


Superspreaders: A Lurking Danger in the Community

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Abstract

A “superspreader” refers to an unusually contagious organism infected with a disease. With respect to a human borne illnesses, a superspreader is someone who is more likely to infect other humans when compared to a typically infected person. The existence of human superspreaders is deeply entrenched in history; the most famous case being that of Typhoid Mary. Through contact tracing, epidemiologists have identified human superspreaders in measles, tuberculosis, rubella, monkeypox, smallpox, Ebola hemorrhagic fever, and SARS. The recent outbreak of Coronavirus disease (COVID-19) has shifted the focus back on the superspreaders. We herein present a case report of a COVID-19 superspreader with a hitherto unusually high number of infected contacts. The index case was a 33 year old male who resided in a low income settlement comprising of rehabilitated slum dwellers and worked as a healthcare worker (HCW) in a tertiary care hospital and had tested positive for COVID-19. On contact tracing, he had a total of 125 contacts, of which 49 COVID-19 infections had direct or indirect contact with the index case, qualifying him as a “superspreader.” This propagated infection led to an outbreak in the community. Contact tracing, testing and isolation of such superspreaders from the other members of the community is essential to stop the spread of this disease and contain the COVID-19 pandemic.

Keywords

community, contagious, COVID 19, infection, outbreak, superspreader

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Introduction

A “superspreader” refers to an unusually contagious organism infected with a disease.¹ With respect to a human borne illnesses, a superspreader is someone who is more likely to infect other humans when compared to a typically infected person. Such superspreaders are of major concern for epidemiologists and public health experts. The concept of superspreaders is not just limited to human species. Many authors have reported the existence of superspreaders in different animal species like water buffaloes (brucellosis), deer mice (Sin Nombre Virus) etc.^{2,3}

The existence of human superspreaders is deeply entrenched in history; the most famous case being that of “Typhoid Mary” who despite herself being asymptomatic, ended up infecting 51 individuals between 1900 and 1907, 3 of whom eventually died.⁴ Through contact tracing, epidemiologists have identified human superspreaders in measles, tuberculosis, rubella, monkeypox, smallpox, Ebola

hemorrhagic fever, and SARS.^{1,5-8} There are multiple explanations for the occurrence of superspreaders and super-spreading events, including asymptomatic patients, patients with increased disease severity, increased viral load, prolonged viral shedding, atypical disease and extensive social interactions.¹

The recent outbreak of Coronavirus disease (COVID-19) has shifted the focus back on the superspreaders. We herein present a case report of a COVID-19 superspreader with a hitherto unusually high number of infected contacts.

