

Potenciais riscos da importação de camarão à carcinicultura e ao ecossistema brasileiros, em decorrência do trânsito de novos vírus e variantes virais.

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Considerações sobre o congelamento



Preservation of viral genomes in 700-y-old caribou feces from a subarctic ice patch

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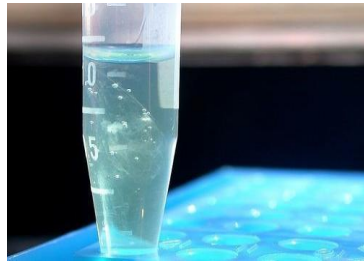
Edited by Peter Palese, Icahn School of Medicine at Mount Sinai, New York, NY, and approved September 30, 2014 (received for review June 6, 2014)

Verificação da existência de vírus infectivos em camarões congelados.

1 - Aquisição do camarão congelado



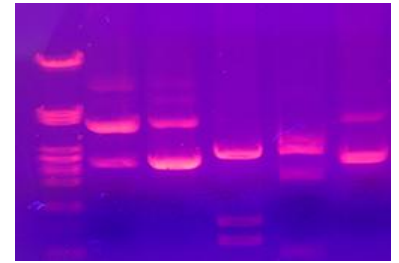
2 - Extração de DNA e RNA do tecido



3 - Reação de PCR



4 - Identificação dos positivos para o vírus



5 - Camarões congelados positivos para o(s) vírus



6 - Produção de lisado (batido)



7 - Injeção ou oferta como alimento para camarões saudáveis



8 - Verificação dos sintomas



The detection of White Spot Syndrome Virus (WSSV) and Yellow Head Virus (YHV) in imported commodity shrimp

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Accepted 2 October 1997

Abstract

Transmission of exotic pathogens occurs through a variety of means, including migration with humans and animals, rapid transit by land, sea or air or through the shipment of infected frozen food products. White Spot Syndrome Virus (WSSV) and Yellow Head Virus (YHV) have caused mass mortalities of cultured shrimp in Asia beginning in 1992. In 1995, these viruses appeared for the first time in the Western Hemisphere causing high mortalities in farm reared shrimp in Texas, USA. The purpose of this study was to determine if WSSV and YHV are present in frozen shrimp products imported into the United States from Asia. Infectivity assays, transmission electron microscopy (TEM), and polymerase chain reaction (PCR) showed these viruses were detectable

Table 1

Results from tests performed using grocery store purchased shrimp

Source and date	Species	Tests performed			Results
		PCR		Southern ^b	
		N/L	Lo ^a		
Fry's: Tucson, AZ, 9/30/95	<i>Panaeus monodon</i>	X			+ WSSV: PCR
WCAC ^c : Tucson, AZ, bioassay: 12/8/95	<i>Panaeus stylirostris</i>	X	X		+ WSSV: PCR + YHV: TEM
Von's: Pasadena, CA, 11/25/95	<i>P. monodon</i>	X	X	X	+ WSSV: PCR and Southern
Minute Market: Seattle, WA, 12/2/95	<i>P. monodon</i>	X	X	X	– WSSV: PCR and Southern
Smith's: Tucson, AZ, 3/5/96	<i>Panaeus californiensis</i>	X	X	X	– WSSV: PCR and Southern
Reay's: Tucson, AZ, 4/17/96	<i>P. californiensis</i>	X	X	X	– WSSV: PCR and Southern
Safeway: Tucson, AZ, 4/17/96	<i>P. monodon</i>	X	X	X	– WSSV: PCR and Southern
Albertson's: Tucson, AZ, 4/29/96	<i>P. monodon</i>	X	X	X	+ WSSV: PCR and Southern
ABCO: Tucson, AZ, 5/9/96	<i>P. monodon</i>	X	X	X	– WSSV: PCR and Southern
HEB's: Harlingen, TX, 5/25/96	<i>P. monodon</i>	X	X	X	– WSSV: PCR and Southern
Albertson's: Tucson, AZ, 6/6/96	<i>Macrobrachium rosenbergii</i>	X	X	X	+ WSSV: PCR and Southern
ABCO: Tucson, AZ, 6/8/96	<i>P. monodon</i>	X	X	X	+ WSSV: PCR and Southern

X: Assay run.

^aN/L = Nunan/Lightner primers; Lo = Lo et al. primers.^bSouthern blot analysis using N/L probe.^cWest Campus Agricultural Center.



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Frozen Commodity Shrimp: Potential Avenue for Introduction of White Spot Syndrome Virus and Yellow Head Virus

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TABLE 1.—Results of polymerase chain reaction (PCR) assays for white spot syndrome virus (WSSV) and reverse transcriptase PCR assays for yellow head virus (YHV) in frozen commodity shrimp from the U.S. retail market. Abbreviations are as follows: NFI = National Fishery Institute; ND = not described. “White tiger” is a pale variety of *P. monodon* that has been given this name for marketing purposes. A minus sign indicates a negative test result (no band observed on the gel); a single plus sign indicates a weakly positive test result (band observed from undiluted template); three plus signs indicate a strong positive test result (band observed from first or second dilution of template with differences in intensity); and four plus signs indicate a very strong positive test result (band observed from undiluted and diluted templates without any difference in intensity).

