

Risk factors leading to COVID-19 cases in a Sydney restaurant

Adam Capon,^{1,2} Jody Houston,¹ Rebecca Rockett,^{3,4} Vicky Sheppard,^{1,5} Sandra Chaverot,¹ Alicia Arnott,^{3,6} Tiana Parashko,¹ Mark Ferson^{1,7}

On 13 January 2020, the first case of COVID-19 appeared in Australia¹ and as of 14 January 2021, 28,658 cases had been identified in Australia and more than 92 million cases worldwide. The causative agent of COVID-19 is a novel betacoronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Transmission of SARS-CoV-2 has been reported in a number of settings, including restaurants. Indoor dining has been identified as a higher risk environment for SARS-CoV-2 transmission.² However, few studies provide evidence defining the risk factors associated with transmission in restaurant environments. The published studies of restaurant outbreaks linking between three and 10 cases have focused on airflow modelling to explain person-to-person transmission.³⁻⁵ However, for these studies, little is known about the potential misclassification of exposure due to other sources of transmission.

On 28 July 2020, South Eastern Sydney Local Health District, Public Health Unit (PHU) was notified of the first of what would become 20 SARS-CoV-2 positive cases epidemiologically linked to a restaurant in Sydney. All 20 cases were patrons present at the restaurant on 25 July 2020, the day of COVID-19 onset for an infectious staff member. A further five staff members also became cases and had multiple days of exposure to the infectious staff member.

Upon notification of a positive case of SARS-CoV-2, the PHU, under the *NSW Public*

Abstract

Objective: To explore the factors associated with the transmission of SARS-CoV-2 to patrons of a restaurant.

Methods: A retrospective cohort design was undertaken, with spatial examination and genomic sequencing of cases. The cohort included all patrons who attended the restaurant on Saturday 25 July 2020. A case was identified as a person who tested positive to a validated specific Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) nucleic acid test. Associations were tested using chi-squared analysis of case versus non-case behaviours.

Results: Twenty cases were epidemiologically linked to exposure at the restaurant on 25 July 2020. All cases dined indoors. All cases able to be genomic sequenced were found to have the same unique mutational profile. Factors tested for an association to the outcome included attentiveness by staff, drink consumption, bathroom use and payment by credit card. No significant results were found.

Conclusion: Indoor dining was identified as a key factor in SARS-CoV-2 transmission, and outdoor dining as a way to limit transmission.

Implications for public health: This investigation provides empirical evidence to support public health policies regarding indoor dining.

Key words: COVID-19, restaurant, dining, transmission, SARS-CoV-2

Health Act 2010, initiates public health control measures. Where an outbreak is identified, these public health measures will include an outbreak investigation. For this outbreak, the investigation involved genomic sequencing of the virus infecting all cases, on-site inspections and semi-structured interviews of key restaurant staff, including the index case. The purpose of these interviews was to discover staff movements on 25 July along with factors that could provide insight into possible transmission risks. The index case was questioned on usual and specific behaviours undertaken on 25 July. The on-

site inspection involved confirming spatial layouts, patron locations and examining adherence to procedures designed to reduce potential disease transmission along with identifying source points of potential transmission. The genomic testing was to provide confirmatory evidence of the transmission between cases.

The staff member had onset of symptoms on 25 July but had also worked during their infectious period on 23 and 24 July. All inside patrons and staff from the three infectious days were quarantined as close contacts, however, cases arose only among patrons and

1. South Eastern Sydney Local Health District, South Eastern Sydney Public Health Unit, New South Wales

2. School of Public Health, Faculty of Medicine and Health, The University of Sydney, New South Wales

3. Westmead Hospital, Centre for Infectious Diseases and Microbiology, Public Health, New South Wales

4. Marie Bashir Institute for Infectious Diseases and Biosecurity, The University of Sydney, New South Wales

5. School of Public Health, Faculty of Medicine and Health, The University of Sydney, New South Wales

6. Institute of Clinical Pathology and Medical Research, Centre for Infectious Diseases and Microbiology Laboratory Services, New South Wales

7. School of Public Health and Community Medicine, University of New South Wales

Correspondence to: Dr Adam Capon, South Eastern Sydney Local Health District, South Eastern Sydney Public Health Unit, Locked Bag 88 Randwick NSW 2031; e-mail: adam.capon@health.nsw.gov.au

Submitted: January 2021; Revision requested: April 2021; Accepted: May 2021

The authors have stated they have no conflicts of interest.

