**THE USE OF ENVIRONMENTAL DNA METHODS FOR DETECTION OF  
OIE LISTED AQUATIC ANIMAL DISEASES**

A discussion paper developed by the OIE Aquatic Animal Health Standards Commission (Aquatic Animals Commission) for Member comments.

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**1. Summary**

The monitoring of aquatic systems using environmental DNA (eDNA) is a rapidly advancing research field that will provide opportunities for cost-effective, non-destructive methods to screen for pathogenic agents, including those of wild aquatic populations where samples may be difficult or undesirable to obtain.

The Aquatic Animals Commission is aware that eDNA methods are being applied for detecting the causative agents of several OIE listed diseases. As these methods are available and currently in use, the Commission has agreed that it would be advisable for guidance to be provided on appropriate application of eDNA methods and potential limitations.

The Commission notes that, as accurate estimates of diagnostic performance are not available for designing surveillance programmes using eDNA assays, data obtained from eDNA methods are unlikely to be suitable to support declarations of freedom from listed diseases. Confirmation of infection with listed diseases could also not be made using eDNA methods because a positive result does not demonstrate that a susceptible host animal(s) is infected.

Positive eDNA results could, however, provide evidence amounting to suspicion of infection such as presence of the pathogen in the sample, perhaps in a different lifecycle stage, or different host. This application of eDNA methods may be particularly useful for the monitoring of high-value or rare animals as an alternative to collection of tissue samples. It has a potential role in early detection of disease incursion in wild populations or under circumstances when infection is not likely to result in observable clinical signs. However, following suspicion, based on positive eDNA, samples obtained directly from aquatic animals need to be tested – described in the relevant disease-specific chapters of the *Manual of Diagnostic Tests for Aquatic Animals* (*Aquatic Manual*) to confirm or exclude the case.

The application of eDNA methods for a given purpose should be considered carefully. Methods should be chosen with consideration given to all relevant factors including the surveillance objective, the target pathogen, the reliability of the method, and the environment to be sampled. It is important that the implications of positive results be considered in advance of applying an eDNA method as any positive results may require that surveys involving direct sampling and testing of susceptible animal be conducted to confirm or exclude a suspect case. eDNA methods will not be an appropriate choice for many aquatic animal disease surveillance purposes.

This document is intended to explore the potential use of eDNA methods with respect to the standards of the OIE *Aquatic Animal Health Code* (*Aquatic Code*) and *Aquatic Manual* and to outline benefits and limitations.

The use of an eDNA method for the detection of *Gyrodactylus salaris* has been included in *Aquatic Manual* Chapter 2.3.3 Infection with *Gyrodactylus salaris[[1]](#footnote-1)*. The inclusion of this method conforms with the conclusions of this discussion paper.

**2. Definitions for eDNA**

Numerous definitions for eDNA exist (e.g. Bass *et al*., 2015; Diaz-Ferguson & Moyer, 2014; Thomsen & Willerslev, 2015). Most definitions regard eDNA as detectable short DNA fragments from a living organism derived from cellular components or fluids secreted into the abiotic components of surrounding environment (i.e. water, air, sediments).

For the purposes of this document we define eDNA as: “nucleic acids of pathogenic agents extracted from ‘true’ environmental samples (such as water, soil, sediment, biofilm)”. Directly host-derived material such as faeces, sloughed cells, and mucous, are excluded from this definition. Once extracted from the environmental sample, target eDNA fragments can be detected using a variety of molecular methods (Diaz-Ferguson & Moyer, 2014). Furthermore, eDNA can be sequenced directly as metagenetic libraries or after PCR amplification of specific target gene regions (Bass *et al*., 2015).

The actual performance of eDNA based detection depends on the sample collection and processing methodology (e.g. volume filtered, presence and removal of PCR inhibitors), biological processes (e.g. rates of shedding, temporal variation) and abiotic factors (analyte degradation, hydrodynamic factors). It is important to evaluate these factors empirically so that the results can be properly interpreted. It is only with a clear understanding of how these factors influence the probability of pathogenic agent detection that eDNA-based detection can be used reliably in a variety of settings (Brunner, 2020).

**3. Objectives**

This paper considers i) the benefits and ii) limitations of eDNA pathogenic agent detection methods, iii) validation of eDNA methods, iv) the conditions for inclusion of an eDNA method in a disease-specific chapter of the *Aquatic Manual* and v) use of eDNA evidence as diagnostic criteria.

