



European Union Reference Laboratory for Fish Diseases

National Veterinary Institute, Technical University of Denmark, Copenhagen

EURL for Fish Diseases

Report of the Inter-Laboratory Proficiency Test 2015

for identification and titration of

VHSV, IHNV, EHNV, SVCV and IPNV (PT1)

and identification of

CyHV-3 (KHV), SAV and ISAV (PT2)

**Organised by the
European Union Reference Laboratory for Fish Diseases,
National Veterinary Institute, Technical University of Denmark,
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PT Reg. no.: 515



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Introduction

A comparative test of diagnostic procedures was provided by the European Union Reference Laboratory (EURL) for Fish Diseases. The test was divided into proficiency test 1 (PT1) and proficiency test 2 (PT2).

PT1 was designed to primarily assess the identification of the fish viruses causing the notifiable diseases: viral haemorrhagic septicaemia virus (VHSV), infectious hematopoietic necrosis virus (IHNV), and epizootic haematopoietic necrosis virus (EHNV) or related rana-viruses and in addition the fish pathogenic viruses: spring viremia of carp virus (SVCV) and infectious pancreatic necrosis virus (IPNV) by cell culture based methods. PT2 was designed for assessing the ability of participating laboratories to identify the fish pathogens: infectious salmon anaemia virus (ISAV), salmon alphavirus (SAV) and Cyprinid herpesvirus 3 (CyHV-3) (otherwise known as koi herpes virus – KHV) by biomolecular methods (PCR based). 45 laboratories participated in PT1 while 44 participated in PT2 of which 34 participated in identifying SAV.

The tests were sent from the EURL in mid-September 2015.

Both PT1 and PT2 are accredited by [DANAK](#) under registration number 515 for proficiency testing according to the quality assurance standard DS/EN ISO/IEC 17043. This report covers both the results of PT1 and PT2.

PT1 consisted of five coded ampoules (I-V). These ampoules contained IHNV, VHSV alone and in a co-infection setting, ECV and sterile cell culture medium (Eagles MEM with 10%FBS) (see table 1). The proficiency test was designed to primarily assess the ability of participating laboratories to identify any of the fish viruses VHSV, IHNV, EHNV, SVCV, and IPNV ([Council Directive 2006/88/EC Annex IV part II](#) and [Commission Implementing Directive 2014/22/EU of 13 February 2014](#)); bearing in mind that the test ampoules also could contain other viruses (e.g. other fish rhabdoviruses, ranaviruses, or birnaviruses). In addition the participants were asked to quantify the viruses in PT1 by titration in order to assess the susceptibility of their fish cell lines for virus infection. Participants were encouraged to use their normal standard laboratory procedures. However, the identification should be performed according to the procedures laid down in [Commission Decision 2015-1554](#) and by using fish cell cultures followed by e.g. ELISA, PCR, immunofluorescence (IFAT) or neutralisation test.

If ranavirus was present in any of the ampoules, it was mandatory to perform sequence analysis or a restriction endonuclease analysis (REA) of the isolate in order to determine if the isolate was EHNV or another ranavirus and it was recommended to follow the procedures described in [Chapter 2.3.1 in the OIE Manual of Diagnostic Tests for Aquatic Animals 2015](#). Laboratories were encouraged to identify VHSV and IHNV isolates as far as possible by means of genotyping in addition to the standard methods. It was recommended to use the genotype notification described in [Einer-Jensen et al. \(2004\)](#) for VHSV and either method as mentioned in the IHN chapter of the 2013 version of the [OIE manual on Aquatic Animal Diseases](#) (Emmenegger et al. (2000)) or in [Kurath et al. \(2003\)](#) for IHNV. Laboratories were encouraged to submit all sequencing results used for genotyping the isolates.

PT2 consisted of four coded ampoules (VI-IX). One ampoule contained CyHV-3 (KHV), one contained SAV, one contained ISAV and one contained sterile cell culture medium (Eagles MEM with 10%FBS), see table 9. The test was designed to primarily assess the ability of participating laboratories to identify the notifiable fish pathogens ISAV and KHV (listed in [Council Directive 2006/88/EC, Annex IV](#) and Commission Implementing Directive 2014/22/EU) if present in the ampoules, bearing in mind that the test ampoules could also contain other pathogens. For 2015 the EURL decided that the panel of pathogens to be investigated should be expanded to include Salmonid Alphavirus (SAV)-. Since SAV is not a listed disease in the European legislation, all participants were free to decide if they would be testing for SAV or not. Each participant was asked to declare whether they would test or not. The EURL would then take care of calculating the score accordingly.

Participants were expected to use their normal PCR or real-time PCR methods for detection of the pathogens. Regarding SAV analysis, participants can refer to the [OIE manual Chapter 2.3.5b. — Infection with salmonid alphavirus](#) . It was not mandatory to grow KHV and ISAV on cell cultures in this test, but the viruses were not inactivated and, thus, it might had been possible to replicate them in cell cultures.

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 providers of the proficiency test have included comments to the participants if relevant. An un-coded version of the report is sent to the European Commission.

Participants were asked to download an excel sheet from the EURL web site (<http://www.eurl-fish.eu/>) to be used for reporting results and to be submitted to the EURL electronically. Additionally, participants were requested to answer a questionnaire regarding the accreditation status of their laboratory. Collected accreditation data will not be presented in this report but will be presented at the 20th Annual Workshop of the NRLs for Fish Diseases week 22, 2016 in Copenhagen. Participants were asked to reply latest November 13th 2015.

Distribution of the test

The test was sent out according to current international regulations for shipment of diagnostic specimens UN 3373, “Biological substance, Category B”. All proficiency tests parcels were delivered by courier and when possible participants were provided with a tracking number so they were able follow the shipment.

Shipment and handling

Within one day, the tests were delivered to 22 participants; 14 more tests were delivered within the first week; 3 more within the first two weeks; 5 further within three weeks and the last test was delivered within 35 days (Figure 1). All the parcels were sent without cooling elements.

A relatively high stability was demonstrated to characterize the lyophilized pathogens in glass ampoules as described in the [PT 2012 report](#).

Extra parcels were kept at 4°C in order to be able to provide fast substitutes in case of damage during transport.

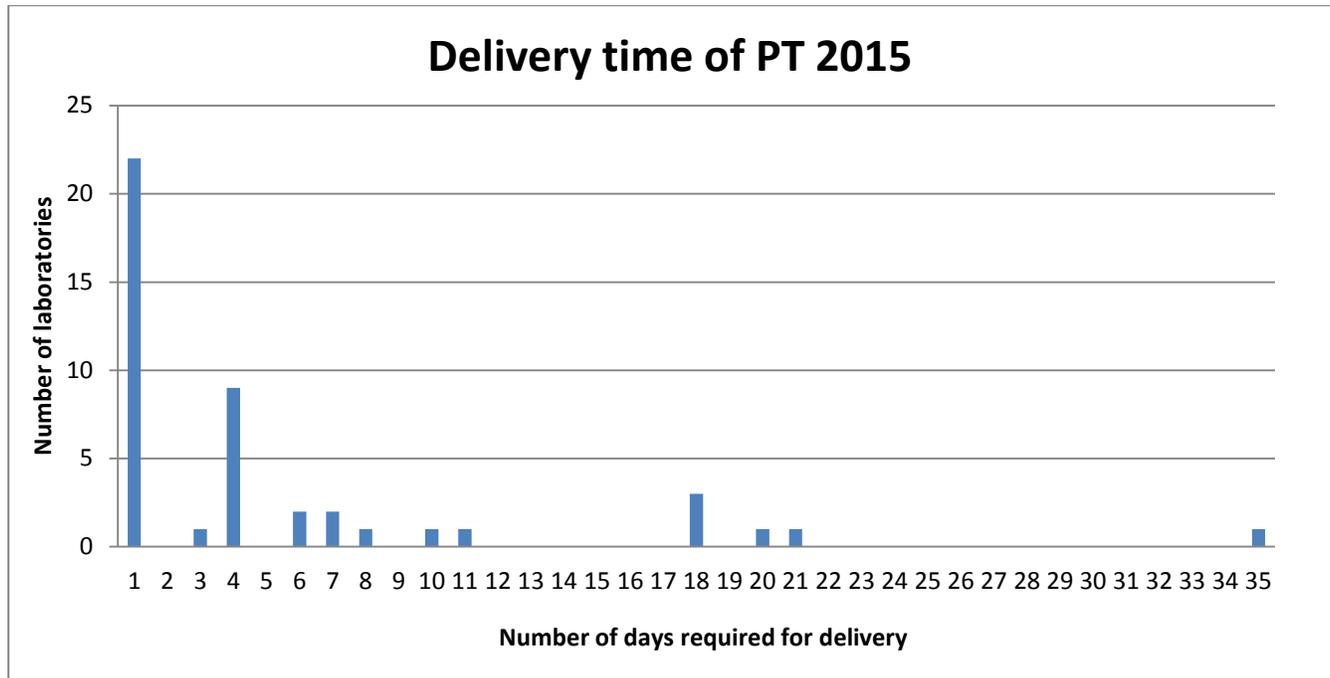


Figure 1. Transport time for the parcels to reach the participants.

Participation

PT1 and PT2: 45 laboratories received the annual proficiency test. 43 of the participants submitted results within the deadline, 2 participants got the deadline extended due to delivery problems or technical problems in the laboratory. Figure 2 show how many laboratories that participated in the proficiency test from 1996 to 2015.

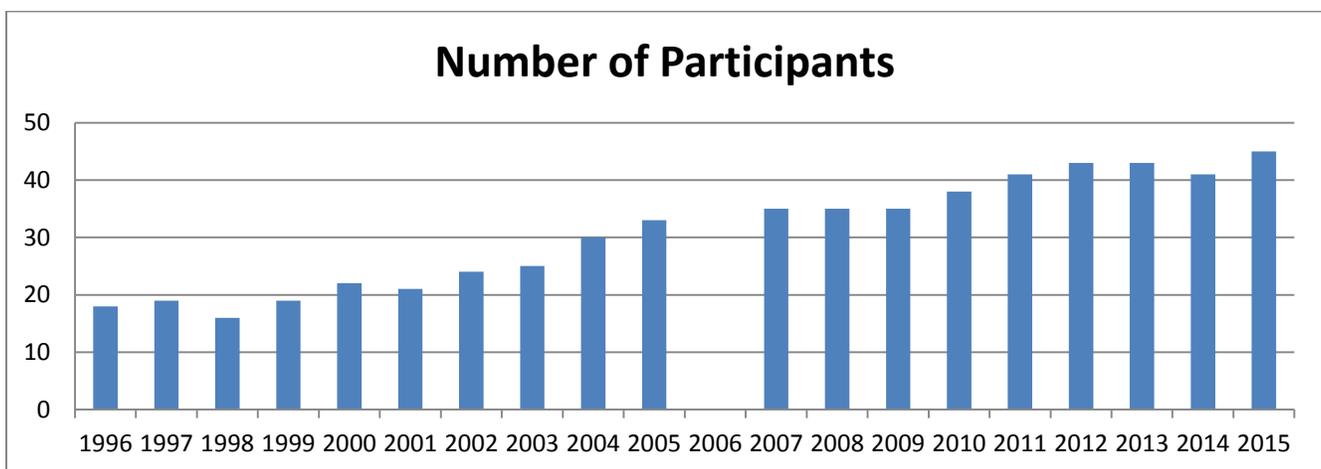


Figure 2. Participants in the EURL proficiency test over the years.

Table 1. Content of each ampoule with reference to culture conditions and major publications of the included viruses.

| Code | Specifications/References |
|--------------|--|
| Ampoule I: | <p><u>IHNV 32/87</u> Received from: First French isolate (April 1987) from rainbow trout. Cell culture passage number: 9 passages in EPC. GenBank accession numbers: J265717 AY524121 (G-gene), FJ265711 (N gene).. Reference on isolate: <i>Hattenberger-Baudouy et al. 1989 Baudin Laurencin F (1987)</i></p> |
| Ampoule II: | <p><u>VHSV strain 1P8:</u> Marine isolate (1996) from herring (<i>Clupea harengus</i>) caught in the Baltic Sea. (Mortensen et al. 1999). Cell culture passage number: 7 Genotype Ib. GenBank accession numbers: AY546573 (G-gene) and GQ325430, AY356652 (N-gene) www.fishpathogens.eu ID number: 2251 Reference on isolate: (Mortensen et al. 1999). References on sequences: Campbell et al. (2009) Einer-Jensen et al. 2004. Snow et al. (2004).</p> |
| Ampoule III: | <p><u>European Catfish virus (ECV), Isolate 562/92</u> Italian isolate from catfish suffering high mortality. Received from Dr. G. Bovo, ISZ-Ve, Padova, Italy. Cell culture passage number: 7 GenBank accession number: FJ358608 Reference on isolate: Bovo et al. (1993). Reference on sequence: Holopainen et al. (2009).</p> |
| Ampoule IV: | <p><u>BLANK</u> Supernatant from NON infected BF-2 cells</p> |

| Code | Specifications/References |
|--------------------------|--|
| Ampoule V ¹ : | <p><u>VHSV strain, DK-5151 + IHNV 32/87</u></p> <p><u>VHSV DK-5151 (Rindsholm, 1992)</u> Danish freshwater VHSV isolate from rainbow trout. Cell culture passage number: 4 in BF-2 and 6 in EPC.</p> <p>.</p> <p>Genotype Ia (Ejner-Jensen et al. 2004).</p> <p>References: Olesen et al. 1993 Ejner-Jensen et al 2004 GenBank accession number: AF345859.1</p> <p><u>IHNV 32/87</u></p> <p>Received from: First French isolate (April 1987) from rainbow trout.</p> <p>Accept for using the isolate: <input checked="" type="checkbox"/></p> <p>Cell culture passage number: 9 passages in EPC.</p> <p>GenBank accession numbers: J265717 AY524121 (G-gene), FJ265711 (N gene)..</p> <p>Reference on isolate: <i>Hattenberger-Baudouy et al. 1989, Baudin Laurencin F (1987)</i></p> |

¹ A specific description of ampoule V content is provided further in the text

Testing of the PT1 test

The PT1 test was prepared and tested according to protocols accredited under DS/EN ISO/IEC 17043. Prior to distribution the EURL tested 5 ampoules of each virus preparation by titration in 4 cell lines (BF-2, EPC, RTG-2 and FHM), to ascertain a satisfactory titre in the preferred cell line and homogeneity of content of ampoules (Table 2 and Figure 4).

The lyophilisation procedure is known to determine some reduction especially for VHSV. Previous experience reported during the past Proficiency tests demonstrated a rather high stability for SVCV, EHNV and IPNV serotype Sp. We have previously shown that lyophilised virus kept in glass sealed ampoules is stable for more than half a year when kept at room temperature ([Inter-Laboratory Proficiency Test report 2007](#)).

We have furthermore shown that lyophilised virus in glass sealed ampoules is stable after exposure to 30°C for 24 hours ([Inter-Laboratory Proficiency Test report 2010](#))

In 2011 we have shown that lyophilised virus in glass sealed ampoules is stable when temperature raised from 20-42°C over a period of 5 hours ([Inter-Laboratory Proficiency Test 2011](#))

The identities of the viruses in all 5 ampoules were checked and confirmed before shipment by ELISA, IFAT, serum neutralisation tests (SNT), RT-PCR/Q-PCR. After shipment the stability of the content in the ampoules were assessed by titrating the virus on cell cultures, and identifying it by ELISA, furthermore PCR based tests were performed on the original content of all the ampoules.

During results receipt 24 of 44 participating laboratories reported the detection of an additional rhabdovirus in ampoule V, being a SVCV or a SVCV-like isolate.

Different analyses were therefore initiated by the EURL to assess and corroborate the presence of this virus in ampoule V.

Direct RT-PCR on re-suspended content of 4 ampoule V replicates both using diagnostic and sequencing primer sets as described by Koutná et al. (2003) and Stone et al., (2003) all tested negative.

Re-suspended content in ampoule V was following inoculated on BF-2; EPC, RTG-2 and FHM cell lines. Harvested supernatant tested by SVCV-ELISA and both SVCV RT-PCR protocols tested negative. However an IFAT analysis performed using polyclonal antibody K42 raised against pike fry rhabdovirus (Jørgensen et al. 1989) provided a positive staining.

Further examinations were then initiated as re-suspended content of ampoule V was inoculated on BF-2-; EPC-, RTG-2- and FHM cell lines, respectively with polyclonal neutralizing antisera against VHSV and IHNV and cells were incubated at 24°C, a temperature considered not permissive to the growth of VHSV and IHNV.

