Supplementary Table 2. Estimates of evolutionary divergence rate between the amino acid (A) and nucleotide (B) sequences of the polyprotein of the assembled genomes. The rate variation among sites was modelled with a gamma distribution (shape parameter = 1). The actual number of differences are provided in the parentheses.

A	BG_1_poly	BG_2_poly	BG_3_poly	BG_4_poly	BG_5_poly	BG_6_poly
BG_1_poly	0 (0)	0 (0)	0 (0)	0 (0)	0.00206(2)	0.00206(2)
BG_2_poly		0 (0)	0 (0)	0 (0)	0.00206(2)	0.00206(2)
BG_3_poly			0 (0)	0 (0)	0.00206(2)	0.00206(2)
BG_4_poly				0 (0)	0.00206(2)	0.00206(2)
BG_5_poly					0 (0)	0 (0)
BG 6 poly						0 (0)

В	BG_1_poly	BG_2_poly	BG_3_poly	BG_4_poly	BG_5_poly	BG_6_poly
BG_1_poly	0 (0)	0 (0)	0 (0)	0 (0)	0.00308 (9)	0.00308 (9)
BG_2_poly		0 (0)	0 (0)	0 (0)	0.00308 (9)	0.00308 (9)
BG_3_poly			0 (0)	0 (0)	0.00308 (9)	0.00308 (9)
BG_4_poly				0 (0)	0.00308 (9)	0.00308 (9)
BG_5_poly					0 (0)	0 (0)
BG_6_poly						0 (0)