Purpose of review
The aim of the study was to provide an update on foodborne viral infections describing illness burden, the main aetiological agents (enteric viruses, hepatitis viruses and emerging and zoonotic viruses) and advances in virus detection in foods.

Recent findings
Norovirus (NoV) is the most common viral foodborne pathogen globally (125 million cases and 35,000 deaths). The role of the asymptomatic food handlers in contributing to NoV outbreaks is becoming increasingly clear, with up to one-quarter of outbreaks attributable to them. Handwashing with soap and water remains the best method for removing NoV from fingers. Risk assessment for transmission of emerging viruses through the food chain should include consideration of all means by which food could post a hazard, that is not just consumption. New technologies have demonstrated the widespread nature of viral contamination in the food chain, but this does not necessarily correlate with the risk of disease. Finally, understanding people’s knowledge and behaviour is just as important as understanding virus characteristics and epidemiology when assessing risks of foodborne transmission.

Summary
The predominant viruses transmitted through food tend to be those for which humans are the natural hosts, so that effective control measures need to prevent exposure of foods to human faeces.

Keywords
foodborne disease, gastroenteritis, hepatitis A virus, norovirus, risk assessment
30 genotypes have been described to date [7]. NoVs are highly infectious, and exposure does not lead to long-lasting protection or broad cross-protection against different genotypes. It has been suggested that genotype profiles may be useful for foodborne attribution of NoV and in recent estimates it was calculated that 14% of all NoV outbreaks may be related to the consumption of contaminated food [8].

High-risk food vehicles include fresh produce and oysters as well as transmission via symptomatic, infected food handlers. NoVs bind to Histo Blood Group Antigens (HBGAs), and differences in the expression of HBGAs are important determinants of susceptibility to NoV infection and disease. Animal NoVs also use carbohydrates as host cell binding molecules. Although HBGAs are unlikely to be the only factors mediating binding and entry of NoVs to host cells, differences in the binding of carbohydrates between animal and human NoVs may have a role in the observed host restriction. NoV binding to carbohydrates is also linked to the risk of foodborne transmission; NoVs specifically bind to HBGA-like molecules present in oysters’ guts and, more recently, specific binding of NoV-like particles to HBGA-like carbohydrates present in the cell wall of lettuce has been demonstrated [9].

The association between infected, symptomatic food handlers and the risk of cross-contamination to food is a well-established cause of outbreaks. Increasingly, however, asymptomatic, infected food handlers are emerging as important sources of foodborne NoV outbreaks [10].

NoV and sapovirus (SaV) share similar characteristics. They have similar structures, transmission routes and clinical presentations. They are both frequently detected in faecally contaminated waters and shellfish. However, there are few rigorously investigated outbreaks of SaV linked to foodborne transmission [11,12]. One important difference between them is that, unlike NoV, there is no evidence that SaVs bind to HBGAs, and no differential patterns of susceptibility to SaV infections have been identified [13]. These differences may also contribute, to some extent, to their limited foodborne transmission.

Similarly, there are relatively few foodborne outbreaks linked to rotavirus [14,15], although the virus can be found on, for example, crops [16]. The current rollout of rotavirus vaccines is likely to contribute to further reduction in the risk of contamination of foods through reduced infection and shedding. There is also limited evidence of foodborne transmission of astrovirus, which, like rotavirus, is primarily transmitted person-to-person [17,18].

There is a wide range of other viruses that are shed in faeces and so could, in theory, cause foodborne illness. For example, aichi viruses are frequently found in contaminated waters, and seroprevalence studies have demonstrated high levels of exposure to these viruses globally, although foodborne transmission has been limited primarily to the consumption of shellfish, principally in Asia. The role in human infection and disease of viruses such bocavirus, cardiovirus, cosavirus, klassevirus, picobirnavirus and torovirus is not yet established [19].

**HEPATITIS VIRUSES**

The WHO estimated that in 2010 hepatitis A virus (HAV) caused approximately 14 million cases and 28,000 deaths globally [6]. During 2013/2014 the largest ever documented foodborne HAV outbreak in Europe occurred [20]. The outbreak affected more than 1500 patients in 13 European Union/European Economic Area countries, and was associated with consumption of several different types of frozen berries. In a retrospective analysis of outbreaks in Europe over a 30-year period (1983–2013), consumption of frozen berries was increasingly associated with reported NoV and HAV outbreaks and contamination events, especially after 2003 [22].

Hepatitis E virus is increasingly recognised as a foodborne pathogen, which has been associated...
with consuming processed pork and can also be found in wild game meat and shellfish [23–27].

