Antigenic dynamics analysis and vaccine recommendation for human influenza (A(H3N2), A(H1N1), B-Yamagata and B-Victoria) viruses based on PREDAC-like methods

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Summary

Computational methods to predict antigenic clusters for human influenza viruses (A(H3N2), A(H1N1), B-Yamagata and B-Victoria) have been developed in our lab (named as PREDAC-H3, PREDAC-H1, PREDAC-B, respectively).The method for influenza A(H3N2) has been demonstrated to be helpful in influenza vaccine recommendations (Du, et al., Nature Communications,2012,3:709). Here, based on the influenza HA1 protein sequences downloaded from GISAID and Influenza Virus Resource, we used the PREDAC methods to analyze the antigenic dynamics of human influenza viruses in recent years and make our recommendations for vaccines of the viruses. The results show that the antigenic clusters HK14, CA09, BR08 and PH13 dominated in the current for influenza A(H3N2), A(H1N1),B-Victoria and B-Yamagata viruses, respectively. No novel antigenic clusters were observed for all of them. Therefore, there is no need to update the influenza vaccines.

Antigenic dynamics and vaccine recommendation for human influenza A(H3N2) viruses

Figure 1A shows the antigenic evolution of influenza A(H3N2) viruses by antigenic cluster from 2008 to 2017, while Figure 1B shows the antigenic dynamics of the viruses in the same period. Obviously, in the last year, antigenic cluster HK14 dominated much. No new antigenic cluster was observed. However, the antigenic cluster HK14 have been dominant for three years since the season of 2014-2015. New antigenic clusters are very likely to appear in this year.

