

(REVIEW ARTICLE)



Environmental virology linked to waterborne diseases and foodborne pathogens: Human and animal food viruses

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Abstract

Foodborne illnesses constitute a serious global one health issue. The transmission of foodborne viruses can occur due to inadequate hygiene of food, lack of basic sanitation, poor personal hygiene and consumption of raw or undercooked food. This study aims overview about environmental virology linked to waterborne diseases and foodborne pathogens in human and animal food viruses. Thus, epidemiological studies have proposed some emerging pathogens as possible transmitters of contaminated water ingestion based on biochemical properties and viral structures such as: *Picornaviridae* (polioviruses, enteroviruses, coxsakiviruses, hepatitis A viruses and echoviruses), *Adenoviridae* (adenoviruses), *Caliciviridae* (noroviruses, caliciviruses, astroviruses), and *Reoviridae* (reoviruses and rotaviruses). These viruses can cause gastrointestinal, liver and central nervous system disorders. In controlling foodborne infections, accurately identifying sources of contamination is a significant challenge, given the complexity of the food production chain. The lack of adequate monitoring and neglect of good health practices contribute to the spread of these infections. Large-scale immunization has contributed to the reduction of enteric outbreaks and eradication of cases in many regions of the world as a prevention of hepatitis A and poliomyelitis. However, challenges such as the lack of effectiveness in inspecting viruses in food increase the risk of outbreaks and epidemics, with emphasis on Noroviruses as the main causes of these infections today. Investment in vaccine research and development has been a fundamental strategy to reduce these statistics, especially in vulnerable groups. Moreover, the implementation molecular-based tools and wastewater-based epidemiology studies to high-throughput for aquatic biomonitoring should be up to date to avoid the risk and impact on public health and aquatic environments. Novel perspectives to control of waterborne viruses has been introduced in continuous surveillance programs for ecosystems monitoring.

Keywords: Foodborne viruses; Waterborne diseases; Ecosystems monitoring; Environmental virology and one health

1. Introduction

Waterborne virus-based illness may be transmitted through adenovirus, astrovirus, hepatitis A and E viruses, rotavirus, norovirus and other caliciviruses, and enteroviruses, including coxsackieviruses and polioviruses which they possibility associated with drinking water contamination. polyomaviruses and cytomegalovirus have been already detected in urine samples that can also be another source of contamination through water [1].

In terms of the treatment of water supply two disinfectants such as free chlorine - a stronger disinfectant to pathogen inactivation, and monochloramine have been applied to avoid the cross-contamination in the water distribution system

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[1]. Epidemiological studies have been proposed some pathogens which may be transmitted by ingestion of contaminated water such as Hepatitis A (HAV), Hepatitis E (HEV) viruses and enteric viruses including adenovirus, astrovirus, rotavirus, calicivirus, Norwalk and other Small round structured viruses (SRSV) [2].

Enteric viruses can be transmitted by food, water, fomites, and human contact [3]. Waterborne diseases are usually acquired, through the ingestion of contaminated water or shellfish. Enteric virus groups may be considered emerging waterborne pathogens, based on their biochemical properties and viral structural belong to the families *Picornaviridae* (polioviruses, enteroviruses, coxsakieviruses, hepatitis A virus, and echoviruses), *Adenoviridae* (adenoviruses), *Caliciviridae* (noroviruses, caliciviruses, astroviruses, and small round-structured viruses), and *Reoviridae* (reoviruses and rotaviruses).

In environmental samples of seawater, freshwater and also sewage have been reported the presence of infectious virus for up to 120 days in these aquatic environments. Moreover, the virus survival had also been detected for up to 100 days in soil samples at temperature 30°C. The prevalence of animal-specific enteroviruses and adenoviruses in hosts had been reported in aquatic environments and may be used as potential tools in water quality management in the waterborne diseases' studies [3].

