

1 **Supplemental Material**

2 **FIGURES**

3 **Fig. S1.** HRSV-A phylogenetic tree constructed from the sequences of the second HVR  
4 of *G* using the maximum likelihood method with the best model (GTR + G).

5 A phylogenetic tree was constructed using the maximum likelihood method with 1000  
6 iterations for the bootstrap using MEGA version 7.0.26. Only bootstrap values greater  
7 than 70% are shown. The evolutionary distances were computed using the p-distance  
8 method and the scale bar represents the number of nucleotide substitutions per site.  
9 Strains detected at Hospital O are shown in red and those detected at Hospital H are shown  
10 in blue. The strains circulating in different countries are shown in purple. The  
11 representative strains of each genotype are shown in green.

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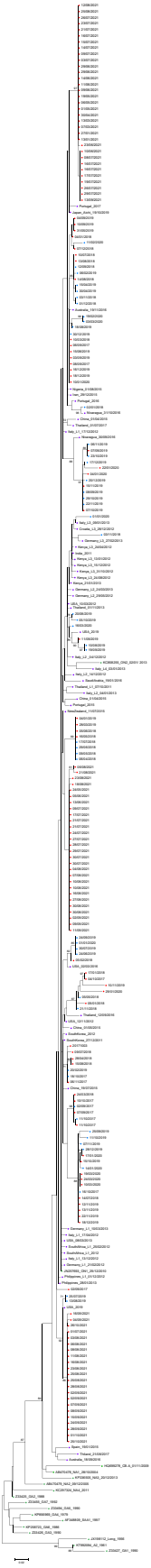
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19 **Fig. S2.** Details of the time-scaled maximum clade credibility tree using the best model  
20 (GTR) of the second HVR of *G* from HRSV-A constructed using the Bayesian Markov  
21 chain Monte Carlo (MCMC) method under the exponential molecular clock. Only  
22 posterior probabilities greater than 0.8 are shown. Strains detected at Hospital O are  
23 shown in red and those detected at Hospital H are shown in blue. The strains circulating  
24 in different countries are shown in purple. Representative strains of each genotype are  
25 shown in green.

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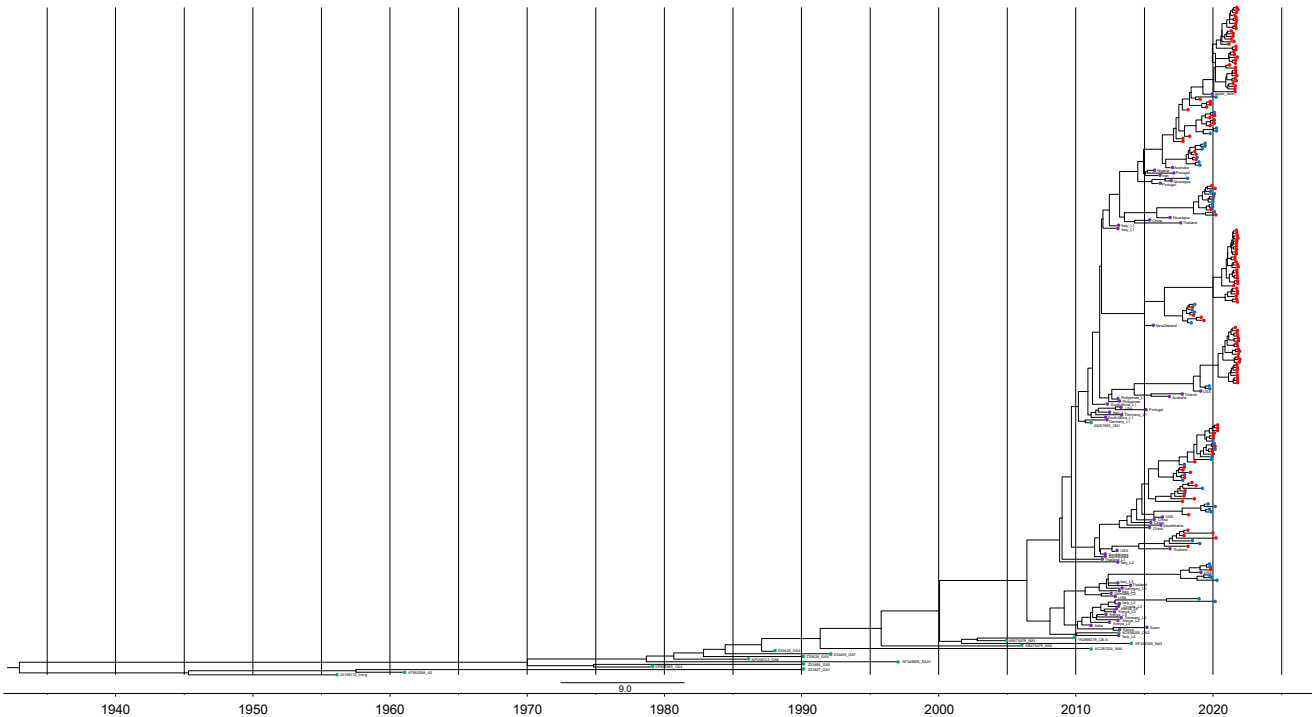
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# HRSV-A