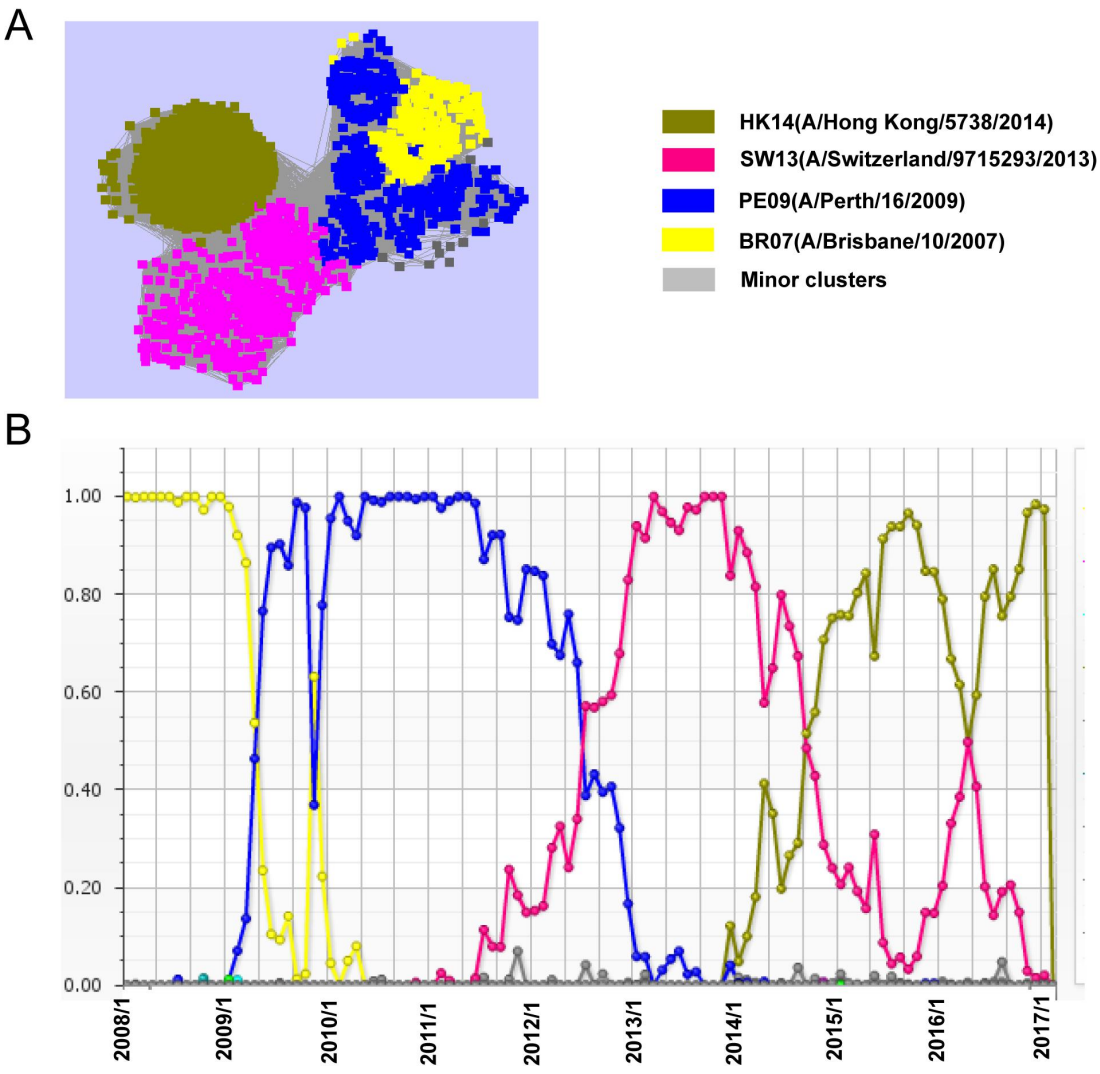


Figure 1: the antigenic correlation network (A) and dynamics (B) of human influenza A(H3N2) viruses from Jan 1st,2008 to Feb 12th,2017. Both the network and plot were colored by antigenic clusters according to the legend.

Antigenic dynamics and vaccine recommendation for human influenza A(H1N1) viruses

Although WHO has updated the influenza vaccine for the pandemic H1N1 viruses in last year, by our antigenic cluster analysis, there has been only one antigenic cluster observed since its emergence in 2009.

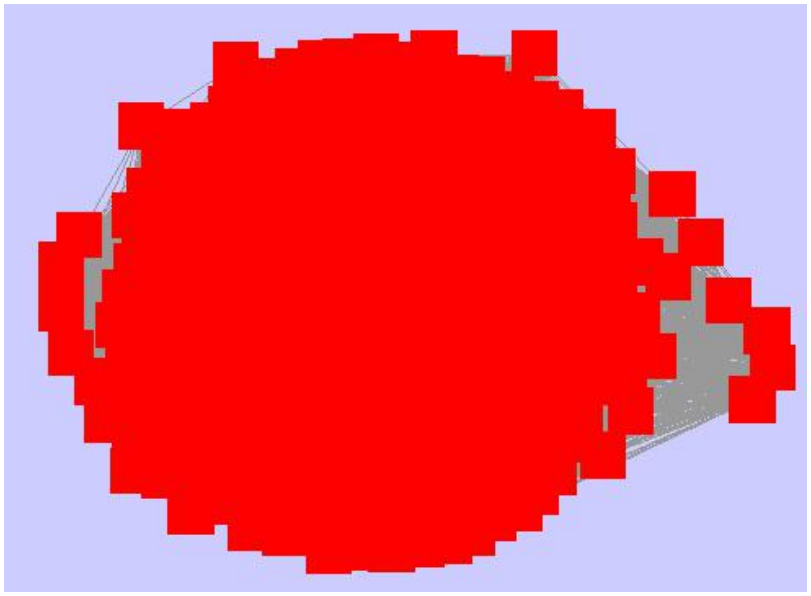


Figure 2: the antigenic correlation network for human influenza pandemic H1N1 viruses from 2009 to 2017. Only one antigenic cluster (named as CA09) has been observed since its emergence.

Antigenic dynamics and vaccine recommendation for human influenza B-Victoria viruses

Figure 3A shows the antigenic evolution of influenza B-Victoria viruses by antigenic cluster from 2000 to 2017, while Figure 3B shows the antigenic dynamics of the viruses in the same period. The antigenic cluster BR08 has been dominant for eight years since 2009.No new antigenic cluster was observed.

