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COVID-19 POTENTIAL TO INFECT 4.44% INDIAN POPULATION

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ABSTRACT

Background: Quantitative characterisation of any contagious diseases could help in making effective strategy to prevent further spreading of the disease. Despite the rapid research in prevention of spreading COVID-19, yet there is no quantitatively information about spatiotemporal epidemiology and epidemic intensity of COVID-19. Therefore, we aimed to quantitatively characterize spatiotemporal epidemiology and epidemic intensity of COVID-19 in Indian geography by determine it's infectability rate, efficacy rate, transmission rate and likelihood of total populations to be infected with COVID-19 in India.

Method: Novel statistical model was designed to quantitatively characterize spatiotemporal epidemiology and epidemic intensity of COVID-19. A Retrospective Cohort study was carried out online and offline in Indian geography using a COVID-19 transmission questionnaires sheet that comprises five mandatory questions. The collected offline as well as online data was then entered into a Microsoft excel sheet to obtain primary data and secondary data required for the mathematical model to calculate quantitative data of spatiotemporal epidemiology and epidemic intensity of COVID-19 in India geography.

Result and Discussion: Total 539 responses were analysed in the current study out of 557 received responses between April-2021 to May-2021. Average reproductive number of secondary cases was found 0.77. Infectability rate of COVID-19 patient was found 38.11% while healthy person has 21.08% risk of becoming infected if they expose to the Primary case. J-Index and H-Index were found 55.32% and 4.44%, respectively, indicating that COVID-19 disease outbreaks as severe epidemic disease in India and has potential to infect ~4.44% Indian population.

Conclusion: Higher infectability rate (38.11%) of COVID-19 patient and higher efficacy rate (21.08%) of healthy individual to be infected with COVID-19 outbreak it a severe epidemic in India. COVID-19 potential to infect about 4.44% Indian population, at present, COVID-19 already infected ~2.13% Indian population, which is about 50% of the anticipated population to be infected i.e., 4.44%.

KEYWORDS: COVID 19, Prevention, Epidemiology, Epidemic, Mathematical Model, Corona, Treatment

1.0 INTRODUCTION

On December 31, 2019, the novel corona virus disease (COVID 19) outbreak was came to light when China informed WHO about a cluster of pneumonia patients due to unknown causes in the city of Wuhan.^{1,2} COVID 19 has claimed 3.73 million deaths and 173 million confirmed cases since its inception.³ On March 11, 2020, the World Health Organization declared the Novel Coronavirus Disease (COVID-19) outbreak an epidemic.⁴

Quantitative characterisation of epidemiology of any contagious diseases could help in making effective strategy to prevent further spreading of the disease. At present, there is no statistical model that could quantitative characterize epidemiology of any contagious diseases and forecast whether a novel contagious disease would being outbreak an epidemic or not in a near future. Currently, only R naught (R_0), a mathematical term, is used to estimate the expected number of new cases from exposure to a single case, assuming that all individuals in a given population are susceptible.⁵ This is the only way to forecast how contagious an infectious disease is. Furthermore, the data gathering process for R naught computation is time-consuming and complicated since it necessitates locating every person who has been exposed to an infected patient.⁵

Despite the rapid research in prevention of spreading COVID-19, yet there was no quantitatively information about spatiotemporal epidemiology and epidemic intensity of COVID-19. Therefore, we aimed to quantitatively characterize spatiotemporal epidemiology and epidemic intensity of COVID-19 in India geography by determine it's infectability rate, efficacy rate, transmission rate, intensity of epidemic and likelihood of total populations to be infected with COVID 19 in India as geographical location. We set out new statistical model that would require minimal data collection only from a primary case and that can be carried out within a short period of time. The present model can be applied to determine quantitatively information about spatiotemporal epidemiology and epidemic intensity of COVID-19 in any region in the world as well as for any new disease other than COVID-19. The outcome of quantitative information about spatiotemporal epidemiology and epidemic intensity of COVID-19 or any other contagious in any region of the world could help health organisations, governments, health workers, household members, and policymakers to take necessary preventive measures in a timely manner to break the ongoing epidemic, i.e., COVID 19 at present or to avoid any future epidemic or pandemic of any novel contagious disease.