**4. Review of published eDNA methods for the detection of aquatic animal pathogenic agents**

A literature review was undertaken to assess the application of eDNA methods for the detection and study of pathogens and parasites of aquatic animals. Thirty-three publications reporting the use of eDNA to detect thirteen OIE listed pathogenic agents were identified (see Appendix 1, Table 1 for details). Methods have been developed for the detection of the causative agents of OIE listed pathogenic agents of amphibians, crustaceans, fish and molluscs. The majority of publications concern the detection of the listed pathogenic agents in wild aquatic animal populations, notably infection with *Aphanomyces astaci*, infection with *Batrachochytrium dendrobatidis*, infection with *B. salamandrivorans*, infection with *Ranavirus* species, infection with *G. salaris*.

A further thirteen publications were found that targeted other specific pathogenic agents (e.g. *Microcytos mackini*), groups of pathogenic agents (e.g. of ornamental fish) or applied eDNA methods to broader areas of study (e.g. water-borne transmission of viruses) (see Appendix 1, Table 2 for details).

**5. Benefits eDNA methods for the detection of aquatic animal pathogenic agents**

eDNA detection is a promising tool that can be used to complement direct sampling of aquatic animals for surveillance. eDNA methods offer some benefits compared to direct sampling and testing of aquatic animals, including, but not limited, to the following:

1. eDNA methods do not require destructive sampling of aquatic animal hosts. They may be particularly useful for rare or valuable aquatic animals, or difficult to collect wild animals (e.g. Rusch *et al*., 2018).
2. eDNA methods do not require handling of animals, avoiding the stress associated with obtaining non-destructive tissue samples (Brunner, 2020).
3. Sample collection and sample processing time and associated costs may be reduced substantially compared to collection and processing of individual animal samples (Rusch *et al*., 2018).
4. As environmental samples may contain analyte from the entire, or a large percentage of a target captive population, many fewer samples may be required to detect a pathogenic agent (compared to individual animal samples), even when diagnostic sensitivity of the eDNA method is low (Brunner, 2020).
5. The same environmental sample can be analysed for the presence of hosts (e.g. see Rusch *et al*., 2018) and multiple pathogens.
6. eDNA methods could be used for assessment of potential introduction pathways where sampling of hosts is not possible (e.g. ballast water).

**6. Limitations of eDNA methods**

Limitations to the application of eDNA based pathogenic agent detection include, but are not limited to, the following:

1. Very little target pathogen DNA may be available in the environmental sample due to dilution in the environment and degradation of nucleic acids. This may negatively impact the sensitivity of the method (Brunner, 2020).
2. The concentration of target DNA in an environmental sample will vary due a range of factors such as host density, prevalence and intensity of infection, sampling method (e.g. for water volume sampled, filter pore size, storage conditions) and environmental conditions (e.g. amount of organic matter). Sensitivity of eDNA methods may, therefore, vary more between localities, surveys undertaken at different time points and target taxa than direct sampling and testing of animal tissues (Brunner, 2020).
3. There are formal frameworks to assess diagnostic performance of tests using animal-derived samples, but these have not been developed for eDNA methods. This means that the design of surveys to demonstrate freedom from infection using eDNA methods is problematic.
4. A positive detection of target pathogen DNA in an environmental sample may be more likely to result from a source of contamination not representative of viable pathogen (e.g. inactivated pathogen from heat treated products) compared with animal-derived samples. Similarly, it may not indicate infection of a host animal with the target pathogenic agent.

**7. Validation of eDNA methods**

There is an increasing likelihood that disease management decisions will be made based on results from eDNA studies. It is thus imperative that data generated by eDNA studies is reliable, defendable and executed with high quality assurance standards (Klymus *et al*., 2019). Empirical validation of eDNA-based pathogen detection should focus on understanding the causes and consequences of variation in test characteristics across sampling conditions and needs to take into consideration a clear understanding of what is being sampled/assayed for in the case of each pathogen of interest.

Chapter 1.1.2. of the *Aquatic Manual* describes the principles and methods of validation of diagnostic assays for infectious diseases. The recommendations of this chapter are intended for diagnostic testing of animal-derived samples; however, the principles and many of the methods are applicable to eDNA methods. It is recommended that the general principles and methods of Chapter 1.1.2. be applied to the validation of eDNA detection methods for OIE listed diseases. It should be noted that the process of sample collection, the concentration of target DNA, the DNA extraction, the sensitivity and other performance (indicators) should be emphasised and validated.