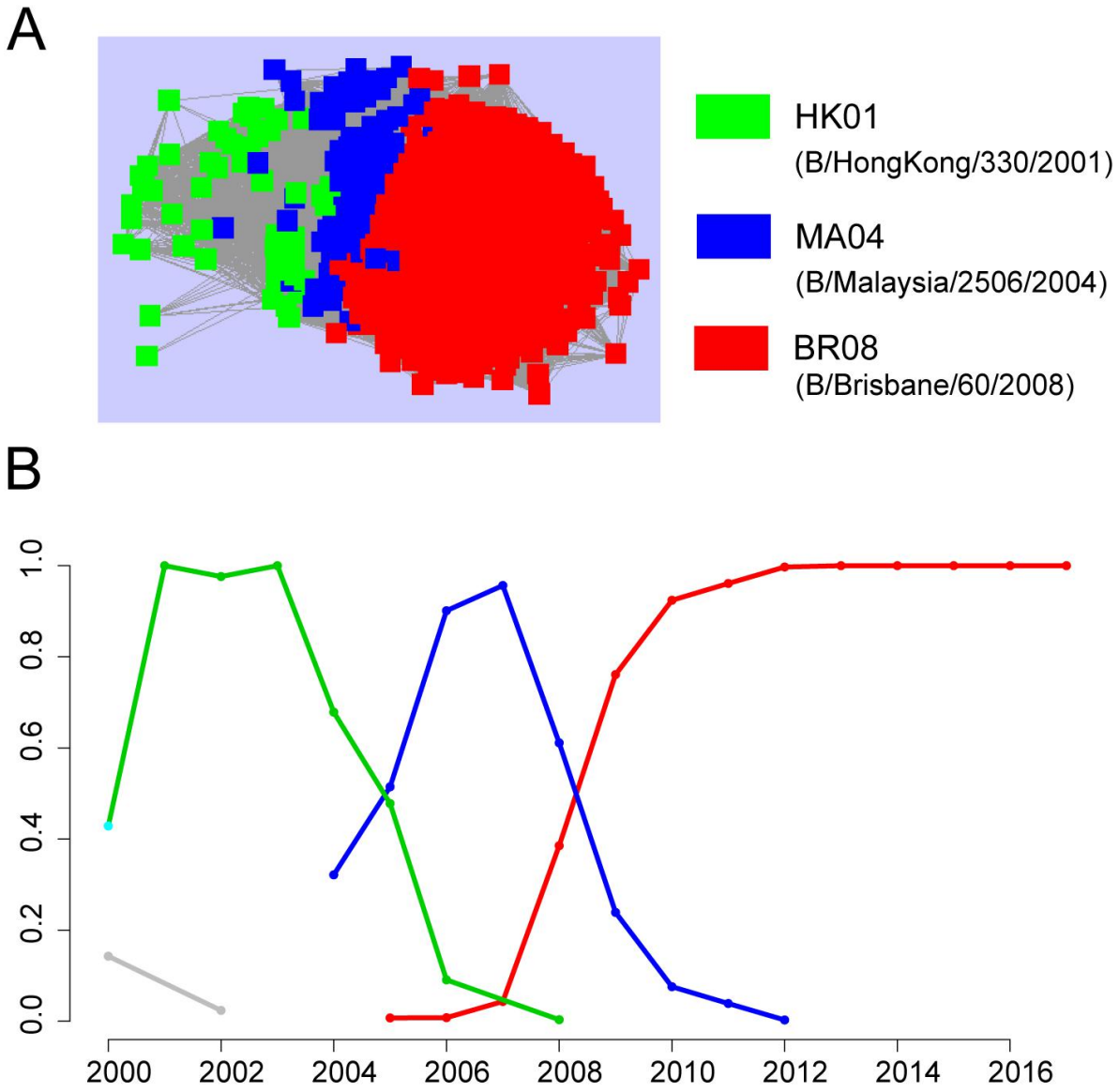


Figure 3: the antigenic correlation network (A) and dynamics (B) of human influenza B-Victoria viruses from Jan 1st, 2000 to Feb 12th,2017. Both the network and plot were colored by antigenic clusters according to the legend.

