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VIRUSES IN FOOD: SCIENTIFIC ADVICE TO SUPPORT RISK MANAGEMENT ACTIVITIES

MEETING REPORT

World Health Organization

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Declarations of interest

All participants completed a Declaration of Interest form in advance of the meeting. None was considered to present any potential conflict of interest.

FOREWORD

Members of the Food and Agriculture Organization of the United Nations (FAO) and of the World Health Organization (WHO) have expressed concern regarding the level of safety of food at both national and international level. Increasing foodborne disease incidence over recent decades seems, in many countries, to be related to an increase in disease caused by micro-organisms in food. This concern has been voiced in meetings of the Governing Bodies of both Organizations and in the Codex Alimentarius Commission. It is not easy to decide whether the suggested increase is real or an artefact of changes in other areas, such as improved disease surveillance or better detection methods for microorganisms in patients or foods. However, the important issue is whether new tools or revised and improved actions can contribute to our ability to lower the disease burden and provide safer food. Fortunately, new tools that can facilitate actions seem to be on their way.

Over the past decade, risk analysis—a process consisting of risk assessment, risk management and risk communication—has emerged as a structured model for improving our food control systems, with the objectives of producing safer food, reducing the number of food-borne illnesses and facilitating domestic and international trade in food. Furthermore, we are moving towards a more holistic approach to food safety, where the entire food chain needs to be considered in efforts to produce safer food.

As with any model, tools are needed for the implementation of the risk analysis paradigm. Risk assessment is the science-based component of risk analysis. Science today provides us with in-depth information on life in the world we live in. It has allowed us to accumulate a wealth of knowledge on microscopic organisms, their growth, survival and death, even their genetic make-up. It has given us an understanding of food production, processing and preservation, and of the link between the microscopic and the macroscopic world, and how we can benefit as well as suffer from these microorganisms. Risk assessment provides us with a framework for organizing these data and information and gaining a better understanding of the interaction between microorganisms, foods and human illness. It provides us with the ability to estimate the risk to human health from specific microorganisms in foods and gives us a tool with which we can compare and evaluate different scenarios, as well as identify the types of data necessary for estimating and optimizing mitigating interventions.

Microbiological risk assessment (MRA) can be considered as a tool that can be used in the management of the risks posed by foodborne pathogens, including the elaboration of standards for food in international trade. However, undertaking an MRA, particularly quantitative MRA, is recognized as a resource-intensive task requiring a multidisciplinary approach. Nevertheless, foodborne illness is one of the most widespread public health problems, creating social and economic burdens as well as human suffering., it is a concern that all countries need to address. As risk assessment can also be used to justify the introduction of more stringent standards for imported foods, a knowledge of MRA is important for trade purposes, and there is a need to provide countries with the tools for understanding and, if possible, undertaking MRA. This need, combined with that of the Codex Alimentarius for risk-based scientific advice, led FAO and WHO to undertake a programme of activities on MRA at international level.

The Nutrition and Consumer Protection Division (FAO) and the Department of Food Safety, Zoonoses and Foodborne Diseases (WHO) are the lead units responsible for this initiative. The two groups have worked together to develop MRA at international level for application at both

national and international level. This work has been greatly facilitated by the contribution of people from around the world with expertise in microbiology, mathematical modelling, epidemiology and food technology, to name but a few.

This Microbiological Risk Assessment series provides a range of data and information to those who need to understand or undertake MRA. It comprises risk assessments of particular pathogen–commodity combinations, interpretative summaries of the risk assessments, guidelines for undertaking and using risk assessment, and reports addressing other pertinent aspects of MRA.

We hope that this series will provide a greater insight into MRA, how it is undertaken and how it can be used. We strongly believe that this is an area that should be developed in the international sphere, and the work to date clearly indicates that an international approach and early agreement in this area will strengthen the future potential for use of this tool in all parts of the world, as well as in international standard setting. We would welcome comments and feedback on any of the documents within this series so that we can endeavour to provide member countries, the Codex Alimentarius and other users of this material with the information they need to use risk-based tools, with the ultimate objective of ensuring that safe food is available for all consumers.

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ABBREVIATIONS

CCFH	Codex Committee on Food Hygiene
CoV	Coronavirus
DNA	Deoxyribonucleic acid
FAO	Food and Agriculture Organization of the United Nations
FBVE	Foodborne Viruses in Europe [network]
GII.4	Genogroup II.4 [strains of NoV]
GAP	Good agricultural practice/Good aquaculture practice
GHP	Good hygiene practice
GMP	Good manufacturing practice
HACCP	Hazard analysis and critical control point [system]
HAV	Hepatitis A virus
HEV	Hepatitis E virus
HRV	Human Rotavirus
IID	Infectious intestinal disease
JEMRA	Joint FAO/WHO Expert Meetings on Microbiological Risk Assessment
NASBA	Nucleic acid sequence-based amplification
NoV	Norovirus
PCR	Polymerase chain reaction
QMRA	Quantitative Microbiological Risk Assessment
RASFF	[European] Rapid Alert System for Food and Feed
RIVM	National Institute for Public Health and the Environment [the Netherlands}
RNA	Ribonucleic acid
RT-PCR	Reverse transcriptase-polymerase chain reaction
SARS	Severe Acute Respiratory Syndrome
SARS-CoV	Severe Acute Respiratory Syndrome-causing Coronavirus
ssDNA	Single stranded Deoxyribonucleic acid
ssRNA	Single stranded Ribonucleic acid
VWA	Food and Consumer Product Safety Authority [the Netherlands]
WHO	World Health Organization
CI	Confidence Interval

EXECUTIVE SUMMARY

This report draws attention to the threat of viruses as a risk to public health when they are present in food. Viruses require special attention because they behave differently from bacteria, and because currently used control measures typically either have not been validated and there is not a good understanding of their efficacy towards viruses, or are not effective in controlling virus contamination. Data from recent studies have shown that foodborne viral infections are very common in many parts of the world despite the measures already in place to reduce bacterial contamination.

While the meeting concluded that viruses play a major role in the burden of infectious intestinal disease, it was noted that under-reporting, the lack of surveillance systems and the inability of existing systems to determine the proportion of disease that is transmitted by foodborne routes relative to other common routes make it difficult to estimate the proportion of viral illness that is foodborne. Nevertheless, the meeting sought to prioritize the virus-commodity combinations of greatest public health concern. Prioritization was done according to the following criteria: disease severity; incidence/prevalence; probability of exposure; trade impact; public health cost; and ability to control foodborne infections. The meeting concluded that the virus-commodity combinations of highest priority are Noroviruses and hepatitis A virus in shellfish, fresh produce and prepared foods. This list is based on current knowledge, which is acknowledged as being incomplete. However, the establishment of these combinations is important as we seek to develop mitigation and intervention strategies.

The characteristics of foodborne viruses present new challenges for risk managers. It is important to note that there are clear differences in morphology, infectivity, persistence and epidemiology between viruses and the common foodborne bacteria. Control of viral hazards often requires measures different to those typically employed to combat bacterial hazards. Thus, an important consideration for risk managers is that current food hygiene guidelines, which have been optimized for prevention of bacterial infections, may not be effective for viruses. Another point for consideration is that mitigation of one virus would probably help in preventing other viruses, as they often have a common source.

In terms of virus detection, there has been much progress in recent years and it can be concluded that well established methods to detect enteric viruses in contaminated foods exist and are used in many countries. However, there is a lack of harmonization among methods. Although there is some work ongoing to try and address this, harmonization efforts are primarily focused on virus detection in bivalve molluscs, while additional efforts aimed at other foods, particularly fresh produce and prepared foods, are needed.

The meeting identified three major routes of viral contamination of foods: i) human sewage and faeces; ii) infected food handlers; and iii) animals for zoonotic viruses. However, large-scale outbreaks are often the result of a combination of several transmission routes. Thus the meeting recommended that intervention strategies should be focused on the priority virus-commodity combinations. Where possible, these combinations should be reviewed for a specific region using the specified criteria, and revised as new information and data become available.

With regard to risk management, the meeting made a number of recommendations:

- The use of routine sewage monitoring to screen human transmission patterns and identify the potential for a greater likelihood of contamination during primary production should be evaluated.

- Emerging viruses should be monitored, particularly when new problems arise, in an effort to assess the potential for foodborne transmission. The specific research needs to address this question should be defined at the early stages of their emergence.

- New and existing pre- and post-harvest processing technologies should be assessed for their viricidal potential in high-risk food products. Conducting an analysis in an effort to systematically understand virus persistence and inactivation in different food commodities is recommended.

- Virus-commodity-specific guidance would assist risk managers in better addressing the issue of foodborne virus contamination and in anticipating measures needed in the event of outbreaks.

- Food producers and risk managers must be aware of the potential for outbreaks. In the event of an outbreak, they should understand the need for complete cooperation with investigators in an effort to identify effective corrective actions and reduce the public health impact of the event.

- To adequately control foodborne viral infections it will be necessary to: heighten awareness of the potential for transmission by infected food handlers; optimize and standardize methods for detection of foodborne viruses and foodborne disease outbreaks; enhance laboratory-based surveillance to detect large common-source outbreaks at an early stage; develop quality control measures specifically for virus control; take into consideration the role of viruses as foodborne pathogens in the development of HACCP plans; inform consumers of the risks presented by foodborne viruses; and better understand transmission and risk through the application of risk assessment.

MEETING REPORT

1. INTRODUCTION

1.1 Background

In recent years, viruses have been increasingly recognized as important causes of foodborne disease. One category of implicated foods is those that are minimally processed, such as bivalve molluscs and fresh produce. These are typically contaminated with viruses in the primary production environment. In addition, many of the documented outbreaks of foodborne viral illness have been linked to contamination of prepared, ready-to-eat food by an infected food handler.

While in many countries viruses are now considered to be an extremely common cause of foodborne illness, they are rarely diagnosed, as the analytical and diagnostic tools for such viruses are not widely available. However, much progress has been made in recent years in terms of the methodology available for detection and identification of viruses in both food and clinical samples. Such developments should contribute towards improving the assessment of the actual burden of foodborne disease linked to viruses, as well as improving strategies for the prevention and control of virus contamination in foods and the associated risks.

Viruses can be passed on to humans in different ways, but the major foodborne viruses are those that infect via the gastrointestinal tract and are excreted in faeces and, in some cases, in vomitus. Noroviruses (NoV) are the most common cause of foodborne viral gastroenteritis worldwide, and Hepatitis A virus (HAV), which can also be transmitted by foodborne routes, continues to pose an international health threat. Rotaviruses, Enteroviruses and Astroviruses are also important, albeit to a lesser extent (Koopmans and Duizer, 2004). Common symptoms of viral gastroenteritis include vomiting and diarrhoea. Asymptomatic infections are common. While contaminated food has been clearly implicated in viral infections in humans, the proportion of infections that can be attributed to the consumption of contaminated food is not known.

At the international level, the Codex Alimentarius Commission (the international food standards setting agency) is considering the types of risk management tools that it could develop to assist countries in their efforts to protect consumer health from foodborne viral illness. In considering its priorities for future work, the 38th Session of the Codex Committee on Food Hygiene (CCFH) agreed that viruses were an important food safety concern. However, at that time the committee considered that it did not have an adequate scientific understanding of the field in order to make an informed decision on the priority virus-commodity combinations on which future work should focus. In order to gain better insight into this subject and to facilitate the decision-making process, the Committee requested FAO/WHO to convene an expert meeting on "Viruses in Food", the output of which would be considered by the 39th Session of the Committee, in 2007.

1.2 Objectives

FAO and WHO convened an Expert Meeting, on 21–24 May 2007, in Bilthoven, The Netherlands, in collaboration with the Dutch National Institute for Public Health and the Environment (RIVM) and the Dutch Food and Consumer Product Safety Authority (VWA),

to review the current state of knowledge on viruses in foods and their public health and trade impacts. The objective was to provide advice and guidance on the virus-commodity combinations of particular concern, the issues that need to be addressed by risk managers, and the options available to them. In addition, the experts were asked to identify further scientific information needed to undertake risk assessment, and to provide scientific advice on managing the risks associated with viruses in foods.

The Terms of Reference provided by the CCFH to FAO and WHO for this work were:

- To review the current state of knowledge on viruses in food and their public health and trade impacts;

- To review availability, feasibility and the practical consequences of using analytical methods for detecting viruses; and

- To review existing risk profiles (including the state of knowledge on current or future risk management options) and other relevant information pertinent to the evaluation of risks associated with viruses in food.

In order to fulfil the above terms of reference, the specific objectives of the expert meeting were:

- To provide the basis for the identification and selection of viruses and product combinations to be addressed in future risk management work;

- To identify the key issues currently faced by risk managers in terms of addressing the problems associated with viruses in food;

- To provide guidance on the different options for management strategies that will be proposed by CCFH and the impact of possible options considered by CCFH in the development of a risk management document;

- To provide guidance on the scientific advice needed for such activities as well as a suggested road map for future work; and

- To identify the data and information needed (data gaps) for risk assessment activities.

This would provide guidance for research needs designed for and targeted to the provision of scientific advice.

1.3 Scope

This meeting considered viruses that are or have the potential to be transmitted to humans via food. Water was considered in the context of being used as an ingredient in food (e.g. in reconstituted milk), in food production (e.g. irrigation water), processing, transport (e.g. packing ice) or preparation. Thus, virus transmission to humans via direct consumption of drinking water was not within the scope of this meeting.