2.0 METHOD

2.1 Sample Size

To calculate more precise information about the epidemiology of COVID 19, it is desirable to have more accurate information about the sample size (number of persons) that comes in close

proximity to a COVID 19 patient. Current evidence suggests that the COVID 19 spreads largely among people who are close to one another, often within 1 meter (short-range). This fact indicating that the likelihood of a COVID 19 infected patient to infect an outsider (relative, coworker, or unknown person) is at least similar to infecting family members living in the same residence with the COVID 19 patient. Furthermore, because the chance of the outsider being come into contact with more than one COVID 19 patient, there is a risk of data gathering errors from the outsider. As a result, to collect more precise and accurate data in the shortest period of time, we traced sample size exclusively from family members living in the same house with the COVID 19 patient as a reliable source instead of tracing the entire hierarchy of all proximity contact of 1st, 2nd, 3rd,n number of covid 19 infected patient, given that the ability of a COVID 19 infected patient to infect a healthy person is unaffected by sample size (number of people), whether they are family members or any outsiders who come in close proximity to the COVID 19 patient.

2.2 Research Design

A retrospective cohort study was undertaken with only the necessary data collected utilising a Covid 19 transmission questionnaires sheet. Only those respondents with a family member who had never been infected with COVID 19 previous to January 2021 but was infected for the first time in January 2021 or later were surveyed online and offline. The partition of respondents in this retrospective cohort study was completely voluntary, anonymous and consensual. Flexibility was provided in the online circulating form to reject the form without providing information, as well as in the offline mode to decline to offer information, i.e., no respondent was forced to fill out or provide information. Although we did not collect any personal information about COVID 19 patients, such as their names, address, or phone number, ethical committee approval was taken since we were concerned about their privacy.

We utilised Google Forms for the online mode since it allowed us to have an unlimited number of respondents. Because Google Forms is a user friendly for surveying in India, it was widely used and implemented in this study due to the respondents' familiarity and comfort. The online questionnaires were created in Google Forms, and the URL to the Google Form was posted publicly on social media sites such as Facebook and WhatsApp in order to solicit replies from online participants. The questionnaires were prepared in a bilingual format, comprising English (International Language) and Hindi (Indian National Language) for ease of comprehension by responders in various parts of India. For the offline mode, members of our research team called friends, relatives, friends of friends, relatives of friends, friends of relatives, relatives of relatives and visited individual homes and a few hospitals to track COVID 19 patients and gather the necessary information. The acquired offline as well as online data was then entered

into a Microsoft excel sheet for easy data tracing from one location. All people who filled out the google form and submitted offline information in response to the questions were deemed research participants.

2.3 Research Method

There are five mandatory questions on the Covid 19 transmission questionnaires sheet. The first question primarily seeks information about whether the respondent was first infected with COVID 19 (Primary Case) in January 2021 or later, the second question primarily seeks information about the total number of family members who stayed in the same house with the primary case, and the third, fourth, and fifth questions seek information on the number of family members infected with COVID 19 (Secondary Cases) who are under the age of ten years, who are between the ages of ten and fifty years, and who are over fifty years old while living in the same house with the primary case, respectively.

The collected information was retrieved as follows to obtain primary data and secondary data. The primary data was retrieved from the COVID 19 transmission questionnaires as follow while secondary data calculated from the primary data:

- Step 1: Total number of Primary Cases (PC) = Sum of answer to question 1
- Step 2: Total number of family members including Primary Cases (TF) = Sum of answer to question 2
- Step 3: Total number of Secondary Cases (SC) = sum of answer to question 3 + sum of answer to question 4 + sum of answer to question 5.

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3.0 MATHEMATICAL MODEL

To quantitatively characterize spatiotemporal epidemiology and epidemic intensity of COVID-19 or any other contagious disease, we developed new statistical model as follow that would require minimal data collection only from a primary case and that can be carried out within a short period of time.