Design and reporting standards are available for diagnostic accuracy studies for methods utilising aquatic animal-derived samples (e.g. Laurin *et al*., 2018). Many of the design and reporting considerations are also applicable to eDNA methods and it is recommended that these standards be applied for eDNA diagnostic accuracy studies.

Additional to the guidance described above, design and reporting considerations have been published specifically for eDNA methods (e.g. Doyle & Uthicke, 2020; Goldberg *et al*., 2016; Klymus *et al*., 2019). Many of these studies report on considerations for detection of macro-organisms rather than pathogenic agents; however, the considerations are generally relevant for eDNA detection methods for pathogenic agents. This guidance will be of particular use for the field collection, processing and preservation of eDNA samples.

**8. Minimum requirements for inclusion of an eDNA method in the *Aquatic Manual***

It is recognised that the validation pathway described in Chapter 1.1.2. of the *Aquatic Manual* and the design and reporting standards described by Laurin *et al*., 2018 (see above) are not met by many diagnostic methods currently included in the *Aquatic Manual*. Indeed, many assays included in the *Aquatic Manual* may be validated only to level 1 or 2 of the validation pathway described in Chapter 1.1.2. of the *Aquatic Manual*.

For this reason, the Commission proposes that the following minimum reporting requirements be met for an eDNA method to be considered for inclusion in the *Aquatic Manual* [Adapted from Goldberg *et al*., (2016)]:

1. The intended purpose or application of the assay or protocol needs to be clearly defined (note that appropriate purposes of use for eDNA methods in the context of OIE standards are discussed further in section 9).
2. Description of sample collection methods and precautions taken to eliminate contamination, including collection volume, container material, negative controls, number of replicates and sampling locations/depth.
3. Description of the methods used to concentrate the target DNA (precipitation/filtration), filter type (if applicable) and filtering location (e.g. in the field).
4. Description of sample preservation and storage (method, temperature, duration).
5. Description of the DNA extraction process including protocol adjustments, contamination precautions, negative controls, and internal positive controls.
6. Description of the molecular detection method and optimisation according to (Bustin *et al*., 2009). Furthermore, assays should be validated (Level 1) in an environmental matrix according to its purpose of use.

**9. Potential application of eDNA detection methods in the** **disease-specific chapters of the *Aquatic Manual***

The disease-specific chaptersof the *Aquatic Manual* recommend tests to identify suspect cases and to confirm suspicion for apparently healthy (or those of unknown health status) and clinically affected animals. Apparently healthy populations may fall under suspicion, and therefore be sampled, if there is an epidemiological link(s) to an infected population. Geographic proximity to, or movement of aquatic animals or aquatic animal products or equipment, etc., from a known infected population equate to an epidemiological link. Alternatively, healthy populations are sampled in surveys to demonstrate freedom.

The following points describe the suitability of evidence from eDNA detection methods for inclusion as case definition criteria in section 6 of the disease-specific chapters of the *Aquatic Manual.*

**a) Apparently healthy animals**

**i) Definition of suspect case in a population of apparently healthy animals**

*Suitable as a criterion*. A positive result obtained from an eDNA method recommended in the *Aquatic Manual* is considered to provide adequate evidence to be included as a criterion for a suspect case when known susceptible species exist in the environment from which the sample was taken.

**ii) Definition of confirmed case in apparently healthy animals**

*Not suitable as a criterion.* A positive result obtained from an eDNA method recommended in the *Aquatic Manual* is not considered to provide appropriate evidence to confirm a case in apparently healthy animals. Methods utilising animal derived samples are considered more appropriate for criteria to confirm a case. Evidence to confirm a case in apparently healthy animals must meet the requirements of Section 6.1.2. of the relevant disease-specific chapter of the *Aquatic Manual*. eDNA evidence will not be included as a criterion within this section.

**b) Clinically affected animals**

**i) Definition of a suspect case in clinically affected animals**

*Suitable as a criterion.* Taking an environmental sample to investigate the cause of disease in a population of clinically affected animals is not generally recommended as samples from clinically affected animals are more likely to lead to pathogenic agent detection and are more suitable for disease

investigation. However, under some circumstances, an eDNA method may detect a pathogenic agent and lead to the recognition of previously unobserved or unassociated clinical signs of disease. In these circumstances, a positive result obtained from an eDNA method recommended in the *Aquatic* *Manual* is considered to provide adequate evidence to be included as a criterion for a suspect case.