1.4 Introduction to viruses

Viruses are very small microorganisms, ranging in size from 0.02 to 0.4 micrometres in diameter, whereas bacteria generally range in size from 0.5 to 5 micrometres. In addition to size, other (structural and biological) properties of viruses may vary greatly, both among viruses and between viruses and bacteria. In contrast to bacteria, which are free living, viruses use the host cells to replicate. Viruses are diverse; for example, the virus genome can be DNA or RNA, in

double- or single-stranded form. The virus particle can vary from a relatively simple structure consisting of a non-enveloped genome with a single protein coat, as is the case for most foodborne viruses, to a rather complex structure consisting of a segmented genome, encapsulated in a complex protein capsid and enveloped by a membrane. The structure of the virus particle is linked to the environmental resistance of the virus, with the more complex structure particles being less resistant.

Viruses cause a wide range of diseases in plants, animals and humans. Individual viruses cause specific patterns of illness, as each group of viruses has its own typical host range and cell preference (tropism). Viruses can be transmitted in different ways. For instance, they can be transmitted via the respiratory route, as might occur by droplets (aerosols) generated when an infected person coughs, or by the faecal-oral route which occurs when faecal material from an infected individual is inadvertently consumed. Virus transmission by sexual intercourse, contact with contaminated blood products, contact with infected animals (zoonotic viruses) or via vectors such as mosquitoes or ticks (arthropod-borne (Arbo-) viruses) have also been documented.

The viruses most frequently involved in foodborne infections are NoV and HAV, but other viruses such as Human Rotavirus (HRV), Hepatitis E virus (HEV), Astrovirus, Aichi virus, Sapovirus, Enterovirus, Coronaviruses, Parvovirus and Adenovirus can also be transmitted by food and anecdotal evidence suggests the list of foodborne viruses may be even longer. Based on the symptoms of infection, these viruses can be grouped into those that cause gastroenteritis (NoV, HRV, Astroviruses, Aichi virus Adenoviruses and Sapoviruses), enterically transmitted hepatitis (caused by HAV and HEV, which migrate to the liver, where they manifest disease), and a third group which replicates in the human intestine, but only cause illness after they migrate to other organs such as the central nervous system (Enterovirus). All of these viruses are shed in human faeces and are infectious for humans when ingested via the oral route. Most of these viruses are small spheres (particles), with a single-stranded positive-sense RNA genome and without an envelope; exceptions include the Rotaviruses, which are double-stranded RNA; Adenoviruses and Parvoviruses, which are DNA viruses; and the Coronaviruses, which contain an envelope. In general these viruses are persistent in the environment and are able to resist (mild) food production processes routinely used to inactivate or control bacterial pathogens in contaminated foods. In addition, some viruses may occasionally be transmitted via food, although their typical mode of transmission is different, as has been documented for Severe Acute Respiratory Syndrome (SARS)-causing Coronavirus (SARS-CoV) and Highly Pathogenic Avian Influenza (HPAI) virus.

Some noteworthy characteristics of foodborne viruses and the associated infections and illnesses are listed below.

- Viruses need to enter living cells in order to be able to replicate. Unlike bacteria, they will never replicate in food. Consequently, viruses will never cause deterioration of the product and the organoleptic properties of the food will not change due to viral contamination.

- Only a few viral/infectious particles (1 to 100) are needed to cause infection and produce illness.

- High numbers of viral particles are shed in the stools of infected persons (e.g. exceeding 10^7 particles per gram of stool in cases of clinical disease, with up to 10^{11} particles per gram of stool in the case of HRV).

- Viruses transmitted by the faecal-oral route have been shown to be hardy and to persist in the environment. Most foodborne viruses do not have an envelope and are therefore quite stable outside of the host, and demonstrate resistance to extremes of pH (acid and alkaline), drying, radiation, etc.

- The transmission of zoonotic viruses via food, as is common for many bacterial pathogens, e.g. *Salmonella* and *Campylobacter* spp., is uncommon for viruses, with the exception of HEV.

- NoV and HAV are very infectious and person-to-person spread is the most common transmission route. Secondary spread of these viruses after introduction by, for example, foodborne contamination, is common and often results in larger prolonged outbreaks. Therefore, outbreaks caused by foodborne introduction of NoV or HAV may not be recognized by the point-source profile characteristic of many bacterial foodborne outbreaks. In addition, foodborne contamination may be the result of infected food handlers who unknowingly transmit their infections to food. Also, viruses frequently cause extensive secondary spread, which is less common for the well known bacterial pathogens such as *Salmonella* and *Campylobacter*.

These characteristics of foodborne viruses present new challenges for risk managers. It is important to note that there are clear differences in morphology, infectivity, persistence and epidemiology between viruses and the common foodborne bacteria. Control of viral hazards often requires measures different to those typically employed to combat bacterial hazards. Thus, an important consideration for risk managers is that current food hygiene guidelines, which have been optimized for prevention of bacterial infections, may not be effective for viruses.

2. FOODBORNE VIRAL ILLNESS – BURDEN OF DISEASE AND VIRUSES OF CONCERN

2.1 Identification of foodborne viruses of main concern

Virology is a complex world. Viruses belonging to at least 10 families have been associated with foodborne illness, causing various diseases (Table 1). These range from self-limiting diarrhoeal disease to severe liver disease leading to hospitalization. The best estimates of the burden of foodborne disease associated with viruses are available for viruses causing gastroenteritis (also known as "gastric flu", winter vomiting disease, diarrhoea and vomiting, and infectious intestinal diseases [IID])

Table 1. Viruses that are, or have the potential to be, transmitted via food and their site of infection in the human body.

Site of Infection	Virus
Neural tissue and nervous system	Enterovirus, Nipah virus, Poliovirus*, Parechovirus*, Tick-borne encephalitis virus*
Respiratory system	HPAI-H5N1, SARS-CoV
Liver	HAV, HEV
Intestinal system	NoV, HRV, Sapovirus, Astrovirus, Adenovirus, Aichi virus

Note: Enteric viruses can also be airborne, bloodborne (including vector-borne) or sexually transmitted.
* While these viruses have the potential to be transmitted via food they were not considered further by the meeting.

However, while all the viruses listed in Table 1 have the potential to cause a foodborne illness, the extent to which they lead to a foodborne disease, the severity of that disease and the level of information available to confirm this varies substantially. Therefore, in order to identify viruses of greatest concern from a food safety perspective, a set of criteria was established. These criteria indicate that the viruses:

- Cause a high incidence of foodborne viral disease, based on currently available data.

- Cause severe disease including significant mortality worldwide.

- Have the potential for foodborne transmission and to pose a significant threat to public health.

Each virus identified in Table 1 was evaluated against these criteria. This evaluation took note of all currently available scientific information for these viruses, with specific emphasis on foodborne transmission and the severity of the illness. In instances where such information was limited, as is the case with emerging viruses, primary consideration was given to the potential of the virus to cause foodborne disease. The viruses were divided into two groups according to these criteria: group 1 viruses are those that met one or more of the aforementioned criteria, and group 2 viruses are those that met none of the criteria. Group 1 viruses were considered to be a priority in terms of foodborne viral disease, while group 2 were not considered to be a priority in terms of food safety at the current time. No attempt was made to rank the viruses within

group 1 as this is likely to vary from country to country and will be dependent on the level of data available. As more information becomes available on these and other viruses, it will be necessary to review this evaluation. The outcome of this evaluation is presented in Table 2.

Table 2. Evaluation of potential foodborne viruses against the three pre-defined criteria to identify the viruses of main concern from a food safety perspective.

Clinical syndrome	Priority group*	Basis of priority ranking (based on current level of knowledge)
Gastroenteritis		
Norovirus	1	High incidence, most common foodborne virus
Group A Rotavirus	1	Sometimes foodborne, severe infection in infants/children
Group B, C Rotavirus	2	
Enteric Adenovirus	2	
Sapovirus	2	
Astrovirus	2	
Aichi virus	2	
Hepatitis		
Hepatitis A	1	Sometimes foodborne, severe infection
Hepatitis E	1	Potential public health impact, emerging infection in developed countries, plausible foodborne transmission as potential foodborne zoonoses from pigs
Neurological infection		
Enterovirus	2	
Nipah virus	1	Bat virus, can cause emerging infections in pigs, humans, foodborne transmission
Respiratory infection		
HPAI virus H5N1	1	Potential public health impact, emerging infection, plausible foodborne transmission but direct exposure to infected chickens main risk factor
SARS Coronavirus	1	Potential public health impact, emerging infection, foodborne transmission

NOTES: * Group 1 viruses met one or more of the pre-defined criteria. Group 2 viruses met none of the pre-defined criteria.

2.1.1 Hepatitis A (HAV)

The incidence of HAV infection varies considerably among and within countries. In most developing countries, where hepatitis A infection is endemic, the majority of persons are infected in early childhood, when the infection is generally asymptomatic. Virtually all adults are immune. In developed countries, however, HAV infections are less common as a result of improved standards of living. Very few persons are infected in early childhood, and the majority of adults remain susceptible to infection by HAV. Later in life, HAV infection may result in a more severe disease outcome. As a result, the potential risk of outbreaks of HAV is increased in these regions (Koopmans and Duizer, 2004; Pintó and Sáiz, 2007).

2.1.2 Norovirus (NoV)

NoV infections occur all year round, and cause illness in people of all ages. Illness overall is relatively mild, but more severe illness and death occurs in risk groups such as the elderly or people with underlying disease. Clear seasonal peaks are observed when looking at reported outbreaks, but these are particularly associated with healthcare infections rather than foodborne infections (these occur in winter in Europe, Australia, New Zealand, Japan and the United States of America). Where available, data suggest a dominant role for NoV in outbreaks of foodborne illness, hence the ranking in Table 2. Foodborne NoV outbreaks are detected year-round. They have been associated with a broad range of food items, but three categories are currently recognized: (i) outbreaks caused by infected food handlers; (ii) outbreaks due to contaminated bivalve molluscs; and (iii) outbreaks due to contaminated produce (berries, green onions).

2.1.3 Human Rotavirus (HRV)

HRV are a leading cause of viral gastroenteritis in infants and children worldwide, causing a severe dehydrating illness. In developing countries, HRV diarrhoea is an important cause of death in young children as a result of the rapid dehydration caused by production of a viral toxin that requires aggressive treatment. The primary mode of transmission for HRV, worldwide, is person-to-person spread, but in areas with poor hygienic situations waterborne and foodborne spread are likely to play a role.

2.1.4 Hepatitis E virus (HEV)

HEV is long known as an endemic disease in areas with poor hygienic conditions, causing acute self-limiting hepatitis. In pregnant women, illness is often severe, with a high risk of mortality. HEV is recognized as a major cause of viral hepatitis in humans in developing countries. Transmission in high endemic regions is generally via faecally contaminated water and large outbreaks have been documented. HEV infection has been considered a travel-related disease in developed countries. However, there is now increasing evidence of locally acquired HEV infections in humans in these countries. Recently, a variant of HEV discovered in pigs worldwide has been linked to cases of HEV infections in humans without a history of foreign travel. Foodborne transmission through consumption of raw or undercooked meat has been documented, but it is unclear how important this mode of transmission is in the epidemiology. The presence of HEV RNA and infectious HEV has also been shown in commercially available pig livers in Japan, the USA and the Netherlands (Yazaki et al., 2003; Feagins et al., 2007; Rutjes et al., 2007).

2.1.5 Emerging viruses (Nipah virus, Highly Pathogenic Avian Influenza (HPAI) virus, SARS-causing Coronavirus)

The potential for foodborne transmission is a concern with every new emerging infection, and ruling out such concerns is often difficult. Although initially considered to be unlikely, faecal-oral spread in particular conditions has been proven for the primarily respiratory pathogens Nipah virus, HPAI virus and SARS-CoV. Infectious avian influenza virus has been cultured from frozen exported meat, raising questions about the possible dissemination of such viruses via the food chain. Although this mode of spread is considered to be rare, the potential consequences of such spread dictated that such viruses be considered by the meeting.

2.2 Estimating the burden of foodborne viral illness

Estimating the global burden of foodborne viral illness requires a global overview of the incidence of such illness. Figure 1 provides an overview of current knowledge in this regard, and clearly indicates the data gaps and limitations faced.
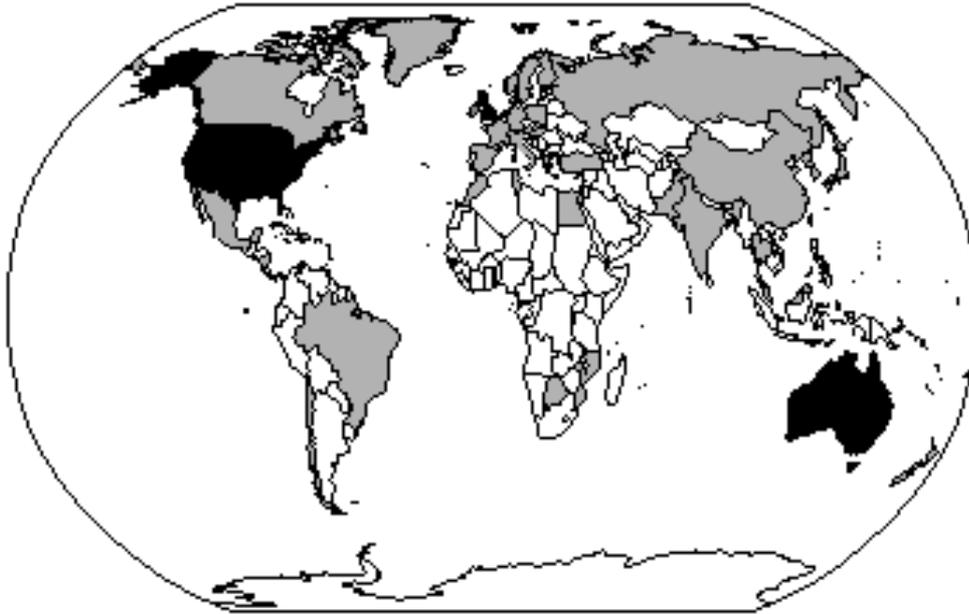
Figure 1. Global overview of the availability of data on the incidence of foodborne viral illness. Note: The background information on which the overview is based is presented in Annex 1.