An isolate was finally obtained and tested with the two PCR protocols mentioned above, where only the more generic test performed with sequencing primers tested positive.

The amplicon was sequenced and the sequence analysis blasted against the ones retrieved from the other participants.

Sequence analysis finally confirmed that the additional isolate from Ampoule V obtained from cell culture at non permissive temperature for the growth of VHSV and IHNV, was 99% identical to the tench rhabdovirus S64 (Jørgensen et al. 1989).

The VHSV isolate DK-5151 in Ampoule V was retrieved from a large virus panel produced in 2009 which included a number of various fish pathogenic viruses and among these the S64 isolate. Our theory is that the DK-5151 vial was contaminated with S64 during this production, but as this happened in our previous facilities in Aarhus we have not been able to exactly trace the procedures followed at that time.

Table 2. PT1:

Titres in ampoules I to V stored in the dark tested on four cell lines at different time points:

- Before lyophilisation, (stored at 4°C).
- After lyophilisation and before shipment (median titre of 5 replicates), (stored at 4°C), the variation of the titre of the 5 replicates was within 1 log in the same cell line.
- After deadline for handling in results and five months after lyophilisation, (1 ampoule), (stored at 4°C).

| Ampoul No. | Cell line | Titre before Lyophilisation | Titre after Lyophilisation and before shipment | Titre after deadline for handling in results (and five months after lyophilisation) (storage 4°C in the dark) |
|--|-----------|-----------------------------|--|---|
| | | TCID ₅₀ /ml | TCID ₅₀ /ml | TCID ₅₀ /ml |
| Ampoule I: IHNV, 32/87 | BF-2 | 1,3E+03 | 1,9E+02 | <1,9E+02 |
| | EPC | 8,6E+06 | 4,0E+05 | 2,7E+05 |
| | RTG-2 | 8,6E+05 | <1,9E+02 | 8,6E+03 |
| | FHM | 1,9E+06 | 8,6E+04 | 2,7E+04 |
| Ampoule II: VHSV, 1p8 | BF-2 | 1,9E+06 | 2,7E+04 | 2,7E+03 |
| | EPC | < 1,9E+02 | <1,9E+02 | <1,9E+02 |
| | RTG-2 | < 1,9E+02 | <1,9E+02 | <1,9E+02 |
| | FHM | 2,7E+06 | 5,9E+04 | 2,7E+04 |
| Ampoule III: ECV, 562/92 | BF-2 | 1,9E+07 | 1,3E+06 | 1,3E+05 |
| | EPC | 1,3E+06 | 1,3E+05 | 1,3E+03 |
| | RTG-2 | 1,3E+03 | 8,6E+02 | 2,7E+03 |
| | FHM | 2,7E+03 | <1,9E+02 | <1,9E+02 |
| Ampoule IV: Blank, BF2 cell supernatant | BF-2 | < 1,9E+02 | <1,9E+02 | <1,9E+02 |
| | EPC | < 1,9E+02 | <1,9E+02 | <1,9E+02 |
| | RTG-2 | < 1,9E+02 | <1,9E+02 | <1,9E+02 |
| | FHM | < 1,9E+02 | <1,9E+02 | <1,9E+02 |
| Ampoule V: VHSV, DK-5151 + IHNV, 32/87 | BF-2 | 2,7E+08 | 8,6E+06 | 1,9E+06 |
| | EPC | 1,9E+08 | 8,6E+06 | 4,0E+06 |
| | RTG-2 | 1,3E+08 | 8,6E+06 | 2,7E+06 |
| | FHM | 1,3E+08 | 4,0E+06 | 4,0E+06 |

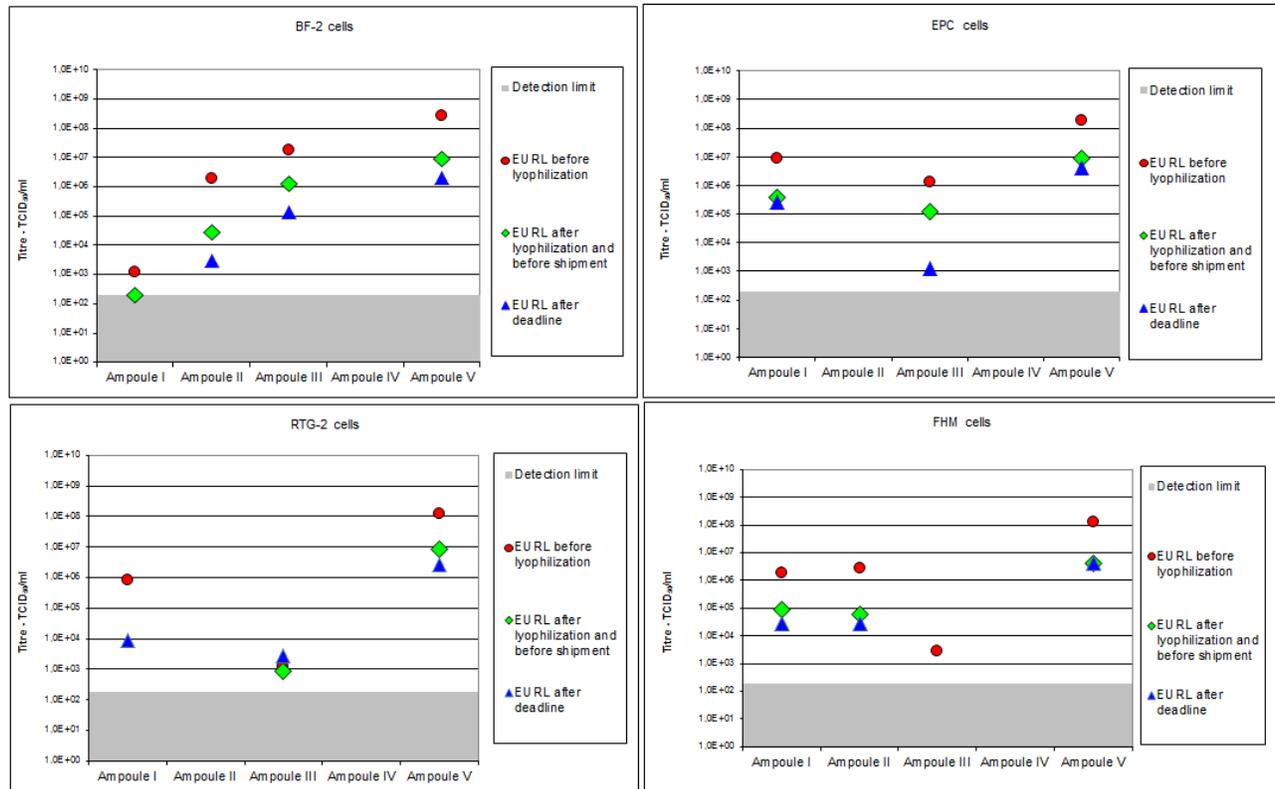


Figure 4. Virus titers in different cell lines:

Before lyophilisation, After lyophilisation-before shipment and After minimum 3 months after lyophilisation (storage 4°C in the dark) (1 ampoule).

Virus identification and titration

Participants were asked to identify the content of each ampoule by the methods used in their laboratory which should be according to the procedures described in [Commission Decision 2015-1554](#), i.e. by cell culture followed by ELISA, IFAT, neutralisation test and/or RT-PCR/Q-PCR. Identification results of the content of the 5 ampoules at the participating laboratories are summarised in table 3.

Participants were also asked to assess the viral load in the ampoules by conducting titrations. The titration procedures were described in the instructions enclosed with the test. All titres were calculated by the EURL based on the crude data submitted by each participant and given as Tissue Culture Infective Dose 50% per ml (TCID₅₀/ml). The titre of the re-dissolved virus was multiplied by a factor of 10 to compensate for the dilution of the original volume of virus in the ampoules (200 µl virus + 200 µl lactalbumin in vials re-dissolved in a total of 2.0 ml cell culture medium). Viruses titration results obtained in the participating laboratories are summarised in tables 4 to 8. The titres obtained from each participating laboratory are represented graphically. In Figures 5-8, all titres submitted by the participants for each cell line and ampoule, respectively are compared to each other. On these figures, the median titre and the 25% and 75% inter quartile range is displayed. In this way, the titres obtained by each laboratory are plotted in relation to the combined submitted data set and each participating laboratory should be able to compare the sensitivity of their cell lines to the sensitivity of those used by the other participating laboratories. CHSE-214 cells are not displayed

graphically or commented on in this report as only 6 laboratories used these cells. Laboratories with the required facilities were encouraged to examine and identify the genotype of the virus isolates. It was not mandatory to perform these analyses for VHSV and IHNV. However, for ranaviruses it is mandatory to perform a sequence or restriction endonuclease analysis of the isolate in order to determine if the isolate is EHNV.

Table 3. Inter-Laboratory Proficiency Test, PT1, 2015 - Virus identification and score obtained by participants.

| Laboratory code number | Score 10/10 | Answer received at EURL | Ampoule I | Ampoule II | Ampoule III | Ampoule IV | Ampoule V |
|------------------------|-------------|-------------------------|---|--|---|--|---|
| | | | IHNV 32/87 | VHSV 1P8 | ECV 562/92 | Blank BF-2 cell supernatant | VHSV DK-5151 + IHNV 32/87 |
| 46 | 10/10 | 09.11.15 | IHNV | VHSV | ESV | Negative | VHSV, IHNV, TenRV |
| 45 | 10/10 | 06.11.15 | IHNV | VHSV | ESV | no virus detected | VHSV & IHNV |
| 44 | 8/10 | 12.11.15 | IHNV | VHSV | RANA (ESV/ECV) | No virus growth | VHSV SVCV RANA (ECV/ESV) |
| 43 | 8/8 | 30.11.15 | IHNV | VHSV | no IHNV, no VHSV, no SVCV, no IPNV ⁴ | no CPE | IHNV, VHSV, SVCV |
| 42 | 9/10 | 13.11.15 | IHNV | VHSV | Rana V ² | No virus | VHSV IHNV SVCV |
| 41 | 10/10 | 11.11.15 | IHNV | VHSV | ESV | Negative | IHNV + VHSV |
| 40 | 10/10 | 13.11.15 | IHNV | VHSV | European sheatfish ranavirus | not IHNV, VHSV, EHNV, Ranavirus, IPNV, SVCV | VHSV and IHNV |
| 39 | 10/10 | 11.11.15 | IHNV | VHSV | ESV | | VHSV and IHNV |
| 38 | 10/10 | 13.11.15 | IHNV | VHSV | Ranavirus not EHNV ¹ | Not VHSV, not IHNV and not Ranavirus (see comment) | VHSV and IHNV |
| 37 | 8/10 | 12.11.15 | IHNV | VHSV | Not VHSV, IHNV, IPNV, SVCV ⁴ | Virus not found | VHSV, IHNV |
| 36 | 10/10 | 13.11.15 | IHNV | VHSV | Ranavirus ¹ | No virus detected | IHNV, VHSV & PFRV |
| 35 | 10/10 | 12.11.15 | IHNV genogroup M/Eur1 | VHSV genotype Ib | European catfish virus ECV | no virus | VHSV genotype Ia, IHNV genogroup M/Eur1, Pikefry-like rhabdovirus |
| 34 | 10/10 | 26.10.15 | IHNV | VHSV | ECV / ESV | negative for all viruses tested | IHNV + VHSV + PFR-like virus |
| 33 | 9/10 | 12.11.15 | rhabdovirus, IHNV France 1987: IHNV 32/87, genogroup Europe | rhabdovirus, VHSV Denmark 1996: DK/1e62, DK/1p8, DK/1p12, sub/genogroup Ib | ranavirus, ECV/ ESV | | rhabdovirus, VHSV Denmark DK/5151 Rindsholm, sub/genogroup Ia |
| 32 | 10/10 | 13.11.15 | IHNV | VHSV | ECV or ESV | NO VHSV NO IHNV NO EHNV | VHSV & IHNV |
| 31 | 9/10 | 13.11.15 | IHNV | VHSV | ESV | Negativ | VHSV+SVCV |
| 30 | 9/10 | 11.11.15 | IHNV | VHSV | ECV | No virus detected | VHSV and SVCV |
| 28 | 9/10 | 13.11.15 | IHNV | VHSV | Ranavirus not EHNV (ECV) | Negative | VHSV + Sprivirus (TenRV) |

Report on the Inter-Laboratory Proficiency Test 2015
for identification of VHSV, IHN, EHN, SVCV and IPNV (PT1) and identification of KHV, SAV and ISAV (PT2)

| Laboratory code number | Score 10/10 | Answer received at EURL | Ampoule I | Ampoule II | Ampoule III | Ampoule IV | Ampoule V |
|------------------------|-------------|-------------------------|---------------------------|----------------------------|--|--|---|
| | | | IHN 32/87 | VHSV 1P8 | ECV 562/92 | Blank BF-2 cell supernatant | VHSV DK-5151 + IHN 32/87 |
| 27 | 10/10 | 16.11.15 | IHN | VHSV | ESV | Negative | VHSV+IHN+SVCV |
| 26 | 10/10 | 13.11.15 | IHN | VHSV | Ranavirus ¹ | | VHSV, IHN, Pike fry-like rhabdovirus |
| 25 | 9/10 | 12.11.15 | IHN | VHSV | EHN ³ | no VHSV/ no IHN/no EHN/ no IPNV/ no SVCV | VHSV/IHN/SVCV |
| 24 | 10/10 | 12.11.15 | IHN | VHSV | RANAVIRUS ¹ | NEGATIVE | VHSV, IHN |
| 23 | 10/10 | 13.11.15 | IHN | VHSV | Ranavirus ¹ | No IHN, VHSV, Ranavirus, SVCV or IPNV detected | VHSV, IHN & SVCV |
| 22 | 9/10 | 13.11.15 | IHN viable virus detected | VHSV viable virus detected | EHN viable virus detected ³ | No viruses detected | IHN and VHSV viable virus detected |
| 21 | 10/10 | 10.11.15 | IHN | VHSV | Ranavirus (ECV or ESV) | No virus detected | IHN and VHSV |
| 20 | 10/10 | 13.11.15 | IHN | VHSV | Ranavirus ¹ | 0 | VHSV/SVCV/IHN |
| 19 | 9/10 | 13.11.15 | IHN | VHSV | EHN ³ | No Virus | IHN, VHSV, PFRV |
| 18 | 10/10 | 13.11.15 | IHN | VHSV | ECV | Negative for VHSV, IHN, IPNV, EHN, ranavirus, SVCV | VHSV, IHN |
| 17 | 10/10 | 13.11.15 | IHN | VHSV | Ranavirus ¹ | Negative | VHSV, IHN, SVCV |
| 16 | 10/10 | 13.11.15 | IHN | VHSV | ESV/ECV | Negative | VHSV IHN Rhabdovirus |
| 15 | 8/10 | 10.11.15 | IHN | VHSV | EHN ² | Negative | VHSV |
| 14 | 9/10 | 13.11.15 | IHN | VHSV | EHN | No Viruses isolated by BF2/EPC cell culture | IHN/VHSV |
| 13 | 10/10 | 13.11.15 | IHN | VHSV | Ranavirus ¹ | / | VHSV, IHN |
| 12 | 10/10 | 13.11.15 | IHN | VHSV | ESV (very closely related to EHN) | | IHN, VHSV |
| 11 | 10/10 | 12.11.15 | IHN | VHSV | Ranavirus ¹ | negative | VHSV, IHN & Tench rhabdovirus(or Pike fry/like rhabdovirus) |
| 10 | 9/10 | 12.11.15 | IHN | VHS | EHN | Negative | IHN, VHS |
| 9 | 10/10 | 12.11.15 | IHN | VHSV | Ranavirus ESV | No virus | IHN, VHSV, SVCV/like* |
| 8 | 9/10 | 13.11.15 | IHN | VHSV | Ranavirus ² | Negative | VHSV, IHN |
| 7 | 10/10 | 10.11.15 | IHN | VHSV | EHN ¹ | no virus found | VHSV, IHN, SVCV |

