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Noroviruses (NoVs) are a major cause of foodborne outbreaks of acute gastroenteritis in humans. Transmission of NoV is commonly linked to the consumption of oysters as they accumulate viruses through filter feeding in faecal-contaminated water. The NoV genogroups (G), GI, GII and GIV infect humans. While GI and GII have often been verified as causative agents of oyster-transmitted illness, GIV is rarely detected and has so far not been confirmed in outbreaks related to oysters. The aim of this study was to determine whether NoVs from oysters implicated in a disease outbreak were linked to the GI, GII and GIV found in the stool samples from infected patients. NoVs were quantified in the oyster samples using Taqman real-time RT-PCR and characterised by sequencing of the partial capsid region. The results confirmed the presence of GI, GII and GIV in the oysters in levels between 101 - 103 detectable genome copies/g of digestive tissue. Sequences of the NoV strains found in oysters clustered with GI.3, GI.6, GII.7 and GIV.1, and showed 87, 79, 79 and 90% nucleotide identity to the respective genotypes found in patients. This discrepancy in sequence identity is not surprising and is probably due to the contamination of the oysters with multiple strains discharged with sewage. To our knowledge, this is the first study characterising NoV GIV in outbreak related oysters. Our results confirm the inherent challenges of establishing the linkage between NoV strains in patients and foods contaminated by sewage.

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