**ii) Definition of confirmed case**

*Not suitable as a criterion.* A positive result from an eDNA method recommended in the *Aquatic Manual* would not be included as a criterion for the confirmation of a pathogenic agent in clinically affected animals (or apparently healthy animals, see point 9.a.ii above). Any positive eDNA test would require further investigation involving the collection and testing of animal tissues as stipulated in the relevant disease-specific chapter of the *Aquatic Manual*. Evidence to confirm a case in clinically affected animals must meet the requirements of Section 6.2.2. of the relevant disease-specific chapter of the *Aquatic Manual*. eDNA evidence will not be included as a criterion within this section.

**10. Discussion**

The key limitations of eDNA is the lack of validation and diagnostic performance data, meaning that negative results cannot be used to demonstrate disease freedom and positive results always require confirmation using animal samples (Brunner, 2020). Nevertheless, there are circumstances where the advantages of environmental, over animal, sampling means that eDNA approaches can be usefully integrated into a surveillance programme.

A country or zone claiming freedom from a specified pathogenic agent(s) are required to have in place an early detection system for disease incursion. Farmer reporting of morbidity and mortality is a key component of an early detection system. Farmed populations can act as sentinels for wild populations only if they are epidemiologically connected (i.e. through shared water). Otherwise active surveillance in wild populations is required as morbidity or mortality is unlikely to be reported (especially as dead or dying animals are likely to be quickly scavenged or predated). Animal sampling of wild populations can present considerable logistical challenges, especially if populations are remote, sparse or if low numbers make destructive sampling undesirable. eDNA based pathogenic agent detection methods overcome many of the challenges of sampling wild aquatic animals (Kamoroff & Goldberg, 2017; Trebitz *et al*., 2017).

Infection with some listed pathogenic agents, under certain conditions or in some host species, will not invariably cause detectable clinical signs. Early detection systems that rely on observations by farmers (or others) of mortality or morbidity are ineffective in these circumstances and active surveillance would be required. Sampling farmed animals on a frequent basis, and at a level to detect a low prevalence, presents considerable logistical challenges and the cost is likely to be unacceptable. eDNA methods can offer a viable alternative (Trujillo-Gonzalez *et al*., 2019a) for active surveillance for pathogens which may not reliably cause observable clinical signs. They have the additional advantage that the sample will contain analyte from a large percentage, if not the entire, captive population. Thus relatively few environmental, compared with animal samples, are needed (provided sufficient DNA can be extracted).

**11. Conclusions**

1. eDNA methods may have utility for enhancing passive surveillance systems for early detection; particularly in circumstances where conditions are not conducive to clinical expression of disease, or populations are not under sufficient observation to detect clinical disease should it occur.
2. eDNA methods may have utility for rare, valuable or difficult to collect wild aquatic animals, where direct sampling of animals is undesirable or cost prohibitive. They may also provide cost advantages for disease monitoring programs in production environments.
3. There are currently no frameworks to allow evaluation of diagnostic performance of eDNA methods in a manner similar to animal-derived samples. For this reason, evidence from eDNA detection methods cannot be utilised as evidence for self-declaration of freedom from disease.
4. eDNA methods will be considered for inclusion in disease-specific chapters of the *Aquatic Manual*, if minimum disease and reporting standards as described in this paper are met.
5. Positive results from an eDNA method that has been included in the *Aquatic Manual* will be considered as an appropriate criterion for a suspect case of a disease.
6. The application of eDNA methods for a given purpose should be considered carefully with respect to the pathogen to be tested, the environment to be sampled, the reliability of the method and the implications of positive results that may require surveys of susceptible animal populations to confirm or exclude a suspect case.
7. Positive results from an eDNA methods that has been included in the *Aquatic Manual* will not be considered as an appropriate criterion for a confirmed case of a disease in either apparently healthy or clinically affected animals.

**References**

Alzaylaee H., Collins R.A., Rinaldi G., Shechonge A., Ngatunga B., Morgan E.R. & Genner M.J. (2020). Schistosoma species detection by environmental DNA assays in African freshwaters. *PLOS Neglect. Trop. Dis.,* 14:e0008129.

Audemard C., Reece K.S. & Burreson E.M. (2004). Real-Time PCR for Detection and Quantification of the Protistan Parasite *Perkinsus marinus* in Environmental Waters. *Appl. Environ. Microbiol.,* **70**, 6611–6618.