This is an open access article under the terms of the Creative Commons Attribution-NonCommercial-NoDerivs License, which permits use and distribution in any medium, provided the original work is properly cited, the use is non-commercial and no modifications or adaptations are made.

Aust NZ J Public Health. 2021; 45:512-16; doi: 10.1111/1753-6405.13135

staff who attended the restaurant on 25 July. Potential transmission routes that emerged from these initial investigations centred on person-to-person transmission by droplets including patron seating location, actions that exposed patrons to the index case staff member (assistance in signing in, ordering) and transmission by fomites, e.g. drink consumption (the index case prepared and served several types of drinks), use of the same bathroom as the case, paying by credit card that was handled by the case and use of salt and pepper shakers. All food was served to share therefore determining exposure to specific foods was not considered informative. These themes formed the basis of the second phase of the investigation – a quantitative survey of all patrons who attended the restaurant on 25 July 2020 along with a spatial examination of patron seating location and index case movements. This second phase is reported below.

Methods

At the time of the outbreak, restaurants in New South Wales (NSW) were required by law to collect patrons' contact details for contact tracing purposes, with patrons providing these details to the restaurant (signing in). Using this data provided by the restaurant, 208 patrons were identified as having visited the restaurant on 25 July 2020. All 208 patrons were invited to take part in the investigation.

Staff who worked on 25 July were not invited to take part in the investigation as they had multiple days of exposure to the infectious staff member and differing interactive behaviours to the index case from the dining public.

On 30 October 2020, an invitation was made via telephone interview by trained contact tracers for all 208 patrons to participate in the investigation. To ensure maximum participation, at least six attempts to contact each patron were made over multiple days and times. On the third attempt, patrons were provided with call back details, before a further three attempts were made. For those successfully contacted, participation required the completion of a questionnaire that examined the location of the patron in the restaurant, actions of staff, and behaviours of the patron.

The venue contained indoor and outdoor dining as well as an indoor bar area. Patrons were asked whether they dined indoors, outdoors or had a drink at the bar only.

Further questions involved understanding if the patrons were greeted by a member of staff on arrival to the restaurant, whether a staff member assisted the patron in signing in, whether a staff member explained the menu to them and if the patrons ordered the meal. The gender of the staff member for each of these actions was sought to help identify potential exposure to the index case. Patrons' behaviours included the consumption of cocktails, spirits, beer, wine, coffee, soft drink, sparkling water and/or tap water, use of the bathroom, use of salt and pepper shakers and providing payment for their meal. Finally, basic demographic information (age, identifying gender and smoking status) was sought.

In the analysis, we combined certain responses to examine the strength of association between aggregated exposures and risk of SARS-CoV-2 infection. These included if a staff member (of the same gender as the index case) both greeted and helped the patron with their sign in, if a staff member (of the same gender as the index case) both stood next to the patron to explain the menu and took the order from the patron, and if the patron drank any alcohol.

Responses were entered into REDCap and analysed in SAS Enterprise Guide 7.0. The analysis involved descriptive and inferential statistics. Descriptive statistics included attack rates that were calculated based on the number of cases divided by the total number of patrons identified. Inferential statistics involved chi-squared tests with an outcome variable of positive SARS-CoV-2 infection and predictor variables being the risk factors identified in the questionnaire or time of day at the restaurant. Fisher's exact test was used to determine significance where cell counts were six or under. Given the low case numbers, adjusted regression analysis was not feasible.

A spatial examination was undertaken to determine if seat proximity to the index case could be considered a risk factor in this environment. This involved interviewing the index case and the 20 subsequent cases regarding their movements on 25 July and reviewing restaurant records such as seating allocations. The examination was undertaken separately for lunch and dinner sittings.

Genome sequencing was performed and analysed as previously described;⁶ whole genome amplification was attempted on all available specimens. The resulting phylogeny of the outbreak sequences was rooted to the reference strain; GISAID EPI_ISL_413856.

