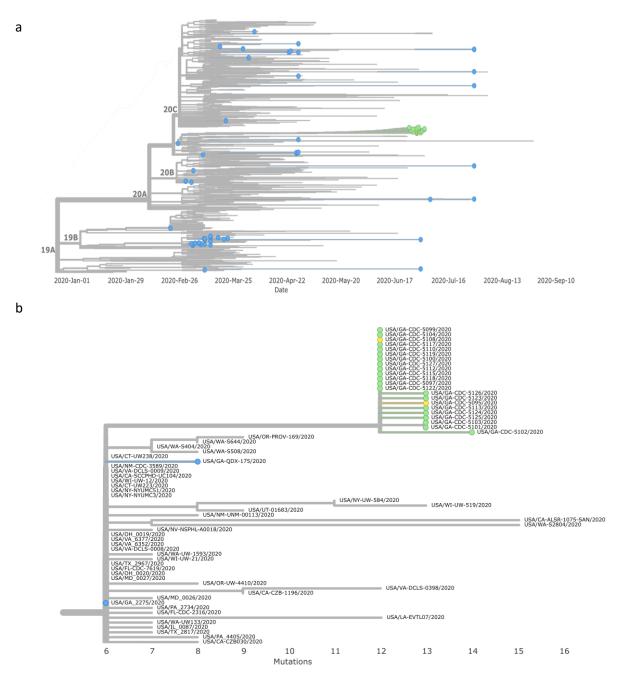
or working at a school or daycare, or having close contact (within 6 feet for \geq 15 minutes) with a person who tested positive for SARS-CoV-2, including other camp attendees.



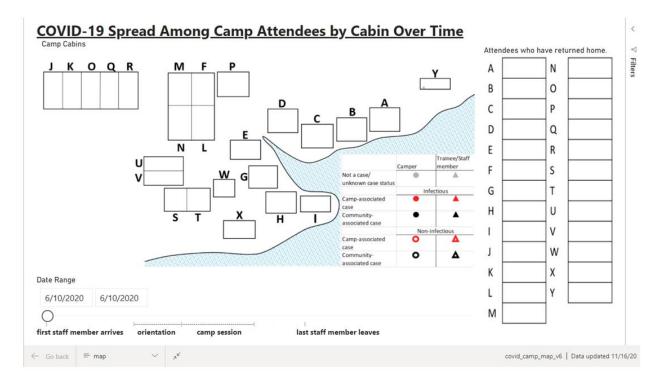


*Cases were asymptomatic or missing symptom information †Case had symptoms but missing onset date

eFigure 2. Phylogenetic Analysis of Samples Obtained from Camp Attendees (n=22) and Selected Sequences from Georgia and other US states



a) Overall divergence tree representing genomes of select COVID-19 cases in the United States since January 2020. Selected sequences from Georgia and other US states were downloaded from GISAID on September 28, 2020. Yellow indicates isolated from community-associated cases, green indicates isolates from camp-associated cases and blue represents SARS-CoV-2 sequences from Georgia. b) Zoom-in view of the divergence tree showing all 22 isolates clustered within 0–2 single nucleotide polymorphisms (SNPs) of another case isolate.



eVideo 1. COVID-19 Spread Among Camp Attendees by Cabin Over Time

^aCommunity-associated cases and camp-associated cases appear as black and red, respectively, during their infectious period (two days before symptom onset or date of first positive specimen until 10 days after symptom onset or date of first positive specimen).

^bMap is not drawn to scale. Grouped cabins in the map indicate shared entryways and common spaces. The size of cabin shape does not correspond to cabin size.

^cSix cabins with three persons or less were not shown in this figure. Two of these cabins did not house any cases.