

Electronic Supplementary Material

A multi-center study on Molecular Epidemiology of Human Respiratory Syncytial Virus from Children with Acute Lower Respiratory Tract Infections in the Mainland of China between 2015 and 2019

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Table S1. List of the RSV *G* gene sequences identified in this study.

Table S2. List of the RSV *G* gene sequences downloaded from GenBank.

Table S3. Distribution of the potentially O-glycosylated sites among the HVR-2 sequences of genotype ON1 collected in the mainland of China between 2015 and 2019.

Position	219	220	227	228	231	270	275	277	281	283
Amino acid	T	T	T	T	T	S	S	S	T	S
G-scores	0.86	0.65	0.72	0.62	0.73	0.51	0.53	0.68	0.51	0.65

Table S4. Distribution of the potentially O-glycosylated sites among the HVR-2 sequences of genotype BA9 collected in the mainland of China between 2015 and 2019.

Position	218	222	227	228	232	236	240	244	245	246	249	250	255	257	260	265	280	281	285	294	297	298	300	304
Amino acid	T	T	T	T	T	T	T	T	S	T	S	T	T	S	T	S	T	T	S	T	S	T	T	S
G-scores	0.58	0.64	0.74	0.89	0.85	0.86	0.80	0.53	0.78	0.78	0.69	0.65	0.66	0.76	0.56	0.55	0.59	0.60	0.59	0.51	0.78	0.59	0.50	0.60