KEY: ■ Population-based estimates for foodborne viral illness
■ Published studies among groups within population related to food and/or anecdotal outbreak data
□ No data available or unknown, or data not yet identified in the literature

In contrast to many of the diseases caused by foodborne bacteria, determining the incidence of foodborne viral illness is difficult, in part because foodborne viruses of concern are also spread efficiently from person-to-person, with the exception of HEV. Therefore, in addition to incidence figures, estimates of the proportion of all illness attributed to food consumption are needed.

In many, perhaps most, countries epidemiological surveillance systems for the most common of the foodborne viruses, NoV, simply do not exist. However, even where available, the data are often insufficient to reliably estimate the fraction of illness that is foodborne. The high rate of secondary spread of viruses is a further complication in obtaining reliable estimates of the proportion of viral illness that can be attributed to foodborne contamination.

The epidemiological surveillance data that is currently available severely underestimates the incidence of foodborne viral diseases. This was well illustrated by an infectious intestinal

diseases study (IID) undertaken in the United Kingdom to determine the population incidence of IID. This showed that routine surveillance in the United Kingdom only detected 1 in 1562 Norovirus infections (Wheeler et al., 1999). There are a number of reasons for this, including the following: NoV causes a sporadic and self-limiting disease for which medical treatment is frequently not sought; clinical diagnostic methods are lacking; and there is a lack of thorough investigation of outbreaks. To obtain such data, specific population-based studies are needed. Since such studies are costly, few have been conducted. Furthermore there are almost no data available on virus prevalence in food on the market. Thus, there are insufficient data to reliably estimate the fraction of illness that is foodborne. A few, specific population-based studies have been conducted to demonstrate the burden of enteric pathogens in the community. These are summarized in Table 3.

Such studies have produced estimates of the incidence of viral disease, which vary widely when compared. The currently available estimates of foodborne illness (Table 3) all make assumptions and use extrapolation from different data sources. Nevertheless, all essentially conclude that viruses are an important cause of foodborne illness. Estimates of the proportion of viral illness attributed to food are in the range of a few percent (around 5%) for HAV to 12–47% for NoV. This translates to estimated numbers of foodborne viral illness cases ranging from approximately 13 000 per million to 30 000 per million persons. Telephone surveys in the USA and Australia have also shown that such illness is common. No such data are available from developing countries, but reports from the literature suggest that foodborne viral illness occurs worldwide.

Table 3. Available estimates for burden of foodborne illness attributed to virus contamination of food. This table summarizes population-based estimates for foodborne viral illness. Note that different approaches were taken in each of the studies; it is therefore not possible to make a direct comparison between the outputs of each study.

Country	Population size (approx.)	Incidence (range/95%CI)				Burden of viral illness	Source
		Viral infections ($\times 10^3$)	Bacterial infections ($\times 10^3$)	Bacterial Intoxications ($\times 10^3$)	Parasitic infections ($\times 10^3$)		
USA[1]	300 million	9200	3715	460	357	1 in 33	Mead et al., 1999
Australia	20 million	470 (95%CI 210–740)	886 (95%CI 590–1310)	64 (0-86)	66 (18-114)	1 in 43	Hall et al., 2005
Netherlands	16 million	90 (range 50–130)	283 (range 82–146)	114 (range 35–236)	25 (range 0–50)	1 in 178	DeWit et al., 2003; Kreijl et al., 2006
UK[2]	60 million	77 (range 70–84)	659 (510–807)	221 (range 98–345)	4 (range 4–5)	1 in 780	Adak, Long and O'Brien, 2002
New Zealand	4 million	17	86	15	Not estimated		Lake et al., 2000
Japan	126 million	13.5 (95%CI 3.4-23.6)	12.7 (95%CI 8.8–16.6)	1.8 (95%CI 1.4–2.2)	No data available	1 in 9333	Report from Ministry of Health, Welfare and Labour

Notes: (1) No range or confidence interval was reported, and paper was based on rather crude estimates and extrapolations. (2) Range was based on numbers reported in 2 investigated years.

Almost no information is available for rates of hospitalization or death associated with these agents. Estimates provided by Mead et al. (1999) suggested that, in the USA, two-thirds of all foodborne illnesses, one-third of hospitalizations for foodborne disease and 7 percent of deaths from foodborne disease were viral, predominantly NoV. A recent study in The Netherlands suggests that NoV deaths in the elderly have been severely underestimated, and more robust estimates are needed for other parts of the world (van Asten et al., paper submitted). A recent study to estimate the burden of foodborne disease for New Zealand ranked NoV among the top three causes of foodborne disease in the country (Cressy & Lake, 2007).

Figure 1, which illustrates data availability, exemplifies the limitations in attempting to provide a global perspective of foodborne viral illness. As a result, the meeting concluded that there are insufficient data from developing countries to determine whether the observations from elsewhere can be considered representative of the global situation. Targeted studies of viral gastroenteritis across the world have confirmed that NoV are also a significant cause of illness among developing country populations, and that outbreaks may occur. It remains to be seen if the relative scarcity of data on outbreaks from these regions is due to lack of data or whether they reflect differences in their epidemiology.

2.3 Data from outbreak reporting

Outbreaks of viral foodborne disease have occurred in all parts of the world where studies have been conducted. However, data for developing countries are scarce, with the exception of studies on HRV infection in children. It is likely that many cases of disease also occur sporadically, although there are virtually no data to quantify the degree of sporadic transmission.

NoV are currently being extensively studied and knowledge on this group of viruses is rapidly expanding. Rates of reported NoV outbreaks in Europe, for example, range from <1 to 20 per million persons per year. The foodborne proportion of these outbreaks ranges from 1% to 69%, reflecting differences in the focus of the surveillance. A key point to recognize, however, is that surveillance systems across the world differ greatly and therefore a comparison of reported rates of outbreaks between countries at present is of limited value. A more standardized approach would contribute significantly to our understanding of the scale of the problem.

The use of molecular typing techniques for NoV has contributed to a deeper understanding of their epidemiology. Overall trends in NoV reporting show the dominance of genogroup II.4 (GII.4) strains, particularly in healthcare settings. GII.4 NoV seem to rapidly evolve and replace each other in a manner similar to the influenza virus. There are indications of increased virulence and impact of the new variants, including higher mortality rates, which may even cause fatal infections. A global comparison of trends in the epidemiology of GII.4 is currently underway.

Outbreaks associated with non-GII.4 strains show less seasonality. The same is observed for foodborne outbreaks, i.e. they are observed year-round. When comparing foodborne outbreaks with outbreaks in health care settings, a wider diversity of NoV stains is observed for the former.

Occasionally, international NoV outbreaks occur in multiple countries. In the Foodborne Viruses in Europe (FBVE) network dataset, they are distinguishable as distinct peaks: one in 2000/2001 and one in 2005/2006. These peaks were associated with multicountry shellfish- and raspberry-related outbreaks, respectively. However, the question of how such international outbreaks occur remains unanswered. There is no formal international requirement to report outbreaks to a central agency and the large majority of foodborne virus outbreaks are not formally investigated and recorded, even at the individual country level. The European Rapid

Alert System for Food and Feed (RASFF) has received reports of 23 outbreaks and/or contamination events during the period 2001-2007 associated with raspberries and molluscan bivalves, in which viruses were involved, but the level of evidence for related outbreaks is mostly incomplete. International foodborne outbreaks are more often, but not exclusively, caused by non-GII.4 viruses. Because of the severe limitations of outbreak reporting, at both the individual country and international level, the existing databases (such as FBVE and RASFF), whilst illustrating the problem with foodborne viruses, should be regarded as a large underestimation of the true extent of illness. Further studies are required to better define the true burden of human illness from foodborne viruses.

3. ROUTES OF TRANSMISSION AND THE IMPACT OF VIRAL CHARACTERISTICS ON THEIR CONTROL

3.1 Transmission routes

The viruses that met the first two criteria for identification of viruses of greatest concern from a food safety perspective, as defined in the previous chapter, are spread mainly by the faecal-oral route. As such, humans become infected following the ingestion of viruses present in faecally-contaminated foods. These viruses enter the gastrointestinal tract, surviving the acidic conditions in the gut, and initiate an infection. Consequently, major foodborne viral disease outbreaks are caused by viruses from humans that are excreted in high numbers in human faeces, where the levels of virus shedding can exceed 10^7 infectious viral particles per gram of stool. Another important factor affecting foodborne transmission is the stability of viruses outside the host. Although foodborne viruses show varying resistance to different environmental stresses such as acid, heat, drying, pressure, disinfectants and ultraviolet radiation, they are generally tough-natured and survive well in the environment. There is therefore considerable potential for food contamination along the food chain continuum. For example, various reports have clearly provided strong evidence of "foodhandler" transmission for NoV and HAV. There is less definitive evidence for "foodhandler" transmission of other enteric viruses found in humans, such as HRV, and emerging viruses, such as HEV.

A separate category is the animal viruses that are able to cause illness in humans. The viruses of potential risk to human health may enter the food chain through animal products, as well as when virus-laden animal manure contaminates food. Once such viruses have entered the human population, further spread may occur between humans. Animal viruses with the potential for foodborne transmission include HEV, HPAI virus H5N1, SARS CoV and Nipah virus.

Accordingly, and as described below, there are three major routes of viral contamination of foods. However, it is worth noting that large-scale outbreaks are often the result of a combination of several transmission routes. For example, the virus is introduced in a sensitive population by food, water or an asymptomatic shedder, which is followed by efficient spread of the virus through the susceptible population by direct person-to-person contact or via a contaminated environment.

3.1.1 Human sewage and faeces

The possibility of acquiring viruses through contact with untreated sewage has long been recognized, beginning with the detection of HAV infections in sewage treatment workers (Cadilhac and Roudot-Thoraval, 1996). It is now known that some commonly used methods of sewage treatment may not be sufficient to effectively remove or inactivate viruses. Various studies in Europe, Japan and the USA showed that treated sewage was still positive for human enteric viruses (van de Berg et al., 2005; Villar et al., 2007; Laverick, Wyn-Jones and Carter, 2004; Silva et al., 2007; Gregory, Litaker and Noble, 2006; la Rosa et al., 2007; Myrmel et al., 2006; Ueki et al., 2005). Direct contact with human sewage is the normal route of contamination for bivalve molluscs. It can also be a cause of pre-harvest contamination of fresh produce items through the use of sewage-contaminated waters in irrigation, washing, as fertilizer or for agrochemical application.

A specific concern with sewage-related contamination is that it can result in the food becoming contaminated with multiple viruses. As a result, people may become infected with more than one virus strain simultaneously (le Guyader et al., 2006a; Symes et al., 2007). The presence of related virus strains (in general within one genus) replicating in a single host (cell) may provide an environment conducive to the evolution of new virus strains. This can occur in one of two ways. One process is called recombination and has been demonstrated for the NoVs (Reuter et al., 2006; Bull, Tanaka and White, 2007). Although there is currently no evidence that recombinant NoVs have properties that differ from the "original" virus strains (Simmonds, 2006), the unpredictable behaviour of recombinant viruses is a potential concern in terms of food safety. For HRV, another process called genomic re-assortment in the progeny of two viruses after co-infection of a single cell may lead to new viruses. Additionally, the introduction of animal Rotaviruses into the human population (zoonosis) may occur (Iturriza-Gomara et al., 2001). All these mechanisms contribute to the diversity of virus strains individually and in combination.

3.1.2 Infected food handlers:

In people with enteric virus infections, viruses are typically detected in stools at levels exceeding 10^7 virus particles per gram. The virus titre or amount of virus particles in vomitus are not known. Infected individuals may start shedding viruses from as early as 12 hours after exposure (e.g. NoV) and continue for up to several weeks depending on the virus type (Rockx et al., 2002). It is therefore quite possible that infected people may shed the virus before even developing symptoms, and long after recovery. In addition, asymptomatic infections are quite common. For example, in a community study in the Netherlands, evidence of NoV shedding was found in 5.2% of controls, i.e. persons without gastrointestinal complaints (de Wit et al., 2001) and in 19% of people without gastrointestinal illness in an outbreak setting (Vinje, Altena and Koopmans, 1997). A recent study in the United Kingdom found even higher levels of asymptomatic shedding (Amar et al., 2007).

The hands of food handlers may become contaminated with human enteric viruses if the handlers are shedding viruses in their faeces, changing diapers or cleaning toilet areas, and are not practising appropriate personal hygiene. These same viruses can be readily transmitted from human skin (hands) to foods and inanimate surfaces (Bidawid, Farber and Sattar, 2000; Bidawid et al., 2004), which serve as a secondary source of contamination if they come in contact with food. Virus contamination as a consequence of human handling can occur at virtually any stage of the farm-to-fork continuum. For example, produce items can be handled by human hands during harvest, packing, distribution, and at retail establishments or homes. At the same time, retail food handlers and food preparers in the home can contaminate highly handled "prepared" foods with viruses immediately prior to consumption.

A second important factor in food handler-associated spread of viruses is vomiting. NoV infections often lead to projectile vomiting, with very abrupt onset. Several outbreaks resulting from exposure to virus-containing vomitus have been documented. The formation of aerosols in an area where a person has vomited can lead to widespread contamination of the environment and objects within, including utensils. However, the relative contribution of fomites and surfaces to the propagation of NoV infections is not known (Boone and Gerba, 2007). Persistence of viruses in a contaminated environment, and their resistance to cleaning and disinfection are factors that may contribute to this mode of transmission.