Sample lot	Source	Origin	Species or name	Count size	Gross signs	PCR detection results
1	Retail	Asian	<i>P. monodon</i>	71–90	Reddish with white spots	++++ WSSV + YHV
2	NFI	Thailand	<i>P. monodon</i>	61–70	ND	+++ WSSV – YHV
3	NFI	Thailand	“White tiger”	57–60	ND	+++ WSSV – YHV
4	NFI	Thailand	<i>P. monodon</i>	31–40	ND	+ WSSV – YHV
5	NFI	Thailand	<i>P. monodon</i> and “white tiger”	31–40	ND	+ WSSV – YHV
6	NFI	Thailand	<i>P. monodon</i>	61–70	ND	+ WSSV + YHV
7	NFI	Thailand	“White tiger”	51–60	ND	– WSSV – YHV
8	Retail	Thailand	<i>P. monodon</i>	41–50	Reddish with white spots	++++ WSSV – YHV
9	Retail	Thailand	<i>P. monodon</i>	31–40	Reddish	– WSSV – YHV
10	Retail	Thailand	<i>P. monodon</i>	41–50	Reddish	+ WSSV + YHV

Transmission of white spot syndrome virus (WSSV) to *Litopenaeus vannamei* from infected cephalothorax, abdomen, or whole shrimp cadaver

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ABSTRACT: Shrimp viruses can remain infectious in frozen shrimp tissue and have been found in frozen commodity shrimp. Therefore, the threat of viral outbreaks in wild and cultured shrimp via frozen commodity shrimp exists. Because frozen shrimp are imported with and without the cephalothorax, more knowledge is needed concerning the infectivity of a cephalothorax relative to that of an abdomen. We compared the mortality rates from shrimp exposed to a WSSV-infected cephalothorax, abdomen, or whole shrimp cadaver. Estimates of transmission coefficients from the exposures to the infected cephalothorax, abdomen, or whole shrimp were also calculated because the transmission coefficients account for differences in the initial doses. In addition, we compared the variability in infectivity of pieces of shrimp by feeding 24 equal sized pieces of cephalothorax and

Detection of White Spot Syndrome virus and Yellowhead virus in prawns imported into Australia

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Objective To determine whether viable White Spot Syndrome virus (WSSV) or Yellowhead virus (YHV) were present in prawn products imported into Australia.

Procedure A sample of fourteen uncooked prawns was obtained from a consignment imported from southeast Asia. Each of the prawns was examined for WSSV by polymerase chain reaction (PCR), and then a bioassay was conducted in which a 10% homogenate of cuticular epithelium from each of the prawns was inoculated intramuscularly into healthy challenge prawns (*Penaeus monodon*) from Australia. The latter were then monitored for clinical signs of disease, and tissue samples were processed for electron microscopy, histological examination and for detection of WSSV by in situ hybridization (ISH) using a commercial kit. Limited numbers of haemolymph samples from inoculated challenge prawns were also examined by PCR for the presence of WSSV and YHV. All work was

mortality with up to 90% of prawns dying within 2 to 4 days of the outbreak of disease. WSD is caused by WSSV, a large, enveloped, bacilliform double-stranded DNA virus that morphologically resembles a baculovirus, but which has now been proposed as the type species of the new family *Whispoviridae*.⁷ Preliminary diagnosis of the disease is achieved by histopathological examination with a definitive diagnosis made by ISH using WSSV-specific nucleic acid probes. PCR may also be used to confirm a tentative diagnosis.⁸

YHD is also an economically important disease of farmed prawns because, like WSD, it is usually associated with extensive mortality and severe production losses.^{9,10} It is caused by YHV, a single-stranded RNA virus that, it is proposed, belongs to the family *Coronaviridae*.¹¹ A PCR has also been developed for its detection.⁸ In Australia, two yellowhead-like viruses have been

WHITE SPOT SYNDROME VIRUS IN FROZEN SHRIMP SOLD AT MASSACHUSETTS SUPERMARKETS

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ABSTRACT One of the most damaging viral diseases affecting the shrimp aquaculture industry is white spot disease (WSD) caused by white spot virus (WSSV), which causes high morbidity and mortality rates in penaeid shrimp and other crustaceans. The rapid spread of WSSV within wild and cultured stocks of shrimp may be caused by unregulated processing, disposal of infected imported shrimp, or the use of contaminated broodstock. The risk of introducing this virus to cultured and wild shrimp and other native species of crustaceans in the United States warrants investigation. The aim of this study is to determine the prevalence of WSSV in frozen commodity shrimp sold at four stores in the Boston area belonging to different supermarket chains. Samples from two size classes were collected in two different batches a month apart. Polymerase chain reaction was used to amplify a portion of the WSSV genome using a commercial PCR kit (ShrimpCare, DiagXotics). WSSV positive samples were visualized by electrophoresis and amplified product of selected samples was sequenced. Results showed a range of 0% to 38.7% for WSSV prevalence rate in the test populations, with an overall prevalence of 4.7%. Significant ($P < 0.001$) differences in WSSV prevalence were observed between shrimp from the two batches purchased a month apart, the two size classes, and the four test stores. Country of origin seemed to dominate the results. Sequence analysis confirmed the presence of WSSV genome in PCR-positive samples. Results provide preliminary evidence that an appreciable proportion of the shrimp sold in Massachusetts' supermarkets are carrying WSSV, and this constitutes a substantial risk of importation of this virus into the local environment. Further investigation is necessary to determine the risk of release of this virus into native fresh and marine water environments in Massachusetts and throughout the United States.

