

## Supplementary Information

# A ROLE FOR THE ANTI-VIRAL HOST DEFENSE MECHANISM IN THE PHYLOGENETIC DIVERGENCE IN BACULOVIRUS EVOLUTION

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<i>B.mori</i>	414	ALKRCEPYKKQEKKVVFNRCTNHWFDFDDTKLCVSLGYYYGIHYMIYLTLAKNETLDDDELWYT	478
<i>B.mandarina</i>	414	.....	478
<i>A.californica</i>	413	.....I.....A.....F.....Q.....I.....H.....	477
<i>M.vitrata</i>	411	.....DRI.....A.....E.....N.....S.....F.....F.....Q.....S.....F.....	475
<i>A.pernyi</i>	407	..E..R..FTTRGVAI..NL..D..HC..KGVNPy..M..S..A..F..KF..SSDAH..EC..DP..F..	470
<i>B.mori</i>	479	YENVMALNLPPDIVCKGFFRKLENVTGVNLVFNGKNYQIVKKEDDLFKLVKSNCYKLSNIKFNN	543
<i>B.mandarina</i>	479	.....	543
<i>A.californica</i>	478	.....H.....T.....	542
<i>M.vitrata</i>	476	.....K..SS.....H.....T.....R.....	540
<i>A.pernyi</i>	471	.K..A..ECEV..LLVLGQA..I..V..Q..T..I..EH..D..Y..FNN..P..Q.....	535
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<i>B.mori</i>	544	WKLYLYTTYGVYNLFTNSFHSNCFPFLGGTLPQTLKKPTDEEYLPEDAFNYMLSTSTDEL	603
<i>B.mandarina</i>	544	.....	603
<i>A.californica</i>	543	.....H.....V.....S.....F.....K.....A.....	602
<i>M.vitrata</i>	541	.....H.....V.....S.....F.....K.....SD.....V.....	600
<i>A.pernyi</i>	536	..M..H..K.....VI..DE..Y.....M..G..F..R..D..PP.....V..A..T..AE..R	595

**S1 Fig. Amino acid sequence alignment of the P143-ScH regions from five nucleopolyhedroviruses; *Bombyx mori* NPV (*B. mori*), *Bombyx mandarina* NPV (*B. mandarina*), *Autographa californica* MNPV (*A. californica*), *Maruca vitrata* NPV (*M. vitrata*) and *Antheraea pernyi* NPV (*A. pernyi*). Sequences that differ from the *Bombyx mori* NPV P143 sequence are indicated for each amino acid residue, whereas identical sequences are represented by dots. The amino acid residues targeted for mutagenesis in this experiment are marked by asterisks.**