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Vectors and reservoir hosts of covert mortality nodavirus (CMNV) in shrimp ponds

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Abstract

Covert mortality nodavirus (CMNV) is the pathogen that has been identified as the cause of viral covert mortality disease (VCMD) in marine and brackish water shrimp. Recent outbreaks of this disease have resulted, and continue to result, in substantial production and economic losses to shrimp aquaculture producers in China and elsewhere. To explore potential vectors and reservoir hosts of CMNV, we collected fifteen species of invertebrates from shrimp ponds affected by VCMD. Samples were tested through the use of: reverse transcription loop-mediated isothermal amplification (RT-LAMP), reverse transcription nested PCR (RT-nPCR) followed by gene sequencing, histopathology, and in situ RNA hybridization (ISH). The results of RT-LAMP and RT-nPCR assay indicated that CMNV positive samples were identified in eleven species including brine shrimp *Artemia sinica*, a barnacle *Balanus sp.*, the rotifer *Brachionus urceus,* the amphipod *Corophium sinense Zhang*, the Pacific oyster *Crassostrea gigas*, a hermit crab *Diogenes edwardsii*, the common clam *Meretrix lusoria*, a ghost crab *Ocypode cordimundus*, the hyperiid amphipod *Parathemisto gaudichaudi*, a fiddler crab *Tubuca arcuata,* and an unidentified gammarid amphipod. The alignment of CMNV RNA-dependent RNA polymerase gene sequences from