1.1 Human Food Viruses

In the late 19th and early 20th centuries, medical researchers such as Dr. Rudolf Virchow and William Osler conceptualized that human health and animal health were closely linked. The concept of one health unites human care, animal and environmental, as a successful strategy for public health efforts and ensuring the well-being of populations. Food safety is a high public health issue and need studies about human and animal food viruses. The risk of microbiological contamination by the presence of viruses in crustaceans is very relevant for food safety. In a retrospective study in the Netherlands (2013-2017), RT-qPCRs were detected in 31.6% of oyster samples and 53.1% of mussel samples [4].

1.2 Animal Food Viruses

The porcine epidemic diarrhea virus (PEDV) caused an alert and aroused the risk in the swine population since 2013 [4]. Although the virus was described initially in the United States, its origin was in China confirmed by the phylogenetic studies [4].

RNA viral genome was detected in samples of rectal swabs of animals infected by PEDV. After consumption of the feed contaminated the pigs has showed clinical signs in the gastrointestinal tract as vomiting and diarrhoea comproving that the animal feed as a vehicle for transmission of viral diseases and it had confirmed in experiments involving environmental swabs by feed dust and feed ingredients [4].

The transmission of *African swine fever virus* (ASFV) was comproved after consumption of purposefully contaminated feed and liquid with the virus in 12 feed ingredients and offered to ingestion of the naïve pigs. Another virus as *pseudorabies virus* (PRV) and *classical swine fever virus* (CSFV) had been also inoculated experimentally in feed ingredients and it was detected in samples of organic soybean meal, lysine, choline, vitamin D, moist and dry pet food [4].

The presence of each virus was reported in two specific ingredients as conventional soybean meal and pork sausage casings. A lot of chemical strategies of treatment as formaldehyde and high temperature to mitigate the risk of contamination and inactive the virus had been implemented as security protocol in feed [4].

2. Waterborne diseases

Waterborne disease commonly include the Human adenoviruses (HAdVs), Noroviruses (NoVs), Hepatitis A (HAV), Hepatitis E (HEV), parvoviruses, enteroviruses and Rotaviruses (RVs). Infectious viruses in upon exposure recreational waters constitutes a public health risk which adenoviruses as an indicator of bathing water quality. Transmission routes for enteric viruses may be person to person, foodborne or waterborne associated with poor hygiene conditions. In the past, waterborne pathogens were measured by detection of faecal bacterial indicator organisms (FiOS) [5].

Cell culture-based methods like monolayer plaque assays may be able to estimate the levels of concentrations of some viruses in surface waters but for viral detection it had been showed some disadvantages. Nowadays, the detection of enteric viruses in waters bathing is by molecular methods such as Reverse Transcription (RT-PCR) or nucleic acid

sequence-based amplification (NASBA) which amplify RNA/DNA for monitoring and/or surveillance of enteric viruses in recreational waters [5, 6, 7].

Viral mRNA targeting assay and integrated cell culture polymerase chain reaction (ICC-PCR) used to detect both DNA viruses and RNA viruses (ICC/RT-PCR) quantifications methods of enteroviruses serotypes detect in several transmission sources like sewage [6, 7].

Waterborne outbreaks have been reported mainly by noroviruses which are the most important cause of viral gastroenteritis disease. Concentration of samples type like freshwater and marine water have been performed by glass wool filtration and by nitrocellulose membrane filtration, respectively [5, 7].

There are many sources of water such as wastewater, seawater, freshwaters, groundwater, drinking water and recreational water which have been detected enteric viruses [7]. Otherwise, until this moment there hasn't been demonstrated the evidence of the possibility of SARS-CoV-2 would be transmitted by contaminated drinking-water [8].

Faecal contamination is a vehicle for pathogenic viruses spread through water environments. The most important waterborne enteric viruses belong to the families *Caliciviridae* (Norovirus), *Picornaviridae* (Enterovirus and HAV) and *Adenoviridae* (Adenovirus). These viruses are more resistant to environmental conditions, water treatments and disinfectants than enveloped viruses like coronavirus. Moreover, there are another group of viruses (enveloped virus) have been detected in water environments such as *Orthomyxoviridae* (Influenza virus), *Paramyxoviridae* (measles virus, mumps virus, respiratory syncytial virus), *Herpesviridae*, *Coronaviridae* and others [8].