3.1.3 Zoonotic transmission

For the purposes of this report, the term zoonotic infection refers to an animal virus infecting humans. For example, when an oyster acts as a passive carrier of human enteric viruses that cause infection in consumers, that oyster would be considered a vehicle of infection. Should an oyster accumulate an animal virus (such as HEV from pig faeces contaminating the environment) and subsequently transmit it to a human, the oyster would still be considered a vehicle, but the infection would be zoonotic. Similarly, transmission of an animal virus to humans by consumption of infected meat or other animal product would be considered a zoonotic infection. There is evidence that HEV can be transmitted by raw meat and liver of deer and wild boar (Tei et al., 2003, 2004; Takahashi et al., 2004; Matsuda et al., 2003). The virus has also been detected in pig meat, organs and faeces. HEV is present in pig populations across the world, but the importance of their zoonotic transmission remains unclear. For example, studies looking at risk factors for HEV infection in recently diagnosed patients in the USA, the United Kingdom and the Netherlands have not been able to show evidence for direct foodborne infection. However, infectious HEV has been detected and characterized from commercial pig livers sold in local grocery stores in the USA, Japan and the Netherlands (Yazaki et al., 2003; Feagins et al., 2007; Rutjes et al., 2007).

HPAI-H5N1 virus has been detected in poultry meat products (Tumpey et al., 2002; Mase et al., 2005; Swayne and Beck, 2005; Promkuntod, Antarasena and Prommuang, 2006) and data from infections and disease in felines and canines suggests that exposure via ingestion may lead to infection (Kuiken et al., 2004; Songserm et al., 2006). Based on the detection of HPAI-H5N1 in eggs and poultry meat and the possibility of infection by ingestion, the potential for foodborne transmission to humans cannot be excluded. The evidence for SARS Coronavirus transmission though faecal spread comes from an incident in a housing complex in Hong Kong, where a large group of people became infected as a result of faecal spread due to a faulty sewage system. It is unknown if the route of infection in these patients was oral or if they inhaled the virus-containing aerosols. However, a considerably high proportion of SARS patients from this outbreak had diarrhoeal disease and oral infection could not be ruled out (McKinney, Gong and Lewis, 2006). Nipah virus infection in humans and pigs as a result of consumption of contaminated fruit has been documented (Luby et al., 2006; Chua, 2003).

3.2 Impact of virus characteristics on their control

Viruses, unlike bacteria, are strict intracellular parasites and can not replicate in food or water. Therefore, viral contamination of food will not increase during processing, transport or storage, and the contaminated products will look, smell and taste normal. However, most food- or water-borne viruses are more resistant to heat, disinfection and pH extremes than are most vegetative bacteria. Consequently, even low levels of virus contamination may persist in a product to the point of consumption, and additionally, many of the foodborne viruses require only a low infectious dose to cause disease.

3.2.1 Persistence of foodborne viruses

A factor affecting overall disease risk is the stability of some of the foodborne viruses in the environment. For example, HRV in aerosols, generated while vomiting, and thought to play a role in the transmission of those viruses, were found to survive in the air for up to 9 days at 20°C (Sattar et al., 1984). Viruses may also persist for extended periods (1 to 60 days for 100-fold reduction in infectivity) on several types of materials commonly found in institutional and domestic environments, such as paper, cotton cloth, aluminium, china, glazed tile, latex and

polystyrene (Abad, Pinto and Bosch, 1994). Adenoviruses were found to survive for up to 35 days on a plastic surface in a low relative humidity environment (Nauheim et al., 1990). This relationship between virus survivability and humidity differs by virus: high relative humidity favours the survival of Enteroviruses, while low humidity favours survival of HAV and HRV (Mbithi, Springthorpe and Sattar, 1991; Sattar et al., 1986, 1988). This relationship illustrates the need for virus-specific data on survival and inactivation. Finally, in artificially contaminated water, viruses may survive for prolonged periods of time. For example, poliovirus and Rotavirus have been reported to survive in mineral water at 4°C (Biziagos et al., 1988). In dried faeces, HAV remained infectious for 30 days when stored at 25°C and 42% relative humidity (Holliger and Ticehurst, 1996). Research has shown that enteric viruses can persist in shellfish and marine sediments for several weeks or months (Greening et al., 2003a; Le Guyader et al., 2006b; Sobsey et al., 1988), and that depuration processes cannot be relied upon for complete virus removal (Lees, 2000; Loisy et al., 2005). In addition, enteric viruses can persist on fresh produce, sometimes for periods exceeding the shelf-life of the product itself (Croci et al., 2002).

3.2.2 Stability of foodborne viruses during processing

Enteric viruses are recalcitrant to many of the commonly used food processing and preservation methods. For example, foodborne viruses tend to survive for prolonged periods of time at pH values as low as 3 to 4 and as high as 9 to 10. However, differences are observed among the different viruses. In general, it has been observed that HAV and HRV are more resistant to inactivation than enteric Adenovirus and poliovirus. In addition, however, significant differences in virus survival have been reported under different processing and substrate conditions. For example, standard milk pasteurization conditions should inactivate HAV, but much more extensive processing times are required to achieve similar levels of HAV inactivation in bivalve molluscs. Enteric viruses are resistant to ionizing radiation, requiring doses that have a negative effect on the organoleptic qualities of the product. As a general rule, washing of produce, either with water alone or in conjunction with a disinfection agent, generally removes only 1–2 $\log_{10}$ of the viral contamination load. Refrigeration and freezing have little impact on virus survival, and freezing is actually an effective virus preservation method (reviewed by Papafragkou, D'Souza and Jaykus, 2006).

Because of concerns about virus persistence in food processing, effective control strategies need to focus on prevention of contamination. Such prevention will have to occur at the pre-harvest level for some products (bivalve molluscs, fresh produce for raw consumption), and at the post-harvest phase for others (prepared and ready-to-eat foods). The persistence of viruses in foods contaminated at either phase is well documented in the epidemiological literature.

However, it is worth noting that higher resistance to environmental or food processing conditions is not the only factor contributing to the probability of foodborne transmission. If viruses infect foods at the end of the foodchain, long-term survival is not necessary, but acid resistance and the ability to infect the gastrointestinal tract are more important. Indeed, these factors are believed to be relevant for potential foodborne transmission of larger enveloped viruses such as avian influenza viruses (e.g. H5N1, *Orthomyxoviridae*; ~300 nm, enveloped), Nipah viruses (*Paramyxoviridae*; 120–500 nm, enveloped), and Coronaviruses (SARS-causing Coronavirus; 170 nm, enveloped) (Luby *et al.,* 2006).

3.2.3 Decontamination of hands

Foodborne viruses like NoV and HAV are excreted in stools at levels frequently exceeding 10^7 PCR-detectable units per gram of stool (i.e. over 10^4/mg). Although the degree of efficacy for

hand sanitizers varies by virus and study design, no agent is able to completely eliminate enteric viruses from hands (usually defined as a 4 $\log_{10}$ reduction in virus infectivity (Steinmann, 2004; Bidawid et al., 2004); many result in only a 1 to 2 $\log_{10}$ drop in virus titre (Sattar et al., 2002; Bidawid et al., 2004; Mattison et al., 2007). Consequently, it is conceivable that considerable numbers of infective viruses will remain when hand sanitizers are used instead of proper hand washing (Bidawid, Farber and Sattar, 2000). There are no convincing data to support the advice to use alcohol-based hand disinfectants instead of traditional hygienic hand washing with streaming water and towel drying.

3.2.4 Decontamination of surfaces

Environmental persistence is likely to be an important consideration for foodborne virus outbreaks. The survival and transferability of human enteric viruses on environmental surfaces depends on several factors, including temperature, relative humidity, type of surface and virus type. Although data differ based on experimental design and virus type, enteric viruses can generally persist on surfaces under ambient conditions of temperature and moisture for a period of days to weeks; they are also transferred between surfaces or hands with relative ease. Of course, cleaning and disinfection of surfaces is important for control of virus transmission during food preparation. However, as is the case for hand disinfection, most surface disinfectants lack efficacy against enteric viruses. In fact, it is well recognized that the majority of chemical disinfectants used in both institutional and domestic environments do not effectively inactivate HAV (reviewed by Papafragkou, D'Souza and Jaykus, 2006).

3.2.5 Difficulties in establishing the impact of control measures on the infectivity of foodborne viruses

As yet, NoV can not be grown in routine tissue culture systems, so it is not possible to test the effects of control measures on their infectivity. Therefore data on inactivation and persistence of viruses have to be inferred using model surrogate viruses. The validity of data obtained using Feline calicivirus (FCV), which are respiratory pathogens and are less stable at low pH than enteric viruses, continues to be debated. Currently, the murine Norovirus (MuNoV) is being evaluated as a model for human caliciviruses since preliminary results indicate improved survivability of MuNoV when exposed to reduced pH, a property more consistent with the behaviour of the human NoV (Cannon et al., 2006).

In most instances, HAV and HRV are more resistant to inactivation by commonly used food preservation and processing methods, in comparison with enteric Adenovirus and poliovirus. Similar data for the human NoV are lacking by virtue of the fact that these viruses cannot be cultured *in vitro*. HAV in particular has demonstrated the greatest resistance to heat, desiccation, pH extremes and ionizing radiation, and it may be a conservative surrogate to use in this regard (ILSI, 2002). Notable exceptions are for ultraviolet radiation, for which Adenoviruses have shown the highest resistance (Thurston-Enriquez et al., 2003) and high pressure processing, for which poliovirus has displayed an unexpectedly high degree of resistance (Kingsley, Meade and Richards, 2002). In all cases, it must be realized that a model is only indicative of reality and cannot be relied upon to provide undisputed evidence of the response of all relevant viruses to specific control measures. Indeed, the exquisite interplay between virus type, commodity and processing conditions emphasizes the need for independent evaluation of virus behaviour as a function of all of these variables.

To definitively establish the efficacy of control measures, quantitative assays capable of discriminating viable from non-viable (or inactivated) viruses are necessary. Fortunately, such

viability/infectivity assays are available for HAV, FCV, MuNoV, human enteric Adenovirus, Astroviruses, Rotaviruses, and (many) Enteroviruses. While not routinely done, these assays are available and operational at several laboratories around the world.

4. CURRENT STATUS OF METHODOLOGY AND ITS IMPACT ON DETECTION AND CONTROL

4.1 Current status of methodology

Recent years have shown a considerable increase in the development and number of methods for the detection of foodborne viruses in different food matrices, reflecting the recognition of the increased significance of foodborne viral diseases. Currently, methods for virus detection in bivalve molluscan shellfish are well established and accredited by national bodies in a number of countries, and are in the process of being validated for international accreditation. Recently, the number of available detection methods for foodborne viruses in other food matrices has also increased, reflecting the recognition of the significance of foodborne viral disease.

As procedures for detection of viruses in these food matrices are diverse, there is a need to validate their use. Validated methods provide a standardized means by which to conduct outbreak investigations, and can serve as a valuable tool in audits of good agricultural practices (GAP), as well as for monitoring the efficacy of intervention strategies. (Boxman, 2007). At present, the number of detection methods for foodborne viruses in different matrices (notably matrices other than shellfish) reflects the growing recognition of the significance of enteric viruses as causes of foodborne disease. Well established methods for the detection of viral contamination in bivalves are available and accredited by national bodies in a number of countries. For other products (fresh produce, ready-to-eat foods) the methodology is not as well advanced. Nonetheless, standardized sensitive methods for NoV and HAV detection in selected food matrices (soft fruits, leafy greens and bottled water) are currently being validated in the CEN/TAG4 committee of the European Union. General rules for the application of PCR for the detection of microorganisms in food samples have been elaborated in Europe by the European Committee for Standardization (CEN).

4.2 Challenges in the development of appropriate methodology

Similar to many bacterial pathogens, viruses are typically present at low levels in contaminated foods; however, unlike most bacterial pathogens, most foodborne viruses cannot readily be enriched by culture methods. Fortunately, molecular-based assays can be used to detect the viral nucleic acid. However, these assays are not without their own complexities, including the (i) the presence of low numbers of highly infectious viruses, necessitating the sampling and testing of large volumes of food; (ii) the need to extract and concentrate viruses prior to detection; and (iii) the need for the extracts to be free of substances that might inhibit or interfere with virus detections methods. Direct detection and identification of viruses in food is also difficult because of the large variety and complexity of foods and the heterogeneous distribution of contaminating viruses in the food milieu. And, of course, molecular detection does not necessarily indicate the presence of infectious viruses, but merely the presence of (fragments of) the viral genome.

Consequently, procedures for virus recovery from food will depend upon the origin, type and history of the food specimen. For example, foods associated with outbreaks of viral infection due to contagious food handlers will often be contaminated at the surface. This can also be the case for produce items that are contaminated by irrigation water, improper handling or cross-

contamination. Uptake of human viruses by roots and into the ingested part of the plant is also suggested, but not well studied.

Filter-feeding bivalve molluscs (e.g. oysters, mussels, clams) have a long history of association with viral foodborne disease. These animals actively accumulate viruses from water contaminated with human excrement. Viruses become trapped in the digestive tissue of the mollusc and are actually concentrated. In this case, the contaminants are internalized, creating additional difficulties for recovery of the virus for subsequent detection. The same mechanism of virus concentration occurs when bivalves harbour zoonotic viruses.

