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Research Article

A BRIEF HISTORY OF *White spot syndrome virus* AND ITS EPIDEMIOLOGY IN BRAZIL

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ABSTRACT

White spot syndrome virus (WSSV) is considered the most threatening infectious agent in shrimp aquaculture. Since its first occurrence in 1992, this pathogen has caused economic losses approach one billion US dollars per year. WSSV is a tailed, rod-shaped nucleocapsid, double stranded DNA virus, which belongs to *Nimaviridae* family. In this report, it is presented a concise overview on WSSV first occurrence and the different features of the virus. Besides, it is reported an update on epidemiology with special attention to its occurrence in Brazil.

Keywords: White spot syndrome virus, Brazil, epidemiology, virus disease
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A Brief history

The first record of the disease caused by *White spot syndrome virus* (WSSV) was made in Japan between march and october 1993, when farms with the kuruma shrimps (*Marsupenaeus japonicus*) presented 80% of mortality and shrimps displayed clinical signs as abnormal red discolouration and small white spots on the body. This event took place after the importation of juvenile shrimps from China to japanese farming systems (Nakano et al. 1994). After experimental inoculations using filtered extracts of homogenized lymphoid organs from sickened specimens, it was possible to trigger the disease in healthy animals, suggesting that the responsible agent was a virus (Nakano et al. 1994). Furthermore, histopathological comparison of this disease with other well-known diseases affecting penaeid shrimp suggested that this is a new infectious disease, in penaeid shrimp where the aetiological agent might be a virus (Momoyama et al. 1994). Further, electron microscopy revealed the presence of a baciliform, enveloped and large (84 x 226 nm) virus, similar to various baculovirus species. This new virus was temporarily named RV-PJ (*Rod-shaped nuclear virus of P. japonicus*), although its taxonomical position was ascertained by analyzing the structure of the genomic DNA (Inouye et al. 1994).

There are reports since 1992 demonstrating the occurrence of outbreaks by this virus in *P. japonicus* in Taiwan (Chou et al. 1995). There the disease was characterized by causing 100% of mortality in shrimp farming, displaying lethargy and great similarity with the outbreak in Japan. In 1993, a white spot syndrome was observed in *Penaeus monodon e Fenneropenaeus penicillatus* in Taiwan as well, with negative impacts on the shrimp farming industry (Chou et al. 1995).

Also there, experiments confirmed that this was a rod-shaped (baciliform) double-stranded DNA virus with approximately 330 X 87 nm in diameter (Chou et al. 1995; Wang et al. 1995). Due to the presence of white spots on the shrimp carapaces and appendage, some authors have suggested the name "white spot syndrome". Besides, the main feature on the morphology of this virus is the presence of tail-like *appendix* at one end of the virion (Wang et al. 1995). Based on genetic and morphological features, the virus was described within the *Nudibaculoviridae* family, genus *Baculovirus* (Non-occluded Baculovirus – NOB). The name Baculovirus associated with white spot syndrome (WSBV) was proposed for the isolate PmNOBIII (*Penaeues monodon* non-occluded baculovirus III) to indicate PmNOBIII related agents (Wang et al. 1995).

During experimental infections of *P. monodon* with *Yellow head virus* (YHV), it was observed that a batch of infected animals with a virus similar to NOB (Wongteerasupaya

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et al. 1995). Transmission electron microscopy analysis revealed that those animals were infected with YHV and another unknown virus which generated basophilic intranuclear inclusions (unlike YHV, which presents eosinophilic inclusions). Isolation and purification of the nucleic acid from the so far new virus yielded double-stranded DNA of approximately 168 kbp. As this virus caused ectodermal and mesodermal infection, it was convenient to name it as Systemic Ectodermal and Mesodermal Baculovirus (SEMBV) (Wongteerasupaya et al. 1995).

A *nested*-PCR protocol was designed in order to identify this virus in penaeids (Lo et al. 1996a). These authors designated the virus as White spot baculovirus (WSBV). To date, this technique has been recommended by the World Organization for Animal Health (OIE) and widely used for detection of this infectious agent. From 1998, the virus was finally named as *White spot syndrome virus* (WSSV) (Lightner et al. 1998). However, its previous classification, in the Baculoviridae Family, was no longer accepted due to the lack of molecular data (Murphy et al. 1995).

