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## Gut virome and its emerging role in inflammatory bowel disease

Rahat Khatoon Khokhar, Abdulqadir J Nashwan

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### Abstract

Inflammatory bowel disease (IBD) is a progressive multifactorial inflammatory disease of the gut. The cause of IBD is yet unknown. Some researchers have shown that genetic factors, environmental factors, and the gut microbiome are significant considerations. Our gut contains gut virome and gut bacteria, which vary among individuals due to some factors. The gut virome is a substantial component of the microbiome. This editorial explores the emerging role of gut virome in IBD.

**Key Words:** Inflammatory bowel disease; Pathogenesis; Gut virome; Bacteriophage; Eukaryotic viruses

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**Core Tip:** Inflammatory bowel disease (IBD) is a chronic multifactorial inflammatory disease involving the gastrointestinal tract. The exact etiopathogenesis is unknown, but gut microbiome dysbiosis is believed to be a cornerstone in triggering disease progression. The gut virome forms a significant part of the microbiome and participates in health and disease conditions. Until 2015, researchers paid little attention to their role in IBD. Subsequently, numerous studies have followed this line of inquiry, using advanced techniques to clarify this role. Herein, we emphasize the viral populations in the gut and their predicted roles in the etiopathogenesis of IBD based on current studies.

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## INTRODUCTION

Inflammatory bowel disease (IBD), which is also known as ulcerative colitis (UC) or Crohn's disease (CD), is present in 1% of the population[1]. According to Le Berre *et al*[2], UC tends to have a genetic predisposition. At birth, the gut microbiome is not fully developed, but as the baby grows, it increases in number. The gut microbiota contains bacteria, fungi, viruses, and archaea. A narrative review by Manos[3] shows that disruption in gut microbiota plays a crucial role in the pathogenesis of multiple diseases like IBD and gastro-oesophageal reflux disease. It also reveals that dysregulation of imperative bacteria redesigns the constituents of bile acid that can exacerbate the progression of IBD. Some research has shown that gut bacteria help build mucosal immunity towards IBD, whereas an imbalance between good and bad bacteria leads to progressive tissue injury. Harmful bacteria such as *Escherichia coli* can lead to the production of inflammatory mediators[4]. The gut virome plays a crucial role in the gut microbiome. However, its imbalance can lead to the pathogenesis of IBD[5]. According to recent studies, the gut virome can be correlated with the etiology of diabetes mellitus[6]. Consequently, further studies reveal that gut virome plays a significant role in childhood diarrhea, and it eventually causes early stages of pediatric IBD[7]. Hetta *et al*[8] also showed that active phages that can kill the bacterial host cell are primarily seen in patients with IBD.

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## FACTORS INFLUENCING IBD

The human gastrointestinal tract (GIT) nurtures a complex community of bacteria, viruses, fungi, protists, and other microorganisms. Studies have shown that the virome is crucial in normal infant development[9]. Hetta *et al*[8] say in their research that the physical appearance of a human, like height, weight, age, and body mass index, can influence the gut virome. Other factors like nutrition, lifestyle, and medication are essential in determining gut virome abundance. It is also concluded that dysbiosis and inflammation related to IBD co-exist. Many factors like genetic makeup, environment, drugs, smoking, diet, mental health, and others influence the occurrence of IBD. It is also shown that a low-fiber diet switches the gut microbiome from digesting the fiber derived glycans to mucous-derived glycans, leading to the eruption of the mucous membrane and better infiltration of pathogens into the blood. Hetta *et al*[8], after going through multiple studies, found that gut phages can impact IBD pathogenesis. It can change the gut phage community so that some specific phages are more prevalent in patients with CD and UC than in healthy people. However, randomised controlled trial verification is still needed. It can cause changes in gut microbiota, leading to a decreased population of good bacteria and an elevated concentration of dangerous bacteria such as *E. coli* and *Fusobacteria*. Gut phages can even cause alterations in the immune response of the body. All this literature is supported by very scanty research.

Eukaryotic viruses reside in the human GIT and remain quiet for ages. Once reactivated by any stimuli tends to cause deterioration in gut microbiota, leading to IBD pathogenesis. Thus, there is a critical need for more research on the association between IBD and gut phages. Hetta *et al*[8] did a fantastic job describing the association between gut virome and IBD. Their work is commendable as it resolves many queries related to gut virome and IBD. However, it is tough to differentiate viral DNA in microbiological practice because viruses possess wide diversity, low genomes, and rapid rates of mutations. In addition to that, viruses are also difficult to grow as they rely on host cells for energy and multiplication. Hence, the host cell should also be extracted. Metagenomic analysis is a tricky procedure, but with recent technologies like VIP and VirFinder, it has become more doable. Also, problematic cultivations of GIT microorganisms, critical DNA sequencing, perplexing recognition, and differentiation of viral specimens have made this association very exhausting and laborious.

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## CONCLUSION

IBD is a chronic progressive inflammatory disease that consists of two parts: UC and CD. The precise cause of IBD is idiopathic. Hetta *et al*[8] described the correlation between gut virome dysbiosis and its impact on the progression of IBD. They also elaborate on the role of gut phages and eukaryotic viruses in the pathogenesis of IBD. Therefore, further innovative research is warmly welcomed.

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## FOOTNOTES

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