The methods for the detection of viruses in food specimens can usually be separated into different phases:

- *Specimen preparation*: virus concentration methods are designed to achieve reduction in sample volume with recovery of virus and elimination of matrix-associated interfering substances. Sample manipulations depend on the behaviour of viruses to act as proteins in solutions, to co-sediment by simple centrifugation when adsorbed to larger particles, and to remain infectious at extremes of pH and/or in the presence of organic solvents. Typical methods include combinations of filtration, centrifugation, adsorption, elution, solvent extraction, precipitation and/or organic flocculation. These are usually followed by a nucleic acid extraction step. On occasion, a direct nucleic acid extraction method without preceding virus extraction from the food is employed.

- *Viral nucleic acid detection:* conventional RT-PCR, real-time RT-PCR, nucleic acid sequence-based amplification (NASBA) or micro-arrays, or a comparable sensitive method of detection may be applied.

The efficiency of the virus and/or nucleic extraction method(s) used greatly influences the ability to detect viral contamination in a food. The efficiency of the extraction method(s) may be evaluated by the co-extraction of a processing control virus such as Mengovirus, MuNoV or FCV. These candidate controls should be similar to the target virus(es) in physico-chemical characteristics, have low pathogenic potential, and be absent from the sample or the laboratory environment.

Conventional nucleic acid amplification methods have recently been replaced with real-time platforms, which improve the efficiency and time to results of the analytic process while decreasing the risk of cross-contamination that might contribute to false positive results. Oligoprobes are the principal means for specific amplicon detection in real time PCR assays. Quantitative analysis is possible with this analytical approach. Nonetheless, the method is not fail-safe. Residual matrix-associated inhibitory substances may remain, necessitating the use of an internal amplification control (ssRNA) which is used to alert the analyst to false positive results occurring because of amplification failure.

Another difficulty to overcome is the high degree of genetic variability for the NoVs, which complicates the selection of appropriate RT-PCR primers and probes. The accumulation of additional sequence data over the last several years has aided in the development of more broadly reactive reagents. It remains to be seen how this technical difficulty can be overcome when developing standard operating procedures for food testing.

Ideally, a virus detection method for food must be simple, sensitive, practical and robust. The method applied should allow an efficient elimination of inhibitors for molecular detection assays and should be applicable to a large variety of food items. The difficulties described above imply that most testing of foods for viral contamination is done in highly equipped laboratories

with well-trained personnel. At present, only virus detection in shellfish is done more than incidentally, and a European group of laboratories is trying to develop an ISO method for NoV detection in shellfish.

Clearly, detection of foodborne viral contamination is much more difficult, and hence costly, in comparison with either the detection of foodborne bacterial pathogens or the detection of enteric viruses in clinical (faecal) samples, which harbour much higher levels of viruses.

5. SELECTION OF PRIORITY VIRUS COMMODITY COMBINATIONS AND THE MAIN SOURCES OF CONTAMINATION

As described in Chapter 3, three main routes of virus contamination of food can be distinguished, namely contamination of food with sewage or human faeces during primary production; handling of food by an infected person; and contamination of food with viruses of animal origin (zoonotic infections). With these three routes in mind, the expert meeting sought to identify the virus-commodity combinations of greatest concern, as well as the main sources of contamination for each of the commodities, based on currently available data.

It should be noted that the degree of evidence and supporting data vary considerably. Foodborne viral outbreaks are investigated with varying degrees of rigour, depending on location of the event, size and scope, ease of trace back, and resources to support epidemiological investigation and microbiological testing. Large events with wide, multi-state or multi-national implications are frequently investigated. Smaller, local, events may or may not be investigated, and the results of such investigations rarely make it into the scientific literature. It should be noted that the priority combinations identified in this document are based on currently available data. As new data become available, particularly from developing countries, additional virus-commodity combinations may be identified.

5.1 Virus-commodity combinations

As noted in Chapter 2, HAV, NoV, and HRV, and emerging viruses (HEV, HPAI-H5N1 virus, SARS-CoV and Nipah virus) were identified as the viruses of primary concern in terms of foodborne transmission. Based on these viruses, the expert meeting sought to identify virus-commodity combinations of concern by considering available information on estimates of the incidence of foodborne disease linked to a specific commodity and the level of evidence for the importance of that commodity in causing viral foodborne disease. Potential regional differences in the assessment of priorities were also considered.

Based on these, the following combinations were selected:

- NoV and HAV in bivalve molluscan shellfish (including oysters, clams, cockles and mussels);

- NoV and HAV in fresh produce;

- NoV and HAV in prepared foods;

- HRV in water for food preparation[1]; and

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[1] Water (used for drinking, ice production, or in food processing): Enteric virus contamination in drinking water has been documented for many years and is beyond the scope of this document. However, water and ice used in processing and packaging of food can be a potential source of contamination. When contaminated water is used to reconstitute food products (such as dried or powdered milk, infant formula, or juice), virus transmission may occur. Both edible ice and packing ice, if made from contaminated water, can also be a source of virus contamination of food.

- Emerging viruses and their associated commodities (e.g. HPAI and poultry, HEV and porcine products, Nipah virus and fruit).

5.2 Main sources of contamination for priority virus-commodity combinations.

Knowledge of the route of contamination is critical in understanding the most effective mechanisms of intervention. Intervention strategies may be generic or specific. In an effort to provide a basis for the development of control and mitigation technologies and strategies, the virus-commodity combinations were characterized and assessed according to the most likely source(s) of contamination[2]. This approach also provides a logical framework upon which to consider further efforts in risk ranking or risk assessment, or both.

It was recognized that more than one route of transmission may lead to the contamination of a commodity; however, transmission routes are not of equal significance when considering the different commodity-virus combinations. In addition, transmission routes cannot be considered absolutely equivalent for various countries. For example, viral contamination of foods by insects (as mechanical vectors) is considered possible in developing countries based on similar data for the transmission of bacterial foodborne pathogens, although specific data for viruses are not available. Similarly, it is well documented that waterborne transmission of HRV is a major children's health issue in the developing world; in the absence of data on the transmission of HRV via food, it seems plausible that under certain conditions (e.g. reconstitution of baby food with HRV -contaminated water) foodborne transmission can occur. Pre-harvest contamination of produce may occur when items are picked by infected field workers or when contaminated irrigation water is used in their production. However, data on the latter route of contamination do not exist. While cooking is usually adequate to destroy any viruses present, post-cooking contamination might occur, for example from infected food handlers.

5.2.1 NoV and HAV and bivalve molluscan shellfish (including oysters, clams, cockles and mussels)

For shellfish, the major, well-documented route of contamination is via faecal contamination of harvesting areas. Handling by infected individuals could theoretically result in contamination (during shucking), but this was considered to be of relatively minor relevance for this combination. Viruses have been observed to persist for at least 8 to 10 weeks in contaminated live shellfish and can be detected in shellfish gut tissue. Recent evidence has shown that NoV bind specifically to shellfish tissue receptor sites (Le Guyader et al., 2006b), which could explain why viruses persist after depuration. Furthermore, studies indicate that there may even be a risk of infection if contaminated shellfish are consumed (lightly) cooked (Croci et al., 2005; Hewitt and Greening, 2004).

5.2.2 NoV and HAV and fresh produce

For fresh produce, handling by infected food handlers and contact with sewage-contaminated water (during irrigation or agrochemical application, with possible uptake) are considered to be

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[2] Naturally occurring events that can result in cross-contamination during production, processing, and preparation (such as very heavy rainfall, floods and the movement of insects and rodents that may inadvertently serve as vehicles to spread contamination) were considered but not taken into account in these initial categories.

the main sources of contamination. Fresh produce is now grown on a large scale in many countries and is transported globally. Viral outbreaks associated with contaminated green onions and raspberries, as well as other produce items, are well documented (Hjertqvist et al., 2006; Falkenhorst et al., 2005; Korsager et al., 2005; Cotterelle et al., 2005; Le Guyader et al., 2004; Amon et al., 2005; Dentinger et al., 2001; CDC, 2003). The contamination of the produce may occur either at the pre-harvest stage (water, infected pickers) or at the post-harvest phase (food handlers). A recent study suggests that viral particles from the water can be taken up into green onions during the growing process (Chancellor et al., 2006). This observation needs follow-up to determine if it is of practical relevance, because such contamination would not be detected with any of the methods currently in use.

Data on the relative contribution of pre- and post-harvest contamination, or contaminated water vs. food handlers, are lacking. There are only limited guidelines for the quality of irrigation waters, and, in some regions of the world, irrigation waters can be contaminated with human sewage. Work on faecal-orally transmitted parasites (*Cryptosporidium* and *Giardia*) has shown that irrigation waters may contain these faecal parasites (Robertson et al., 2001). This was not a rare event, because the investigators detected *Cryptosporidium* in lettuce and mung bean sprouts, and *Giardia* on dill, lettuce, mung bean sprouts, radish sprouts and strawberries. A recent study developed a quantitative microbial risk assessment model for estimating the annual risk of enteric virus infection associated with consuming raw vegetables that have been overhead irrigated with non-disinfected secondary treated reclaimed water. According to the authors, it is currently estimated that, worldwide, at least 20 million hectares of agricultural land are irrigated with raw, treated or partially diluted (i.e. possibly contaminated) wastewater. The model showed that the mean annual risk of infection varies for different crops, with annual risk of infection ranging from 10^{-3} to 10^{-1} when reclaimed-water irrigation ceased 1 day before harvest and from 10^{-9} to 10^{-3} when it ceased 2 weeks before harvest (Hamilton et al., 2006).

5.2.3 NoV and HAV and prepared foods

For this virus-commodity combination, infected food handlers are the main sources of contamination, although the relative contribution of hand versus surface contamination (resulting from vomiting or cross-contamination from other contaminated foods handled on the same surface) remains to be established. In all instances where a person carrying a virus comes into contact with food, contamination might occur, and, due to the stability of these pathogens, they are likely to survive in many foods that do not receive a terminal heating step prior to consumption (Koopmans and Duizer, 2004).

When viral contamination occurs because of poor personal hygiene of a food handler who has direct contact with the food, the contamination will be localized in spots (focally). Infections caused by focally contaminated foodstuffs are most likely to be recognized as foodborne when the contamination has occurred at the end of the food chain (i.e. at retail or in the home). Several such outbreaks, with hundreds of cases, have been described (Gotz et al., 2002; de Wit et al., 2007). Prepared foods are at greatest risk of contamination by this route, and include delicatessen and bakery products, salads and other ready-to-eat foods. NoV outbreaks associated with these products have been reported (Parashar and Monroa, 2001; de Wit et al., 2007). Surface contamination, either by faecal deposition or by aerosolized vomitus may also cause foodborne outbreaks. Since vomiting is a symptom of NoV infection in 70 to 80% of the cases, it can be an efficient mode of virus spread, directly via aerosols, or indirectly via contamination of food items or via contamination of the environment or surfaces, with subsequent cross-contamination of foods (Patterson et al. 1997; Marks et al., 2003; deWit et al., 2007).

Although not definitively documented, it is likely that surface contamination with viruses is less important relative to direct contamination by the hands of an infected food worker.

5.2.4 HRV and water for food preparation

HRV infections occur globally, and the virus is the leading cause of gastroenteritis in infants and young children worldwide. HRV has its most serious effects in developing countries, with estimates of 600 000 diarrhoea-related deaths occurring annually, 80% of them in developing countries. Children become dehydrated and require medical intervention and hospitalization. Forty-two unique HRV strains have been identified based on their combination of VP7 and VP4 (viral proteins, determining G and P typing) varieties; only five account for more than 90% of HRV worldwide. Although person-to-person transmission is most common, there is ample documentation of the potential for virus transmission via drinking water and water used for food preparation (Villena et al., 2003; Martinelli et al., 2006). There are no data on relative contribution of water-for-food as a source of HRV infections in resource-poor countries. For high-income countries, this is thought to be negligible.

5.2.5 Emerging viruses in selected commodities

Emerging viruses were considered separately. This group of pathogens has either newly appeared in a population or has existed before and is rapidly increasing in incidence, geographical range or public health impact. Although there is scant evidence on transmission of these viruses via food, it is likely to be rare, relative to other transmission routes, and will probably be restricted to one or only a few food products or items. For example, HPAI virus in undercooked poultry or eggs, HEV in porcine organs or muscle tissue and Nipah virus in date palm sap are postulated to be foodborne. Another emerging virus for which this mode of transmission may be relevant is SARS-CoV. All four viruses happen to be zoonotic viruses, but limited epidemiological data exist that support their transmission by the consumption of contaminated foods. Although HEV has been shown to be foodborne in Japan, data from other countries have not been able to actually prove HEV illness as a result of food consumption, and the exact transmission patterns remain to be established. Nonetheless, foodborne transmission is plausible. Nipah virus was shown to affect people slaughtering pigs. Whether eating produce from infected pigs can transmit the Nipah virus is not known. Nipah virus was shown to affect children eating fruits contaminated with urine from bats shedding the viruses, and three outbreaks in Bangladesh have been linked to consumption of fresh date palm sap, a local sweet delicacy, which had been contaminated by bats (Luby et al., 2006). It is important to recognize that, for most of the emerging foodborne pathogens, contaminated food is not the sole or even a likely vehicle of transmission, but the potential for foodborne transmission should be considered in epidemiological studies that aim to describe the modes of transmission. The finding of virus-contaminated poultry meat as a potential source of HPAI-H5N1 virus has sparked discussions about the need for food testing. The meeting agreed that this would be unrealistic, given the low probability and the lack of reliable methods. Prevention of such transmission could be safeguarded by full compliance with veterinary avian influenza control and prevention guidelines (FAO/OIE, 2006; FAO/VSF-CICDA, no date; WHO, 2007, EFSA, 2006; IAFP, 2005).

