A Brief Report on the Transmission Dynamics of the Severe Acute Respiratory Coronavirus-2 (SARS-CoV-2)

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Abstract

Global public health is now at a full risk due to the COVID-19 pandemic caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Lots of studies have already been already conducted on the various aspects of SARS-CoV-2 regarding its mode of transmission, genomic characterization, epidemiology and pathogenesis; the drug designing and vaccine development, etc. The superfluous transmission of the virus is increasing day by day; and therefore, the study of the viral transmission dynamics may demand an important aspect in order to create a public health sustainability during such pandemic. Current review focused on SARS-CoV-2 transmission dynamics and presented the progress of research on this very field briefly.

Keywords: Severe Acute Respiratory Coronavirus-2 (SARS-CoV-2); Transmission Dynamics; Pandemic; Public Health

Background: Study on COVID-19 Pathogenesis

The COVID-19 pandemic by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has already accounted for 702642 deaths out of 18614177 infected cases globally, with the typical mild symptoms to the severe ones including the acute respiratory syndrome (ARDS) [1-4]. The dreadfulness of SARS-CoV-2 is being noticed to be far higher than the Middle East respiratory syndrome coronavirus (MERS-CoV) outbreak in 2012 and the severe acute respiratory syndrome coronavirus (SARS-CoV) epidemic in 2003, probably due to the host immunity evasion strategies employed by the SARS-CoV-2 and unfortunately no specific drug (except some broad-spectrum anti-virals) has been developed against COVID-19 so far [3,5-7]. An array of studies has been already conducted on mode of transmission, viral pathogenesis and epidemiology and concomitantly exclusive research is in full swing for designing novel drug(s) using computer simulations, animal culture and patient trials along with the development of several vaccine platforms against COVID-19 [4,5,7-10]. The genomic characterization of SARS-CoV-2 as well as the possible virulence proteins especially the spike (S) proteins, nucleocapsid (N) proteins and the non-structural proteins (nsps) have been identified together with their receptor binding domains (RBDs) and the viral fusion mechanism (with the aid of the membrane-associated type II transmembrane serine protease or TMPRSS2) into the host [5,7-9]. The host receptors for viral entry prior to pathogenesis, i.e. the angiotensin-converting enzyme 2 (ACE2) for the SARS-CoV-2 and SARS-CoV and the dipeptidyl peptidase 4 (DPP4) for MERS-CoV are already well known [5]. The induction of renin-angiotensin-aldosterone system (RAAS) by ACE2 protein has also been investigated which in turn promotes the pro-inflammatory cytokine storm as the cause of event of the viral pathogenesis [5-10]. In association to such genomic and immunological studies, investigations, mostly through the mathematical and computational modeling and simulations on the transmission rate of SARS-CoV-2 have also been undertaken by the scientists in

order to draw the necessary measures to protect the mass public health. Current review briefly presented such studies on the COVID-19 dynamics which in turn may partially help to identify the key parameters of such dreadful pandemic.

Focus of current review: Quantification of transmissibility of SARS-CoV-2

The relevant origins of the coronaviruses have been well identified by several groups, and it's known that SARS-CoV and MERS-CoV originated from bats and then SARS-CoVs were transmitted to humans from market civets while the MERS-CoV originated from the dromedary camels [2,5]. The present reason of COVID-19 pandemic lies under the human-to-human transmission via the respiratory droplets of SARS-CoV-2 particles, global travelling and certain underlying medical conditions [2]. However, the spread of SARS-CoV-2 is currently devastating the global public health and hence, researchers are trying to plot the viral spreading dynamics using several variables in computational simulation studies [11].

Due to the apparently high transmission rate of SARS-CoV-2 with concomitant infection oriented rapid deaths, several groups have been trying to ponder all the aspects of COVID-19 transmission including the calculation of rate of the transmission dynamics through the simulated model like the susceptible-exposed-infectious-recovered (SEIR) model, adopted by Fang and colleagues using algorithm [11,12]. Indeed, the key epidemiological parameters associated with such study is to calculate the basic reproduction number, expressed as R_0, which is also known as the average number of the secondary infections instigated by one SARS-CoV-2 infected patient during the whole infectious episode [13]. Interestingly, R_0 can also be defined as the expected number of the surplus cases and hence the R_0 value reflects the magnitude of disease severity, i.e. the high value of R_0 means the quick rate of disease transmission [11,13]. R_0 governs the aptitude of an epidemic, the magnitude of disease transmission especially in the absence of the preventive measures, and interestingly, projects the possible scope of the control measures to reduce such spread of the disease-causing agents. Thus, the R_0 value can be taken as the best epidemic tool for the measurement of the transmission potential of a disease [13,14]. In addition, the simultaneous derivation of the effective reproductive number (R) is also required under different settings of the pandemic [11]. Indeed, the R value amounts the secondary cases induced by the original infectious case once the epidemic starts and continues; and it has already been noticed that the exponential growth (i.e. viral reproduction rate) is preceded by the early outbreak frequency [11,12].

A value of R_0 less than 1 is indicative of the self-limiting trait of any etiological agent, meaning that the corresponding disease may eventually be mitigated [11]. In case of SARS-CoV-2, the mean estimation of R_0 has been reported to be within 2.24 to 3.58 and such a substantial high value compared to 1 is clearly inherent with the colossal pandemic potential as is currently seen all over the world [12]. Besides R_0 and R, estimation of the time-varying reporting rate, expressed as $r(t)$, is also important parameter for the measurement of the transmission dynamics [12]. The other parameters of the study of viral transmission dynamics include frequency of exposure (k), probability of infection per exposure (b_0) and the average recovery time (T_i), which in turn reveal that viral dynamics is actually correlated with the viral numbers [11,15]. After the latency followed by the entry of the virus particles into a host, approximately 3 - 4 days have been estimated for the infectiousness of the virus through the doubling at every 3 days quadruplication at every 7 days, million-fold (10^6) multiplication within 2 months and the billion fold (10^9) multiplication within 3 months considering that 1000-fold growth (1 to 10^3) requires at least 10 doublings [15,16].

Based on these discussions, it is understood that there are several benefits of studying such transmission dynamics besides the genomic or immunological research. The updated R_0 estimates may impart the effective evaluation of the control measures which are being taken against COVID-19 pandemic. Moreover, as suggested by Fang and colleagues, from the knowledge on the transmission dynamics parameters may help COVID-19 mitigation in various ways as such the frequency of exposure can be controlled by isolation; the infection per exposure can be counteracted by wearing protective suit; and finally, the average recovery time can be minimized by the treatment strategy [11]. Besides, the knowledge of the viral mutation rate ($\sim 10^{-6}$ mutations/site/cycle) also came from such study on transmission

dynamics which in turn may infer on single infection(s) [15]. As known from several reports, the R_0 value as well the R values project the severity of the pandemic, and these values may also focus on viral spread potential as well as can be used for modelling of the epidemic curve [11,16].

Conclusion

Predictive epidemiology about the COVID-19 pandemic largely depends on the knowledge on the viral dynamics simply expressed in the viral multiplication cycles, viral numbers and the viral RNA shedding. Along with the knowledge on SARS-CoV-2 genomic characterization, pathogenesis, the host immune system evasion strategies, the viral transmission dynamics is thus essential. Several comprehensive reports are already available in this field especially focusing on the basic reproduction number and effective reproduction number; however, further projection on the viral reassortment connecting to the transmission dynamics would be effective to understand the detailed about the rapid transmission severity of the virus.

Grant Support

Nil

Conflict of Interest

Authors have declared that they have no conflict of interest.

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