Research Square

Preprints are preliminary reports that have not undergone peer review.
They should not be considered conclusive, used to inform clinical practice,
or referenced by the media as validated information.

Hemagglutinin genetic characteristics of the influenza B virus Victoria lineage in Fujian Province from 2015 to 2022，China

Qi LIN
Fujian Center for Disease Control and Prevention Priority Laboratory for Zoonoses Research of Fujian
Yuqing YAN
Fujian Center for Disease Control and Prevention Priority Laboratory for Zoonoses Research of Fujian
Yanhua ZHANG
Fujian Center for Disease Control and Prevention Priority Laboratory for Zoonoses Research of Fujian
Jingjing WU
Fujian Center for Disease Control and Prevention Priority Laboratory for Zoonoses Research of Fujian
Hongbin Chen
chb@fjcdc.com.cn
Fujian Center for Disease Control and Prevention Priority Laboratory for Zoonoses Research of Fujian

Research Article

Keywords: Influenza B virus, Victoria lineage, Hemagglutinin, Sequence analysis

Posted Date: April 11th, 2023

DOI: https://doi.org/10.21203/rs.3.rs-2722108/v1

License: This work is licensed under a Creative Commons Attribution 4.0 International License. Read Full License

Additional Declarations: No competing interests reported.

Abstract

Objective

This study analyzed the molecular characteristics of hemagglutinin(HA) of the influenza B virus (IBV) Victoria lineage in Fujian Province from 2015 to 2022.

Methods

Fujian flu surveillence data during 2015.1.1-2022.3.31 were collected through China's Disease Prevention and Control Information System and counted.The strains were obtained from canine kidney passaged cells or chicken embryo culture isolates of influenza-like cases from the 2015–2022 Influenza Network Surveillance System.The virus nucleic acid was extracted, and the HA gene fragment was amplified by RT-PCR and sequenced .MEGA5.0, Net NGlyc 1.0 Server software to analyse genetic characteristics.

Results

From 2015 to 2022, the HA gene of the influenza B virus Victoria lineage in Fujian Province had three nucleotide lengths, 1758 bp、1752 bp and 1749 bp respectively.The HA gene differential loci are mainly involved in the antigenic determinant clusters 120-loop, 150-loop, 160-loop, 190-helix and several receptor binding sites(RBS).145, 166 and 197 glycosylation sites are more diverse relative to other glycosylation sites.

Conclusion

The variation of the HA gene of influenza B virus Victoria lineage in Fujian Province from 2015 to 2022 is diversifying and the number of variant loci is increasing year by year, and research should continue to be strengthened to provide basic data for the prevention and control of the epidemic in Fujian Province.

Background

Influenza B viruses are single-stranded negative-stranded RNA viruses of the orthomyxoviridae family. It can be divided into two major lineages according to their antigenic and genetic characteristics, represented by the strains B/Yamagata/16/88 and B/Victoria/2/87, referred to as the Yamagata and Victoria lineages respectively[-].During the 1990s, the spread of the Victoria lineage almost ceased, except for outbreaks found in Africa, but has dominated globally since the early 2000s[-]Influenza B is somewhat epidemiologically distinct from influenza A. Knowledge of the global epidemiology and disease burden of influenza B remains to be improved, particularly outside Europe and the United States[]. Like the influenza A virus, the influenza B virus relies on mutations in the viral outer membrane proteins, particularly the heavy chain HA1 gene for haemagglutinin, to alter antigenic properties to evade existing immune protection by antibodies, thus continuing to cause influenza epidemics []. Studies of antigenic and genetic analyses of pandemic viruses from many regions of the world have shown that the evolutionary pattern of influenza B viruses is more complex[]. HA is the main antigen of the virus, which is not only related to the body immunity, but also the molecular basis for the antigenic variation of influenza.n this study, the HA gene characteristics of influenza B virus Victoria lineage in Fujian Province from 2015–2022 were analysed at the molecular biological level to provide reference for the development of influenza epidemic prevention and control measures.

Materials And Methods

Sources of data and specimens

Influenza surveillance data in Fujian Province from 2015.1.1 to 2022.3.31 collected by the Chinese Information System for Disease Control and Prevention. The strains were sourced from influenza-like cases monitored by the influenza network in Fujian Province from 2015–2022 and isolated and cultured from canine kidney passaged cells or chicken embryos.

