



# Current knowledge and limitations of eDNA as a monitoring tool for European eel

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Biology and Environmental Science - Bachelor's Programme  
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## Abstract

Monitoring organisms and ecosystems is essential to provide baseline information against which we can evaluate changes and extremes. This is especially important for critically endangered species, such as the European eel (*Anguilla anguilla*). Today we monitor European eel by the means of trawling, netting and electrofishing, among other methods. eDNA is a relatively new, non-invasive and non-lethal monitoring method that analyses what organisms reside in a system based on what DNA can be found in environmental samples. The aim of this study was to explore the use of eDNA in the monitoring of fish, with emphasis on the European eel. A literature search was performed and the 22 articles reviewed were divided into nine categories, based on the perceived area of use. The most common category was using eDNA to detect European eel (11 studies). Using eDNA to estimate abundance and/or biomass was less common (4 studies) and the results of these studies were less consistent. Using eDNA to confirm absence, detect parasites, and detect hybridization were the least common categories (1 study each). The lack of knowledge surrounding how to estimate abundance and/or biomass with eDNA seems to be the largest challenge to using eDNA in current eel monitoring programs and will likely be investigated more in the future.

*Key words: Anguilla anguilla, literature review, presence, distribution, biomass, migration, barriers*

## Sammanfattning

Övervakning av organismer och ekosystem är avgörande för att ge grundläggande information mot vilken vi kan utvärdera förändringar och extremer. Detta är särskilt viktigt för akut hotade arter, såsom den europeiska ålen (*Anguilla anguilla*). Idag övervakar vi den europeiska ålen med hjälp av bland annat trålning, nätfiske och elfiske. eDNA är en relativt ny, icke-invasiv och icke-dödlig övervakningsmetod som analyserar vilka organismer som finns i ett system baserat på vilket DNA som kan hittas i miljöprover. Syftet med denna studie var att undersöka användningen av eDNA till övervakning av fisk, med fokus på den europeiska ålen. En litteratursökning utfördes och de 22 granskade artiklarna delades in i nio kategorier, baserat på det upplevda användningsområdet. Den vanligaste kategorin var att använda eDNA till att detektera europeisk ål (11 studier). Det var mindre vanligt att använda eDNA till att uppskatta antal och/eller biomassa (4 studier) och resultaten av dessa studier var mindre konsekventa. De minst vanliga kategorierna var att använda eDNA till att bekräfta frånvaro, detektera parasiter och detektera hybridisering (1 studie vardera). Bristen på kunskap kring hur man uppskattar antal och/eller biomassa med eDNA verkar vara den största utmaningen för att kunna använda eDNA i nuvarande ålövervakningsprogram och kommer sannolikt att undersökas mer i framtiden.

*Nyckelord: Anguilla anguilla, litteraturstudie, förekomst, utbredning, biomassa, migration, vandringshinder*

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# 1. Introduction

## 1.1 Monitoring ecosystems and organisms

Our need to monitor the status of organisms and ecosystems is largely explained by our survival and quality of life being dependent on these ecosystems and the services they provide. Without high-quality ecological information, collected continually over long periods of time, we would be unable to document and provide baselines against which change or extremes can be evaluated, and guide evidence-based environmental legislation (Lindenmayer & Likens 2010).

Monitoring is also necessary to ensure that management efforts and policy have their intended effect and are cost-effective (Lovett et al. 2007). Limited budgets and efforts require trade-offs, and we cannot monitor everything all the time. However, monitoring marine and freshwater systems is especially important, since fisheries support the livelihoods of many people and provide a major source of protein for humans. This is the largest extractive use of wildlife in the world (Radinger et al. 2019).

Monitoring can provide information at community level and/or population level and often focuses on parameters such as species richness, food web structure, genetic diversity, exploited fish stocks, size and age structure, growth, condition, and presence or abundance of for example threatened species (Radinger et al. 2019). Fish, in comparison to other taxonomic groups, have been and continue to be underrepresented in biological monitoring despite their high diversity. This is likely because of them living in water, which requires more specialized sampling methods compared to monitoring terrestrial systems (Radinger et al. 2019). Sampling methods include both capture (e.g. netting, trapping and electrofishing) and non-capture techniques (e.g. hydroacoustic surveys and environmental DNA), each with their costs and benefits, such as some methods being lethal and others not (Radinger et al. 2019).

## 1.2 eDNA

One of the monitoring methods that do not require capture, and is hence non-lethal, is eDNA (environmental DNA). It refers to a mixture of genomic DNA secreted, excreted, exuded and/or discharged by an organism to the environment it inhabits. The genomic material can originate from hair, scales, epithelial cells, faeces and/or mucus and is sampled from the environment, e.g. water or sediment (Karlsson 2024).

