Co-circulation of Three Recombinant Norovirus Genogroup II Genotype 4 Variants, 2014—2016, Hong Kong, China

Martin C.W. Chan, Kirsty Kwok, Tin-Nok Hung, Lok-Yi Chan and Paul K.S. Chan

Correspondence: Dr. Martin Chan, PhD (martin.chan@cuhk.edu.hk)

Department of Microbiology, Faculty of Medicine, Chinese University of Hong Kong, Hong Kong, China

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Background

Norovirus is a leading cause of acute gastroenteritis and food-borne illnesses worldwide. All age groups are affected but certain groups, including infants, young children, the elderly, and the immunocompromised are particularly vulnerable to more severe clinical outcome. Norovirus is genetically diverse and one genotype known as GII.4 has been globally-circulating in the past two decades. New variants of norovirus GII.4 emerged every 2 to 4 years and they were usually associated with surge in norovirus outbreaks. The most recent pandemic GII.4 variant was called Sydney 2012 (GII.4 Sydney) that has already emerged for over 4 years. Close molecular surveillance of norovirus gastroenteritis is important to detect the next pandemic GII.4 variant.

Materials and Methods

Hong Kong is a coastal city in southern part of China. Starting from March 2014, our team has established a molecular surveillance of **in-patients of all ages** with laboratory-confirmed norovirus gastroenteritis in our hospitals. All norovirus GII.4 cases were subjected to partial RNA-dependent RNA polymerase (RdRp) gene genotyping and full-length capsid (VP1) gene was determined by Sanger sequencing. Virus genotype and variant assignment were performed using RIVM's online Norovirus Genotyping Tool. Phylogenetic inference was performed using the neighbour-joining statistical model.

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Results

- From March 2014 to February 2017, a total of 1129 stool samples were collected from 1109 patients. The median age was 3 years (interquartile range: 1—44 years). Norovirus VP1 genotype was determined from 991 (89.4%) cases.
- **Top 3 circulating VP1 genotypes were GII.4 (n=527; 53.2%), GII.17 (n=180; 18.2%), and GII.2 (n=88; 8.9%) (Figure 1)**.
- All GII.4 strains belonged to VP1 Sydney, except for two strains that were classified into New Orleans. RdRp genotyping of VP1 Sydney revealed 3 genotypes: **GII.Pe (n=496; 94.1%), GII.P16 (n=21; 4.0%), and GII.P4 New Orleans (n=8; 1.9%)**.
- GII.P16 was first detected in January 2016 whilst GII.P4 New Orleans was detected sporadically throughout the study period **(Figure 2)**.
- Phylogenetic analysis of VP1 showed that GII.4 strains with different RdRp genotypes formed distinct clusters and those carried GII.P4 New Orleans were most distant from the prototype strain of GII.4 Sydney **(Figure 3)**.

Conclusions

- We report co-circulation of three recombinant norovirus GII.4 variants from March 2014— February 2017 in Hong Kong. **The predominant variant was GII.Pe_GII.4 Sydney.**
- **In sharp contrast, GII.P16_GII.4 Sydney** that emerged in the winter of 2015/16 and accounted for a majority of outbreaks in the US **remained a minority in Hong Kong.**
- Close monitoring of the spread of the 2 emergent recombinant GII.4 variants is needed.

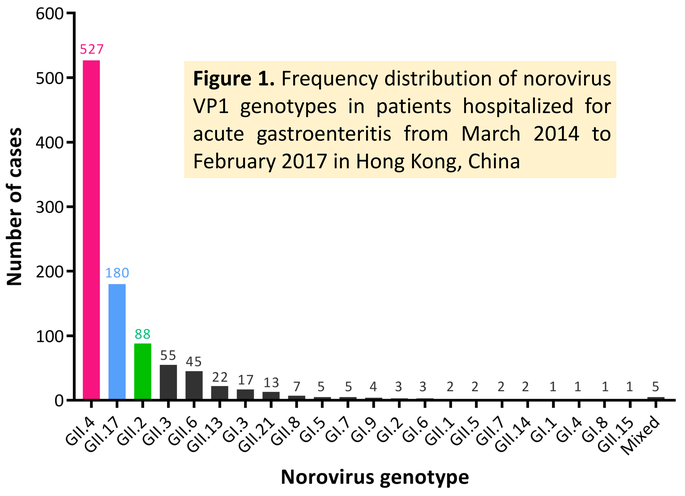

Figure 1. Frequency distribution of norovirus VP1 genotypes in patients hospitalized for acute gastroenteritis from March 2014 to February 2017 in Hong Kong, China

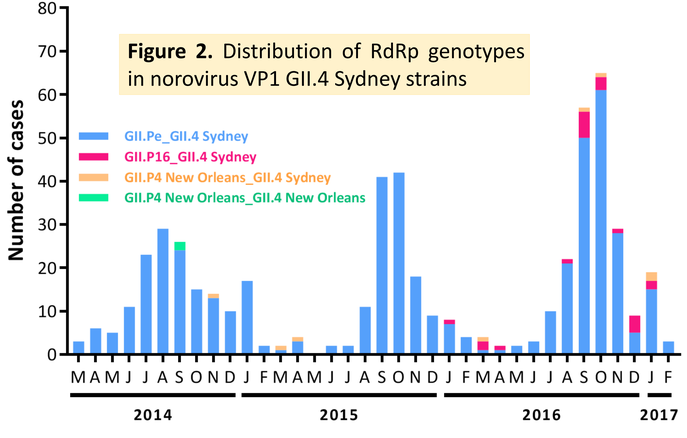

Figure 2. Distribution of RdRp genotypes in norovirus VP1 GII.4 Sydney strains

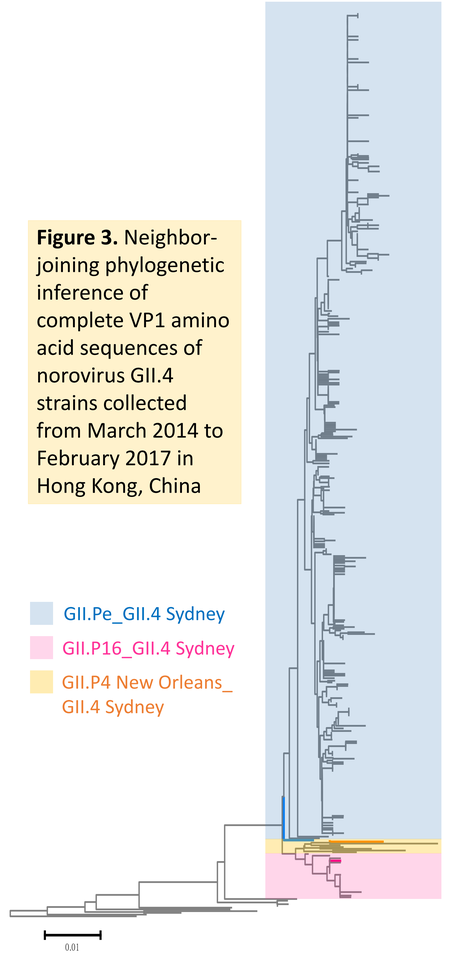

Figure 3. Neighbor-joining phylogenetic inference of complete VP1 amino acid sequences of norovirus GII.4 strains collected from March 2014 to February 2017 in Hong Kong, China