



Could Perturbation of Gut Microbiota Possibly Exacerbate the Severity of COVID-19 via Cytokine Storm?

Ramachandran Vignesh^{1,2}, Chinnamedu Ravichandran Swathirajan², Zaw Htet Tun¹, Marimuthu Ragavan Rameshkumar³, Sunil Suhas Solomon^{2,4} and Pachamuthu Balakrishnan^{2*}

¹ Preclinical Department, Faculty of Medicine, Royal College of Medicine Perak, Universiti Kuala Lumpur, Ipoh, Malaysia, ² Infectious Diseases Laboratory, YR Gaitonde Centre for AIDS Research and Education (YRG CARE), Chennai, India, ³ Laboratory Division, Indian Council of Medical Research-National Institute of Epidemiology (ICMR-NIE), Indian Council of Medical Research, Chennai, India, ⁴ Department of Medicine, Johns Hopkins University School of Medicine, Baltimore, MD, United States

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*Correspondence:

Pachamuthu Balakrishnan
bala@yrgcare.org

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INTRODUCTION

The coronavirus disease-19 (COVID-19) pandemic caused by the Severe Acute Respiratory Syndrome Coronavirus-2 (SARS-CoV-2) continues to be a global threat (1). Studies have shown that COVID-19 patients also presenting with gastrointestinal symptoms and SARS-CoV-2 RNA has been detected in stool specimens from patients with severe disease (2–4). One of the pressing scientific questions that remain unanswered is, why the elderly population and those with underlying conditions are at more risk of developing severe COVID-19 complications than the younger population. Gastrointestinal manifestations play a major role in exacerbating proinflammatory cytokines due to disturbance of gut lining by SARS-CoV-2. Here, we discuss the possible role of the gut microbiota and the dysbiosis leading to exacerbated COVID-19 severity and cytokine storm.

GUT IMMUNOLOGY AND MICROBIOTA

The human body is inhabited by a cornucopia of microorganisms, with a rough estimate of about 38 trillion bacteria and gut remains the most densely and diversely colonized organ (5). The gut microbiota play an arterial role in maintaining immune homeostasis. The mucosal immune system, mainly the mucosa-associated lymphoid tissue such as gut-associated lymphoid tissue (GALT) and bronchial-associated lymphoid tissue, is very important since it acts as the primary line of defense against infections (6). GALT includes Peyer's patches, appendix and isolated lymphoid follicles of the intestinal mucosa. Crosstalk between immune cells of the GALT and gut microbiota is essential to modulate the immune system. The role of gut microbial products in maintaining the balance between regulatory T cell and effector T cell response has been extensively reviewed (7). Furthermore, Short Chain Fatty Acid (SCFA), a product of commensals' fermentation of fibre-rich diet, is also essential to facilitate the efficient migration