KEY WORDS: white spot syndrome virus, WSSV, frozen commodity shrimp

White-spot syndrome virus (WSSV) introduction into the Gulf of Mexico and Texas freshwater systems through imported, frozen bait-shrimp

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ABSTRACT: We analysed 20 boxes of, frozen imported bait-shrimp (China: *Parapenaeopsis* sp. and *Metapenaeopsis* sp.) and 8 boxes of native, frozen bait-shrimp (Gulf of Mexico: *Litopenaeus setiferus* and *Farfantepenaeus duorarum*) by RT-PCR or PCR for Taura syndrome virus (TSV), yellowhead virus/gill-associated virus (YHV/GAV), white-spot syndrome virus (WSSV) and infectious hypodermal and hematopoietic necrosis virus (IHHNV). All 28 boxes of shrimp were negative for TSV, YHV/GAV and IHHNV; 2 boxes of imported bait-shrimp were WSSV-positive by 3 different PCR assays. Intramuscular injection of replicate groups of SPF (specific pathogen-free) *L. vannamei* juveniles with 2 different tissue homogenates prepared from the 2 WSSV-positive bait boxes resulted in 100 % mortality of the test shrimp within 48 to 72 h post-injection. No mortality occurred among injected negative control groups. Histological and *in situ* hybridization analyses of 20 moribund treatment-shrimp demonstrated severe WSSV infections in each sample. Oral exposure of SPF *L. vannamei* postlarvae, PL (PL 25 to 30 stage; ~0.02 g) to minced tissue prepared from the 2 WSSV-positive bait-lots did not induce infection, possibly because of an insufficient infectious dose and/or viral inactivation resulting from multiple freeze-thaw cycles of the bait-shrimp during PCR testing. Use of an electric drill and collection of drill-tailings (tissue from ~20 to 30 shrimp) from frozen blocks of shrimp was successfully employed as an alternate tissue-sampling method without thawing. Our findings indicate that imported WSSV-infected bait shrimp, originating from China, are being sold in Texas for the purpose of sport fishing and represent a potential threat to freshwater and marine crustacean fisheries, as well as to coastal US shrimp farms.

KEY WORDS: White-spot syndrome virus · PCR · Histopathology · Bait-shrimp · Disease transmission · Biosecurity · Penaeid shrimp

White-spot syndrome virus diagnostics in frozen shrimp stocks imported to Mexico

Diagnóstico del virus del síndrome de la mancha blanca en lotes de camarones congelados importados a México

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This article describes white-spot syndrome virus (WSSV) diagnostics in 50 shrimp frozen stocks imported to Mexico from the USA. Frozen stocks cover various shrimp species and have different origins. Routine histological techniques and polymerase chain reaction (PCR)-based molecular analysis were used to document this disease. One frozen shrimp stock containing only *Penaeus aztecus* from the USA was detected as WSSV-positive using these non-conventional samples. Feasibility of frozen shrimp analysis is discussed since current viral detection is conducted in fresh shrimps before their marketing and/or re-importation. The role of frozen commodities in viral mobility and introduction into Mexico was also discussed.

Keywords: WSSV; frozen shrimp; diagnostic diseases



Susceptibility of juvenile European lobster *Homarus gammarus* to shrimp products infected with high and low doses of white spot syndrome virus

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ABSTRACT: White spot syndrome virus (WSSV) is the most important pathogen known to affect the sustainability and growth of the global penaeid shrimp farming industry. Although most commonly associated with penaeid shrimp farmed in warm waters, WSSV is also able to infect, cause disease in and kill a wide range of other decapod crustaceans, including lobsters, from temperate regions. In 2005, the European Union imported US\$500 million worth of raw frozen or cooked frozen commodity products, much of which originated in regions positive for white spot disease (WSD). The presence of WSSV within the UK food market was verified by means of nested PCR performed on samples collected from a small-scale survey of supermarket commodity shrimp. Passage trials using inoculum derived from commodity shrimp from supermarkets and delivered by injection to specific pathogen-free Pacific white shrimp *Litopenaeus vannamei* led to rapid mortality and pathognomonic signs of WSD in the shrimp, demonstrating that WSSV present within commodity shrimp was viable. We exposed a representative European decapod crustacean, the European lobster *Homarus gammarus*, to a single feeding of WSSV-positive, supermarket-derived commodity shrimp, and to positive control material (*L. vannamei* infected with a high dose of WSSV). These trials demonstrated that lobsters fed positive control (high dose) frozen raw products succumbed to WSD and displayed pathognomonic signs associated with the disease as determined by means of histology and transmission electron microscopy. Lobsters fed WSSV-positive, supermarket-derived commodity shrimp (low dose) did not succumb to WSD (no mortality or pathognomonic signs of WSD) but demonstrated a low level or latent infection via PCR. This study confirms susceptibility of *H. gammarus* to WSSV via single feedings of previously frozen raw shrimp products obtained directly from supermarkets.

