European Union Reference Laboratory for Fish and Crustacean Diseases
NATIONAL INSTITUTE OF AQUATIC RESOURCES, TECHNICAL UNIVERSITY OF DENMARK

Report of the

17th Annual Workshop of the National Reference Laboratories for Crustacean Diseases

Kgs. Lyngby, Denmark

May 28th 2026

Organized by the European Union Reference Laboratory for Fish and Crustacean Diseases, National Institute of Aquatic Resources, Technical University of Denmark, Kgs. Lyngby

Contents

Introduction and short summary

The 17th Annual Workshop of the National Reference Laboratories for Crustacean Diseases was held on 28th of May 2026. There were 67 participants attending the workshop in person, representing 34 countries.

The workshop was held back-to-back with the 30th Annual Workshop for National Reference Laboratories for Fish Diseases and a special session for NRLs in EU and EEA on the implementation of the Animal Health Law.
The workshop was opened with "Welcome and announcements" by section leader for fish and shellfish diseases at DTU Aqua, Britt Bang Jensen. The first session entitled "Update on EU listed crustacean diseases and their control" started with Coordinator of the EURL for Crustacean Diseases Shyam Kokkattunivarthil Uthaman giving an update on the disease and surveillance situation of crustacean diseases in EU countries based on the results obtained from the Survey and Diagnosis questionnaire. This was followed by a talk from NRL of the Netherlands Janneke Allart on investigations of mortality event associated with *V.harveyi* in a shrimp held in a research facility.

The second session had the title: "Results from ongoing research on crustacean diseases". *Mostafa Rakhshani* from Guent University gave an update on a new media for cultivating shrimp cell lines and virological examinations. Later on, two contributions from University of Bern were given. First Julius Hermanns provided an overview of the validation of three molecular assays for the detection of *A.astaci*, then Eliane Jemmi described the results of in vivo challenge trials with Crayfish plague where sex determined differences in the susceptibility.
After a coffee break, Tin Škugor from Croatia provided insights into model which combines host, pathogen and climate change to investigate spread of *A.astaci* in future.
The session was finished with a presentation from Valentina Paolini from the Italian NRL, which presented characterization of *A.astaci* strains in white-clawed crayfish.

Session III had the title "Update from the EURL for Crustacean Diseases" and started with the coordinator for EURL for crustacean diseases *Shyam K Uthaman*, who gave a talk on the participation and expected results of the interlaboratory proficiency tests for crustacean diseases in 2026. Finally, Head of EURL for fish and crustacean diseases Niccoló Vendramin presented the EURL activities in 2025 and plans for 2026.

Lone Madsen and Anna Luisa Farias Alencar from DTU Aqua took minutes from the meeting, and Niccoló Vendramin assembled the report.

We would once again like to thank all the presenters for their great contributions, without them the meeting would not have been a success. The workshop was organized by Niccoló Vendramin and Shyam K Uthaman, with the help from the rest of the fish and shellfish diseases section at the National Institute of Aquatic Resources, DTU Aqua. The meeting next year is planned to be held in person at the end of May 2027.

We wish to thank all of you for participating and we are looking forward to seeing you next year.

Niccoló Vendramin and Shyam Uthaman

Programme

Thursday May 28th
Annual Workshop of the National Reference Laboratories for Crustacean Diseases

9.30 – 9:40	Welcome and announcement *Britt Bang Jensen, DTU, Denmark*

SESSION I: Update on EU listed crustacean diseases and their control

Chair: Britt Bang Jensen and Minutes: Anna Luiza Farias Alencar

09:40 – 10:00	Survey and diagnosis of shrimp production and diseases in Europe 2025 *Shyam K Uthaman, DTU, Denmark*
10:00 – 10:20	Case study of *Vibrio harvey* infection in penaeid shrimp in a research facility *Jannekke Allaart, WUR - The Netherlands*

SESSION II: Results from ongoing research on crustacean diseases

Chair: Shyam K Uthaman and Minutes: Lone Madsen

10:20 – 10:40	A new shrimp medium and DNA and RNA transfections in primary shrimp cell line *Mostafa Rakhshani Nejad, Ghent University, Belgium*
10:40 – 11:00	Comparison of three published PCR assays for *Aphanomyces astaci* detection to determine diagnostic sensitivity and specificity, as well as limit of blank (LoB) and limit of detection (LoD) *Julius Hermannns, UNIBE, Switzerland*
11:00 – 11:20	Unexpected sex differences in crayfish plague disease susceptibility *Eliane Jemmi, UNIBE, Switzerland*
11:20 – 11:40	**Coffee Break**
11:40 – 12:00	Host-pathogen dynamics under climate change: Uncovering the potential distribution of crayfish and the crayfish plague pathogen *Aphanomyces astaci* using Species Distribution Modelling *Tin Škugor, PBF, Croatia*
12:00 – 12:20	Development on the genetic characterization of *Aphanomyces astaci* from Italian crayfish plague outbreaks in white-clawed crayfish *Valentina Paolini, IZSVe, Italy*