3. Enteric viruses commonly found in water

3.1 Hepatitis A virus (HAV)

Member of the *Picornaviridae* family and *Hepatovirus* genus. Despite a nucleotide diversity similar to that of other picornaviruses, HAV exists as a single serotype, with human strains divided into three genotypes (I, II and III) and seven subgenotypes (IA, IB, IC, IIA, IIB, IIIA and IIIB). The subgenotype IIIA have been reported to be more severe in hepatitis cases with high levels of hospitalization.

The specific symptomatology is characterized by jaundice, acholic stools, choluria and non-specific symptoms such as fever, nausea, vomiting, abdominal pain and tiredness. The asymptomatic associated cases usually occur in children up to 5 years of age. Viral transmission occurs via the fecal-oral route through ingestion of contaminated water or food. HAV has already been detected in contaminated drinking and recreational water. In addition to other sources of water such as wells, sewage, rivers and streams. The emergence of a new serotype HAV-related viruses zoonotic origin had been detected in aquatic animal. This virus is very stable at pH 1-3, heat resistant at 60°C for 1 hour and resistant to denaturing.

3.2 Hepatitis E virus (HEV)

Classified in the *Herpesviridae* family and the *Herpesvirus* genus. The Hepatitis E virus is spread via the fecal-oral route by ingesting contaminated food and water. Seven genotypes of mammalian HEV have been documented within subgenus *Orthoherpevirus* A which host species are: human (HEV-1 and HEV-2); pig, wild boar, rabbit, deer and mongoose (HEV-3); human and pig (HEV-4); wild boar (HEV-5/6); and camel (HEV-7). Moreover, *Orthoherpevirus* B predominantly infects chickens, *Orthoherpevirus* C rats and ferrets, and *Orthoherpevirus* D bats.

3.3 Rotavirus

Member of the *Reoviridae* family and *Rotavirus* genus. The spread of the virus is via the fecal-oral route. Its transmission occurs through direct contact with the infected person, through the ingestion of contaminated water, consumption of contaminated food. There is a high concentration of the virus in the patient's feces, which is another source of contamination. Its highest prevalence is in less developed countries. The virus is stable at pH 3-9, thermostable at 50°C and is resistant to solvents.

3.4 Adenovirus

Enteric adenoviruses belong to *Adenoviridae* family and *Mastadenovirus* genus. These viral pathogens are very stable at acidic pH, resistant to ether and chloroform treatments. The virus is transmitted by direct contact, fecal-oral, and contaminated water such as sewage samples and poor water supply. The transmission of adenoviruses in recreational

waters and swimming pools as responsible for causing outbreaks of conjunctivitis has already been reported. The virus is persistently excreted through the pharynx and feces for long periods. The disease usually manifests as a mild illness with diarrhea and vomiting [3]. Adenoviruses as human pathogens (Figure 1) and Adenoviruses as animal pathogens (Figure 2) linked viruses, host/infections and diseases associated are shown below.