37 **Fig. S3.** HRSV-B phylogenetic tree constructed from sequences of the second HVR of *G*  
38 using the maximum likelihood method with the best model (GTR + G).

39 The phylogenetic tree was constructed using the maximum likelihood method with 1000  
40 iteration for the bootstrap using MEGA version 7.0.26. Only bootstrap values greater than  
41 70% are shown. Evolutionary distances were computed using the p-distance method and  
42 the scale bar represents the number of nucleotide substitutions per site. Strains detected  
43 at Hospital O are shown in red and those detected at Hospital H are shown in blue. The  
44 strains circulating in different countries are shown in purple. Representative strains of  
45 each genotype are shown in green.

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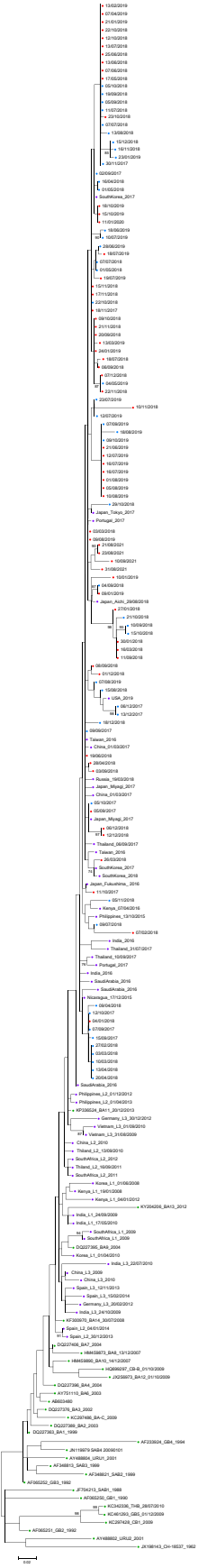
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55 **Fig. S4.** Details of the time-scaled maximum clade credibility tree using the best model  
56 (GTR) of the second HVR of *G* from HRSV-B constructed using the Bayesian Markov  
57 chain Monte Carlo (MCMC) method under the exponential molecular clock. Only  
58 posterior probabilities greater than 0.8 are shown. Strains detected at Hospital O are  
59 shown in red and those detected at Hospital H are shown in blue. The strains circulating  
60 in different countries are shown in purple. Representative strains of each genotype are  
61 shown in green.

