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**Glossary**

**Hepatitis A virus** A 27–32 nm, nonenveloped, positive-sense single-stranded RNA virus with a 7.5-kb genome and a capsid with icosahedral symmetry. This virus is classified in the Picornaviridae family under the genus *Hepatovirus*. The virus causes a classic hepatitis syndrome that is less severe than hepatitis A and B and does not result in subsequent chronic disease. Nonetheless, it is one of the more severe of the foodborne viral illnesses.

**Hepatitis E virus** A positive-sense single-stranded RNA virus, hepatitis E virus is transmitted by the fecal–oral route and is endemic in the developing world. Clinical symptoms are very similar to those of hepatitis A virus infection, but with more severe consequences to infected pregnant women. Its increasing recognition in industrialized countries suggests that hepatitis E virus may be an emerging foodborne pathogen.

**Human enteric viruses** A functional, rather than taxonomic, group of viruses that infect humans by ingestion of infectious particles. Many virus families are represented by the enteric viruses, which are most commonly transmitted by the fecal–oral route.

**Norovirus** One of four genera within the Caliciviridae family. Human noroviruses are the most common cause of acute viral gastroenteritis in industrialized countries, and also the leading cause of foodborne illness. These are nonenveloped icosahedral viruses approximately 27 nm in diameter and having a genome consisting of a single strand of positive-sense RNA of 7.4–8.3 kb in length. Based on amino acid homology of the viral capsid protein, the *Norovirus* genus can be further subdivided into five genogroups.

**Positive-sense RNA** Single-stranded RNA molecule that can be translated directly, without need for modification.

**Reverse transcription-quantitative polymerase chain reaction (RT-qPCR)** A modification of the DNA amplification method qPCR intended to be applied to RNA. This is accomplished by preceding the qPCR with a RT step that produces a double-stranded DNA copy of the RNA. RT-qPCR is a commonly used method to detect the genomes of human enteric viruses, as these typically consist of single-stranded RNA.

**Virus** A small infectious agent that can only replicate in a live host cell, i.e., an obligate intracellular pathogen. Viruses consist of one or more nucleic acid molecules (genome) surrounded by a protective protein coat (capsid); some viruses are further surrounded by a lipid bilayer or envelope.

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**Introduction**

Human enteric viruses are the most common cause of foodborne illness worldwide. These viruses comprise a functional, rather than taxonomic group, almost all of which are nonenveloped (lacking a lipid outer layer) and transmitted by the fecal–oral route. From an epidemiological perspective, human noroviruses (*HuNoV*) are now considered the most important of the foodborne viruses, causing 58% of foodborne illnesses of known etiology in USA. Hepatitis A virus (*HAV*) is also important as it causes perhaps the most severe of the viral foodborne diseases. There are other important viruses that can be transmitted by foodborne routes, although their significance is less well characterized.

Viruses are obligate intracellular parasites that require the metabolic machinery of the host cell to replicate. They are tissue tropic (enteric viruses infect the gastrointestinal tract) and species specific, so human enteric viruses infect humans but not other animals, and vice versa. Enteric virus particles are shed in extremely high numbers in the feces of infected individuals, and hence their transmission is usually due to the fecal–oral route. However, epidemiological evidence suggests that NoV particles are also shed in vomitus and this may significantly increase transmissibility of these viruses, especially if virus particles become aerosolized during vomiting events. In general, enteric viruses are highly infectious and typically disease can be caused by a small number (perhaps 10–100) of infectious virus particles.

Human enteric viruses are spread in a number of ways: by person-to-person contact; through contact with contaminated inanimate objects (fomites); or by consumption of contaminated food or water. Most cases of foodborne viral disease are caused by consumption of foods that have been handled or prepared by infected food handlers who have not practiced adequate hygiene, particularly after using the restroom. Contamination can also occur preharvest, as a consequence of exposure to human feces (sewage) during irrigation or fertilization of fresh produce, or during production of molluscan shellfish.
Although the disease caused by the common foodborne viruses is rarely life threatening, the sheer volume of cases places severe burden on the public health system. This article will summarize the early days of food virology, outline key characteristics of important and emerging foodborne viruses, and discuss epidemiological surveillance and control of these important agents of foodborne disease.