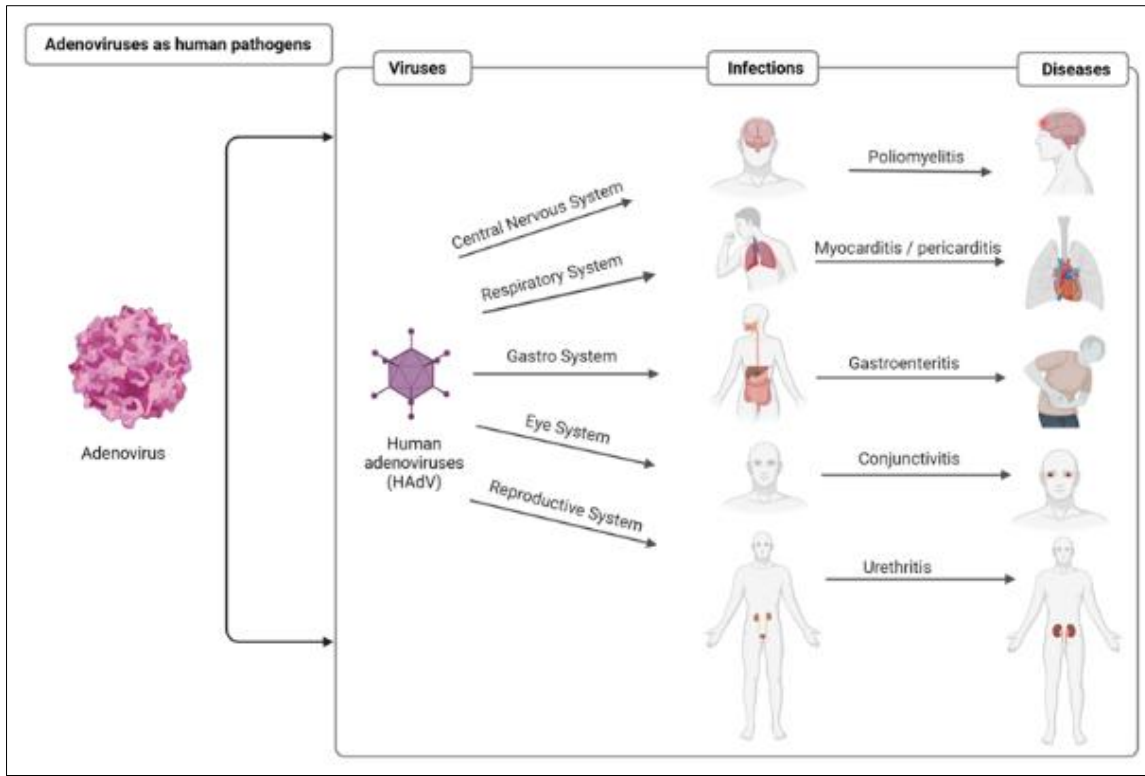


Figure 1 Human adenoviruses (HAdV) linked viral tropism and clinical manifestations of the disease. This figure was created and designed by the author using scientific image and illustration software with publication license into journals

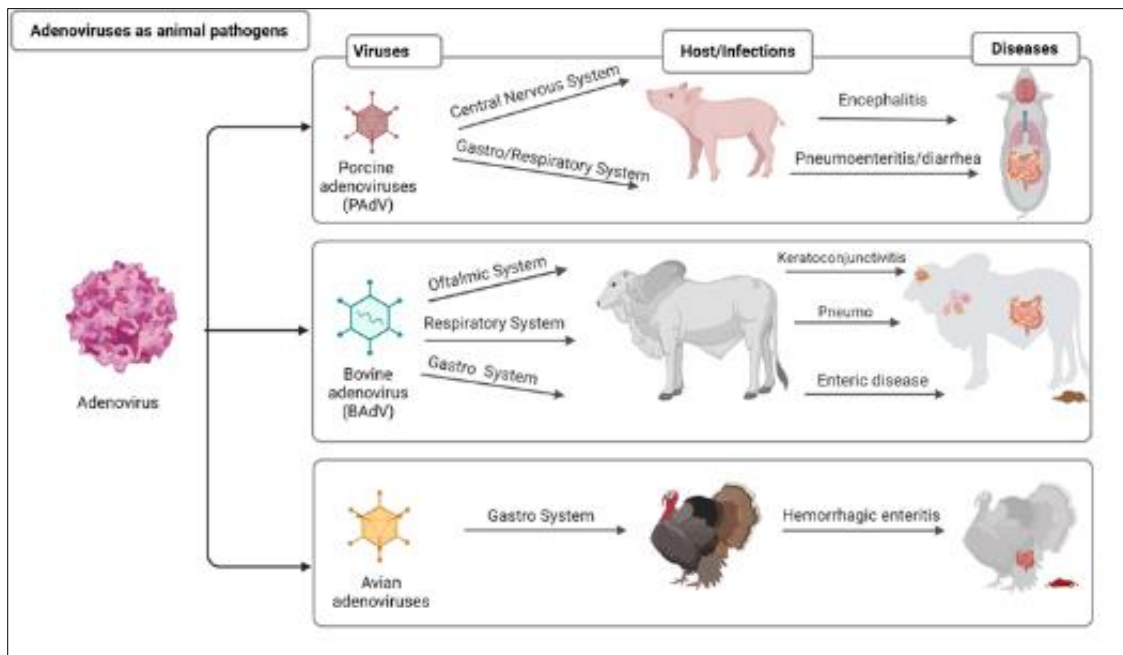


Figure 2 Animal adenoviruses associated viral tropism of the host species and clinical manifestations of the disease. This figure was created and designed by the author using scientific image and illustration software with publication license into journals

