# A ROLE OF GUT MICROBIOME IN DIABETIC PATIENTS WITH INFLAMMATORY BOWEL DISEASE AS WELL AS COVID-19 INFECTION

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**ABSTRACT:**

Microbial population had intense to have an infection on humans particularly commensals. Now there was a wide range of knowledge on diabetic as well as progression and immune function about the immunological studies.Nowadays the most priority was given to RNA viral genome or otherwise virome.Gene 16srRNA was used to analyse the specific bacteria in patients who are infected with the viral load. SARS-CoV-2 is newly emerging virus which causative agent of Corona virus (COVID-19). A phylogenetic analysis of SARS-CoV-2 is highly sub-clade with SARS-CoV. The immunological symptoms of COVID-19 are dysregulation of cytokine production, improper functioning of various organs and the barrier leakage.

**Keywords:** SARS-CoV-2, COVID-19, RNA viruses, Immune system

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## INTRODUCTION

Microbial communities had intense to have an infection on humans particularly commensals[1-3]. Now there was a wide range of knowledge about the progression and immune function about the immunological studies. Normal microbial flora plays a vital role in skin, tissues, and various organs of human body. Microorganisms which harbours in a barrier surfaces, including respiratory and gastrointestinal tract, are collectively known as "microbiome". The term virome isalso a part of microbiome, which also includes other organisms viz., bacterial and archaeal organisms, mycobiome, meiofauna such as protists and metazoans[3].Most often the eukaryotic virome was likely to be underestimated eventually by metagenomes but RNA viruses highly ignored[4-6]. RNA viruses of humans as well as animal pathogens like influenza, rotavirus, hepatitis C virus and arboviruses. Nowadays the most priority was given to RNA viral genome or otherwise virome. Some of the enteric viruses which have been contributed within the intestine for the development and predatory history of inflammatory bowel diseases[7].Bacteriophages are viruses which are specific to the bacteriaon whom they pre-exist to play a vital role in stabilizing the balance of microorganisms in each and every environment exclusively to the human intestine[8-10]. Many of the pathogenic viruses are influencing by altering the gut microbiota and can cause severity among the humans as well as animals. Especially, the pandemic SARS-CoV – 2 were primarily found in the respiratory tract and a recently recorded that they found in the human faeces[11]. Gene sequences in viral genome plays an important role in identification of the pathogenesis of the particular viruses viz., coronavirus (COVID-19), Norovirus, Hepatitis and Herpes viruses[12-15]. In different combinations of microbiota as well as mycobiota of viral genome H1N1 and SARS-CoV-2 of infected patients were yields lack of various fungal as well as bacterial species compared to the healthy controls[10]. In viral diseased states which indicates with the clinical parameters like diarrhoea and lymphocyte count.

## ROLE OF RNA VIRUSES IN GUT MICROBIOME

Portal of entry for Influenza viruses in the host through upper respiratorytract (URT) and it can modify the microbial ingredients of the URT significantly followed by the

infection. Due to increased colonization of viral infection, there was drastically decreased in growth of normal healthy bacteria like Prevotella sps and anaerobes. Gene 16srRNA was used to analyse the specific bacteria in patients who are infected with the viral load. SARS-CoV-2 is newly emerging virus which causative agent of Corona virus (COVID-19). A phylogenetic analysis of SARS-CoV-2 is highly sub-clade with SARS-CoV[16]. It is a world pandemic, we urgently required for potential therapeutic strategies to combat with the disease. A very few clinical studies insist that COVID-19 mainly proceeds with gastrointestinal disorders which followed by the respiratory tract. During the gastrointestinal symptoms, the normal healthy bacteria may alter during the COVID-19 infection. Likely, diarrhoea is considered as one of the major consequences of this viral infection[9]. Usually, the gut microbiome alters by the usage of intrinsic factors like antibiotics, cigarette smoking and now they included viral infections[8].The major role of gut microbiota is mostly targeting the dysbiosis which helps to control the progression or development of COVID-19.The immunological symptoms of COVID-19 are dysregulation of cytokine production, improper functioning of various organs and the barrier leakage. SARS-CoV mostly infect the surface cell receptors with the help of binding a viral spike protein to the host cells and it has less affinity when compared with SARS-CoV – 2[15]. There was a two site of entry for viruses, one is the gut and another through respiratory tract. On former they suggest because of food contamination with intestinal expression of ACE2 due to fecal-oral transmission[12]. During this pandemic outbreak, COVID-19 infected patients, mostly shed the RNA viral genome was detected in the stool samples and no longer was detected in the respiratory tract by using Real Time PCR technology.

. As seen during previous coronavirus outbreaks, around half of all COVID-19 patients have detectable SARS-CoV-2 RNA in their stools - even when it is no longer found in the respiratory tract[17-19]. More number of trials has been initiated to follow the adverse effects on personalized food or medicine which includes prebiotics or probiotics to combat with the current therapeutic methods[18]. There was a reduction of proinflammatory cytokines IL-6 and insulin resistance due to the consumption of nondigestible carbohydrates. Similarly increased the level of plasma cytokines and IL-10 with the intake of high amylose maize starch.

**CONCLUSION WITH FUTURE PRESPECTIVES OF VIROME**

Eukaryotic viruses like Herpes viruses and Noroviruses were carry their viral genes and inducing the severity of Inflammatory Bowel Disease (IBD) among humans as well as animals[6]. In case of IBD cases, the isolation of viral genomes is purified from faces. Virome can alter the gut microbiome present in the intestine of human and also, they suggested a positively associated with the certain disease. The authors from different studies were showed that they were able to assign only 15% of the sequences to the viral taxonomy [7]. The two abundant viruses Caudovirales and Microviridae. The former has been observed less from Los Angeles and no evidence found on the latter viral genome. Five bacterial specific subtypes viz., Lactococcus, Lactobacillus, Enterococcus, Clostridium and Streptococcus were positively associated with the virus Caudovirales of Crohn's patients[5,8]. In many of the studies, the researchers are stated that they are unable to correlate with specific bacterial taxonomy and therefore the bacteriophage – bacteria correlation was not validated yet. In future it has been rectified by segregation of different viral genomes using Next Generation sequencing (NGS) technology. So that it can be identify the pathogenic genetical variability which affects the gut microbiome in large numbers and also enhance the severity of the particular disease.

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