A new virus has been discovered that is likely spread by the drinking water route. Originally suspected in a shellfish-associated outbreak of diarrhea in Japan in the late 1980s, new evidence supports that the Aichi virus causes widespread disease in humans. The virus has now been identified in sewage samples collected in the United States and isolated from patients with acute diarrhea worldwide. Questions remain as to the occurrence, public health impact and potential treatment of these previously undescribed human viruses.

**Worldwide impacts**

Diarrhea is one of the leading causes of mortality in the world, with approximately two million deaths per year. Most of these fatal infections occur in the developing world in children under the age of five. An additional 1.4 billion cases of diarrhea are estimated to occur each year in both the developed and developing world. Therefore, mitigating the global burden of diarrheal illness is a primary public health goal. Complicating control efforts is the fact that approximately 40 percent of diarrheal illness is due to unidentified causative agents. Viruses pose the greatest challenge in disease surveillance since they must be grown in a complimentary host cell and many cannot be cultured in the laboratory. In addition, human viruses are constantly emerging. Since the first discovery of the infectious Yellow Fever virus in 1901, approximately three to four new species of viruses have emerged every year. To complicate matters further, two-thirds of the known human viruses can also infect animals (including mammals and birds), which creates additional challenges in controlling their transmission in the environment.

**Emerging pathogens**

Aichi viruses are members of the genus Kobuvirus in the family of Picornaviridae. There are over 200 serotypes of picornaviruses, including rhinovirus, poliovirus and enterovirus. While picornaviruses can cause a wide range of illnesses, including colds, rashes, meningitis and diarrhea, Aichi viruses appear to be enteric, meaning their primary route of infection is the gut, resulting in diarrheal illness. Like other enteric viruses, Aichi virus is shed in the feces of infected individuals and thus completes the cycle of transmission via the fecal/oral route. Ingestion of contaminated food and water (via drinking, bathing or recreational exposures), in addition to contact with contaminated hands or surfaces, are known routes of enteric virus transmission.

Aichi viruses have been isolated worldwide, including Asia, Europe, South America, Africa and the US. Human exposure also appears to be widespread, given that 80 to 99 percent of adults express sera antibodies to the virus. Although a seropositive reaction suggests previous exposure and an immune response to infection, infection does not necessarily mean illness occurred. Aichi virus infection in patients with diarrhea appears to be low but it has been isolated from children with diarrhea in several countries. One study collected fecal samples from 445 children, aged zero to six years, who were hospitalized at the Shanghai Children’s Hospital, People’s Republic of China, with acute diarrhea. Aichi virus was detected in only eight (1.8 percent incidence) of the examined stool samples. All eight of these Aichi virus-positive samples were further screened for common diarrheal agents, including norovirus, sapovirus, rotavirus, astrovirus and various types of adenoviruses. Only one sample tested positive for an agent of possible co-morbidity, which was astrovirus. In addition to the 445 sick children, 92 healthy children, aged two to five years old, from three Shanghai City childcare centers served as a negative control population. None of the healthy children’s stool tested positive for Aichi virus. Although little is known about the microbiome of the gut, this evidence suggests that Aichi virus is more than a commensal or symbiotic microbe in humans but rather a common pathogen.

**Environmental monitoring**

Clinical evidence of novel virus infections leading to previous cases of unexplained diarrhea has led to an increase in environmental monitoring for related pathogens. Recently, a study in Japan surveyed river water and wastewater for the prevalence of Aichi viruses by collecting monthly samples for a year. Using tests to target the genetic sequences of the viruses, 100 percent (12/12) and 92 percent (11/12) of the wastewater samples were positive, before and after conventional treatment, respectively. Sixty percent (36/60) of river water samples were also positive—a higher rate than that of noroviruses, which are thought to be the dominant cause of all food and waterborne outbreaks in the US. Similarly, two never before recognized viruses have recently been isolated from the feces of dogs with diarrhea. The canine kobuvirus is a close genetic relative of human Aichi viruses and has been isolated from both healthy and diarrheal dogs. Given that dogs have been shown to transmit other viruses to humans (i.e., rotavirus), their role in the zoonotic transmission of additional viruses has been questioned. Regardless of the potential for novel virus emergence from dogs to people, the need for better characterization of unrecognized viruses in the human realm of exposure is warranted.
Future tracking tools

Utilizing tools in genetic sequencing, novel viruses can now be recognized within a complex mixture of microbial communities, such as those found in the gut and the environment. Using these tools, scientists have recently characterized an additional human virus, known as saliviruses. Saliviruses are genetically similar to the Aichi virus and they too have been identified in stool samples around the globe, including Nigeria, Tunisia, Nepal and the US. The presence of these viruses in stool was statistically significant to the association with unexplained cases of gastroenteritis. The association between saliviruses and diarrhea adds additional evidence that new, emerging members of the Picornaviridae family of viruses may account for a large portion of the unexplained cases of diarrhea worldwide. While most enteric viruses are susceptible to conventional drinking water disinfectant treatment (i.e., chlorine), in addition to ultraviolet light and ozone treatment, it is not uncommon for them to exhibit variable resistance.

Conclusion

Although the emergence of new human viruses is certain, few global surveillance tools are in place to track disease prevalence or identify risk factors of public health importance related to novel pathogens. The recently discovered additions to the picornavirus family are relatively mild pathogens; however, the threat of more virulent pathogen mutation and emergence is also anticipated (i.e., avian influenza). Thus, the continued development of tracking tools promises to aid in identification of future hazards and lead to improved responses toward control.

References


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