This is a recently developed method, gaining traction after the turn of the millennia, judging by the usage of the term “eDNA” by the Google Books Ngram

Viewer (Figure 2). Ogram et al. (1988) coined the term early in its' discovery when studying how DNA molecules adhere to soil particles, making it easier to measure microbial activity and genetic diversity. The first study in which eDNA was used to monitor a macro-organism was published in 2008, with the aim of detecting the invasive American bullfrog (*Rana catesbeiana*) in Europe using freshwater samples (Ficetola et al. 2008). The use of the method in monitoring aquatic ecosystems has since then dramatically increased and multiple species have been the focus of study – amphibians, fishes, mammals and reptiles among others (Rees et al. 2014).

In aquatic environments the eDNA method usually consists of collecting water samples, filtering the water with a very fine-pored filter, extracting the DNA from the filter, and amplifying the DNA-sequence of one or several target species using PCR (Figure 1) (Rees et al. 2014). This can be done using different methods. qPCR is often used to identify a single target species, such as rare, threatened or invasive species. Metabarcoding is used to monitor species compositions within a biological community, since this method targets all species in the sample (Harper et al. 2018).

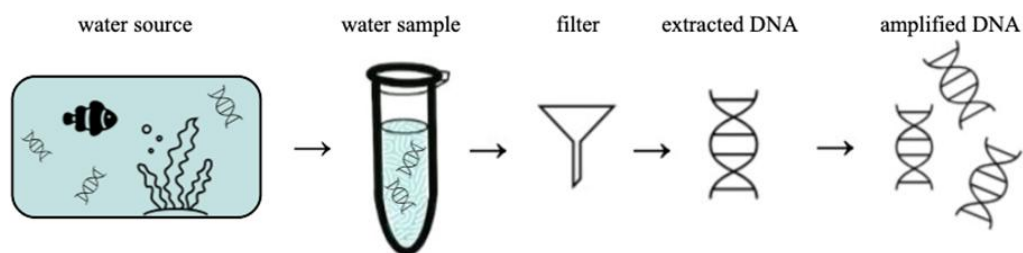


Figure 1. Visualization of the eDNA process (sampling, filtering the sample, extracting DNA, and amplifying DNA)

Since eDNA is a relatively young research field (Figure 2), much is still unknown about the nature of eDNA, especially regarding its' persistence in aquatic ecosystems, the rate of dispersal and degradation, and the relationship between eDNA-concentration and biomass or abundance. This limits its' impact as a monitoring tool. Abiotic factors such as radiation, temperature and pH all affect the breakdown of DNA into smaller fragments, which coincides with biodegradation through enzymatic action and bacterial activity (Joseph et al. 2022). Studies done in both marine and freshwater systems suggest that the dispersal of eDNA is highly variable, both in distance from the source and in depth, and factors affecting the dispersal remain unclear (Jo et al. 2025). In the case of lotic systems with flowing water, eDNA-concentrations are usually higher within or directly downstream of the source, and decreases with increasing distance from the source, but to which extent seemingly varies with species and/or taxon (e.g. Chucholl et al. 2021, Sansom & Sassoubre 2017). Using eDNA-

concentration to estimate biomass or abundance is further complicated by biotic factors. The DNA production and shedding rates of organisms varies depending on the metabolic rate and size among individuals experiencing the same environment, as well as feeding and diet (Rourke et al. 2022). Species distribution and density or seasonal behaviours such as reproduction and migration will also result in spatial and temporal variations in eDNA concentrations (Rourke et al. 2022).

