

Continuous Emergence and Disappearance of Sub-lineages of Norovirus GII.4 Sydney 2012 during 2012-2016 in Hong Kong

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About Us

Background

- Human noroviruses are the leading causes of acute gastroenteritis affecting all age groups worldwide.
- Norovirus GII.4 variants emerged every 2 to 4 years. The latest variant emerged in 2012 and was called Sydney 2012.
- Mechanism of GII.4 molecular evolution remains elusive.

Aim

- To study phylodynamics of norovirus GII.4 Sydney 2012

Results

- Overall, strains in the 2012/13 season formed a genetically **diverse central pool of haplotypes** from which 5 major sub-lineages (SL1-SL5) emerged (**Figure 1**).
- SL1**: First emerged in the 2012/13 season, SL1 became the major sub-lineage in the 2013/14 season and then waned and disappeared completely in the 2015/16 season.
- SL2 and SL3**: First emerged in the 2013/14 season, both became the major sub-lineage in the 2014/15 season with reduced detection in the 2015/16 season.

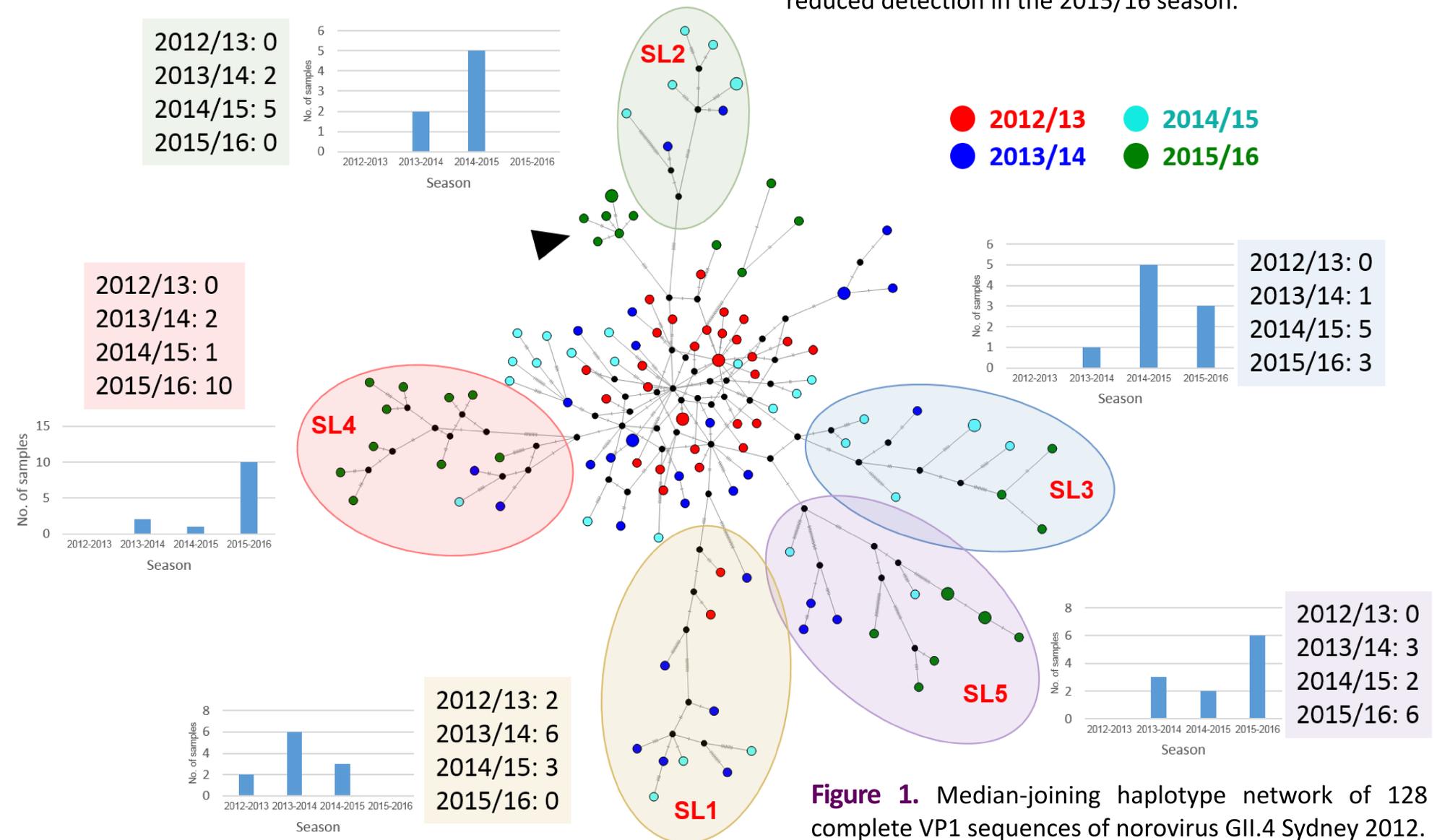


Figure 1. Median-joining haplotype network of 128 complete VP1 sequences of norovirus GII.4 Sydney 2012.

Methods

- From August 2012 to March 2016, 461 GII.4 Sydney 2012 strains were obtained from hospitalized cases in Hong Kong.
- Complete major capsid viral protein 1 (VP1) sequences were determined in 348 (75.5%) cases by either **Sanger sequencing** or **next-generation sequencing of amplicons on illumina's MiSeq platform**.
- A subset of 32 VP1 sequences were selected in each of the 4 norovirus seasons for analysis (e.g., from July 2013 to June 2014; in total 128 sequences).
- Phylogenetic inference was performed using median-joining haplotype network analysis by PopART v1.7.

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(cont'd from Results)

- SL4 and SL5**: First emerged in the 2013/14 season, both expanded progressively and became key sub-lineages in the 2015/16 season.
- A new cluster of strains arose from the central pool in the most recent 2015/16 season with potential to develop into a new sub-lineage (Figure 1, black arrow).**

Conclusions

Our findings show that norovirus GII.4 Sydney 2012 undergoes rapid genetic diversification during spread and displays continuous emergence and disappearance of sub-lineages. Norovirus GII.4 strains are continuously exploring nucleotide sequence space in a boom-and-bust cycling pattern for a new evolutionary more advantageous variant.