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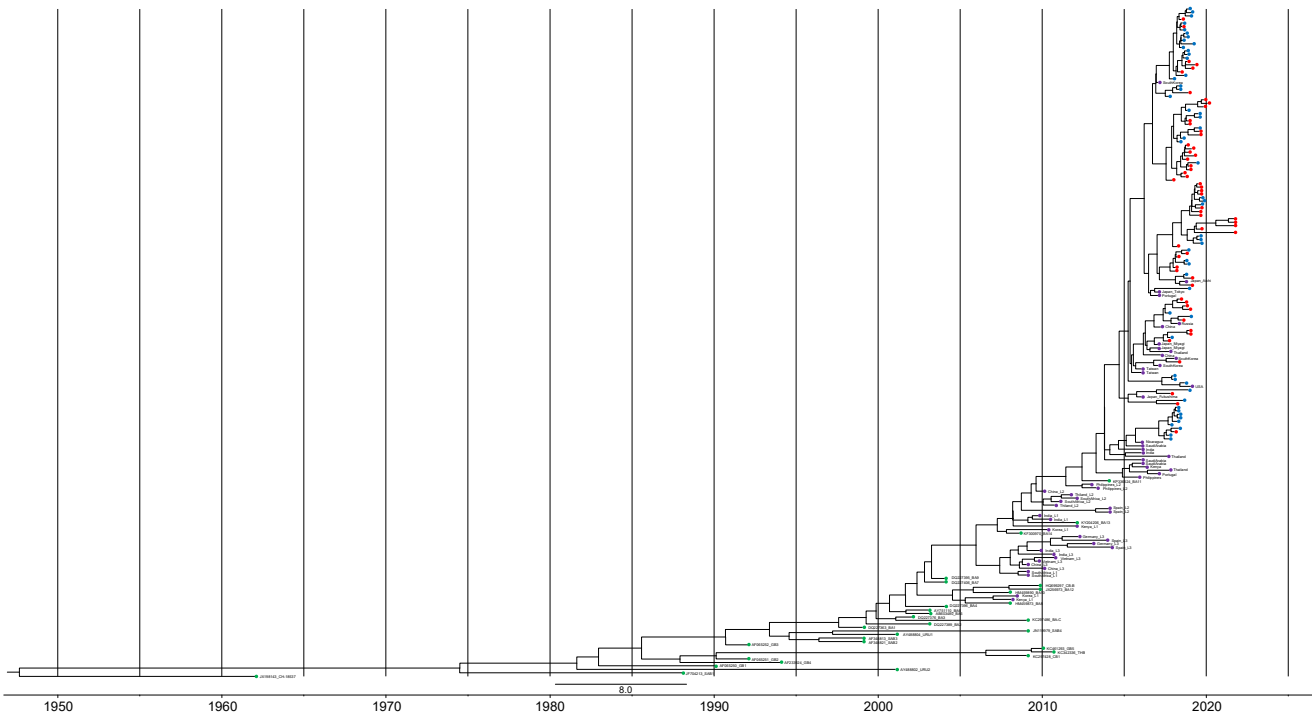
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# HRSV-B





73 **TABLES**

74 **Table S1.** Evolutionary rates of the analyzed HRSV-A and HRSV-B strains.

Subtype	Mean rate (95 % HPD) (substitution/site/year)
HRSV-A	$3.54 \times 10^{-3}$ ( $2.74\text{--}4.37 \times 10^{-3}$ )
HRSV-B	$6.02 \times 10^{-3}$ ( $4.56\text{--}7.42 \times 10^{-3}$ )

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76 **Table S2.** Ratio of the same array and pairwise distance per cluster of HRSV-A and

77 HRSV-B detected at Hospital O in 2021.

Cluster	HRSV-A			HRSV-B
	1	3	4	2
Ratio of same array	23/33 and 9/33	24/28 and 2/28	20/22	2/4
Pairwise distance	0.006	0.012	0.006	0.02

78 Clinical strains of HRSV-A and HRSV-B in 2021 included several strains with exactly

79 the same sequence in each cluster, and the pairwise distance was also low.

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81 **Table S3.** Pairwise distance of HRSV-A and HRSV-B clusters detected at Hospitals O

82 and H during 2017–21.

Cluster	HRSV-A							
	1	2	3	4	5	6	7	8
Pairwise distance	0.042	0.027	0.027	0.012	0.054	0.051	0.030	0.042

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Cluster	HRSV-B					
	1	2	3	4	5	6
Pairwise distance	0.053	0.066	0.033	0.015	0.059	0.010

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85 **Table S4.** Details of the sequences used for constructing phylogenetic trees using the  
86 maximum likelihood (ML) method, Bayesian Markov chain Monte Carlo (MCMC)  
87 method, and genome network analysis.

<b>Table S4.</b> Details of the sequences used for constructing phylogenetic trees using the maximum likelihood (ML) method, Bayesian Markov chain Monte Carlo (MCMC) method, and genome network analysis.						
Accession Number	Country/Year of isolation	Subgroup	Genotype	ML method	MCMC method	Network analysis
KT992094	Australia/1961	A		✓	✓	
JX198112	USA/1956	A		✓	✓	
Z33427	Uruguay/1990	A	GA1	✓	✓	
Z33425	Uruguay/1988	A	GA2	✓	✓	
Z33426	Uruguay/1990	A	GA3	✓	✓	
KP856969	USA/1979	A	GA4	✓	✓	
Z33494	Uruguay/1990	A	GA5	✓	✓	
KP258723	USA/1986	A	GA6	✓	✓	
Z33455	Spain/1992	A	GA7	✓	✓	
AF348809	South Africa/1997	A	SSA1	✓	✓	
AB470478	Japan/2004	A	NA1	✓	✓	
AB470479	Japan/2005	A	NA2	✓	✓	
KP336505	China/2013	A	NA3	✓	✓	
KC297324	China/2011	A	NA4	✓	✓	
HQ699278	South Korea/2009	A	CB-A	✓	✓	
JN257693	Canada/2010	A	ON1	✓	✓	✓
KC858255	Italy/2013	A	ON2	✓	✓	✓
JX198143	USA/1962	B		✓	✓	
JF704213	South Africa/1998	B	SAB1	✓	✓	
AF348821	South Africa/1999	B	SAB2	✓	✓	
AF348813	South Africa/1999	B	SAB3	✓	✓	
JN119979	Cambodia/2009	B	SAB4	✓	✓	
AY488804	Uruguay/2001	B	URU1	✓	✓	