3.5 Norovirus (NoVs)

NoVs are currently recognized as the cause of outbreaks of nonbacterial gastroenteritis, and also as an important cause of gastroenteritis sporadic in children and adults. It belongs to the *Caliciviridae* family and *Norovirus* genus. Virions have a capsid and a nucleic acid, measuring about 27 to 30 nm in diameter and do not have a viral envelope. The nucleocapsid is rounded and exhibits icosahedral symmetry. The viral genome consists of a linear molecule of single-stranded RNA of positive polarity and serve as mRNA. The complete genome contains approximately 7.5 kb; composed of 45%-56% cytosine + guanine (C + G). Norovirus genomic organization and localization of the three ORFs and the Pol region has been used to design the primer pools used in RT-PCR for the identification of genogroups and genotypes.

NoVs are genetically and antigenically highly diverse agents distributed into seven genogroups (GI to GVII) with altogether more than 30 genotypes distributed worldwide, and with GI, GII and GIV infecting humans. GII, genotype 4 (GII.4) periodically emerging for the majority of cases worldwide. Norovirus is spread by contaminated water and food and person-to-person contact. The disease often affects adult individuals. They are associated with outbreaks in confined or close contact places such as hospital environments, on ships, nursing homes, homes and schools. This virus is an important cause of viral gastroenteritis. The most common symptoms are vomiting, diarrhea and moderate stomach cramps. High numbers of viruses are disseminated in their feces, over 10^{10} NoV genome copies per gram (gc/g) of stool, and other hand about of 3×10^7 virus particles are released in a single episode of vomiting. A new variant (GII.17) causing outbreaks has recently emerged in China and Japan replacing the previously dominant GII.4 genotype. There are presently several on-going efforts to develop vaccines - intranasal vaccination with virus-like particles (VLP) - to prevent NoV GI.1 (Norwalk virus) infections to target multiple genotypes of interest NoV [2]. Quantitative levels of NoV RNA have been assessed in mussels and oysters collected and risk associated with the consumption of raw and undercooked shellfish along the food chain in the Netherlands [9].

Consumption of leafy greens and fresh herbs has been associated with several foodborne outbreaks including human norovirus (HuNoV) [10]. MNV and HuNoV GI were detected based on the RT-qPCR ORF1/ORF2 primer system. Extraction approach based on magnetic silica beads is very effective at recovering HuNoV GI and GII from leafy greens [10].

3.6 Astrovirus

Human astroviruses belong to the *Astroviridae* family, *Mamastrovirus* genus. Astrovirus transmission is fecal-oral and infection usually occurs through direct contact with infected people, ingestion of contaminated food and water, and fomites. The infection produces clinically acute gastroenteritis and the typical symptom is watery diarrhea that may be accompanied by vomiting, fever, anorexia, abdominal pain and dehydration.

3.7 Enterovirus

Classified in the *Picornaviridae* family and the *Enterovirus* genus. Human enteroviruses include polioviruses, coxsackieviruses A, B, echoviruses, and enteroviruses. Enteroviruses are transmitted via the fecal-oral route and infection occurs through ingestion of contaminated food or water. Enteroviruses can cause a variety of diseases such as polio, aseptic meningitis, childhood diarrhea, and myocarditis (Figure 3). Enteroviruses as animals pathogens as bovine and porcine enteroviruses affected in central nervous, respiratory, reproduction and gastro system inducing disorders or irreversible lesions (Figure 4). These viruses are very stable and resistant to detergents, proteolytic enzymes, solvents and chlorination. They are frequently detected in recreational waters however most cases are underreported [3].