Antigenic dynamics and vaccine recommendation for human influenza B-Yamagata viruses

Figure 4A shows the antigenic evolution of influenza B-Yamagata viruses by antigenic cluster from 2000 to 2017, while Figure 4B shows the antigenic dynamics of the viruses in the same period. PH13 dominated completely in the last year. No new antigenic cluster was observed. However, the antigenic cluster PH13 has been dominant for 3 years since 2014. New antigenic clusters are likely to emerge in this year.

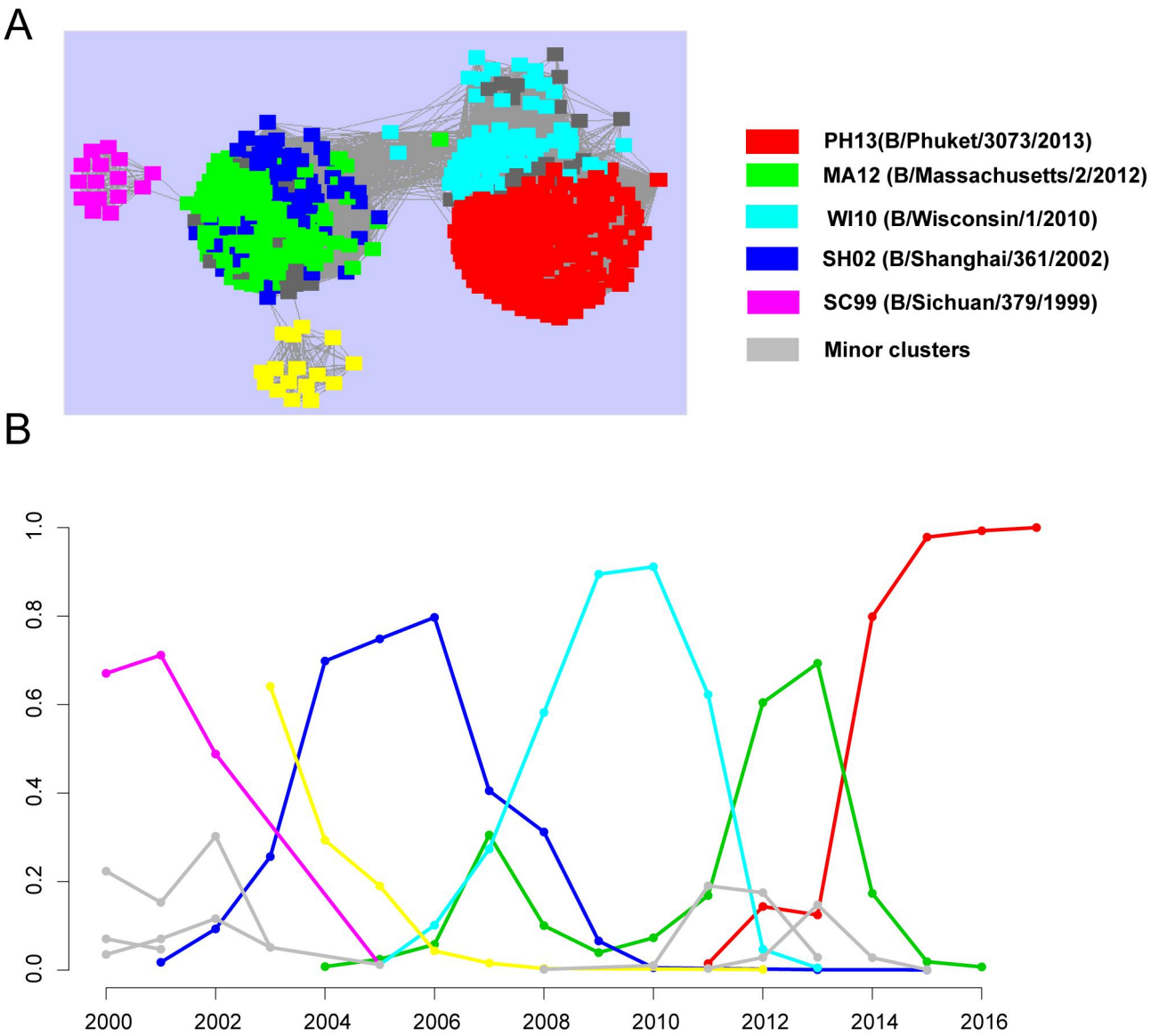


Figure 4: the antigenic correlation network (A) and dynamics (B) of human influenza B-Yamagata viruses from