Bass D., Stentiford G.D., Littlewood D.T.J. & Hartikainen H. (2015). Diverse Applications of Environmental DNA Methods in Parasitology. *Trends Parasitol.,* **31**, 499–513.

Bastos Gomes G., Hutson K.S., Domingos J.A., Chung C., Hayward S., Miller T.L. & Jerry D.R. (2017). Use of environmental DNA (eDNA) and water quality data to predict protozoan parasites outbreaks in fish farms. *Aquaculture,* **479**, 467–473.

Bastos Gomes G., Hutson K.S., Domingos J.A., Infante Villamil S., Huerlimann R., Miller T.L. & Jerry D.R. (2019). Parasitic protozoan interactions with bacterial microbiome in a tropical fish farm. *Aquaculture,* **502**, 196–201.

Bernhardt L., Myrmel M., Lillehaug A., Qviller L. & Weli S. (2020). Filtration, concentration and detection of salmonid alphavirus in seawater during a post-smolt salmon (*Salmo salar*) cohabitant challenge. *Dis. Aquatic. Org.,* **144**, 61–73.

Brannelly L.A., Wetzel D.P., Ohmer M.E.B., Zimmerman L., Saenz V. & Richards-Zawacki C.L. (2020). Evaluating environmental DNA as a tool for detecting an amphibian pathogen using an optimized extraction method. *Oecologia,* **194**, 267–281.

Brunner J.L. (2020). Pooled samples and eDNA-based detection can facilitate the “clean trade” of aquatic animals. *Sci. Rep.,* **10**, 10280.

Bustin S.A., Benes V., Garson J.A., Hellemans J., Huggett J., Kubista M., Mueller R., Nolan T., Pfaffl M.W., Shipley G.L., Vandesompele J. & Wittwer C.T. (2009). The MIQE Guidelines: Minimum Information for Publication of Quantitative Real-Time PCR Experiments. *Clin. Chem.,* **55**, 611–622.

Diaz-Ferguson E.E. & Moyer G.R. (2014). History, applications, methodological issues and perspectives for the use environmental DNA (eDNA) in marine and freshwater environments. *Rev. Biol. Trop.,* **62**, 1273–1284.

Doyle J. & Uthicke S. (2020). Sensitive environmental DNA detection via lateral flow assay (dipstick) – A case study on corallivorous crown-of-thorns sea star (*Acanthaster cf . solaris*) detection. *Environ. DNA*, 1–20.

Fossoy F., Brandsegg H., Sivertsgård R., Pettersen O., Sandercock B.K., Solem Ø., Hindar K. & Mo T.A. (2020). Monitoring presence and abundance of two gyrodactylid ectoparasites and their salmonid hosts using environmental DNA. *Environ. DNA,* **2**, 53–62.

Goldberg C.S., Turner C.R., Deiner K., Klymus K.E., Thomsen P.F., Murphy M.A., Spear S.F., McKee A., Oyler-McCance S.J., Cornman R.S., Laramie M.B., Mahon A.R., Lance R.F., Pilliod D.S., Strickler

K.M., Waits L.P., Fremier A.K., Takahara T., Herder J.E. & Taberlet P. (2016). Critical considerations for the application of environmental DNA methods to detect aquatic species. *Methods Ecol. Evol.,* **7**, 1299–1307.

Gregory A., Munro L.A., Snow M., Urquhart K.L., Murray A.G. & Raynard R.S. (2009). An experimental investigation on aspects of infectious salmon anaemia virus (ISAV) infection dynamics in seawater Atlantic salmon, *Salmo salar* L. *J. Fish Dis.,* **32**, 481–489.

Hall E.M., Crespi E.J., Goldberg C.S. & Brunner J.L. (2016). Evaluating environmental DNA-based quantification of ranavirus infection in wood frog populations. *Molec. Ecol. Resour.,* **16**, 423–433.

Haramoto E., Kitajima M., Katayama H. & Ohgaki S. (2007). Detection of koi herpesvirus DNA in river water in Japan. *J. Fish Dis.,* **30**, 59–61.

Holt C., Foster R., Daniels C.L., Van Der Giezen M., Feist S.W., Stentiford G.D. & Bass D. (2018). *Halioticida noduliformans* infection in eggs of lobster (*Homarus gammarus*) reveals its generalist parasitic strategy in marine invertebrates. *J. Invertebr. Pathol.*, **154**, 109–116.

Honjo M.N., Minamoto T. & Kawabata Z. (2012). Reservoirs of Cyprinid herpesvirus 3 (CyHV-3) DNA in sediments of natural lakes and ponds. *Vet. Microbiol.,* **155**, 183–190.

