

Evolutionary analysis of Human Respiratory Syncytial Virus in Myanmar, 2015-2018



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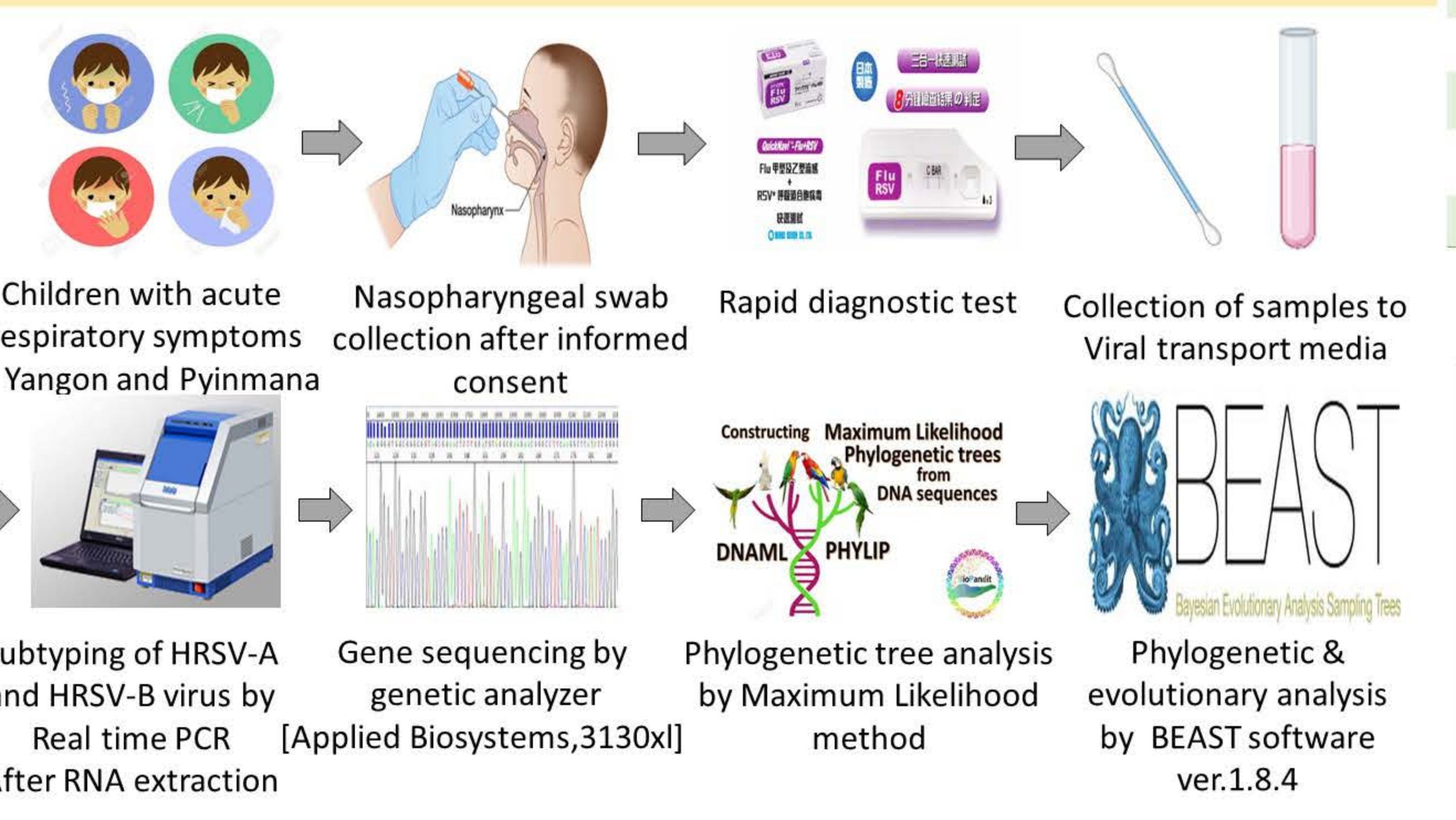
Background

- ◆ Genetic evolution of Human Respiratory syncytial virus (HRSV), especially G gene encoding attachment protein, plays a crucial biological role for faster viral replication, which may elicit strong resistance to herd immunity.
- ◆ In Myanmar, there are no previous studies done to characterize genotypes and to assess evolution of HRSV.

Aim

- ❖ To clarify the clinical manifestations of HRSV infections in outpatients, and seasonality of HRSV in Myanmar
- ❖ To assess the evolution of HRSV in Myanmar by studying genetic variations of the 2nd hypervariable region (HVR) of the G gene of the virus.