Report on the Inter-Laboratory Proficiency Test 2015
for identification of VHSV, IHNV, EHNV, SVCV and IPNV (PT1) and identification of KHV, SAV and ISAV (PT2)

| Laboratory code number | Score 10/10 | Answer received at EURL | Ampoule I | Ampoule II | Ampoule III | Ampoule IV | Ampoule V |
|------------------------|-------------|-------------------------|------------|------------|---|-----------------------------|--|
| | | | IHNV 32/87 | VHSV 1P8 | ECV 562/92 | Blank BF-2 cell supernatant | VHSV DK-5151 + IHNV 32/87 |
| 6 | 8/10 | 12.11.15 | IHNV | Sterile | ECV | Sterile | IHNV & VHSV |
| 5 | 8/10 | 13.11.15 | IHNV | VHSV | Ranavirus was identified by conventional RT/PCR and then REA was applied as given by OIE manual to identify ECV | IHNV | VHSV, IHNV, SVCV |
| 4 | 10/10 | 13.11.15 | IHNV | VHSV | European sheatfish virus | NEGATIVE | VHSV and IHNV |
| 3 | 9/10 | 06.11.15 | IHNV | VHSV | Ranavirus, not EHNV ¹ | Negative | VHSV & TenRV |
| 2 | 9/10 | 13.11.15 | IHNV | VHSV | Ranavirus ¹ (Not EHNV, see sequencing result) | negative | VHSV |
| 1 | 10/10 | 12.11.15 | IHNV/M | VHSV I/b | European sheatfish virus | no virus detected | mixed infection: tench rhabdovirus; IHNV; and VHSV |

- 1: Correct sequence and answered ESV in sequences sheet.
2: Genomic analysis not performed
3: Correct sequence, wrong answer after blast.
4: Did not perform test for Ranavirus

Table 4. Inter-Laboratory Proficiency Test, PT1, 2015 – Results of titration of ampoule I.

| <i>Ampoule I - IHNv 32/87</i> | | | | | |
|-------------------------------|---|-----------|-----------|-----------|-----------|
| Laboratory code number | Virus Identification | Titre in | | | |
| | | BF-2 | EPC | RTG-2 | FHM |
| 46 | IHNv | < 1,9E+02 | 1,9E+05 | 2,7E+03 | N/A |
| 45 | IHNv | < 1,9E+02 | 8,6E+04 | < 1,9E+02 | N/A |
| 44 | IHNv | < 1,9E+02 | 1,9E+04 | 5,9E+02 | N/A |
| 43 | IHNv | < 1,9E+02 | 2,7E+04 | N/A | N/A |
| 42 | IHNv | 1,3E+04 | 1,3E+03 | N/A | N/A |
| 41 | IHNv | < 1,9E+02 | 4,0E+05 | 5,9E+03 | 5,9E+05 |
| 40 | IHNv | 2,7E+03 | 8,6E+04 | N/A | N/A |
| 39 | IHNv | N/A | 2,7E+03 | 8,6E+02 | 2,7E+02 |
| 38 | IHNv | < 1,9E+02 | 2,7E+05 | 2,7E+05 | 4,0E+05 |
| 37 | IHNv | 1,3E+03 | 4,0E+04 | N/A | N/A |
| 36 | IHNv | < 1,9E+02 | 5,9E+04 | N/A | N/A |
| 35 | IHNv genogroup M-Eur1 | 1,3E+03 | 5,9E+05 | N/A | N/A |
| 34 | IHNv | < 1,9E+02 | 1,3E+06 | 5,9E+04 | N/A |
| 33 | rhabdovirus, IHNv France 1987: IHNv 32/87, genogroup Europe | < 1,9E+02 | 1,0E+04 | < 1,9E+02 | < 1,9E+02 |
| 32 | IHNv | < 1,9E+02 | 5,9E+04 | N/A | N/A |
| 31 | IHNv | < 1,9E+02 | 8,6E+05 | N/A | N/A |
| 30 | IHNv | < 1,9E+02 | 2,7E+06 | N/A | N/A |
| 28 | IHNv | 2,7E+02 | 2,7E+05 | N/A | N/A |
| 27 | IHNv | 8,6E+02 | 4,0E+05 | N/A | N/A |
| 26 | IHNv | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 25 | IHNv | < 1,9E+02 | 1,9E+05 | N/A | N/A |
| 24 | IHNv | N/A | 5,9E+05 | 2,7E+04 | N/A |
| 23 | IHNv | < 1,9E+02 | 2,7E+04 | N/A | N/A |
| 22 | IHNv viable virus detected | N/A | 4,0E+04 | N/A | 4,0E+05 |
| 21 | IHNv | 5,9E+02 | 8,6E+03 | N/A | N/A |
| 20 | IHNv | 5,9E+02 | 1,9E+03 | N/A | N/A |
| 19 | IHNv | N/A | 2,7E+04 | < 1,9E+02 | 1,3E+04 |
| 18 | IHNv | 2,7E+02 | 1,9E+05 | 4,0E+02 | 5,9E+05 |
| 17 | IHNv | N/A | 4,0E+04 | 8,6E+03 | N/A |
| 16 | IHNv | 1,3E+03 | 4,0E+02 | N/A | N/A |
| 15 | IHNv | 2,7E+04 | 1,9E+05 | N/A | N/A |

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| Laboratory code number | Virus Identification | Titre in | | | |
|------------------------|----------------------|-----------|-----------|-----------|-----------|
| | | BF-2 | EPC | RTG-2 | FHM |
| 14 | IHNV | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 13 | IHNV | 4,0E+03 | 1,3E+03 | 1,3E+03 | 1,3E+03 |
| 12 | IHNV | < 1,9E+02 | 8,6E+03 | N/A | N/A |
| 11 | IHNV | < 1,9E+02 | 1,9E+03 | < 1,9E+02 | < 1,9E+02 |
| 10 | IHNV | < 1,9E+02 | 1,3E+03 | < 1,9E+02 | < 1,9E+02 |
| 9 | IHNV | < 1,9E+02 | 8,6E+05 | < 1,9E+02 | 8,6E+05 |
| 8 | IHNV | < 1,9E+02 | N/A | N/A | 5,9E+04 |
| 7 | IHNV | 1,9E+02 | 1,3E+06 | N/A | N/A |
| 6 | IHNV | N/A | 1,3E+05 | N/A | 4,0E+05 |
| 5 | IHNV | < 1,9E+02 | 1,3E+04 | N/A | N/A |
| 4 | IHNV | 1,3E+03 | 1,3E+05 | N/A | N/A |
| 3 | IHNV | 4,0E+03 | N/A | N/A | 1,3E+05 |
| 2 | IHNV | < 1,9E+02 | 1,3E+04 | N/A | 4,0E+04 |
| 1 | IHNV-M | 1,9E+04 | 1,3E+04 | 1,3E+04 | 8,6E+03 |

N/A: Cell line not applied by the participating laboratory for titration of the virus

| | BF-2 | EPC | RTG-2 | FHM |
|--------------------|----------|----------|----------|----------|
| Median titre | <1,9E+02 | 4,1E+04 | 7,2E+02 | 4,1E+04 |
| Maximum titre | 2,7E+04 | 2,7E+06 | 2,7E+05 | 8,6E+05 |
| Minimum titre | <1,9E+02 | <1,9E+02 | <1,9E+02 | <1,9E+02 |
| 25% quartile titre | <1,9E+02 | 9,9E+03 | <1,9E+02 | 2,7E+02 |
| 75% quartile titre | 1,1E+03 | 2,3E+05 | 7,9E+03 | 4,1E+05 |

Table 5. Inter-Laboratory Proficiency Test, PT1, 2015 – Results of titration of ampoule II.

| <i>Ampoule II - VHSV 1P8</i> | | | | | |
|------------------------------|--|-----------|-----------|-----------|-----------|
| Laboratory code number | Virus Identification | Titre in | | | |
| | | BF-2 | EPC | RTG-2 | FHM |
| 46 | VHSV | 2,7E+03 | 4,0E+02 | < 1,9E+02 | N/A |
| 45 | VHSV | 4,0E+03 | < 1,9E+02 | 1,9E+03 | N/A |
| 44 | VHSV | 1,9E+04 | 1,3E+03 | 8,6E+03 | N/A |
| 43 | VHSV | 2,73E+03 | < 1,9E+02 | N/A | N/A |
| 42 | VHSV | 8,6E+03 | 5,9E+02 | N/A | N/A |
| 41 | VHsv | 1,3E+04 | < 1,9E+02 | < 1,9E+02 | 2,7E+04 |
| 40 | VHSV | 1,3E+04 | 5,9E+03 | N/A | N/A |
| 39 | VHSV | N/A | 1,9E+02 | 1,3E+03 | 1,9E+03 |
| 38 | VHSV | 1,3E+04 | < 1,9E+02 | < 1,9E+02 | 2,7E+04 |
| 37 | VHSV | 2,7E+03 | 1,3E+03 | N/A | N/A |
| 36 | VHSV | 2,7E+03 | 4,0E+02 | N/A | N/A |
| 35 | VHSV genotype Ib | 8,6E+03 | 4,0E+02 | N/A | N/A |
| 34 | VHSV | 5,9E+04 | < 1,9E+02 | < 1,9E+02 | N/A |
| 33 | rhabdovirus, VHSV Denmark 1996: DK-1e62, DK-1p8, DK-1p12, sub-genogroup Ib | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 32 | VHSV | 1,3E+03 | < 1,9E+02 | N/A | N/A |
| 31 | VHSV | 4,0E+03 | 1,3E+04 | N/A | N/A |
| 30 | VHSV | 8,6E+03 | 1,9E+02 | N/A | N/A |
| 28 | VHSV | 1,9E+04 | 1,9E+02 | N/A | N/A |
| 27 | VHSV | 8,6E+03 | < 1,9E+02 | N/A | N/A |
| 26 | VHSV | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 25 | VHSV | 4,0E+05 | < 1,9E+02 | N/A | N/A |
| 24 | VHSV | N/A | 1,9E+04 | 5,9E+03 | N/A |
| 23 | VHSV | 8,6E+03 | < 1,9E+02 | N/A | N/A |
| 22 | VHSV viable virus detected | 4,0E+04 | 5,9E+03 | N/A | 8,6E+03 |
| 21 | VHSV | 4,0E+03 | < 1,9E+02 | N/A | N/A |
| 20 | VHSV | 1,9E+02 | 1,9E+02 | N/A | N/A |
| 19 | VHSV | N/A | 4,0E+02 | < 1,9E+02 | < 1,9E+02 |
| 18 | VHSV | 4,0E+04 | 1,9E+03 | 5,9E+03 | 2,7E+02 |
| 17 | VHSV | N/A | 8,6E+05 | 4,0E+04 | N/A |
| 16 | VHSV | 2,7E+03 | < 1,9E+02 | N/A | N/A |

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| Laboratory code number | Virus Identification | Titre in | | | |
|------------------------|----------------------|-----------|-----------|-----------|-----------|
| | | BF-2 | EPC | RTG-2 | FHM |
| 15 | VHSV | 2,7E+04 | 1,3E+04 | N/A | N/A |
| 14 | VHSV | 2,73E+02 | < 1,9E+02 | N/A | N/A |
| 13 | VHSV | 1,3E+04 | 1,3E+04 | 1,3E+04 | 1,3E+04 |
| 12 | VHSV | 4,0E+04 | 5,9E+02 | N/A | N/A |
| 11 | VHSV | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 10 | VHS | < 1,9E+02 | 1,26E+03 | < 1,9E+02 | < 1,9E+02 |
| 9 | VHSV | 1,9E+04 | 8,6E+02 | 1,3E+04 | < 1,9E+02 |
| 8 | VHSV | 2,7E+03 | N/A | N/A | 1,3E+04 |
| 7 | VHSV | 2,7E+04 | < 1,9E+02 | N/A | N/A |
| 6 | Sterile | N/A | 1,9E+02 | N/A | 1,9E+02 |
| 5 | VHSV | 1,9E+03 | 8,6E+02 | N/A | N/A |
| 4 | VHSV | 1,3E+04 | 5,9E+02 | N/A | N/A |
| 3 | VHSV | 2,7E+04 | N/A | N/A | 4,0E+02 |
| 2 | VHSV | 2,7E+03 | < 1,9E+02 | N/A | < 1,9E+02 |
| 1 | VHSV I-b | 1,9E+03 | 2,7E+02 | < 1,9E+02 | < 1,9E+02 |

N/A: Cell line not applied by the participating laboratory for titration of the virus

| | BF-2 | EPC | RTG-2 | FHM |
|--------------------|----------|----------|----------|----------|
| Median titre | 8,6E+03 | 1,9E+02 | <1,9E+02 | 1,9E+02 |
| Maximum titre | 4,0E+05 | 8,6E+05 | 4,0E+04 | 2,7E+04 |
| Minimum titre | <1,9E+02 | <1,9E+02 | <1,9E+02 | <1,9E+02 |
| 25% quartile titre | 2,7E+03 | <1,9E+02 | <1,9E+02 | <1,9E+02 |
| 75% quartile titre | 1,9E+04 | 1,1E+03 | 5,9E+03 | 8,6E+03 |

Table 6. Inter-Laboratory Proficiency Test, PT1, 2015 – Results of titration of ampoule III.

| <i>Ampoule III - ECV 562/92</i> | | | | | |
|---------------------------------|----------------------------------|----------|-----------|-----------|-----------|
| Laboratory code number | Virus Identification | Titre in | | | |
| | | BF-2 | EPC | RTG-2 | FHM |
| 46 | ESV | 4,0E+05 | 4,0E+05 | < 1,9E+02 | N/A |
| 45 | ESV | 4,0E+05 | 4,0E+04 | 1,3E+05 | N/A |
| 44 | RANA (ESV/ECV) | 1,9E+04 | 4,0E+03 | 1,9E+04 | N/A |
| 43 | no IHN, no VHSV, no SVC, no IPNV | 5,87E+04 | 2,73E+04 | N/A | N/A |
| 42 | Rana V | 1,3E+05 | 4,0E+03 | N/A | N/A |
| 41 | ESV | 1,9E+05 | 1,9E+03 | < 1,9E+02 | 1,3E+03 |
| 40 | European sheatfish ranavirus | 4,0E+06 | 4,0E+05 | N/A | N/A |
| 39 | ESV | N/A | 1,3E+05 | 1,9E+04 | 4,0E+03 |
| 38 | Ranavirus not EHN | 4,0E+05 | 4,0E+04 | 4,0E+04 | 2,7E+02 |
| 37 | Not VHSV,IHN, IPNV,SVC | 8,6E+05 | 2,7E+04 | N/A | N/A |
| 36 | Ranavirus | 5,9E+03 | 5,9E+03 | N/A | N/A |
| 35 | European catfish virus ECV | 1,3E+05 | 1,3E+05 | N/A | N/A |
| 34 | ECV / ESV | 2,7E+05 | 5,9E+04 | 1,9E+02 | N/A |
| 33 | ranavirus, ECV/ ESV | 6,8E+03 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 32 | ECV or ESV | 1,3E+05 | 4,0E+04 | N/A | N/A |
| 31 | ESV | 2,7E+05 | 4,0E+04 | N/A | N/A |
| 30 | ECV | 2,7E+03 | 4,0E+02 | N/A | N/A |
| 28 | Ranavirus not EHN (ECV) | 4,0E+05 | 8,6E+03 | N/A | N/A |
| 27 | ESV | 1,9E+06 | 8,6E+05 | N/A | N/A |
| 26 | Ranavirus | 2,7E+05 | 5,9E+05 | 8,6E+05 | < 1,9E+02 |
| 25 | EHN | 2,7E+04 | 1,9E+04 | N/A | N/A |
| 24 | RANAVIRUS | N/A | 8,6E+02 | 5,9E+02 | N/A |
| 23 | Ranavirus | 8,6E+05 | < 1,9E+02 | N/A | N/A |
| 22 | EHN viable virus detected | 4,00E+05 | N/A | N/A | N/A |
| 21 | Ranavirus (ECV or ESV) | 1,9E+04 | 5,9E+03 | N/A | N/A |
| 20 | Ranavirus | 4,0E+04 | 1,3E+03 | N/A | N/A |
| 19 | EHN | N/A | 1,9E+04 | < 1,9E+02 | 5,9E+03 |
| 18 | ECV | 1,3E+05 | 2,7E+03 | 4,0E+06 | 1,9E+05 |
| 17 | Ranavirus | N/A | 5,9E+03 | < 1,9E+02 | N/A |
| 16 | ESV/ECV | 1,9E+05 | 2,7E+02 | N/A | N/A |
| 15 | EHN | 1,9E+05 | 5,9E+04 | N/A | N/A |

