Note

Screening of pathogens from a biosecured pacific white shrimp (Penaeus vannamei) farm in Kattur, Tamil Nadu

K. SARAVANAN1, R. MARY LINI2 AND S. K. OTTA3*
1ICAR-Central Island Agricultural Research Institute, P. O. Box No. 181, Port Blair - 744 101 Andaman and Nicobar Islands, India
2ICAR-National Bureau of Fish Genetic Resources, Canal Ring Road, Telibagh, P. O. Dilkusha, Lucknow - 226 002 Uttar Pradesh, India
3ICAR-Central Institute of Brackishwater Aquaculture, 75, Santhome High Road, Raja Annamalai Puram Chennai - 600 028, Tamil Nadu, India
e-mail: subhendu@ciba.res.in

ABSTRACT

Screening for presence of various pathogens were carried out in one of the biosecurity maintained shrimp farms in Kattur Village of Tamil Nadu. Sampled shrimps exhibited pinkish discolouration of the body, pale hepatopancreas and antennal cut indicating bacterial infection. Similarly, there was also large scale size variation and reduced growth compared to the days of culture. Samples were screened for bacterial and four (including three OIE-listed) viral pathogens. The samples were also subjected to histopathological investigations. Based on the biochemical tests, the isolated bacteria was identified as Vibrio parahaemolyticus. Metalloprotease gene-specific PCR further confirmed the isolates to be V. parahaemolyticus. PCR was carried out to further investigate the early mortality syndrome/acute hepatopancreatic necrosis disease (EMS/AHPND) strain status of these isolates and were found to be negative. The samples were found to be positive for white spot syndrome virus (WSSV) by second step PCR and infectious hypodermal and haematopoietic necrosis virus (IHHNV) by direct PCR. All these were negative for monodon baculovirus, yellow head virus and gill associated virus. Infection of samples by WSSV and IHHNV were further confirmed by histopathology. The finding of the present study indicated the reduction in growth and size variation due to bacterial infection by V. parahaemolyticus and viral infection by IHHNV. Though biosecurity was maintained in the farm, the pathogens are suspected to be transmitted through the seed or improper pond preparation.

Keywords: Biosecurity, Diagnosis, Pathogens, Penaeus vannamei

Shrimp culture is an ever growing popular food producing sector in India. Penaeus vannamei Boone, 1931 is one of the economically important penaeid shrimp which is extensively cultivated in many countries including India during the past few years. India was a leading exporter of black tiger shrimp until this market was virtually replaced by P. vannamei. The success of culturing this exotic species using imported specific pathogen free (SPF) stocks in the Indian sub-continent has led to more farmers adopting this species in the country (Regunathan and Kitto, 2011). Cultivation of penaeid shrimp in Asia has changed dramatically since 2002 because of the widespread adoption of this species.

With intensification of penaeid aquaculture industry, occurrence of diseases has increased which poses a major risk and primary constraint to the growth of shrimp culture industry in many parts of the world including India. Important shrimp viral diseases caused by white spot syndrome virus (WSSV), hepatopancreat parvo-like virus (HPV), infectious hypodermal haematopoietic necrosis virus (IHHNV), yellow head virus (YHV) and monodon baculo virus (MBV) have been reported from India (Manivannan et al., 2002; Bondad-Reantaso et al., 2005; Flegel, 2006; Kalaimani et al., 2013). To date, In India WSSV remains the most important virus causing mass mortalities in shrimp farms, leading to severe economic losses (Rai et al., 2009). IHHNV is one of the major viral pathogens of penaeid shrimps worldwide (Lightner and Redman, 1998). Though IHHNV infection does not cause mortality in stocks of P. vannamei and Penaeus monodon, it can result in a disease condition, which is characterised by reduced growth as well as deformities of cuticle and rostrum (Bell and Lightner, 1984; Kalagayan et al., 1991; Primavera and Quitonito, 2000). Recently Otta et al. (2014) reported WSSV and IHHNV infection from P. vannamei farms in Tamil Nadu. Except for a few reports, there is no information available on the diseases of P. vannamei from Indian shrimp culture. With this background, the present investigation was undertaken to screen for the presence of various pathogens in one of the biosecurity maintained shrimp farm at Kattur Village of Tamil Nadu.
P. vannamei samples were collected from a shrimp farm at Kattur Village in Minjur Taluk, Thiruvalloor District of Tamil Nadu (Fig. 1). The ponds were having bird and crab fence. Adequate reservoir ponds were there for preliminary water treatment and release into ponds. Entry to the farm was regulated through partial sanitisation. Samples were collected from two different shrimp ponds and screened for various pathogens. Samples were collected using cast net, four from each corner and one from the middle of each pond. Pooled samples from each pond were taken for pathogen screening. For PCR analysis, samples were collected in 90% ethanol. Samples for histopathological analysis were fixed with Davidson’s fixative (Bell and Lightner, 1988).