A total of 75 strains were randomly selected from Fujian Province from 2015 to March 2022 according to their distribution in different years and cities. In most years, the number of strains was 12 per year.Less than 12 strains in 2015 due to low numbers of early strains and in 2020 due to over-concentration of areas.Details are 2 strains in 2015, 12 strains in 2016, 12 strains in 2017, 12 strains in 2018, 12 strains in 2019, 10 strains in 2020, 12 strains in 2021, and 3 strains in January-March 2022. There are 67 cell culture strains and 8 chicken embryo culture strains.

Extraction Of Viral Nucleic Acid

Extraction of Viral Nucleic Acid
The viral RNA was extracted using the Nucleic Acid Extraction System in accordance with the instructions of the Viral RNA Extraction Kit from Tianlong Technology (Suzhou) Co., Ltd.

Primer Design And Synthesis

The sequences of primers are shown in Table 1 and were synthesized by SunYa Biotechnology (Shanghai) Co., Ltd.

Table 1
HA gene amplification primers for influenza B virus

Primer name	Sequence (5'-3')
B-HA-UniF	GGGGGGAGCAGAAGCAGAGC
B-HA-UniR	CCGGGTTATTAGTAGTAACAAGAGC

Rt-pcr Amplification And Sequencing

Nucleic acids were amplified with the SuperScript III One-step RT PCR System with platinum Taq High Fidelity DNA Polymerase kit (Invitrogen, USA). PCR instrument (Applied Biosystems Veriti Thermal Cycler, USA) amplification reaction procedure: 45℃ 60 min; 94℃ 2 min; 94℃ 30s, 44℃ 30s, 68℃ 3min, 5cycles; 94℃ 30s, 57℃ 30s, 68℃ 3min, 31cycles; 68℃ 7 min. The amplification products sequencing was completed by Beijing Novogene Technology Co., Ltd.

Sequence Analysis And Phylogenetic Tree

The sequences of influenza strains from Fujian Province were spliced using CLC Genomics Workbench 11.0 software and compared with WHO-recommended influenza vaccine strains from the Northern Hemisphere to analyse differences in amino acid sites, antigenic determinant clusters and receptor binding sites. The WHO recommends the Northern Hemisphere Victoria lineage vaccine strain B/Brisbane/60/2008 (GISAID:EPI902456)for 2015–2018, B /Colorado /06/2017(NCBI:CY236607.1)for 2018–2020 and B/Washington/02/2019 (GISAID: EPI1368874) for 2020–2022.

Download 98 strains of virus from different years and provinces in China from the GenBank database of the National Biotechnology Information Center (NCBI) (https://www.ncbi.Nlm.nih.gov/)of the United Statesand the database of the Global Shared Avian Influenza Data Initiative(GISAID) (https://gisaid.org/).They are 9 strains in 2015, 13 in 2016, 14 in 2017, 13 in 2018, 14 in 2019, 10 in 2020, 14 in 2021 and 11 in 2022.These 98 strains were combined with 75 strains from Fujian Province and 3 vaccine strains for a total of 176 strains to construct a Maximum Likelihood Evolutionary Tree using MEGA5 with JTT-Model, Bootstrap Reps set to 1000.The datasets generated and analysed during the current study are available in the NCBI and GISAID repository(isolate ID numbers are presented in Additional file1: Table S1).

Glycosylation site

Prediction of glycosylation sites in 75 strains from Fujian Province using Net NGlyc 1.0 Server online analysis software.

Results

Analysis of influenza epidemic in Fujian Province from 2015 to 2022

The results of PCR identification of original specimens of influenza-like cases from the influenza network surveillance in Fujian Province from 2015 to 2022 are detailed in Table 2 and Fig. 1.Compared to the number of original specimens positive for PCR of influenza-like cases in Fujian Province in 2015–2019 (3523–5551), the number in 2020 (930) is significantly and substantially lower.Compared to 2020, the number in 2021 (2514) is significantly higher, all in the Victoria lineage.The Victoria lineage remained at a high level in January-March 2022 (2006, 99.80%). The proportion of Victoria lineage (40.40%, 46.08%, 100% and 99.80%, respectively) surpassed the other types as the dominant endemic strain in 2016, 2019, 2021 and 2022 (January-March).Taken together, this indicates that the Victoria linage dominated most years in Fujian Province from 2015–2022.

