

Table 1. Summary demographic information of sequenced RSV-A strains in north Viet Nam during 2017-2020.

	Year of sample collection				Total
	2017	2018	2019	2020	
SARI cases	512	421	367	263	1563
Positive RSV cases	185	109	78	66	438
RSV-A cases	99	59	31	45	234
Sequenced RSV-A cases	19	14	12	11	56
Genotype ON1	19	13	10	11	53
Genotype non-ON1	0	1	2	0	3
Demographic information of sequenced RSV-A					
Sex					
Male	13	9	7	7	36
Female	6	5	5	4	20
Age group					
<1	13	8	4	2	27
1-< 2	5	5	7	6	23
2-< 5	1	1	1	3	6

Table 2. Positively selected amino acid substitution sites of the RSV-A G gene in north Viet Nam, 2017-2020.

Positively selected site	FEL ^a	SLAC ^b	MEME ^c	FUBAR ^d
T113I	√			√
N178G			√	√
G232K		√	√	
Y273del	√	√		√
L274del	√	√	√	√

The value of p-value <0.05 with FEL, SLAC, MEME, and the posterior probability of 0.95 with FUBAR were considered to be statistically significant and indicated as the symbol ($\checkmark$).

^a FEL: Fixed Effects Likelihood

^b SLAC: Single-Likelihood Ancestor Counting

^c MEME: Mixed Effects Model for Episodic Diversifying Selection

^d FUBAR: Fast Unconstrained Bayesian AppRoximation