SESSION III: Update from the EURL for crustacean diseases

12:20 – 12:40	EURL proficiency test for crustacean diseases 2026 *Shyam K Uthaman, DTU, Denmark*
12:40 – 13:00	EURL Work done in 2025 and ideas and plans for 2026 *Niccoló Vendramin, DTU, Denmark*

Next meeting and end of 17th Annual Workshop

End of Crustacean workshop

SESSION I: Update on EU listed crustacean diseases and their control

Chair: Britt Bang Jensen

Surveillance and diagnostics of crustacean diseases in Europe 2025

Shyam K Uthaman, Niccolò Vendramin and Thomas Weise

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Abstract

As part of being the EURL for crustacean diseases, we see it as our obligation to collect and disseminate data on the disease situation for crustacean production in Europe. To that end we send out an inquiry to all European NRLs for crustacean diseases to:

1) Report the number of farms belonging to each health status according to COMMISSION DELEGATED REGULATION (EU) 2020/689.

2) Report any outbreaks in the country of EU listed crustacean diseases, as well as health problems related to other crustacean diseases.

3) Report the number of samples tested for WOAH listed crustacean diseases and how many of these gave a positive result.

4) Describe the current status of crustacean aquaculture in the country, as well as the strategy used for surveillance of crustacean diseases.

Data from 17 countries have so far been obtained and will be compared to the data received for since 2019.
An overview of health situation of crustacean farmed in Europe and trends will be discussed.

White muscle tissue and increased mortality in *L. vannamei*

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Abstract

Shrimps were sent from a research facility in the Netherlands two weeks after arrival of the animals at the facility. The shrimps showed a white discoloration of the muscle tissue and an increased mortality (10%). The symptoms can be caused by several pathogens like *Vibrio harveyi*, *Photobacterium damselae*, infectious myonecrosis virus and *Penaeus vannamei* nodavirus. The shrimps were necropsied and a bacterial culture was initiated. Both *V. harveyi* and *P. damselae* were cultured from the shrimps. The bacteria were also cultured from healthy animals and from post-larvae. An antibiogram was performed and both *V. harveyi* and *P. damselae* seemed to be sensitive to tetracyclin, flumequine and florfenicol. A treatment with oxytetracycline was performed, based on earlier experience with a *V. harveyi* outbreak in fish. After the treatment, no *V. harveyi* or *P. damselae* was cultured from shrimps from the different aquariums. Also the new stock of post-larvae was negative for *V. harveyi* or *P. damselae.* This case is an example of a clear diagnosis and a sufficient antibiotic treatment of *L. vannamei* shrimps.

SESSION II: Results from ongoing research on crustacean diseases

Chair: *Shyam K Uthaman*

A New Shrimp Cell Culture Medium and DNA/RNA Transfection in Primary Shrimp Cells

Mostafa Rakhshaninejad, Liping Zheng, Hans Nauwynck

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Abstract

The lack of continuous shrimp cell lines remains one of the major limitations in shrimp health research, disease studies, and aquaculture biotechnology. Reliable *in vitro* systems are needed to study host-pathogen interactions, immune responses, viral replication, and cellular mechanisms under controlled laboratory conditions. This work addresses this bottleneck through two complementary approaches: the development of an improved crustacean cell culture medium and the optimization of DNA and RNA transfection methods in primary shrimp cells.

First, a new culture medium was developed to better support the growth and maintenance of crustacean cells. The medium was optimized for key culture requirements, including ionic balance, osmotic conditions, nutrient composition, amino acids, vitamins, and energy sources. Using primary shrimp lymphoid organ cultures, the medium supported cell attachment, monolayer formation, cell survival, and improved culture performance over time. These improvements provide a stronger foundation for maintaining shrimp cells *in vitro* and for performing downstream experimental manipulations.