Materials & Methods



Results

Table 1. Positivity of HRSV subgroups by year in Myanmar, 2015-2018

	2015 (n,%)	2016 (n,%)	2017 (n,%)	2018 (n,%)	Total (n,%)
Number of samples	356 (100)	629 (100)	328 (100)	388 (100)	1701 (100)
HRSV positive by RDT	12 (3.4)	185 (29.4)	52 (15.9)	167 (43.0)	416 (24.5)
HRSV positive by RT-PCR	6 (100)	38 (100)	52 (100)	148 (100)	244 (100)
HRSV-A	6 (100)	33 (86.8)	3 (5.8)	42 (28.4)	84 (34.4)
HRSV-B	0	4 (10.5)	49 (94.2)	105 (70.9)	158 (64.8)
HRSV-A and B	0	1 (2.7)	0	1 (0.7)	2 (0.8)

Table 2. Base line characteristics of HRSV-A & HRSV-B subgroups in Myanmar, 2015-2018

Variables	HRSV-A (n=84)	HRSV-B (n=158)	HRSV-A and B (n=2)	Total(n=244)
Age (years)				
Median	0.6	1.2	2.1	1
(Interquartile range)	(0-1.4)	(0.7-2.1)	(1.18-3.06)	(0.5-2)
<1year	34 (40.5%)	37 (23.4%)	1 (50.0%)	72 (29.5%)
From ≥1year to <5years	50 (59.5%)	121 (76.6%)	1 (50.0%)	172 (70.5%)
Sex	(n,%)	(n,%)	(n,%)	(n,%)
Male	42 (50.0%)	81 (51.3%)	2 (100.0%)	125 (51.2%)
Female	42 (50.0%)	77 (48.7%)	0	119 (48.6%)
Symptoms	(n,%)	(n,%)	(n,%)	(n,%)
Cough	62 (81.6%)	137 (98.6%)	2 (100.0%)	199 (92.6%)
Wheezing	6 (7.9%)	2 (1.4%)	0	8 (3.7%)
Rhinorrhoea	54 (71.1%)	136 (97.8%)	1 (100.0%)	190 (88.4%)
Dyspnoea	0	2 (1.4%)	0	2 (0.9%)

