



Complete Genome Sequences of Four Major Viruses Infecting Marine Shrimp in Egypt

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ABSTRACT The genome sequences of four economically important shrimp viruses, *Penaeus stylirostris densovirus 1*, hepatopancreatic parvovirus, yellow head virus, and gill-associated virus, are reported here. Genome data are fundamental for epidemiological studies in determining the origins of these viruses detected for the first time in Egypt and in developing disease management strategies.

Penaeus semisulcatus and *Marsupenaeus japonicas* are the two native shrimp species in Egypt cultured since the 1980s. With the introduction of *Fenneropenaeus indicus*, a nonnative species, shrimp farmers started experiencing disease outbreaks. Laboratory diagnosis revealed the presence of *Penaeus stylirostris densovirus 1* (PstDENV1), hepatopancreatic parvovirus (HPV), yellow head virus (YHV), and gill-associated virus (GAV). The genome sequences of these viruses are presented here.

Total DNA and RNA were extracted from pleopods and hepatopancreas of shrimp using DNeasy and RNeasy minikits (Qiagen). Samples that tested positive by PCR (PstDENV1 and HPV) and reverse transcription-PCR (RT-PCR) (YHV and GAV) were taken for cloning. DNA and cDNA were digested with restriction enzymes, and plasmid libraries were made before taking recombinant clones for shotgun sequencing using an ABI 3730XLS sequencer (Macrogen, Inc.). Contigs were generated and aligned to the viral reference genomes to separate viral contigs from shrimp genome contigs. Sequences were examined using Chromas version 1.45 (1) and BioEdit 7.0.9, open reading frames (ORFs) were annotated using BLASTn, and Geneious R11 and multiple alignments were performed using CLUSTALW.

PstDENV1 and HPV are classified in the family *Parvoviridae*, genus *Brevidensovirus* (2). Altogether, 11 PstDENV1 contigs 3,530 to 3,912 nucleotides (nt) long were generated. Each sequence contained ORFs encoding nonstructural (NS) proteins NS1 and NS2 and coat protein, as reported for other PstDENV1 isolates (3, 4). A pairwise comparison of PstDENV1-Egypt isolates to the reference strain (GenBank accession number [AF218266](#)) (5) showed 92.33% to 100% identity.

The genome sizes of 10 HPV-Egypt isolates varied from 5,685 to 6,336 nt. All but one isolate (GenBank accession number [KT316245](#)) contained three ORFs in the order of NS2, NS1, and VP, similar to the reference strain (6). HPV-Egypt isolates showed 80.62% to 100% identity to the reference sequence (RefSeq accession number [NC_007218](#)) (6). The [KT316245](#) isolate presented left (partial), middle, and right ORFs and showed 100% identity to an isolate from Madagascar (7).

The YHV and GAV are bacilliform, enveloped, positive, single-stranded RNA (ssRNA) viruses in the family *Roniviridae*, genus *Okavirus* (8). The genome of YHV-Egypt was 26,662 nt containing 3 ORFs (9). ORF1 encodes a polyprotein containing a 3C-like protease (nt 8571 to 9422) domain and a ribosomal frameshift slippery motif (AAAUUUU) (nt 12254 to 12260) that joins ORF1 and ORF2 (10). ORF2 encodes a p20 nucleocapsid protein, a helicase domain (nt 16688 to 17534), and an RNA-dependent

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DNA polymerase motif (nt 14291 to 15046). ORF3 (nt 20939 to 25984) encodes a polyprotein that generates two envelope glycoproteins (9, 11). YHV-Egypt showed 100% identity to an isolate from Thailand (GenBank accession number [FJ848674](#)).

The genome of GAV-Egypt was 26,253 nt, containing 4 ORFs (12). ORF1a contains a 3C-like protease (nt 8535 to 9386) domain and the ribosomal frameshift slippery motif AAAUUUU (nt 12215 to 12221) (13, 14). ORF1b contains an RNA-dependent DNA polymerase motif (nt 14252 to 15007) and a helicase domain (nt 16136 to 17515) (15). ORF2 encodes p20 nucleocapsid protein (nt 20183 to 20617), and ORF3 contains a polyprotein (nt 20630 to 25597) of unknown function (12, 16). GAV-Egypt showed 100% identity to an Australian isolate (GenBank accession number [AF227196](#)) (13). The genome data are valuable in determining the origins of these viruses in Egypt.

Data availability. The whole-genome sequences of the four viruses from Egypt have been deposited in GenBank under accession numbers [KT316249](#), [KT316250](#), [KT316251](#), [KT316252](#), [KT316253](#), [KT316254](#), [KT316256](#), [KT316257](#), [KT316258](#), [KT316259](#), and [KT316260](#) for PstDNV1; [KR492908](#), [KR492909](#), [KR492910](#), [KR492911](#), [KT316240](#), [KT316241](#), [KT316242](#), [KT316243](#), [KT316244](#), and [KT316245](#) for HPV; [KT316279](#) for GAV; and [KT316278](#) for YHV.

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