Table 1. Commodity shrimp tested for presence of white spot syndrome virus (WSSV) by nested PCR

Species	Origin	Source and description	Nested PCR (% positive)
<i>Litopenaeus vannamei</i>	Ecuador	Supermarket; headless, shell off	65
<i>L. vannamei</i>	Honduras	Supermarket; headless, shell off	80
<i>Penaeus monodon</i>	Indonesia	Supermarket; headless, shell off	0
<i>L. vannamei</i>	Thailand	Supermarket; headless, shell off	5
<i>P. monodon</i>	Thailand	Supermarket; headless, shell off	0
<i>P. monodon</i>	Vietnam	Supermarket; headless, shell off	100
<i>P. monodon</i>	Bangladesh	Market; whole animal	0
<i>P. monodon</i>	Bangladesh	Market; whole animal	0
<i>P. monodon</i>	Bangladesh	Market; headless, shell on	0
<i>L. vannamei</i>	Brazil	Market; whole animal	0
<i>L. vannamei</i>	China	Market; headless, shell on	0
<i>P. monodon</i>	India	Market; whole animal	0
<i>P. monodon</i>	Indonesia	Market; whole animal	0
<i>L. vannamei</i>	Indonesia	Market; whole animal	0
<i>Farfantepenaeus notialis</i>	Senegal	Market; headless, shell on	0
<i>P. monodon</i>	Vietnam	Market; headless, shell on	20

Mecanismos identificados para a transferência potencial de vírus em produtos congelados importados para populações domésticas de estoques de camarão cultivado ou selvagem.

→ A liberação de resíduos líquidos ou sólidos não tratados de plantas de importação e processamento de camarão diretamente para as águas costeiras,

→ Eliminação inadequada de resíduos sólidos de camarão. Importando e processando em aterros, nos quais o lixo está acessível para gaivotas e outras aves marinhas,

→ O uso de camarão importado como isca por pescadores esportivos.



Considerações sobre a carga viral

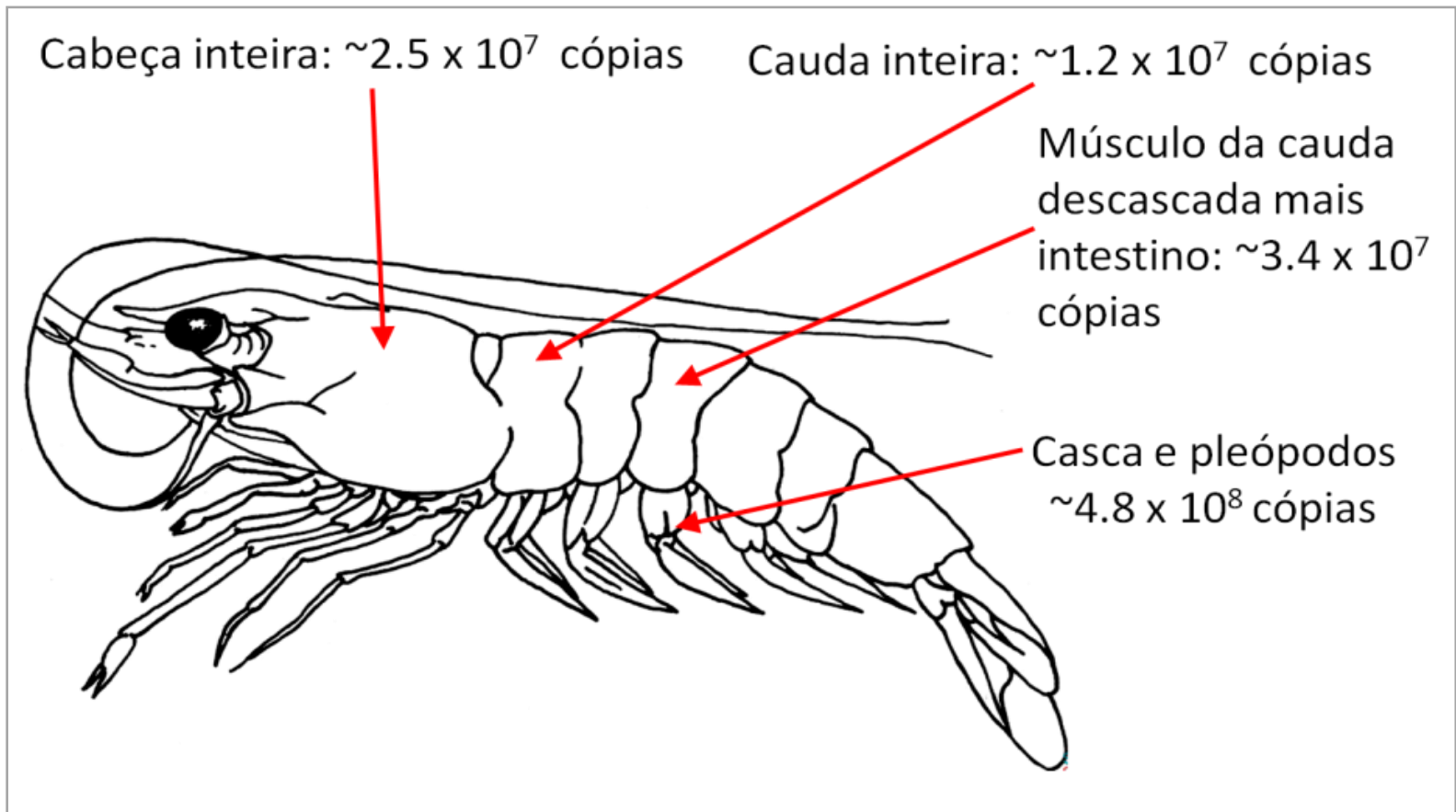


Figura 1 - Principais partes do camarão e respectivas cargas virais considerando uma infecção severa pelo vírus causador da síndrome da mancha branca (WSSV). Os números correspondem ao número de cópias do DNA viral em um micrograma de DNA total extraído de cada uma das partes do camarão (adaptado dos dados revisados por Oidtmann e Stentiford, 2011).

