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Genetic Analysis of Human Norovirus Strains in Japan in 2016-2017.

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Abstract

In the 2016/2017 winter season in Japan, HuNoV GII.P16-GII.2 strains (2016 strains) emerged and caused large outbreaks of acute gastroenteritis. To better understand the outbreaks, we examined the molecular evolution of the *VPI* gene and *RdRp* region in 2016 strains from patients by studying their time-scale evolutionary phylogeny, positive/negative selection, conformational epitopes, and phylodynamics. The time-scale phylogeny suggested that the common ancestors of the 2016 strains *VPI* gene and *RdRp* region diverged in 2006 and 1999, respectively, and that the 2016 strain was the progeny of a pre-2016 GII.2. The evolutionary rates of the *VPI* gene and *RdRp* region were around 10^{-3} substitutions/site/year. Amino acid substitutions (position 341) in an epitope in the P2 domain of 2016 strains were not found in pre-2016 GII.2 strains. Bayesian skyline plot analyses showed that the effective population size of the *VPI* gene in GII.2 strains was almost constant for those 50 years, although the number of patients with NoV GII.2 increased in 2016. The 2016 strain may be involved in future outbreaks in Japan and elsewhere.

KEYWORDS: RNA-dependent RNA polymerase; capsid; epitope mapping; molecular evolution; norovirus; phylogeny

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A Food Poisoning Outbreak Due to Food Handler-Associated Contamination with the Human Norovirus GII.P16-GII.2 Variant Strain in Italian Cuisine in Tokyo during the 2016/17 Winter Season.

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KEYWORDS: Norovirus; food poisoning outbreak; variant

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