- Primary Case refers to a first member in the family who diagnosed with COVID 19 infection. Secondary Case refers to those family members who are infected with COVID 19 after they comes in close exposure to Primary Case while living in the same house with the Primary Case.
- **Transmission rate** refers to average reproductive number of secondary cases generated from direct exposure to a Primary case. It can be calculated by

$$\text{Transmission Rate (T)} = \frac{\text{Total number of Secondary Cases (SC)}}{\text{Total number of Primary Cases (PC)}}$$

- **Efficacy rate** refers to ability of a healthy individual to becoming infected after exposure to an infected patient. It calculates the average number of secondary cases generation from the total number of populations that expose to primary cases. It can be calculated by

$$\text{Efficacy Rate (E)} = \frac{\text{Total number of Secondary Cases (SC)}}{\text{Total number of populations that exposes to primary cases (TP)}}$$

wherein, TP can be calculated by

$$\text{TP} = \text{TF} - \text{PC},$$

wherein, TF stand for total number of family members including Primary cases.

- **Percentile Efficacy rate (%E)** can be calculated by multiplying efficacy rate with 100.
- **Infectability rate** refers to the ability of the infected patient to infect a healthy person. It can be calculated by

$$\text{Infectability Rate (I)} = \frac{\text{Transmission Rate (T)} / S}{\text{Average number of populations that exposes to primary cases (P)}}$$

wherein, S can be calculated by

$$S = \frac{\text{Efficacy Rate (E)}}{\frac{\text{Total Number of Case (PS)}}{\text{Total number of family member (TF) including Primary Cases}}}$$

wherein, PS = PC + SC,

wherein, P can be calculated by

$$P = \frac{\text{Total number of Population that expose to Primary Case (TP)}}{\text{Total number of Primary Cases (PC)}}$$

- **Percentile Infectability rate (%I)** can be calculated by multiplying infectability rate with 100.
- **J Index (J)** is percentile prediction to know the epidemic intensity of any contagious infectious disease, i.e., novel or existing disease. It is a percentile ratio of efficacy rate to infectability rate.

$$\text{J Index} = \frac{\% \text{ Efficacy Rate (\%E)}}{\% \text{ Infectability Rate (\%I)}}$$

- **H Index (H)** is the last step of the model to calculate likelihood of total populations to be infected with the contagious diseases, i.e., COVID-19, in the particular geographical location. It can be calculated by

$$H \text{ Index (H)} = \frac{\text{Transmission Rate (T)} / \frac{\text{Average number of population that expose to Primary Case (P)}}{K}}{K} \times 100$$

wherein,

K is the average number of populations that generating a new secondary case after exposure to the primary case and it can be calculated by

$$K = \frac{\text{Total number of Population that expose to Primary Case (TP)}}{\text{Total number of Secondary Cases (SC)}}$$

- **Validation and Limit Set Out for the Mathematical Model:** The value of the Primary Case (PC), the total number of populations exposed to the Primary Case (TP), and the total number of family members (TF) are the independent value and will remain constant in the actually traced sample size, i.e. they cannot change even though the epidemic intensity of contagious disease vary. Secondary cases (SC) are generated exclusively from the total number of healthy members who exposed to the primary case (TP), i.e. total number of secondary cases is one of the characteristics that can fluctuate depending on the epidemic intensity of the contagious disease within traced sample size, may be from 1 to maximum is the total number of healthy members who exposed to the primary case. Thus, to validate the model, the value of secondary cases (SC) was varied from 1 %, 5 %, 10 %, 20 %, 35 %, 50 %, 75 %, 95 % and to maximum 100 % of total number healthy members exposed to primary case (TP), then Infectability rate, J index, and H index were calculated to validate the model and determine its limitations.

4.0 RESULT

On January 27, 2020, India reported the first COVID 19 case.⁶ As shown in figure 1, total we traced 557 families in between April 2021 to May 2021, with none of the families had a COVID 19 infection prior to January 2021. A total of 539 responses were analysed in the current study out of 557 received responses, with 18 responses being excluded due to mismatched information (13 responses) and a few respondents living alone at home (5 responses). 143 responses were received online, 89 responses were received by visiting a hospital, 182 responses were received by visiting an individual's home, and 125 replies were received by phone.

Table 1 summarise the primary data derived from the responses received and the secondary data calculated from the primary data as per the mathematical model.