For microbiological analysis, hepatopancreas, haemolymph and gut were directly dissected out and inoculated into Zobell marine agar and TCBS agar plates and Zobell marine broth (HiMedia, Mumbai, India). Pure culture of the predominant isolate was obtained by repeated streaking till individual colonies were obtained. Colonies from TCBS plates were subjected to biochemical tests for identification of Vibrio sp. as per Alsina and Blanch (1994).

For bacterial DNA extraction for PCR amplification, hepatopancreas and stomach tissues were collected and separately inoculated into the alkaline peptone water of 50 ml each and then kept at 30°C in shaking incubator for 5 h. After incubation, 5 ml culture was taken for bacterial DNA extraction using CTAB (Bruce et al., 1993). Briefly, the culture was first centrifuged at 8000 rpm for 5 min, supernatant was removed and the pellet was re-suspended in 50 µl distilled water. From this, 10 µl was taken and 567 µl of TE buffer, 30 µl of 10% SDS and 3 µl of 20 mg ml⁻¹ proteinase K were added. The contents were mixed thoroughly and kept at 37°C for 1 h. After incubation, 100 µl of 5 M NaCl and 80 µl of CTAB/NaCl solution was added, mixed thoroughly and again incubated for 10 mins at 65°C. Equal volume of chloroform/isoamyl alcohol was added and centrifuged at 12000 rpm for 5 min. Again the clear aqueous phase was transferred to a fresh tube and 0.6 volume of isopropanol was added into it and centrifuged at 12000 rpm for 5 min to precipitate the DNA. From this, supernatant was removed, pellet was washed with equal volume of 70% ethanol and air dried. This pellet was suspended in 20 µl distilled water. The extracted DNA was used for PCR reaction. To obtain crude bacterial DNA extract, 10 µl of bacterial pellet was directly resuspended into 100 µl of distilled water and then boiled for 10 mins in a water bath. From this, 1 µl of crude extract was used for PCR reaction.

For V. parahaemolyticus species confirmation, PCR was carried out with metalloprotease gene-specific VPM primers (Luan et al., 2007). To determine the EMS/AHPND status, PCR was carried out as described by Flegel and Lo (2014). The reaction volume of 25 µl containing 2x master mix (Biorad, Germany), gene specific forward and reverse primers (10 pm), 1 µl template DNA and PCR grade water was amplified in a thermocycler (Biorad, Germany). The details of primers and PCR cyclic conditions are detailed in Table 1. PCR products (5 µl each) were resolved on 1.5% gel and photographed with a gel documentation system (Biorad).

For histopathological analysis, whole animal was first injected with Davidson fixative at hepatopancreas, 3rd and 6th segments and then preserved in Davison fixative. Totally three different tissues namely gill, hepatopancreas and pleopods were taken for this study. The tissue samples were processed in automatic tissue processor (Leica, Germany), embedded in paraffin wax, sections were cut using rotary microtome (Thermo Fisher Scientific, Germany), mounted on glass slides and stained using hematoxylin and eosin (Bell and Lightner, 1988).

The collected shrimp samples had pinkish discoloration of the body, pale hepatopancreas and antennal cut (Fig. 2 and 3) indicating bacterial infection with large scale size variation and reduced growth compared to the days of culture.

