



# Inter-laboratory proficiency test 2020

## Detection of White Spot Syndrome Virus in Shrimp Pleopods

**Organised by the**

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Distribution Date:	12/07/2020
Report Date:	04/12/2020
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## Introduction

A comparative test of diagnostic procedures for the detection of White Spot Syndrome Virus (WSSV) in shrimp was provided by the European Union Reference Laboratory (EURL) for Fish and Crustacean Diseases at DTU AQUA in accordance with EC Directive 2006/88. The invitation to participate in this year's proficiency test was sent to 27 laboratories including 20 NRLs of EU Member States. 25 laboratories including 18 NRLs of EU Member States accepted the invitation to participate and send in their test results.

Each laboratory was given a code number to ensure discretion. The code number of each participant is supplied to the respective laboratories with this report. Furthermore, the EURL-team has included comments to the participants if relevant. An un-coded version of the report is sent to the European Commission.

## Sample Preparation

Viral inoculates of WSSV were obtained from the Cefas laboratory in Weymouth, UK, who originally obtained them from the OIE reference laboratory at the University of Arizona, USA. The OIE isolate of WSSV (UAZ 00-173B) was generated in *Penaeus vannamei* from an original outbreak in *Fenneropenaeus chinensis* in China in 1995. Subsequent passages of this isolate into naïve *P. vannamei* held at Cefas have demonstrated continued infectivity of this isolate.

A WSSV inoculum was prepared by grinding half of a shrimp carcass infected with WSSV in a mortar with a small amount of sand and 4 ml PBS. PBS was added to a total volume of 4 ml per gram of shrimp tissue and the inoculum was then centrifuged at 3000 g for 30 minutes and frozen at -80°C in 2 ml aliquots. Before use, the inoculum was diluted 1:20 with PBS and sterile filtered through a 0.22 µm sterile filter mounted on a syringe. WSSV infected shrimp carcasses were prepared by direct intramuscular injection of 100 µl WSSV inoculum into specific pathogen free (SPF) *P. vannamei*. During the following days, dead and moribund shrimp were removed from the experimental tanks. The shrimp were kept in a flow-through system with artificial sea water with a salinity of ca. 20 ppt and a temperature of ca. 26°C.

All 10 pleopods were removed from newly dead animals and fixed in 70 % ethanol for molecular analysis, with each matching set of pleopods stored in the same tube (i.e. 5 tubes per shrimp). Pleopods from SPF shrimp served as WSSV negative samples. Prior to distribution the EURL tested one set of pleopods from each individual shrimp to ensure that infection had resulted in a satisfactory titre that was measurable with standard PCR based methods.

Multiple NRLs received pleopods from the same shrimp.

Shrimp were confirmed as WSSV positive and WSSV negative by real-time PCR using the following procedure.

## Diagnostic method

### Extraction of DNA from Pleopods

DNA was extracted using an Indimag Pathogen kit (Indical Bioscience) on an Indimag 48s extraction machine. Half of a pleopod was homogenized using bead beating with a 5 mm metal bead in 200 µl PBS in a TissueLyser II (QIAGEN) for 2 x 2 min. The DNA was then purified using the manual enclosed in the kit.

### WSSV real-time PCR

Based on Durand & Lightner (2002).

2 µl template DNA was added to a PCR tube containing: 10 µl Luna® Universal Probe qPCR Master Mix (New England Biolabs), 0.8 µl forward primer (10 µM), 0.8 µl reverse primer (10 µM), 0.4 µl Taqman Probe (10 µM) and 6 µl molecular grade water. The PCR profile is one cycle of 94°C for 15 minutes, followed by 50 cycles of 94°C for 15 seconds and 60°C for 60 seconds.

Primer sequences were WSS1011F: 5'-TGG-TCC-CGT-CCT-CAT-CTC-AG-3', WSS1079R: 5'-GCT-GCC-TTG-CCG-GAA-ATT-A-3', Taqman Probe: 5'-AGC-CAT-GAA-GAA-TGC-CGT-CTA-TCA-CAC-A-3' with fluorescent dyes 6-Carboxyfluorescein (6-FAM) on the 5' end, Iowa Black FQ (IBFQ) on the 3' end and an internal ZEN quencher between the 9<sup>th</sup> and the 10<sup>th</sup> base. All primers were manufactured by Integrated DNA Technologies.

A positive PCR control was included, which consisted of a synthesized gBlocks gene fragment representing the WSSV PCR amplicon.