Second, genetic delivery strategies were evaluated to enhance the proliferative potential of primary shrimp lymphoid organ cells. Telomerase reverse transcriptase was identified in *Penaeus vannamei*, and conserved functional domains were confirmed. Its expression declined during cultivation, suggesting a relationship with cellular senescence. DNA transfection was improved by testing different promoters, with the shrimp elongation factor 1 alpha promoter showing the best performance. However, DNA-based expression remained limited and did not significantly improve cell culture parameters. In contrast, mRNA-based delivery was much more efficient. Non-replicating mRNA reached 14% transfection efficiency at 72 hours, while self-replicating mRNA reached 20% at 7 days after transfection. Importantly, both mRNA approaches significantly increased cell number and mitotic activity in primary shrimp cells.

Together, these findings show that improved culture conditions combined with efficient RNA-based transfection can enhance the growth potential of primary shrimp cells. This work represents an important step toward more reliable shrimp cell culture platforms and provides a basis for future development of continuous crustacean cell lines for aquaculture research and disease control.

Q : Have you tried infection studies with e.g. WSSV to see if the transfected cells support higher division and propagation of cells compared to non-transfected cells?

A: not in this case – but normally the lab has done a thing like that in other cases

Q: Have you tried cultivating other cells in the medium? E.g. muscle cells or others?

A: Tried lymphoid cells and ovary cells – not any others. Have tried the nephro-complex (???). Also tried other medium but not successful

Q: Have you tested cells from other crustaceans besides shrimp on this Hanamora medium?

A: Not on this medium but in the past tried culturing lobsters??? (I did not get his answer to this).

Comparison of three published PCR assays for *Aphanomyces astaci* detection to determine diagnostic sensitivity and specificity, as well as limit of blank (LoB) and limit of detection (LoD)

Julius Hermanns[1], Eliane Jemmi[1], Nicolas Diserens[1], Ramona Lüthi[1], Simone Roberto Rolando Pisano[1], Ana Bielen[2], Heike Schmidt-Posthaus[1], Gary Delalay[1]

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Abstract

Aphanomyces astaci, the pathogen responsible for crayfish plague, has caused the decline and extinction of native crayfish populations in Europe. Crayfish plague is notifiable in Switzerland and listed by the World Organisation for Animal Health.

Although various molecular methods have been developed to diagnose the presence of *A. astaci* in crayfish tissue, no gold standard is available yet, and a comprehensive comparison of the suitability of the different methods for diagnostic purposes is lacking. To fill this gap, we first calculated the limit of blank (LoB) and the limit of detection (LoD) of two available qPCR assays (Vrålstad et al. 2009, modified by Strand et al. 2013, and Strand et al. 2023). LoB was estimated using 96 samples of *A. astacus* negative for *A. astaci* with three replicates per sample. LoD was estimated according to Klymus et al. (2020) using artificial gene fragments (gBlocks^{TM}) in two-fold dilution series with 24 replicates each. Additionally, we determined the diagnostic sensitivity and specificity of both qPCR assays and of a conventional PCR from Oidtmann et al. 2006 using Bayesian latent class modelling (BLCM) on crayfish from two populations (n = 40 and n = 96, respectively) with differing *A. astaci* prevalence. For each assay, triplicates were analysed for each sample. The BLCM by Pereira Da Silva et al. (2017) was computed in R using JAGS and accounted for replicate-level data and dependency between tests.

LoB was calculated as 0 copies/reaction for the Strand assay and 0.639 copies/reaction for the modified Vrålstad assay. LoD for the Strand assay was calculated with 2.3 copies/reaction and 3.7 copies/reaction for the modified Vrålstad assay. Both qPCR assays showed a much higher estimated diagnostic sensitivity (~80%) than the PCR by Oidtmann (~55%). The assays by Strand and Oidtmann showed a higher estimated specificity (~97%) than the assay by Vrålstad (~94%).

Based on our results, we would recommend the use of the qPCR assay by Strand for diagnostic purposes.

Q: How does it affect the results that this was done on two different crayfish species (noble crayfish and signal crayfish)? Primarily because the probability of being infected is different in those two species

A: Limitations on how many populations that could be chosen between. Signal crayfish was the largest one. Need to know how PCRs behave to low pathogen loads when it comes to surveillance. Therefore, it is good to have something in between (neither very low nor very high)

Q: Have you tried any of the tested assays on the digital PCR?