**The History of Food Virology**

Poliovirus was the first enteric virus to be widely recognized, causing foodborne disease outbreaks in the early 1900s associated with the consumption of contaminated raw milk. Raw milk outbreaks of poliomyelitis continued until the 1950s, when an effective vaccine was introduced. Molluscan shellfish-associated outbreaks of hepatitis were also reported in the 1950s and 1960s. The cause of this disease was HAV, which was identified as an enterically transmitted infectious agent when Dr. Saul Krugman intentionally fed mentally disabled children purified fecal extracts prepared from symptomatic patients; the children subsequently developing classic hepatitis symptoms. During the same era, foodborne outbreaks of nonbacterial gastroenteritis were recognized and although a viral etiology was suspected, it remained difficult to confirm.

This changed when, in 1972, Dr. Albert Kapikian identified the first virus to be associated with acute nonbacterial gastroenteritis. Appropriately named ‘Norwalk virus’ because of its association with an outbreak in Norwalk, OH, in USA, this virus was the first of many that would ultimately be identified as members of the genus *Norovirus (NoV)* within the Caliciviridae family. Electron microscopy was used to identify the Norwalk virus, and this method, which requires virus loads $>10^6$ particles per g of stool, is still used to this day.

The absence of culture methods for both HuNoV and HAV was a major impediment to further study of these agents. In 1987, Dr. Theresa Cromeans developed a method to propagate HAV, ushering in a new era for studying this virus. This method, as well as cultivation methods for the vaccine strain of poliovirus, eventually allowed for the quantification of infective virus plaque forming units and facilitated studies on detection and control of enteric viruses in water and foods, with a particular focus on molluscan shellfish. Dr. Dean Clier, who served as a professor at the University of Wisconsin in Madison and at the University of California in Davis, provided much of the foundation on which current principles in food virology are based.

In 1990, Dr. Mary Estes team at Baylor College of Medicine sequenced the full Norwalk virus, and many other NoV genomes have been characterized since then. With knowledge of nucleic acid sequence and the rapid adoption of molecular biological methods, scientists were suddenly presented with new tools to study human enteric viruses. Particularly important was the nucleic acid amplification method polymerase chain reaction (PCR), which was readily adapted to the detection of RNA viruses by preceding PCR with a reverse transcription (RT) step, hence the designation RT-PCR. Conventional RT-PCR methods, followed by Southern hybridization were quickly developed for the detection of these viruses in clinical (fecal) samples and foods, particularly molluscan shellfish. These were later replaced by more rapid and sensitive quantitative real-time RT-PCR (RT-qPCR) methods.

Although promising, the utility of these molecular amplification methods for virus detection in food and environmental samples was limited by low levels of contamination; high levels of matrix-associated inhibitory substances that interfered with nucleic acid amplification; and the lack of broadly reactive primers and probes for HuNoV. In addition, the development of an *in vitro* cultivation system for HuNoV has remained elusive. Cultivable surrogate viruses (e.g., feline calicivirus and murine norovirus) have been used in a variety of studies but their behavior does not always mimic that of HuNoV. These impediments to the study of HuNoV continue to this day.

The epidemiological importance of HuNoV came to the forefront in 1999 when Mead et al. (1999) suggested that viruses, not bacteria, were the leading cause of foodborne illness of known etiology. This study prompted expanded epidemiological surveillance activities in Europe. The Mead et al. (1999) publication, along with some high profile outbreaks in the late 1990s and early 2000s, also focused attention on foods other than molluscan shellfish as significant causes of foodborne viral gastroenteritis. In fact, we now know that foods such as salads, bakery products, and sandwiches are responsible for more NoV and HAV infections than are molluscan shellfish. Fresh produce (berries and green onions) have also emerged as important vehicles of infection. The association of disease with foods such as these suggest that the hands of infected food handlers are arguably the most common source of the virus contamination for many if not most foods. Recent epidemiological data continue to support the fact that viruses, particularly HuNoV, are the most common cause of foodborne disease of known etiology in USA.