### Distribution

Each laboratory participating in the proficiency test received a pair of pleopods from each of two infected and three non-infected animals. Multiple NRLs received pleopods from the same shrimp. The test samples were sent out according to current international regulations for shipment of diagnostic specimens UN 3373, "Biological substance, Category B". All proficiency tests were delivered by courier.

### Expected results

Participants were asked to identify the infection status of the content of each of the six received tubes by the method used in their laboratory. The infection status of the tube contents is shown in Table 1.

**Table 1.** Expected results of the proficiency test.

Sample ID	Sample type	WSSV infection status
Sample XX-001	<i>P. vannamei</i> pleopods in EtOH	Positive (UAZ 00-173B)
Sample XX-002	<i>P. vannamei</i> pleopods in EtOH	Negative
Sample XX-003	<i>P. vannamei</i> pleopods in EtOH	Negative
Sample XX-004	<i>P. vannamei</i> pleopods in EtOH	Positive (UAZ 00-173B)
Sample XX-005	<i>P. vannamei</i> pleopods in EtOH	Negative

### Actual results

Results were received from all 25 participating laboratories.

- 20 laboratories correctly diagnosed all samples, 5/5 (100 %).
- 4 laboratories correctly diagnosed 4/5 samples (80 %).
- 1 laboratory correctly diagnosed 0/5 samples (0 %).

The following methods were used by the participants:

- 12 laboratories used nested PCR methods (Lo et al. 1996)
- 10 laboratories used real time PCR (Durand & Lightner 2002)
- 3 laboratories used both methods
- 3 laboratories verified the identity of at least one of the obtained PCR products by sequencing.

A detailed overview of the results is shown in table 2.

**Table 2.** Proficiency test results submitted by the individual laboratories. Reported cycle thresholds for qPCR is shown in brackets (for the EURL this is based on an average of all samples used for the test). Samples diagnosed as negative for WSSV are marked as -ve while samples diagnosed as positive for WSSV are marked as +ve. Diagnoses that did not match the expectations are shown in red.

Laboratory Code	Method	XX-001	XX-002	XX-003	XX-004	XX-005	Score
<b>EURL</b>	qPCR	+ve (17.6)	-ve	-ve	+ve (17.6)	-ve	
<b>1</b>	Nested PCR	+ve	-ve	-ve	+ve	-ve	5/5
<b>2</b>	Nested PCR	+ve	-ve	-ve	+ve	-ve	5/5
<b>3</b>	Nested PCR	+ve	-ve	-ve	+ve	-ve	5/5
<b>4</b>	This NRL has outsourced its crustacean diagnostics to FLI in Germany						
<b>5</b>	Nested PCR	+ve	-ve	-ve	+ve	-ve	5/5
<b>6</b>	qPCR	+ve (16)	-ve	-ve	+ve (18)	-ve	5/5
<b>7</b>	Nested PCR	+ve	-ve	-ve	+ve	-ve	5/5
<b>8</b>	Nested PCR	+ve	-ve	+ve	+ve	-ve	4/5
<b>9</b>	Nested PCR	-ve	+ve	+ve	-ve	+ve	0/5
<b>10</b>	This NRL did not participate in the WSSV proficiency test						
<b>11</b>	Nested PCR + qPCR	+ve (14.2)	-ve	-ve	+ve (14.9)	-ve	5/5
<b>12</b>	Nested PCR	+ve	-ve	-ve	+ve	-ve	5/5
<b>13</b>	qPCR	+ve (16.0, 15.5)	-ve	-ve	+ve (16.1, 15.2)	+ve (32.7, 34.0)	4/5
<b>14</b>	Nested PCR	+ve	-ve	-ve	+ve	-ve	5/5
<b>15</b>	qPCR	+ve (18.5, 18.4)	-ve	-ve	+ve (18.4, 18.4)	-ve	5/5
<b>16</b>	Nested PCR	+ve	-ve	+ve	+ve	-ve	4/5
<b>17</b>	This NRL has outsourced its crustacean diagnostics to The Netherlands						
<b>18</b>	Nested PCR + qPCR	+ve (13.8)	-ve	-ve	+ve (14.1)	-ve	5/5
<b>19</b>	Nested PCR	+ve	-ve	-ve	+ve	-ve	5/5
<b>20</b>	Nested PCR + qPCR	+ve (16.5)	-ve	-ve (39.7)	+ve (20.5)	-ve	5/5
<b>21</b>	qPCR	+ve (14)	-ve	-ve	+ve (17)	-ve	5/5
<b>22</b>	qPCR	+ve (15.5)	-ve	-ve	+ve (18.2)	-ve	5/5
<b>23</b>	qPCR	+ve (11.3)	-ve	-ve	+ve (9.1)	-ve	5/5
<b>24</b>	qPCR	+ve (26.0)	-ve	-ve	+ve (13.6)	+ve (32.4)	4/5
<b>25</b>	qPCR	+ve (18.02)	-ve	-ve	+ve (15.6)	-ve	5/5
<b>26</b>	Nested PCR	+ve	-ve	-ve	+ve	-ve	5/5
<b>27</b>	qPCR	+ve (19.8)	-ve	-ve	+ve (15.1)	-ve	5/5
<b>28</b>	qPCR	+ve (18.2)	-ve	-ve	+ve (20.6)	-ve	5/5

