Quantitative relationship of two viruses (MrNV and XSV) in white-tail disease of *Macrobrachium rosenbergii*

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**ABSTRACT:** *Macrobrachium rosenbergii* nodavirus (MrNV) and extra small virus (XSV) were purified from diseased freshwater prawns *M. rosenbergii* and used to infect healthy post-larvae (PL) by an immersion method. Three groups of prawns were challenged with various combined doses of MrNV and XSV. Signs of white-tail disease (WTD) were observed in Groups 1 and 2, which had been challenged with combinations containing relatively high proportions of MrNV and low proportions of XSV. By contrast there was little sign of WTD in Group 3, which had been challenged with a higher proportion of XSV than MrNV. A 2-step Taqman real-time RT-PCR was developed and applied to quantify viral copy numbers in each challenged PL. Results showed that genomic copies of both viruses were much higher in Groups 1 and 2 than they were in Group 3, indicating that MrNV plays a key role in WTD of *M. rosenbergii*. The linear correlation between MrNV and XSV genome copies in infected prawns demonstrated that XSV is a satellite virus, dependent on MrNV, but its role in pathogenicity of WTD remains unclear.

**KEY WORDS:** *Macrobrachium rosenbergii* · Nodavirus · Extra small virus · Real-time RT-PCR · White-tail disease

**INTRODUCTION**

The giant freshwater prawn *Macrobrachium rosenbergii* de Man is one of the most economically important crustaceans in freshwater aquaculture in China, but it is also cultured widely in areas of the Caribbean and in other Asian countries. Since 1990, white-tail disease (WTD) has been prevalent in the main culture areas such as Thailand, Guadeloupe, the Antilles, China and India (Nash et al. 1987, Anderson et al. 1990, Arcier et al. 1999, Tung et al. 1999, Qian et al. 2002, Sahul Hameed et al. 2004). Two kinds of viral particles have been isolated from WTD prawns; one is a nodavirus (*M. rosenbergii* nodavirus or MrNV) and the other a smaller virus associated with MrNV (called extra small virus or XSV) (Qian et al. 2003, Shi et al. 2004). Both viruses have been well characterized. MrNV is 26 to 27 nm in diameter, icosahedral and non-enveloped with a genome consisting of 2 linear ssRNA fragments (3 and 1.2 kb). XSV is 15 nm in diameter, icosahedral and non-enveloped, and possesses a linear ssRNA genome of 0.9 kb encoding 2 overlapping structural proteins of 16 and 17 kDa (Shi et al. 2004, Sri Widada & Bonami 2004, Bonami et al. 2005).

Various methods have been developed to detect MrNV and XSV. A sandwich enzyme-linked immunosorbent assay (S-ELISA) and 3 complementary genome-based methods, i.e. dot-blot hybridization, in situ hybridization and reverse transcriptase-polymerase chain reaction (RT-PCR), are available for the detection of MrNV (Romestand & Bonami 2003, Sri Widada & Bonami 2004, Bonami et al. 2005).
and RT-PCR were also developed to detect XSV (Sri Widada et al. 2004). More recently, Voganandhan et al. (2005) established a 1-step multiplex RT-PCR to detect MrNV and XSV simultaneously. These methods have facilitated the diagnosis of WTD.

Due to the small size and absence of an RNA-dependent RNA polymerase (RdRp) gene in the XSV genome, it was believed that XSV is a satellite virus (Sri Widada & Bonami 2004). In our previous studies, MrNV and XSV were always found co-located in the connective tissues of diseased prawns (Qian et al. 2003, Shi et al. 2004). Experimental infection with a mixture of the 2 viruses demonstrated that WTD in Macrobrachium rosenbergii could be attributed to one or both of them. Without purification and separation of MrNV and XSV, the role and relationship of these 2 viruses in WTD of M. rosenbergii remains uncertain.

In this study, MrNV and XSV were purified and separated from diseased Macrobrachium rosenbergii and used to infect healthy post-larvae (PL). Real-time RT-PCR was developed and used to quantify copy numbers of the 2 viruses in challenged PL and investigate their role and relationship in WTD.

