Emergence and Predominance of a Fast-mutating and Putatively Immune-escaped Novel Variant of Norovirus Genogroup II Genotype 17 in Hospitalized Gastroenteritis, 2014—2015, Hong Kong

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Background/Objective

Norovirus is the leading cause of acute gastroenteritis. Phylogenetically, norovirus is classified into at least 5 genogroups and nearly 40 genotypes. One genotype, known as genogroup II genotype 4 (GII.4), has been the major circulating genotype and is associated with most hospitalized (i.e., severe) norovirus gastroenteritis. Beginning from December 2014, there was an increase in the number of hospitalized norovirus gastroenteritis attributed to a GII.17 instead of the usual GII.4 genotype. Here, we aim at characterizing the recent norovirus GII.17 genotype.

Method

This study included all laboratory-confirmed cases of norovirus gastroenteritis in our ongoing, hospital-based norovirus surveillance between March 2014 and February 2015. Age distribution of GII.4 and GII.17 cases were compared. Complete GII.17 viral protein 1 (VP1) sequencing was performed. Phylogenetic inference was made using maximum likelihood method. GII.17 VP1 substitution rate was estimated using root-to-tip and BEAST analyses. Mutations in putative antigenic epitopes of GII.17 VP1 were mapped through homologous modelling.

Result

A total of 355 hospital cases of norovirus gastroenteritis were studied. Virus genotype was known in 320 (90.1%) cases. During December 2014-February 2015, GII.17 cases outcompeted GII.4 cases (65.2% versus 21.4%; $p<0.0001$). GII.17 cases were older than GII.4 cases (median age [interquartile range], 53 [9-75] versus 3 [1-11] years; $p<0.0001$). Phylogenetic analysis suggested the recent GII.17 represented a novel variant that we named "GII.17 Hong Kong 2014". Residue substitutions and insertion were observed in 4 of 5 inferred antigenic epitopes on GII.17 VP1 which has an estimated substitution rate of 2.4x10-2 nucleotide substitutions/site/year. Two sequential GII.4-GII.17 infections were noted.

Conclusion

The fast-mutating and putatively immune-escaped novel norovirus GII.17 Hong Kong 2014 lineage causes severe gastroenteritis in all age groups, including previously less vulnerable population. The epidemic spread of a rare norovirus genotype underlines the highly dynamic and unpredictable nature of norovirus genotype circulation that may complicate vaccine development.