

Cruising with Noroviruses

Jan Vinjé, Ph.D.
University of North Carolina,
Chapel Hill, NC, USA.

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Statens Serum Institut
Cantina, Buildn. 37, room 1
5 Artillerivej, 2300 Cph. S.

Abstract:

Noroviruses (NoVs) are the most commonly identified cause of outbreaks and sporadic cases of acute gastroenteritis. Recent estimates of the proportion of foodborne illness showed that 50% of all foodborne outbreaks would be associated with noroviruses if all specimens were tested. Outbreaks of NoV have been caused by contaminated food and/or drinking water, person-to-person virus transmission, and airborne droplets of infected vomitus. Noroviruses can be separated into five genogroups on the basis of sequence comparison of a partial region of RNA dependent polymerase and capsid of the genome. Genogroups I, II, and IV (GI, GII, and GIV) are associated with infections in humans. A key problem in the detection of NoV is the great nucleotide diversity of strains that makes it difficult to design one set of primers to detect all strains with equal efficiency. More sensitive and reliable techniques are required to detect NoV in environmental samples, food, and water, in which viral loads are typically much lower than those found in clinical samples. In early human volunteer studies it was known that some individuals could not be infected with Norwalk virus and the recent discovery that humans lacking ABH histo-blood group antigens cannot be infected demonstrated that these antigens likely serve as receptors for Norwalk virus and perhaps other NoVs docking and entry. It appears that various NoV strains exhibit different patterns of attachment to ABH histo-blood group antigens. Although the mechanism behind the striking increase in the number of outbreaks in recent years predominantly caused by GII.4 is unknown, emergence of recombinant strains as well as possible animal reservoirs may play an important role how these viruses genetically evolve. The purpose of this presentation is to provide an overview on the latest developments in classification, sensitive detection as well as genetic typing of noroviruses.

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for veterinær- og
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Formand:
Overlæge, dr.med.
Anders Fomsgaard
Godthåbsvej 87
2000 F

E-mail:
AFO@ssi.dk

Internet:
www.virologi.dk

Danish Society for
Virology

President:
Anders Fomsgaard,
MD, DSc(med.)

Godthåbsvej 87
DK-2000 F

AFO@ssi.dk
www.virologi.dk