A: This is pending – but as long as it is not known if there are no known false negative/positive results, it is hard to do this

Unexpected sex differences in crayfish plague disease susceptibility

Eliane Jemmi[1], Ana Bielen[2], Sandra Hudina[2], Simone Roberto Rolando Pisano[1] & Heike Schmidt-Posthaus[1]

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Abstract

Crayfish plague, caused by the oomycete *Aphanomyces astaci*, is one of the major drivers of native European crayfish decline and poses a major threat to *Astacus astacus* populations. Host-pathogen interactions in freshwater ecosystems are strongly influenced by environmental conditions, particularly temperature, which affects both host immune responses and pathogen virulence. As part of a larger study investigating the effects of different temperature regimes on crayfish plague dynamics, a pilot infection trial was conducted to establish suitable infection conditions and evaluate host responses under controlled laboratory conditions.

A total of 60 juvenile *Astacus astacus* (6 females and 4 males per treatment group) were individually maintained at 18°C and experimentally infected with five *Aphanomyces astaci* zoospore concentrations ranging from 0 to 3000 spores/ml. Mortality was monitored daily over a 21-day period, and infection load was assessed using qPCR. Female crayfish showed markedly earlier and higher mortality compared to males. In females, cumulative mortality reached 100% within 8-10 days post-infection at several infection doses, whereas mortality in males did not exceed 50% and generally occurred later in the experiment. In addition, Ct values were positively associated with time to death for several infection doses, suggesting that individuals surviving longer generally exhibited lower pathogen burdens over the course of infection.

The pronounced sex-related differences observed in the pilot trial were not reproduced in the subsequent large-scale infection experiment involving > 200 crayfish exposed to 500 spores/ml under four different temperature regimes. The observed pattern may therefore reflect batch effects or variability among experimental groups, although potential sex-dependent differences in susceptibility cannot be excluded, particularly under different infection doses. Sex-biased infection outcomes have been described across a wide range of host-pathogen systems, with susceptibility differing between sexes depending on species, pathogen type, reproductive investment, and environmental conditions.

Despite its limited scale, the pilot study revealed clear dose-dependent mortality dynamics and highlighted the importance of accounting for potential sex-related variation in host responses. Accordingly, the ongoing large-scale experiment includes sex-specific analyses together with investigations of immune- and stress-related gene expression under different temperature regimes to examine how temperature-dependent host immune responses may contribute to variation in susceptibility to *Aphanomyces astaci* infection.

Q: how do you inoculate the crayfish with the pathogen?

A: produce spores in the lab, count them and add spores to the water, wait one week and then change the water (this means a one-week challenge with a known amount of spores in the water).

Q: Any specific organ sensitivity to this pathogen?

A: Soft tissues are sensitive – therefore pleopods etc will be used for testing. Lesions and soft tissues are good entry points for Aphanomyces.

Q: Have you considered doing histopathology on the reproductive organs?

A: Have not taken samples for histology. Think it is an interesting thought. Will consider this in future samplings/experiments.

Host-pathogen dynamics under climate change: Uncovering the potential distribution of crayfish and the crayfish plague pathogen *Aphanomyces astaci* using Species Distribution Modelling

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Abstract

Crayfish plague, caused by the oomycete *Aphanomyces astaci* Schikora, 1906, represents one of the most important causes of decline of native crayfish populations in Europe. Ongoing climate change is expected to significantly affect freshwater crayfish worldwide via distribution shifts of both indigenous (ICS) and non-indigenous (NICS) crayfish species. However, the role of climate change in shaping the future distribution and spread of *A. astaci* remains unknown. Therefore, we have applied species distribution modelling (SDM) to assess the potential current and future habitat suitability of *A. astaci* and its crayfish hosts in Croatia (four ICS and two NICS). First, input presence data for both the hosts and the pathogen were compiled. Distribution data for different ICS and NICS in Croatia have been assembled by combining historical and recent occurrence records. For the pathogen, we have performed *A. astaci*-specific qPCR-based detections in ethanol-preserved crayfish specimens collected between 1998 and 2025 across Croatia, and combined the obtained data with literature records, yielding in total of 112 *A. astaci*-positive localities. Next, we modelled the current and future potential distribution of the hosts and pathogen using 13 environmental predictors and the maximum entropy (MaxEnt) approach. Future projections were based on Shared Socioeconomic Pathways (SSP) scenarios for the 2100 period and four different General Circulation Models (GCMs). Environmental niche occupied by *A. astaci* (visualised with PCA based on the environmental variables) overlapped with and encompassed the combined environmental range of all analysed host species. Suitable habitats for both ICS and NICS were projected to decrease and shift north-northwest under future climatic conditions, in line with their current overall adaptation to temperate climatic regimes. Future climatic suitability for *A. astaci* decreased less than suitability for individual host species, although its distribution was also predicted to shift north-northwest, following the potential future distribution of hosts. Overall, our results suggest that climate change alone is unlikely to promote further spread of NICS or crayfish plague, at least among hosts that are adapted to temperate climate as those analysed in our study. Finally, while our models focused on temperate species currently present in Croatia, it would be beneficial to also analyse the environmental niche of thermotolerant hosts and their associate *A. astaci* lineages since they might pose higher climate driven risks. Notably, *Procambarus clarkii*, a thermotolerant NICS, is expanding its range across Europe, with recent reports from neighboring Slovenia.