**HuNoV**

HuNoV are the most common cause of acute gastroenteritis in industrialized countries. Scallan et al. (2011b) estimate that these viruses are responsible for approximately 58% of foodborne disease of known etiology in USA. This amounts to 5.5 million infections per year, resulting in approximately 50,000 hospitalizations and 300 deaths. These numbers reflect only those diseases of known etiology; if foodborne disease of unknown etiology were included, as well as other transmission routes, these estimates would be staggeringly high. For example, of the more than 170 million cases of gastroenteritis that occur in USA each year, the etiology of only about one-fifth of them is confirmed, leaving an estimated 140 million cases of gastroenteritis caused by unspecified agents. Owing to the frequency of NoV infection, it is likely that a large proportion of these are also caused by HuNoV. Similar data are available from Europe.

The taxonomy of NoV has changed substantially over the past 15 years, and what was originally called the ‘Norwalk-like’ virus group is now classified as the *NoV* genus, one of four genera within the Caliciviridae virus family. The other genus in this family causing disease in humans is *Sapovirus*, also shown to cause gastroenteritis. HuNoV are a nonenveloped icosahedral
viruses approximately 27 nm in diameter and having a genome consisting of a single strand of positive-sense RNA of 7.4–8.3 kb in length. The genome encodes three open reading frames (ORF): ORF1 encodes a nonstructural polyprotein that contains the genes for p48, NTPase, p22, VPg, protease, and RNA polymerase; ORF2 encodes the viral capsid protein; and ORF3 encodes a small basic structural protein of unknown function.

Based on nucleic acid sequence analysis, the NoV genus can be further classified into five genogroups, designated GI, GII, GIII, GIV, and GV, based on >60% amino acid homology of the viral capsid protein. Human infections are caused almost exclusively by genogroups GI and GII, with the vast majority caused by GII strains. Each genogroup can be further classified into genotypes, based on a >80% amino acid homology in the capsid protein. Currently, 8 GI strains and 19 GII strains have been identified. The genetic cluster GII.4 is the most significant of the genotypes, having predominated in outbreaks around the world for over a decade. However, strains other than GII.4 are most often the cause of foodborne disease outbreaks.

Outbreaks of NoV have involved food products including molluscan shellfish, fresh fruits and vegetables, and ‘ready-to-eat’ (RTE) foods. Epidemiologically speaking, it appears that RTE foods are the most common cause of foodborne NoV outbreaks, although high-profile outbreaks have occurred in produce items such as berries. In healthy adults, the incubation period for NoV infection ranges from 24 to 48 h, with symptoms lasting 12–72 h. The disease is gastrointestinal in nature, typically presenting with vomiting (hallmark symptom), diarrhea, and abdominal cramps that may or may not be accompanied by fever. In certain at-risk groups, particularly the elderly, NoV infection can result in a much more severe disease, with symptoms lasting as long as 6 weeks. The hospitalization rate for HuNoV infection is estimated to be 0.03% and the mortality rate is less than 0.1%. Nonetheless, the sheer numbers of cases make these viruses one of the leading causes of foodborne disease hospitalizations and deaths. No antiviral strategy exists for prevention or treatment of NoV illness. As is the case for all enteric diseases, infected individuals should be treated to maintain hydration and electrolyte balance.