Table 2
Composition ratio of different types of influenza surveillance in Fujian Province from 2015 to 2022

Type	2015	2016	2017	2018	2019	2020	2021	2022 (Jan-Mar)
B/Victoria	9.28% (327/3523)	40.40% (1988/4921)	9.15% (360/3935)	8.18% (349/4269)	46.08% (2558/5551)	37.42% (348/930)	100.00% (2514/2514)	99.80% (2006/2010)
B/Yamagata	38.52% (1357/3523)	9.77% (481/4921)	26.02% (1024/3935)	31.32% (1337/4269)	0.04% (2/5551)	0.11%(1/930)	0.00% (0/2514)	0.00% (0/2010)
A(H3)	50.75% (1788/3523)	27.8% (1368/4921)	48.26% (1899/3935)	5.06% (216/4269)	27.44% (1523/5551)	37.96(353/930)	0.00% (0/2514)	0.2%(4/2010)
A(H1)pdm09	1.45% (51/3523)	22.03% (1084/4921)	16.57% (652/3935)	55.45% (2367/4269)	26.45% (1468/5551)	24.52% (228/930)	0.00% (0/2514)	0.00% (0/2010)

Amino Acid Variation Of Ha Gene

The antigenic determinant of HA protein of influenza B virus mainly consists of four regions: 120-loop(116–137), 150-loop (141–150), 160-loop (162–170) and 190-helix (197–205), and the 120-loop of the Victoria lineage includes sites 75 and 77[]. The receptor binding sites (RBS) includes 190-helix (196–205), 240-loop (240–245), 140- loop (136–143), Phe-95, Trp-158, His-194, and Tyr-205[]. Differences in amino acid sites between the 75 Fujian Province strains

compared to previous years of northern hemisphere vaccine strains. Only the differences in the antigenic determinant cluster sites and receptor binding sites (RBS) are presented in Table 3. There were also some scattered amino acid differences outside the antigenic determinant cluster.

From 2015 to 2022, there were three circulating strains of HA gene with nucleotide length (1758bp, 1752bp and 1749bp). The prevalent strain 1752bp exhibits a deletion of 2AA at loci 162, 163 (Δ2)[]. The 1749bp prevalent strain exhibited a deletion of 3AA at loci 162, 163, 164 (Δ3).

The high number of loci and strains involved in the difference in strains from 2015–2022 in Fujian Province was 120-loop, followed by 150-loop, 160-loop, 190-helix, and RBS.New variant loci E128K and G133R add in 2019–2020, reverting to E128 and G133 in 2021–2022. New variant loci P241Q add in 2021, reverting to P241 in 2022. New variant loci K136E add in 2019–2022. New variant loci H122N/Q, A127T, E128K, P144L, N150K, S197D, K203R add in 2021–2022. The I117V, N129G/D and S197N variant loci were the same as the vaccine strain. The comprehensive analysis shows that the variation of the HA gene in the Victoria lineage in Fujian Province from 2015 to 2022 is diversified and the variant loci are increasing year by year.

Table 3
Variation of HA gene in influenza B virus Victoria lineage in Fujian Province from 2015 to 2022

	120-loop						120-loop RBS	150-loop RBS	150-loop				160-loop			
Vaccine strain / Year	117	122	127	128	129	133	136	141	144	146	147	150	162	163	164	169
B/Brisbane/60/2008	I	H	A	E	N	G	K	G	P	I	T	N	K	N	D	A
B/Colorado/06/2017	V	.	.	.	G	.	.	.	.	.	.	.	–	–	.	.
B/Washington/02/2019	V	.	.	.	D	R	E	.	.	.	.	.	–	–	–	.
2015 (2 strains)	0	0	0	0	0	0	0	0	0	2(V)	0	0	0	0	0	0
2016 (12 strains)	10(V)	0	0	0	12(D)	0	0	0	0	0	0	0	0	0	0	0
2017 (12 strains)	12(V)	0	0	0	12(D)	0	0	0	0	1(V)	0	0	0	0	0	0
2018 (12 strains)	12(V)	0	0	0	10(D)□ 2(G)	0	0	0	0	0	1(I)	0	2(-)	2(-)	0	0
2019 (12 strains)	12(V)	0	0	1(K)	10(D)□ 1(G)	11(R)	11(E)	0	0	0	0	0	12(-)	12(-)	11(-)	0
2020 (10 strains)	10(V)	0	0	1(K)	7(D)	10(R)	10(E)	0	0	0	0	0	10(-)	10(-)	10(-)	0
2021 (12 strains)	11(V)	2(N)□ 2(Q)	2(T)	0	12(D)	0	12(E)	1(R)	2(L)	0	0	12(K)	12(-)	12(-)	12(-)	0
2022 (3 strains)	3(V)	3(Q)	3(T)	0	3(D)	0	3(E)	0	3(L)	0	0	3(K)	3(-)	3(-)	3(-)	1(T)