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| Laboratory code number | Virus Identification | Titre in | | | |
|------------------------|---|-------------|-------------|-----------|-----------|
| | | BF-2 | EPC | RTG-2 | FHM |
| 14 | EHN | 126491,1064 | 1264,911064 | N/A | N/A |
| 13 | Ranavirus | 2,7E+05 | 1,3E+05 | 2,7E+05 | 1,3E+05 |
| 12 | ESV (very closely related to EHN) | 2,7E+05 | 8,6E+05 | N/A | N/A |
| 11 | Ranavirus | 1,86E+03 | 1,86E+04 | < 1,9E+02 | 1,26E+03 |
| 10 | EHN | 1,26E+03 | 4,00E+03 | < 1,9E+02 | 2,73E+03 |
| 9 | Ranavirus ESV | 2,7E+05 | 2,7E+05 | 1,3E+05 | 2,7E+05 |
| 8 | Ranavirus | 8,6E+04 | N/A | N/A | < 1,9E+02 |
| 7 | EHN | 8,6E+06 | 5,9E+05 | N/A | N/A |
| 6 | ECV | N/A | 5,9E+05 | N/A | 1,9E+04 |
| 5 | Ranavirus was identified by conventional RT-PCR and than REA was applied as given by OIE manuel to identified ECV | 2,7E+04 | 2,7E+04 | N/A | N/A |
| 4 | European sheatfish virus | 2,7E+05 | 8,6E+05 | N/A | N/A |
| 3 | Ranavirus, not EHN | 2,7E+04 | N/A | N/A | 1,9E+03 |
| 2 | Ranavirus (Not EHN, see sequencing result) | 1,3E+05 | 1,3E+04 | N/A | 8,6E+03 |
| 1 | European sheatfish virus | 2,7E+05 | 8,6E+04 | 5,9E+03 | 1,9E+03 |

N/A: Cell line not applied by the participating laboratory for titration of the virus

| | BF-2 | EPC | RTG-2 | FHM |
|--------------------|---------|----------|----------|----------|
| Median titre | 1,9E+05 | 2,7E+04 | 3,2E+03 | 2,3E+03 |
| Maximum titre | 8,6E+06 | 8,6E+05 | 4,0E+06 | 2,7E+05 |
| Minimum titre | 1,3E+03 | <1,9E+02 | <1,9E+02 | <1,9E+02 |
| 25% quartile titre | 3,7E+04 | 4,0E+03 | <1,9E+02 | 1,0E+03 |
| 75% quartile titre | 3,0E+05 | 1,3E+05 | 1,0E+05 | 1,1E+04 |

Table 7. Inter-Laboratory Proficiency Test, PT1, 2015 – Results of titration of ampoule IV.

| <i>Ampoule IV - Blank, BF-2 cellesupernatant</i> | | | | | |
|--|--|-----------|-----------|-----------|-----------|
| Laboratory code number | Virus Identification | Titre in | | | |
| | | BF-2 | EPC | RTG-2 | FHM |
| 46 | Negative | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | N/A |
| 45 | no virus detected | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | N/A |
| 44 | No virus growth | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | N/A |
| 43 | no CPE | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 42 | No virus | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 41 | Negative | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 40 | not IHN, VHSV, EHN, Ranavirus, IPNV, SVCV | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 39 | | N/A | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 38 | Not VHSV, not IHN and not Ranavirus (see comment) | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 37 | Virus not found | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 36 | No virus detected | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 35 | no virus | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 34 | negative for all viruses tested | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | N/A |
| 33 | | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 32 | NO VHSV NO IHN NO EHN | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 31 | Negativ | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 30 | No virus detected | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 28 | Negative | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 27 | Negative | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 26 | | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 25 | no VHSV/ no IHN/ no EHN/ no IPNV/ no SVCV | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 24 | NEGATIVE | N/A | < 1,9E+02 | < 1,9E+02 | N/A |
| 23 | No IHN, VHSV, Ranavirus, SVCV or IPNV detected | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 22 | No viruses detected | < 1,9E+02 | < 1,9E+02 | N/A | < 1,9E+02 |
| 21 | No virus detected | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 20 | 0 | 4,0E+02 | < 1,9E+02 | N/A | N/A |
| 19 | No Virus | N/A | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 18 | Negative for VHSV, IHN, IPNV, EHN, ranavirus, SVCV | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 17 | Negative | N/A | < 1,9E+02 | < 1,9E+02 | N/A |
| 16 | Negative | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 15 | Negative | < 1,9E+02 | < 1,9E+02 | N/A | N/A |

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| Laboratory code number | Virus Identification | Titre in | | | |
|------------------------|---|-----------|-----------|-----------|-----------|
| | | BF-2 | EPC | RTG-2 | FHM |
| 14 | No Viruses isolated by BF2/EPC cell culture | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 13 | - | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 12 | | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 11 | negative | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 10 | Negative | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 9 | No virus | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |
| 8 | Negativ | < 1,9E+02 | N/A | N/A | < 1,9E+02 |
| 7 | no virus found | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 6 | Sterile | N/A | < 1,9E+02 | N/A | < 1,9E+02 |
| 5 | IHNV | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 4 | NEGATIVE | < 1,9E+02 | < 1,9E+02 | N/A | N/A |
| 3 | Negative | < 1,9E+02 | N/A | N/A | < 1,9E+02 |
| 2 | negative | < 1,9E+02 | < 1,9E+02 | N/A | < 1,9E+02 |
| 1 | no virus detected | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 | < 1,9E+02 |

N/A: Cell line not applied by the participating laboratory for titration of the virus

| | BF-2 | EPC | RTG-2 | FHM |
|--------------------|----------|----------|----------|----------|
| Median titre | <1,9E+02 | <1,9E+02 | <1,9E+02 | <1,9E+02 |
| Maximum titre | 4,0E+02 | <1,9E+02 | <1,9E+02 | <1,9E+02 |
| Minimum titre | <1,9E+02 | <1,9E+02 | <1,9E+02 | <1,9E+02 |
| 25% quartile titre | <1,9E+02 | <1,9E+02 | <1,9E+02 | <1,9E+02 |
| 75% quartile titre | <1,9E+02 | <1,9E+02 | <1,9E+02 | <1,9E+02 |

Table 8. Inter-Laboratory Proficiency Test, PT1, 2015 – Results of titration of ampoule V.

| <i>Ampoule V - VHSV/IHN</i> | | | | | |
|-----------------------------|---|----------|----------|---------|---------|
| Laboratory code number | Virus Identification | Titre in | | | |
| | | BF-2 | EPC | RTG-2 | FHM |
| 46 | VHSV, IHN, TenRV | 2,7E+05 | 5,9E+06 | 4,0E+05 | N/A |
| 45 | VHSV & IHN | 1,9E+06 | 1,9E+06 | 4,0E+06 | N/A |
| 44 | VHSV SVC RANA (ECV/ESV) | 2,7E+06 | 2,7E+06 | 1,3E+06 | N/A |
| 43 | IHN, VHSV, SVC | 5,87E+05 | 8,62E+05 | N/A | N/A |
| 42 | VHSV IHN SVC | 5,9E+04 | 5,9E+03 | N/A | N/A |
| 41 | IHN + VHSV | 4,0E+06 | 8,6E+06 | 8,6E+05 | 8,6E+06 |
| 40 | VHSV and IHN | 2,7E+06 | 1,9E+07 | N/A | N/A |
| 39 | VHSV and IHN | N/A | 1,9E+06 | 1,3E+05 | 1,9E+05 |
| 38 | VHSV and IHN | 5,9E+06 | 5,9E+06 | 4,0E+06 | 5,9E+06 |
| 37 | VHSV, IHN | 1,9E+05 | 4,0E+05 | N/A | N/A |
| 36 | IHN, VHSV & PFR | 1,9E+06 | 4,0E+06 | N/A | N/A |
| 35 | VHSV genotype Ia, IHN genogroup M-Eur1, Pike-fry-like rhabdovirus | 8,6E+05 | 1,3E+07 | N/A | N/A |
| 34 | IHN+VHSV+PFR-like virus | 2,7E+07 | 5,9E+07 | 2,7E+06 | N/A |
| 33 | rhabdovirus, VHSV Denmark DK- 5151 Rindsholm, sub- genogroup Ia | 1,5E+04 | 4,6E+04 | 6,8E+03 | 4,6E+03 |
| 32 | VHSV & IHN | 1,3E+06 | 5,9E+05 | N/A | N/A |
| 31 | VHSV+SVC | 8,6E+05 | 2,7E+06 | N/A | N/A |
| 30 | VHSV and SVC | 8,6E+06 | 1,3E+07 | N/A | N/A |
| 28 | VHSV + Sprivirus (TenRV) | 2,7E+06 | 1,9E+06 | N/A | N/A |
| 27 | VHSV+IHN+SVC | 5,9E+06 | 2,7E+06 | N/A | N/A |
| 26 | VHSV, IHN, Pike fry-like rhabdovirus | 1,9E+05 | 1,9E+05 | 2,7E+05 | 4,0E+05 |
| 25 | VHSV/IHN/SVC | 2,7E+04 | 5,9E+04 | N/A | N/A |
| 24 | VHSV, IHN | N/A | 1,3E+07 | 5,9E+06 | N/A |
| 23 | VHSV, IHN & SVC | 5,9E+06 | 4,0E+06 | N/A | N/A |
| 22 | IHN and VHSV viable virus detected | 4,0E+06 | 4,0E+06 | N/A | 4,0E+07 |
| 21 | IHN and VHSV | 2,7E+05 | 2,7E+05 | N/A | N/A |
| 20 | VHSV/SVC/IHN | 1,3E+04 | 1,9E+04 | N/A | N/A |
| 19 | IHN, VHSV, PFR | N/A | 4,0E+05 | 2,7E+05 | 1,3E+06 |
| 18 | VHSV, IHN | 2,7E+06 | 4,0E+06 | 8,6E+06 | 1,3E+07 |
| 17 | VHSV, IHN, SVC | N/A | 5,9E+06 | 4,0E+04 | N/A |

Report on the Inter-Laboratory Proficiency Test 2015
for identification of VHSV, IHNV, EHNV, SVCV and IPNV (PT1) and identification of KHV, SAV and ISAV (PT2)

| Laboratory code number | Virus Identification | Titre in | | | |
|------------------------|---|----------|----------|-----------|-----------|
| | | BF-2 | EPC | RTG-2 | FHM |
| 16 | VHSV IHNV Rhabdovirus | 1,3E+05 | 5,9E+03 | N/A | N/A |
| 15 | VHSV | 5,9E+05 | 1,9E+06 | N/A | N/A |
| 14 | IHNV/VHSV | 1,9E+05 | 400 | N/A | N/A |
| 13 | VHSV, IHNV | 5,9E+05 | 1,3E+06 | 1,3E+05 | 1,3E+05 |
| 12 | IHNV, VHSV | 8,6E+04 | 5,9E+06 | N/A | N/A |
| 11 | VHSV, IHNV & Tench rhabdovirus (or Pike fry-like rhabdovirus) | 1,86E+06 | 2,73E+05 | 5,87E+04 | 1,26E+05 |
| 10 | IHN, VHS | 1,26E+04 | 2,73E+04 | < 1,9E+02 | < 1,9E+02 |
| 9 | IHNV, VHSV, SVCV-like* | 2,7E+06 | 1,3E+06 | 1,9E+06 | 8,6E+05 |
| 8 | VHSV, IHNV | 1,9E+06 | N/A | N/A | 2,7E+06 |
| 7 | VHSV, IHNV, SVCV | 8,6E+06 | 8,6E+06 | N/A | N/A |
| 6 | IHNV & VHSV | N/A | 1,3E+07 | N/A | 4,0E+07 |
| 5 | VHSV, IHNV, SVCV | 5,9E+05 | 8,6E+07 | N/A | N/A |
| 4 | VHSV and IHNV | 2,7E+06 | 1,3E+07 | N/A | N/A |
| 3 | VHSV & TenRV | 5,9E+06 | N/A | N/A | 8,6E+06 |
| 2 | VHSV | 5,9E+05 | 8,6E+05 | N/A | 1,3E+06 |
| 1 | mixed infection: tench rhabdovirus; IHNV; and VHSV | 8,6E+05 | 4,0E+06 | 1,3E+05 | 8,6E+05 |

N/A: cell line not applied by the participating laboratory for titration of the virus

| | BF-2 | EPC | RTG-2 | FHM |
|--------------------|---------|---------|----------|----------|
| Median titre | 1,1E+06 | 2,7E+06 | 3,4E+05 | 1,3E+06 |
| Maximum titre | 2,7E+07 | 8,6E+07 | 8,6E+06 | 4,0E+07 |
| Minimum titre | 1,3E+04 | 4,0E+02 | <1,9E+02 | <1,9E+02 |
| 25% quartile titre | 2,5E+05 | 4,0E+05 | 1,3E+05 | 1,9E+05 |
| 75% quartile titre | 2,7E+06 | 5,9E+06 | 2,5E+06 | 8,6E+06 |

Figure 5. Virus titres obtained in BF-2 cells. The titre (red diamond) of each participating laboratory (country code) using BF-2 cells illustrated for ampoule I, II, III, IV and V. The detection level (grey shadow), median (blue line), 75% quartile (upper yellow line) and 25% quartile (lower yellow line) are plotted on all graphs. For participants failing to obtain any titre, no red diamond is shown.