Results

Of the 208 patrons who attended the restaurant on 25 July, 179 (19 cases and 160 non-cases) participated in the investigation. Nine patrons declined and 20 were unable to be contacted. The median age of participants was 37 years with no difference in median age between case (37 years) and non-case (37 years) groups. Participants were more likely to identify as female (60%) with similar proportionality of females in the case (58%) and non-case (60%) groups. The majority of patrons dined indoors ($n=163$, attack rate 12%) and a small number dined outdoors, none of whom became cases ($n=14$, attack rate 0%). Only two patrons smoked while in attendance at the restaurant. Figure 1 displays the epidemiological curve of symptom onset for the 19 cases; for asymptomatic cases, the date of the first positive test was used.

Cases tended to arise in groups that ate at or near the bar, or along the path the infectious staff member walked from the bar to the entrance. Even among larger dining groups, no more than two cases arose from a seating.

Chi-squared analysis of reported risk factors did not identify any statistically significant risk factors (Table 1).

The restaurant operated with two-hour dining bookings spaced across the day to involve a total of six sittings for the day. The index case worked across all six sittings (three lunch, three dinner). Ninety-seven patrons sat for lunch and 111 sat for dinner sessions. The index case appeared to become more infectious throughout the day, although not significantly, with seven cases identified through the lunch period (attack rate 7%) and 13 cases during the dinner period (attack rate 12%; $p=0.27$), see Figures 2 and 3. The restaurant was vacated between the lunch and dinner sessions for a complete clean and re-set. The index case was reported to be predominantly located behind the bar area and between the bar and guest entrance (marked in red, Figures 2 and 3).

Figures 2 and 3 show cases predominantly seated where the index case would walk between the bar and guest entrance to greet new patrons.

Complete SARS-CoV-2 genomes were sequenced from eight of the 20 cases within the outbreak as well as the index case (Case 1), see Figure 4. Using the pangolin typing systems, all nine sequences were classified as lineage D.2, which was the predominant locally acquired lineage at the time of the outbreak.⁷ The same mutational profile was

uncovered in each genome when compared to the originally reported Wuhan strain (NCBI Accession: MN908947.3). Mutations at positions (non-synonymous changes shown in brackets) C241T, A1163T (ORF1ab I300F), C3037T, T7540C, C14408T, G15535T (ORF1ab K590N), G16647T (ORF1ab R5461L), C18555T (ORF1ab T6097I), C22480T, G22992A (Spike S477N), G23401A, A23403G (Spike D614G), G28881A (Nucleocapsid R203K), G28882A, G28883C (Nucleocapsid G204R). Only one genome, Case 5, contained an additional single nucleotide polymorphism at position G8861A (ORF1ab V2866M). Genomes generated were uploaded to the Global Initiative on Sharing All Influenza Data (GISAID) database with the accession numbers; EPI_ISL_513355, EPI_ISL_513377, EPI_ISL_513376, EPI_ISL_513375, EPI_ISL_544956, EPI_ISL_545023, EPI_ISL_526121, EPI_ISL_513374, EPI_ISL_490038 (first sequenced case of SARS-CoV-2 lineage D.2 in NSW).

Discussion

Australia is in a unique situation in that it is one of only a few countries with high testing rates to confirm the low background rate of SARS-CoV-2 infection within the community. Having little to no community transmission of SARS-CoV-2 infection provides confidence that SARS-CoV-2 transmission occurred within the restaurant environment and was not circumstantial to patrons being newly infected within the community and meeting in this one location by chance.

We found that only those who dined indoors became infected with the SARS-CoV-2 virus. Further, the attack rate varied throughout the day, with a higher attack rate as the day progressed.

We believe that indoor transmission is a key finding. The index case greeted, seated and prepared drinks behind the bar for all patrons, regardless of whether the patron was seated indoors or outdoors, indicating that the indoor environment posed a greater risk. The staff member did, however, take orders and serve drinks to indoor patrons only. Nonetheless, the lack of cases among outdoor patrons supports the strategies of moving dining and other activities to outdoor or well-ventilated places to reduce the risk of SARS-CoV-2 transmission.

The second finding is seeing the increase in attack rate as the day progressed. Patrons had a consistent duration of exposure throughout the day (two hours), but the attack rate was

Figure 1: Epidemiological curve of outbreak cases.