Considerações sobre o tipo de material genético viral

CHAPTER 2.2.4.

TAURA SYNDROME

ssRNA vírus!!!
Altas taxas de
mutação!

1. Scope

Taura syndrome (TS) is a virus disease of penaeid shrimp caused by infection with Taura syndrome virus (TSV) (3, 15, 27, 42). The principal host species in which TSV can cause significant disease outbreaks and mortalities are

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2.3.2. Prevalence

In regions where the virus is enzootic in farmed stocks, the prevalence of TSV has been found in various surveys to range from 0 to 100% (5, 24, 25).

2. [unclear]

2.3.3. Geographical distribution

TS is widely distributed in the shrimp-farming regions of the Americas and South-East Asia (4, 5, 8, 19, 27, 28, 37, 45, 56, 58, 63).

The Americas: following its recognition in 1992 as a distinct disease of cultured *P. vannamei* in Ecuador (6, 23), TS spread rapidly throughout many of the shrimp-farming regions of the Americas through shipments of infected PL and broodstock (5, 7, 19, 27, 28). Within the Western Hemisphere, TS and TSV have been reported from virtually every penaeid shrimp-growing region in the Americas and Hawaii (1, 5, 53). TSV is enzootic in cultured penaeid shrimp stocks on the Pacific coast of the Americas from Peru to Mexico, and it has been occasionally found in some wild stocks of *P. vannamei* from the same region (31, 34). TSV has also been reported in farmed penaeid stocks from the Atlantic, Caribbean, and Gulf of Mexico coasts of the Americas, but it has not been reported in wild stocks from the these regions (19, 27, 28, 30).

Asia: TSV was introduced into Chinese Taipei in 1999 with infected imported Pacific white shrimp,

Considerações sobre diferentes variantes virais



Fitness and virulence of an ancestral White Spot Syndrome Virus isolate from shrimp

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Abstract

White Spot Syndrome Virus, the type species of the virus family *Nimaviridae*, is a large dsDNA virus infecting shrimp and other crustaceans. Genomic analysis of three completely sequenced WSSV isolates identified two major polymorphic loci, “variable region ORF14/15” and “variable region ORF23/24”. Here, we characterize a WSSV isolate originating from shrimp collected in Thailand in 1996 (TH-96-II). This isolate contains the largest WSSV genome (~312 kb) identified so far, mainly because of its sequences in both major polymorphic loci. Analysis of “variable region ORF14/15” suggests that TH-96-II may be ancestral to the WSSV isolates described to date. A comparison for virulence was made between TH-96-II and WSSV-TH, a well characterized isolate containing the smallest genome (~293 kb) identified at present. After injection of the isolates into *Penaeus monodon* the mortality rates showed that the median lethal time (LT₅₀) of TH-96-II was approximately 14 days, compared to 3.5 days for WSSV-TH. When both isolates were mixed in equal amounts and serially passaged in shrimp, WSSV-TH outcompeted TH-96-II within four passages. These data suggest a higher virulence of WSSV-TH compared to TH-96-II. The molecular basis for the difference in virulence remains unclear, but a replication advantage of the 19 kb smaller WSSV-TH genome could play a role.

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Keywords: White Spot Syndrome Virus; WSSV common ancestor; Polymorphic loci; Competitive fitness; Virulence

Virulence and genotypes of white spot syndrome virus infecting Pacific white shrimp *Litopenaeus vannamei* in north-western Mexico

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were evident. Using mortality data, the four WSSV strains grouped into three virulence levels. The Mx-F strain (intermediate virulence) and the Mx-C strain (high virulence) showed more genetic differences than those observed between the Mx-G (low-virulence) and Mx-H (high-virulence) strains, in ORF94 and ORF125. The application of high-viral-load inocula proved useful in determining the different virulence phenotypes of the WSSV strains from the Eastern Pacific.

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Novel, closely related, white spot syndrome virus (WSSV) genotypes from Madagascar, Mozambique and the Kingdom of Saudi Arabia

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ABSTRACT: White spot syndrome virus (WSSV) is highly pathogenic to penaeid shrimp and has caused significant economic losses in the aquaculture industry around the world. During 2010 to 2012, WSSV caused severe mortalities in cultured penaeid shrimp in Saudi Arabia, Mozambique and Madagascar. To investigate the origins of these WSSV, we performed genotyping analyses at 5 loci: the 3 open reading frames (ORFs) 125, 94 and 75, each containing a variable number of tandem repeats (VNTR), and deletions in the 2 variable regions, VR14/15 and VR23/24. We categorized the WSSV genotype as {N₁₂₅, N₉₄, N₇₅, ΔX_{14/15}, ΔX_{23/24}} where N is the number of repeat units in a specific ORF and ΔX is the length (base pair) of deletion within the variable region. We detected 4 WSSV genotypes, which were characterized by a full-length deletion in ORF94/95, a relatively small ORF75 and one specific deletion length in each variable region. There are 2 closely related genotypes in these 3 countries: {6₁₂₅, del₉₄, 3₇₅, Δ5950_{14/15}, Δ10971_{23/24}} and {7₁₂₅, del₉₄, 3₇₅, Δ5950_{14/15}, Δ10971_{23/24}}, where del is the full-length ORF deletion. In Saudi Arabia, 2 other related types of WSSV were also found: {6₁₂₅, 7₉₄, 3₇₅, Δ5950_{14/15}, Δ10971_{23/24}} and {8₁₂₅, 13₉₄, 3₇₅, Δ5950_{14/15}, Δ10971_{23/24}}. The identical patterns of 3 loci in these 4 types indicate that they have a common lineage, and this suggests that the WSSV epidemics in these 3 countries were from a common source, possibly the environment.

