

Electronic Supplementary Material

Meta-transcriptome profiling of Novel Invasive Pest *Spodoptera frugiperda* in Yunnan, China

Junming Shi^{1,2}; Weiwei Li^{3,4}; Yunyu Wang^{3,4}; Quanyan Chen³; Fei Deng¹✉

1.State Key Laboratory of Virology and National Viruses Resource Center, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China

2.University of Chinese Academy of Sciences, Beijing 100049, China

3.Kunming Institute of Zoology Chinese Academy Sciences, Kunming 650223, China

4.Yunnan Agricultural University, Kunming 650201, China

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Table S1. General statistical indexes of RNA-Seq raw sequence reads and assembled contigs

Overall evaluation of RNA-seq	Value
Total size (Gb)	30.3
Paired reads	43093070
Average length of reads (nt)	145
GC percentage (%)	40.45
Assembly evaluation	Value
Number of transcripts	531181
Muti-position matched	30295516
Perfect matched	6902422
Unmapped pairs	5895132
Percentage of mapped reads	86.32%
N50 of transcripts (nt)	647
Max length of transcripts (nt)	71803
Min length of transcripts (nt)	201
Transcripts with homologous in NR/trEMBL	204751 (38.5%)

Table S2. Primers used in this study.

Reference virus and mapped gene	PCR primers (5' to 3')	Amplicon size (bp)
<i>Autographa californica</i> nucleopolyhedrovirus strain E2 (hypothetical protein)	F: TATAATGTTGATAGTACAGAG R: GGATGGCACGACAGGCGTGCC	370
<i>Clanis bilineata</i> nucleopolyhedrovirus (P87/VP80)	F: TTCTAGGCAAGTTTGTATT R: TTCTCTATGTATGGGAATA	390
<i>Helicoverpa armigera</i> granulovirus (hypothetical protein HaGV_gp053)	F: ATCAAAGAAGAGCTATGAT R: CGTGTATTCCACGACATGG	252
Serratia phage Eta_0034 (hypothetical protein)	F: GTTGTTCATGGATCGAAT R: AGAAGCAGTTAACCCCAAC	234
<i>Spodoptera frugiperda</i> rhabdovirus (L protein)	F: AAGTGGGATCTTCTATACT R: TGGGGTCACCCCACCCTGG	262
<i>COI</i>	F: GTAGGTACTTCTTTAAGTTTATT R: AAAATATATACTTCAGGATGTCC	610
<i>Tip</i>	F: GGTGAAATCTCCCCTGCTATG R: AATTTTATTACCTGCTGTGG	310