



Coronavirus Model with Territorial Vulnerability Parameters

Sangeetha Choudhary*

Department of Biotechnology, Andhra University, Visakhapatnam, India

EDITORIAL NOTE

After the emergence of the first cases in Wuhan, China, the novel coronavirus (2019-nCoV) infection has rapidly opened to other provinces, neighbouring countries and eventually has become a worldwide terror. It's indeed a matter of great concern to review the transmission dynamics of this virus. The potential and severity of a plague and providing critical information for identifying the type of disease interventions and intensity are often well understood by the unknown basic reproduction number. A stochastic model is often used to estimate this number with possible safeguard on uncertainties. The challenge is to forecast unseen future simulated data for 3 different scenarios at a short time points. We estimate current levels of transmissibility, over variable time points under different levels of interventions and use that to forecast near-future incidence. The forecasted values of incidence are often used for determining the near future mortality also.

World Health Organization (WHO) declared COVID-19 as a plague disease on March 11, 2020. Comparison of genome sequences from diverse locations allows us to spot the genetic diversity among viruses which could help in ascertaining viral virulence, disease pathogenicity, origin and spread of the SARS-CoV-2 between countries. The aim of this study is to figure out the genetic diversity among Indian SARS-CoV-2 isolates. Initial examination of the phylogenetic data of SARS-CoV-2 genomes (n=3123) from different continents deposited at GISAID (Global Initiative on Sharing All Influenza Data) revealed multiple origin for Indian isolates. An in-depth analysis of 449 viral genomes derived

from samples representing countries from USA, Europe, China, East Asia, South Asia, Oceania, Middle East regions and India revealed that the bulk Indian samples are divided into two clusters (A and B) with cluster A showing more similarity to samples from Oceania and Kuwait and thus the cluster B grouping with countries from Europe, Middle East and South Asia. Diversity analysis of viral clades, which are characterized by specific non-synonymous mutations in viral proteins, discovered that the cluster A Indian samples belong to I clade (V378I in ORF1ab), which is an Oceania clade with samples having Iran connections and thus the cluster B Indian samples belong to G clade (D614G in Spike protein), which is an euclade. The study also emphasizes the importance of pathogen genomics through phylogenetic analysis to urge viral genetic diversity and understand the viral transmission dynamics with eventual grasp on viral virulence and disease pathogenesis.

The COVID-19 pandemic has been an emerging threat to global public health. Despite the important roles of the gut-lung axis within the antiviral immunity, only limited information is currently available concerning COVID-19-specific changes within the gut microbiome. This review summarizes recent knowledge of intestinal dysbiosis related to COVID-19 patients and its potential contribution to the respiratory symptoms through the gut-lung axis. We also discuss the likelihood of prophylactic and therapeutic use of probiotics in COVID-19, including our ongoing trial using *Lactobacillus plantarum*, which is understood to possess a good variety of immunomodulatory activity against respiratory viral infections.

Correspondence to: Sangeetha Choudhary, Department of Biotechnology, Andhra University, Visakhapatnam, India, E-mail: sangeetha987@gmail.com

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