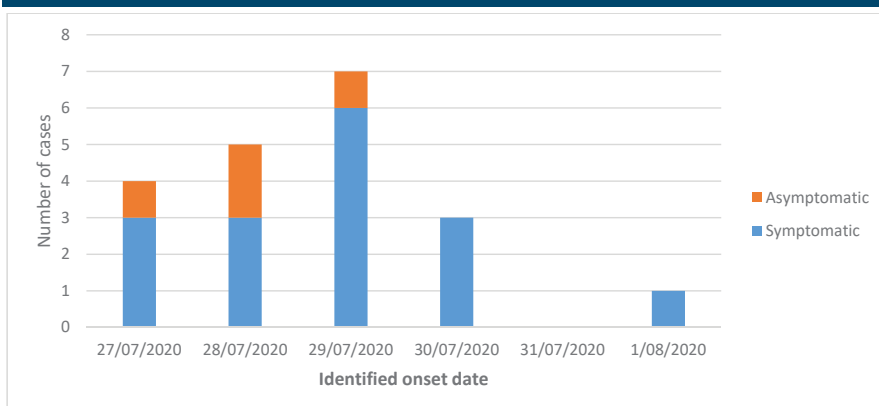


Table 1: Relative risk of SARS-CoV-2 infection from potential risk factors.

Risk factors	RR	CI	P value
Identifying as female	0.9	0.4–2.2	0.85
Greeted by a member of staff on arrival*	1.8	0.7–4.6	0.25
Dined indoors	#	#	0.19
Helped to sign in by a member of staff*	1.4	0.4–4.7	0.47
Member of staff stood next to patron to explain the menu*	0.4	0.06–3.2	0.69
Ordered their meal from the wait staff*	0.8	0.2–3.3	1
Drank a cocktail	0.9	0.4–2.3	0.89
Drank a spirit	2.9	1.1–7.7	0.06
Drank a beer	2.1	0.8–5.3	0.16
Drank a wine	0.6	0.2–1.3	0.18
Drank a coffee	1.6	0.5–4.9	0.43
Drank a soft drink	1	0.2–7.0	1
Drank sparkling water	0.6	0.2–1.6	0.29
Drank tap water	1.9	0.7–5.0	0.19
Went to the bathroom*	0.6	0.2–2.0	0.47
Handled the salt and pepper grinders	0.8	0.1–5.9	1
Paid by card	1	0.4–2.4	0.9
Were greeted and helped to sign in by staff*	0.8	0.1–5.2	1
Staff member* stood next to and took the order from the patron	0.8	0.1–5.5	1
Drank Alcohol	1.2	0.3–4.8	1

Notes:

*of the same gender as the index case

unable to be calculated due to zero cases dining outdoors

higher for those who dined in the evening compared to the afternoon, to a rate similar to that reported in many households.⁸ One possible explanation is that the index case became more infectious as the day progressed. Alternate explanations are the possibility of declining hand hygiene by the index case or environmental contamination built up during the day, increasing the risk of fomite exposure for those who dined in the evening. This would be consistent with the greater dispersed pattern of cases through the restaurant during the evening but would be counter to the reported cleaning protocols in place and current evidence that fomites are an unusual source of infection.⁹

We found that for 16 of the 20 cases, the incubation period was four days or less

(Figure 1), this being less than the reported average incubation period of five days in the literature.¹⁰ We are confident that this incubation period is accurate, given the low background rate of SARS-CoV-2 infection within the community at the time. This may add further weight to our hypothesis of environmental contamination built up during the day and therefore patrons receiving a large amount of virus that may have possibly reduced their incubation period.

The investigation examined a number of hypothesised routes of transmission, but it was unable to significantly associate any route to confirmed infection. This result, while disappointing, is not surprising given the lack of power in the investigation. Post hoc power calculations showed the investigation was

underpowered, with the power to detect a real association ranging from 3% to 54%, with a median of 6%. Being able to clearly attribute 20 cases to a single exposure on the basis of traditional and molecular epidemiology is a valuable opportunity to develop evidence around SARS-CoV-2 transmission.

The consumption of spirits was close to a significant association with infection, and this could be seen as a plausible mechanism of transmission as the index case had responsibility for making and delivering

spirits. This weak association also had the highest power to detect an effect (54%). However, it is possible this could also be due to chance, given the number of associations tested in this analysis.