Afterwards, WSSV genomic segments containing ribonucleotide redutase (RR) genes and repeated regions were analyzed in order to investigate its taxonomic status (van Hulten et al. 2000a). Thus, it was further established that the RRs from baculovirus and WSSV did not share a common ancestor, showing that this vírus belongs to a new family. Later on, two major proteins of WSSV were identified: VP28 and VP26 associated to the envelope and nucleocapsid, respectively. The protein sequences were deposited in Genbank under the accession numbers: AF173993 (VP28) e AF173992 (VP26) (van Hulten et al. 2000b). Usually, viral proteins are well conserved among members from the same family. However, neither VP28 nor VP26 shares significant homology with other known structural proteins from Baculovirus available on databases. These results indicated the possibility that WSSV might belong to a new viral family, *Whispoviridae* (van Hulten et al. 2000b; van Hulten et al. 2000c).

The complete sequence of the double-stranded, circular DNA genome of WSSV was determined in 2001 (van Hulten et al. 2001; Yang et al. 2001). Both authors described a genome size ranging from 292 to 305 kb and containing 181 to 184 major open reading frames (ORF) besides, a low similarity with available sequences in database. Only a few genes have shown some degree of homology with herpesvirus genes (Yang et al. 2001). Together with phylogenetic analysis of the DNA polymerase, these informations have confirmed previous reports of a new viral family (van Hulten et al. 2001). Further phyogenetic studies based on WSSV codifying genes of polymerase DNA, major ribonucleotide redutase (RR1), ribonucleotide redutase R2, protein kinase and endonuclease revealed that WSSV is not related to other viral families (van Hulten et al. 2001).

Thus, based on phylogenetic analysis, the International Committee on Taxonomy of Viruses (ICTV) included WSSV as the type species of the genus *Whispovirus* within the newly recognized family *Nimaviridae* ("nima" is the Latin name for "thread") due to the physical feature of the virus, which is a tail-like polar projection (Mayo 2002).

Morphology

WSSV virions have an ovoid to bacillar morphology with a long envelope extension at one extremity (Chou et al. 1995; Wang et al. 1995; Wongteerasupaya et al. 1995). Enveloped particles have about 350 x 130 nm with size variations ranging from 300 to 400 nm length and 110 to 140 nm in diameter. The appendage at the extremity measures 270 to 310 nm in length and about 30 nm in diameter (Durand et al. 1996). The virion is surrounded by a 6-7 nm thick loose-lifting outer lipid layer, with a trilaminar envelope (Durand et al. 1997; Nadala et al. 1998; Wongteerasupaya et al. 1995). The nucleocapsid is slightly striated and its dimensions are 180–420 in length and 54–85 nm in diameter, indicating that it is tightly packed within the virion (Durand et al. 1997).

Major viral proteins

Over the past decade, several studies have been carried in order to identify viral proteins from WSSV. Major structural proteins on the envelope and capsid, as well as non-structural proteins have been successfully identified. The structural proteins compose the viral particle, besides having an important role on viral assembly and virus entry. On the other hand, non-structural proteins are involved in the process of viral replication and inhibition of host cell function (Liu et al. 2006).

The major structural proteins present on the envelope are: VP28, VP19 (van Hulten et al. 2000b), VP466 (Huang et al. 2002a), VP76 (Huang et al. 2005), VP124 (Zhu et al. 2005), VP281 (Huang et al. 2002b), VP110 (Li et al. 2006), VP22 (Zhang et al. 2002), VP31 (Li et al. 2006), VP76 (Huang et al. 2005), VP36B, VP38A, VP51B, VP53A (Tsai et al. 2006), VP150, VP52A, VP52B, VP41A, VP41B (Xie et al. 2006). Proteins located on the viral envelope are mainly involved in the attachment to the host cell and entry. Several other proteins were identified in the nucleocapsid, such as VP26, VP24 (van Hulten et al. 2000b), VP15 (van Hulten et al. 2002), VP35 (Chen et al. 2002), VP51, VP76 (Wu & Yang 2006), VP136A (Tsai et al. 2006). Non-structural proteins like VP9 (Liu et al. 2006) WSV021 (Zhu et al. 2007) e WSV477 (Han et al. 2007) are involved in the transcription, regulation of viral replication and viral DNA replication, respectively.

Genome

Two complete genome sequences were established for isolates from Tailand (van Hulten et al.

2001) and China (Yang et al. 2001). A third sequence, from Taiwan, is available in the GenBank under the accession number AF440570. Genome size was reported differently for each isolate: 292,967 nucleotides for WSSV-TH (van Hulten et al. 2001), 305,107 nucleotides for WSSV-CH (Yang et al. 2001) and 307,287 for WSSV-TW (AF440570). Notwithstanding, these three sequences are very similar among them, and the biggest difference is a gene deletion of approximately 13 kb (WSSV-TH) and 1 kb (WSSV-CH) in the same genomic region, in relation to WSSV-TW (position 31134-31135) (Marks et al. 2003; Marks et al. 2004). The second biggest difference among the three isolates is genetic variation located at the 22961-23619 genomic region of WSSV-TH (genomic segment responsible for codifying ORF14 and 15) (Marks et al. 2004).

