

Parallel Session 2: Implementing Research Findings in Clinical Practice

T2a - Role of Gastrointestinal Tract and Gut Microbiota in Pathogenesis of Coronavirus Disease 2019 (COVID-19): A Missing Site for Viral Replication & Transmission

Prof NG Siew-chien^{1,2,3}

¹*Department of Medicine and Therapeutics, The Chinese University of Hong Kong, Hong Kong SAR, China*

²*Institute of Digestive Disease, State Key Laboratory of Digestive Diseases, LKS Institute of Health Science, The Chinese University of Hong Kong, Hong Kong SAR, China*

³*Center for Gut Microbiota Research, Faculty of Medicine, The Chinese University of Hong Kong, Hong Kong SAR, China*

The role of gut microbiota in pathogenesis of COVID-19 is largely unknown. We evaluated gut bacterial and viral microbiota in COVID-19 patients and its association with disease severity and outcomes and determined the effect of SARS-CoV-2 on gut inflammation and ACE2 expression by a prospective case control studies including 50 hospitalised patients with laboratory-confirmed SARS-CoV-2 infection, 30 patients hospitalized with community-acquired pneumonia, and 30 healthy individuals. 73.3% of COVID-19 patients had SARS-CoV-2 nucleic acid detected in faeces during hospitalization (median 3.86×10^3 copies per mL inoculum). 46.7% showed active SARS-CoV-2 infection with strikingly higher coverage the 3' vs 5' end of SARS-CoV-2 genome in faecal viral metagenome profile, even after disease resolution. Patients with COVID-19 had altered bacterial and viral microbiota, compared with healthy controls ($P < 0.05$), which persisted up to 6 months after recovery. Several gut commensal bacteria with known immunomodulatory potential e.g. *Faecalibacterium prausnitzii*, *Eubacterium rectale* and bifidobacteria and two Pepper-derived RNA virus species (RNA virus) were underrepresented in COVID-19 patients. Depletion of these bacterial and viral taxa was associated with more severe disease as well as elevated concentrations of inflammatory cytokines and blood markers ($P < 0.05$).

Our study showed that there was prolonged and active SARS-CoV-2 virus in the faeces of COVID-19 patients, even after recovery, which highlights the threat of potential fecal-oral viral transmission. We, for the first time, identified several biomarkers of gut bacterial and viral microbiota specific to COVID-19, and elucidate their associations with disease severity and host immune response. This will allow potential therapeutics to modulate the gut microbiota to reduce severity and complication of COVID-19.

Project Number: COVID190111

Parallel Session 2: Implementing Research Findings in Clinical Practice

T2a - Novel Strategies to Facilitate Early Detection, Prevention and Intervention for Long-term Health Problems Related to COVID-19 (NoviTor-COVID Study)

Prof Francis CHAN Ka-leung^{1,2,3}

¹ *Department of Medicine and Therapeutics, The Chinese University of Hong Kong, Hong Kong SAR, China*

² *Institute of Digestive Disease, State Key Laboratory of Digestive Diseases, LKS Institute of Health Science, The Chinese University of Hong Kong, Hong Kong SAR, China*

³ *Center for Gut Microbiota Research, Faculty of Medicine, The Chinese University of Hong Kong, Shatin, Hong Kong SAR, China*

In order to study the effect of COVID-19 on the development of co-morbidities (**Programs 1-2**) and to examine the impact of a novel digital mental health (DMH) platform on neuropsychiatric disorders (**Program 3**); and evaluate the role of a novel oral microbiome replacement therapy on reducing chronic comorbidities in COVID-19 survivors; and the impact of gut microbiota on immunity to COVID-19 vaccination (**Program 4**), we performed a total of 4 studies: prospective cohort studies (**Programs 1-2**); (ii).Prospective cohort and pre-post observational study (**Program 3**); (iii).a mixed randomized, placebo-controlled (**Program 4a**) and prospective cohort design (**Program 4b**) including COVID-19 survivors, healthy controls and subjects going to receive COVID-19 vaccines. We hoped to evaluate the incidence and trajectory of various COVID-19 complications and neuropsychiatric disorders, the effect of modulation of gut microbiota on long-term complications associated with COVID-19 and the seroprevalence of SARS-CoV-2 specific antibodies after COVID-19 vaccines.

Project Number: COVID1903002

Parallel Session 2: Implementing Research Findings in Clinical Practice

T2a - Modulation of Gut Microbiota to Enhance Health and Immunity in Vulnerable Individuals During COVID-19 Pandemic

Dr Joyce MAK Wing-yan^{1,2}

1 Department of Medicine and Therapeutics, The Chinese University of Hong Kong, Hong Kong SAR, China

2 Institute of Digestive Disease, The Chinese University of Hong Kong, Hong Kong SAR, China

Elderlies and patients with type 2 diabetes mellitus (DM) have a higher risk of developing severe COVID-19 infection and mortality. Gut microbiota has been linked to the pathogenesis of COVID-19 and to our immune function. We aimed to evaluate the efficacy of modulating gut microbiota with a microbiome immunity formula in vulnerable subjects (patients with underlying type 2 DM and elderlies) in improving immune functions, reducing adverse events associated with COVID-19 vaccines, and reducing hospitalisation in susceptible individuals during the COVID-19 pandemic. A 12-month double-blinded, randomised controlled trial on the use of a microbiome immunity formula vs. Placebo in enhancing health and immunity in patients with Type 2 DM and a 12-month, open-labelled, randomised controlled comparing 3-month vs. 6-month regimen of microbiome immunity formula in elderly individuals will be performed to assess the proportion of subjects achieving restoration of gut dysbiosis at 6 months, adverse events associated with COVID-19 vaccines and number of unplanned hospitalisation and clinic visits.

Project Number: COVID19F07