Q: Where the host is, the pathogen is present according to Tin – can the pathogen be there without the host being there – any chance for this?

A: The pathogen can only survive a few days without the host. Therefore, it seems not to be the case.

Q: Why the selection of 3 degrees and 5 degrees in the model?

A: Chosen due to what is known – variety of factors known according to temperature rise in connection with climate change

Genetic diversity of *Aphanomyces astaci* in recent Italian crayfish plague outbreaks in white-clawed crayfish

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Abstract

The oomycete *Aphanomyces astaci* is the aetiological agent of crayfish plague, a disease that has been causing severe damage to the native European freshwater crayfish populations. In Europe, this pathogen has been extensively studied to evaluate its genetic diversity, but data regarding the Italian peninsula are still limited. Therefore, IZSVe performed genotyping and haplotyping analyses to characterise the *A. astaci* strains involved in seven recent crayfish plague outbreaks in Italy. These mortalities occurred between 2018 and 2025 in white-clawed crayfish (*Austropotamobius pallipes* complex) populations from northern and central Italian regions. Isolation of the oomycete was possible from two cases, whereas for the other outbreaks only frozen or ethanol-fixed crayfish were available. For the genotyping analysis, DNA extracted from the crayfish cuticle and from the isolates was tested. For a more accurate haplotyping analysis, in the absence of isolates, DNA extraction was performed from the muscle tissue, thus minimising contaminations from other oomycetes present on the crayfish cuticle. Genotyping and haplotyping were performed using nuclear-specific molecular markers analysed by real-time PCR and mitochondrial markers assessed by endpoint PCR followed by Sanger sequencing, respectively. Our study indicates that four outbreaks were caused by genotype group D; haplotype d1 was identified in three sites, in central Italy, and d2 in one site, in northern Italy. Genotype group B with haplotype b was identified in one site in northern Italy. In the remaining two cases, from northern and central Italy, we found the rare combination of genotype group B with haplotype a, which to our knowledge was previously reported only in central Europe (Danube River and Czech Republic) and USA (Pennsylvania). These results expand our knowledge about the genetic diversity of *A. astaci* in Italy and highlight the importance of combining multiple molecular markers to study this pathogen.

Acknowledgement: This study was supported by EU LIFE Programme: LIFE-CLAW, Crayfish Lineages Conservation in North-western Apennine (LIFE18 NAT/IT/000806).

Q: To get the isolates, what is a suitable sample size? It is hard to manage to isolate Aphanomyces due to overgrowth of bacteria etc.

A: Have only received frozen samples for some of the samplings. In other two cases – received frozen samples but thereafter asked for more samples and asked for moribund animals.

Do not immediately plate from the animals but clean them and keep them in water – wait for a couple of days – then you will be able to see something that looks like Aphanomyces (in comparison to saprolegnia) and then plate this. Thereby you can avoid overgrowth.

SESSION III: Update from the EURL for crustacean diseases

Chair: Niccoló Vendramin

2026 Inter-laboratory Proficiency Test for Crustacean diseases

Shyam Kokkattunivarthil Uthaman, Charlotte Bjørner Larsen, Argelia Cuenca, and Niccolò Vendramin

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Abstract

In March 2026 an inter-laboratory proficiency test for White Spot Syndrome Virus (WSSV), Taura Syndrome Virus (TSV) and Yellow Head Virus genotype 1 (YHV1) was organized by the EURL for Fish and Crustacean Diseases. The test material consisted of FTA cards incubated with tissue extracts of WSSV-infected shrimp, TSV-infected shrimp, YHV-1 infected shrimp or non-infected shrimp. The participants are asked to identify the WSSV, TSV and YHV positive samples among nine test samples. 20 laboratories in 19 EU member states and 6 laboratories from Non-EU countries were signed up for the test. The expected pathogen in each FTA card will be presented.

Q : Storage of the FTA cards at -20 or -80 degrees for long time storage?