MATERIALS AND METHODS

Post-larvae. Five-d-old healthy Macrobrachium rosenbergii PL, with no history of WTD, were purchased from a hatchery in Wuhan (Hubei Province, China). The PL were reared in 50 × 38 × 23 cm disinfected tanks and fed powdered eggs 3 times a day. Excreta and food remains were removed daily. Water temperature was controlled at 25 to 27°C, and the tanks were gently aerated. Two-thirds of the freshwater was exchanged each day.

MrNV and XSV purification. Infected PL were collected from a hatchery in Zhejiang Province (China) and stored at −70°C. Purification was performed as described previously (Bonami et al. 2005). Briefly, the PL were homogenized in PBS buffer (pH 7.4) and clarified at 10 000 × g for 25 min. The resultant supernatant was centrifuged at 160 000 × g for 4 h at 4°C. The pellets were resuspended in PBS, followed by extraction 2 to 3 times with Freon (1,1,2-trichloro-2,2,1trifluoroethane). Then, the aqueous layer was centrifuged at 160 000 × g for 4 h. The 2 viruses were separated with a 15 to 30% (w/v in PBS) sucrose gradient, followed by a CsCl gradient. The viruses were quantified by real-time RT-PCR as indicated below. The purified virions were stored at −70°C.

Experimental infections. The 5-d-old PL were reared for 3 d and starved for 1 d before challenge. RT-PCR with MrNV- and XSV-specific primers was performed to confirm the health of the PL. Three groups of healthy PL were challenged with different combinations of the 2 purified viruses—Group 1: 3.49 × 10^{13} MrNV and 9.82 × 10^{11} XSV ml⁻¹ (i.e., MrNV:XSV = 36:1); Group 2: 1.75 × 10^{13} MrNV and 2.23 × 10^{12} XSV ml⁻¹ (i.e., MrNV:XSV = 8:1); Group 3: 4.20 × 10^{9} MrNV and 3.48 × 10^{12} XSV ml⁻¹ (i.e., MrNV:XSV = 1:830). A control group was treated with PBS only. The PL (81 for each group) were immersed in a virus suspension or PBS solution for 15 min and then transferred to freshwater tanks. The leftover virus suspensions were mixed with the powdered eggs used to feed the PL over the following 3 d. Clinical signs were monitored daily. PL exhibiting white muscle were recorded and transferred to a separate tank. Seven PL were sampled from each group on Day 8 post-immersion (p.i.), and the remainder were harvested on Day 24 p.i. for storage at −70°C.

RNA extraction. Total RNA was extracted from whole PL with TRIzol reagent (Invitrogen) according to the manufacturer’s protocol. The final RNA was resuspended in 40 to 50 μl DEPC water and stored at −70°C. For RNA extraction from viral particles, virus suspensions were digested with 200 μg ml⁻¹ Proteinase K in 10 mM Tris-HCl, 10 mM EDTA (pH 8.0) and 0.5% SDS at 37°C for 1 h. RNA was extracted successively with phenol, phenol/chloroform/isoamyl alcohol (25:24:1, v/v/v) and chloroform/isoamyl alcohol (24:1, v/v), and then precipitated with 2.5 vol of absolute ethanol after addition of 0.3 M sodium acetate (final concentration) at −20°C for 2 h, followed by washing with 75% ethanol and dissolving as above.

Primers and probes. The primers and probes (Table 1) for MrNV and XSV detection were designed using Primer Express software (Version 2.0, Applied Biosystems) and targeted the MrNV RNA1 and XSV sequences, respectively (GenBank Nos. AY231436 and DQ174318). Taqman probes were labeled with the fluorescent reporter dye 6-carboxy-fluorescein (FAM) and the quencher 6-carboxy-3,4,5,6-tetra-methylrhodamine (TAMARA) at the 5'- and 3'-ends, respectively. The primers for 18S rRNA were designed from Macrobrachium rosenbergii 18S rRNA (AY461599). The amplicon sizes for MrNV RNA1, XSV and 18S rRNA were 75, 69 and 213 bp, respectively.