Although some immunologically based commercial methods are available for detection of HuNoV in clinical samples, they are licensed in only some parts of the world. This is largely because of poor sensitivity due to the lack of broadly reactive antibodies that will detect all HuNoV strains. The high degree of genetic diversity for the NoV has historically complicated the development of broadly reactive RT-qPCR methods. Four ‘regions’ of the NoV genome have been used for primer design (designated regions A, B, C, and D). These regions are generally conserved among HuNoV strains of the same genogroup. The ORF-1–ORF2 junction (just downstream of region B) seems to be the most conserved and is frequently used for genogroup-specific detection. For strain comparison (as might be appropriate in outbreak investigation), primers corresponding to the NoV capsid region (region D) are usually used. Commercial RT-qPCR method detection methods are available for use in the food and environmental sector, but in all cases, substantial sample preparation to concentrate the viruses and remove the sample matrix is required before the application of RT-qPCR for detection. Taken together, HuNoV detection in clinical, food, and environmental samples is not done routinely and there are wide regional variations in protocols. This highlights the need for standardized methods of detection and consistency of surveillance and disease reporting across countries.

**HAV**

HAV is a 27–32 nm, nonenveloped, positive-sense single-stranded RNA virus with a 7.5-kb genome and capsid having icosahedral symmetry. This virus is classified in the Picornaviridae family under the genus *Hepatovirus*. Unlike other RNA viruses, the HAV genome is highly conserved, with only 1–4% amino acid variation. Human isolates of HAV comprise a single serotype, but sequence heterogeneity within the VP1/2A can be used to differentiate HAV into seven unique genotypes. Of these seven genotypes, genotypes I and III predominate in human disease. Transmitted primarily by contact with the blood of infected individuals or through male homosexual relations, only approximately 5% of HAV cases are foodborne, with transmission almost always in keeping with the fecal–oral route. Once infected, the disease incubation period averages 4 weeks (range of 2–6 weeks). Disease initially presents with a prodrome that includes fever, headache, nausea, vomiting, and diarrhea. These symptoms progress 1–2 weeks later into inflammation of the liver and jaundice. Hospitalization occurs in 35.1% of cases, with mortality rates estimated at 2.4%. Infected young children are frequently asymptomatic, while disease severity increases with age. Hepatitis A infection is endemic in developing regions of the world, and foods imported from third world countries where sewage treatment and hygiene advancements are still developing pose an increased risk to naïve consumers in developed countries.

Like NoV, outbreaks of HAV have involved food products including molluscan shellfish, fresh fruits and vegetables, and RTE foods. For example, in 1988 approximately 300 000 people in China contracted HAV from consuming partially cooked clams that had become contaminated by release of raw sewage in the proximity of the harvest area. Within the fresh produce category, products such as raspberries, strawberries, lettuce, and green onions have caused outbreaks, some quite sizable. A good example is the 2003 US outbreak when green onions served at a single Pennsylvania restaurant resulted in more than 600 HAV cases, with 124 hospitalizations, and 3 deaths. Fresh produce most likely becomes contaminated by the use of human sewage-contaminated irrigation water, because of human defecation in production fields, and/or from the hands of infected food handlers during harvest or preparation phases of the farm-to-fork continuum. Still, the most common cause of HAV foodborne outbreaks in general is poor personal hygiene of infected food handlers. Fortunately, an effective vaccine that provides lifelong immunity is now available suggesting that as the immunized population grows the disease will eventually go the route of poliovirus, although it may take decades before this is realized.

Because HAV has a degree of genetic and antigenic homogeneity, its detection is much easier than that of HuNoV. Clinical assays that detect antibodies against HAV are commercially available, and for food and environmental samples,
RT-qPCR using primers targeting the highly conserved VP1/2 A junction or 5' untranslated region of the viral genome are used. As is the case for NoV, substantial preanalytical sample processing must be done when applying these methods to complex sample matrices and this remains the limiting factor in the routine detection of HAV in foods.

Rotaviruses

Rotaviruses are the leading cause of infantile diarrhea worldwide and are responsible for more than 500,000 deaths annually, the majority of which occur in developing countries. These viruses are 70–75 nm in diameter and contain 11 segmented double-stranded RNA molecules encased in a double-layered protein coat of icosahedral symmetry. The 11 genome segments range in size from 667 bp (segment 11) to 3302 bp (segment 1), for a total of 18.5 kb. Each of the segments encodes a single protein, with the exception of segments 9 and 11 which encode two proteins. A total of six structural viral proteins form the virus particle (termed VP1, VP2, VP3, VP4, VP6, and VP7), whereas a further five nonstructural proteins (termed NSP1–NSP5) are responsible for RNA replication, packing, and other functions. Interestingly, NSP4 is an enterotoxin that induces diarrhea. At least seven different rotavirus groups exist (A–G) based on VP6 reactivity with monoclonal antibodies.