A: FTA cards can be stored at 4 degrees Celsius, or minus 20 degrees for longer storage.

EURL for Crustacean Diseases, work done in 2025

Niccolò Vendramin and the EURL team

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Abstract

The duties of the EURL are described in the REGULATION (EU) 2017/625 (OCR). The duties mainly concern the crustacean cat A and C diseases given in (EU) 2018/1882 : White Spot Disease (WSD), Taura Syndrome (TS) and Yellow Head Disease (YHD).

The facilities supporting the activities of the EURL are placed in the DTU Campus in Kgs. Lyngby, and placed in the institute DTU AQUA, National Institute of Aquatic Resources.

The 15th Annual Workshop of the National Reference Laboratories for Crustacean Diseases was held online on 30th of May 2024. There were 68 participants attending the workshop in person, representing 34 countries. There were three sessions, with 12 presentations.

The annual proficiency test for crustacean diseases (PT) included WSSV, TSV, YHV samples with 25 laboratories including 18 NRLs of EU Member States accepted the invitation to participate and send in their test results for diagnostic assays not derogated to other laboratories. The full reports with the results and the identification of NRLs will be submitted to the Commission, whereas each participant has received a coded version of the report and a certificate of participation with an indication of performance.

During 2024, resources were again used to collate data on surveillance, health categorisation and diagnostics in EU; to identify and characterise selected virus isolates; to type, store and update a library of listed virus isolates; to supply reference materials to NRLs; to provide training courses in laboratory diagnosis; to update the EURL website (www.eurl-fish.eu), to provide consultancy to NRL´s and finally to attend international meetings and conferences.

The EURL provided help in supporting NRL for diagnosing WSSV in wild Crayfish.

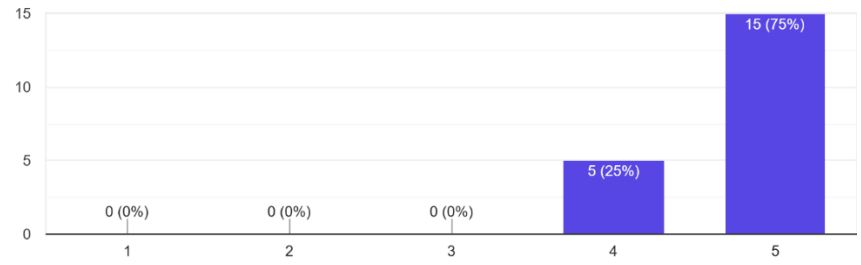
Significant efforts were put into the technical advisory to EFSA in working groups for vector species for listed crustacean diseases. From the laboratory side, the EURL further assessed the analytical characteristics (specificity and sensitivity) of the following methods by participating in Inter-Laboratory proficiency test provided by CSIRO in IMNV, AHPND, IHNNV.

Workshop evaluation

A questionnaire was delivered to the participants asking to evaluate various aspects of the workshop. An overview of the 20 questionnaires retrieved is shown below. Specific comments are going to be considered for the next annual workshop organization.

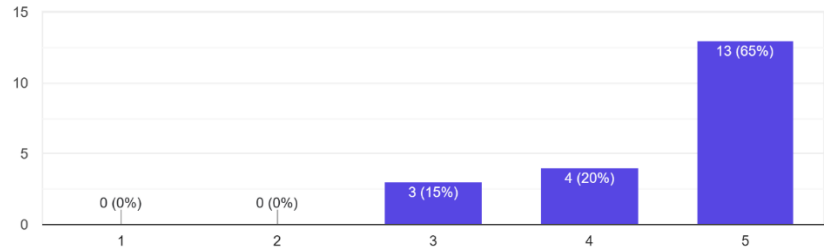
SESSION I:Update on EU listed crustacean diseases and their control- quality of the presentations

20 responses



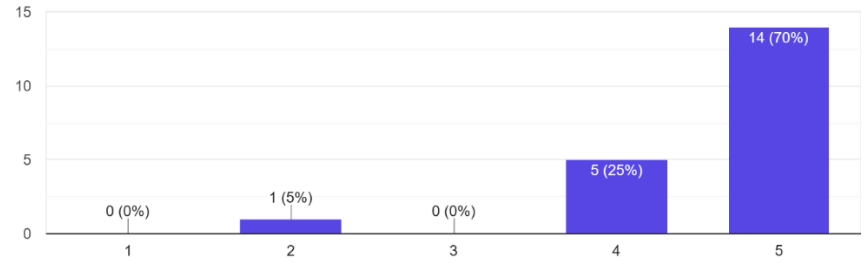
SESSION I:Update on EU listed crustacean diseases and their control- relevance for you