Honjo M.N., Minamoto T., Matsui K., Uchii K., Yamanaka H., Suzuki A.A., Kohmatsu Y., Iida T. & Kawabata Z. (2010). Quantification of cyprinid herpesvirus 3 in environmental water by using an external standard virus. *Appl. Environ. Microbiol.,* **76**, 161–168.

Huver J.R., Koprivnikar J., Johnson P.T.J. & Whyard S. (2015). Development and application of an eDNA method to detect and quantify a pathogenic parasite in aquatic ecosystems. *Ecol. Appl.,* **25**, 991–1002.

Jorgensen L., Von G., Nielsen J.W., Villadsen M.K., Vismann B., Dalvin S., Mathiessen H., Madsen L., Kania P.W. & Buchmann K. (2020). A non-lethal method for detection of *Bonamia ostreae* in flat oyster (*Ostrea edulis*) using environmental DNA. *Sci. Rep.,* **10**, 1–9.

Julian J.T., Glenney G.W. & Rees C. (2019). Evaluating observer bias and seasonal detection rates in amphibian pathogen eDNA collections by citizen scientists. *Dis. Aquat. Org.,* **134**, 15–24.

Kamoroff C. & Goldberg C.S. (2017). Using environmental DNA for early detection of amphibian chytrid fungus Batrachochytrium dendrobatidis prior to a ranid die-off. *Dis. Aquat. Org.,* **127**, 75–79.

Klymus K.E., Merkes C.M., Allison M.J., Goldberg C.S., Helbing C.C., Hunter M.E., Jackson C.A., Lance R.F., Mangan A.M., Monroe E.M., Piaggio A.J., Stokdyk J.P., Wilson C.C. & Richter C.A. (2019). Reporting the limits of detection and quantification for environmental DNA assays. *Environ. DNA*, 1–12.

Kongrueng J., Yingkajorn M., Bunpa S., Sermwittayawong N., Singkhamanan K. & Vuddhakul V. (2015). Characterization of *Vibrio parahaemolyticus* causing acute hepatopancreatic necrosis disease in southern Thailand. *J. Fish Dis.* **38**, 957–966.

Lafferty K.D. & Ben-Horin T. (2013). Abalone farm discharges the withering syndrome pathogen into the wild. *Front. Microbiol.,* **4**, 1–5.

Laurin, E., Thakur, K.K., Gardner, I.A., Hick, P., Moody, N.J., Crane, M. & Ernst, I. (2018). Design standards for experimental and field studies to evaluate diagnostic accuracy of tests for infectious diseases in aquatic animals. *J. Fish Dis.,* **41**, 729–749.

Mahon A.R., Horton D.J., Learman D.R., Nathan L.R. & Jerde C.L. (2018). Investigating diversity of pathogenic microbes in commercial bait trade water. *PeerJ*., 6:e5468.

Miaud C., Arnal V., Poulain M., Valentini A. & Dejean T. (2019). eDNA increases the detectability of ranavirus infection in an alpine amphibian population. *Viruses,* **11**, 1–15.

Mosher B.A., Huyvaert K.P., Chestnut T., Kerby J.L., Madison J.D. & Bailey L.L. (2017). Design- and model-based recommendations for detecting and quantifying an amphibian pathogen in environmental samples. *Ecol. Evol.,* **7**, 10952–10962.

Natividad K.D.T., Nomura N. & Matsumura M. (2008). Detection of White spot syndrome virus DNA in pond soil using a 2-step nested PCR. *J. Virol. Methods,* **149**, 28–34.

Oidtmann B., Dixon P., Way K., Joiner C. & Bayley A.E. (2018). Risk of waterborne virus spread – review of survival of relevant fish and crustacean viruses in the aquatic environment and implications for control measures. *Rev. Aquacult.,* **10**, 641–669.

Pierson T.W. & Horner A.A. (2016). Environmental DNA (eDNA) sampling for amphibian pathogens. Southeastern Partners in Amphibian and Reptile Conservation (SEPARC), Disease, Pathogens and Parasites Task Team: Information Sheet #19.

Polinski M.P., Meyer G.R., Lowe G.J. & Abbott C.L. (2017). Seawater detection and biological assessments regarding transmission of the oyster parasite *Mikrocytos mackini* using qPCR. *Dis. Aquat. Org.,* **126**, 143–153.

