Isolated norovirus GII.7 strain within an extended GII.4 outbreak.

Abstract:

Noroviruses are a major cause of viral gastroenteritis and have been detected with increasing prevalence in recent years. Currently, two main genogroups GI and GII with an increasing number of subtypes are differentiated. Because of a high genetic variability new variants emerge constantly allowing epidemiological tracing of viruses from year to year and location to location. A 282 bp sequence at the 5’end of the capsid gene was analyzed in isolates originating from the University hospital, Technische Universität München. Phylogenetic analysis was based on 20 GII positive samples from an outbreak in March/April 2006 and 8 samples from the following winter season 2006-2008. In the initial outbreak two distinct genotypes were identified. The GII.4 strain 2006a found in the majority of outbreaks in 2006 worldwide was isolated from all but two patients. These two individuals were infected with a GII.7 strain clustering mainly with isolates from Asia. Of note, they excreted noroviral RNA for 81 and 27 days, respectively. Longitudinal analysis of an extended 1381 bp sequence revealed positive selection in the P2 domain. The variant was very similar to GII.7 strains isolated in 1990 and 1994 suggesting slow evolution with evidence of recombination according to the SimPlot analysis. Strains found in the following years 2006-2008 clustered around the isolate GII.4 2006b, characterized in the spring of 2006 and reaching a high prevalence.
in 2006-2007. The results provide an insight into norovirus evolution at a University hospital over 3 years and describe intraindividual evolution within a patient infected chronically.