Jan 1st, 2000 to Feb 12th,2017. Both the network and plot were colored by antigenic clusters according to the legend.

Materials and Methods

1 Data

All the HA1 protein sequences for four kinds of human influenza viruses were downloaded from GISAID and Influenza Virus Resource databases on Feb 12th, 2017. The yearly number of HA1 protein sequences used for each kind of virus was displayed in Figures 5-8 below.

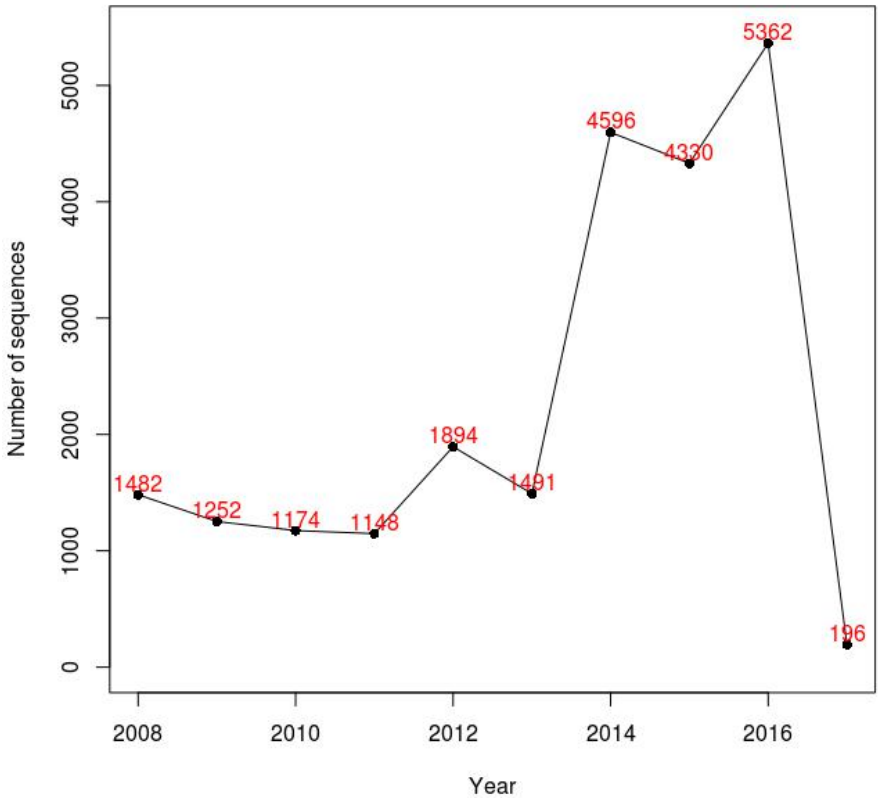


Figure 5: the yearly number of HA1 protein sequences used in this study for human influenza A(H3N2) viruses from 2008 to 2017. The numbers in red listed the detailed number of sequences.