3.8 Anelovirus

Classified in the *Anelloviridae* family and the *Alphatorquevirus* genus. Torquetenovirus is present in a variety of body fluids, which suggests that transmission occurs through the parenteral route, contact with contaminated blood, and by the fecal-oral route. Torque Teno Virus (TTV) has been detected with high prevalence reaching 90% of the world population and high viral load can be found in sewage samples and water from polluted rivers [6].

3.9 SARS-CoV-2

Coronavirinae includes four genera, Alpha (α -CoVs strains HCoV-229E and HCoV-NL63), Beta (β -CoVs strains HCoV-HKU1 and HCoV-OC43), Gamma and Delta-coronavirus (La Rosa, 2020). Severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East respiratory syndrome coronavirus (MERS-CoV), and SARS-CoV-2 are also classified as betacoronaviruses. Most recent reported occurrences in different countries on several continents had been documented according to tracking of variants (VOC Delta GK (B.1.617.2 + AY)) [11].

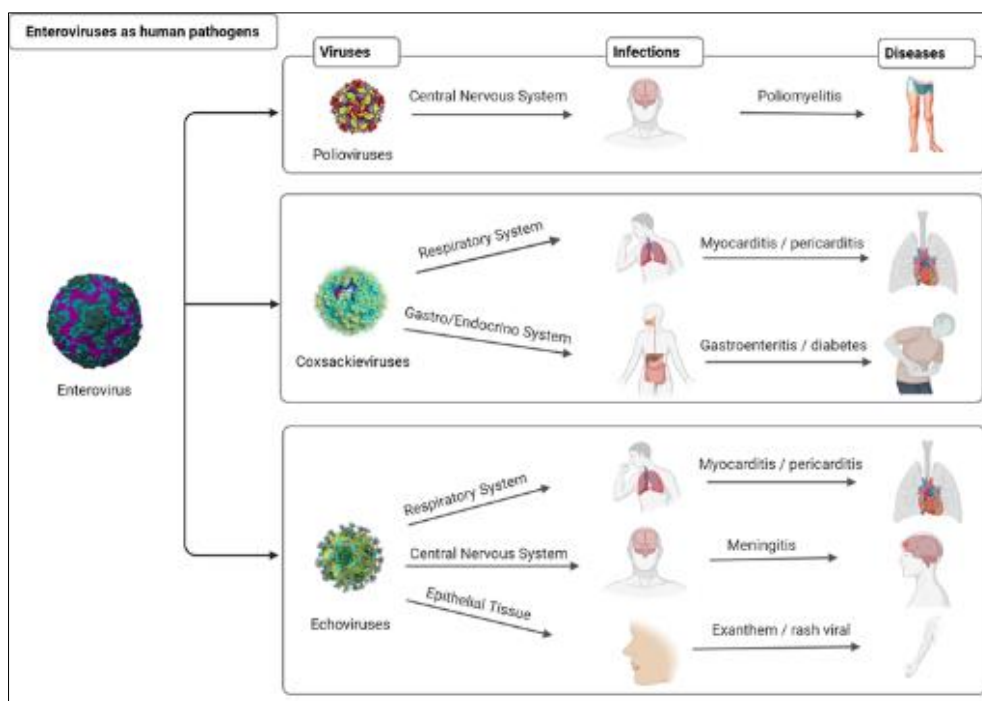


Figure 3 Human enteroviruses linked viral tropism and clinical manifestations of the disease. This figure was created and designed by the author using scientific image and illustration software with publication license into journals