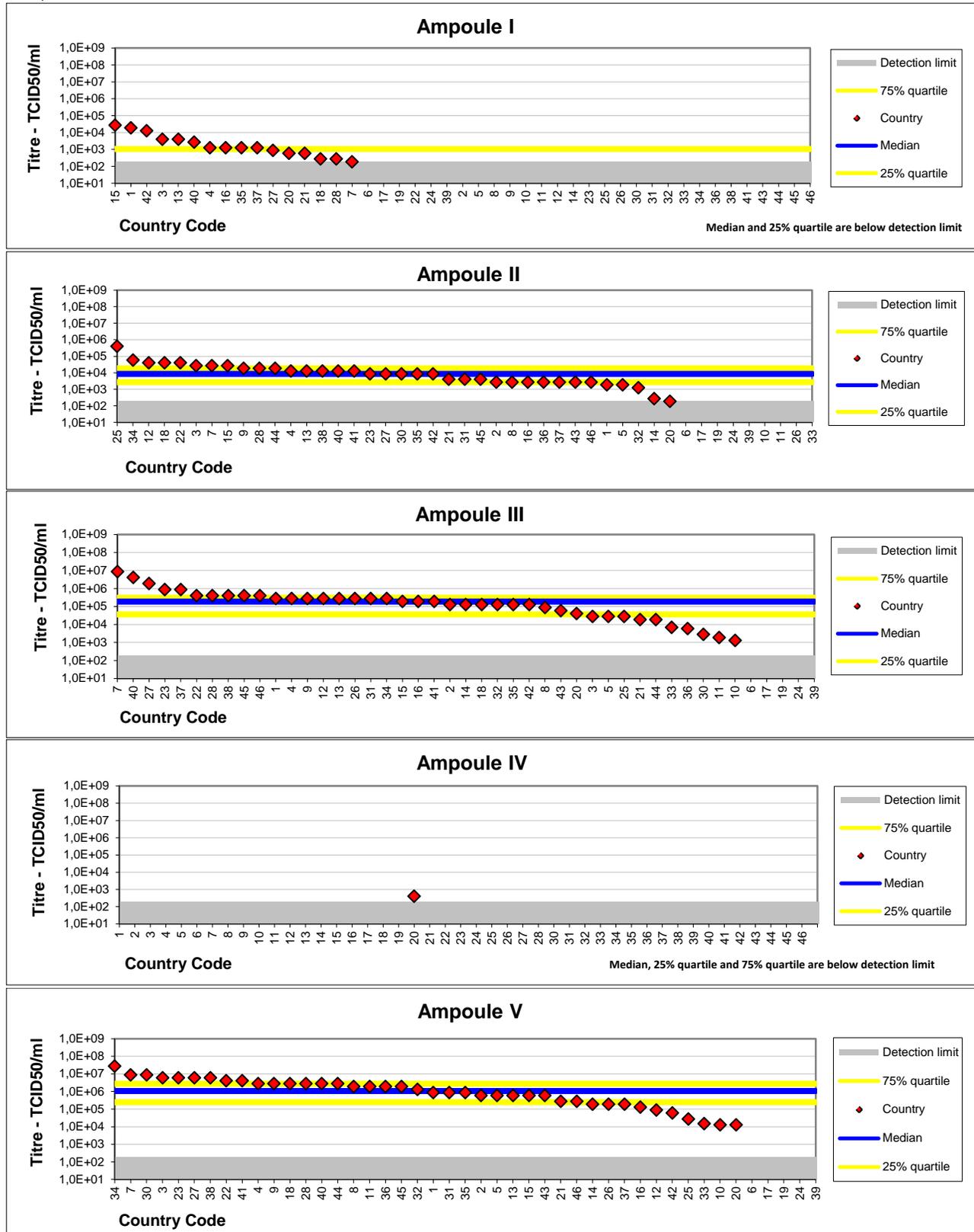


Figure 6. Virus titres obtained in EPC cells. For further details see Figure 5

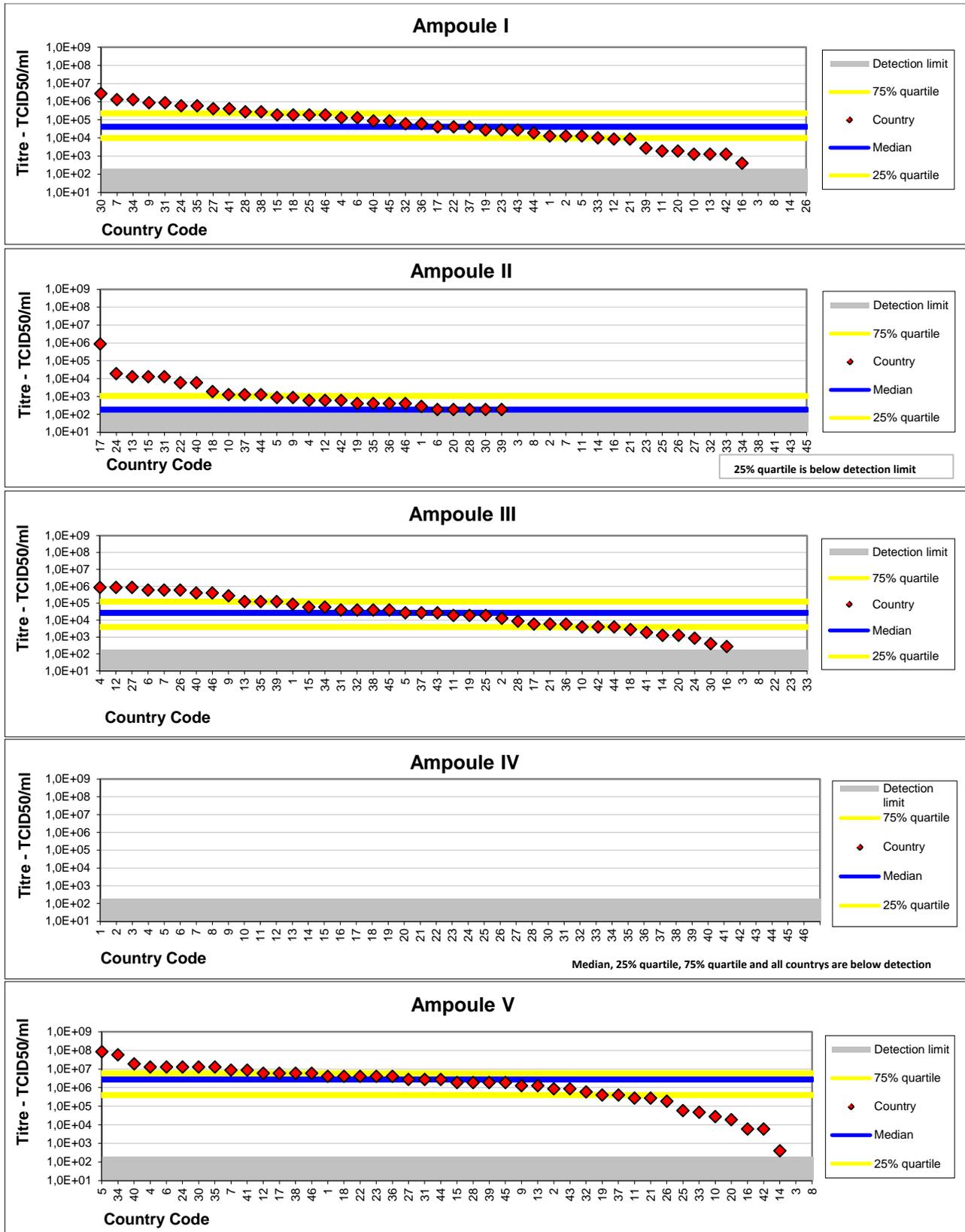


Figure 7. Virus titre obtained in RTG-2 cells. For further details see Figure 5

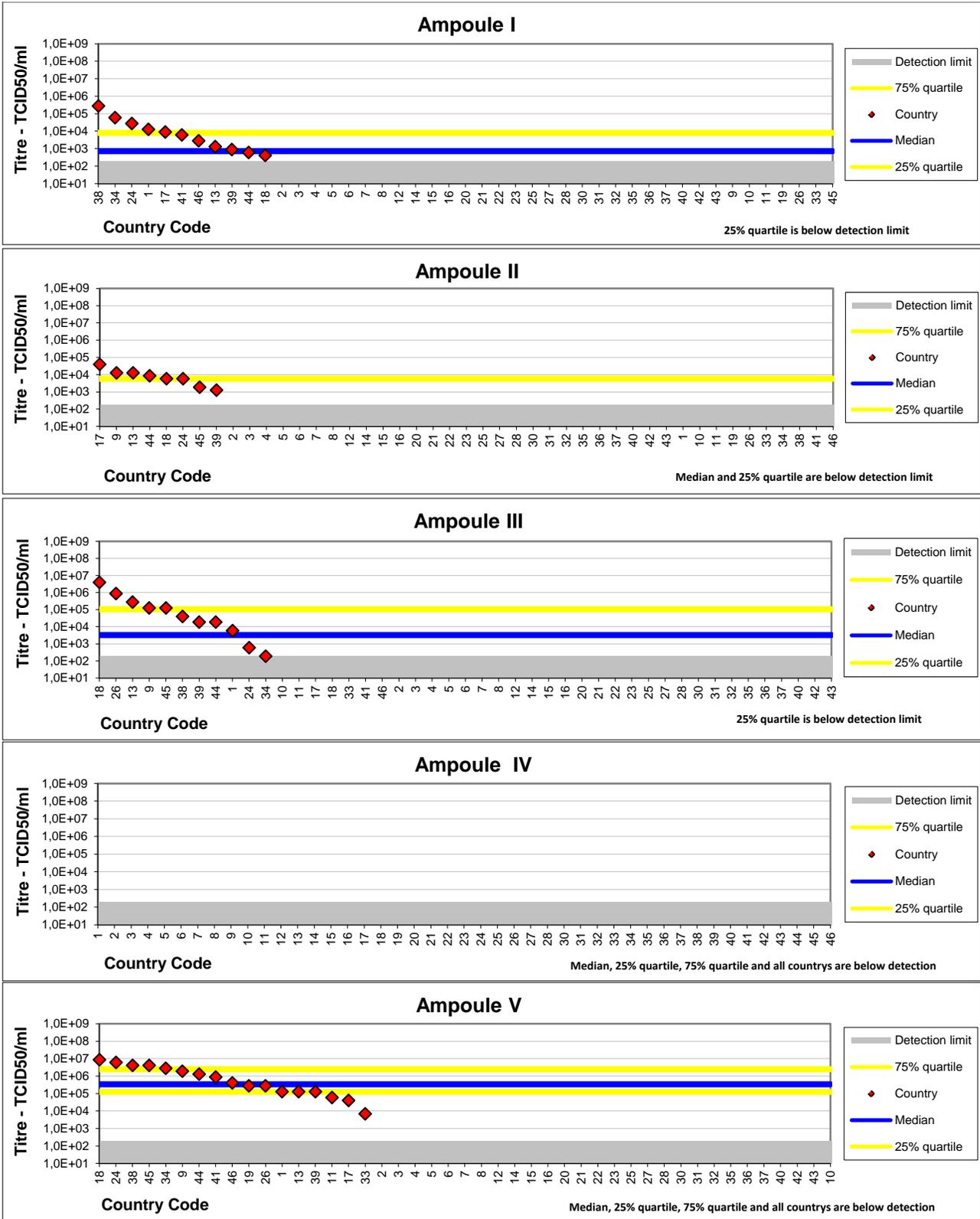
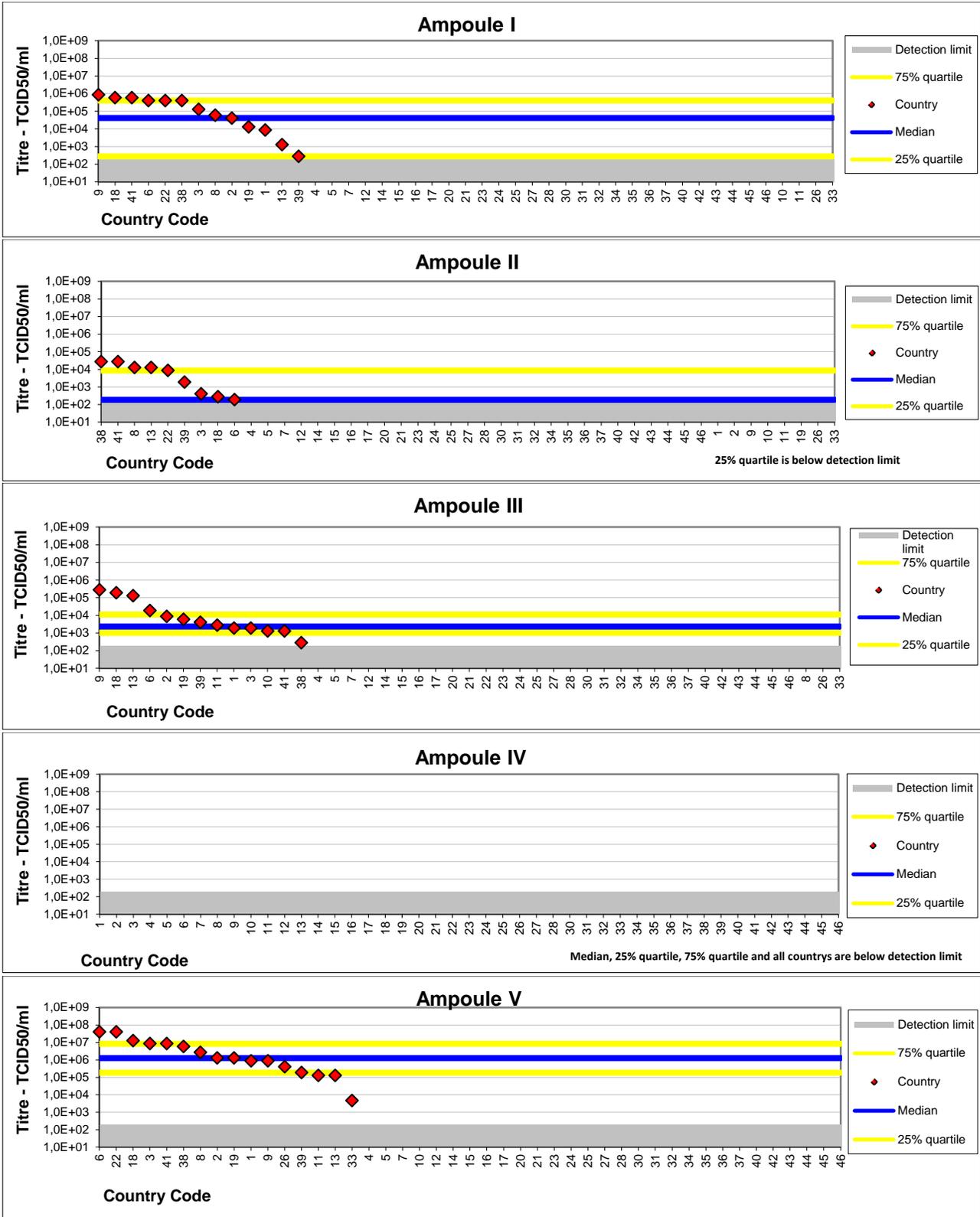


Figure 8. Virus titres obtained in FHM cells. For further details see Figure 5



Identification of content

- 29 laboratories correctly identified all viruses in all ampoules
- 43 of the participants submitted the spreadsheet within the deadline, 2 participants got the deadline extended due to delivery problems or technical problems in the laboratory.

Ampoule I – IHNV

- All 45 laboratories correctly isolated and identified IHNV

Ampoule II - VHSV

- 44 laboratories correctly identified VHSV
- 1 laboratory did not isolate any viruses.

Ampoule III – ECV

- 35 laboratories correctly isolated and identified ECV
- 3 laboratories correctly isolated Rana-virus but did not identify it – of which 1 by agreement does not have to sequence.
- 5 laboratories isolated Rana-virus but identified it as EHNV.
- 2 laboratories does not perform test for Ranaviruses.

Ampoule IV – BLANK

- 44 laboratories correctly identified 'not IHNV, not VHSV, not IPNV, not SVCV, not EHNV'
- 1 Laboratory isolated and identified IHNV

Ampoule V – VHSV + IHNV (+SVC-like)

- 37 laboratories correctly isolated and identified both VHSV and IHNV
- 7 laboratories isolated and identified only VHSV
- 1 laboratory isolated and identified VHSV and Rana-virus
- 24 laboratories isolated and identified SVC-like virus

Scores

Starting with proficiency test 2003 we have provided a scoring system for the identification part of the proficiency tests. We have assigned a score of 2 for each correct answer/identification, giving the possibility for obtaining a maximum score of 10 (Table 3).

Ampoule I: IHNV identification was given the score 2. IHNV not identified was given the score 0. Incorrectly finding of “no virus” or additional types of viruses than those included in the ampoule scored 0, even though the included virus (IHNV) was amongst the identified viruses.

Ampoule II: VHSV identification was given the score 2. VHSV not identified was given the score 0. Incorrectly finding of “no virus” or additional types of viruses than those included in the ampoule scored 0, even though the included virus (VHSV) was amongst the identified viruses.

Ampoule III: ECV/ESV identification backed up by genomic analysis was given the score 2. Ranavirus answer for this ampoule with a genomic analysis showing ECV/ESV was given the score 2. Ranavirus/iridovirus as the only answer (without genomic analysis) was given the score 1. EHNV identification (with or without genomic analysis) was given the score 1.

Ampoule IV: Identification “no virus”, “Blank”, “not IHNV, not VHSV, not IPNV, not SVCV, not EHNV” or similar answer was given the score 2. Incorrectly finding of virus in the ampoule was given the score 0.

Ampoule V: Identification of both VHSV and IHNV was given the score 2. Identification of VHSV, IHNV and SVCV or SVCV/PFR-like was given the score 2. VHSV identification only was given the score 1. VHSV and SVCV identification only was given the score 1. Incorrectly finding of “no virus” or additional types of viruses other than VHSV, IHNV and SVCV/PFR-like virus scored 0 even though VHSV and IHNV was amongst the identified viruses.

Out of 45 laboratories participating in the PT 1 2015, 27 obtained maximum score. Serotyping and genotyping of VHSV and IHNV and submission of sequencing results are not a mandatory part of the test and is not included in the score of participants.

Cells applied for solving the test

Within the panel of cell lines available in the legislation the following ones were used by the participants:

- 39 laboratories used BF-2 cells
- 43 laboratories used EPC cells
- 18 laboratories used RTG-2 cells
- 17 laboratories used FHM cells
- 6 laboratories used CHSE-214 cells

- 10 laboratories used four cell lines (BF-2, EPC, RTG-2 and FHM)

- 7 laboratories used tree cell lines:
 - 4 laboratories used BF-2 cells in combination with EPC cells and RTG-2 cells
 - 1 laboratory used BF-2 cells in combination with EPC cells and FHM cells
 - 2 laboratories used RTG-2 cells in combination with EPC cells and FHM cells

- 28 laboratories used two cell lines:
 - 22 laboratories used BF-2 cells in combination with EPC cells
 - 2 laboratories used RTG-2 cells in combination with EPC cells
 - 2 laboratories used BF-2 cells in combination with FHM cells
 - 2 laboratory used EPC cells in combination with FHM cells

The combination of EPC and FHM cells or BF-2 and RTG 2 as well is not valid according to [Commission Decision 2015-1554](#). The laboratories using these combinations are encouraged to include the use of BF-2 cells and EPC or FHM.