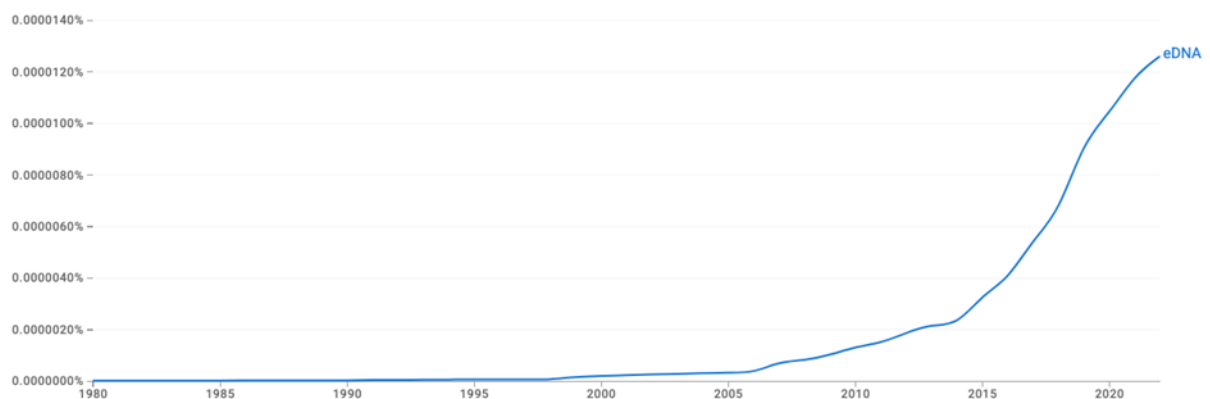


Figure 2. Usage trend of the term 'eDNA' from 1980 and onward. The graph was generated by Google Books Ngram Viewer. It shows a dramatic increase in the use of the term, starting in the early 2000s, that has not yet peaked. (Michel\* et al. (2010). Google Books Ngram Viewer: eDNA. [graph] [https://books.google.com/ngrams/graphcontent=eDNA&year\\_start=1980&year\\_end=2022&corpus=en&smoothing=3](https://books.google.com/ngrams/graphcontent=eDNA&year_start=1980&year_end=2022&corpus=en&smoothing=3) [2026-04-28]).

### 1.3 European eel (*Anguilla anguilla*)

The European eel (*Anguilla anguilla*) is a facultatively catadromous fish that breeds and spawns in the marine waters of the Sargasso Sea area and carries out the remainder of its' life cycle in fresh, brackish and coastal waters (IUCN 2018). The exact mechanisms by which leptocephali, eel larvae, reach the European and north African coasts, and exactly how adult silver eels (sexually mature eels, ready for spawning migration) undertake the spawning migration back to the Sargasso Sea, are largely unknown and complicate the monitoring of e.g. survival and recruitment (IUCN 2018).

The European eel is classified as critically endangered by The IUCN Red List of Threatened Species (IUCN 2018). Compared to the 1960-1979 reference level, its' recruitment index has dropped significantly, with 98.7% in the North Sea recruitment data series and 92,8% elsewhere in the Europe series when measured in 2024 (ICES 2025). Commercial landings (of all eel life stages) report a long-term declining trend, from around 10 000 tons in the 1960s to above 2000 tons this past decade, that continues to decline (ICES 2025). Several natural and

anthropogenic threats can explain this decline in recruitment, such as climate change, change in oceanic currents, migration barriers, habitat loss and degradation, pollution, parasites, predation and unsustainable exploitation (IUCN 2018). An EU-wide recovery plan for the species was adopted in 2007, instructing EU-member states to develop and implement Eel Management Plans to reduce anthropogenic mortalities, and implementing monitoring programmes is one of many important measures (IUCN 2018).

Today, most life stages of European eel are monitored using a large range of methods, with regards to recruitment, restocking, production, growth, mortality and spawning migration. Individuals are captured to measure size, age, gender and origin (i.e., naturally recruited or imported-restocked), etc. (Fiskbarometern, 2026). In Sweden, glass eels arriving from the Sargasso Sea are monitored using a special kind of trawl as part of the “International Bottom Trawl Survey”, and by trawling at openings for cooling water at nuclear power plants. Elvers (immature eels, generally shorter than 30 cm) are monitored in freshwater by capturing them at migration barriers using different types of eel ladders and collectors and via electrofishing. Yellow eels (the residential growth phase of adult eels) are generally monitored via fyke-net fishing and/or electrofishing. Silver eels are often monitored when leaving freshwater systems using different types of traps catching downstream migrating eel and via automatized fish camera counters with AI-algorithms, which can automatically identify species and size. Altogether, the gathered information is used for the national and international stock assessments (Fiskbarometern, 2026). In addition, eels are also collected from commercial fisheries to collect individual level data. Currently there is no standardized implementation of eDNA in the monitoring of European eel (Fiskbarometern, 2026).

## 1.4 Research Question

This study investigates the following research questions: 1. How is eDNA used in the monitoring of fish, with emphasis on the European eel (*Anguilla anguilla*)? 2. Which monitoring parameters can be assessed using eDNA? This was done by gathering a wide variety of studies in which eDNA had been used to monitor European eel, in vitro and in situ, and dividing them into categories based on their perceived area of use. The purpose of this study was hence to gather and summarize important information regarding eDNA as a monitoring tool for European eel, to establish how far research within the field of eel monitoring using eDNA has come, and to identify research gaps within the field. This information will hopefully aid in future monitoring and conservation efforts of the European eel, if not at least showcase what research is necessary in order to utilize eDNA as a monitoring method for the species in the future.