**EMERGING AND ZOONOTIC VIRUSES**

Several emerging viruses have posed questions about potential foodborne transmission in recent years. These include SARS coronavirus, H1N1 influenza and, currently, Zika virus. When assessing potential risks through the food chain it is important to think widely. This means not confining considerations purely to consumption of contaminated foodstuffs but also other means by which food could pose a hazard, for example through cutaneous transmission by handling meat to occupational groups like veterinary surgeons or abattoir workers, or through bodily secretions other than faeces, such as urine, saliva and (breast) milk. Often key data are lacking, and the degree of uncertainty around risk assessment is very high. Nevertheless, the process of performing a risk assessment points out important data gaps and can help to target rapid research.

There is, as yet, no direct evidence for foodborne transmission of SARS coronavirus or influenza H1N1 through food. Although there is a theoretical risk from both agents, which have the potential to be

<table>
<thead>
<tr>
<th>Virus</th>
<th>Virus family</th>
<th>Genome</th>
<th>Host</th>
<th>Symptoms</th>
<th>Main route of transmission</th>
<th>Documented frequency of foodborne transmission</th>
<th>Source of food contamination</th>
</tr>
</thead>
<tbody>
<tr>
<td>Norovirus</td>
<td>Caliciviridae</td>
<td>ssRNA</td>
<td>Human</td>
<td>Gastroenteritis</td>
<td>Faecal–oral</td>
<td>High</td>
<td>At source (faecal contamination)</td>
</tr>
<tr>
<td>Sapovirus</td>
<td>Caliciviridae</td>
<td>ssRNA</td>
<td>Human</td>
<td>Gastroenteritis</td>
<td>Faecal–oral</td>
<td>Rare</td>
<td>At source (faecal contamination)</td>
</tr>
<tr>
<td>Astrovirus</td>
<td>Astroviridae</td>
<td>ssRNA</td>
<td>Human</td>
<td>Gastroenteritis</td>
<td>Faecal–oral</td>
<td>Rare</td>
<td>At source (faecal contamination)</td>
</tr>
<tr>
<td>Aichi virus</td>
<td>Picornaviridae</td>
<td>ssRNA</td>
<td>Human</td>
<td>Gastroenteritis</td>
<td>Faecal–oral</td>
<td>Rare</td>
<td>At source (faecal contamination)</td>
</tr>
<tr>
<td>Rotavirus</td>
<td>Reoviridae</td>
<td>dsRNA</td>
<td>Human</td>
<td>Gastroenteritis</td>
<td>Faecal–oral</td>
<td>Rare</td>
<td>At source (faecal contamination)</td>
</tr>
<tr>
<td>Hepatitis A virus</td>
<td>Picornaviridae</td>
<td>ssRNA</td>
<td>Human</td>
<td>Hepatitis</td>
<td>Faecal–oral</td>
<td>Increasingly recognised</td>
<td>At source (faecal contamination)</td>
</tr>
<tr>
<td>Hepatitis E virus</td>
<td>Hepeviridae</td>
<td>ssRNA</td>
<td>Human</td>
<td>Hepatitis</td>
<td>Faecal–oral</td>
<td>Low/unknown</td>
<td>At source (faecal contamination)</td>
</tr>
</tbody>
</table>

**Table 1.** Key characteristics of foodborne viral infections
found in the food chain, the main risk is considered to be likely to come from direct contact with infected animals [19].

Infective Zika virus particles have been demonstrated to be present in breast milk with high viral loads [28]. As vertical transmission via breastfeeding for other arboviruses (dengue, West Nile and Yellow Fever) has been suggested previously, there needs to be very close scrutiny of the potential for transmission of Zika infection via this route.

It is thought that zoonotic viruses like simian herpes viruses, simian immunodeficiency virus and simian foamy viruses can enter the food chain through the butchering of wildlife for bush meat [19,29]. To underline this, the index case in the 2014/2015 Ebola epidemic in West Africa was thought to be an 18-month-old child in Guinea who had contracted the disease through eating or handling bush meat [21]. In general, butchering infected animals is considered the most likely high-risk activity because the viruses are possibly inactivated by cooking [19].

Raw date palm sap has been shown to be the contaminated food vehicle in two outbreaks of Nipah virus (NiV) infection in Bangladesh [30,31]. These outbreaks demonstrate that it is insufficient to consider only virus biology and epidemiology. In a very important follow-up study, researchers who investigated these outbreaks surveyed the date palm sap consumption habits of rural residents and the factors associated with consuming date palm sap [32**]. They showed that survey respondents’ knowledge of NiV was low, that they did not understand the risks of NiV, and that they were likely to drink sap when it was available [32**]. This shows the critical importance of understanding people’s knowledge and behaviour when assessing risks of foodborne transmission.