All virus genomes sequenced from this transmission event carried the same mutational profile, with only one patron gaining an additional single nucleotide polymorphism, strongly supporting transmission events within the restaurant. The SARS-CoV-2 lineage detected in this outbreak

– D.2 – was the only lineage circulating in the Australian community during this time period. However, community transmission during this outbreak was low with only 86 COVID-19 cases reported in NSW in the epidemiological week ending on 25 July 2020.¹¹ Interestingly, this genome contained the D614G mutation that has been suggested to increase the transmissibility of SARS-CoV-2.¹² In addition, the outbreak lineage contains the spike protein mutations S477N, which is within the receptor-binding domain and may reduce the neutralising antibody response.¹³ The combination of traditional and genomic epidemiology provides additional evidence when investigating outbreaks of SARS-CoV-2.

An interesting point is the timing of the infectiousness of the index case. The index case acquired the infection from a customer who dined at the restaurant on 22 July. According to current evidence, a person can be infectious 48 or even 72 hours prior to the onset of symptoms.¹⁴ Following standard Australian public health guidelines in place at the time, all patrons of the restaurant during the index case infectious period (48 hours prior to onset, i.e. from 23 July) were followed up and placed in home quarantine for two weeks after their dining date. However, despite being potentially infectious and working at the restaurant on the 23 and 24 July, no transmission of SARS-CoV-2 infection occurred until the day of symptom onset (25 July), in contrast to some studies that highlight peak infectivity prior to symptom onset, and confirming infectivity during symptom onset.¹⁴⁻¹⁷

Figure 2: Lunchtime sittings identifying case locations.

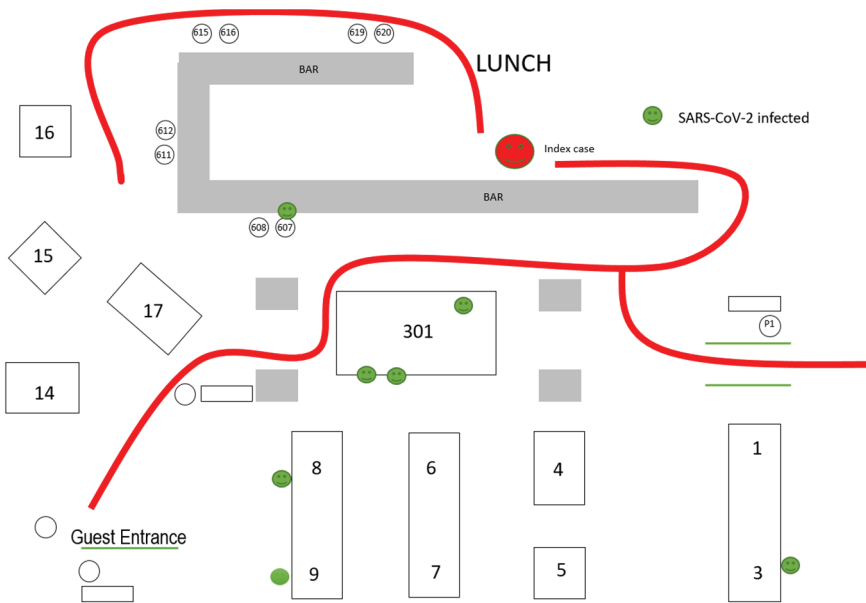


Figure 3: Dinner sittings identifying case locations.



Limitations

This paper has a number of limitations. While we are confident that transmission of SARS-CoV-2 infection occurred on 25 July, it is possible that some cases could have been infected by the household member with whom they were dining at the restaurant. However, as these cases had similar onset dates, the more credible explanation is infection on 25 July with slightly differing incubation periods.

The investigation relied on the recall of the index case and patrons regarding movements through the restaurant environment and other behaviours and as such may have been subject to recall bias. Objective measurement of these factors through the examination of CCTV footage was not possible as such footage was unavailable.

In order to maintain confidentiality, we could not identify the index case to patrons. We were therefore required to analyse our data by the gender of the index case. Other staff of the same gender were working on 25 July and this may have led to some of the data being subject to exposure misclassification. However, the work pattern of the index case was different to those staff of the same gender. Using this, we developed our questionnaire to minimise any potential exposure misclassification.

