Comparative Analysis of Target Regions into the White Spot Syndrome Virus (WSSV) Genome in Two Species of Crustaceans

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Introduction: White Spot Syndrome Virus (WSSV) has caused great mortality rates and economic losses to shrimp farming worldwide. WSSV can infect several species of cultivated shrimp as well as different species of crustaceans which can become alternative reservoirs for the pathogen. Variable Number Tandem Repeats (VNTRs) (open reading frame [ORF] 75, 94, 125) found in WSSV genome have been proposed as suitable molecular markers both for genotyping and epidemiological studies. This study aims to compare the utility of these VNTR as epidemiological markers for genotyping WSSV isolates from different crustacean species, as well to comparatively assess the virulence between them.

Material and Methods: Samples from native crab (Chasmagnathus granulata) and farmed shrimp (Litopenaeus vannamei) were collected in Santa Catarina between 2005 and 2008. DNA was extracted from gill and epithelium tissues following standard laboratory protocols. All the samples were diagnosed as positive for WSSV after a two-step Polymerase Chain Reaction (PCR) survey. PCR assays were performed accordingly for each of the tree selected VNTRs and the products were visualized on 1% agarose gels. PCR products were purified and sequenced using an automatic DNA sequencer.

Results and Discussion: The amplified products showed the expected size for all VNTRs. Sequencing analysis revealed no differences in the VNTRs among the samples as well as in comparison to other geographic isolates. Conclusions: No differences were detected in any of the three target regions. This lack of mutations maybe due either to the short interval of time between sampling, or to the fact that the chosen VNTRs may not be the most suitable genome region to asses and identify differences between WSSV isolates in such scenario. Analysis of other VNTRs may further contribute to understand the behavior and virulence of WSSV in the field.

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