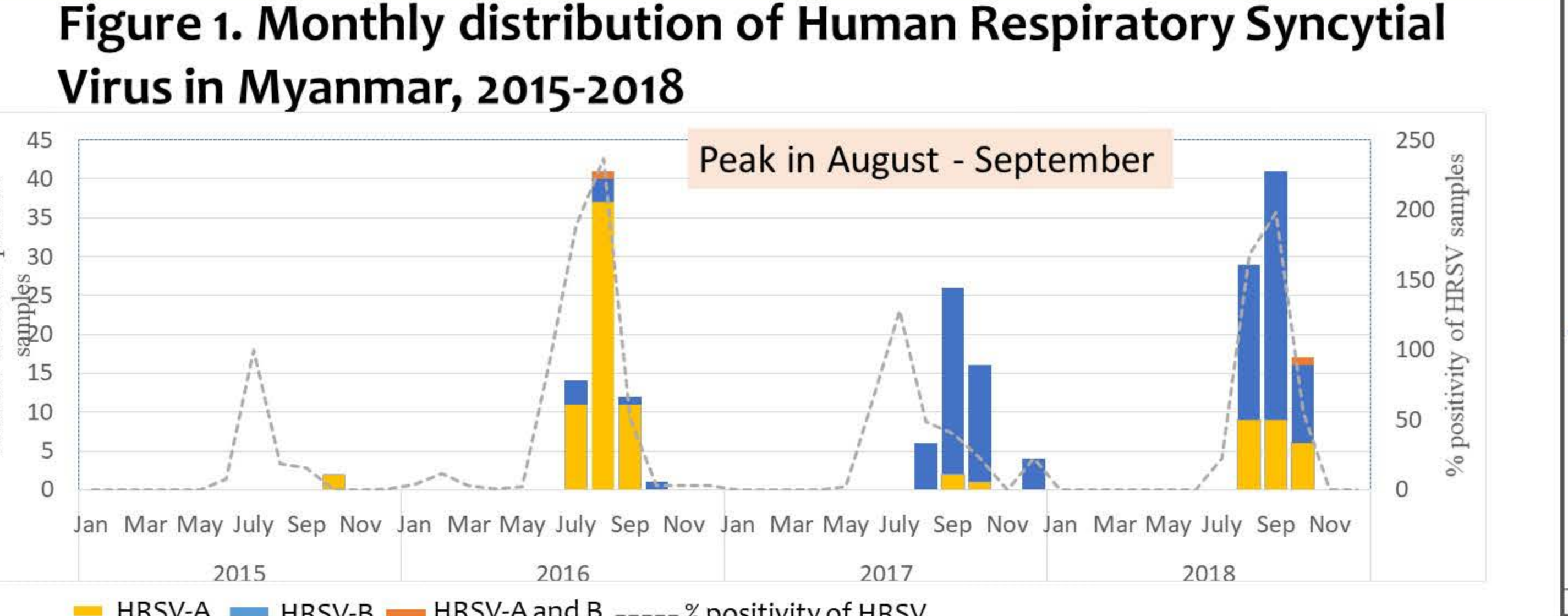


Figure 2: Phylogenetic trees of G gene of HRSV-A and HRSV-B strains from Myanmar and reference strains, 2015-2018