20 responses



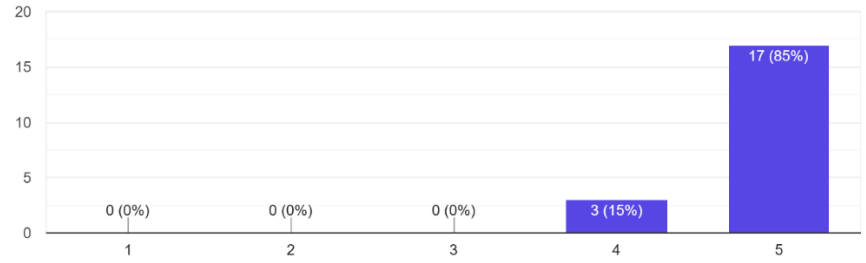
SESSION I:Update on EU listed crustacean diseases and their control- increase of your knowledge

20 responses



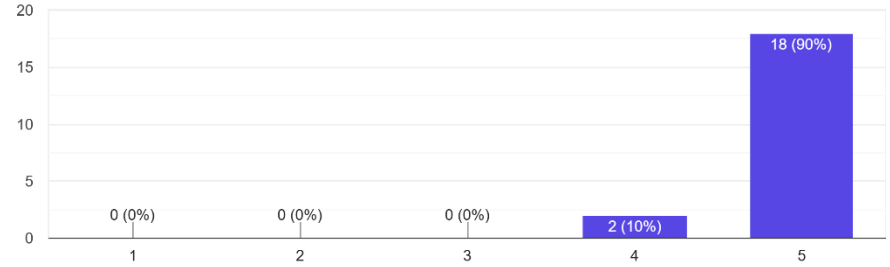
SESSION I:Update on EU listed crustacean diseases and their control- overall score

20 responses



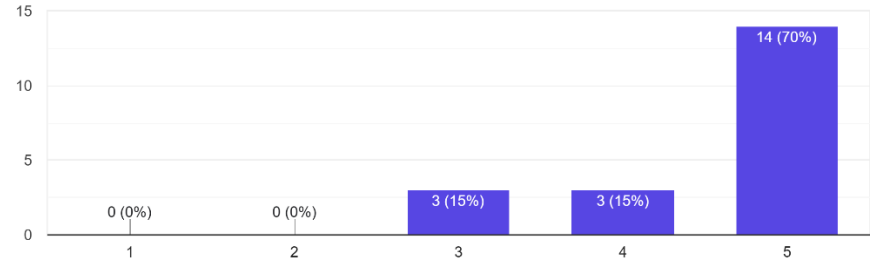
SESSION II:Results from ongoing research on crustacean diseases- quality of the presentations

20 responses



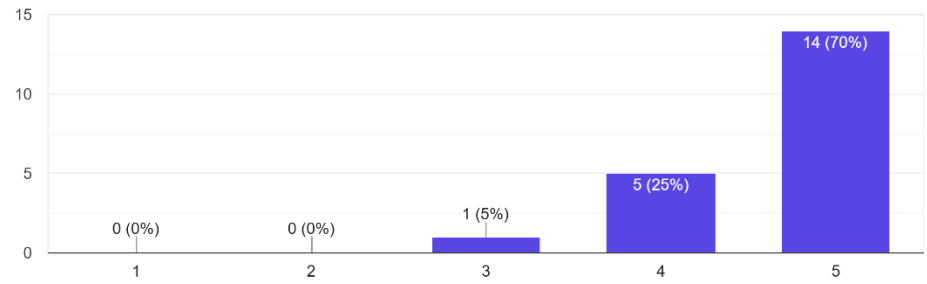
SESSION II:Results from ongoing research on crustacean diseases- relevance for you

20 responses



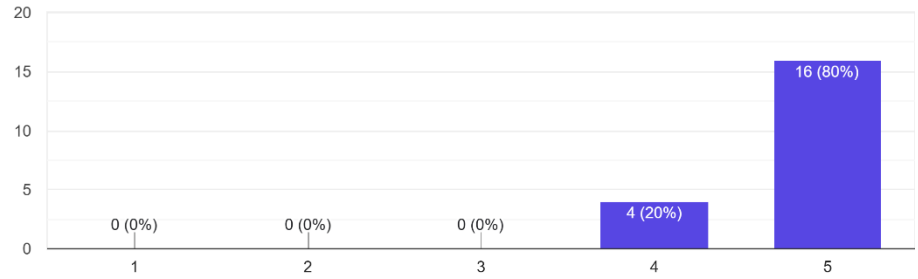
SESSION II:Results from ongoing research on crustacean diseases- increase of your knowledge