6. RISK ASSESSMENT – AVAILABLE KNOWLEDGE AND FEASIBILITY

6.1 Introduction

The risk analysis framework, which includes risk assessment, has been defined and characterized by the Codex Alimentarius Commission (CAC, 1999). Numerous microbiological risk assessments of pathogen-food commodity combinations have already been undertaken at both the national and international level, but these have focused on bacterial rather than viral hazards.

The data requirements for a quantitative risk assessment are quite rigorous. Consideration was given as to whether or not there is enough information to contemplate undertaking risk assessment on a viral-commodity basis for each of the virus-commodity groups of concern. The expert meeting concluded that we are not yet at the point of undertaking a full quantitative risk assessment. Nevertheless, the experts also believed that data gaps do not necessarily preclude the use of risk assessment approaches in addressing foodborne viral problems.

6.2 Availability of data for risk assessment

Several critical reviews regarding the availability of data for virus-commodity risk assessment have already been undertaken or are underway. The Food Standards Agency in the United Kingdom have reviewed data needs for risk assessment of NoV in bivalve molluscs and fresh produce, and identified specific data gaps that need to be addressed before such work could be undertaken (HPA, 2004). A risk profile of viruses in foods has been prepared in New Zealand (Greening et al., 2003b) and another is under preparation in the USA. The meeting considered this issue from a global perspective for each of the virus-commodity combinations of concern.

The availability of data potentially of use for risk assessment varies from one part of the world to another. It also varies in terms of the viruses and products of concern. The data needed for risk assessment can be separated according to the three primary risk assessment steps: hazard identification; hazard characterization; and exposure assessment.

6.2.1 Hazard identification

On a global basis, the incidence and severity of both HAV and HRV are well documented, although this does not mean that every country has the same degree of information or quality of data. With regard to the NoV, the global picture is less clear. While there is some very good information from developed countries, data from developing countries is limited, although an increasing number of reports and anecdotal evidence confirm its occurrence in these regions. Information on the severity of the illness caused by NoV is available, although less extensive than that for HRV and HAV. However, as indicated in Chapter 2, while the foodborne route of transmission has been well documented, particularly for HAV and NoV, the proportion of viral disease attributable to food is less clear. With respect to HRV our knowledge is lacking regarding the incidence and severity of the disease contracted from exposure to water used for food preparation and processing.

An important question for all foodborne viruses is whether severity of disease differs by route of exposure (foodborne versus other routes), or between normal, healthy individuals and those in vulnerable groups (e.g. the young, malnourished, elderly, pregnant and immunocompromised). Such data play an important role in risk assessment, particularly in hazard characterization, where consideration has to be given to differences in susceptibility of different population groups, and, indeed, whether such groups should be addressed separately.

With regard to emerging viruses (HEV, HPAI-H5N1 virus, SARS-CoV and Nipah virus) much of the information, with the exception of that for HEV, comes from developing countries. However, while information on the incidence and severity of illness is available, major data gaps exist in terms of the linkage to foodborne transmission.

6.2.2 Exposure assessment

Exposure assessment requires information on the routes of exposure; prevalence and levels of virus in the foods of concern; the characteristics of the virus and its behaviour and survival along the exposure pathway; as well as information on consumer practices and consumption of the food of concern.

Our understanding of the source and routes of contamination of food commodities varies according to the commodity itself. In the case of bivalve molluscs, there is a good level of information, which clearly identifies the primary source of contamination for both NoV and HAV as environmental (sewage or human faeces) in nature, occurring at the site of production and/or harvest. While there is always the potential for post-harvest contamination of bivalve molluscs, there is little available evidence, and this was considered of minor importance in the overall likelihood of contamination in this commodity.

With regards to produce, the available information is less definitive. The potential routes of contamination have been identified as via sewage-contaminated water or via poor personal hygiene of individuals handling the produce. Contamination could occur during production, harvest or packing, via both of these routes, but generally the production and harvesting phases are considered more likely. With regard to HAV and fresh produce, there is a body of data suggesting that handlers and pickers are the primary mode of transmission. For NoV in produce, the relative importance of these two routes of transmission is less clear.

In terms of prepared foods, food handlers have been identified as the most likely source of virus. While virus contamination may also originate from, for example, preparation surfaces or other food ingredients, the relative importance of fomite transmission to food is less clear. Food handlers can contaminate food either from faeces (NoV and HAV) or vomitus (NoV). At this stage, the faecal route is better characterized. More information is needed on the relative importance of vomitus, given that projectile vomiting is an important symptom of illness and may serve as a source of virus to both foods and surrounding fomites. Even though human faecal material is the main source of HRV, transmission of this virus by foodborne routes is poorly characterized. For emerging viruses, there is relatively good information on their most common sources, which has implicated them as potential foodborne pathogens, but beyond that there is very little additional information.

With regard to contamination of foods, the greatest amount of data exists for HAV and NoV in bivalve molluscs. Nonetheless, little quantitative data exists relative to virus load. In the case of produce and prepared foods, there is much less information available. For HRV in water, the extent of information on prevalence is high if drinking water is used for food preparation (e.g. reconstitution of powdered infant formula) and processing, as well as for packing, since data on

viruses in drinking water are relatively abundant (WHO, 2004). Prevalence data on the emerging viruses is quite limited, even for HEV. This is clearly a major constraint in terms of risk assessment, particularly when risk assessment is designed to evaluate mitigation strategies. Nevertheless, as indicated in Chapter 4, progress has been made in methodology and therefore the collection of quantitative data, particularly for bivalve molluscs, is now feasible.

An important component of exposure modelling is the human factor. In most countries, there are guidelines for the safe production, processing and preparation of foods. However, access to and compliance with these guidelines differs by country, and to a certain extent by facility (farm, processor, retail establishment) and individual worker. For example, bare hand contact (gloving) recommendations are only as good as compliance with those recommendations. Field workers can only practice good personal hygiene if they are provided access to adequate facilities to do so. These factors need to be considered in exposure assessment. For the developed world, a limited number of studies are available in this regard; virtually nothing is known about compliance rates nor access to adequate hygiene facilities in the developing world.

In some countries in Europe, North America and the southwest Pacific, the consumption patterns (amounts and frequencies) for bivalve molluscs and of produce eaten raw are well documented. There is much less data available from a global perspective, and it is likely that there are dramatic regional differences in food consumption patterns as well as food preparation practices. Data regarding consumption patterns, preparation practices and behaviours have been collected in some countries for bacteriological risk assessment, so these may be transferable to virus risk assessment.

6.2.3 Hazard characterization (dose-response)

In terms of dose-response relations, which are required for quantitative microbiological risk assessment, data are available on NoV dose-response in human volunteers (Lindesmith et al., 2003, 2005). However, even these studies are limited in their ability to extrapolate to infectious virus, as there are no data on the infectivity of NoV, since no cell culture systems are available (Duizer et al*.,* 2004). For HAV and HRV, some human volunteer studies using vaccine strains have been done, but not in combination with food matrices, and also not with low doses of virus (Teunis et al. 1996). However, separate studies have looked at the levels of infectious HAV particles in bivalve molluscs. For emerging viruses such as HEV, no studies are known that could result in reliable dose-response estimates. Overall, for some viruses such as NoV, the potential for obtaining new dose-response data is high because of ongoing human challenge studies. For other viruses, particularly those causing severe disease, the likelihood of obtaining such data is minimal. A consistent problem is the lack of any sort of dose-response data in which challenge has occurred in conjunction with the food matrices, as matrix effects have been shown to modify the dose-response relationship.

6.3 Existing risk assessments of foodborne viruses

The meeting was aware of one risk assessment project underway in the USA to look at the role of food handlers in viral transmission from faeces. While acknowledging that vomitus from sick handlers, which was not included here, is probably as important as the faecal route, the meeting considered that despite data limitations such a modelling approach does have a value in providing insight into risk management options. For example, the USA model highlighted the need for more than one intervention, the need for highly efficient interventions, and the importance of compliance with mitigation measures (Mokhtari and Jaykus, 2006).

While the experts were not aware of any risk assessments that specifically looked at a virus-

commodity combination where the source of contamination is sewage, a risk assessment of HRV in drinking water is underway by the WHO drinking water group. A risk assessment model that looks at the transmission of enteric viruses from irrigation water via raw vegetables has also been undertaken (Hamilton et al., 2006). Although not explicitly considered by the meeting, it was anticipated that such a risk assessment could provide a strong basis for any future virus-food risk assessments that consider sewage as the source of contamination.

6.4 Potential application of risk assessment to foodborne viruses

Although virus-commodity combinations are a new challenge for risk assessment, much can be learnt from bacterial pathogen-commodity risk assessments. While the current lack of quantitative data means that a comprehensive quantitative risk assessment of any virus-commodity combination is not yet feasible, the meeting considered that this does not preclude the use of risk assessment approaches in addressing foodborne viral problems. Risk assessment provides a structured and logical framework within which data are critically analysed and considered. Where actual data are not available, assumptions can be made, although such assumptions must be clearly identified and stated. Conceptual models can also be developed as a means of providing insights into modes of transmission and exposure pathways. It was also noted that the process of risk assessment itself is frequently iterative in nature. With these factors in mind, the experts considered that a stepwise approach can be used to the application of risk assessment in this area.

Exposure assessments can provide greater insight into routes of transmission (Mokhtari and Jaykus, 2006). There is already an adequate amount of information available to develop conceptual models for this element of viral risk assessment. One of the first uses of risk assessment could be in the identification of data needs and prioritization of research.

7. RISK MANAGEMENT CONSIDERATIONS

7.1 Introduction

The protection of consumer health is the primary objective of risk managers. In working to achieve such an objective, there are a number of issues to be considered that will influence the manner in which the problem of foodborne viruses is addressed. For example, the commodities of concern for foodborne transmission identified earlier, namely bivalve molluscs, fresh produce (e.g. berries, salads, green onions) and prepared foods, contribute significantly to volume and value in international trade. This means that the risk associated with foodborne viruses can lead to international outbreaks of illness or huge economic losses, or both. Also, production systems for these commodities may vary substantially from country to country, or even region to region, posing another challenge for risk management.

7.2 Trade aspects of commodities of concern

7.2.1 Bivalve molluscs

In 2005, bivalves represented 10% of total world fishery production, but 26% in volume and 14% in value of total world aquaculture production. World bivalve production (capture and aquaculture) has increased substantially in the last fifty years, going from nearly 1 million tonne in 1950 to about 14.1 million tonne in 2005. This growth is mainly due to the increase in aquaculture production, which was particularly rapid in the 1990s. World bivalve aquaculture production grew from more than 3.3 million tonne in 1990 to nearly 12 million tonne in 2005, with an average growth rate of 5.6% per year during this period. In 2005, about 84% of the total bivalve production in the world was cultured (11.9 million tonne). China is by far the leading producer of bivalves, producing 9.5 million tonne in 2005, representing 70% of total bivalve production and 80.2% of total bivalve aquaculture production. All of the Chinese bivalve production is by aquaculture. Chinese bivalve production has skyrocketed over the last 30 years, going from 178 000 tonne in 1970 to 9.5 million tonne in 2005.

In 2005, 38.9% of total bivalve aquaculture production consisted of oysters. Clams cockles and arkshells represented the second main group of bivalves cultured (35.2%) followed by mussels (15.1%) and scallops and pectens (10.7%). In 2005, 97.0% of oyster production originated from aquaculture. This share was 93% for mussels, 86% for clams, cockles and arkshells and 64% for scallops and pectens. In terms of value, scallops are the most important species (38% of value), but these rarely cause foodborne viral infections because consumption is limited to the muscle tissue, which is almost always cooked before consumption. Mussels are the next most important species in value (33%). Clams and oysters are relatively less important. The share of scallops has stayed stable over the years, while the importance of the mussel trade has increased at the expense of clams. Total trade in mussel reached a new record in 2004, at 270 000 tonne. In 2004, 70% of total mussel exports was live, fresh or chilled mussel, 14% was frozen, 11% canned and limited quantities were sold as cured product. The share of live mussel in total trade increased substantially in the last decade, while frozen and canned mussels have lost in market share.

7.2.2 Fresh produce

The challenge to supply seasonal, perishable products to consumers throughout the year has favoured international trade in fresh produce. The value and volume of trade in this sector varies according to commodity. Fresh produce for raw consumption, such as berries, leafy vegetables and spring onions, are all widely produced or gathered, and traded extensively.

It is difficult to quantify the size of production of leafy vegetables globally; however, data from the FAO statistical database FAOSTAT indicate that developed countries produced over 9 million tonne of lettuce and chicory in 2006, while 14 million tonne of these two categories were produced in developing countries (FAOSTAT, 2007). Interestingly, this represented a doubling of the production in developing countries since 1996. Production of spinach has also doubled in developing countries in the last 10 years (FAOSTAT, 2007). In many countries, leafy vegetables are now produced on an industrial scale, with production, harvesting and packing taking place practically on a 24-hour basis. There is an increasing demand for these commodities as a result of efforts to promote better nutrition and address the double burden of malnutrition. Some of the vegetables in this commodity group are also being introduced into countries where they were not commonly grown or consumed previously, particularly developing countries, where they are often produced for export. The export value of lettuce and chicory more-or-less doubled between 1995 and 2005, with a 50% increase in volume of product exported. The volume of spinach exported in the same period increased by 80%, with more than a three-fold increase in export value (FAOSTAT, 2007).