![Fig. 2. Pinkish colouration on the body (left) with normal shrimp (right)](image-url)
Table 1. Details of primers used in the study

| Pathogen/ Disease | PCR step   | Primer sequence (5'-3')                          | Product size (bp) | PCR cycle conditions                                                                 | Reference                        |
|-------------------|------------|--------------------------------------------------|-------------------|---------------------------------------------------------------------------------------|----------------------------------|
| EMS/ AHPND        | Single step| F TCACCCGAATGCTCGCTTGAGG<br>R CGTCGCTACTGCTAGCTGAAG | 700               | 94ºC 5 min, 30 cycles of 94ºC 30 s, 60ºC 30 s, 72ºC 60 s and 72ºC for 10 min          | Flegel and Lo (2014)             |
|                   |            |                                                   |                   |                                                                                        |                                  |
| Vibrio parahaemolyticus | Single step | VPM-1 CAGCTACCAGAAACACAGCTA<br>VPM-2 TCCTATCGAGACTCTCTCAAC | 675               | 94ºC 5 min, 30 cycles of 94ºC 30 s, 60ºC 30 s, 72ºC 45 s and 72ºC for 10 min         | Luan et al. (2007)               |
|                   |            |                                                   |                   |                                                                                        |                                  |
| WSSV              | First step | F1 ATCATGGCTGCTTCACAGAC<br>R1 GCTGGAGAGGACACAAAGACAT | 982               | 94ºC 4 min, 39 cycles of 94ºC 1 min, 55ºC 1 min, 72ºC 2 min and 72ºC for 5 min        | Kimura et al. (1996)             |
|                   | Second step| F2 TCTTCATCGAGCTACTGC<br>R2 TAAGCTATCCAGTATCAGG | 570               |                                                                                        |                                  |
| IHNV              | Single step| 356F ATCGGTTCACATCTGGA<br>356R TCCTATCGAGACTCTCAAC | 356               | 95ºC 5 min, 35 cycles of 95ºC 30 s, 55ºC 30 s, 72ºC 1 min and 72ºC for 7 min          | Nunan et al. (2000); Tang et al. (2007) |
|                   |            | 392F GGGCGAACCAGAAATCACTTA<br>392R ATCCGGAGGAATCTGATGTG  | 392               |                                                                                        |                                  |
| MBV               | First step | F1 CGATTCATATCGGGCGGAAATA<br>R1 TTCGCACTGCACCTCAGAGAT | 533               | 95ºC 5 min, 39 cycles of 95ºC 30s, 65ºC 30 s, 72ºC 1 min and 72ºC for 7 min           | Belcher and Young (1998)         |
|                   | Second step| F2 TCCAATCGCGTCTGCGATCT<br>R2 CGCTATCGGGGACACAGTCTCAAC | 361               | 95ºC 5 min, 39 cycles of 95ºC 30 s, 60ºC 30 s, 72ºC 1 min and 72ºC for 7 min          |                                  |
| YHV-GAV           | First step | GY1 GACATCACTCCAGAACAACATCTG<br>GY4 GTGAACTGCTTGCAGACTGAGACG | 794               | 95ºC 5 min, 34 cycles of 95ºC 1 min, 66ºC 1 min, 72ºC 1 min and 72ºC for 5 min        | Wongteerasupaya et al., (1997); Cowley et al. (2004) |
|                   | Second step| GY2 CATCTGCTCCAAGGCGCGTCTATGA<br>GY3 ACCTCTTCTGGAACAGATGACG<br>GY6 GTAGTAGGAGAGTGACACCTAT | YHV - 277<br>GY3 - 406 |                                                                                        |                                  |