Phylogenetic Tree Analysis

Figure 2 shows that the Clade 1 branch of the evolutionary tree contains three length prevalent strains.The Clade 1 branch HA nucleotide length is mostly 1758bp.The △2 branch has only 4 strains (3 strains in Fujian Province and 1strain in other province; 3 strains in 2018 and 1strain in 2019). The △3 branch contains strains from Fujian Province as well as from other provinces for the years 2019–2022.

In 2015–2020, the Fujian Province and the vaccine strains are located in Clade 1. In 2021–2022, the Fujian Province and other province strains are located in Clade 2.Clade2 branch is different from the branch of vaccine strains B/Washington/02/2019, B/Colorado/06/2017, B/Brisbane/60/2008 (Clade1), which indicates that there is a certain distance of evolutionary differentiation, suggesting that the matching degree of vaccine strains may be reduced.The N150K, G184E/K, and N197D loci began to differ in 2020, and the Clade1 to Clade2 transition suggests a change in prevalence.In addition to the large branches there are still a few scattered small branches in the evolutionary tree, suggesting localised population differences in infection.(See Fig. 2 for details).

Glycosylation Sites

Table 4 shows that the eight glycosylation loci of the HA gene 25, 59, 233, 304, 492, 518, 531 and 563 of the Fujian Province strain are relatively conserved. In contrast, the 145, 166, 171 and 197 glycosylation loci showed differential diversification. For example, there was no glycosylation at locus 197 in 2021–2022, whereas in previous years only individual strains were not glycosylated. 145 and 166 glycosylation loci differed in amino acids of individual strains, and only one strain was glycosylated at locus 171.

Table 4
Glycosylation sites of HA gene of influenza B virus Victoria lineage in Fujian Province from 2015 to 2022

Glycosylation site	Amino acid	Remarks
25	NVTG (75 strains)	/
59	NCTD (75 strains)	/
233	NQTE (75 strains)	/
304	NKSK (75 strains)	/
492	NQTC (75 strains)	/
518	NITA (75 strains)	/
531	NHTI (75 strains)	/
563	NVSC (75 strains)	/
145	NITN (71 strains), NVTN (3 strains), and no glycosylation site (1 strain)	No glycosylation. (B / Fujian-Yanping / 1651 / 2018 C2); NVTN(B/Fujian-Cangshan / 1487 / 2015 C1, B /Fujian-Hanjiang / 31 / 2015 C2, B /Fujian-Xiangcheng / 1228 / 2017 C1).
166	NKTA (74 strains), NKTT (1 strain)	NKTT (B / Fujian-Gulou / 1152 / 2022 E1)
171	NSST (1 strain), No glycosylation(74 strains)	NSST (B / Fujian-Fengze / 11273 / 2021 C2)
197	NETQ (56strains),No glycosylation(19 strains)	19 strains without glycosylation (1 strain in 2016, 1 in 2017, 2 in 2020 and all 15 strains in 2021–2022).

Discussion

Victoria lineage has been prevalent in Fujian Province every year since 2015, and has surpassed influenza A in several years. The sharp decline in the number of influenza cases in Fujian Province after 2020 and the fact that only the Victoria lineage will be prevalent in 2021–2022 are both directly related to the impact of the international environment.The emergence of a pandemic caused by SARS-CoV-2 and the implementation of various social and health measures have kept most people out of circulation. Influenza testing has decreased by 99% as of April 2020, and the SARS-CoV-2 pandemic has led to a significant reduction in cases of influenza A and B viruses globally[]. The current high level of population movement and the speed of circulation make the mutation of the virus more complex. The complex interplay of viral, host and ecological factors shapes the spatial and temporal incidence and evolution of human influenza viruses, and the influence of the surrounding environment on local areas of Fujian Province cannot be ignored. Multiple factors make it impossible to distinguish between strains from Fujian Province and other provinces in the same year.