The median titre calculated from the submitted results of each ampoule and in each cell line is illustrated in Figure 11.

It appears that:

Ampoule I (IHNV) replicates equally well on EPC and FHM cells, less efficiently on RTG-2 and not at all on BF-2 cells.

Ampoule II (VHSV Ib) replicate well on BF-2 cells, whereas its viral content was barely detectable on EPC and FHM cells, finally did not grow at all on RTG-2.

Ampoule III (ECV) replicates well on all four cell lines, however it grows best on BF-2 cells.

Ampoule V (VHSV + IHNV) replicates equally well on all four cell lines, which probably have to due to the fact that the two viruses replicates best on different cell lines.

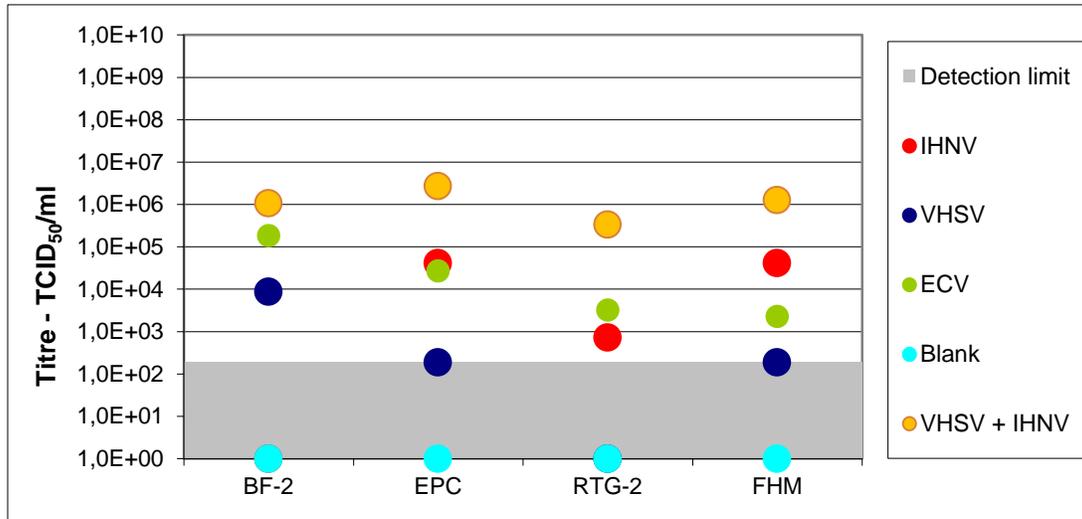


Figure 9. Median virus titres obtained by the participants in 4 different cell lines.

Genotyping and sequencing

In previous proficiency tests provided by the EURL, we have encouraged participants to genotype the identified viruses though it has not been a mandatory task. As ranaviruses are included in the test, it is mandatory to do sequence or REA analysis in order to discriminate EHN from the non-listed ranaviruses. For IHNV and VHSV we still encouraged participants to genotype isolates according to the notification described in [Einer-Jensen et al. \(2004\)](#) for VHSV and in [Kurath et al. \(2003\)](#) and [Emmenegger et al., 2000](#) for IHNV but this was not an obligatory task.

AMPOULE I - IHNV

27 laboratories sequenced correctly IHNV in ampoule 1

- 18 laboratories partially sequenced the Glycoprotein Gene according to protocol from Emmenegger et al., 2000
- 1 Laboratory sequenced the full G Gene with in house developed primer sets
- 1 laboratory targeted the G gene according to the protocol provided by Miller et al., 1998
- 2 laboratories targeted the G gene according to the protocol provided by Kolodziejek et al., 2008
- 1 laboratory targeted the G gene according to Williams K. et al., 1999
- 1 laboratory reported to sequence the G protein without providing a protocol
- 1 laboratory targeted the Nucleocapsid protein according to protocol by Bergmann et al 2000
- 1 laboratory targeted the Nucleocapsid protein according to the protocol provided in the OIE manual 2006
- 1 laboratory referred to OIE Manual of 2006 without providing specifics for targeted region and primer sets
- 1 laboratory sequenced the NV region

It has to be specified that some participants used more than one protocol for sequencing the isolate.

AMPOULE II- VHSV

25 laboratories sequenced correctly VHSV in ampoule 4

- 6 laboratories targeted the G gene according to the protocol from Einer-Jensen et al., 2004
- 10 laboratories targeted the Nucleocapsid protein according to protocol from Snow et al., 2004
- 1 laboratory targeted the Nucleoprotein gene according to protocol from Bergmann et al., 2000
- 2 laboratory targeted the G gene according to protocol from Hedrick et al., 2003
- 1 laboratory targeted the G gene according to Miller et al. 1998
- 1 laboratory targeted the G gene according to Williams et al., 1999.
- 1 laboratory targeted the G gene according to OIE manual 2009
- 1 laboratory referred to OIE manual (non-specified year)
- 2 laboratories used unpublished results targeting the G gene

It has to be specified that some participants used more than one protocol for sequencing the isolate.

AMPOULE III - EHNV

35 laboratories sequenced ECV in ampoule III,

- 11 laboratories targeted the Major Capsid Protein MCP according to the protocol provided by Hyatt et al., 2000.
- 1 laboratory targeted the Major Capsid Protein MCP according to the protocol provided by Ohlemeyer et al., 2011
- 2 laboratories targeted the Major Capsid Protein MCP according to the protocol provided by OIE Manual 2011
- 1 laboratory targeted the Major Capsid Protein MCP according to protocol provided by Marsh et al., 2002
- 19 laboratories targeted the Major Capsid Protein MCP according to protocol provided by Holopainen et al, 2009
- 1 laboratory targeted the Polymerase according to the protocol provided by Holopainen et al, 2009
- 1 laboratory targeted the Major Capsid Protein MCP according to the protocol provided by Bigarre et al. 2008
- 1 laboratory targeted the Major Capsid Protein MCP without providing a protocol of reference
- 2 laboratories referred to OIE manual without providing details on protocol

It has to be specified that some participants used more than one protocol for sequencing the isolate.

AMPOULE V

Ampoule V – IHNV

24 laboratories sequenced IHNV isolate in Ampoule V

- 9 laboratories partially sequenced the Glycoprotein Gene according to protocol from Emmenegger et al., 2000
- 1 Laboratory sequenced the full G Gene with in house developed primer sets
- 1 laboratory targeted the Nucleocapsidprotein according to protocol by Bergmann et al 2000
- 3 laboratories targeted the G gene according to the protocol provided by Kolodziejek et al., 2008
- 5 laboratories targeted the G gene according to OIE manual
- 2 laboratories targeted the N gene according to OIE manual
- 1 laboratory targeted the G gene according to Williams et al., 1999
- 1 laboratory targeted the G gene without providing protocol of reference
- 1 laboratory provided the primersets without referring to a protocol
- 1 laboratory did not provide a protocol

It has to be specified that some participants used more than one protocol for sequencing the isolate.

Ampoule V – VHSV

25 laboratories sequenced the VHSV isolate included in Ampoule V

- 6 laboratories targeted the G gene according to the protocol from Einer-Jensen et al., 2004
- 7 laboratories targeted the Nucleocapsid protein according to protocol from Snow et al., 2004
- 1 laboratory targeted the Nucleocapsidprotein according to protocol by Bergmann et al 2000
- 1 laboratory targeted the G gene according to the protocol provided by Miller et al., 1998
- 1 laboratory targeted the G gene according to Williams et al., 1999
- 1 laboratory targeted the G gene according to Hedrick et al., 2003
- 1 laboratory targeted the G gene according to Raja-Halli et al., 2006
- 1 laboratory sequenced both N and G gene according to OIE manual
- 2 laboratories provided primer sets without reference and target region
- 2 laboratory targeted the g gene region with an “in house” developed protocol
- 1 laboratory sequenced the product obtained by qPCR analysis from Jonstrup et al., 2012.

It has to be specified that some participants used more than one protocol for sequencing the isolate.

Ampoule V – Tench rhabdovirus

9 Laboratories sequenced a rhabdovirus identified as tench rhabdovirus using protocols designed by Stone et al., 2003. This virus was not expected to be included in Ampoule V of the Interlaboratory Proficiency test 2015, a specific paragraph address this issue in the report.

Résumé and concluding remarks PT1

. 49% of parcels were delivered by the shipping companies within 1 day after submission and 80% was delivered within 1 week. It was, however, unfortunate that six parcels were more than 2 weeks on the way and one of these was 35 days on the way before delivered to the laboratory primarily due to border controls.

This year ECV was included. 43 participants were able to identify Ranavirus of these laboratories 38 correctly identified 'Ranavirus' or 'not EHNv'. 40 laboratories performed sequencing and among these 35 identified 'ESV/ECV' correctly.

In this report (Figures 5-8), all the viral titres submitted by participants are compared to each other. In this way, the titres obtained by each laboratory are plotted in relation to the combined submitted data set and each participating laboratory is able to compare the sensitivity of its cell lines to the sensitivity of those used by the other participants. We recommend all participants to evaluate the sensitivity of the cells used in their laboratory in relation to the diagnostic purpose.

The EURL provides the annual proficiency test, collates the data and process the figures so that individual laboratories can see how they perform 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 will also take the opportunity to provide a comment 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.

It was unexpected and quite unfortunate that the PFR/ tenchRV like virus – S64- showed up in Ampoule V.

The presence of this rhabdovirus was confirmed in the ampoules V in addition to the expected VHSV strain DK-5151 + IHNV strain 32/87. The virus identified was Tench Rhabdovirus S64. The scoring system has been adjusted on the background of the finding from the participants and the final confirmation conducted at the EURL. This issue has been taken seriously into consideration by the EURL and managed both with the participants and DANAK the accreditation body that audit the QA system at DTU.

The results presented in this report will be further presented and discussed at the 20th Annual Workshop of National Reference Laboratories for Fish Diseases to be held 31th of May - 1st of June 2016 in Copenhagen, Denmark.

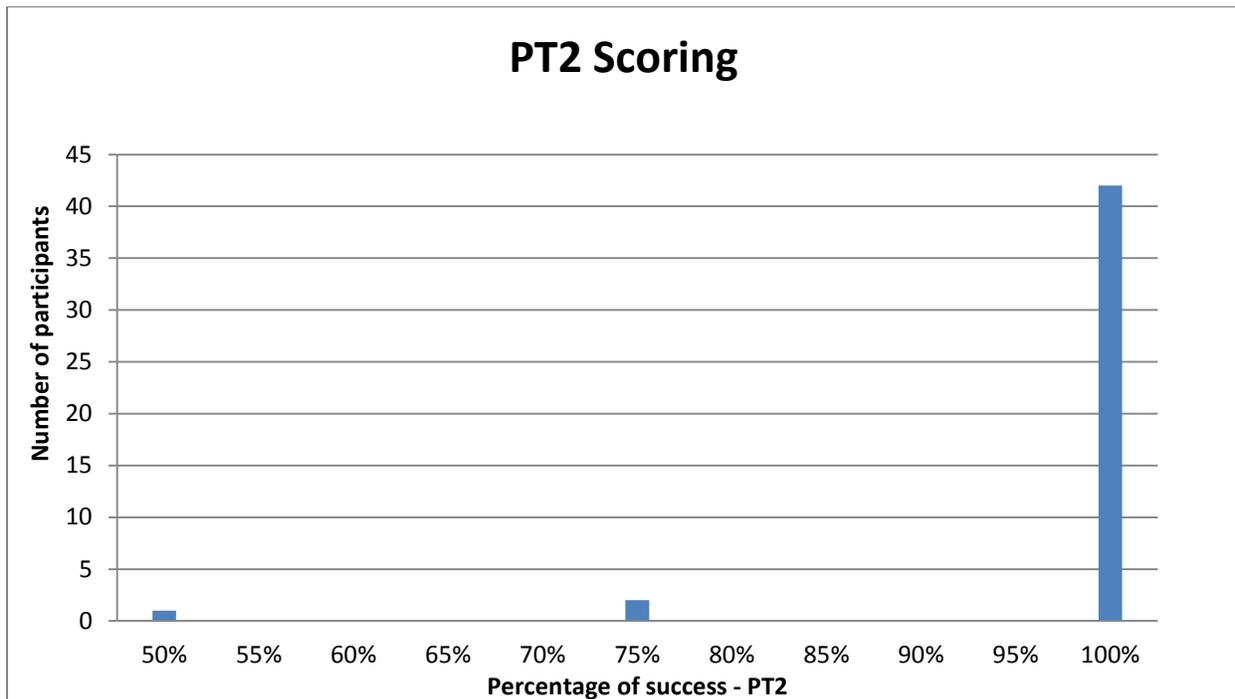
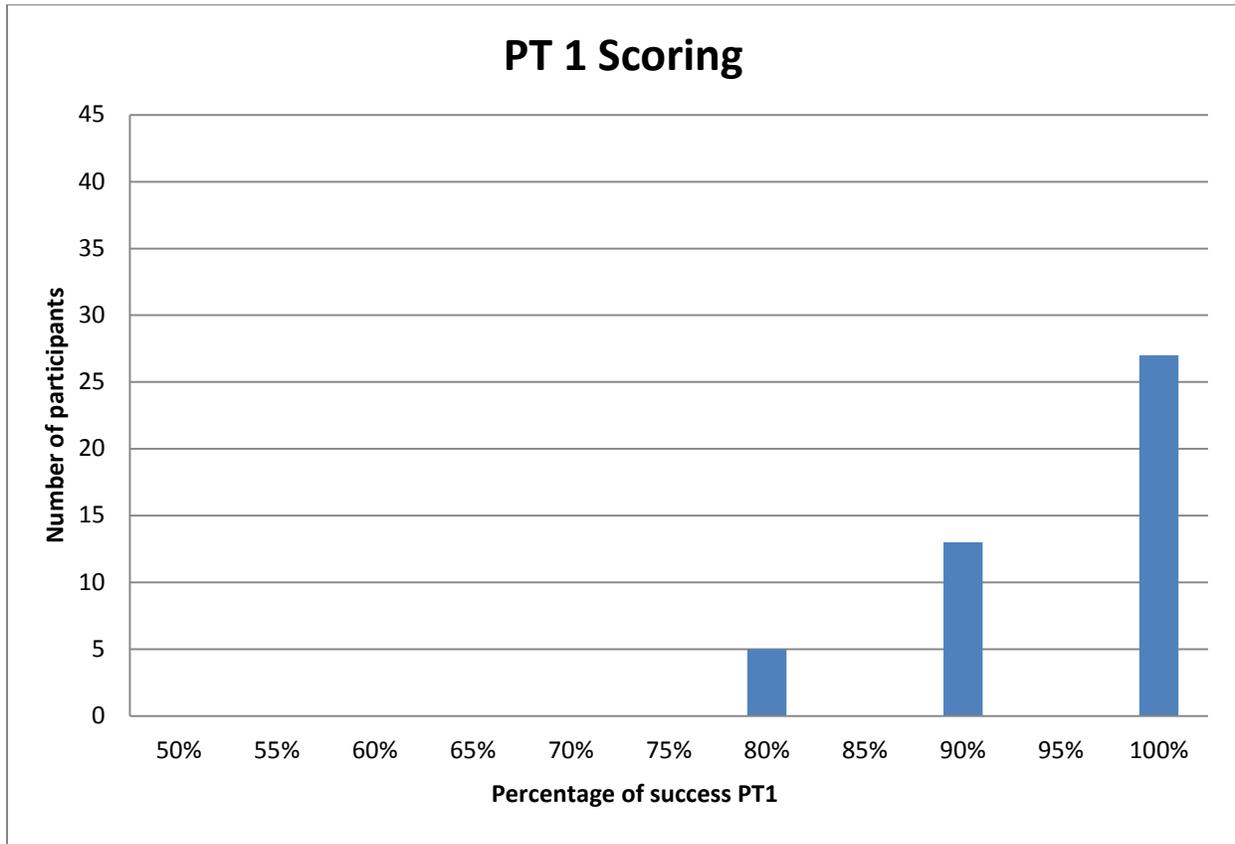


Figure 10 "a" and "b" Success-rate of participating laboratories 2015

Proficiency test 2, PT2

Four ampoules containing lyophilised cell culture supernatant were delivered to the same laboratories that participated in PT1 with the exception of one that participated only in PT1.

