

A CASE STUDY OF INTRA-FAMILY CLUSTERING OF COVID-19 IN INDIA

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ABSTRACT

Background: With unprecedented COVID-19 disease-related morbidity and mortality globally, understanding the transmission dynamics of this disease is of paramount importance for disease control efforts. Despite the lockdown in India, there has been reported an ever-increasing number of infected cases, suggesting clustering of cases. As our first 25 cases belonged to a single family we undertook the study with the objective of finding the cluster dynamics by charting the family tree. **Methods:** We conducted a retrospective case study of twenty-five confirmed COVID-19 disease cases belonging to a single-family in rural Maharashtra, India. Four members of the family returned from foreign travel and developed COVID-19 symptoms and tested positive by RT-PCR of throat swab on day 7 of their travel. A contact investigation of 52 household members revealed 21 new infections and all 24 members of the family were placed in hospital quarantine. **Results:** Of the 25 cases, 11(44%) were male and 14 (56%) were female; 2 were children. Of the 23 adults, 7 (30%) were asymptomatic at diagnosis while 16 (70%) had only mild symptoms. All were placed on a course of hydroxychloroquine, azithromycin, and oseltamivir; none required intensive care admission. All tested negative on repeated throat swab on day 14 of quarantine and were discharged. **Interpretation and Conclusion:** Our case study of the intrafamily transmission of COVID-19 in rural Maharashtra highlights how clustering of cases occurs within families that could become a potential source of high transmission. Clustering of cases within families and communities may in part explain the rise in COVID-19 cases despite lockdown in India.

KEYWORDS: COVID-19, clusters, intra-family, transmission.

INTRODUCTION

By mid-April of 2020, over 1.92 million cases of COVID-19 disease from the SARS-CoV-2 virus have been reported in 210 countries and territories, indicating the unprecedented rapid spread of the disease globally.^[1] Data to-date indicate that disease spectrum ranges from asymptomatic phase to severe pneumonia and acute respiratory distress syndrome with a relatively high mortality rate among high-risk groups such as elderly, and those with comorbidities (e.g. diabetes, hypertension).^[2,3,4] Furthermore, the transmissibility of the virus remains high mainly by droplets, as well as, by contact with contaminated surfaces.^[5]

India reported its first COVID-19 case on 30 January 2020 in Kerala, which rose to three cases by 3 February 2020; all were students who had returned from Wuhan, China.^[6] Thereafter, India adopted the WHO-recommended strategy of identifying COVID-19 cases among foreign travellers and quarantined those with symptoms and who tested positive as well as recommended self-isolation.^[7] On March 22nd complete

3- week lockdown was announced to curb the transmission of COVID-19.^[7] Despite these bold measures, India's case count breached 20,000 (and <3% mortality) by 23rd April and the disease trajectory appear to follow in the same direction as that of many affected countries (Italy, United States). Clustering of cases within families and communities may in part explain the rise in COVID-19 cases despite lockdown in India. In this report, we describe a case study of the intrafamily transmission of COVID-19 disease providing insights into the clustering of cases within a family.

MATERIAL AND METHODS

We conducted a retrospective study of twenty-five confirmed COVID-19 disease cases belonging to a single-family in rural Maharashtra. These cases were hospitalized for COVID-19 diagnostics, as well as, for quarantine at the teaching tertiary care center that was converted into a dedicated COVID-19 hospital that is affiliated with Government Medical College, Miraj.

On day 5 of their return from Saudi Arabia, four members of the family sought health check-up for COVID-19. They were recommended home quarantine as they had no symptoms. Two days later (7 days after their return), all developed fevers and returned to the medical facility and were kept on isolation. Oropharyngeal swab for Reverse transcription-polymerase Chain Reaction (RT-PCR) came back positive for the four travellers. Soon after, 52 household contacts were tested for COVID-19, of which 21 family members turned positive. All positive cases were placed in the COVID-19 hospital facility for initiation of treatment, as well as, for quarantine. The demographic, clinical, and laboratory data from medical records were abstracted. The RT-PCR of oropharyngeal swabs was done at the National Institute of Virology, Pune, which is an accredited National Organization. The Institutional Ethics Committee of Government Medical College, Miraj, approved the study.