International trade in berries is extensive, although the volumes may be small compared to other produce. For example, approximately 500 000 tonne of strawberries and 120 000 tonne of raspberries and related berries were exported in 2005. Also, berries are often frozen before export, but this does not mean that the hazards have been eliminated. Outbreaks linked to berries have an economic impact, particularly on producer countries. For instance, an outbreak in North America linked to raspberries from Guatemala resulted in a loss of market for this Central American country (Calvin, Avendaño and Schwentesius, 2004). Spring onions are traded internationally. The HAV outbreak in the USA in 2003 led to a decrease in the market price of green onions, and a shut down of the American market for some Mexican producers. The food safety concerns led to a drop in demand for Mexican green onions and estimated losses of US$ 10.5 million for Mexican growers in a two-week period in November 2003 (Calvin, Avendaño and Schwentesius, 2004). Although HAV was not isolated from suspected farms in Mexico, practices that could contribute to contamination of the product were identified. This was an impetus for the implementation of GAPs among the producers and as a requirement for opening of export markets.

7.3 Challenges for risk management

Since molluscan shellfish and fresh produce are predominantly products with short shelf life and are consumed without much processing, there are limited options for post-harvest management.The most common route of contamination of bivalve molluscs and fresh produce is at the stage of primary production. Though there are also bacterial hazards associated with these foods, or the management options for these hazards, when they exist or are implemented may not adequately address the viral hazards. Furthermore, currently used microbiological quality control criteria do not reliably predict the presence or absence of viruses. A management option like prevention of sewage contamination of shellfish growing areas requires coordinated efforts of agencies dealing with sewage treatment, the environment and fisheries. Although sewage

contamination control and remediation is expensive and complicated, it is vitally important as a long-term strategy for sustainable bivalve mollusc production. Monitoring for the presence of enteric viruses in production areas may also be valuable, but standardized and validated methods to achieve such monitoring are currently not available. Controlled purification methods, such as depuration and relaying, cannot assure the safety of molluscan shellfish. It is important that areas of production are protected from sewage contamination and that elimination of viruses during treatment is optimized. More specific and user-friendly guidance in this area, which would inform risk managers about the risk of viral contamination in foods, the sources of such contamination and effective mitigations, would be a valuable resource.

For fresh produce, growing methods differ. Nonetheless, a common concern is the quality of water used for irrigation, fertilization and pesticide application, and during harvest and packing. Beyond this, soil amendments and other inputs to production, as well as personal hygiene of pickers, are critical considerations. Water for irrigation must be of the highest quality that is available in quantities sufficient to support production. If available water presents significant risks of virus contamination of the crop the water needs to be decontaminated prior to application or use, or else an alternative source found. Food controls or guidance need to be elaborated to address this issue.

Another important consideration is the fact that for fresh produce and molluscan shellfish, virus survival generally exceeds the shelf life of the product, frequently longer than bacterial contaminants can survive. Therefore, both existing and any proposed controls for microbiological contamination need to be assessed in the light of their effectiveness for reducing or inactivating virus contaminants. For instance, freezing will only minimally influence virus infectivity in a product. Currently, there are large data gaps about the specific agricultural practices used in many countries and the degree to which countries or regions have adopted GAP programmes, and compliance with such programmes. For those countries that do have GAP programmes, the extent of compliance is variable. It is also unknown whether recommended GAPs aimed at controlling bacterial contamination are equally effective in reducing viral contamination.

Management of virus risks from food preparation depends on knowledge of effective hand and environmental decontamination procedures, and on conditions of virus carriage by food handlers. Data gaps exist in this area, and should be addressed to inform effective risk management. It is critical that adequate sanitary facilities are available to food handlers. Food handlers should maintain a high degree of personal cleanliness and they and their supervisors must be adequately trained. Special challenges arise in small businesses, where one person performs all functions, and also in high turnover/low cost operations. In these cases, risk managers need to consider how to better control the unique challenges presented by viruses. In addition, in the case of contamination by food handlers, the level of contamination may vary depending upon the amount of virus being shed by an infected individual. Variations in level of contamination may also occur due to the focal nature of such contamination. This combination of focal contamination and variable and poorly understood patterns of shedding create additional challenges for risk managers. Additionally, testing as a means of control is not yet available due to the limited availability of diagnostic methods and the lack of any culture systems for most of the wild-type enteric viruses.

Trade in commodities known to be linked to virus hazards may be affected whenever there are reported cases, even from other unrelated sources. The European Rapid Alert System for Food and Feed (RASFF) has alerted countries to suspected viral contamination of food in international trade or foodborne viral illness, but the quality of information provided is often

limited and guidance on the relevance of data on viruses in food is missing. In addition, trace-back that would help further identify possible risks to consumers is not commonly considered (this is data that can be derived directly from an overview of RASFF reports on possible virus contamination or foodborne illness). International sharing of data coupled with product tracing and trace-back can help restore consumer confidence when products are implicated in outbreaks, but there are no agreed guidelines and standard or harmonized procedures to do this internationally. Certainly, routine sharing of information between food safety authorities and public health authorities of food producing and importing countries can help in this regard. At present, no such systems exist, although integrated analysis of data from illness reports and virus identification is increasingly used to link cases related to food. So far, such systems have been or are being used regionally, mostly in research settings (Foodborne Viruses in Europe (FBVE) network, operating since 2000 (Koopmans *et al.*, 2003); Calicinet CDC, launched in 2008; The Australian and New Zealand Norovirus surveillance system, established in 2006).

7.4 Risk management options

Risk management options will vary according to the commodity, and the system and conditions of production. It is critical to understand that options currently in use to inactivate or control the proliferation of bacterial hazards of concern may not be effective against viruses. Some possible options and issues for consideration by risk managers for each of the commodities of concern are outlined below.

In many instances, control of viral contamination in foods needs to focus on prevention of contamination (e.g. preventive measures at source, sewage treatment or in food handling), rather than destruction of the pathogen through the use of various food processes. In fact, for viral contamination of both molluscan shellfish and fresh produce, there are no realistic post-harvest risk management options except cooking. Furthermore, with the main focus to date being on bacterial hazards in foods, there is simply not a good understanding of how risk management systems such as HACCP or monitoring programmes can be optimized to address viruses in foods. For example, monitoring activities, conducted at the pre-harvest phase, could provide useful information for managing potential virus contamination of molluscs and produce, if a suitable indicator of viral contamination could be identified as the target for such monitoring programmes or if reliable methods for detection of human pathogenic viruses were available. A suitable indicator has yet to be identified, but methods for virus detection in shellfish and/or water are promising for monitoring purposes. Also, the relatively recent recognition of foodborne viruses as a significant hazard has caught some of the sectors of the food industry off guard as producers, processors, retailers, food handlers and consumers struggle to become better informed about these agents and their transmission. Expanded educational efforts are an important early step in addressing the problem of foodborne viruses. This is particularly important for ready-to-eat foods and foods that are often handled by multiple people just prior to consumption. Some of the commodity-specific issues are summarized below:

7.4.1 Bivalve molluscs

The role of sewage in virus contamination of bivalves clearly highlights the need for collaboration between public health and food safety authorities and environmental and wastewater treatment authorities to adequately address the problem of sewage contamination in bivalve mollusc growing areas.

The establishment of criteria or standards for viruses in bivalve molluscs and their culture waters was considered to have potential, but as a tool for monitoring the impact of control

measures rather than for end-product testing. However, this requires the availability of reliable analytical methods. Much progress has been made to improve our ability to detect and even quantify viral contamination in bivalve molluscs, meaning that this may be a feasible option in the near future.

Bivalve mollusc purification or depuration is not an effective means to control foodborne viruses, particularly when regulated based on the degree of removal observed for the classic bacterial faecal indicators. The use of these controlled purification methods at the international level as food controls should be re-evaluated in the context of managing enteric virus contamination.

Freezing is not an effective means to control foodborne viruses.

Monitoring for virus occurrence in production areas could be an effective control strategy, and should be evaluated in conjunction with the availability of reliable analytical methods.

Batch testing of foods for absence of viruses is not recommended.

Good Aquaculture Practice (GAP) guidelines should emphasize that aquaculture operations should not be established in areas susceptible to sewage contamination In some parts of the world, such areas have been classified, e.g. "Class A" areas in the European Union, or FDA-approved areas in the USA.

7.4.2 Fresh produce

Understanding the relative importance of the various contamination routes is critical in the selection of effective risk management options. While a number of potential routes have been identified for virus contamination of fresh produce, further studies should be undertaken to establish the relative contribution to contamination from manual harvesting (picking), soil amendments, irrigation, washing, etc.

There are currently no internationally recognized guidelines on the microbiological quality of irrigation water used for fresh produce production. While related guidance documents exist, such as the WHO guidelines for the safe use of wastewater, excreta and greywater (WHO, 2006), clear guidance with regard to irrigation water would be beneficial.

Manual harvesters of fresh produce should adhere to the requirements of the Codex Alimentarius General Principles of Food Hygiene regarding personal hygiene.

Good Agricultural Practices (GAPs), Good Hygienic Practices (GHPs) and Good Manufacturing Practices (GMPs) need to take into account the risk posed by foodborne viruses, and establish guidelines for the quality of irrigation water.

7.4.3 Handling

Food handlers play an important role in the transmission of foodborne viruses. Elaboration of international guidance regarding practices for furloughing ill employees and guidelines for their return to work would be valuable to risk managers.

Personal hygiene, particularly hand washing, remains a key intervention strategy in food preparation premises, and must be reinforced on a near constant basis.

Existing hand and surface sanitizers have poor efficacy against most enteric viruses. There is a need for improved sanitizers that can achieve at least 4 $\log_{10}$ inactivation of the most important foodborne viruses.

Food handlers and their supervisors can—and need to be—educated regarding risks from foodborne viruses and risk reduction strategies.

Risk-based environmental monitoring of food premises for foodborne viruses may be an effective control strategy, particularly when contamination is suspected (such as after a vomiting event), and should be evaluated in conjunction with the availability of reliable analytical methods.

Risk managers need to consider how to better control the risks posed by food businesses using poorly qualified or untrained staff with high turnover.

8. CONCLUSIONS AND RECOMMENDATIONS

8.1 Conclusions

8.1.1 Viruses of concern and burden of foodborne viral disease

Infectious intestinal disease (IID) is common, and viruses play a major role in its burden. Only a fraction of cases are reported to existing national surveillance systems, and many countries have no surveillance at all. In addition, traditional surveillance is not currently able to determine the proportion of IID that is transmitted by foodborne routes relative to other common routes, further complicating estimation of the proportion of viral illness that is foodborne.

Foodborne viruses belong to at least 10 different families. Based on the current state of knowledge, three priority areas have been defined:

- Foodborne viruses with the highest incidence - NoV. Estimates of the burden of disease due to NoV have been attempted in a few countries. These estimates range from 11 to 3067 cases per 100 000 persons per year. Data from at least four continents show that this is a major public health issue worldwide, although data from developing countries are sparse.

- Foodborne viruses that cause severe disease and significant mortality - HRV and HAV.

- Emerging viruses of a zoonotic nature which have been linked to food or postulated to be transmitted via food - HEV, Nipah virus, HPAI-H5N1 virus.

8.1.2 Virus behaviour in food and the environment

Most foodborne viruses of concern are non-enveloped. Because of this structure, they tend to be more persistent in the environment and less susceptible to intrinsic and extrinsic parameters commonly used in food preservation (refrigeration, freezing, pH, etc.). HAV can persist on raw food, such as fresh produce, beyond the shelf life of the product, and long enough in the environment to cause concern for additional spread.

Freezing and refrigeration temperatures preserve viruses and are believed to be the single most important parameter that increases the persistence of foodborne viruses in the environment. Heat and drying can be used to inactivate viruses, but there are virus-to-virus differences in susceptibility to these processes. The food matrix can influence relative survival to heat and desiccation.

The foods most commonly associated with foodborne viral infections include fresh produce, raw bivalve molluscs and prepared ready-to-eat foods that do not undergo any viricidal processes prior to consumption. The food type influences both the likelihood of contamination and the persistence of certain viruses, thus providing an indication of why certain foods are more often linked to certain viruses than others.

Alcohol-based hand disinfectants are not effective for virus inactivation compared with traditional hygienic hand washing practices.

Overall, it was concluded that HAV and HRV are more resistant to inactivation than enteric

Adenovirus and poliovirus, but it must be noted that significant differences in survival rates were found for different environmental and substrate conditions. Because they remain non-culturable, similar data for the human NoV relies on the use of surrogates, which may or may not accurately mimic the behaviour of human strains.

8.1.3 Routes of transmission

The main routes for the introduction of viruses in high-risk commodities have been assessed:

- For fresh produce, the main routes of contamination are through contaminated water (used for irrigation, agrochemical application or wash water); the use of human sewage as fertilizer; and manual (human) handling during and post-harvest. However, the relative contribution of each is not known.

- For bivalve molluscs consumed raw, the main route of contamination is through faecal contamination of the waters in which they are growing. The contamination most commonly occurs through sewage discharge, run-off from agriculture, and point source contamination of the immediate surrounding of the growing areas.

- For prepared ready-to-eat foods, the main route of contamination is via infected food handlers practicing poor personal hygiene during food preparation and serving.

8.1.4 Methodology

There has been much progress in recent years, and it can be concluded that well established methods to detect enteric viruses in contaminated shellfish exist. However, there is a lack of harmonization among methods. Although there is some work ongoing which is attempting to address this, harmonization efforts are primarily focused on virus detection in bivalve molluscs, and additional efforts aimed at other foods are needed.

For food other than shellfish, current methods can only be recommended in support of outbreak investigations, due to low sensitivity of tests (many false-negatives).

Since most foodborne viruses can not be cultured *in vitro*, detection methods are based on techniques of molecular amplification. Molecular methods remain important tools, even though they are unable to discriminate between infectious and non-infectious viruses.