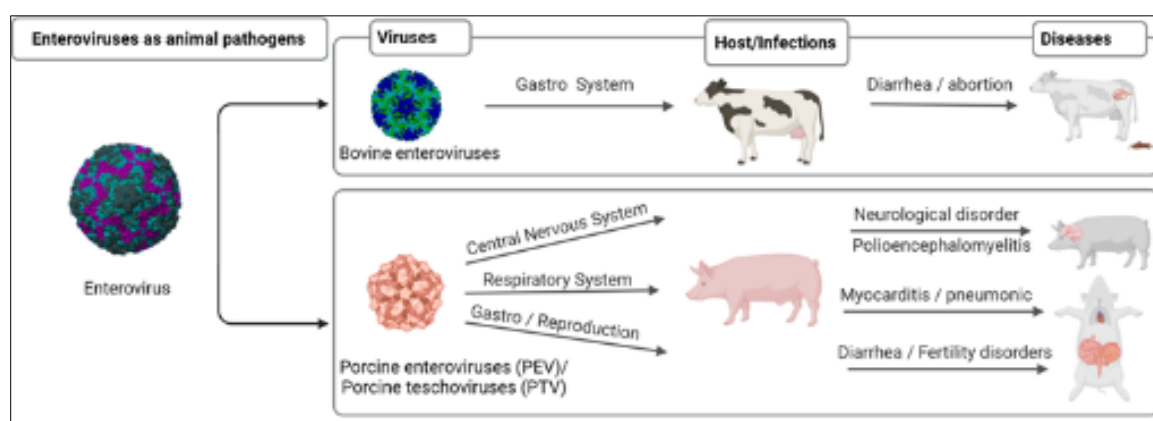


Figure 4 Enteroviruses as animals pathogens cause in several animal species as bovine and pig’s disorders or lesions in central nervous, respiratory, reproduction and gastro system. This figure was created and designed by the author using scientific image and illustration software with publication license into journals.

Phylogeny of SARS-like *betacoronaviruses* including SARS-CoV-2, showing 49 genomes design by *Nextstrain* [11]. Classical and Next-Generation Biotechnological platforms for SARS-CoV-2 vaccine candidates licensed and Real-time tracking of SARS-CoV-2 evolution had been constantly monitored by epidemiological surveillance applied metagenomic tools [11].

Occurrence of coronavirus in water environments has been documented. The SARS-CoV-2 spread from an infected individual through air and waterborne pathways and their environmental factors as role of transmission routes has been reported [12]. RNA SARS-CoV-2 can survive up to 2-3 days in sewage water and up to 10 days in tap water [8].

There are many sources of water such as wastewater, seawater, freshwaters, groundwater, drinking water and recreational water which have been detected enteric viruses [8]. Otherwise, until this moment there hasn’t been demonstrated the evidence of the possibility of SARS-CoV-2 would be transmitted by contaminated drinking-water [8].

The effect of thermal processing on the inactivation method of human coronaviruses results no change or no detectable cytopathic effect SARS-CoV into cell culture medium. Thermal processing (heating at 75°C (15–60 min) is the main way to inactivate SARS-CoV-2. Moreover chilling and freezing are inappropriate ways to reduce coronavirus infection because SARS-CoV is stable at 4°C in clinical specimens for many weeks and also could survive about 2 years on stool at –80°C and for many weeks in clinical specimens at –70°C. The use of disinfectants like chlorine and sodium hypochlorite solution, decrease the SARS- CoV viability (>3 log₁₀) after 5 min the use of food preservation methods to establish coronavirus inactivation [13].

4. Conclusion

Integrated epidemiological surveillance actions adopted in conjunction with prevention measures such as:

- Implementation of good hygiene practices,
- Food handling,
- Adequate hygiene of utensils and personnel,
- Training of professionals involved in the food chain,
- Consumer education on food safety measures and
- The application of traceability systems are fundamental strategies to guarantee food safety within the scope of public health [14].

So, this overview supports the importance of water-based epidemiology monitoring of viral contamination to prevention of waterborne diseases and adopted prophylactic measures in order to mitigating the environmental risks [14]. Moreover, the implementation molecular-based tools and wastewater-based epidemiology studies to high-throughput for aquatic biomonitoring should be up to date to avoid the risk and impact on public health and aquatic environments. Novel perspectives to control of waterborne viruses has been introduced in continuous surveillance programs for ecosystems monitoring.

Compliance with ethical standards

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Disclosure of conflict of interest

There is no conflict of interest.

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