Preparation of quantitative standards. The amplicons of MrNV RNA1 and XSV were cloned into pGEM-T easy vector (Promega). The plasmid DNA was extracted with a plasmid miniprep kit (Omega Bio-Tek). The amplicon of 18S rRNA by RT-PCR was purified using an EZNA gel extraction kit (Omega Bio-Tek). Copy numbers were calculated according to DNA concentrations using a Lambda 25 UV/VIS spectrometer (Perkin-Elmer). The DNA stock solutions were aliquoted and stored at −20°C. One aliquot was serially diluted 10-fold and used in real-time PCR with
either a Taqman probe (MrNV RNA1 and XSV) or SYBR Green I dye (18S rRNA).

**Two-step real-time RT-PCR.** Reverse transcription was performed in a 10 µl volume. An aliquot of 3 µl RNA with 10 pmol reverse primer and 2.8 µl of diethylpyrocarbonate-treated H2O were first denatured at 70°C for 10 min, then immediately quenched on ice and subsequently added to the RT mixture consisting of 0.6 mM each of the 4-deoxynucleoside triphosphates, 8 U RNasin (BioStar) and 80 U M-MLV reverse transcriptase (Promega). The reverse transcription reaction was conducted at 42°C for 60 min, followed by heating to 70°C for 5 min and holding at 4°C.

Real-time PCR assays for MrNV and XSV with Taqman probes were conducted in a DNAEngine OPTICON machine (MJ). The final PCR mixture (25 µl) contained 0.4 µM each of forward and reverse primers, 80 nM Taqman probe, 0.5 U of Taq polymerase (BioStar) and 5 µl cDNA. The thermal cycling conditions were: 94°C for 5 min, then 50 cycles of 94°C for 30 s and 58°C for 30 s. Fluorescence was measured after each cycle. In the real-time PCR assay with SYBR Green I dye (OPE Tech) to quantify 18S rRNA, the amplification profile was 94°C for 5 min, followed by 40 cycles of 94°C for 30 s, 57°C for 30 s, 72°C for 30 s and 84°C for 5 s for plate reading to collect fluorescence data. A melting curve from 16 to 94°C was generated after the last extension step at 72°C for 10 min.

**Statistical analysis.** The coefficient of variation of the real-time RT-PCR assays and standard error of the mean were calculated using Microsoft Excel 2000 and SPSS Version 10.0, respectively. Significant differences were determined using an independent-samples t-test, and correlation analysis was carried out using a bivariate correlation test with SPSS software.

### RESULTS

**Sensitivity and reproducibility of real-time PCR assays**

To assess the dynamic range of the real-time PCR assays, DNA plasmids, or amplicons, were serially diluted 10-fold and tested 3 times in triplicate. Standard curves were constructed by plotting the logarithm of copy number against measured C_T (threshold cycle) values (Fig. 1). The curves covered a linear range of 50 to 5.0 × 10^8, 45.8 to 4.58 × 10^8 and 9.11 × 10^5 copies per reaction (25 µl) for MrNV, XSV and 18S rRNA, respectively. The linear correlations (R^2) between the C_T and the log of the copy number were 0.997, 0.998 and 0.999 for the 3 curves, respectively.

Reproducibility of the methods was evaluated by intra- and inter-assay variation. Each point for the serial 10-fold dilutions represented triplicate samples for 3 independent runs. The results are summarized in Table 2. In fact, Taqman probe real-time PCR could detect <10 copies per reaction, but the coefficient of variation exceeded 5% (data not shown).

### Table 1. Primers (FP: forward; RP: reverse) and probes used in real-time RT-PCR (MrNV: Macrobrachium rosenbergii nodavirus; XSV: extra small virus). Tm: annealing temperature