KEY WORDS: WSSV genotyping · Variable number of tandem repeats · VNTR analysis · Variable-length deletion · Africa · Saudi Arabia

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GENOTYPING OF WHITE SPOT SYNDROME VIRUS (WSSV) AND INFECTIOUS HYPODERMAL AND HEMATOPOIETIC NECROSIS VIRUS (IHHNV) IN ECUADORIAN CULTURED SHRIMP

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The phylogenetic analysis of the Ecuadorian IHHNV samples and viral isolates from other shrimp producer countries showed that the Ecuadorian isolates were classified in the infectious IHHNV group and suggesting the presence of different genotypes circulating within the country. On the other hand, variable number of tandem repeat (VNTR) analysis of ORF94 for the WSSV genome also showed high levels of genetic variation with distinct numbers of repeat units (RUs) of VNTRs (Table 1). The comparison of the variable region ORF14/15 showed variable length for the presence of indels in the Ecuadorian samples. We found novel strains of WSSV with a unique insertion in comparison with WSSV isolates from other shrimp producer countries.

Genotyping of white spot syndrome virus (WSSV) geographical isolates from Brazil and comparison to other isolates from the Americas

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markers for genotyping. WSSV-infected shrimp *Litopenaeus vannamei* were collected in 2 Brazilian regions (Santa Catarina and Bahia) from 2005 to 2008. DNA was extracted and PCR of the variable regions was performed, followed by sequencing. All Santa Catarina samples showed the same number of repeats for the minisatellites analyzed. Bahia samples showed a different pattern for the regions, indicating that there are at least 2 different WSSV genotypes in Brazil. Both Brazilian isolates have an 11 453 bp deletion in ORF 23/24 when compared with WSSV-TW (Taiwan), which has the full sequence for this locus. The Brazilian WSSV isolates were compared with WSSV isolates from

An alternative set of oligonucleotide primers for WSSV genotyping

Jéssica M. P. Pereira^{1,3}; Emília N. V. de Souza ^{1,2}; Jéssica R. B. Candido ^{1,2}; Márcia D. A. Dantas ^{1,3}; Allan R. D. Nunes ^{1,3}; Karina Ribeiro ²; Dárlío I. A. Teixeira ²; Daniel C. F. Lanza^{1,3}

1 - Laboratório de Biologia Molecular Aplicada, Universidade Federal do Rio Grande do Norte, Natal, RN, Brazil.

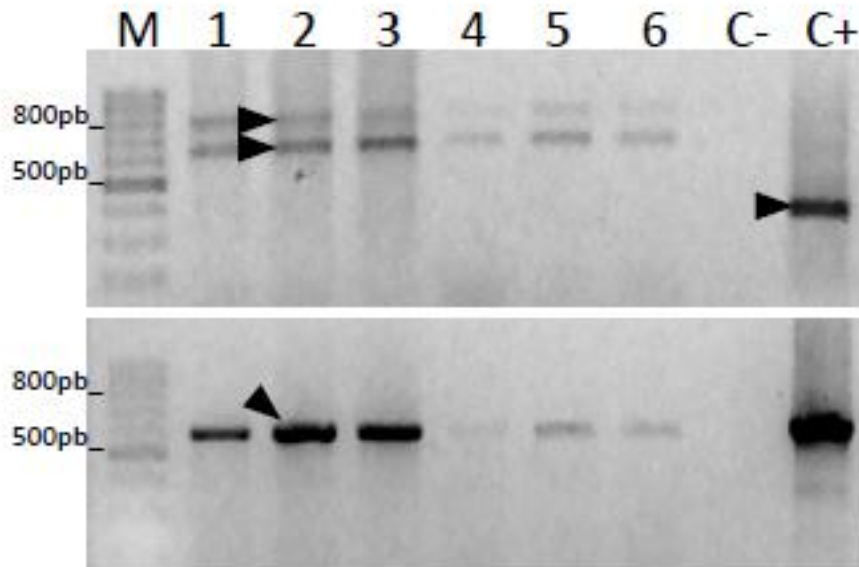
2 - Escola Agrícola de Jundiaí, Universidade Federal do Rio Grande do Norte, Macaíba, RN, Brazil.

3 - Programa de Pós-Graduação em Bioquímica, Universidade Federal do Rio Grande do Norte, Natal, RN, Brazil.

