Supplemental Table S4. Former sub-genotypes within class I and class II that did not pass the updated classification criteria (either one of 5% nucleotide distance, branch support equal or above 70%, at least 4 independent isolates) and were merged. The sub/genotype designation follows the newly proposed nomenclature and the former names are provided in parenthesis.

Distance between groups is below 5%

Class I	
	1.2 (1c)
1.2 (1d)	3.68

Class II genotype VI	
	VI.1.2.1.1.1 (VIn)
VI.1.2.1.1.1 (VIa)	3.46

Class II genotype X	
	X (Xa)
X (Xb)	4.83

Class II genotype XVII	
	XVII (XVIIb)
XVII (XVIIa)	4.59

Class II genotype VII	
	VII.1.1 (VIIe)
VII.1.1 (b+j+d+ℓ)	4.21

Class II genotype VII	
	VII.1.1 (VIId+VIIℓ)
VII.1.1 (VIIb+VIIj)	4.68

Class II genotype VII	
	VII.1.1 (VIIj)
VII.1.1 (VIIb)	3.31

Lack of branch support or sufficient number of epidemiologically independent isolates

Class II genotype VII	
	VII.2 (VIIi)
VII.2 (VIIh+VIIk)	9.61

Class II genotype VII	
	VII.2 (VIIk)
VII.2 (VIIh)	11.10

Class II genotype V	
	V (Vd)
V.1 + V.2 (Vb+Vc)	9.96

Class II genotype XXI	
	XXI (VI ℓ)
XXI.1+XXI.2 (VIg+m+i)	13.24