## 2. Method

The approach of this study was similar to that of a semi-systematic review and the process was similar to the guidelines described by Snyder et al. (2019). Only peer reviewed articles published in established scientific journals were used in this study. Relevant articles were found by searching thorough different databases accessed via the Swedish University of Agricultural Sciences. This included the databases Primo, Web of Science and Scopus. The open access search tool Google Scholar was also used. The search took place between 2026-03-23 and 2026-04-21.

When using these databases, the search was narrowed down by different combinations of search words and phrases. At first, a wider search was established by using the search words “*Anguilla anguilla* AND eDNA”. The search was specified and narrowed down by using a more extensive search phrase, “(eDNA OR "environmental DNA") AND ("anguilla anguilla" OR "European eel") AND monitor\*”. At a later stage of the search process, AI-search tools were also employed, including Scopus AI (Scopus AI 2026), a tool exclusive to the Scopus database, and Ai2 Asta (Ai2 Asta 2026). When using these tools, search words were not required. Instead, an early iteration of the research question was used; “Is eDNA a useful method for monitoring fish, with emphasis on European eel?”. Scopus-AI delivered a synthesis of relevant information to answer the question, through which all references were accessible. All relevant articles that had not yet been identified via the searches in the aforementioned databases were included. Ai2 Asta produced a list of articles, similarly to any search engine, categorized by how relevant they were to the research question and in what way. From these listed articles, those not yet included and deemed relevant enough (see further details below) were chosen (Figure 3).

The process of selecting articles was dynamic throughout the research process. Initially, only articles with titles related to the research question were chosen. The title had to include both environmental DNA or eDNA and *Anguilla anguilla* or European eel. Later, the search for relevant articles was expanded to studies using eDNA to monitor fish communities, but European eel had to be part of those fish communities, mentioned either in the abstract or in the full text as part of the result. This was checked by using Microsoft Edge’s word search function (command + F) for each article in which European eel was not found within the title or abstract. When analysing the result of this literature search, literature reviews were excluded (Figure 3).

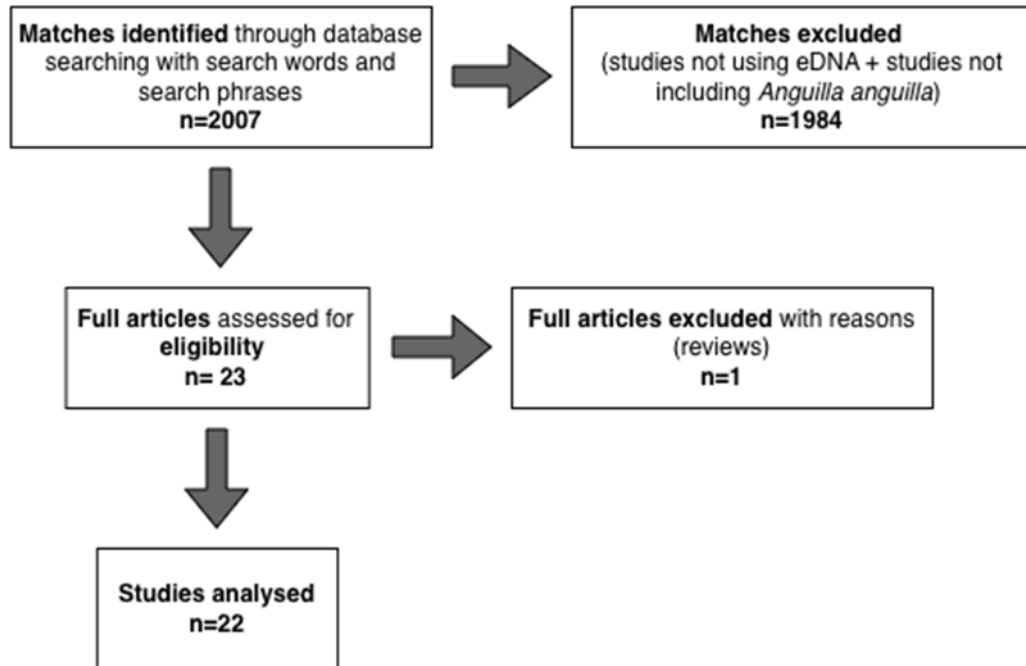


Figure 3. Workflow diagram showing the number of articles at each step of the process (i.e. identified matches, assessed articles, and analysed studies).