TECHNOLOGICAL ADVANCES IN ASSESSING THE RISK OF FOODBORNE TRANSMISSION

Detecting enteric viruses in food relies on molecular methods (RT-PCR principally), which offer sensitive, rapid and specific identification of the presence of the pathogen. Various pre-treatments have been optimised for the successful extraction of virus nucleic acid from food commodities, primarily shellfish, soft berry fruits and salad greens (including a standardised method: ISO/TS 15216-1:2013; Horizontal method for determination of HAV and NoV in food using real-time RT-PCR) [33]. Methods for detecting NoV in composite foods have also been developed, which are important, particularly in circumstances in which food contamination occurs via the food handler [34]. However, the biggest challenge remains correlating the detection of viral nucleic acid with infectivity. Various methods have been developed to assess NoV capsid integrity through measuring the degradation of nucleic acid following heat treatment or chemical treatment [35–37] or the ability to bind HBGA [38]. However, demonstrating that viral nucleic acid is protected by a capsid, or that HBGA binding persists, does not necessarily correlate with the ability of the virus to establish infection. For example, inactivating methods like ultraviolet treatment, or the presence of molecules such as antibodies that can potentially neutralise infectivity, do not result in exposure of the nucleic acid. Also, HBGA-like molecules present in bacteria may potentially mask binding assays.

Caliciviruses other than NoVs have also been used as model systems to study the stability of human NoV and the virucidal effects of disinfectants [39–41]. However, these viruses might not model the basic properties of human NoV accurately, and are not ideal substitutes. Furthermore, data from a recent systematic results review suggest that, based on comparative RT-qPCR data, human NoV is likely to be more resistant to typical food and environmental control measures when compared with cultivable surrogate viruses [42].

Recently, a human NoV in-vitro cell culture system has been developed using B cells and an in-vivo immunocompromised mouse model has been established that supports human NoV replication [43**]. These exciting advances provide, for the first time, the tools that can potentially lead to our understanding of many aspects of human NoV. These include characterising the virus life cycle at the molecular level, developing therapeutic and prophylactic compounds, improving candidate vaccines, assessing the viability and infectivity of viruses found in foods, and helping to assess risks and develop interventions. Despite their significance, neither of these systems is currently developed in a way that allows their widespread use and, at present, low levels of virus replication remain a major challenge.

UNDERSTANDING THE ROLE OF THE MICROBIOME

In the last few years, the role of bacterial flora on enteric virus infections has been an increasing focus of research [44**,45]. In fact, the human NoV B-cell culture model is facilitated by commensal bacteria expressing HBGA-like antigens [43**,46]. From a food safety perspective, binding of HBGA-expressing bacteria may also protect NoV during food processing treatments [47*], and therefore developing or
implementing NoV control measures may also require careful consideration of the presence and risks posed by the presence of certain bacterial species.

**CONTROLLING THE SPREAD OF FOODBORNE VIRUSES**

Viruses associated with transmission via the food chain tend to be those for which humans are the natural hosts, so that effective control measures need to be aimed at preventing exposure of foods to human faeces (Fig. 1). Vaccines against HAV and rotavirus have already been implemented to good effect, and there are now several candidate vaccines for NoV although none is yet close to market. Despite the importance of foodborne transmission of NoV, the predominant mode of spread is person-to-person. Should an effective vaccine become available, one of the challenges will be to establish which population groups should be vaccinated to interrupt transmission most effectively. Similarly, it will be important to understand how broadly reactive any future candidate vaccines might be against different genotypes and emerging variants.

**CONCLUSIONS**

Foodborne viruses cause considerable morbidity and mortality. Controlling them still means relying on good personal and food hygiene, good agricultural practice, post-harvest controls and effective management of human sewage to prevent onward transmission. Handwashing with soap and water remains superior to using alcohol-based hand disinfectants for removing NoV from fingers [48*]. However, hand sanitiser formulations supplemented with urea and citric acid may be more effective against nonenveloped viruses, including NoV [49]. When considering the risk posed by food and the food chain on the transmission of emerging viruses, activities and behaviours beyond food consumption need to be assessed.

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Disclaimer: The views expressed are those of the author(s) and not necessarily those of the NHS, the NIHR, the Department of Health or Public Health England.

Conflicts of interest
There are no conflicts of interest.

REFERENCES AND RECOMMENDED READING

Papers of particular interest, published within the annual period of review, have been highlighted as:
* of special interest
** of outstanding interest


A landmark report documenting, for the first time, the global impact of food-related illness.


An outstanding synthesis of a very wide variety of data to develop global and regional estimates of the burden of foodborne disease covering 31 infectious and chemical hazards.


The first published complete genome sequence of a genogroup V genotype 2 sapovirus strain from a suspected foodborne gastroenteritis outbreak identified using metagenomic sequencing.


33. A very important study demonstrating the crucial importance of people’s knowledge and behaviour when trying to understand exposure to, and hazards from, foodborne pathogens.


Description of a method which may serve as a proxy for discriminating viable versus nonviable noroviruses with potential application to environmental and food surfaces.