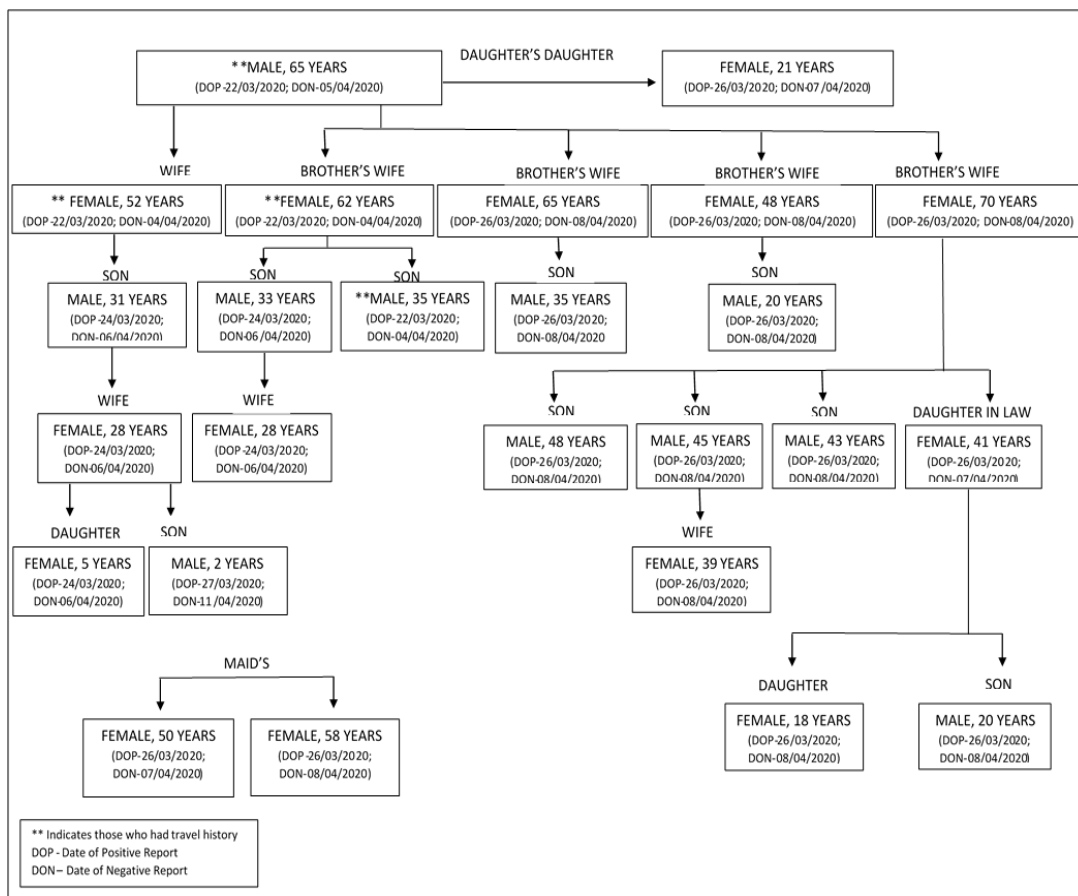
STUDY DESIGN: A retrospective study.

RESULT

Figure 1. Illustrates the family tree and relationship of 25 confirmed COVID-19 cases; 23 were adults and 2 were

children (a 2-year old and 5 years old); 11 (44%) were male and 14(56%) were female (Figure 1). Six members of the family reported hypertension; 2 diabetes; 2 hypothyroidism and one member (65-year-old male) reported coronary vascular disease.

Of the 23 adult confirmed cases 7(7/23, 30%) were asymptomatic and 16 (70%) were mildly symptomatic at the time of admission; cough was seen in 10 (10/23, 43%) cases; sore throat in 6(6/23,46%); fever in 4(4/23, 17%), headache in 2(2/23, 9%) breathlessness in 1 (1/23, 4%), dryness of mouth in 1 (1/23, 4%) and breast engorgement in 1(1/23, 4%)case. The median duration of symptoms was 3 (range 1-5 days) days. Hydroxychloroquine 400 mg twice daily on the first day followed by 200 mg BD for the next 4 days; Azithromycin 500 mg daily for 5 days and oseltamivir 75 mg BD for 5 days was initiated in all adults. Two required intravenous medications and oxygenation during their treatment. All had received the BCG vaccine in childhood. Symptoms lasted for 5 days for those that were symptomatic. None required intensive care unit admissions. A repeat oropharyngeal swab for RT-PCR was negative on Day 14 (of the first test) for all family members.



Legend to figure: Figure 1. Illustrates the family tree and relationship of 25 confirmed COVID-19 cases

DISCUSSION

Our case study of the intrafamily transmission of COVID-19 in rural Maharashtra represents how

clustering of cases occurring within families could become a potential source of high transmission. Rapidly transmitting, the COVID-19 pandemic has been

overwhelming health systems with high demand for care.^[8,9] In India, where the case count is still manageable, our report demonstrates the cluster dynamics that fuel the transmission of COVID-19, providing evidence for implementation of rigorous household contact investigation strategy to mitigate its transmission.

Consistent with prior reports, asymptomatic COVID-19 infection was present among all four returning travellers at their first contact with health systems, which may have provided false security. This resulted in the transmission of the disease among many family members.^[10,11] However, this implies that active case finding and quarantine among both household contacts and casual contacts of the confirmed cases (as has been done with this family) may be an important strategy to reduce the disease burden.^[12] Such hospital-based quarantine may become impractical when the number of cases that need high-level medical care rises and home-based quarantine for asymptomatic infection and mild disease would likely be the most pragmatic option. More importantly, we found that the disease symptoms were milder among all family members. Whether the universal BCG vaccination or the overall younger age of the members contributed to this mild disease spectrum needs to be further studied.^[13] The main limitation of our case study is that it did assess the infection status among all casual contacts, but identifying casual cases will require huge resources. Despite this limitation, this report underscores the immediate need for active case finding to identify and quarantine those with the disease to limit the spread.

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