Along this segment, WSSV-TH and WSSV-TW possess different sequences of 657 and 834 bp, respectively, without homology with any available nucleotide sequence in the database (Marks et al. 2004). The third difference is an insert of 1337 bp in the TW isolate, at the region 254028-254029, which codifies ORF (Marks et al. 2004). Furthermore, there is a small variation related to the number of ORFs 184 (WSSV-TH) an 181 (WSSV-CH), which codify more than 50 proteins (van Hulten et al. 2001; Yang et al. 2001).

Pathogenicity

The vírus infects cells in tissues of ectodermal and mesodermal origins, including: exoskeleton, appendages and inside the epidermis. Signs of WSSV include lethargy, reduction in food consumption, red discoloration of body and appendages and a decrease in hemolymph circulation (Durand et al. 1996; Durand et al. 1997). WSSV-infected shrimp develop white spots ranging from 0,5 – 3,0 mm in diameter, associated to subcuticular epithelial cells dysfunction and abnormal deposits of calcium (Durand et al. 1997). The white spots are not considered a reliable sign for preliminary diagnosis of this disease, since these spots are not always present and similar spots could be produced after bacterial infections, high alkalinity and stress (Sánchez-Paz 2010). On the cellular level the virus causes margination of chromatin and nuclear hipertrophy (Durand et al. 1997).

Host range and vectors

WSSV can infect a very broad host range amongst decapod crustaceans (Escobedo-Bonilla et al. 2008). In addition, there are reports demonstrating the occurrence of the virus in freshwater species like *Macrobrachium rosenbergii* (Chakraborty et al. 2002). Up to date, more than 93 species of arthopods have been reported as hosts or carriers of WSSV, besides rotifers (Yan et al. 2004) and polychaetes (Vijayan et al. 2005). Table 1 shows some reports on crustacean species infected by WSSV.

Table 1: Reports on different crustacean species infected by WSSV

Species	Report
shrimp	
M. japonicus	Inouye et al. 1994; Nakano et al. 1994; Momoyama et al. 1994
P. monodon, F. penicillatus	Chou et al. 1995
Macrobrachium rosenbergii,	Lo et al. 1996b; Chakraborty et al. 2002
P. semisulcatus, Palaemon sp	Lo et al. 1996b
L. setiferus	Lightner 1996; Lightner et al. 1998
F. aztecus, F. duorarum, L. vannamei	Lightner et al. 1998
Metapenaeus monoceros, M. brevicornis, Exopalaemon styliferus	Hossain et al. 2000
Metapenaeus dobsoni, Parapenaeopsis stylifera, Solenocera crassicornis	Hossain et al. 2001
Heterocarpus sp., Aristeus sp., Metapenaeus elegans	Chakraborty et al. 2002
crabs	
Charybdis feriatus, Portunus pelagicus, P. sanguinolentus, Helice tridens	Lo et al. 1996b
Pseudograpsus intermedius	Hossain et al. 2000
Charybdis annulata, C. cruciata, Macrophthalmus sulcatus, Gelasimus marionis nitidus e Metopograpsus messor	Hossain et al. 2001
Cancer pagurus	Corbel et al. 2001
Charybdis hoplites	Chakraborty et al. 2002
Chasmagnathus granulata	Marques et al. 2011, Cavalli et al. 2013

Transmission

WSSV transmission can occur through vertical or horizontal pathways. The presence of viral inclusions in reproductive organs of *P. monodon* broodstock indicates the vertical transmission of the virus (Lo et al. 1997). However, no virus infection was found in mature females, which may imply that infected eggs died by the virus before maturation (Lo et al. 1997). The horizontal transmission can occur among individuals by direct contact, or indirectly, by ingestion of infected organisms.

Epidemiology

Since its first ocurrence in 1992 (Chou et al. 1995), WSSV has been spread worldwide. In 1993, it was confirmed that the virus was disseminated throughout Asia (Inouye et al. 1994; Nakano et al. 1994; Momoyama et al. 1994). In november 1995, the first case of infection by WSSV was described in the New World, affecting a shrimp farming in Texas, USA (Lightner 1996). In Latin

America, the presence of the virus was reported in 1999 in Mexico, Panama, Peru, Costa Rica, El Salvador, Colombia, Nicaragua, Honduras (*Annual animal health status* - http://www.oie.int/hs2/report.asp) and Ecuador (Rodriguez et al. 2003). The first notification of WSSV in shrimp farms in Brazil occurred in 2005, in the states of Santa Catarina (South) (Seiffert et al. 2006) and Ceará (Northeast) (OIE 2005).