Quang N.D., Hoa P.T.P., Da T.T. & Anh P.H. (2009). Persistence of white spot syndrome virus in shrimp ponds and surrounding areas after an outbreak. *Environ. Monit. Assess.,* **156**, 69–72.

Robinson C.V., Uren Webster T.M., Cable J., James J. & Consuegra S. (2018). Simultaneous detection of invasive signal crayfish, endangered white-clawed crayfish and the crayfish plague pathogen using environmental DNA. *Biol. Conserv.,* **222**, 241–252.

Rusch J.C., Hansen H., Strand D.A., Markussen T., Hytterød S. & Vrålstad T. (2018). Catching the fish with the worm: a case study on eDNA detection of the monogenean parasite *Gyrodactylus salaris* and two of its hosts, Atlantic salmon (*Salmo salar*) and rainbow trout (*Oncorhynchus mykiss*). *Parasite. Vector.,* **11**, 333.

Rusch J. C., Mojžišová M., Strand D.A., Svobodová J., Vrålstad T. & Petrusek A. (2020). Simultaneous detection of native and invasive crayfish and *Aphanomyces astaci* from environmental DNA samples in a wide range of habitats in Central Europe. *NeoBiota*, **58**, 1–32.

Salama N. & Rabe B. (2013). Developing models for investigating the environmental transmission of disease-causing agents within open-cage salmon aquaculture. *Aquacult. Env. Interac.,* **4**, 91–115.

Sana S., Williams C., Hardouin E.A., Blake A., Davison P., Pegg J., Paley R., Zhang T. & Andreou D. (2018). Phylogenetic and environmental DNA insights into emerging aquatic parasites: implications for risk management. *Int. J. Parasitol.,* **48**, 473–481.

Spitzen-Van Der Sluijs A., Stark T., Dejean T., Verbrugghe E., Herder J., Gilbert M., Janse J., Martel A., Pasmans F. & Valentini A. (2020). Using environmental DNA for detection of *Batrachochytrium salamandrivorans* in natural water. *Environ. DNA,* **2**, 565–571.

Strand D.A., Holst-Jensen A., Viljugrein H., Edvardsen B., Klaveness D., Jussila J. & Vrålstad T. (2011). Detection and quantification of the crayfish plague agent in natural waters: Direct monitoring approach for aquatic environments. *Dis. Aquat. Org.,* **95**, 9–17.

Strand D.A., Jussila J., Johnsen S.I., Viljamaa-Dirks S., Edsman L., Wiik-Nielsen J., Viljugrein H., Engdahl F. & Vrålstad T. (2014). Detection of crayfish plague spores in large freshwater systems. *J. Appl. Ecol.,* **51**, 544–553.

Thomsen P.F. & Willerslev E. (2015). Environmental DNA – An emerging tool in conservation for monitoring past and present biodiversity. *Biol. Conserv.,* **183**, 4–18.

Trebitz A.S., Hoffman J.C., Darling J.A., Pilgrim E.M., Kelly J.R., Brown E.A., Chadderton W.L., Egan S.P., Grey E.K., Hashsham S.A., Klymus K.E., Mahon A.R., Ram J.L., Schultz M.T., Stepien C.A. & Schardt J.C. (2017). Early detection monitoring for aquatic non-indigenous species: Optimizing surveillance, incorporating advanced technologies, and identifying research needs. *J. Environ. Manage.,* **202**, 299–310.

Trujillo-Gonzalez A., Becker J.A., Huerlimann R., Saunders R.J. & Hutson K.S. (2019a). Can environmental DNA be used for aquatic biosecurity in the aquarium fish trade? *Biol. Invasions,* **22**, 1011–1025.

Trujillo-Gonzalez A., Edmunds R. C., Becker J.A. & Hutson K.S. (2019b). Parasite detection in the ornamental fish trade using environmental DNA. *Sci. Rep.,* **9**, 1–9.

Vilaca S.T., Grant S.A., Beaty L., Brunetti C.R., Congram M., Murray D.L., Wilson C.C. & Kyle C.J. (2020). Detection of spatiotemporal variation in ranavirus distribution using eDNA. *Environ. DNA,* **2**, 210–220.

Vralstad T., Strand D., Rusch J., Toverud O., Johnsen S.I., Tarpai A., Rask-Moller P. & Gjerve A.-G. (2016). The surveillance programme for *Aphanomyces astaci* in Norway 2016. Norwegian Veterinary Institute.