<table>
<thead>
<tr>
<th>Target gene</th>
<th>Primer and probe</th>
<th>Sequence (5’→3’)</th>
<th>Tm</th>
<th>Amplicon (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MrNV RNA1</td>
<td>FP</td>
<td>CAACCTCGGTATGGAACTCAAGGT</td>
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<td>75</td>
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<tr>
<td></td>
<td>RP</td>
<td>AGGAAATAACACGAGAAGAAAGTC</td>
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<td></td>
</tr>
<tr>
<td></td>
<td>Probe</td>
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<tr>
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<td>FP</td>
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<td>69</td>
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<tr>
<td></td>
<td>RP</td>
<td>CTCCAGGAAAGTGCGATACG</td>
<td>58</td>
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<tr>
<td></td>
<td>Probe</td>
<td>CATGCCGCAATGCATCTCGCA</td>
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<tr>
<td>18S rRNA</td>
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<tr>
<td></td>
<td>RP</td>
<td>GTCCCGCATTTGTTATTTTCGTC</td>
<td>57</td>
<td></td>
</tr>
</tbody>
</table>

![Fig. 1. Standard curves for MrNV RNA1, XSV and 18S rRNA real-time PCR assays](image-url)
MrNV, XSV purification and quantification

By sequential sucrose gradient and CsCl isopycnic centrifugation, electron microscopy revealed that MrNV and XSV from the WTD-infected PL were well separated (Fig. 2). However, quantification by Taqman real-time RT-PCR showed that the MrNV fraction (3.16 × 10¹² copies µl⁻¹) still contained 8.90 × 10¹⁰ copies µl⁻¹ of XSV (i.e. about 35 times more MrNV than XSV), while the XSV fraction (3.60 × 10¹¹ copies µl⁻¹) contained 4.34 × 10⁸ copies µl⁻¹ of MrNV (1 single MrNV particle for about 830 XSV particles).

Experimental infection and gross signs of disease

At Day 6 p.i., white spots were observed on the telson of PL in Groups 1 and 2, the groups that were given combined viral doses in which MrNV dominated. The spots then spread to the whole abdominal musculature. White-tail prawns showed decreased activity. The cumulative percentages of white-tail prawns on Day 24 p.i. were >60 and 40%, respectively, for Groups 1 and 2 (Fig. 3). By contrast, many fewer PL showing gross signs of WTD were seen in Group 3 containing PL given combined viral doses in which XSV dominated. Only 2 suspicious prawns whose abdominal muscles were slightly white and semi-transparent were observed on Day 11 p.i. In addition, the average weight of non-white-tail and white-tail prawns in Group 2 decreased by 8 and 22%, respectively, compared with the control group at Day 24 p.i. (data not shown).

Quantification and statistical analysis of MrNV and XSV

Real-time RT-PCR quantification of MrNV and XSV genomic copies in infected tissue (Fig. 4) revealed no significant difference for MrNV copies between Groups 1 and 2 on Days 8 and 24 p.i. (p > 0.05). How-

<table>
<thead>
<tr>
<th>Copy number</th>
<th>Mean C₇ value</th>
<th>Intra-assay CV (%)</th>
<th>Inter-assay CV (%)</th>
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<tr>
<td>RNA1 XSV 18S</td>
<td>RNA1 XSV 18S</td>
<td>RNA1 XSV 18S</td>
<td>RNA1 XSV 18S</td>
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<td>35.40</td>
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Table 2. Evaluation of reproducibility of quantitative real-time PCR assays. C₇ values were determined from 9 replicates; intra-assay coefficients of variation (CV) were determined from 3 replicates of each dilution; inter-assay CVs were determined from 3 independent assays performed on different days (abbreviations for target genes, see Table 1)

Fig. 2. Purified viral particles by transmission electron microscopy (TEM). There are some XSV (black arrows) remaining in the MrNV-containing fraction (a, scale bar: 200 nm) and MrNV (white arrows) remaining in the XSV-containing fraction (b, scale bar: 100 nm)
ever, MrNV copies in Group 3 were significantly lower than they were in Groups 1 and 2 (p < 0.05) on Days 8 and 24 p.i. This corresponded with the fact that Group 3 showed few gross signs of WTD. In the case of XSV, the copy numbers in 3 groups did not show significant differences on Day 8 p.i. (p > 0.05), while on Day 24 p.i., the copies in Group 1 were significantly higher than those in Group 3 (p < 0.05). However, the overall XSV copy numbers were up to 2 logs or more higher than those of MrNV on both days. In the control group, a few samples gave Ct values above background and around 35. These values were distinctly higher than those from infected groups (Ct = 15 to 26) and were considered to result from non-specific amplification (data not shown).