Content of ampoules

The viruses were propagated on each of their preferred cell line and when total cytopathic effect (CPE) was observed, the supernatants were collected and filtrated through a 45 µm filter, mixed with equal volumes of 2% w/v lactalbumin hydrolysate solution and lyophilized in glass ampoules. Before the ampoules were sealed by melting, the pathogen concentration was analysed by the KHV real-time PCR protocol described by [Gilad et al. \(2004\)](#) and the conventional PCR protocol described by [Bercovier et al. \(2005\)](#), the SAV real-time RT-PCR protocol described by [Hodneland et al. \(2006\)](#) and the ISAV real-time RT-PCR protocol described by Snow et al. (2006) and conventional RT-PCR protocol described by [Mjaaland et al. \(2002\)](#).

The details of the virus isolates used in the proficiency test 2 are outlined in table 9.

Table 9. Content in each ampoule with reference to culture conditions and major publications of the included pathogens.

| Code | Specifications/References |
|--------------|--|
| Ampoule VI | <p>KHV, (CyHV-3) Koi Herpesvirus (CyHV-3): KHV-TP 30 (syn: KHV-T (for Taiwan)). KHV-TP 30 was isolated from koi in Taiwan and cloned for producing large plaques by Dr. Peiyu Lee, Institute of Medical Biotechnology, Central Taiwan University of Science and Technology, Dakeng, BeiTung District, TaiChung City 406, Taiwan in-2005. The isolate was provided by Dr. Sven M. Bergmann, Friedrich-Loeffler-Institut (FLI), Federal Research Institute for Animal Health, Südufer 10, 17393 Greifswald-Insel Riems, Germany</p> |
| Ampoule VII | <p>SAV 6 * Pancreas Disease Virus, Ireland F104596 GenBank accession numbers: EF675499 (nsp3 gene); EF675547 (E2 gene)</p> <p>*: In the result sheet submitted by the EURL one week after deadline for submission of the PT-2 results the SAV isolate was nominated as SAV1- this is not correct, according to E Fringuelli, H M Rowley, J C Wilson, R Hunter, H Rodger and D A Graham Journal of Fish Diseases 2008, 31, 811–823 doi:10.1111/j.1365-2761.2008.00944.x the correct name is SAV6</p> |
| Ampoule VIII | <p>BF-2, cells Supernatant from NON Infected BF-2 cells</p> |
| Ampoule IX | <p>ISAV, FO/01/01/HPR13. ISAV virus kindly provided by Debes Christiansen, The Faroe Islands Genotype: HPR13 GenBank accession numbers: AJ440970 Cunningham CO et al., 2002 Christiansen et al. J., 2011</p> |

Testing of the test

The PT2 test was prepared and tested according to protocols accredited under DS/EN ISO/IEC 17043. Prior to the distribution we tested 5 ampoules of each virus preparation, by PCR (Bercovier et al. (2005)) and real-time PCR (Gilad et al. (2004)) for KHV, by RT-PCR (Mjaaland et al. (1997)) and real-time RT-PCR (Snow et al. (2006)) for ISAV and by RT-PCR (Fringuelli et al. (2008)) and real-time RT PCR (Hodneland et al. (2006)) for SAV, to ascertain identity and homogeneity of the content in the ampoules (Figure 11). As a result all the standard deviations were below 1 Ct. value. Furthermore, minimum 3 months after lyophilisation and storage in the dark at 4°C, the content of the ampoules were tested to assess their stability (Table 10 and Figure 12).

Conventional PCR/RT-PCR fragments were sequenced and so was the HPR region of the ISAV isolate.

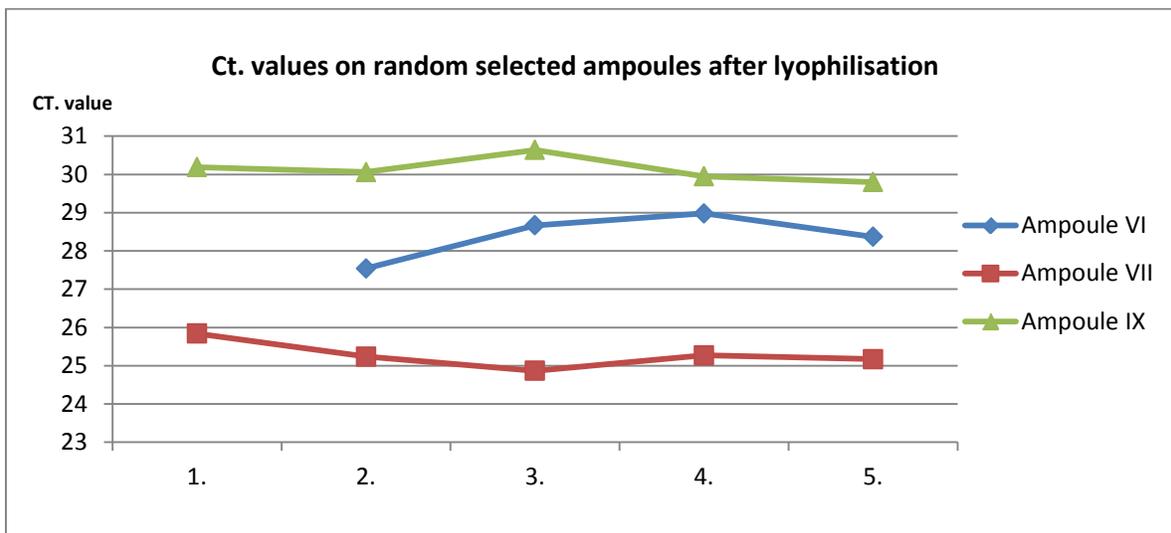


Figure 11, Ampoule VI (CyHV-3), VII (SAV) and IX (ISAV) tested shortly after lyophilisation to assess homogeneity of the content.

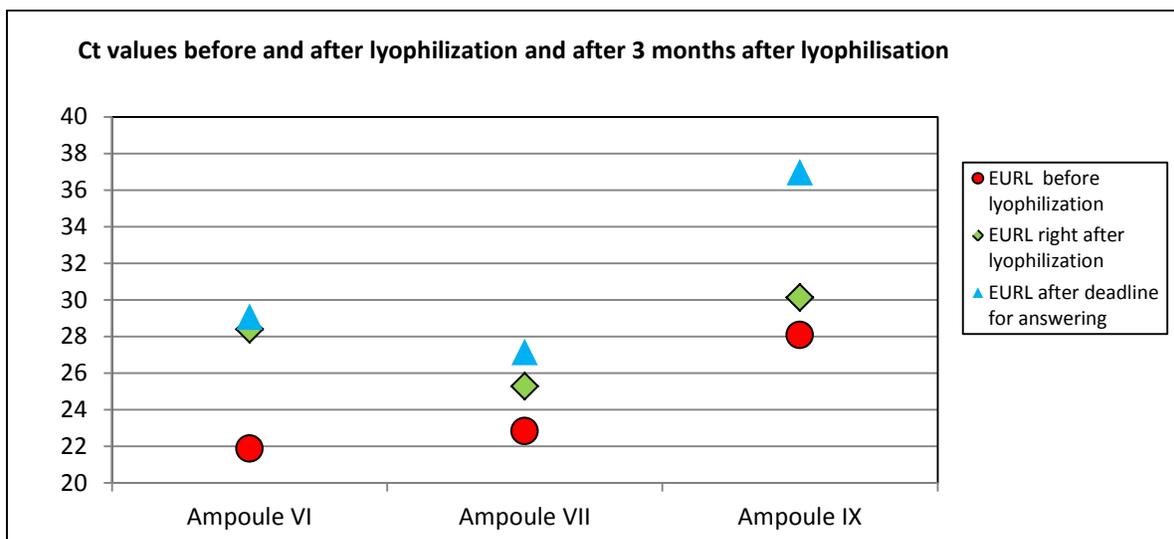


Figure 12, Ampoule VI, VII and IX tested before and after lyophilisation and after deadline for handling in results.

Table 11, Ct-value of ampoules VI, VII and IX tested before and immediately after lyophilisation and after deadline for handling in results.

| Ampoule No. | Content | | EURL Ct. value before lyophilization | EURL Ct. value right after lyophilization | EURL Ct. value after deadline for answering |
|-------------|----------------|---|--------------------------------------|---|---|
| Ampoule VI | KHV | a | 21,87 | 27,54 | 29,08 |
| | | b | | | |
| | | c | | 28,67 | |
| | | d | | 28,98 | |
| | | e | | 28,37 | |
| | Average | | 21,87 | 28,39 | 29,08 |
| Ampoule VII | SAV | a | 22,83 | 25,84 | 27,16 |
| | | b | | 25,24 | |
| | | c | | 24,87 | |
| | | d | | 25,27 | |
| | | e | | 25,17 | |
| | Average | | 22,83 | 25,28 | 27,16 |
| Ampoule IX | ISAV | a | 28,08 | 30,19 | 36,98 |
| | | b | | 30,06 | |
| | | c | | 30,64 | |
| | | d | | 29,95 | |
| | | e | | 29,80 | |
| | Average | | 28,08 | 30,13 | 36,98 |

The lyophilisation procedure caused a significant virus reduction (mainly in ampule VI and IX) as detected by real-time PCR or real-time RT-PCR.

For each ampoule no other pathogens than the expected were detected.

Pathogen identification

In PT2, Participants were asked to identify any of the fish viruses ISAV and KHV (both listed in [Council Directive 2006/88/EC](#)) if present in the ampoules, bearing in mind that the test ampoules also could contain other viruses. Participants were expected to use their normal PCR or real-time PCR methods for detection of KHV and their normal RT-PCR or real-time RT-PCR methods for detection of ISAV. It was not mandatory to grow KHV and ISAV on cell cultures in this test, but the viruses had not been inactivated and should thus be viable. This year the panel of pathogens to be investigated were expanded to include SAV – Salmonid Alpha Virus. Since this is not a listed disease in the European legislation the participation was voluntary and therefore the participants were asked to declare if the ampoules were tested for SAV or not. Regarding methods for detection of SAV the participants were notified that they could refer to the OIE manual chapter 2.3.5b – Infection with Salmonid alpha virus. In order to obtain uniform answers, participants were requested to download a spreadsheet available from the [EURL web page](#), insert results in this and return by email. The results from participating laboratories are shown in table 11.

Table 11. Inter-Laboratory Proficiency Test, PT2, 2015 - Virus identification.

| Laboratory code number | Score | Answer received at EURL | Ampoule VI | Ampoule VII | Ampoule VIII | Ampoule IX |
|------------------------|-------|-------------------------|---------------------------|---------------------------|--|----------------------------|
| | | | KHV (CyHV-3) | SAV | Sterile | ISAV (HPR13) |
| 46 | 8-8 | 09.11.15 | KHV | SAV | Negative | ISAV |
| 45 | 8-8 | 06.11.15 | KHV | SAV | no virus detected | ISAV |
| 44 | 8-8 | 12.11.15 | KHV | no pathogen found | no pathogen found | ISAV |
| 43 ² | | 30.11.15 | 0 | 0 | 0 | 0 |
| 42 ¹ | 6-8 | 13.11.15 | KHV | NO VIRUS | RNA VIRUS, no rhabdo or birna virus | ISAV |
| 41 | 8-8 | 11.11.15 | KHV | SAV | Negative | ISAV |
| 40 ¹ | 8-8 | 13.11.15 | KHV | not KHV nor ISAV | not KHV nor ISAV | ISAV |
| 39 | 6-8 | 11.11.15 | KHV | 0 | 0 | ISAV + KHV |
| 38 | 8-8 | 13.11.15 | KHV | SAV | Not ISAV, not KHV, not SAV | ISAV |
| 37 ¹ | 8-8 | 12.11.15 | KHV | no KHV no ISAV | no KHV no ISAV | ISAV |
| 36 | 8-8 | 13.11.15 | KHV | SAV | No virus detected | ISAV |
| 35 | 8-8 | 12.11.15 | KHV | SAV | no virus | ISAV HPR13 |
| 34 | 8-8 | 26.10.15 | KHV | SAV | negative for all viruses tested | ISAV |
| 33 | 8-8 | 12.11.15 | KHV | SAV | 0 | ISAV |
| 32 | 8-8 | 13.11.15 | KHV | SAV | NO KHV NO ISA NO SAV | ISAV |
| 31 | 8-8 | 13.11.15 | KHV | SAV | NEGATIV | ISAV |
| 30 ³ | 8-8 | 11.11.15 | No virus detected | SAV | No virus detected | ISAV |
| 28 | 8-8 | 13.11.15 | KHV | SAV | Negative | ISAV |
| 27 | 8-8 | 16.11.15 | KHV | SAV | Negative | ISAV |
| 26 | 8-8 | 13.11.15 | KHV | SAV | - | ISAV |
| 25 ¹ | 8-8 | 12.11.15 | KHV | Not KHV, Not ISAV | Not KHV, Not ISAV | ISAV |
| 24 ¹ | 8-8 | 12.11.15 | KHV | Negative for KHV and ISAV | Negative for KHV and ISAV | ISAV |
| 23 | 8-8 | 13.11.15 | KHV | SAV | No KHV ISAV or SAV detected | ISAV |
| 22 | 8-8 | 13.11.15 | KHV viable virus detected | SAV viable virus detected | No viruses detected | ISAV viable virus detected |
| 21 | 8-8 | 10.11.15 | KHV | SAV6 | No virus detected | ISAV |
| 20 | 8-8 | 13.11.15 | KHV | SAV | 0 | ISAV |
| 19 | 8-8 | 13.11.15 | KHV | SAV | No Virus | ISAV |
| 18 | 8-8 | 13.11.15 | KHV | SAV | negativ for KHV, ISAV, SAV | ISAV |
| 17 ¹ | 8-8 | 13.11.15 | KHV | Negative | Negative | ISAV |
| 16 ¹ | 8-8 | 13.11.15 | KHV | Not ISAV Not KHV | Not ISAV Not KHV | ISAV |
| 15 | 8-8 | 10.11.15 | KHV | SAV | Negative | ISA |
| 14 ⁴ | 8-8 | 13.11.15 | KHV | KHV negative | KHV negative | KHV negative |
| 13 | 8-8 | 13.11.15 | KHV | SAV | - | ISAV |
| 12 | 8-8 | 13.11.15 | KHV | SAV | Not detected | ISAV |
| 11 | 8-8 | 12.11.15 | KHV | SAV | negative | ISAV |
| 10 ¹ | 8-8 | 12.11.15 | KHV | Negative | Negative | ISAV |
| 9 | 8-8 | 12.11.15 | KHV | SAV | Not virus detected | ISAV HPR-deleted |
| 8 | 8-8 | 13.11.15 | KHV | SAV | Negativ | ISAV |
| 7 | 4-8 | 10.11.15 | KHV | no ISAV, SAV or KHV | SAV | ISA |
| 6 | 8-8 | 12.11.15 | KHV | SAV | Negative | ISAV |
| 5 | 8-8 | 13.11.15 | KHV | SAV | Virus was not detected. | ISAV |
| 4 | 8-8 | 13.11.15 | KHV + | Alphavirus + | Negative (for ISAV/SAV and cyprinid herpes virus inc. KHV) | ISAV + |
| 3 | 8-8 | 06.11.15 | KHV | SAV | Negative | ISAV |
| 2 | 8-8 | 13.11.15 | KHV | SAV | negative | ISAV |
| 1 | 8-8 | 12.11.15 | KHV | SAV | not ISAV, KHV, SAV | ISAV |

¹Did not test for SAV, ² Did not participate in PT2, ³ Did not test for KHV, ⁴ Did only test for KHV

All laboratories were encouraged to sequence the HPR region of ISAV isolates. However, this was not a mandatory task.

It was requested that the pathogens in the samples were not forwarded to third parts without having contacted the EURL for permission in advance.

Identification of content

- 44 laboratories submitted results
- 31 laboratories correctly identified all four ampoules
- 42 laboratories tested for both two listed pathogens
- 43 laboratories tested for ISAV
- 43 laboratories tested for KHV
- 33 laboratories tested for SAV
- 1 laboratory tested for KHV only
- 1 laboratory that did participate in PT 1 did not participate in PT2

Ampoule VI – KHV

- 43 laboratories correctly identified KHV
- 1 laboratory did not examine for KHV

Ampoule VII – SAV

- 32 laboratories correctly identified SAV
- 11 laboratories did not examined for SAV

Ampoule VIII – BF2 cell supernatant

- 42 laboratories correctly identified 'Not KHV or ISAV'
- 2 laboratory found a virus

Ampoule IX – ISAV

- 42 laboratories correctly identified only ISAV
- 1 laboratories identified ISAV and KHV

Scores

We have assigned a score of 2 for each correct answer (Table 11), giving the possibility for obtaining a maximum score of 8. Incorrectly finding of pathogens not present in the ampoules gives the score 0.