Genomic analysis of the two influenza B virus lineages, Victoria and Yamagata, revealed fundamentally different phylodynamics, determined by the complex relationship between viral transmission, age of infection and receptor binding preference[]. From 2015 to 2022, the sequence length of the HA gene of the Victoria lineage in Fujian Province changed twice, with three nucleotide length strains (1758bp、1752bp and 1749bp), making the epidemiological situation more complex than before, suggesting that the Victoria lineage virus may be under great evolutionary pressure.Moreover, the table of amino acid site variation differences shows that the number of variation in antigenic determinant clusters of prevalent strains gradually increases over time.For a long time after 2010, WHO used B/Brisbane/60/2008 as the northern hemisphere vaccine strain or recommended strain.In contrast, the vaccine strain was changed in two to three years starting in 2018.The Victoria lineage subsequently became the dominant strain in Fujian Province in 2019. It is presumed to be closely related to the emerging epidemic strain (△3) to which the population is not immunized.

Analysis of the Victoria lineage suggests that the population is subject to high selective pressure, allowing it to evade human immunity by acquiring beneficial substitutes for the gene[]. Recently prevalent viruses including the Victoria and Yamagata lineages have relatively high entropy HA residues most often located in the 120-loop region[].Most of the 2015–2022 HA variants of the Victoria lineage strains in Fujian Province involved 120-loop.The 2022 strains from Fujian Province and other provinces are mainly located in Clade2, and differ from the other branches by A127T, P144L, K203R, which are antigenic determinant cluster sites (120-loop, 150-loop, 190-helix) and receptor binding sites, which are important for later herd immunization and screening of vaccine strains. The Clade2 to Clade1 conversion reflects a change in pandemic trend, as evidenced by differences at the N150K, G184E/K, and N197D loci.The new E128K and G133R variant loci are added in Fujian Province from 2019–2020, and E128 and G133 are restored after 2021.Analysis of amino acid substitutions in the HA gene of influenza B virus suggests that new and some old variants may co-transmit in the same epidemic[7]. Whether or not it is associated with alterations in the strain itself, it may affect the human immune response. The complexity of the immune response to influenza in individuals is associated with multiple exposures to different strains, and hosts with different exposure histories may continue to experience different patterns of infection, affecting the ongoing antigenic evolution of influenza viruses[].

It was found that the 145 glycosylation site was located in the 150-loop of the antigen determining cluster, the 166 glycosylation site in the 160-loop of the antigen determining cluster and the 197 glycosylation site in the 190-helix of the antigen-determining cluster, which were more diverse compared to the other glycosylation sites.The immunological impact of altered glycosylation sites, which may lead to structural changes in antigenic epitopes, is twofold: on the one hand, they may induce new immune determinants and induce specific immune responses; on the other hand, they may inhibit immune responses by closing or destroying antigenic epitopes through altered molecular or spatial structures by glycosylation[].Mutations in the N-glycosylation modification site can affect the level of vaccine specific T cells, which are involved in the regulation of antigen presentation and affect their vaccine adjuvant function[].Unlike

the situation in previous years, none of the Fujian Province strains were glycosylated at locus 197 in 2021–2022, suggesting a different trend of immune response to recent infections.

Studies related to the burden of influenza deaths in China have found higher levels of burden in the elderly, in northern regions and in patients infected with influenza A (H3N2) and B virus[].There is a large variation in the ability of Victoria lineage viruses to spread in humans during disease outbreaks, with a higher proportion of the HA gene for Victoria viruses in different genetic backgrounds, which may have important fitness implications[12]. This study suggests that the combination of multiple antigenic determinants and glycosylation sites in the Victoria lineage influences population prevalence, and the phylogenetic tree analysis shows that the evolution of strains has become more complex in recent years.The prevalent strains of the virus are genetically diverse and may not be as effective in preventing infection in people who do not receive an annual flu vaccination.There is increasing pressure to screen for vaccine strains and continuous monitoring will help to understand epidemiological patterns and adjust prevention and control programmes.

Abbreviations

HA hemagglutinin

IBV influenza B virus

RBS receptor binding sites

Declarations

Additional files

Additional files1 Table S1 .The isolate ID numbers of the datasets generated and analysed in the current study are listed in Additional file 1 Table S1 .