The assessment of mask use to limit transmission could not be undertaken as mask use was not mandated by the NSW Government at this time. Further, the assessment of airflow on infection was beyond the scope of this investigation, however, given the pattern of case distribution around the restaurant (Figures 2 and 3), we believe the index case movements around the restaurant to be a greater factor in SARS-CoV-2 spread than the restaurant ventilation.

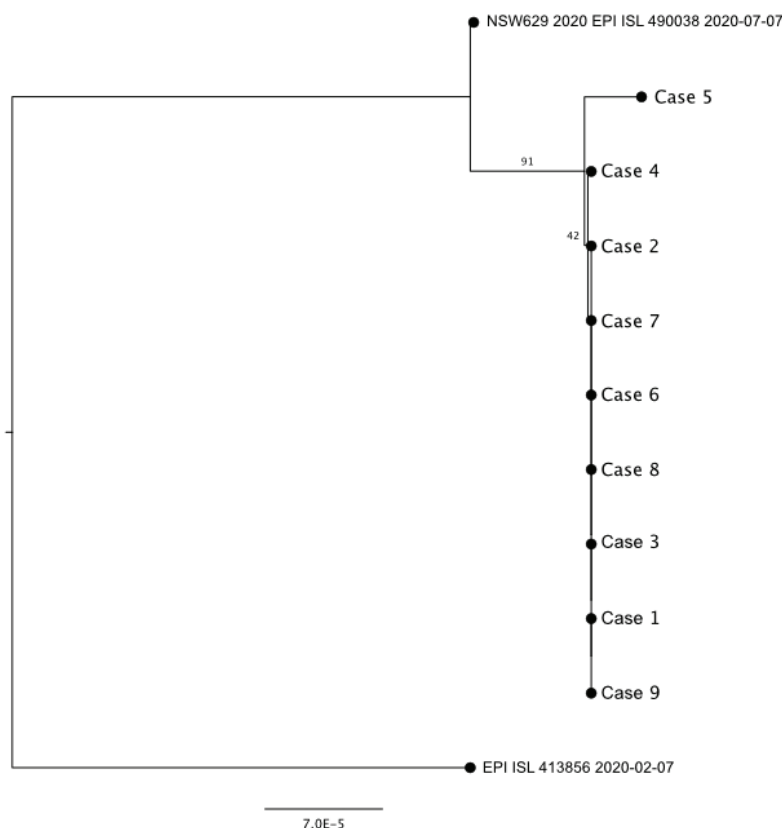
Conclusion and implications for public health

Outdoor dining is a way to reduce the potential transmission of SARS-CoV-2 in the restaurant environment. Very little has been reported on the transmission of SARS-CoV-2 within this environment and this investigation provides empirical evidence to support current public health policies for reducing the risk of the public's exposure to SARS-CoV-2, while at the same time limiting the economic and social impact of the pandemic.

Acknowledgements

The authors thank Alice Zhu, Milica Mihajlovic, Rose Kassolis, Eleanor Sullivan, Nicolas Gonzales, Katrina Pearson, Sue Griffiths, Douglas Knox and Maria Browne at South Eastern Sydney Public Health Unit, Close Contact Tracing Team for data collection and Aneliese Goodwin, Clement Lee, Carl Banting, Connie Lam, Karen-Ann Gray, Eby Sim, Elena Martinez, Mailie Gall, Jenny Draper, Rosemarie Sadsad, Andrew Ginn, Qinning Wang and Vitali Sintchenko at the Microbial Genomics Reference Laboratory, New South Wales Pathology-Institute of Clinical Pathology and Medical Research for SARS-CoV-2 genome sequencing and bioinformatic analysis.

Figure 4: Maximum likelihood phylogeny of the nine SARS-CoV-2 genomes in this outbreak. A reference sequence of the first sequenced case of SARS-CoV-2 lineage D.2 in NSW is also included (NSW629 EPI ISL 490038).