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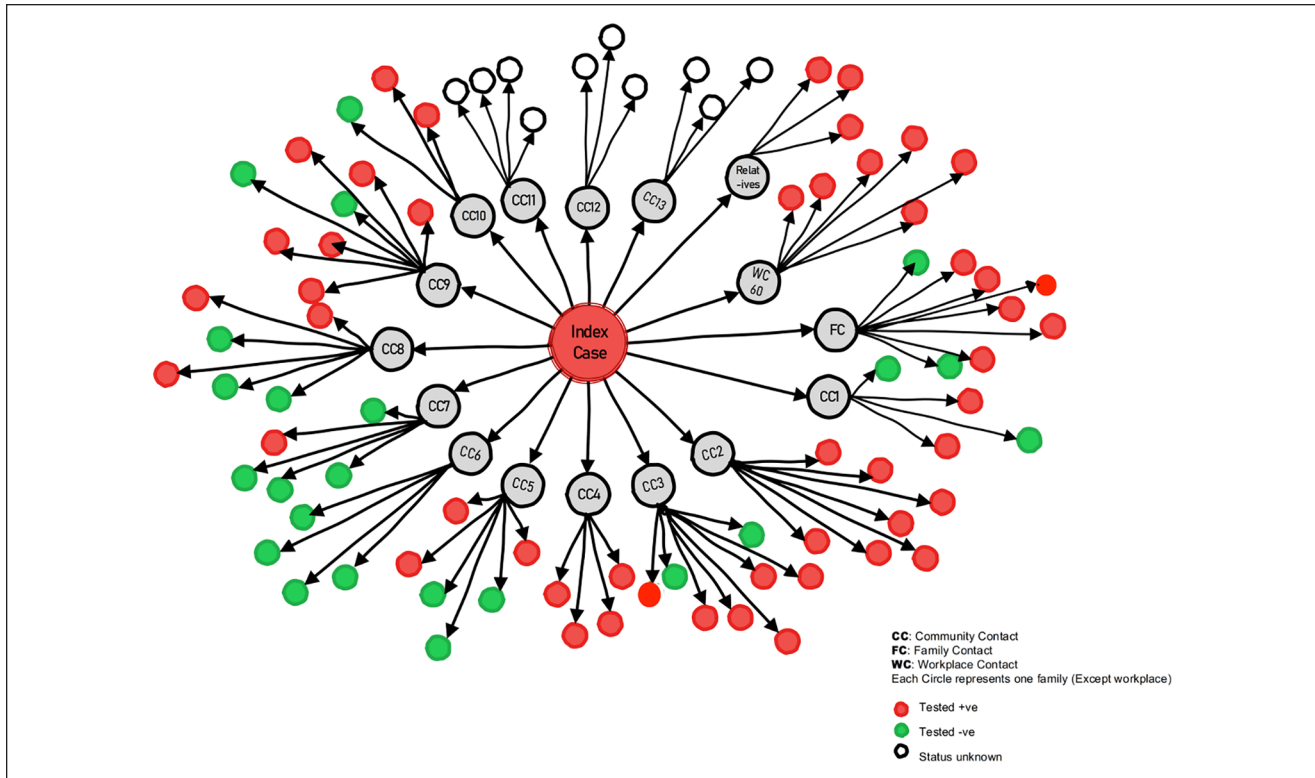


Figure 1. Contact tracing and spread of COVID-19 by Index Case.

Case Presentation

The index case was a 33-year-old male who resided in a low-income settlement comprising of rehabilitated resettlement colony for people residing in urban slum in Chandigarh, India and worked as a healthcare worker (HCW) in a tertiary care hospital. He presented with complaints of fever, cough, and sore throat. His nasopharyngeal swab tested positive for RT-PCR for SARS-CoV2 and he was diagnosed as a case of COVID-19. On contact tracing, he had a total of 11 family contacts, of which 8 were household contacts while the other 3 were his relatives who were staying in a different house, but had visited the index case. Amongst the 8 household contacts, 6 were positive for COVID-19 whereas all 3 contacts in the latter group tested positive for COVID-19. Furthermore, on contact tracing, there was a history of attending a small community function in the locality. In total, the index case had 125 contacts, of which 65 were community contacts and 60 were workplace contacts. All these contacts were screened and 21 community contacts and 3 workplace contacts were found to be symptomatic while the rest were asymptomatic. Testing was done for 55 community contacts and all 60 workplace contacts. A total of 34 community contacts and 6 workplace contacts were positive for COVID-19. Therefore in total, 49 COVID-19 infections had direct or

indirect contact with the index case, qualifying him as a “superspreader” as shown in Figure 1. This propagated infection in the community led to an outbreak in the colony where the index case was residing with 236 cases reported till the date the paper has been submitted for publication, which accounted for more than two-thirds of the total cases in the city. The first contact came positive after 3 days of index case coming positive and the last contact that came positive was after 15 days of index case coming positive. Around 126 male and 110 females were found to be infected from the index case. About 80 contacts were less than 18 years of age while 135 were in age group 19 to 60 while 21 contacts were > 60 years of age. The contacted cases were those who had direct close physical contact of the index case and criteria for PCR testing was as per the testing strategy of Government of India.^{9,10}

Discussion

Since times immemorial, super-spreading events have been documented in many infectious diseases which are shaped by a multitude of host factors (physiological/ behavioral/ immunological), pathogen factors (virulence/ co-infection) and environmental factors (crowding/undiagnosed cases/ multiple hospitalizations or hospital transfers/building dynamics). Based on the earlier studies in infectious disease

epidemiology, it was believed that the chances of all susceptible hosts becoming infected within a population were equal. However, subsequently it was shown that pathogen transmission is not homogenous, with some individuals displaying a higher ability to infect others. Multiple observational and modeling studies favored the concept of the 20/80 rule, which implies that 20% of the individuals within any given population contribute to at least 80% to the transmission potential of a pathogen. This concept was a game changer in infectious disease epidemiology and many host–pathogen interactions were found to follow this empirical rule.¹