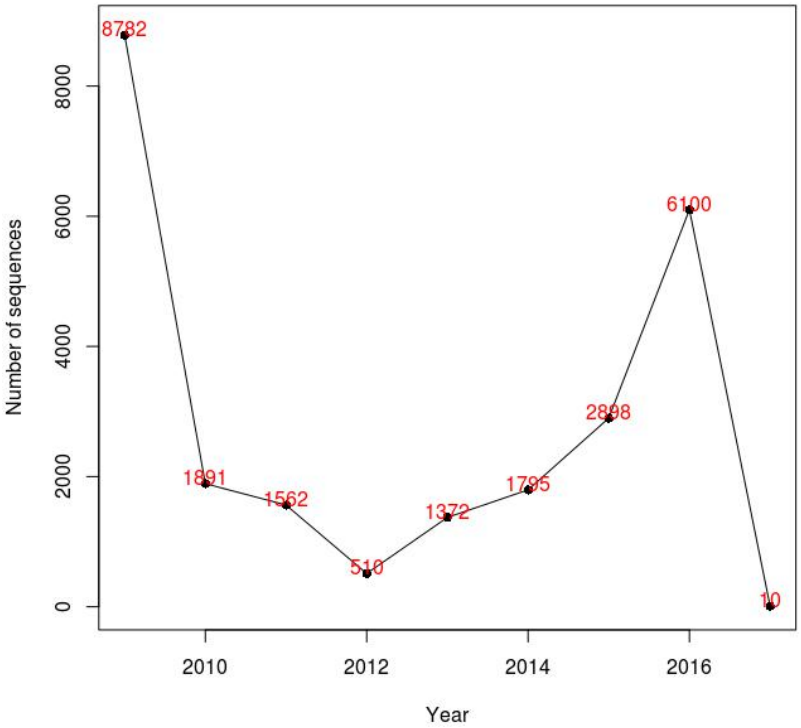


Figure 6: the yearly number of HA1 protein sequences used in this study for human influenza pandemic H1N1 viruses from 2009 to 2017. The numbers in red listed the detailed number of sequences.

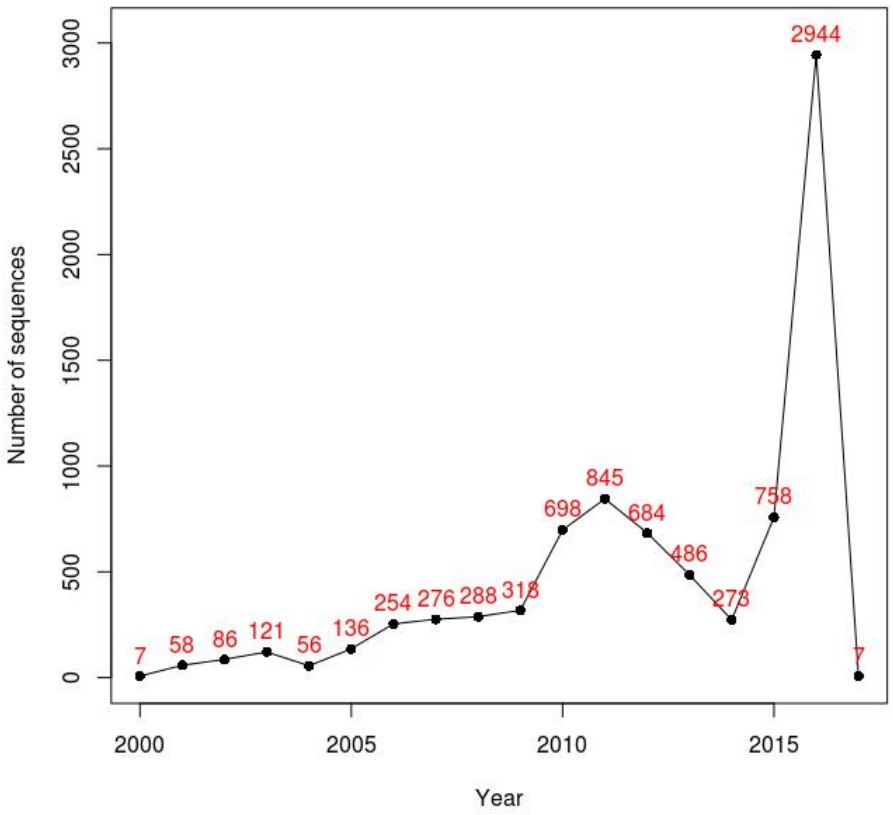


Figure 7: the yearly number of HA1 protein sequences used in this study for human influenza B-Victoria viruses from 2000 to 2017. The numbers in red listed the detailed number of sequences.