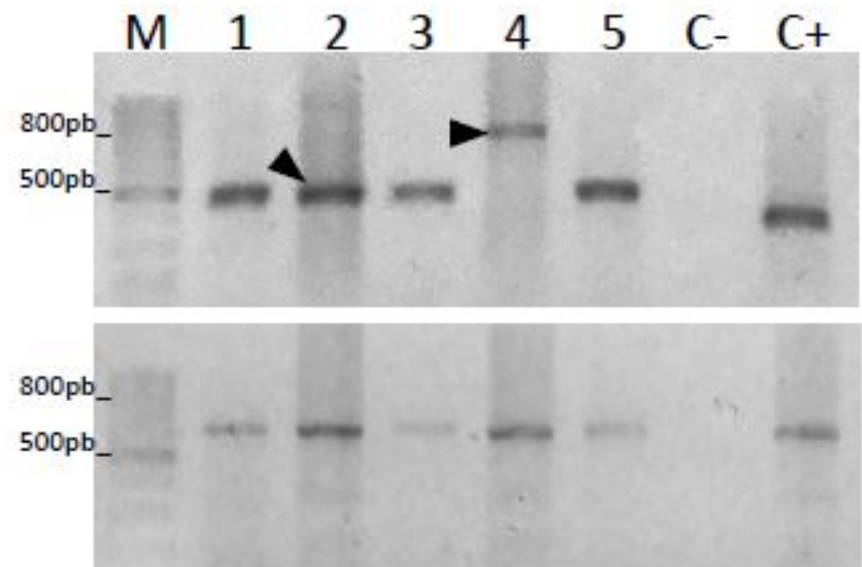
Variantes virais no estado do RN – WSSV

Dados preliminares do nosso grupo

Sul do RN

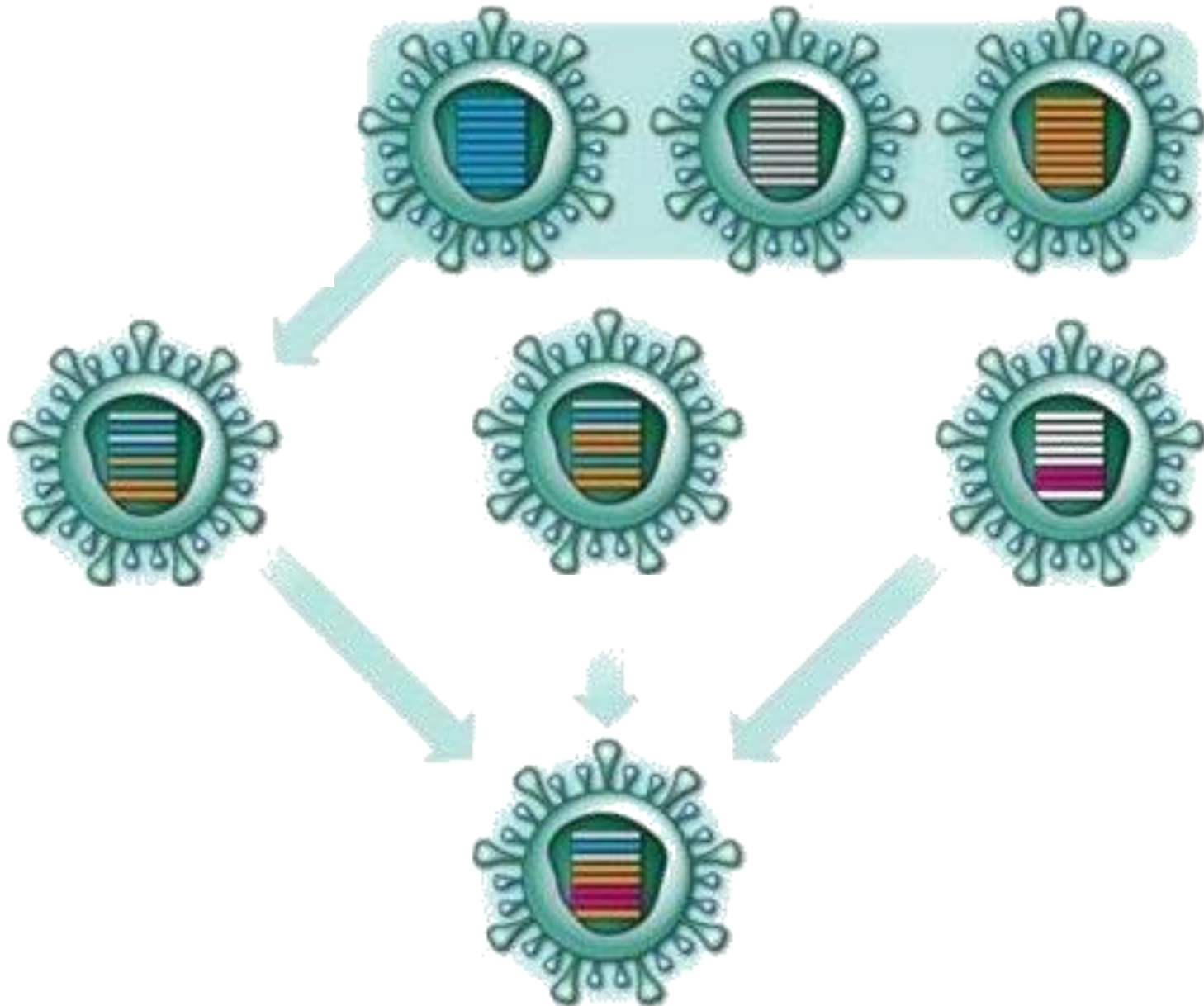


Norte do RN



A variabilidade genética no estado do RN é menor que a observada em outras regiões do mundo.

Recombinação entre genomas virais.



