ISWAVLD 2023
International Symposium of the World Association of Veterinary Laboratory Diagnosticians
29 JUNE-1 JULY 2023
Congress Centre Lyon
Towards the veterinary diagnostics of the future

Main topic :

Challenges and future direction for enteric viruses detection in food

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Introduction
Enteric viruses cause the majority of foodborne diseases and represent a serious public health concern. Among the enteric viruses, human norovirus (NoV) followed by hepatitis virus (HAV) are the main viruses suspected to cause foodborne outbreaks. Hepatitis E virus is recognized as an emerging viral foodborne pathogen that includes zoonotic transmission via pork products. Common symptoms include vomiting, diarrhea, abdominal pain and fever. Through the results obtained in the context of foodborne investigations, we will discuss the limits of current methods and new approaches that could improve diagnosis in food virology.

Methods
Enteric viruses are mainly transmitted through fecal-oral route, by person-to-person contact or by consuming contaminated water and foods consumed raw (such as vegetables, soft berries, shellfish…) or any other food contaminated by a food handler. Food samples analyzed in the frame of outbreak investigations cover the food generally found in institutional catering. Detection methods used in the field of food virology are currently based on a final detection of the viral genome using real-time reverse transcriptase PCR (RT-qPCR). The general strategy for the detection of enteric viruses in food samples consists in three steps: virus extraction, purification of viral RNA and quantitative molecular detection of viral RNA. Due to the complexity of the methods and the presence of substances that can inhibit PCR amplification, comprehensive sets of controls are used. According to the epidemiological studies, 246 suspected food samples, from 56 foodborne outbreaks investigation, were examined for the presence of four human enteric viruses (NoV GI and NoV GII, HAV or HEV) using either methods described in the EN ISO 15216 or in house methods. All viral analysis of food samples were performed with the implementation of process control and external amplification controls according to the ISO procedure.

Results
Eighteen of 56 foodborne outbreaks investigated included at least one positive food sample (16/18 NoV, 1/18 HAV and 1/18 HEV). The genomic levels of four viruses detected ranged from <102 to 107 genome copies per g or per L. By taking account both controls, results were not validated for 204 analyses out of 479 (42%).
The study highlights the need to develop effective molecular methods regardless of the type of food sample. Other ways can be proposed to improve molecular routine diagnosis such as digital PCR, high throughput PCR or metagenomics. In the same way, new molecular or cellular based methods (viability PCR method, real-time cell analysis (RTCA) …) could improve the viral risk assessment in terms of public health.

Conclusions
To conclude, this study showed the interest to optimize molecular methods for the extraction of viruses in different foodstuffs to better identify the association between viral diseases and food consumption. In the future, the development of new approaches for the detection of viral genomes or infectious viruses in food could be very useful for a better viral risk assessment.