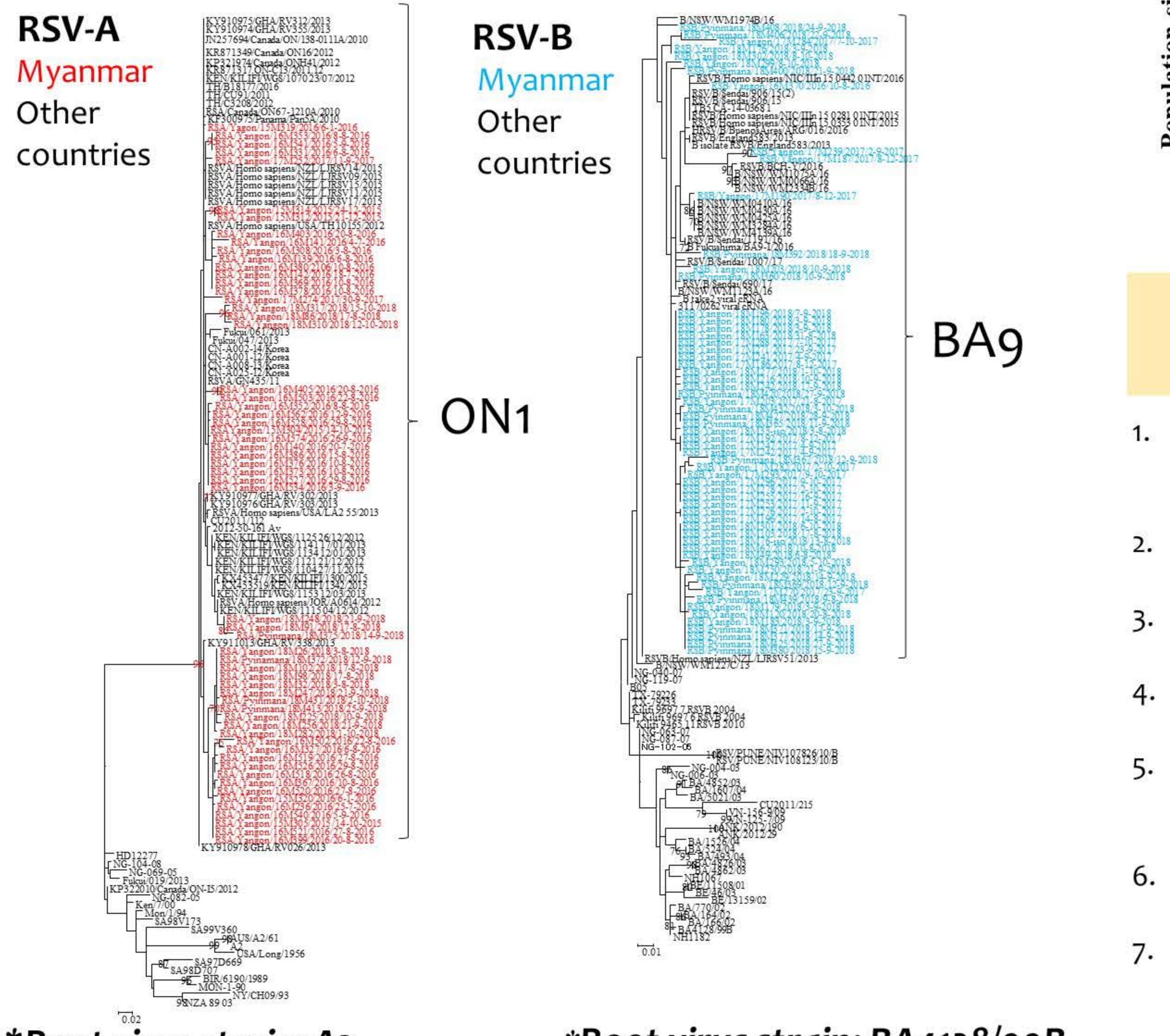
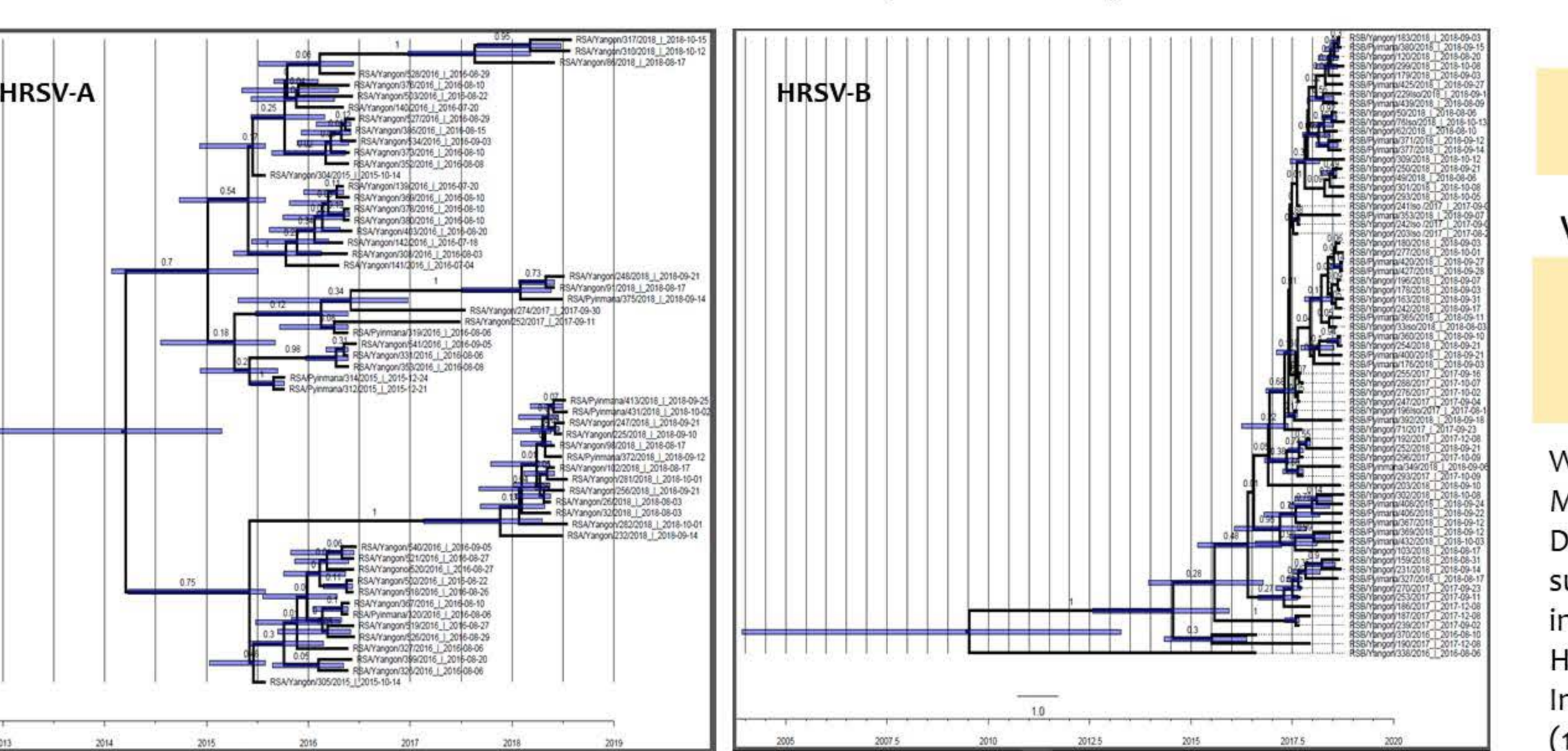
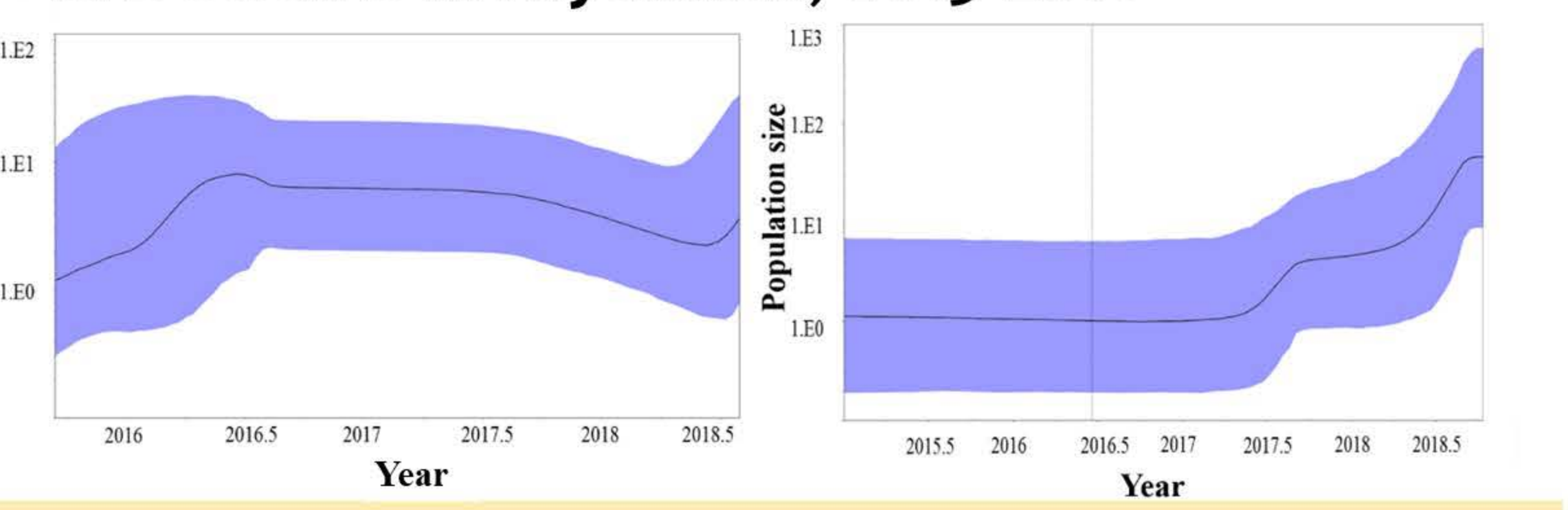