Acknowledgements

We are grateful to the authors and their laboratories for sharing the influenza virus sequences in the GISAID EpiFlu database, and send our sincere acknowledgement to the staff of the Centers for Disease Control and Prevention of Fuzhou District, Xiamen District, Quanzhou District, Zhangzhou District, Sanming District and Nanping District, Fujian, China for their assistance in collecting samples.

Author contribution

Hongbin Chen and **Qi Lin**: Project design, experimental research, data collection, analysis / interpretation data, paper writing, financial support; **Yuqing Yan ,Yanhua Zhang** : implement the research, collected data; **Qi Lin** , and **Jingjing Wu** : data collection, administrative, technical or material support.

Funding

This study was funded by the Fujian provincial health technology project(No.2020QNB015).

Data Availability

The dataset used and analyzed in this study are stored in GISAID/NCBI and FJCDC. The datasets are available upon reasonable requests to the corresponding author.

Ethical approval

The collection of samples was conducted for the control and management of national notifiable diseases, no human or animal researches were conducted, and therefore ethical approval was not required.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

1. Rota PA , Wallis TR , Harmon M W , et al. Cocirculation of two distinct evolutionary lineages of influenza type B virus since 1983. Virology, 1990, 175(1):59-68.
2. Kanegae Y , Sugita S , Endo A , et al. Evolutionary pattern of the hemagglutinin gene of influenza B viruses isolated in Japan: Cocirculating lineages in the same epidemic season[J]. J Virol, 1990, 64(6):2860-2865.DOI：10.1128/JVI.64.6.2860-2865.1990
3. Koutsakos M, Nguyen TH, Barclay WS,et al.Knows and unknows of influenza B. Future Microbiol 2016; 11(1):119-35.

4. Nichols JM, Bourne AJ, Chen H,et al.Sialic acid receptor detection in the human respiratory tract:evidence for widespread distribution of potential binding sites for human and avian influenza viruses. Resp Res 2007; 8(1):73.
5. Caini S,Huang QS,Ciblak MA,et al.Epidemiological and virological characteristics of influenza B: results of the Global Influenza B Study.Influenza Other Respir Viruses.2015;9 Suppl 1(Suppl 1)3-12.
6. Guo Yuanji, Cheng Xiaowen. Influenza virus and experimental techniques . Beijing: China Three Gorges Press, 1997:42-102.
7. Kanegae Y , Sugita S ,Endo A , et al. Evolutionary pattern of the hemagglutinin gene of influenza B viruses isolated in Japan: cocirculating lineages in the same epidemic season.. J Virol, 1990, 64(6):2860-5.
8. Wiley DC, Wilson IA, Skehel JJ. Structural identification of the antibody-binding sites of Hong Kong influenza haemagglutinin and their involvement in antigenic variation. Nature,1981, 289(5796):373-378.
9. Weis W, Brown JH, Cusack S, et al. Structure of the influenza virus haemagglutinin complexed with its receptor, sialic acid. Nature,1988,333(6172):426-431.
10. European Centre for Disease Prevention and Control. Influenza virus characterisation, summary Europe,December 2020. Stockholm: ECDC; 2020. [EB/OL] https: //www. ecdc. europa.eu/ sites/default/files/documents/Influenza-characterisation-report-December2020.pdf.
11. Koutsakos M, Wheatley AK, Laurie K,et al. Influenza lineage extinction during the COVID-19 pandemic?. Nature Rev Microbiol 2021191212741-742 .
12. Vijaykrishna D,Holmes E,Joseph U,et al.The contrasting phylodynamics of human influenza B viruses. eLife.2015;4e05055.
13. Reina J. The Victoria and Yamagata Lineages of Influenza B Viruses, unknown and undervalued. Rev Esp Quimioter 2022353231-235 .
14. Suptawiwat O; Ninpan K;,Boonarkart C, et al.Evolutionary dynamic of antigenic residues on influenza B hemagglutinin. Virology,2017,502:84-96.
15. Cobey S,Hensley SE.Immune history and influenza virus susceptibility. Curr Opin Virol ,2017,22:105-111.
16. Yang Yili, Wu Jun. Progress in investigating the relationship between viral antigen glycosylation and immunity . Chinese Journal of Letters in Biotechnology , 2008,19 (5): 728-730.
17. Guo Peng, Li Changfei, Ju Ying, et al. Effects of N-glycosylation modification on the immunological function of the heat shock protein gp 96 . Chinese Journal of Biotechbology, 2021,37(11):4036-4046.
18. Li Sa, Liu Sijia, Zhu Aiqin, et al. A matic review of the burden of influenza deaths in China . Chinese Journal of Preventive Medicine, 2019, 53(10): 1049-1055.