Waterborne and person-to-person transmission are the most common causes of rotavirus infection; however, transmission via food products has been documented, with infant populations under 5 years of age most often affected. The incubation period preceding disease is approximately 2 days, and symptoms of disease include vomiting, diarrhea, and fever; dehydration is the most common cause of death. Hospitalization rates in USA are estimated at 1.7%, with a mortality rate of less than 0.1%. The World Health Organization (WHO) now recommends the use of second generation rotavirus vaccines worldwide in an attempt to reduce the burden of disease in developing countries.

Emerging Foodborne Viruses

A number of enteric viruses have the capacity to be transmitted by foodborne routes, although this is rarely documented or has not yet occurred. A few of these are described briefly in this section.

Hepatitis E virus (HEV)

HEV is a positive-sense single-stranded RNA virus that is transmitted via the fecal–oral route, generally through the consumption of water and sometimes food that has become contaminated with human feces. This virus is endemic in developing countries, particularly those locations having hot climates. Large waterborne outbreaks have been recorded in many countries, and it is also possible that the virus is transmitted by the consumption of raw or undercooked pork and deer meat. Interestingly, cases of HEV have recently been reported in USA, UK, and Japan, leading to speculation that the geographic range of this virus is increasing and that HEV may become an emerging food and waterborne pathogen in the developed world.

The incubation period for HEV infection ranges from 3 to 8 weeks, with disease symptoms generally lasting several weeks. Frank disease occurs more often in adults, with children often spreading the infection without displaying symptoms. Clinical symptoms are very similar to those of HAV infection, but unlike HAV, the disease is quite severe in pregnant women for whom mortality is approximately 20%. Clinical diagnosis of HEV involves detecting antibodies specific to the virus in the blood of patients displaying the symptoms of hepatitis, or by RT-PCR.

Other Human Enteric Viruses

Other human enteric viruses also have the potential to be transmitted by contaminated food products, although their epidemiological significance is not well understood. The human enteroviruses, including poliovirus, coxsackie, and echoviruses, are nonenveloped particles containing single-stranded positive-sense RNA, with particle diameter of approximately 27 nm. Poliovirus has been all but eradicated in the developed world, coxsackie and echoviruses, which cause a variety of symptoms that can range from gastroenteritis, neurological, and skin manifestations, can be transmitted by foodborne routes, albeit infrequently. Like HuNoV, they are resistant to harsh conditions, making them environmentally persistent.

Astroviruses are 28 nm single-stranded RNA viruses with a star-shaped capsid structure. These viruses cause sporadic disease and outbreaks of diarrhea in children and the elderly, particularly in venues such as day care centers and hospitals. Transmission of these astroviruses by food is uncommon but has been documented for molluscan shellfish. Human adenoviruses are nonenveloped double-stranded DNA viruses that range from 80 to 110 nm in diameter. They can cause gastroenteritis, conjunctivitis, and most frequently, respiratory symptoms. The presence of these viruses in environmental samples such as wastewater, sludge, and drinking water has been reported, and for this reason, their use as an indicator for the presence of human enteric viruses has been proposed. However, the transmission of adenoviruses by foodborne routes has not yet been documented.

Nipah Virus

Nipah viruses belong to the genus Henipavirus in the family Paramyxoviridae, and are relatively large (120–150 nm diameter), enveloped, single-stranded RNA viruses. The Nipah virus was first recognized in 1999 in Malaysia in association with pig farmers who contracted the disease by contact with infected animals. It can also be transmitted by person-to-person contact and can be carried by fruit bats. There have been recorded outbreaks where the vehicle of infection was fruits and vegetables contaminated with the saliva of bats. Other outbreaks have involved direct contact with contaminated pigs or their tissues. Disease symptoms usually include
fever, headache, muscle pain, vomiting, and sore throat. These can progress to pneumonia and other respiratory illnesses. In severe cases, seizure and encephalitis can occur, often resulting in death. Currently, there is no vaccine or treatment for Nipah virus infection, so control of foodborne disease relies on cleaning and disinfection of pig farms, culling animals suspected of being infected, and controlling bat populations.