### 3. Result

The aforementioned search resulted in 22 articles that fit the previously stated criteria. They concerned different areas of study pertaining to eDNA and its' ability to monitor European eel and fish communities. These 22 studies were further divided into nine categories, depending on their area of use and the aims within each study: A) detecting presence, B) confirming absence, C) estimating abundance and/or biomass, D) surveying species composition in fish communities, E) surveying temporal changes and migration, F) surveying spatial distribution, G) detecting parasites, H) detecting hybridization, and I) surveying the effects of barriers on fish communities and fish migration (Table 1). Many of the studies were placed in two or three categories, in cases where multiple areas of use were applicable within a study, e.g. both detecting presence and surveying spatial distribution (Table 1). The number of studies related to each category varied, and most were in category A – detecting presence (Table 1, Figure 4). The search also resulted in several articles about eDNA and other anguillid species, such as Japanese eel (*Anguilla japonica*) and American eel (*Anguilla rostrata*). However, these were not included in this literature analysis because of the lack of time.

*Table 1. Overview of which category (area of use) the resulting 22 articles were placed in, if eDNA had been evaluated for the same area of use and if it worked (with sources listed). The current monitoring methods for each area of use are also listed, except for categories B) Confirming absence, and D) Detecting hybridization, since there were no current methods for the area of use, or the current method was not found. If eDNA has been used to evaluate the area of use is listed in the middle column, and the asterisk (\*) following 'Yes' for category B, G and H indicates that eDNA has been evaluated for the area of use, but only once. If using eDNA worked for the intended purpose is listed in the fourth column, and the asterisks (\*\*) following 'Yes' for category B, G and H indicates that it did work, but only in that one study. For categories C and D, eDNA is stated to work 'To some degree'. This means that the results of the studies included in these categories were inconsistent.*

Area of use	Current monitoring method	Has eDNA been evaluated for Did it work? Source		
		the same area of use?		
A. Detecting presence	Trawling, netting, trapping, electrofishing, automatic counter	Yes	Yes	Weldon et al. (2020), Barco et al. (2022), Fernandez et al. (2026), Vucić et al. (2023), Griffiths et al. (2020), Burgoa Cardás et al. (2020), Knudsen et al. (2019), Monaghan et al. (2026), Griffiths et al. (2025a), Griffiths et al. (2023), Schenekar et al. (2020)

B. Confirming absence	–	Yes*	Yes**	Griffiths et al. (2025b)
C. Estimating abundance and/or biomass	Trawling, netting, trapping, automatic counter	Yes	To some degree	Weldon et al. (2020), Fernandez et al. (2023), Halvorsen et al. (2023), Knudsen et al. (2019)
D. Surveying species composition in fish communities	Trawling, netting, trapping, electrofishing	Yes	To some degree	Barco et al. (2022), Fernandez et al. (2026), Griffiths et al. (2020), Hallam et al. (2023), Schenekar et al. (2020), Cunnington et al. (2024)
E. Surveying temporal changes and migration	Trawling, netting, trapping, automatic counter	Yes	Yes	Hallam et al. (2023), Burgoa Cardás et al. (2020), Griffiths et al. (2025a), Cunnington et al. (2024)
F. Surveying spatial distribution	Trawling, netting, trapping, electrofishing	Yes	Yes	Leerhøi et al. (2024), Vucić et al. (2023), Griffiths et al. (2023), Halvorsen et al. (2020)
G. Detecting parasites	Capture and euthanasia	Yes*	Yes**	De Noia et al. (2020)
H. Detecting hybridization	–	Yes*	Yes**	Crowley et al. (2025)
I. Surveying the effects of barriers on fish communities and fish migration	Netting, trapping, electrofishing	Yes	Yes	Overland et al. (2026), Halvorsen et al. (2020), Griffiths et al. (2025a), Griffiths et al. (2023), Muha et al. (2021)