Figures

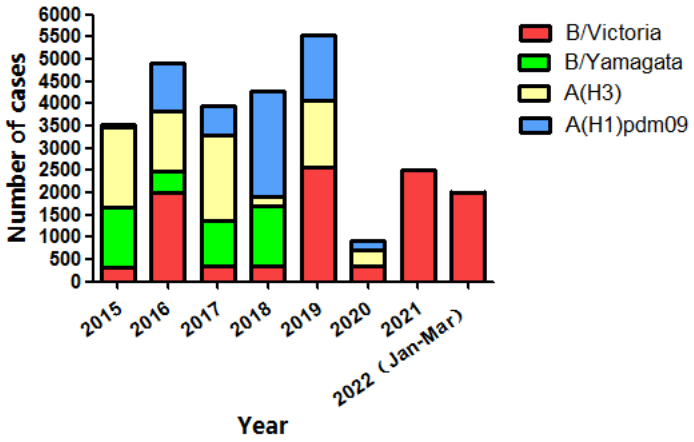


Figure 1

Different types of influenza surveillance in Fujian Province from 2015 to 2022

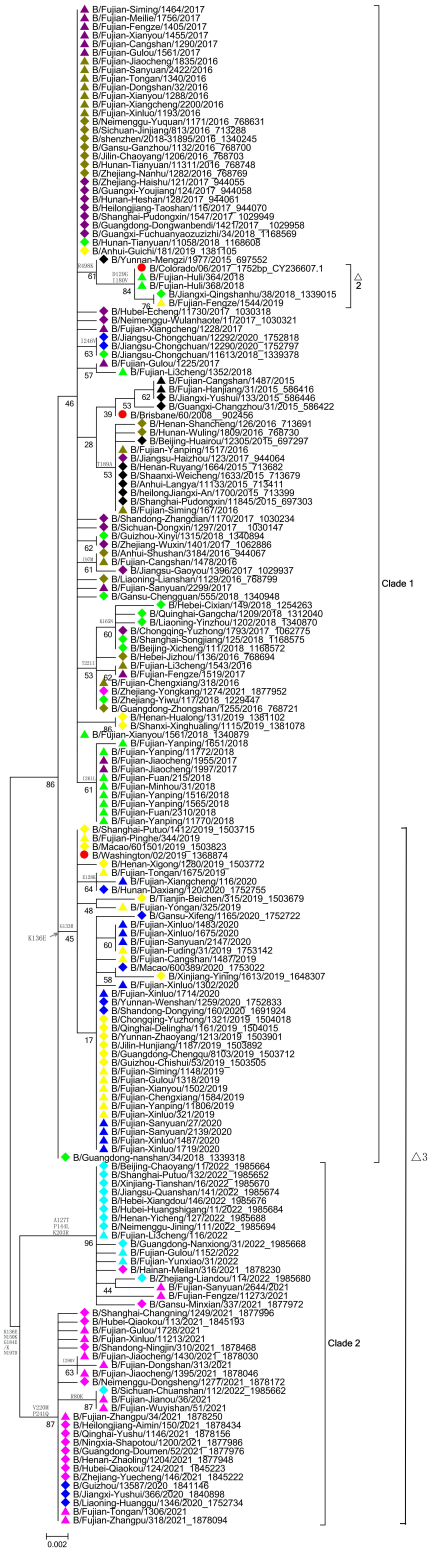


Figure 2

Evolution of HA gene of influenza B virus Victoria lineage in Fujian Province from 2015 to 2022

Note:Black: 2015; Grey: 2016; Dark purple: 2017; Green: 2018;

Yellow: 2019; Blue: 2020; Purple: 2021; Light blue: 2022；Red: vaccine strain

Fujian Province：▲ strains from other provinces: ■ ； vaccine strains:●

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- Additionalfile1TableS1.xls