The reason why certain individuals infect disproportionately large numbers of secondary contacts is still unclear. The most important factors that govern disease transmission are the Individual reproductive number and the Basic reproductive number (R_0).^{11,12} The Individual reproductive number represents the number of secondary infections caused by a specific individual during the time that individual is infectious. On the other hand, the basic reproduction number is the average number of secondary infections caused by a typical infective person in a susceptible population and is calculated by multiplying the average number of contacts in a day by the average probability that a susceptible individual who is exposed will become infected and the duration of infectious period. The importance of both these variables in assessing outbreak severity, and guiding public health interventions cannot be overemphasized.¹³ Another important factor that also plays a significant role in disease transmission is the absence of herd immunity.¹ Herd immunity, by definition, is the indirect protection that immunized community members provide to non-immunized members in preventing the spread of contagious disease. With the increase in the number of immunized individuals, the likelihood of an outbreak decreases as there are fewer susceptible contacts. With time, as the pathogen that confers immunity to the survivors moves through a susceptible population, the number of susceptible contacts declines. Even if susceptible individuals remain, their contacts are likely to be immunized, preventing any further spread of the infection. The presence of co-morbidities like diabetes, hypertension, immunocompromised state may also sometimes influence disease transmission. For comparison, the basic reproduction number of the SARS-CoV2, is between 1.4 and 3.9 which means that in the absence of any preventive measures, the average number of additional people that a single COVID-19 patients will infect ranges from 1.4 to 3.9.¹

The first case of COVID-19 related superspreader was reported as early as February 20th, 2020 from South Korea when the Centers for Disease Control and Prevention Korea (KCDC) reported 70 cases linked to “Patient 31” who had participated in a gathering in Daegu at the Shincheonji Church of Jesus the Temple of the Tabernacle of the Testimony. Over the next few days, the number of cases

quickly rose to 544 among 4400 examined followers of the church.¹⁴ Another superspreader that was reported in New York, USA was a lawyer in New Rochelle who contracted the illness and then spread it to at least 20 other individuals in his community, thereby creating a cluster of nearly 100 cases, which accounted for more than half COVID-19 cases in the state during early March 2020.¹⁵ The latest in the global list of superspreaders is a worker at a fish processing plant in Tema, Ghana who is believed to have infected over 500 other people with COVID-19.¹⁶

In India, limited data is available about superspreaders of SARS-CoV2. There are only anecdotal reports available about a preacher who on returning from Italy and Germany ignored self-quarantine which led to 19 of his relatives testing positive. He reportedly had contact with 550 people which fuelled the Indian government’s fears of an outbreak and led to the quarantine of 40 000 residents from 20 villages in the State of Punjab, India on March 27th, 2020.¹⁷ To the best of our knowledge, our case remains the first reported case of documented COVID-19 superspreader with an unusually high number of secondary infections.

The reason for spreading the infection in this particular case may be because of two reasons. The person was living in a densely populated low-income settlement colony where physical distancing between the individuals is not possible and the high number of community contacts the person had. This coupled with asymptomatic infections was responsible for the late detection and delayed isolation of cases leading to widespread outbreak.

Even though all efforts were made to do contact tracing of the index case, these numbers may not reflect the true story as sometimes the patients are not very forthcoming with their history of contact due to stigma associated with quarantine. Another important limitation in this report was that 10 community contacts belonging to 3 families were only screened and not tested by RT-PCR for COVID-19. Furthermore, in those contacts of asymptomatic cases that were tested negative, repeat testing was not done between Day 5 to Day 14. Repeat testing in such cases is recommended, as it is difficult to assess the last date of exposure in such cases and the limited sensitivity of the RT-PCR test.

To prevent such superspreading events in the community, there is a need for behavior change communication emphasizing on early reporting to health facility if a person develops Influenza-like-illness (ILI) symptoms namely fever ($>100^\circ$ F) and cough, avoiding unnecessary contacts and maintaining a distance of at least 1 m during social interactions in the community, use of masks and frequent hand washing.


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