**Highly Pathogenic Avian Influenza (HPAI) Viruses**

HPAI viruses are large (300 nm diameter), negative sense RNA viruses having a segmented genome and belonging to the Orthomyxoviridae family. Domestic and wild birds are the major reservoir for these viruses. There are virtually hundreds of HPAI strains, however, only four have been shown to cause infection in humans; H5N1, H7N3, H7N7, and H9N2. Disease in humans is typically mild, except for the H5N1 virus, which has been responsible for a number of human deaths following outbreaks. The potential for spread of this virus through the food chain has been of concern because the virus appears to survive on imported meat. There is also concern for the risk of fecal contamination of water that is subsequently used in production agriculture or even for food preparation. However, it has been documented that HPAI is susceptible to thermal processes, meaning that the consumption of properly cooked food poses little risk for HPAI infection.

**Coronavirus**

Coronaviruses are enveloped viruses with positive-sense single-stranded RNA that belong to the family Coronaviridae. The coronavirus that causes sudden acute respiratory syndrome (SARS-CoV) was first recognized as a human pathogen in 2002 in association with an outbreak in China. The virus was subsequently detected in more than 30 other countries, infecting more than 8500 people with a 10% mortality rate. Although generally thought to be spread exclusively by respiratory routes, there is evidence that SARS-CoV can replicate in the small and large intestines, causing diarrhea that results in fecal shedding of the virus. Thus, the fecal–oral transmission route cannot be excluded. However, SARS-CoV is sensitive to fairly mild heat treatment and commonly used disinfectants, suggesting that attention to proper food handling and preparation measures should control foodborne transmission of the virus. Taken together, the spread of SARS-CoV via contaminated food products remains possible but is now considered unlikely.

**Lassa Virus (LV) and Hantavirus (HV)**

LV and HV are RNA viruses that belong to the Arenaviridae and Bunyaviridae families, respectively. LV, which is endemic in sub-Saharan Africa, causes a viral hemorrhagic fever; HV initially presents as a flu-like syndrome that can progress to severe pulmonary disease. The natural reservoir for both of these viruses is the mouse, and although rare, food can potentially be a vehicle of infection if it becomes contaminated with urine and/or feces of mice.

**Epidemiological Surveillance and Burden of Disease**

The US Centers for Disease Control and Prevention (CDC) conducts surveillance of foodborne disease outbreaks, including those caused by HuNoV and HAV, through the National Outbreak Reporting System (NORS). Because the program relies on individual states reporting their data, which is quite variable, the database is incomplete. The NORS system provides some important information that can be used relative to epidemiological attribution estimates, but it only reports on epidemic disease. In the absence of routine clinical diagnostics, it is very difficult to get estimates for endemic HuNoV disease. The CDC has also recently launched CalciNet, a national HuNoV sequence database that may eventually have utility similar to that of the PulseNet system for bacterial foodborne pathogens.

Surveillance for HuNoV illness in Europe has been done by the European Centre for Disease Control and Prevention (ECDC) and the Foodborne Viruses in Europe (FBVE) Network. In Australia, the notification of individual NoV infections is not required, however, the reporting of two or more infections having a time, place, and/or person association, suggesting an outbreak, is required.

In many other countries, foodborne viral disease surveillance is not conducted, making it difficult to estimate the global impact of disease. In a UK study, it was estimated that only 1 in 1562 HuNoV infections was actually reported. This is not surprising due to the mild nature of most infections and the lack of routine clinical diagnostics. Of particular interest is the proportion of HuNoV infections that are caused by contaminated foods as compared to other transmission routes. Getting at these estimates will undoubtedly require targeted epidemiological efforts such as active surveillance and/or case control studies, both of which are expensive and time-consuming. Further, until standardized reporting at the country and international level is established, the true burden of foodborne viral disease will remain unknown.