Figure 3: Time scaled phylogenetic tree of ON1 of HRSV-A and BA9 of HRSV-B using Bayesian Markov Chain Monte Carlo (MCMC) method



Results

Figure 4: Effective population size of HRSV-A and B strains in Myanmar, 2015-2018



Summary

1. During the study period, 416 (24.5%) out of 1701 nasopharyngeal swabs were identified by RDT kit. Of these, 244 samples were positive by real time PCR, 84 (34.4%) were HRSV-A, and 158 (64.8%) were HRSV-B and 2 (0.8%) were mixed infection.
2. HRSV-A was predominant in 2016. However, HRSV-B became predominant in two consecutive years of 2017 and 2018.
3. Higher proportion rate of HRSV cases were found in 1-year old and above than children less than 1-year old (70.5% versus 29.5%).
4. Cough and rhinorrhoea were the main symptoms, observed in 80-90% and 70-100% of HRSV infected children.
5. The monthly distribution of HRSV positive samples showed that HRSV epidemic in Myanmar occurred between July through October and peaked during August and September.
6. Phylogenetic analysis showed that HRSV ON1 strain in RSV-A type and BA9 in RSV-B type is likely to circulate during 2015-2018 in Myanmar.
7. According to Bayesian Markov Chain Monte Carlo (MCMC) method by using Beast software, the time to the most recent common ancestor (tMRCA) was estimated since 2014 (95%HPD- 2012-2015) for HRSV-A and since 2009 (95%HPD- 2004-2012) for HRSV-B.
8. The mean evolutionary rate for HRSV-B (2.12×10^{-2} substitutions/site/year (95%HPD: 8.53×10^{-3} to 3.63×10^{-2}) was slightly faster than HRSV-A (1.39×10^{-2} substitutions/site/year (95%HPD: 6.03×10^{-3} to 2.12×10^{-2}).
9. The estimated effective population size (diversity) of HRSV-A increased from 2015 to 2016, during which ON1 was the dominant genotype and declined in the middle of 2018. In contrast, the diversity of HRSV-B was constant in 2015-2016, and increased in the middle of 2017.

Conflict of interest

We have no conflict of interest.

Acknowledgement

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