The presence of WSSV in wild shrimps was reported by Lo et al. (1996b) in four species of shrimp in Taiwan. Nunan et al. (2001) reported a viral prevalence of 2% in *L. vannamei* caught in the Pacific Ocean, at the offshore of Panama, using dot blot hybridization technique. Different prevalences were reported for *Fenneropenaeus indicus, P. monodon, Metapenaeus* spp e *Scylla serrata* infected in the east coast of India (Vaseeharan et al. 2003). Chapman et al. (2004) described the presence of WSSV in shrimps of South Carolina, USA, in the North Atlantic Ocean. Uma et al. (2005) revealed the presence ranging from 25-50% of WSSV in *Penaeus monodon* breeders from Southeastern India. In Brazil wild shrimp species *Farfantepenaeus brasiliensis* and *F. paulensis* were found to be infected by this virus (Cavalli et al. 2010 and 2011). However, the most austral occurrence of the virus in the South America was registered for wild crustaceans of Bahia Blanca, Argentina (Martorelli et al. 2010).

WSSV in Brazil

In november 2004, *Litopenaeus vannamei* cultivated in ponds (1400 ha.) in Lagoa de Imaruí, Laguna, Southern Brazil, were infected by WSSV. Mortality rates reached 90%, causing economic losses of approximately US$ 3 million at Laguna, Southern Brazil (Seiffert et al. 2006). The disease led to a decrease in shrimp production from 4.189t in 2004 to 480t in 2006 (Seiffert et al. 2006). This was the first report of WSSV in Brazil and notified to World Organization for Animal Health (OIE) in january 2005. In December 2010, OIE brought out another occurrence of the disease in Santa Catarina state. In North coast of Santa Catarina, a great number of *White spot syndrome virus particles*, were visualized by the negative staining technique (Hipolito et al. 2012).

WSSV detection was also reported in Ceará, Pernambuco and Rio Grande do Norte states (Guerrelhas & Teixeira 2012). Viral co-infection with *Infectious myonecrosis* virus (IMNV) and WSSV was also report in Ceara (Feijó et al. 2013). Rio Grande do Norte and Ceará are the major shrimp producers in Brazil, responsible for about 80% of total shrimp production. Therefore, it is necessary special attention concerning management and vírus control in these areas in order to prevent further impacts.

In wild animals, the virus has already been detected in *Farfantepenaeus paulensis* and *F. brasiliensis* in the Atlantic Ocean (Cavalli et al. 2010). Likewise, the presence of viral DNA was confirmed in *F. paulensis* in the Laguna estuarine system (Cavalli et al. 2010) and *Litopenaeus vannamei* from farms in Santa Catarina state (Cavalli et al. 2010; Costa et al. 2010). Moreover, in the southern region, the virus has been detected in wild *F. paulensis* and *L. vannamei* produced in ponds in the Lagoa dos Patos, Rio Grande do Sul state (Cavalli et al. 2011).

The arrival of the virus into the brazilian shrimp cultivation remains not well known. However, an epidemiological study suggests that the entry of the virus in Santa Catarina occurred upon nauplius and postlarvae import from Northeastern Brazil (Costa 2010). The entry of pathogens in shrimp farming occurs mainly due to contaminated food and objects, infected breeders and animals which act as vectors (Fegan & Clifford 2001; Lightner 2005).

In addition, environmental factors such as sudden changes in temperature(Rahman et al. 2006, Rahman et al. 2007), salinity (Liu et al. 2006) an increase in the number of predators and population density, as well as other potentially stressful factors in animal production can trigger the development of diseases. Stress factors may affect appreciably the physiological balance of the aquatic organisms, consequently changing their imune system, thus decreasing their ability to respond to pathogens (Pavanelli et al. 1998).

CONCLUSIONS

For the control of WSSV disease, it is important the use of prophylactic measures in order to prevent the virus transmission. Fish industries must be focused on biosecurity and programs that include the reduction of water exchange as this is a risky management option for shrimp farmers unless both influent and effluent stream are disinfected (Lotz 1997). More strict controls are important on the entry of live animals (tested or not), as they present a potential risk to introduce the infection (Lightner 2005). Import procedures must include a rigorous quarantine and screening for diseases for breeding stocks before their transfer to aquaculture (Flegel & Fegan 2002). In addition to breeders and larvae (Flegel, 2006), the spread of shrimp viruses can include frozen shrimps (Durand et al. 2000, Flegel & Fegan 2002) and ballast water (Flegel & Fegan 2002). Moreover, considering that only few epidemiological researches have been conducted and these indicated the presence of WSSV in Brazil, surveillance studies on the Brazilian coast are necessary in order to better determine the presence of WSSV in wild shrimps and the spreading of the disease in our coast in order to identify the hotspots, or regions relatively free of the virus.

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