Molecular methods, such as reverse-transcriptase polymerase chain reaction (RT-PCR) methods are less time- and labour-intensive and have facilitated the analysis of large numbers of samples. They can also be designed to be quantitative or semi-quantitative. Once validated, these methods will be useful in outbreak investigations, as well as in auditing and monitoring of control systems.

The routine use of virus detection methods for foods is limited to a few laboratories in a few countries. There is a need to transfer this technology to other locations in an effort to promote its more routine use.

8.1.5 Priority virus-commodity combinations

Virus-commodity combinations of the highest priority are NoV and HAV in shellfish, fresh produce for raw consumption and prepared foods. This prioritization is based on current knowledge, which is not complete. However, the establishment of these combinations is important as we seek to develop mitigation and intervention strategies. It should be kept in mind

that mitigation of one virus would probably help in preventing other viruses too, as they often have a common source.

Criteria needed to prioritize the virus-commodity combinations of public health concern were based on categorization of strength of causal evidence, which in turn was based on a limited body of evidence. Prioritization can be done according to the following criteria: disease severity, incidence or prevalence, probability of exposure, trade impact, public health cost, and ability to control foodborne infections

Because of lack of epidemiological information, further ranking of virus-commodity combinations in order of public health priority is not currently possible.

8.1.6 Risk assessment

While fully quantitative risk assessments are not yet feasible, it is currently possible to use risk assessment to gain a better understanding of foodborne viruses. Initially, conceptual models or models addressing specific aspects, such as food handling, can and are being developed. As well as providing insights into routes of transmission, such risk assessments can be used to identify data needs and prioritize research. Thus, it was concluded that a stepwise approach to risk assessment is already feasible.

Although numerous data gaps for risk assessment were identified, it was also concluded that for some virus-commodity combinations (such as NoV and HAV in bivalve molluscs), there is already a solid body of knowledge. More information is always desirable and can be collected, but it is important that the collection of this information is prioritized and structured. Risk assessment can be a useful tool in this regard. While quantitative data on viruses is currently limited, the developments in methodology mean that it is now feasible to address this data gap.

While risk assessment can be undertaken as a research activity, it is more useful when targeted to address specific risk management questions, with the support of risk managers. Interaction between risk assessors and risk managers from an early stage can ensure that resources and risk assessment are directed towards the areas most needed.

8.1.7 Risk management

During primary production, there is a need to gain a better understanding of actual agricultural and aquaculture practices to identify high-risk practices, GAP implementation and compliance rates, and to what extent existing controls are effective against viruses.

Current food safety controls do not specifically address the issue of transmission of viruses by food products, and may be ineffective in controlling virus transmission. This problem may be exacerbated by the potential global health threats posed by new emerging pathogenic viruses should they become transmissible by the faecal-oral route.

The degree of information collected regarding foodborne viral outbreaks is often insufficient to support action to be taken by the relevant food safety authority.

Control measures should be targeted at prevention of contamination (e.g. preventive measures at source, sewage treatment, improved food handling), rather than through food processes, because, for the commodities of concern, there is currently a lack of post-harvest decontamination options. Prevention of environmental sewage and faecal contamination in bivalve mollusc harvesting areas should be a particular focus for risk management activities.

Researchers and risk managers need to be on alert to consider the likelihood of foodborne

transmission of newly emerging viruses.

8.2 Recommendations

8.2.1 Viruses of concern and burden of foodborne viral disease

Current estimates of foodborne viral disease incidence need to be refined. Studies allowing such estimates are needed, particularly in developing countries. Existing data from national reports should be systematically reviewed to identify possible sources of additional information indicating viral foodborne disease

To better compare national estimates, internationally agreed or harmonized standards for outbreak investigations are needed. This should include criteria for the minimum amount of data needed to provide clear evidence of a foodborne link, and protocols for environmental sampling and testing.

Studies of the prevalence and levels of virus contamination of foods commonly implicated in outbreaks need to be completed, and are essential to enable Quantitative Microbiological Risk Assessment (QMRA) to be conducted

An international platform for exchange of data from foodborne outbreaks, including strain sequence information, is needed to improve early detection of international common-source outbreaks.

8.2.2 Methodology

Efforts should be continued to develop simple, sensitive and robust methods, as well reviewing existing methods to ensure they are still relevant, for the detection of viruses in food samples. Sample size should be relevant, reflecting average serving sizes, and limits of detection should be adequate to ensure detection of the low levels of virus anticipated in naturally contaminated foods.

The growing number of methods increases the needs for inter- and intra-laboratory standardization and validation at national and international levels. This should include sampling procedure, detection limit determination, and virus extraction efficiency.

Guidelines for good laboratory practice for molecular-based assays to detect foodborne viruses should be developed to facilitate the dissemination and reliable use of methods for virus detection. This would assist in capacity building worldwide.

Similarly, global and regional reference centres and networks for detection of foodborne viral disease in humans would assist in capacity building for the detection of foodborne viral disease. At present, this is a very low priority, given the importance of other human diseases such as HIV, malaria and tuberculosis.

To improve applicability of molecular methods, better understanding is needed of the persistence of virus infectivity and the public health impact of detection of viral nucleic acids.

Methods for the detection of emerging viruses in clinical samples should be developed and validated for use in foods, should these viruses prove to be foodborne.

8.2.3 Research

Comparative studies should be conducted to determine the most appropriate surrogate viruses for inactivation and persistence studies.

The exact role and proportion of the different routes of contamination need to be assessed.

As food production and distribution are increasingly global, a network approach with partners in developed and developing countries is needed to undertake studies intended to fill in data gaps.

Additional data gaps and research needs are identified in Chapter 9, and should be addressed according to the specific needs of risk managers.

8.2.4 Risk assessment

A global hazard identification for human pathogenic viruses in foods should be conducted as a first step in international risk assessment efforts for viruses in foods.

Given the current lack of data, an incremental approach to virus risk assessment is recommended. This could include:

- The development of conceptual models to provide insights into modes of transmission and exposure pathways, and to identify data needs and prioritize research.

- Further development of the risk assessment model for the contamination route of food handling, with the inclusion of a module to take into account transmission via vomitus.

- Modelling of environmental contamination (sewage, manure) using approaches developed by other disciplines.

- Identification of relevant data and approaches used in bacterial risk assessments that could be applied to virus risk assessment.

- Targeted data collection, reflecting its importance in ensuring the development of relevant risk assessments.

- Specific studies undertaken to facilitate the estimation of dose-response relationships for viruses for which there are no data, and to elucidate the impact of the food matrix on the dose-response relationship.

8.2.5 Risk management

Intervention strategies should be focused on the priority virus-commodity combinations. Where possible these combinations should be reviewed for a specific region using the specified criteria and revised as new information and data become available.

The use of routine sewage monitoring to screen human transmission patterns and identify the potential for a greater likelihood of contamination during primary production should be evaluated.

Emerging viruses should be monitored, particularly when new problems arise, in an effort to assess the potential for foodborne transmission. The specific research needed to address this question should be defined at the early stages of their emergence, in collaboration with researchers with specific knowledge on foodborne virus transmission.

New and existing pre- and post-harvest processing technologies should be assessed for their viricidal potential in high-risk food products. Conducting meta-analysis in an effort to systematically understand virus persistence and inactivation in different food commodities is recommended.

Virus- and commodity-specific guidance would assist risk managers in better addressing the issue of foodborne virus contamination and anticipate measures needed in the event of outbreaks.

Food producers and risk managers must be aware of the potential for outbreaks as a result of virus contamination of food. In the case of an outbreak, they should understand the need for complete cooperation with investigators in an effort to identify effective corrective actions and reduce the public health impact of the event.

To adequately control foodborne viral infections, it will be necessary to heighten awareness concerning the potential for transmission by infected food handlers; optimize and standardize methods for detection of foodborne viruses and foodborne disease outbreaks; enhance laboratory-based surveillance to detect large common-source outbreaks at an early stage; develop quality control measures specifically for virus control; identify and emphasize the role of viruses in HACCP plans; inform consumers of the risks presented by foodborne viruses; and better understand transmission and risk through the application of risk assessment.

International standards for traceability would assist in management of foodborne viral illness, as well as in the identification of areas where specific measures are needed.

The management of some of the foodborne viral problems would benefit from better interaction between different sectors, such as those working in the clinical area, sewage treatment, weather information, and production and processing, particularly in the terms of data sharing that could assist in better targeting of control measures.

9. DATA GAPS

The meeting identified numerous data gaps, which if filled would greatly contribute to the level of knowledge on foodborne viruses.

- The contribution of different transmission routes to the global burden of foodborne viral disease.

- The role of food in certain viral infections is not fully understood. For example, it is not known what role food plays in transmission of HRV in children or in transmission of HEV.

- The role of foodborne transmission in generating new viruses by recombination is likely but not known.

- Methods for rapid assessment of the extent of outbreaks are needed (e.g. based on saliva testing).

- Methods for early discrimination of person-to-person outbreaks from foodborne outbreaks are needed.

- The role of insects (such as flies) as mechanical vectors is not known.

- There is a need to collect additional data to support or refute the role of irrigation water as a means of contamination for fresh-produce items.

- Lack of knowledge on sewage treatment plan efficiency on viruses. Lack of control for sewage discharge.

- Lack of precise information on the occurrence of various virus strains in different types of foods, including zoonotic strains.

- Lack of data on persistence of infectivity and the public health impact of detection of viral nucleic acid during monitoring and testing.

- Absence of knowledge of human consumption patterns and food serving sizes in relation to testing volume.

- Data are needed on the prevalence of viruses in foods implicated in outbreaks.

- Meta-analysis of available data on virus survival and persistence on different food commodities, including thermal inactivation.

- Global agricultural practices, including the use and effectiveness of GAP programmes for virus control.

- The effectiveness of existing control points in food harvesting, processing and handling for virus control.

- Data on behaviour and compliance rates of food handlers.

- The role and probability of foodborne transmission for emerging viruses need to be investigated.

- The role and efficacy of rinsing and food sanitizers in removing virus contamination from produce items needs to be investigated. Similarly, the antiviral properties of currently available surface disinfectants should be investigated.

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ANNEX 1

BACKGROUND INFORMATION TO GLOBAL OVERVIEW OF INCIDENCE OF FOODBORNE VIRAL ILLNESS

(PRESENTED IN FIGURE 1)

Categories:

- Population-based estimates for foodborne viral gastroenteritis.

- Published studies for several population groups and viruses, but not population-based.

- Outbreak data (anecdotal).

- No data available.

Pubmed search parameters:

- Name of the country and virus and food.

- Name of the country and virus and outbreak.

Countries

Countries with population-based estimates for foodborne viral illness

The Netherlands, United States of America, United Kingdom, Australia, New Zealand and Japan (see Table 3).

Countries with published studies among groups within population related to food and/or anecdotal outbreak data

Austria, Canada, Botswana, Brazil, Chile, China, Denmark, Dominican Republic, Egypt, France, Germany, Greece, Hungary, India, Ireland, Israel, Italy, Jamaica, Japan, Korea (Republic of), Malaysia, Mexico, Morocco, Mozambique, Nicaragua, Norway Pakistan, Poland, Russia, Slovakia, Sweden, Switzerland, Taiwan (Province of China), Thailand, Tunisia and Turkey.

Countries for which data was not available, is unknown, or not yet identified in the literature

Afghanistan, Albania, Algeria, Angola, Argentina, Armenia, Azerbaijan, Belgium, Belarus, Belize, Benin, Bhutan, Bolivia, Bosnia Herzegovina, Brunei, Bulgaria, Burkina-Faso, Burundi, Cambodia, Cameroon, Central African Republic, Chad, Colombia, Congo, Côte d'Ivoire, Croatia, Cuba, Cyprus, Czech Republic, Djibouti, Ecuador, El Salvador, Equatorial Guinea, Eritrea, Estonia, Ethiopia, French Guyana, Gabon, Georgia, Ghana, Guatemala, Guinea, Guinea-Bissau, Guyana, Hawaii (USA), Honduras, Iceland, Indonesia, Iran, Iraq, Jordan, Kazakhstan, Kenya, Kyrgyzstan, Kuwait, Laos, Latvia, Lebanon, Lesotho, Liberia, Libya, Lithuania, FYR Macedonia, Madagascar, Malawi, Mali, Mauritania, Moldavia, Mongolia, Namibia, Nepal, Niger, Nigeria, Oman, Panama, Papua New Guinea, Paraguay, Peru, Philippines, Portugal, Qatar, Rumania, Rwanda, Saudi Arabia, Senegal, Serbia, Sierra Leone, Slovenia, Somalia, South-Africa, Sri Lanka, Sudan, Surinam, Swaziland, Syria, Tajikistan,

Tanzania, Togo, Turkmenistan, Uganda, Ukraine, Uruguay, Uzbekistan, Venezuela, Viet Nam, Yemen, former Yugoslavia, Zambia, Zimbabwe,.

Sources of published studies on a country basis. Note that these are only examples of available data, not a complete overview.

USA: (1); Australia: (2); Netherlands: (3, 4); UK: (5); Canada: (6, 7), information sent to WHO; Brazil: (8–12); Mexico: (13); Russia: (14–17); China: (18–23); Japan:(24–26), papers sent to WHO; France: report, (27–29); India: (30, 31); Korea: (32–34); Sweden: (35–37); Chile: (38); Malaysia: (39); Nicaragua: (40); Taiwan (Province of China): (41); Jamaica: (42); Italy (43, 44); Switzerland (45); Germany (46–49); Poland (50); Austria (51, 52); Mozambique (53); New Zealand (54); Tunisia (55); Morocco (56); Pakistan (57); Israel (58); Turkey (59–61); Denmark (62, 63); Greece (64); Hungary (65); Slovakia (66).

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