References

- 2019-nCoV National Incident Room Surveillance Team. 2019-nCoV acute respiratory disease, Australia, Epidemiology Report 1 (Reporting week 26 January - 1 February 2020). *Commun Dis Intell.* (2018).2020;44. doi: 10.33321/cdi.2020.44.13.
- Fisher KA, Tenforde MW, Feldstein LR, Lindsell CJ, Shapiro NI, Files DC, et al. Community and close contact exposures associated with COVID-19 among symptomatic adults ≥ 18 years in 11 outpatient health care facilities - United States, July 2020. *MMWR Morb Mortal Wkly Rep.* 2020;69(36):1258-64.
- Lu J, Gu J, Li K, Xu C, Lai Z, Zhou D, et al. COVID-19 outbreak associated with air conditioning in restaurant, Guangzhou, China, 2020. *Emerg Infect Dis.* 2020;26(7):1628-31.
- Li Y, Qian H, Hang J, Chen X, Hong L, Liang P, et al. Evidence for probable aerosol transmission of SARS-CoV-2 in a poorly ventilated restaurant. *medRxiv.* 2020:2020.04.16.20067728. doi: 10.1101/2020.04.16.20067728
- Kwon KS, Park JI, Park YJ, Jung DM, Ryu KW, Lee JH. Evidence of long-distance droplet transmission of SARS-CoV-2 by direct air flow in a restaurant in Korea. *J Korean Med Sci.* 2020;35(46):e415.
- Rockett RJ, Arnott A, Lam C, Sadsad R, Timms V, Gray K-A, et al. Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling. *Nat Med.* 2020;26(9):1398-404.
- Rambaut A, Holmes EC, O'Toole A, Hill V, McCrone JT, Ruis C, et al. A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. *Nat Microbiol.* 2020;5(11):1403-7.
- Madewell ZJ, Yang Y, Longini IM Jr, Halloran ME, Dean NE. Household transmission of SARS-CoV-2: A systematic review and meta-analysis. *JAMA Netw Open.* 2020;3(12):e2031756-e.
- Meyerowitz EA, Richterman A, Gandhi RT, Sax PE. Transmission of SARS-CoV-2: A review of viral, host, and environmental factors. *Ann Intern Med.* 2021;174(1):69-79.
- McAloon C, Collins A, Hunt K, Barber A, Byrne AW, Butler F, et al. Incubation period of COVID-19: A rapid systematic review and meta-analysis of observational research. *BMJ Open.* 2020;10(8):e039652.
- NSW Health. *COVID-19 Weekly Surveillance Reports - Epidemiological Week 30, Ending 25 July 2020 [30 July 2020].* Sydney (AUST): State Government of New South Wales; 2020.
- Korber B, Fischer WM, Gnanakaran S, Yoon H, Thielier J, Abfalterer W, et al. Tracking changes in SARS-CoV-2 spike: Evidence that D614G increases infectivity of the COVID-19 virus. *Cell.* 2020;182(4):812-27.e19.
- Tea F, Stella AO, Aggarwal A, Darley DR, Pilli D, Vitale D, et al. SARS-CoV-2 neutralizing antibodies; longevity, breadth, and evasion by emerging viral variants. *medRxiv.* 2020:2020.12.19.20248567. doi: 10.1101/2020.12.19.20248567
- Wei WE, Li Z, Chiew CJ, Yong SE, Toh MP, Lee VJ. Presymptomatic transmission of SARS-CoV-2 - Singapore, January 23-March 16, 2020. *MMWR Morb Mortal Wkly Rep.* 2020;69(14):411-5.
- He X, Lau EHY, Wu P, Deng X, Wang J, Hao X, et al. Temporal dynamics in viral shedding and transmissibility of COVID-19. *Nat Med.* 2020;26(5):672-5.
- Lu Q-B, Zhang Y, Liu M-J, Zhang H-Y, Jalali N, Zhang A-R, et al. Epidemiological parameters of COVID-19 and its implication for infectivity among patients in China, 1 January to 11 February 2020. *Euro Surveill.* 2020;25(40):2000250.
- Benefield AE, Skrip LA, Clement A, Althouse RA, Chang S, Althouse BM. SARS-CoV-2 viral load peaks prior to symptom onset: A systematic review and individual-pooled analysis of coronavirus viral load from 66 studies. *medRxiv.* 2020:2020.09.28.20202028; doi: 10.1101/2020.09.28.20202028