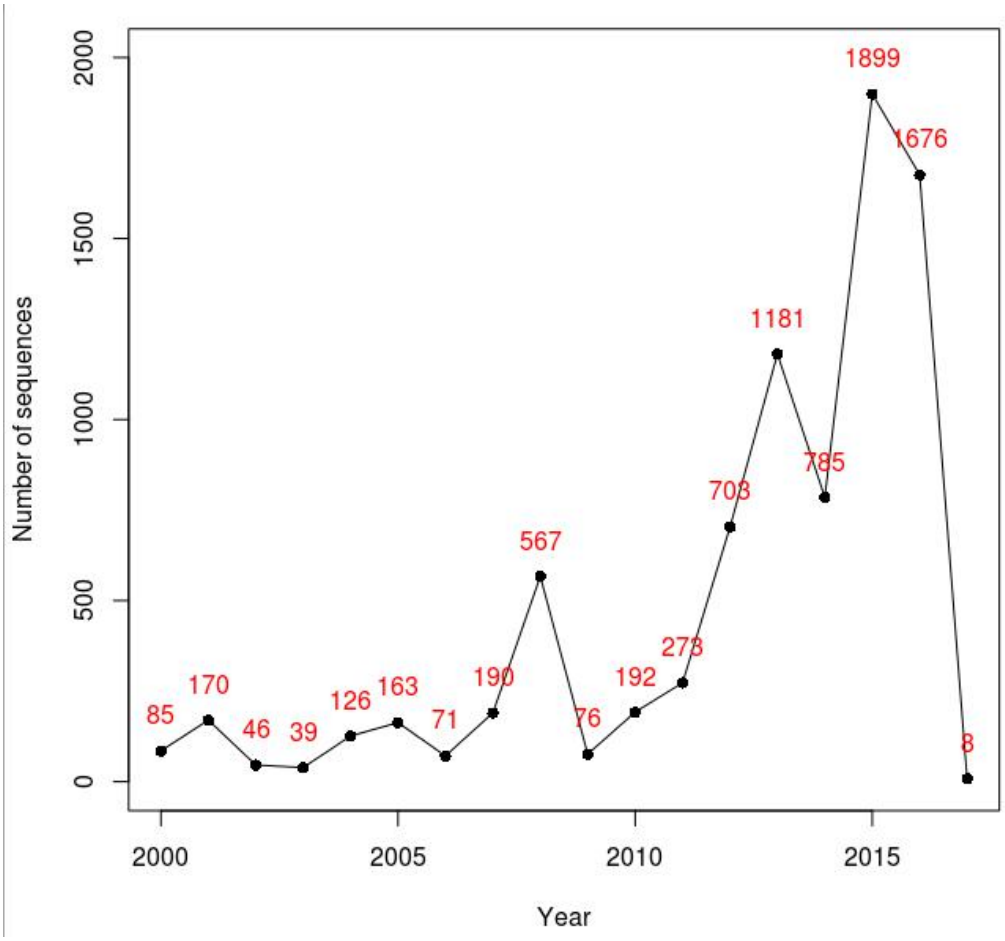


Figure 8: the yearly number of HA1 protein sequences used in this study for human influenza B-Yamagata viruses from 2000 to 2017. The numbers in red listed the detailed number of sequences.

Methods

PREDAC-H3 and PREDAC-H1 were adapted from Du et al.(Du, et al., Nature Communications,2012,3:709) and Liu et al.(Liu, et al., Scientific Reports,2015,5:14171), respectively. The antigenic dynamics plots for influenza A(H3N2) were adapted from our platform PREDAC-H3 (http://biocloud.hnu.edu.cn/influ411/html/index.php). PREDAC-B was developed in our lab (not published).