## Evaluation of results

The error rate of the results received in 2020 is a bit higher than for most previous proficiency tests, which mostly results from one lab diagnosing all five samples wrongly. This result originated from a contamination issue in the lab in question, which has subsequently taken appropriate means to avoid the issue in the future. Of 125 samples tested, nine were not diagnosed correctly (7.2 %). As multiple laboratories received pleopods from the same shrimp, we can evaluate the likeliness of these unexpected diagnoses (see Table 3).

**Table 3.** Diagnoses obtained for each individual pleopod pair. Each shrimp provided five pairs of pleopods labeled A – E. Pleopod pair A was tested by the EURL before sending the samples (B – E). Numbers refer to codes of participating laboratories. Samples diagnosed as negative for WSSV are marked in grey, and samples diagnosed as positive for WSSV are marked in yellow. Samples not used in the test are marked in white.

	Shrimp ID	Pleopod ID				
		A	B	C	D	E
Non-inoculated Shrimp	19-5656-10	EURL	1	2	3	5
	19-5656-11	EURL	6	7	8	9
	19-5656-12	EURL	11	12	13	14
	19-5656-13	EURL	15	16	18	19
	19-5656-14	EURL	20	21	22	23
	19-5656-15	EURL	24	25	26	27
	19-5656-16	EURL	28	1	2	3
	19-5656-17	EURL	5	6	7	8
	19-5656-18	EURL	9	11	12	13
	19-5656-19	EURL	14	15	16	18
	19-5656-22	EURL	19	20	21	22
	19-5656-23	EURL	23	24	25	26
	19-5656-24	EURL	27	28	1	2
	19-5656-25	EURL	3	5	6	7
	19-5656-26	EURL	8	9	11	12
Shrimp inoculated with WSSV	19-5656-74	EURL	1	2	3	5
	19-5656-75	EURL	6	7	8	9
	19-5656-76	EURL	11	12	13	14
	19-5656-77	EURL	15	16	18	19
	19-5656-78	EURL	20	21	22	23
	19-5656-79	EURL	24	25	26	27
	19-5656-80	EURL	28	1	2	3
	19-5656-81	EURL	5	6	7	8
	19-5656-82	EURL	9	11	12	13
	19-5656-83	EURL	14	15	16	18
	19-5656-84	EURL	19	20	21	22
19-5656-85	EURL	23	24	25	26	
19-5656-86	EURL	27	28			

Table 3 highlights that in most cases of falsely diagnosed samples, negative samples were diagnosed as positives, and that the pleopods in question originated from different shrimp, for which the remaining four pairs of pleopods were tested negative for WSSV by four other laboratories (including the EURL). From this analysis we are confident that the samples sent were diagnosed correctly by the EURL, and find that the most likely reason for the unexpected diagnoses is cross-contamination in the laboratory in question. It is also worth noticing that in the two cases where false positives were obtained by qPCR, the Ct values were very high, which indicates the presence of only trace amounts of virus DNA, and further corroborating that the false results originated from sample cross-contamination. It is thus worth highlighting that disease agent diagnostics using PCR based methods is very sensitive and highly prone to cross-contamination issues, and consequently it is important that NRLs take all possible measures to avoid this problem.

The EURL provides the annual proficiency test, collates the data and process the figures so that individual laboratories can see how they fare in relation to the other participants. It is up to the individual laboratory to assess if they perform according to their own expectations and standards. We take the opportunity to provide comments to participants regarding submitted results if relevant. Furthermore, we encourage all participants to contact us with any questions concerning the test or any other diagnostic matters.

The results given in this report will be further presented and discussed at the 11th Annual Workshop of the National Reference Laboratories for Crustacean Diseases to be held 4th – 5th of November as a virtual meeting.

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## References

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- Lo, C. F., et al., 1996. Detection of baculovirus associated with white spot syndrome (WSBV) in penaeid shrimp using polymerase chain reaction. *Diseases of Aquatic Organisms*, 25, 133-141.