Laboratório de Biologia Molecular Aplicada

Identificação molecular de patógenos, bioinformática e inovação

- Foi criado em 2012 tendo como um dos principais objetivos estudar os principais vírus que acometem a carcinicultura;
- Trabalha atualmente com a caracterização de variantes virais, estudo da biologia dos vírus (virologia molecular) e desenvolvendo métodos para identificação molecular de vírus de interesse econômico;
- Foi o primeiro grupo brasileiro a sequenciar os genomas dos vírus IMNV e PstDNV (IHNV) e WSSV;
- Tem como objetivo desenvolver métodos para detecção de patógenos a baixo custo, para implementação no ambiente industrial (laboratórios de PLs, beneficiamento, manejo).

Atualmente temos sistemas desenvolvidos para detecção de:

1. *Penaeus stylirostris* densovirus - *PstDNV*
2. Infectious Myonecrosis Virus - IMNV
3. White Spot Syndrome Virus - WSSV

→ Os sistemas estão adequados à detecção de variantes virais que ocorrem no Brasil e em outras partes do mundo.

Desenvolvimento do sistema Molbit® para gerenciamento de análises moleculares visando redução de custos

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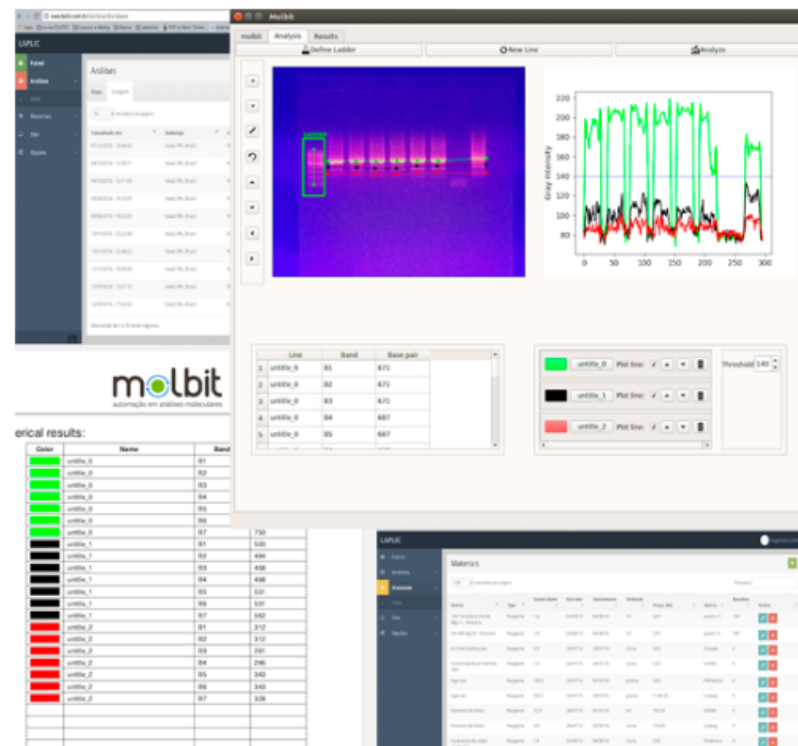
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Simplificando a implementação de análises moleculares em seu laboratório ou empresa.

A identificação pelo DNA é a melhor alternativa para detecção de microorganismos e identificação individual, podendo ser aplicada também em programas de melhoramento genético. A plataforma Molbit é a primeira iniciativa genuinamente brasileira que tem como proposta simplificar e dinamizar a implementação de análises moleculares, por meio da gestão integrada de insumos e análises.

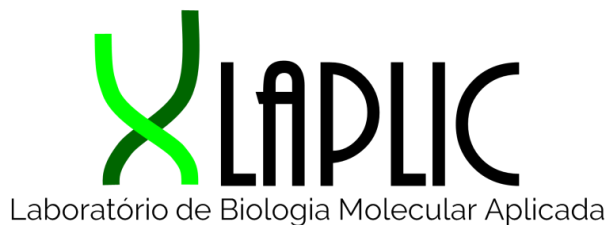
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Parceria Universidade e Empresa

Projeto de extensão PJ 653-2016 – UFRN/FUNPEC – Identificação de patógenos que acometem a carcinicultura

1. Consultoria em análises moleculares;
2. Identificação das variantes virais que ocorrem nas fazendas;
3. Estudos de virulência x variabilidade genética;
4. Desenvolvimento de estratégias para o controle de doenças;
5. Adaptação de tecnologias para inserção no sistema produtivo;
6. Auxílio no programa de melhoramento genético.



Laboratório de Biologia Molecular Aplicada

Identificação molecular de patógenos, bioinformática e inovação

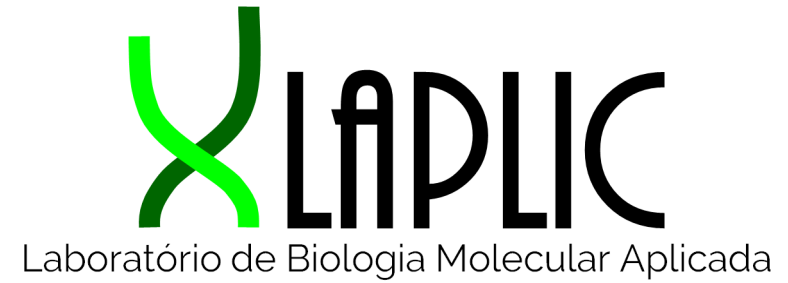


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Natal – 17 de novembro de 2017