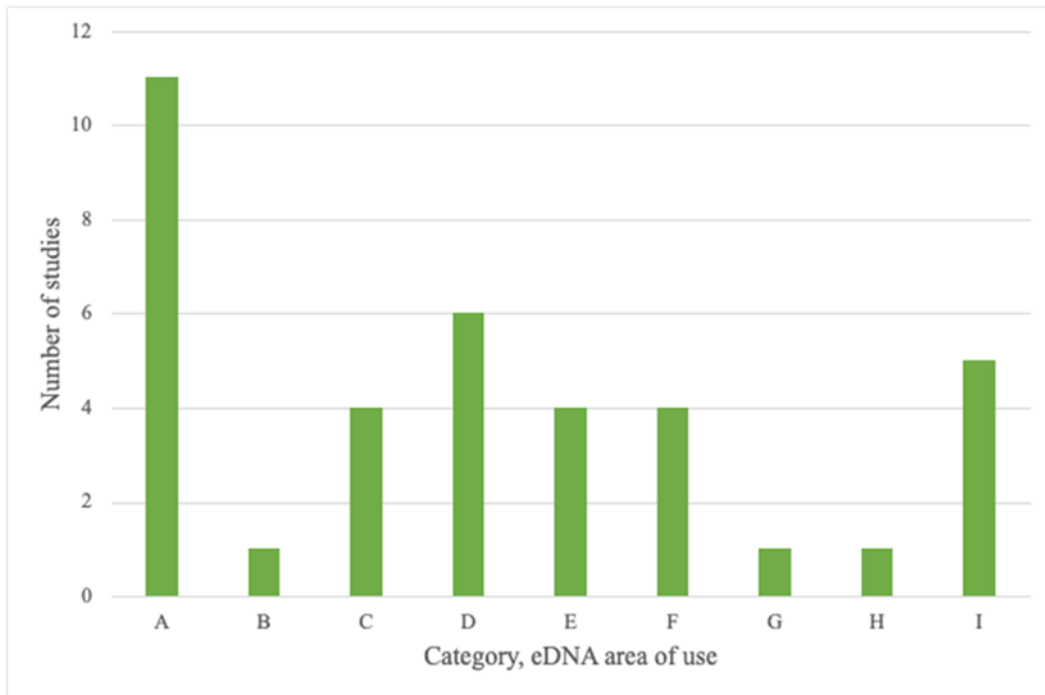


Figure 4. Division of the 22 selected studies of European eel and eDNA between the nine categories, A) detecting presence, B) confirming absence, C) estimating abundance and/or biomass, D) surveying species composition in fish communities, E) surveying temporal changes and migration, F) surveying spatial distribution, G) detecting parasites, H) detecting hybridization, and I) surveying the effects of barriers on fish communities and fish migration. Note that the same study might be present in two or three categories in cases where multiple categories were applicable within a study.

### 3.1 Detecting presence

The largest number of studies (11) concerned eDNA's ability to detect the presence of European eel either on its' own or in comparison to other current monitoring methods such as trawling, netting, and electrofishing (Table 1, Figure 4). Weldon et al. (2020), for example, compared eDNA to fyke netting in five Irish lakes and found that eDNA detected eel in 70 out of 84 water samples and detected eel DNA in lakes were fyke nets caught none. Similarly, Griffiths et al. (2020) studied European eel in pumped river catchments and compared eDNA metabarcoding to electrofishing and seine netting and found that eDNA metabarcoding detected eel in 14 out of 17 sites while the traditional methods only detected eel in 3 out of 17 sites. Although eDNA was less advantageous when studying entire fish communities, it was the only method able to detect European eel, when compared to bottom trawling and seine netting (Knudsen et al. 2019, Fernandez et al. 2026, Barco et al. 2022). Monaghan et al. (2026) compared the sensitivity and sampling effort needed for different eDNA methods

(qPCR and eDNA metabarcoding), and Burgoa Cardás et al. (2020) designed and validated a highly specific eDNA primer, that was able to detect eel DNA at very low concentrations. Vucić et al. (2023) also found that eDNA was a highly specific method for detecting eel in marine, brackish and freshwater.

### 3.2 Surveying species composition of fish communities

Similarly, a relatively larger number of studies (6) focused on if eDNA is an applicable method for surveying the species composition of fish communities, also in comparison to other monitoring methods or on its' own (Table 1, Figure 4). Barco et al. (2022) and Fernandez et al. (2026) found eDNA to be less effective than traditional methods when monitoring an entire fish community. eDNA and the traditional methods identified different parts of the community, or eDNA identified fewer species, but only eDNA was able to identify European eel and other rare or invasive species. However, when Griffiths et al. (2020) compared eDNA to traditional methods, eDNA was able to identify site occupancy to an equal or greater degree for 25 out of 26 species. Hallam et al. (2020) also found that species detection using eDNA across a single year included over 75% of species recorded in a 30-year historical dataset with traditional catch methods in the river Thames. Based on the results in these studies, I categorized eDNA to work “To some degree” when surveying species composition in fish communities (Table 1).

### 3.3 Surveying the effects of barriers on fish communities and fish migration

Five studies concerned using eDNA to survey the effects of barriers on fish communities and fish migration (Table 1, Figure 4). Halvorsen et al. (2020) found that the probability of detecting *A. anguilla* decreased significantly as the distance to the sea increased, and hydroelectric power stations were the only type of barrier to significantly affect the probability, decreasing the probability of detection of eel with eDNA with an increasing number of power stations. Overland et al. (2025) and Muha et al. (2021) studied how barrier removals affected fish populations and found that the removal of a barrier did not lead to a change in fish community diversity or relative abundance (Muha et al. 2021) and that *A. anguilla* was negatively affected (Overland et al. 2025). Overland et al. (2025) also found that eel was more likely to be detected downstream of barriers.

