S106
Symposium
Can metagenomics replace stool culture for surveillance and control of enteric infections?

Stool cultures have traditionally been used to diagnose enteric infections and to detect, investigate and control outbreaks of foodborne enteric infections. With the introduction enteric molecular enteric diagnostic panels, this is rapidly changing. These methods are fast and may help the clinicians decide when and how to treat patients with enteric diseases in a timely fashion. However, these non-culture based methods may be deleterious to the public health response to foodborne diseases because cultures are needed for subtyping to differentiate outbreak related patients from sporadic cases occurring in the society at the same time. Metagenomics, i.e., sequencing all genetic material in the sample, has the potential to serve both public health and diagnostics purposes without culture. The sequencing and bioinformatics technologies are quickly evolving and it may be possible within a foreseeable future to identify and characterize the whole microbial flora in a stool specimen in close to real-time. This way the etiology of the disease of the patient and the subtype including the antimicrobial susceptibility of the pathogen(s) involved could be determined at the same time, thereby speeding up both the diagnostic process and cluster detection for public health. Additionally, metagenomics could transform the way we perceive infectious diseases: since both commensals and pathogens will be sequenced along with the host genome, we will learn more about the virulence and interactions (complementation/enhancement/inhibition) between pathogens and commensals, and pathogens and the host, information that may be used for clinical decision making and public health action. For example, already today we know that patients infected with Shiga toxin (Stx) producing E. coli producing the Stx2a or Stx2d subtypes are more likely to develop Haemolytic Uremic Syndrome (HUS) than patients infected with any other Stx subtype; similarly, we know that non-secretors are resistant to norovirus infections. But can virulence factors produced by a commensal E. coli complement or enhance the virulence of a diarrhoeagenic E. coli? However, before metagenomics may be implemented in clinical and public health practice, a number of issues regarding IT-infrastructure, the sensitivity and specificity of the technology, as well as ethical issues related to using the host genotype in clinical decision making need to be resolved.