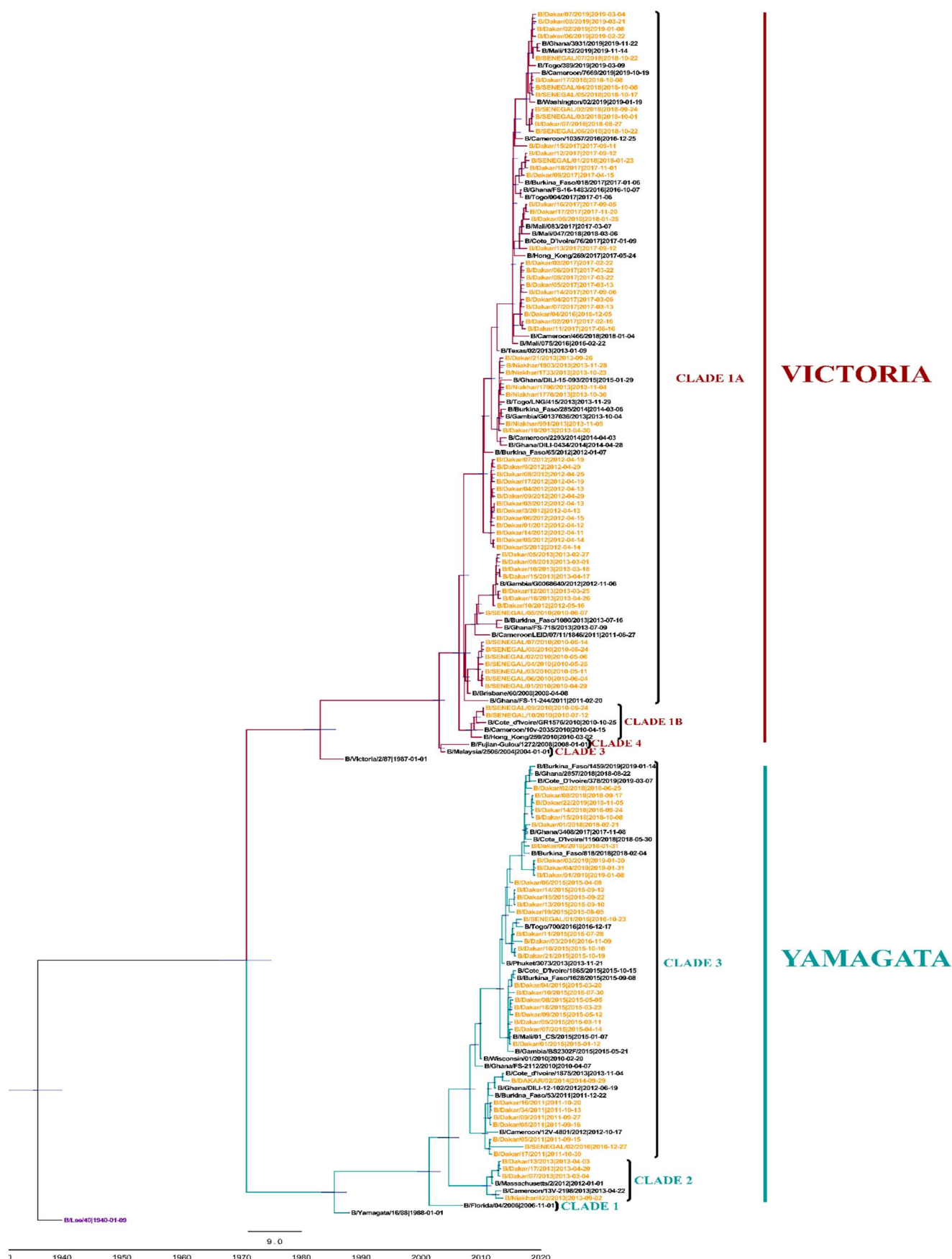


Supplementary Figure S1: Alignment of the amino acid sequences of HA gene (B/Vic) of twelve Senegalese strains that circulated in 2018 and 2019. Vaccine strain B/Brisbane/60/2008 was used as reference strains. Deletion in HA gene are indicated in the orange box.

[1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111111	1111111112]
[0000000001	1111111112	2222222223	3333333334	4444444445	5555555556	6666666667	7777777778	8888888889	9999999990]
[1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890]
#B/Brisbane/60/2008 2008-04-08	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAENAPGGP	YKIGTSGSCP	NITNGNGFFA	TMAWAVPKND	KN	KTATNPLT	
#B/Dakar/17/2018 2018-10-08	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGGP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/SENEGAL/01/2018 2018-01-23	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGGP	YKIGTSGSCP	NITNGNGFFA	TMAWAVPKND	KN	KTATNPLT	
#B/SENEGAL/02/2018 2018-09-24	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGGP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/SENEGAL/03/2018 2018-10-01	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGGP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/SENEGAL/04/2018 2018-10-08	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGGP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/SENEGAL/05/2018 2018-10-17	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGGP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/SENEGAL/06/2018 2018-10-22	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGGP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/SENEGAL/07/2018 2018-10-22	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAENAPGRP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/Dakar/02/2019 2019-01-08	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGRP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/Dakar/06/2019 2019-02-22	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGRP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/Dakar/08/2019 2019-03-21	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGRP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	
#B/Dakar/07/2019 2019-03-04	KIP SARV SIL	HEVRPVTSGC	FPI MHDR TKI	RQLPNLLRGY	EHVRLSTHNV	INAEDAPGRP	YEIGTSGSCP	NITNGNGFFA	TMAWAVPKN	--	KTATNPLT	

Supplementary Figure S2. Phylodynamic tree of HA gene for Senegalese circulating strains. The tree was obtained by the Markov Chain Monte Carlo method using the BEAST software. 200,000,000 steps were required and the GTR + G model was used. Strain B/Lee/1940 was used to root the tree. The Senegalese strains are indicated in orange.



Supplementary Figure S3. Phylodynamic tree of HA gene for Senegalese circulating strains. The tree was obtained by the Markov Chain Monte Carlo using the BEAST software. 200,000,000 steps were required and the GTR + G model was used. Strain B/Lee/1940 was used to root the tree. The Senegalese strains are indicated in orange.

