

Supplementary

Table 1. The pairwise K-2-P distances of the nucleotide sequences of (A) *polh*, (B) *lef-8*, and (C) *lef-9* fragments among *Spodoptera frugiperda* multiple nucleopolyhedrovirus (SfMNPV) isolates.

A:

<i>polh</i> ($\gamma = 1.80^{-1}$)	1	2	3	4	5	6	7	8	9
1 SfMNPV-Hub									
2 SfMNPV_G	0.000								
3 SfMNPV_Ni	0.000	0.000							
4 SfMNPV_IIB1197	0.000	0.000	0.000						
5 SfMNPV_19	0.000	0.000	0.000	0.000					
6 SfMNPV_IIB459	0.000	0.000	0.000	0.000	0.000				
7 SfMNPV_Co	0.002	0.002	0.002	0.002	0.002	0.002			
8 SfMNPV_3AP2	0.002	0.002	0.002	0.002	0.002	0.002	0.004		
9 MabMNPV_K1 ²	0.208	0.208	0.208	0.208	0.208	0.208	0.205	0.205	

B:

<i>lef-8</i> ($\gamma = 0.64^{-1}$)	1	2	3	4	5	6	7	8	9
1 SfMNPV-Hub									
2 SfMNPV_G	0.003								
3 SfMNPV_Ni	0.003	0.000							
4 SfMNPV_IIB1197	0.003	0.000	0.000						
5 SfMNPV_19	0.004	0.004	0.004	0.004					
6 SfMNPV_IIB459	0.003	0.003	0.003	0.003	0.004				
7 SfMNPV_Co	0.001	0.001	0.001	0.001	0.003	0.001			
8 SfMNPV_3AP2	0.013	0.010	0.010	0.010	0.012	0.013	0.012		
9 MabMNPV_K1 ²	0.843	0.843	0.843	0.843	0.843	0.833	0.833	0.859	

C:

<i>lef-9</i> ($\gamma = 200^{-1}$)	1	2	3	4	5	6	7	8	9
1 SfMNPV-Hub									
2 SfMNPV_G	0.007								
3 SfMNPV_Ni	0.007	0.000							
4 SfMNPV_IIB1197	0.007	0.000	0.000						
5 SfMNPV_19	0.007	0.000	0.000	0.000					
6 SfMNPV_IIB459	0.007	0.000	0.000	0.000	0.000				
7 SfMNPV_Co	0.007	0.000	0.000	0.000	0.000	0.000			
8 SfMNPV_3AP2	0.007	0.000	0.000	0.000	0.000	0.000	0.000		
9 MabMNPV_K1 ²	0.232	0.227	0.227	0.227	0.227	0.227	0.227	0.227	

¹ The gamma shape parameter was calculated for each alignment with MEGA v7.0 [1]. ² Mamestra brassicae multiple nucleopolyhedrovirus (MabMNPV) K1 isolate (GenBank: JQ798165.1) [2] was used as an outgroup control.

References

1. Kumar, S.; Tamura, K.; Nei, M. MEGA3: Integrated software for molecular evolutionary genetics analysis and sequence alignment. Briefings in Bioinformatics 2004, 5, 150-163.
2. Choi, J.B.; Heo, W.I.; Shin, T.Y.; Bae, S.M.; Kim, W.J.; Kim, J.I.; Kwon, M.; Choi, J.Y.; Je, Y.H.; Jin, B.R.; and Woo, S.D. Complete genomic sequences and comparative analysis of Mamestra brassicae nucleopolyhedrovirus isolated in Korea. Virus Genes 2013, 47(1), 133-151.