### 3.4 Estimating abundance and/or biomass

A smaller number of studies (4) focused on the use of eDNA in estimating eel abundance and/or biomass (Table 1, Figure 4). Weldon et al. (2020) found a significant positive relationship between eel biomass in individual fyke nets and mean eDNA-concentration in paired water samples taken after the nets had been removed. Halvorsen et al. (2023) instead chose to focus on estimating the number of individuals and did so by using eDNA to detect the haplotypes of individual eels in a closed aquatic environment and in rivers. In the closed environment, eDNA was able to identify all individual haplotypes, and when the method was validated in three riverine environments, it detected 13 different individuals. Fernandez et al. (2023) found that riverine conditions affected the correlation between eDNA-quantity and eel biomass, and Knudsen et al. (2019) found no significant correlation between biomass caught by trawling and eDNA-concentration in water samples taken at the same time. Hence, based on the results in these studies, I categorized eDNA to work “To some degree” when estimating biomass and/or abundance (Table 1).

### 3.5 Surveying temporal changes and migration

Four studies focused on using eDNA to survey temporal changes, such as migration, (Table 1, Figure 4). Hallam et al. (2023) and Burgoa Cardás (2020) both found that eDNA detection corresponded with expected eel migration, e.g. by an increase in relative read abundance (i.e., number of detected eDNA molecules after processing and analysis, Hallam et al. 2023). However, Griffiths et al. (2020) found that seasonal variation in eDNA patterns is not always comparable between river types, but that detections of *A. anguilla* were highest in summer between all different types.

### 3.6 Surveying spatial distribution

The same number of studies (4) concerned using eDNA to survey spatial distribution of eel (Table 1, Figure 4). Vucić et al. (2023), for example, conducted the first known study of eel distribution in the Adriatic Sea using eDNA and found that eel DNA was more frequently detected in marine and brackish habitats than in freshwater habitats. Griffiths et al. (2023) studied the distribution of European eel in freshwater systems and found that the species was limited to lowland freshwater systems, and that the negative correlation between eels and elevation, distance from coast, and number of barriers was significant. Leerhøi et

al. (2024) stood out by using citizen science to monitor the distribution of several fish species (one of them being *A. anguilla*) in Denmark.

### 3.7 Confirming absence, detecting parasites, and detecting hybridization

The categories ‘confirming absence’, ‘detecting parasites’, and ‘detecting hybridization’ were outliers, with one study in each (Table 1, Figure 4). Griffiths et al. (2025b) developed a confidence in absence framework, with the intention of making it possible to confirm the absence of European eel from a location with confidence, using eDNA, aiming to aid in conservation management. However, this model has not yet been validated by others. De Noia et al. (2020) developed and validated a rapid, non-lethal and non-invasive eDNA method to detect the invasive nematode parasite *Anguillicoloides crassus* in the swim bladder of the European eel. Crowley et al. (2025) used eDNA to detect mitochondrial DNA of European eel in Newfoundland, Canada, where the American eel should be the only anguillid species present. The presence of hybrids outside of their normal range, having previously only been found in Icelandic waters, was further confirmed by sequencing the entire genome of several individuals .

### 3.8 Alternative or complimentary method

Of the 22 above mentioned studies, nine suggest eDNA as a complementary or alternative method to other more traditional or targeted methods in their discussion or conclusion (Weldon et al. 2020, Barco et al. 2022, Crowley et al. 2025, Fernandez et al. 2026, Griffiths et al. 2023, Knudsen et al. 2019, Griffiths et al. 2020, Burgoa Cardás et al. 2020, and Fernandez et al. 2023).

## 4. Discussion

In this study, I compiled 22 articles concerning how eDNA can be of use when monitoring European eel. I found that most of these articles (11 out of 22) concerned using eDNA to detect European eel in some way, either on its' own, comparing different eDNA methods to each other, or in comparison to other more traditional monitoring methods. This is unsurprising, as eDNA has been established as a reliable detection method since the early 2010's (Rees, et al. 2014). Studies evaluating the methodology and comparing it to more conventional methods have mostly focused on aquatic taxa such as fishes and amphibians, especially with regards to rare, cryptic, endangered or invasive species (Beng & Corlett 2020). Dejean et al. (2012), for example, demonstrated that eDNA-detection surpassed traditional amphibian survey methods when monitoring the invasive American Bullfrog (*Rana catesbeiana*). Deutschmann et al. (2019) found that eDNA was highly specific for a target species, only amplifying brown trout (*Salmo trutta*) even though rainbow trout (*Oncorhynchus mykiss*) was present in the system. European eel is seemingly a fitting species for eDNA-detection considering its' endangered status and elusive nature, which might explain why many studies chose to focus on this species and method.