Walker S.F., Salas M.B., Jenkins D., Garner T.W.J., Cunningham A.A., Hyatt A.D., Bosch J. & Fisher M.C. (2007). Environmental detection of *Batrachochytrium dendrobatidis* in a temperate climate. *Dis. Aquat. Org.,* **77**, 105–112.

Weli S.C., Bernhardt L.-V., Qviller L., Myrmel M. & Lillehaug A. (2021). Development and evaluation of a method for concentration and detection of salmonid alphavirus from seawater. *J. Virol. Methods,* **287**, 113990.

Wittwer C., Nowak C., Strand D.A., Vrålstad T., Thines M. & Stoll S. (2018a). Comparison of two water sampling approaches for eDNA-based crayfish plague detection. *Limnologica,* **70**, 1–9.

Wittwer C., Stoll S., Strand D., Vrålstad T., Nowak C. & Thines M. (2018b). eDNA-based crayfish plague monitoring is superior to conventional trap-based assessments in year-round detection probability. *Hydrobiologia,* **807**, 87–97.

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**Appendix 1. Publications describing eDNA methods for aquatic animal pathogenic agents**

**Table 1.** Published applications of eDNA methods for the detection of   
OIE listed pathogenic agents of aquatic animals

| **OIE LISTED DISEASE** | **PUBLICATION** |
| --- | --- |
| **Amphibian diseases** | |
| Infection with *Batrachochytrium dendrobatidis* | Brannelly *et al*., 2020; Julian *et al*., 2019; Kamoroff & Goldberg, 2017; Mosher *et al*., 2017; Pierson & Horner, 2016; Walker *et al*., 2007 |
| Infection with *Batrachochytrium salamandrivorans* | Brunner, 2020; Spitzen‐van der Sluijs *et al*., 2020 |
| Infection with Ranavirus species | Hall *et al*., 2016; Julian *et al*., 2019; Miaud *et al*., 2019; Pierson & Horner, 2016; Vilaca *et al*., 2020 |
| **Fish diseases** | |
| Infection with *Gyrodactylus salaris* | Fossoy *et al*., 2020; Rusch *et al*., 2018; |
| Infection with HPR-deleted or HPRO infectious salmon anaemia virus | Gregory *et al*., 2009 |
| Infection with koi herpesvirus | Haramoto *et al*., 2007; Honjo *et al*., 2010; 2012 |
| Infection with salmonid alphavirus | Bernhardt *et al*., 2020; Weli *et al*., 2021 |
| **Crustacean diseases** | |
| Acute hepatopancreatic necrosis disease | Kongrueng *et al*., 2015 |
| Infection with *Aphanomyces astaci* (crayfish plague) | Robinson *et al*., 2018; Rusch *et al*, 2020; Strand *et al*., 2011; 2014; Vralstad *et al*., 2016; Wittwer *et al*., 2018a; 2018b |
| Infection with white spot syndrome virus | Natividad *et al*., 2008; Quang *et al*., 2009 |
| **Mollusc diseases** | |
| Infection with *Bonamia ostreae* | Jorgensen *et al*., 2020 |
| Infection with *Perkinsus marinus* | Audemard *et al*., 2004 |
| Infection with *Xenohaliotis californiensis* | Lafferty & Ben-Horin, 2013 |

**Table 2.** Published eDNA studies of pathogenic agents of aquatic animals not listed by the OIE

|  |  |
| --- | --- |
| **SUBJECT** | **PUBLICATION** |
| Ornamental fish parasite detection | Trujillo-Gonzalez *et al*., 2019b; 2019a |
| Parasitology | Bass *et al*., 2015 |
| Protozoan parasite outbreaks in fish farms | Bastos Gomes *et al*. 2017; 2019 |
| Disease transmission in open water Salmon cages | Salama & Rabe, 2013 |
| Emerging aquatic parasites | Sana *et al*., 2018 |
| Pathogenic microbes in bait | Mahon *et al*., 2018 |
| Waterborne virus detection | Oidtmann *et al*., 2018 |
| *Halioticida noduliformans* in lobsters | Holt *et al*., 2018 |
| *Microcytos mackini* | Polinski *et al*., 2017 |
| Trematode parasite *Ribieroia ondatrae* | Huver *et al*., 2015 |
| *Schistosoma* species | Alzaylaee *et al*., 2020 |

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1. <https://www.oie.int/fileadmin/Home/eng/Health_standards/aahm/current/2.3.03_G_salaris.pdf> [↑](#footnote-ref-1)