

Influenza B in Norway, 2016-2017 season: Lineage differences by region and age, and emergence of B/Victoria lineage deletion variant

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Summary

Among influenza B viruses circulating in Norway during the 2016/2017 season, approx. 80% were of the B/Yamagata lineage. There were, however, marked differences between regions and age groups. Late in the season, we have observed sporadic occurrence of the antigenically distinct B/Victoria lineage deletion variant first reported in North America.

Introduction

Only a small proportion of the influenza viruses circulating in Norway during the 2016/2017 season were type B, with strong influenza A(H3N2) predominance like in most other countries.

The influenza B viruses did, however, persist longer into the late season, reaching peak numbers only in mid-May. Out of approximately 3600 influenza B viruses detected nationally, more than 900 have been available for closer study in the National Influenza Centre (NIC). In this study, we analysed the patterns of geographic and age-group distributions of the different influenza B genetic lineages/groups.

Methods

- Aggregated weekly influenza detection data were submitted from nearly all Norwegian medical microbiology laboratories that test for influenza. These laboratories also forwarded a subset of positive specimens to the NIC.
- In addition, a network of sentinel practices submitted samples from patients with influenza-like illness.
- Reference influenza virus diagnostics was carried out by rRT-PCR, including a duplex assay detecting influenza B viruses by Victoria/Yamagata lineage.
- Haemagglutinin gene sequencing was carried out on a subset of the viruses.

Results

- Out of the 925 influenza B viruses genotyped, nearly 80% belonged to the B/Yamagata/16/1988 HA lineage. However, there was marked geographic heterogeneity (Fig.1). The Victoria/Yamagata lineage proportions conformed to the national data in large parts of the population-rich south-east and in northern Norway. However, in Western Norway Yamagata-lineage viruses accounted for more than 90% predominance. Conversely, in the two southernmost counties, B/Victoria/2/1987-lineage viruses were in majority.
- The two lineages were equally frequent among children less than 10 years old. The Yamagata lineage was particularly predominant among adults 35 years and older (90%) and with the highest incidence in the elderly above 75 years (Fig.2).
- During this season, a new genetic group of B/Victoria-lineage viruses has emerged in North America, with a two-amino acid deletion in the haemagglutinin gene and evidence of antigenic drift. Among 61 Norwegian Victoria-lineage viruses sequenced, six viruses, from cases occurring in different locations in April through June, belong to this genotype. At the time, they represented the first such viruses reported outside of North America. The cases have no apparent epidemiological links and the viruses differ genetically (Fig.3).

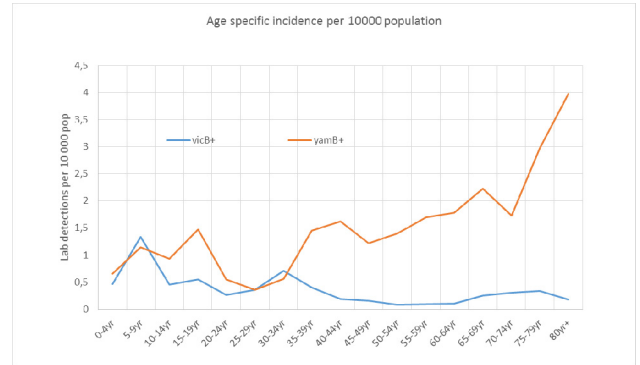


Figure 2: Incidence per 10 000 population of detected influenza B lineages, by 5-year age groups in Norway, 2016/17 season.

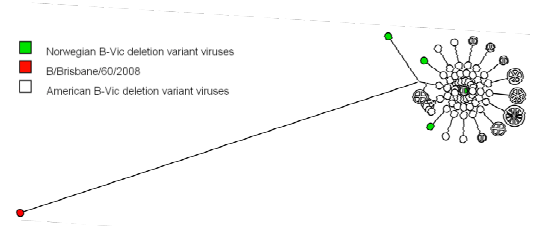


Figure 3: Cluster analysis of HA-encoding sequences of Norwegian and North American B/Victoria lineage viruses carrying the HA1 amino acid 162-163 deletion. Each circle or circle sector represents one virus. Included are the four Norwegian viruses for which complete HA0 sequence was obtained.

Conclusions

- The predominance of the influenza B/Yamagata lineage in Norway this season was most pronounced in older adults and elderly. The Yamagata lineage did not predominate over the Victoria lineage in young adults (20-34 years) and children less than 10 years old.
 - This probably points to different lineage-specific susceptibilities between age groups.
- The lineage distribution varied between regions
 - Geographic differences may have arisen through founder effects, i.e. due to different proportions among the limited sets of viruses introduced at the beginning of the season
- Our findings underscore the importance of population specific data to understand the epidemiology of influenza; nationwide data do not apply to every sub-national locality, and important differences may exist between age groups.
- The late-season detection of the novel influenza B/Victoria-lineage deletion variant in Norway was the first indication that this variant is occurring also outside North America.
- Epidemiological and genetic data indicates that the cases in Norway represented at least two independent virus introductions.
 - If there have been several introductions into one small European country like Norway, the virus variant probably has been dispersed also to other populations where it may persist beyond the end of the Northern Hemisphere season.
 - This makes it less likely that the variant will fade out with the ending of the seasonal influenza virus circulation in northern hemisphere populations.

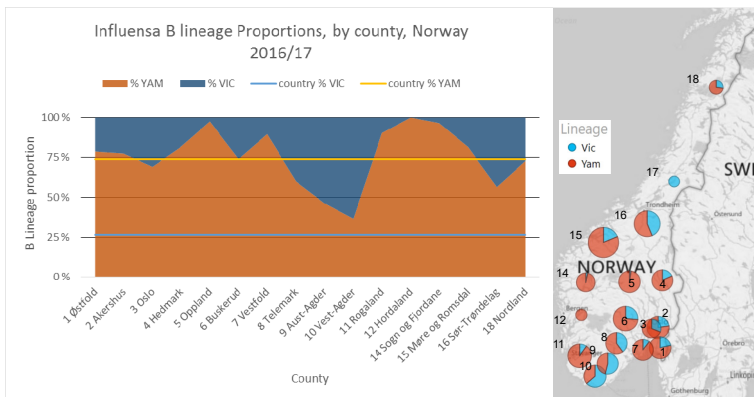


Figure 1: Proportions of influenza B lineages, by county in Norway, 2016/17 season. In the left hand panel, proportions per county are plotted in adjacent order (county numbering is indicated on the map). In the right-hand map, proportions in counties are plotted as pies where the pie size corresponds to number of characterised viruses. The smallest one contain 3 characterisations, the largest contains 91.