When looking at MrNV and XSV copies of individual PL, it seemed that PL showing white tails had relatively higher viral copies than those without white tails (data not shown). Therefore, on Day 24 p.i., PL in Group 2 that showed gross signs of WTD (n = 19) were compared to those (n = 19) from the same group that did not (Fig. 5). It was found that the mean log of MrNV copies in non-white-tail prawns (6.1 × 10^6) was 10 times less than that in white-tail prawns (6.1 × 10^7) (p < 0.05). Accordingly, XSV genomic copies in non-white-tail prawns (6.9 × 10^8) and white-tail prawns (9.7 × 10^9) differed about 14-fold (p < 0.05). At the same time, the transcription of host 18S rRNA of the white-tail group (3.5 × 10^9) was also significantly higher than that of the non-white-tail group (1.6 × 10^9) (p < 0.05), suggesting that viral replication could slightly interfere with transcription of host genes. This was in agreement with results from studies on panicum mosaic virus and its satellite virus infection in which there is a consistently sustained slight reduction of host rRNA expression (Scholthof 1999).

A scatter chart constructed by plotting the log of XSV genomic copies against the log of MrNV genomic copies, divided by the respective 18S rRNA copies of each tested individual (n = 80) (Fig. 6), resulted in a linear plot with a positive Pearson correlation coefficient of 0.729 calculated by SPSS software (p < 0.01).
revealed that the non-white-tail prawns had subclinical infections despite the relatively high viral loads, especially for XSV. This result is in agreement with the work of Sahul Hameed et al. (2004). In their study, the 2 viruses failed to cause clinical signs or mortality when injected into adult prawns, although both were detected in many organs, except eyestalks and the hepatopancreas, by conventional RT-PCR. Such prawns showing no gross signs of disease could act as carriers of the virus and be responsible for virus transmission.

In most cases, the XSV copy numbers were much higher than those of MrNV, indicating an efficient replication of XSV. This large difference in viral loads of XSV and MrNV may lead to misinterpretation of conventional RT-PCR detection results. In a recent report, Yoganandhan et al. (2005) found that some prawns were MrNV negative, but XSV positive by conventional RT-PCR. We detected MrNV in Group 1 prawns on Day 24 p.i. by a multiplex RT-PCR test established in our laboratory (authors’ unpubl. data), but when genomic copies were <10^4, MrNV could not be detected by conventional RT-PCR (data not shown).

To date, 4 plant satellite viruses, satellite tobacco necrosis virus (STNV), satellite maize white line mosaic virus (SMWLMV), satellite tobacco mosaic virus (STMV) and satellite panicum mosaic virus (SPMV) and an animal satellite virus (the chronic bee-paralysis virus-associated satellite) have been recognized by the ICTV (www.ncbi.nlm.nih.gov/ICTVdb/ictv/fr-fst-g.htm). The function of some plant satellite viruses has been well analyzed by transgenetic techniques. The SPMV capsid protein acts as a pathogenicity factor in both host and non-host plants and interferes with suppression of gene silencing (Qiu & Scholthof 2004). STNV was reported to suppress its helper virus replication and ameliorate the symptoms induced by the helper virus in different hosts (Jones & Reichmann 1973, Kassanis 1981, Rodriguez-Alvarado et al. 1994). However, the presence of STMV did not modify (Valverde & Dodds 1986, Valverde et al. 1991) or enhance the symptoms (Rodriguez-Alvarado et al. 1994) in different hosts. Although we have shown that MrNV is important in WTD outbreaks in prawns, the role of XSV in pathogenicity is still unclear and further work is needed to determine whether it plays any role.

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**LITERATURE CITED**


Jones IM, Reichmann ME (1973) The proteins synthesized in tobacco leaves infected with tobacco necrosis virus and satellite tobacco necrosis virus. Virology 52:49–56


Valverde RA, Dodds JA (1986) Evidence for a satellite RNA associated naturally with the U5 strain and experimentally with the U1 strain of tobacco mosaic virus. J Gen Virol 67:1875–1884


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