Table 1: Primary and Secondary Data

Sr. No.	Particulars	Data
Primary Data		
1	Total number of Primary Cases (PC)	539

2	Total number of family members including Primary Cases (TF)	2498
3	Total number of Secondary Cases (SC)	413
Secondary Data		
4	Total number of family members that comes in close exposure to primary COVID 19 infected family members (TP)	1959
5	Average number of populations that exposes to primary cases (Y)	3.63
6	Total Number of Cases (PS)	952
7	Average number of populations that new secondary case (Z)	4.74

Figure 1: Screening of responses received from Research Participants

Table 2 summarise transmission rate, % efficacy rate, % infectability rate, J index (intensity of epidemic) and H index (approx. Indian population to be infected with COVID-19) for Indian Geographical location that calculated utilising the primary data and the secondary data by applying it in the developed mathematical model.

Table 2: Outline of Data generated for Indian Geographical location

Particulars	Data
Transmission Rate (T)	0.77
Percentile Efficacy Rate (E)	21.08%
Percentile Infectability Rate (I)	38.11%
J Index (J)	55.32%
H Index (H)	4.44%

After analysing the data, we discovered that a total of 2498 family members lived in the same residence with 539 Primary Cases. A total of 413 family members were infected with COVID 19, i.e. secondary cases, after they were exposed to 539 primary cases, indicating the transmission rate was found 0.77. The Infectability rate of COVID-19 patient was found 38.11% indicating that each COVID 19 patient (either primary or secondary) has a 38.11% chance of infecting a healthy individual. The efficacy rate was found 21.08%, implying that if a healthy person comes into close contact with a COVID 19 patient, then they have a 21.08% risk of becoming infected. The J index value and H Index value were found 55.32% and 4.44%, respectively, indicating that COVID-19 outbreak as a severe epidemic in India and potential to infect approx. 4.44% India population if necessary preventive measures are not taken on time to break the chain of current COVID 19 epidemics.

H index and J index value were extrapolated to validate the mathematical model and to set up its critical limits based on varying the value of secondary cases (SC) from 1% to a maximum 100% of total number of healthy population that exposed to primary case (TP) and generated data were described in table 3.

Table 3: Extrapolated Data for J Index and H Index

Number of Secondary Cases	Efficacy Rate	Infectability Rate	J Index	H Index
20 (1%)	1.02	22.38	4.56	0.01
98 (5%)	5.00	25.50	19.61	0.25
196 (10%)	10.00	29.42	34.00	1.00
392 (20%)	20.01	37.27	53.69	4.00
413 (Actual)	21.08	38.11	55.31	4.44
686 (35%)	35.02	49.04	71.41	12.26
980 (50%)	50.03	60.81	82.27	25.03
1469 (75%)	74.98	80.38	93.29	56.23
1861 (95%)	95.00	96.08	98.88	90.25
1959 (100%)	100.00	100.00	100.00	100.00

5.0 DISCUSSION

The developed new statistical model is the first model at the present time that quantitatively characterises spatiotemporal epidemiology and epidemic intensity of COVID 19. The unique feature of the present model is that it can provide critical information about the contagious disease with minimal data collection only from a primary case and it could be possible to collect the data within a short period of time.

A retrospective cohort study was undertaken online and offline in Indian geography to collect necessitate data require for the mathematical model to quantitatively characterises spatiotemporal epidemiology and epidemic intensity of COVID 19 in India. After analysing

data from 539 families, we discovered that an average of 3.63 healthy members were exposed to a single primary case, and the average reproductive number of secondary cases from direct exposure to a single primary case was 0.77, indicating that each primary case produced 0.77 new secondary cases. After being exposed to primary cases, 1959 healthy members generated 413 secondary cases, indicating that the efficacy rate of healthy members in becoming infected with COVID 19 was found 21.08 percent, with an average of 4.74 healthy members generating 1 new case after being exposed to primary case.

COVID 19 patients have a 38.11 percent infectability rate, which means that each COVID 19 patient, whether primary or secondary, has a 38.11 percent probability of infecting a healthy person. Many people wonder why, if COVID 19 spreads through intimate contact with COVID 19 infected patients, they did not become infected with COVID 19. Infectability and efficacy rates provide an explanation to this question. Because the infectability rate of COVID 19 patients is 38.11 percent and the efficacy rate of healthy person to be infected with COVID 19 is 21.08 percent, it will never be possible for every healthy person who comes into close contact with the primary case to become infected unless both the infectability and efficacy rates reach 100 percent.