20 responses



SESSION II:Results from ongoing research on crustacean diseases- overall score

20 responses



Comments:

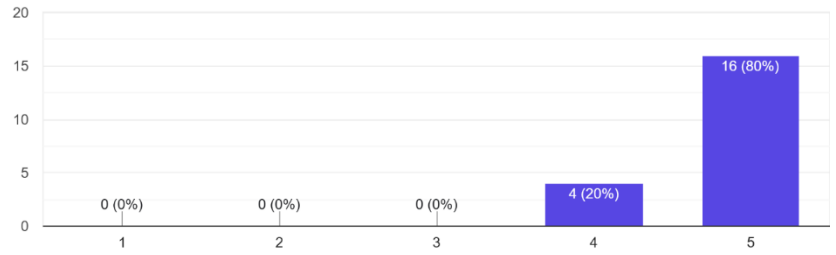
The scientific presentations were very interesting. It was good to see all of this work done by other researchers

Fabulous talks. very informative

Very interesting

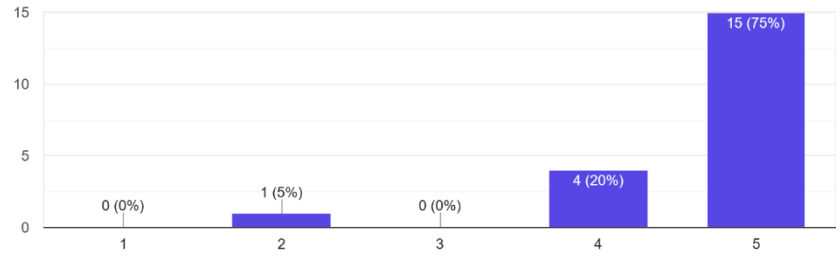
SESSION III:Update from the EURL for crustacean diseases- quality of the presentations

20 responses



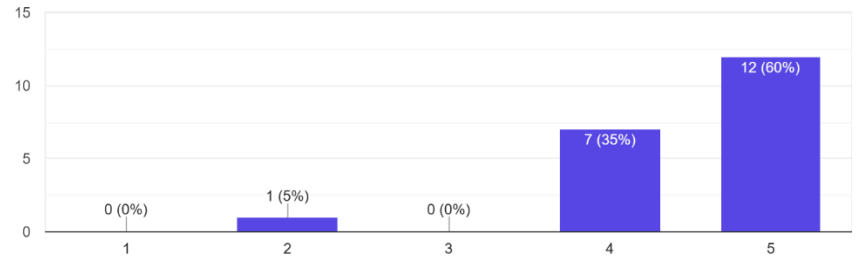
SESSION III:Update from the EURL for crustacean diseases- relevance for you

20 responses



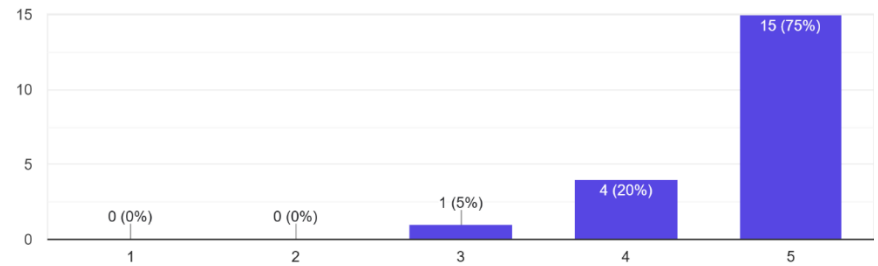
SESSION III:Update from the EURL for crustacean diseases- increase of your knowledge

20 responses



SESSION III:Update from the EURL for crustacean diseases- overall score

20 responses



SESSION III:Update from the EURL for crustacean diseases- comments, feedback, input, response

Good

Greetings and conclusions of the meeting

The tentative dates for the next meeting will be in the end of May 2027. It will be organized as an on-site physical meeting in Lyngby, Denmark. Thanks a lot, to the people arranging the meeting as well as those of you who helped running the meeting by being chair, presenter and/or participant.

We are looking forward to seeing you all next year!

With kind regards,

The EURL fish and crustacean team.