Of the 44 laboratories submitting results 41 laboratories obtained maximum score. The laboratories (there did not test for all viruses) obtained maximum score if they did not find the viruses they tested for in other ampoules than where the virus actual were present. E.g. one laboratory examined for KHV only and found KHV in ampoule VI and 'not KHV' in VII, VIII and IX, this laboratory obtained the score 8 out of 8 possible.

Genotyping of ISAV HPR region and submission of sequencing results was not a mandatory part of the test and is not included in the score of participants.

Methods applied

The following methods were used by the participants:

- 33 laboratories used KHV PCR, among these approx. 21 used the protocol provided by Bercovier et al 2005.
- 26 laboratories used KHV Real-time PCR among these approx. 21 used the protocol from Gilad et al 2004.
- 16 laboratories used both KHV real-time PCR and KHV PCR.

- 25 laboratories used SAV RT-PCR among these approx. 17 used the protocol from Fringuelli et al. 2008.
- 18 laboratories used SAV real-time RT-PCR among these approx. 13 used the protocol from Hodneland et al. 2006.
- 8 laboratories used both SAV real-time RT-PCR and SAV RT-PCR.

- 33 laboratories used ISAV RT-PCR among these the two most used protocols were the ones from Mjaaland et al 2002 and OIE Manual for diagnostic tests for aquatic animals 2009.
- 24 laboratories used ISAV real-time RT-PCR among these approx. 18 used the protocol from Snow et al., 2006.
- 14 laboratories used both ISAV real-time RT-PCR and ISAV RT-PCR

Genotyping and sequencing

Participants were encouraged to sequence the HPR region of possible ISAV isolates though it was not a mandatory task.

- 22 laboratories performed sequencing for KHV
- 33 laboratories performed sequencing for SAV
- 27 laboratories performed sequencing for ISAV

AMPOULE VI KHV:

22 laboratories sequenced the KHV isolate included in Ampoule VI

- 15 laboratories sequenced the Thimidine kinase region using primer sets described in Bercovier et al.2005
- 2 laboratory used primer sets according described in Engelsma et al.,2013
- 1 laboratory provided primer set without describing the protocol
- 1 laboratory did not provide primer sets nor protocol
- 1 laboratory sequenced the sphl gene using primersets described in Gray et al. 2002
- 2 laboratories sequenced the polymerase gene using primersets described in protocol by Stone and Way from CEFAS 2010

AMPOULE VII SAV:

33 laboratories participated in testing ampoules for SAV, which was included in PT2 2015 on a volunteer basis.

Of these, 20 laboratories sequenced the SAV isolate included in Ampoule VII.

- 13 laboratories sequenced the E2 and nsP3 gene using primer sets described in Fringuelli et al., 2008
- 4 laboratories sequenced the E2 region according to Hodneland et al., 2006
- 1 laboratory targeted the RNA polymerase without specifying the protocol
- 2 laboratories provided primersets without reporting the protocol

AMPOULE IX ISAV:

27 laboratories sequenced the ISAV isolate included in Ampoule IX

- 12 laboratories targeted the HPR region using primersets described in Mjaaland et al., 2002
- 1 laboratory targeted the HPR region using primer set described in Cunningham et al., 2002
- 4 laboratories sequenced the partial HA gene according to Kibenge et al., 2009
- 1 laboratory sequenced the HA region according to McBeath et al., 2009
- 3 laboratories sequenced the region using primerset by Christiansen et al. 2011
- 6 laboratories used in house developed primersets protocols

Concluding remarks PT2

This was the first time that the EURL provided a proficiency test on SAV identification. Considering that 33 laboratories participated (of which 32 correctly identified SAV in ampoule VII) this was regarded as a proper initiative that strengthen the diagnostic capacities of the NRLs in detecting emerging pathogens, and it will be included in the coming years as well.

All 43 laboratories testing for KHV identified the virus in ampoule VI.

Out of the 33 laboratories that tested for SAV 32 laboratories identified SAV in ampoule VII.

Out of 44 laboratories 42 laboratories identified Not *KHV* or ISAV in ampoule VIII and there were "only" two false positive.

All 43 laboratories testing for ISAV identified the virus in ampoule IX, though one laboratory also wrongly identified KHV in ampoule IX.

It is an appreciated matter of fact that many laboratories are putting efforts in performing genetic characterization of the isolates through sequence analysis, as it is important that laboratories can discriminate between isolates as e.g. pathogenic ISAV strains with deletions in the HPR region and HPR0 strains, especially after the delisting of ISAV HPR0 (Commission Implementing Directive 2014/22/EU).

Of the 27 laboratories sequencing the ISAV virus all found that the isolate was with deletion in segment 6 and thus not belong to HPR0.

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 20th Annual Workshop of National Reference Laboratories for Fish Diseases to be held 31th of May-1st of June 2016 in Copenhagen, Denmark.

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European Union Reference laboratory for Fish diseases

National Veterinary Institute, Technical University of Denmark, February 2016

References

1. Baudin Laurencin F (1987) IHN in France. *Bulletin of the European Association of Fish Pathologists* 7, 104.
2. Bercovier H., Fishman Y., Nahari R., Sharon S., Zlotkin A., Eyngor M., Gilad O., Eldar A. and Hedrick R. P. 2005 Cloning of the koi herpesvirus (KHV) gene encoding thymidine kinase and its use for a highly sensitive PCR based diagnosis *BMC Microbiology* 2005, 5:13
3. Bigarre L, Cabon J, Baud M, Pozet F, Castric J (2008) Ranaviruses associated with high mortalities in catfish in France. *Bull Eur Assoc Fish Pathol* 28: 163-168
4. Bovo G., Comuzi M., DeMas S., Ceschia G., Giorgetti G., Giacometti P., Cappelozza E. (1993) Isolamento di un agente virale irido-like da pesce gatto (*Ictalurus melas*) d'allevamento. *Boll Soc Ital Patol Ittica* 11:3-10
5. Campbell S., Collet B., Einer-Jensen K., Secombes C. J., M. Snow Identifying potential virulence determinants in viral haemorrhagic septicaemia virus (VHSV) for rainbow trout *Diseases of Aquatic Organisms* Vol. 86: 205–212, 2009 doi: 10.3354/dao02127
6. Christiansen DH, Østergaard PS, Snow M, Dale OB, Falk K. A low-pathogenic variant of infectious salmon anemia virus (ISAV-HPRO) is highly prevalent and causes a non-clinical transient infection in farmed Atlantic salmon (*Salmo salar* L.) in the Faroe Islands. *J Gen Virol.* 2011;92:909–918. doi: 10.1099/vir.0.027094-0
7. COMMISSION IMPLEMENTING DECISION (EU) 2015/1554 of 11 September 2015 laying down rules for the application of Directive 2006/88/EC as regards requirements for surveillance and diagnostic methods
8. Commission Implementing Directive 2014/22/EU of 13 February 2014 amending Annex IV to Council Directive 2006/88/EC as regards infectious salmon anaemia (ISA) Text with EEA relevance
9. Council Directive 2006/88/EC of 24 October 2006 on animal health requirements for aquaculture animals and products thereof, and on the prevention and control of certain diseases in aquatic animals
10. Cunningham CO, Gregory A, Black J, Simpson I, Raynard RS (2002) A novel variant of the infectious salmon anaemia virus (ISAV) haemagglutinin gene suggests mechanisms for virus diversity. *Bull Eur Assoc Fish Pathol* 22(6):366–374
11. Einer-Jensen K, Ahrens P, Forsberg R & Lorenzen N (2004). Evolution of the fish rhabdovirus viral haemorrhagic septicaemia virus. *Journal of General Virology* 85, 1167-1179.
12. Emmenegger E. J, Meyers T. R., Burton T. O., Kurath G. Genetic diversity and epidemiology of infectious hematopoietic necrosis virus in Alaska. *Dis Aquat Organ.* 2000 Apr 20;40(3):163-76
13. Engelsma M. Y., Way K., Dodge M. J., Voorbergen-Laarman M., Panzarin Valentina, Abbadi Miriam, El-Matbouli M., Stone D. M., Skall H. F., Kahns S., Detection of novel strains of cyprinid herpesvirus closely related to koi herpesvirus *Diseases of Aquatic Organisms* — 2013, Volume 107, Issue 2, pp. 113-120
14. Fringuelli, E., Rowley, H. M., Wilson, J. C., Hunter, R., Rodger, H. and Graham, D. A. (2008), Phylogenetic analyses and molecular epidemiology of European salmonid alphaviruses (SAV) based on partial E2 and nsP3 gene nucleotide sequences. *Journal of Fish Diseases*, 31: 811–823. doi: 10.1111/j.1365-2761.2008.00944.x
15. Gilad O, Yun S, Andree KB, Adkison MA, Way K, Willits NH, Bercovier H, Hedrick RP: Molecular comparison of isolates of an emerging fish pathogen, the koi herpesvirus, and the effect of water temperature on mortality of experimentally infected koi. *J Gen Virol* 2003, 84:1-8
16. Gray, W. L., Mullis, L., LaPatra, S. E., Groff, J. M. and Goodwin, A. (2002), Detection of koi herpesvirus DNA in tissues of infected fish. *Journal of Fish Diseases*, 25: 171–178. doi: 10.1046/j.1365-2761.2002.00355.x

17. Hattenberger-Baudouy AM, Danton M, Merle G, Torchy C, de Kinkelin P (1989) Serological evidence of infectious haematopoietic necrosis in rainbow trout from a French outbreak of disease. *Journal of Aquatic Animal Health* 1, 126-134.
18. Hedrick RP, Batts WN, Yun S, Traxler GS, Kaufman J, Winton JR (2003) Host and geographic range extensions of the North American strain of viral hemorrhagic septicemia virus. *Dis Aquat Org* 55:211–220
19. Hodneland K. & Endresen C. (2006). Sensitive and specific detection of salmonid alphavirus using real-time PCR (TaqMan). *J. Virol. Methods*, 131, 184–192.
20. Holopainen R., Ohlemeyer S., Schütze H., Bergmann S.M. & Tapiovaara H. (2009). Ranavirus phylogeny and differentiation based on major capsid protein, DNA polymerase and neurofilament triplet H1-like protein genes. *Dis. Aquat. Org.*, 85, 81–91.
21. Hyatt AD, Gould AR, Zupanovic Z, Cunningham AA, Hengstberger S, Whittington RJ, Kattenbelt J & Coupar BEH (2000) Comparative studies of piscine and amphibian iridoviruses. *Archives of Virology* 145, 301-331.
22. Kibenge, F. S., Godoy, M. G., Wang, Y., Kibenge, M. J., Gherardelli, V., Mansilla, S., Lisperger, A., Jarpa, M., Larroquete, G. & other authors (2009). Infectious salmon anaemia virus (ISAV) isolated from the ISA disease outbreaks in Chile diverged from ISAV isolates from Norway around 1996 and was disseminated around 2005, based on surface glycoprotein gene sequences. *Virology* 396, 88.
23. Jonstrup S P, Kahns S, Skall H F, Boutrup T S and Olesen N J * 2012 Development and validation of a novel Taqman-based real-time RT-PCR assay suitable for demonstrating freedom from viral haemorrhagic septicemia virus Volume 36, Issue 1, pages 9–23, January 2013
24. Jørgensen, P. E. V., Olesen, N. J., Ahne, W., Lorenzen, N. (1989) SVCV and PFR viruses: Serological examination of 22 strains indicates close relationship between the two rhabdoviruses. In Ahne, W., and Kurstak, E. (eds.): *Viruses of lower vertebrates*. 349- 366. Springer Verlag, Berlin, Heidelberg
25. Kolodziejek J, Schachner O, Dürrwald R, Latif M, Nowotny N (2008) “Mid-G” region sequences of the glycoprotein gene of Austrian infectious hematopoietic necrosis virus isolates form two lineages within European isolates and are distinct from American and Asian lineages. *J Clin Microbiol* 46:22–30
26. Koutna M., Vesely T., Psikal I., Hulova J.: Identification of spring viraemia of carp virus (SVCV) by combined RT-PCR and nested PCR. *Dis. Of Aquatic Org.* 55, 229-235 (2003).
27. Kurath G., Garver K. A., Troyer R. M., Emmenegger E. J., Einer-Jensen K. and Anderson E. D. (2003), Phylogeography of infectious haematopoietic necrosis virus in North America *Journal of General Virology* (2003), 84, 803–814
28. Marsh IB, Whittington RJ, O'Rourke B, Hyatt AD & Chisholm O (2002) Rapid differentiation of Australian, European and American ranaviruses based on variation in major capsid protein gene sequence. *Molecular and Cellular Probes* 16, 137-151.
29. McBeath AJA, Bain N, Snow M, 2009. Surveillance for infectious salmon anaemia virus HPR0 in marine Atlantic salmon farms across Scotland. *Diseases of Aquatic Organisms*, 87, 161–169.
30. Miller TA, Rapp J, Wastlhuber U, Hoffmann RW, Enzmann PJ (1998) Rapid and sensitive reverse transcriptase-polymerase chain reaction based detection and differential diagnosis of fish pathogenic rhabdoviruses in organ samples and cultured cells. *Dis Aquat Org* 34:13–20

31. Mjaaland S., Hungnes O., Teig A., Dannevig, B. H., Thorud K., Rimstad E. Polymorphism in the Infectious Salmon Anemia Virus Hemagglutinin Gene: Importance and Possible Implications for Evolution and Ecology of Infectious Salmon Anemia Disease *Virology* Volume 304, Issue 2, 20 December 2002, Pages 379–391
32. Ohlemeyer, S., Holopainen, R., Tapiovaara, H., Bergmann, S.M., & Schütze, H. 2011. Major capsid protein gene sequence analysis of the Santee-Cooper ranaviruses DFV, GV6, and LMBV. *Dis Aquat Org.* 96:195-207.
33. OIE Manual of Diagnostic Tests for Aquatic Animals 2015
34. Olesen, N. J., Lorenzen, N. & LaPatra, S. (1999). Production of neutralizing antisera against viral haemorrhagic septicaemia (VHS) virus by intravenous injections of rabbits. *J Aquat Anim Health* 11, 10–16.
35. Olesen, N.J., N. Lorenzen & P.E.V. Jørgensen (1993) Serological differences among isolates of viral haemorrhagic septicaemia virus detected by neutralizing monoclonal and polyclonal antibodies. *Dis. Aquat. Org.* 16, 163-170.
36. Purcell M. K., Thompson R. L., Garver K. A., Hawley L. M., Batts W. N., Sprague L., Sampson C., Winton J. R., Universal reverse-transcriptase real-time PCR for infectious hematopoietic necrosis virus (IHNV) *Dis Aquat Org* Vol. 106: 103–115, 2013 doi: 10.3354/dao02644
37. Raja-Halli, M., Vehmas, T.K., Rimaila-Pärnänen, E., Sainmaa, S., Skall, H.F., Olesen, N.J., Tapiovaara, H., 2006. Viral haemorrhagic septicaemia (VHS) outbreaks in Finnish rainbow trout farms. *Dis. Aqua. Organ.* 72, 201-211
38. Mjaaland S., Rimstad E., Falk K, and Dannevig B. H. 1997 Genomic Characterization of the Virus Causing Infectious Salmon Anemia in Atlantic Salmon (*Salmo salar* L.): an Orthomyxo-Like Virus in a Teleost *JOURNAL OF VIROLOGY*, Oct. 1997, p. 7681–768
39. Snow M., Bain N., Black J., Taupin V., Cunningham C. O., King J. a., Skall H. F., Raynard R. S. Genetic population structure of marine viral haemorrhagic septicaemia virus (VHSV)[†] *DAO* 61:11-21 (2004)doi:10.3354/dao061011
40. Stone D.M., Ahne W., Denham K.L., Dixon P.F., Liu C-T.Y., Sheppard A.M., Taylor G.R. & Way K. (2003). Nucleotide sequence analysis of the glycoprotein gene of putative spring viraemia of carp virus and pike fry rhabdovirus isolates reveals four genogroups. *Diseases of Aquatic Organisms* 53, 203-210.
41. Williams K., Blake S., Sweeney A., Singer J., Nicholson B.L., 1999. Multiples reverse transcriptase PCR assay for simultaneous detection of three fish viruses. *J. Clin. Microbiol.* 37, 4139–4141.