The current model was validated by altering the value of secondary cases to determine the model's critical limit. The model's limitations as shown in table 4 was set up based on the derived data after altering the value of secondary cases.

Table 4: Mathematical model's critical limit

Epidemic Intensity	Index Value	Description
None	I Index: < 0.1% J Index: < 15%	Indicating that the disease will not outbreak a epidemic.
Mild	I Index: > 0.1% J Index: < 25%	Indicating that contagious disease will not cause an epidemic, but that proper preventative measures must be taken to prevent the spread of contagious disease in the community. At this stage, the disease is expected to affect less than 1% of the population in the respective geographical location.
Moderate	I Index: > 0.5% J Index: < 50%	Indicating that contagious disease is on the edge of becoming an epidemic if essential preventive measures are not done quickly. At this stage, the disease is expected to afflict about 1% of the population in the respective geographical location.
Severe	I Index: > 1.0% J Index: > 50%	Indicating that contagious disease outbreaks an epidemic, necessitating the implementation of

		prompt preventive measures to control the epidemic. At this stage, the disease is expected to affect more than 1% of the population in the respective geographical location.
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In the present case, the J Index value was found 55.32 percent indicating that the COVID 19 disease outbreak as a severe epidemic in India. H Index value was found 4.44 indicating that COVID 19 has potential to infect approximately 4.44 percent the Indian population (approx. 61.8 million population out of 1390 million population) ^{7,8} if necessary preventive measures are not taken quickly to break the chain of current COVID 19 epidemics. At present, COVID 19 has infected around 2.13 percent Indian population (29.6 million population out of 1390 million population), ^{7,8} i.e. which is about 50% of the anticipated population to be infected, i.e., 4.44% Indian population (approx. 61.8 million population, calculated by the present mathematical model's).

COVID 19 is typically transmitted between persons who are in close proximity to one another, generally within 1 meter, according to current evidence. Infection can occur when virus-containing aerosols or droplets are inhaled or come into direct contact with the eyes, nose, or mouth.^{9, 2} A family members staying with COVID 19 infected member has extremely high chance to comes into contact with the saliva droplets or discharge come out from the nose of the COVID 19 infected person when they sneeze or cough. Therefore, the greatest way to prevent transmission is to identify suspicious cases among family members as soon as possible.^{10,11} In most cases, however, the incubation period of COVID-19, which is the interval between virus exposure and symptom onset, is 5-6 days. ^{2, 12, 13} As a result, locating suspected COVID 19 infected members among the family is very difficult until the 5-6 days post the infection with COVID 19, and during this period, healthy family members are exposed to COVID 19 infected member, resulting in the emergence of new covid 19 patients. Therefore, wearing a mask at home, similar to what we do when we go outdoors, and sanitising the house on a regular basis could be a potential strategy for breaking the COVID 19 transmission chain and reducing COVID 19 cases, not just in India but globally. The developed new model can also be applied to determine quantitatively information about spatiotemporal epidemiology and epidemic intensity of any existing or new contagious disease in any region in the world. The outcome of quantitative information about spatiotemporal epidemiology and epidemic intensity of COVID-19 or any other contagious could help health organisations, governments, health workers, household members, and policymakers to take necessary preventive measures in a timely manner to break the ongoing epidemic, i.e., COVID 19 at present or to avoid any future epidemic or pandemic of any novel contagious disease.

6.0 CONTRIBUTORS

- **Jayendrakumar Patel:** Conceptualisation of mathematical model, research design and research method. Data curation, formal analysis and validation of data, investigation, writing first original draft manuscript and editing.
- **Shalin Parikh, Rakesh Patel, Shwetaaben Patel, Ronak Patel, Payalben Patel and Ankita Patel:** Contributed equally in Data curation and formal analysis. Review first original draft manuscript.

7.0 DECLARATION OF INTERESTS

- We declare no competing interests.

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