AY488802	Uruguay/2001	B	URU2	✓	✓	
AF065250	USA/1990	B	GB1	✓	✓	
AF065251	USA/1992	B	GB2	✓	✓	
AF065252	USA/1992	B	GB3	✓	✓	
AF233924	USA/1994	B	GB4	✓	✓	
KC461293	China/2009	B	GB5	✓	✓	
DQ227363	Argentina/1999	B	BA1	✓	✓	
DQ227389	Argentina/2003	B	BA2	✓	✓	
DQ227376	Argentina/2002	B	BA3	✓	✓	
DQ227396	Argentina/2004	B	BA4	✓	✓	
AB603480	Japan/2003	B	BA5	✓	✓	
AY751110	Belgium/2003	B	BA6	✓	✓	
DQ227406	Argentina/2004	B	BA7	✓	✓	
HM459873	Japan/2007	B	BA8	✓	✓	
DQ227395	Argentina/2004	B	BA9	✓	✓	✓
HM459890	Japan/2007	B	BA10	✓	✓	
KP336524	China/2013	B	BA11	✓	✓	
JX256973	Malaysia/2009	B	BA12	✓	✓	
KY204206	Pakistan/2012	B	BA13	✓	✓	
KF300970	Panama/2008	B	BA14	✓	✓	
KC297486	China/2009	B	BA-C	✓	✓	
KC297428	China/2009	B	CB1	✓	✓	
HQ699297	South Korea/2009	B	CB-B	✓	✓	
KC342336	Thailand/2010	B	THB	✓	✓	
MK634184	South Korea/2012	A	ON1	✓	✓	✓
KY654518	Philippines/2013	A	ON1	✓	✓	✓
JX627336	South Korea/2011	A	ON1	✓	✓	✓
KU950651	USA/2012	A	ON1	✓	✓	✓
KX765956	New Zealand/2015	A	ON1	✓	✓	✓
LC530050	Japan/2019	A	ON1	✓	✓	✓
MK749913	Nicaragua/2016	A	ON1	✓	✓	✓
MN306031	USA/2019	A	ON1	✓	✓	✓
MH181987	Kenya/2013	A	ON1	✓	✓	✓
MK749886	Nicaragua/2016	A	ON1	✓	✓	✓

MN630103	USA/2016	A	ON1	✓	✓	✓
MN306048	USA/2019	A	ON1	✓	✓	✓
KU950492	USA/2012	A	ON1	✓	✓	✓
MH447954	Thailand/2013	A	ON1	✓	✓	✓
KJ672448	USA/2013	A	ON1	✓	✓	✓
KC731482	India/2011	A	ON1	✓	✓	✓
MK749881	Nicaragua/2015	B	BA9	✓	✓	✓
MN306044	USA/2019	B	BA9	✓	✓	✓
LC385002	Philippines/2015	B	BA9	✓	✓	✓
LC495297	Japan/2018	B	BA9	✓	✓	✓
MN365581	Kenya/2016	B	BA9	✓	✓	✓
LC488177	Japan/2016	B	BA9	✓	✓	✓
JX912358	Germany/2012	A	ON1	✓	✓	✓
JX912364	Germany/2012	A	ON1	✓	✓	✓
KJ710375	Germany/2013	A	ON1	✓	✓	✓
KJ710380	Germany/2013	A	ON1	✓	✓	✓
KJ710396	Germany/2013	A	ON1	✓	✓	✓
JX988443	Italy/2012	A	GA2	✓	✓	✓
KC858199	Italy/2012	A	GA2/ON1	✓	✓	✓
KC858208	Italy/2012	A	GA2/ON1	✓	✓	✓
KC858249	Italy/2012	A	GA2/ON1	✓	✓	✓
KC858250	Italy/2012	A	GA2/ON1	✓	✓	✓
KC858211	Italy/2013	A	GA2/ON1	✓	✓	✓
KC858222	Italy/2013	A	GA2/ON1	✓	✓	✓
KC858256	Italy/2013	A	ON2	✓	✓	✓
AB846651	Philippines/2012	A	ON1	✓	✓	✓
KC476744	South Africa/2012	A	ON1	✓	✓	✓
JX885730	South Africa/2012	A	ON1	✓	✓	✓
KC342434	Thailand/2011	A	ON1	✓	✓	✓
KF587941	Kenya/2012	A	ON1	✓	✓	✓
KF587952	Kenya/2012	A	ON1	✓	✓	✓
KF587961	Kenya/2012	A	ON1	✓	✓	✓
KF587967	Kenya/2012	A	ON1	✓	✓	✓
KF587976	Kenya/2012	A	ON1	✓	✓	✓