Based on the biochemical tests conducted for isolated bacteria, the species was identified as *Vibrio parahaemolyticus* (Table 2). *V. parahaemolyticus* is the dominant species in shrimp affected by red disease and tail necrosis (Jayasree et al., 2006). The result obtained in this study corroborates that of Alagappan et al. (2010) who found incidence of *V. parahaemolyticus* in shrimp ponds of Tamil Nadu and markedly higher incidence in animal surface and tissue samples. Likewise, pathogenic *V. parahaemolyticus* has been characterised from the infected shrimp samples of Tamil Nadu (Alagappan et al., 2013).
Table 2. Results of biochemical tests

| Amino acid decarboxylase test | Salt tolerance (% NaCl) | G | I | SC | MR | VP | OG | Sugar utilisation |
|-------------------------------|-------------------------|---|---|----|----|----|----|------------------|
|                               |                         | 0 | 3 | 6 | 8  | 10 |     | M   | A  | S   | D  |
| Ly                            | +                       | - | + | + | +  | -  | +  | +   | +  | -   | +  |
| Ar                            | +                       | - | + | + | +  | -  | +  | +   | +  | -   | +  |
| Or                            | +                       | - | + | + | +  | -  | +  | +   | +  | -   | +  |
|                               |                         |   |   |   |    |    |    | M   | A  | S   | D  |

Amino acids used: Ly - Lysine, Ar - Arginine, Or - Ornithine; G - Gelatinase test; I - Indole test; SC - Simmons citrate test; MR-VP - Methyl red-Voges Proskauer test; OG - Ortho-Nitrophenyl-β-galactosidase test; Sugars used: M - Mannitol, A - Arabinose, S - Sucrose, D - D-Glucosamine

Gene-specific PCR (VPM-V. parahaemolyticus Metalloprotease gene) further confirmed the isolates as V. parahaemolyticus (Fig. 4). PCR was carried out to find out the EMS/AHPND strain status of these isolates using AHPND primers and all were found to be negative (Fig. 5). Thus, the results indicated that S/AHPND strain of V. parahaemolyticus (Tran et al., 2013), was not present in the culture system included in this study.

The samples were found to be positive for WSSV by second step PCR (Fig. 6) and IHHNV by direct PCR (Fig. 7). All these were negative for MBV and other exotic pathogens (YHV/GAV) (Fig. 8 and 9). WSSV and IHHNV infections with mortality of P. vannamei in culture ponds of Tamil Nadu was reported by Otta et al. (2014). They also found that the analysed samples were negative for taura syndrome virus, yellow head virus and infectious myonecrosis virus. This supports our result that majority of the vannamei culture is infected by the two viruses namely WSSV and IHHNV. It has also been reported that IHHNV infection on Penaeus vannamei results in development and growth abnormalities (Kalagayan et al., 1991; Lightner et al., 1992) and size reduction (Lightner and Redman, 1998). Similar size variation and growth reduction were also observed in the present samples. However, the typical body abnormality as observed for runt deformity syndrome (RDS) was not found in any of the shrimps during the sampling.
Infection of samples by WSSV and IHHNV was further confirmed by histopathology through the presence of intranuclear inclusion bodies. Typical WSSV inclusion bodies and Cowdry type A inclusion bodies of IHHNV infection were observed in the gills. Likewise, Otta et al. (2014) reported the presence of inclusion bodies for WSSV and IHHNV through histopathological analysis in *P. vannamei*.

The finding of present study indicated the reduction in growth due to *Vibrio parahaemolyticus* and size variation due to IHHNV. *V. parahaemolyticus* was isolated from the shrimp samples as a sole group indicating their pathogenic status. However, the samples were negative for specific EMS strain by PCR. This shows the strain of *V. parahaemolyticus* which cause EMS/AHPND was not present in the culture system selected for this study. Though biosecurity was maintained in the farm, the pathogens are suspected to be transmitted through the seed or improper pond preparation.

**Acknowledgements**

The authors are extremely thankful to the Director, ICAR-CIBA, Chennai for facilities provided to carry out this research. The authors express their deep sense of gratitude to the Director, ICAR-CIARI, Port Blair and the Director, ICAR-NBFGR, Lucknow for their continuous support and encouragement to complete this work.

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Date of Receipt : 13.09.2016
Date of Acceptance : 06.05.2017