**Control of Foodborne Viruses**

As obligate intracellular parasites, enteric viruses cannot replicate in foods or water. In general, if wastewater is adequately treated through primary, secondary, and tertiary steps, and including chlorination, the risk of viral contamination is minimal. When it comes to foods, many measures classically applied to control bacterial growth are not very effective against viruses. For example, exposure to extremes of pH (2.0–10.0) and water activity will have little or no effect on the infectivity of enteric viruses. Refrigeration and freezing actually help to preserve virus infectivity. The efficacy of standard thermal inactivation treatments is dependent on the food matrix and virus studied. As a general rule of thumb, NoV and HAV appear to be less sensitive to heat than are typical Gram-negative bacteria, and more sensitive to heat than spores. High hydrostatic pressure has been recognized as an emerging processing technology for inactivating viruses in molluscan shellfish, however, similar to thermal inactivation, the effectiveness of the treatment is variable and virus specific. Enteric viruses are also notably resistant to ionizing radiation.
Many studies have demonstrated the ability of enteric viruses to survive on abiotic surfaces commonly found in food processing and preparation environments, including stainless steel, aluminum, and polystyrene. Viruses also persist in foods, having been found to survive in shellfish for weeks or months and on the surface of fresh produce for days to weeks. To make matters worse, it is well documented that many common sanitizers used in food processing environments have poor efficacy against nonenveloped enteric viruses, at least when used at manufacturer-recommended concentrations.

It is for this reason, current control measures focus on the prevention of contamination, rather than treatments to inactivate viruses after a contamination event has occurred. The central tenets of control are good hygiene practices in food processing and handling environments, and prevention of contamination in the preharvest environments. Because the decontamination of hands and surfaces in food processing and preparation is critical to preventing virus contamination, an important effort is assuring effective hand decontamination. The best method remains the traditional soap and water wash followed by towel drying. Commercial alcohol-based hand sanitizers should not be used in place of adequate hand washing. Of course, hand washing compliance in retail, institutional, and home settings remains a challenge and must be continuously advocated. There has been interest in further promoting the need for infected food handlers to report illness symptoms and abstain from work during periods of time in which they are actively shedding virus. However, the latter may be difficult in light of emerging evidence suggesting that shedding of HuNoV may persist for weeks after symptom resolution. Adequate cleaning and disinfection of surfaces is also important to preventing virus contamination of foods, but the availability of disinfecting agents with specific activity against the nonenveloped enteric viruses is a pressing need. Also needed are better microbiological indicator systems that have a more direct correlation with virus contamination of water in production environments, as the fecal coliforms and Escherichia coli remain poor indicators for this application. This is particularly relevant for molluscan shellfish and fresh produce production.

Conclusion

Food virology is a relatively young field, at least from the perspective of food safety. The development of molecular techniques during the 1990s, in combination with increased epidemiological surveillance, have raised awareness of the importance of viruses to foodborne illness. Although methodological advancements have been made, much still remains unknown. The lack of a culture system for HuNoV is probably the single most important limiting factor to studying and controlling these viruses. With availability of such a method, or in its absence, availability of better cultivable surrogates or more sensitive detection methods for complex sample matrices, scientists would be able to tackle the challenges associated with trying to control foodborne viruses. Likewise, the availability of routine clinical assays would result in greater awareness of these diseases and improvements in reporting and epidemiological surveillance. The field of food virology is set to grow rapidly in the coming years as scientists tackle these problems with the aid of developing technologies.

See also: Food Safety Assurance Systems: Personal Hygiene and Employee Health. Organisms of Concern but not Foodborne or Confirmed Foodborne: Foot-and-Mouth Disease Virus. Viruses: Hantavirus; Hepatitis A Virus; Hepatitis E Virus; Lassa Fever Virus; Nipah Virus; Norovirus

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