Revealing Hidden Enemies: A Review of Emerging Gastrointestinal Viruses

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To Editor,

Today, many deadly infectious epidemics have been reduced with the improvement of individual and social health levels, the increase of vaccinations, and the use of antibiotics and extensive preventive measures. However, the number of diseases and complications with unknown etiology has long been significant. The advancement of technology in the field of diagnostic apparatuses has improved the science of diagnosis and led to the identification of pathogenic agents, especially infectious agents, at the genus and species level.1

Among idiopathic diseases, gastrointestinal (GI) complications (e.g., gastroenteritis, diarrhea, and the like) are highly common in children and adults; considering that 40% of cases of GI complications are still of unknown etiology, these newly discovered viruses may play a role in the development of GI complications; the rotavirus, human bocavirus, adenovirus, norovirus, and the like are among these agents. In addition, recently, diagnostic methods and tools have been able to shed light on factors that cause digestive complications, leading to the isolation and identification of viruses such as cosavirus, bufavirus, Saffold virus, tusavirus, and salivirus from patients (particularly children) with GI complications.2–4 It seems that the number of these emerging viruses is increasing. Molecular tests and high-accuracy sequencing can identify and distinguish organisms at the strain level. Meta-analysis studies have assessed the association between the prevalence of some GI viruses and clinical symptoms in certain time periods, which were statistically significant in some cases. However, additional tests such as in vitro (cell culture) and in vivo (animal models) histopathology tests are needed to prove their potential role in pathogenesis and appearance of clinical symptoms. On the other hand, the lack of a statistically significant association cannot rule out their role in GI complications, and more studies should be conducted with case-control designs with a large sample size.5

The prevalence of emerging viruses is reported to be low, but this is probably due to the low screening of these viruses due to self-limiting complications and non-specific symptoms. The chances for opportunistic organisms and emerging viruses have been increased with the rise of susceptible hosts during the increased use of immnosuppressants, the increase of HIV, and the change of intestinal microbial flora. Considering the route of oral-fecal transmission of GI viruses, the possibility of outbreaks in susceptible populations with communal living is not far from expected.6

It should be noted that most reports are related to undeveloped and developing regions, which can be associated with poor personal and public sanitary, as well as nutritional poverty because the immune system is affected by nutrition. Furthermore, regarding the studied people’s gender, no significant difference was found between the prevalence rates; however, the prevalence may be higher in boys because they are more exposed to outdoor environments.7 As mentioned earlier, rapid progressions in sequencing technologies, bioinformatics, and metagenomics have led to the discovery of new viruses in recent years. Considering that many newly isolated viruses contain RNA genomes, the real-time polymerase chain reaction technique has been extremely helpful; it is better to consider isolated genotypes for each virus because it can be useful for vaccine designs or therapeutic purposes.8 One of the limitations of the studies that can create a miss-diagnosis and miss-interpretation is co-infection with other GI viruses or even parasites, making it more difficult to interpret whether newly isolated viruses contribute to clinical complications.9

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Competing Interests
All authors declare that they have no competing interests.

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Not applicable.

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