KF057865	Croatia/2012	A	ON1	✓	✓	✓
KU254628	China/2015	A	ON1	✓	✓	✓
KU254631	China/2015	A	ON1	✓	✓	✓
KU254636	China/2015	A	ON1	✓	✓	✓
MH760610	Australia/2016	A	ON1	✓	✓	✓
MN122463	Portugal/2015	A	ON1	✓	✓	✓
MN122526	Portugal/2016	A	ON1	✓	✓	✓
MN122553	Portugal/2017	A	ON1	✓	✓	✓
MH174872	Iran/2015	A	ON1	✓	✓	✓
KU736774	Nigeria/2015	A	ON1	✓	✓	✓
MH447710	Thailand/2017	A	ON1	✓	✓	✓
MH760638	Australia/2016	A	ON1	✓	✓	✓
KT326803	Spain/2015	A	ON1	✓	✓	✓
KX009687	China/2015	A	ON1	✓	✓	✓
MH388034	Saudi Arabia/2016	A	ON1	✓	✓	✓
MH447708	Thailand/2016	A	ON1	✓	✓	✓
MH447714	Thailand/2017	A	ON1	✓	✓	✓
KF246588	India/2009	B	BA9	✓	✓	✓
KF246630	India/2010	B	BA9	✓	✓	✓
HQ711811	South Africa/2009	B	BA9	✓	✓	✓
KC476954	South Africa/2009	B	BA9	✓	✓	✓
HQ699298	Korea/2008	B	BA9	✓	✓	✓
HQ699290	Korea/2010	B	BA9	✓	✓	✓
KF156570	Kenya/2008	B	BA9	✓	✓	✓
KP862466	Kenya/2012	B	BA9	✓	✓	✓
KM402711	Spain/2013	B	BA9	✓	✓	✓
KM402675	Spain/2014	B	BA9	✓	✓	✓
KM873461	Philippines/2012	B	BA9	✓	✓	✓
KM873497	Philippines/2013	B	BA9	✓	✓	✓
KC342339	Thailand/2010	B	BA9	✓	✓	✓
KC342345	Thailand/2011	B	BA9	✓	✓	✓
KC477035	South Africa/2011	B	BA9	✓	✓	✓
KC477096	South Africa/2012	B	BA9	✓	✓	✓
KC297457	China/2010	B	BA9	✓	✓	✓

KJ939921	Vietnam/2009	B	BA9	✓	✓	✓
JX079979	Vietnam/2010	B	BA9	✓	✓	✓
KC297441	China/2009	B	BA9	✓	✓	✓
KC297447	China/2010	B	BA9	✓	✓	✓
KJ690596	India/2009	B	BA9	✓	✓	✓
KF246602	India/2010	B	BA9	✓	✓	✓
KM402683	Spain/2013	B	BA9	✓	✓	✓
KM402745	Spain/2014	B	BA9	✓	✓	✓
KJ710407	Germany/2012	B	BA9	✓	✓	✓
JX967575	Germany/2012	B	BA9	✓	✓	✓
MH447754	Thailand/2017	B	BA9	✓	✓	✓
MH447779	Thailand/2017	B	BA9	✓	✓	✓
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MN122639	Portugal/2017	B	BA9	✓	✓	✓
MN122686	Portugal/2017	B	BA9	✓	✓	✓
MG962341	India/2016	B	BA9	✓	✓	✓
MH476342	India/2016	B	BA9	✓	✓	✓
MK947336	South Korea/2017	B	BA9	✓	✓	✓
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MK947352	South Korea/2018	B	BA9	✓	✓	✓
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MN163125	China/2017	B	BA9	✓	✓	✓
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MK481079	Russia/2018	B	BA9	✓	✓	✓
LC324679	Japan/2017	B	BA9	✓	✓	✓
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