Fewer studies (4 respectively) focused on estimating abundance and/or biomass, surveying temporal changes and migration, and surveying spatial distribution of European eel using eDNA. To differentiate "spatial distribution" and "detecting presence" as two categories, as I did here, was a bit difficult, since surveying spatial distribution of eel is based on being able to detect where they reside in a system. So, the separation of studies into these categories was based on if I found that the purpose of the study was to find out where in a larger system European eel could be found. A study of the spatial distribution of Japanese eel at river basin scale suggested that eDNA is an appropriate tool for this purpose. eDNA detected Japanese eel at nearly all study sites where the species was caught with electrofishing, and where it was expected to be found, but also further up the rivers where electrofishing had not caught any eel (Itakura et al. 2019).

The small number of studies concerning using eDNA to estimate biomass was to be expected, since using eDNA to estimate abundance or biomass is limited by the knowledge gap of how biotic and abiotic factors affect eDNA degradation and detection (Rees et al. 2014). Examples of biotic factors are intraspecific variation in DNA production among individuals experiencing the same environment, stress, metabolism and size, distribution and density of individuals within the environment, feeding and diet, and reproduction and migration. Water flow and temperature, water depth, and degradation due to UV-radiation, pH, microbial activity and enzymatic digestion are considered abiotic factors (Rourke et al. 2022). Some studies have explored if eDNA can provide quantitative information,

e.g. using mock communities or combined conventional surveys with eDNA, but the results of these studies have been varied, both strong and weak or with no clear quantitative estimates (Beng & Corlett 2020). A similar pattern is found among the studies represented in the category, with Weldon et al. (2020) finding a significant positive relationship between eDNA-concentration and eel biomass in individual fyke nets, and Knudsen et al. (2019) finding no significant correlation between eDNA-concentration and biomass caught by trawling. Worth noting is that no eels were caught by trawling in the study made by Knudsen et al. (2019) and that the correlation between eDNA-concentration and biomass thus does not relate to European eel. Although Halvorsen et al. (2023) are seemingly alone in their approach of using the different haplotypes to estimate abundance of individual eels, the method has been used to estimate the abundance of other species. Yoshitake et al. (2021) applied the haplotype-counting method in a study of Pacific bluefin tuna (*Thunnus orientalis*), researching a potential non-invasive method for conducting fish stock surveys, and Dugal et al. 2022 found another potential in non-invasive analysis of population genetics in whale sharks (*Rhincodon typus*) with the help of eDNA samples. With regards to the positive results in the study conducted by Halvarson et al. (2023), it will be interesting to see if more studies of haplotype-counting for the European eel will be made in the future.

Five studies focused on using eDNA to survey the effects of barriers on fish communities and fish migration. Halvorsen et al. (2020) made a particularly interesting finding considering the challenges European eel face in northern Europe. The probability of detecting eel eDNA along the coast of southern Norway decreased significantly with the number of hydroelectric power stations, even when accounting for the effect of distance from the sea (Halvorsen et al. 2020). Currently there are around 2000 hydroelectric power stations in Sweden (Energiföretagen 2023) and migration barriers are considered one of many reasons behind the European eel's declining population (IUCN 2018). Using a similar sampling scheme to Halvarson et al. (2020) when monitoring eel distribution could make it possible to establish which power stations form the most effective migration barriers in Swedish waterways. However, if one were to remove a barrier to improve migration routes it is important to remember to monitor both before and after the barrier removal to ensure that it has the intended effect, as established by both Muha et al. (2021) and Overland et al. (2026), and to do so in a way that accounts for natural variation in population abundance.

## 4.1 Complementary or Alternative?

As mentioned above, nine studies suggested eDNA as a complementary or alternative method to other more traditional methods. But, in what way?

Weldon et al. (2020) suggested that eDNA should complement fyke net data, since fyke nets are a biased sampling method only able to catch eels of a certain size. Fyke nets alone may lead to a false zero if eel numbers are low and netting is infrequent, and eDNA has the potential to detect smaller or newly established local stocks due to its' sensitivity. Barco et al. (2022) suggested that eDNA based fish surveys should be implemented alongside current surveys when monitoring fish populations, as eDNA detected species that trawling had not detected in ten years of monitoring the area, among them European eel. Fernandez et al. (2026) made a similar suggestion; that eDNA data should complement net data, since eDNA is highly effective in detecting rare species, provides taxonomic resolution, and is non-lethal, non-destructive and cost-effective. Griffiths et al. (2023) made the suggestion that eDNA methods can aid in detecting eel in remote areas that are hard to sample otherwise.

Certain limitations might prevent eDNA from replacing traditional monitoring methods. Capture-based methods can easily and with more certainty provide information about fish condition and population structure, and while eDNA is able to provide data on presence and absence, it cannot do so in real time, and there is a higher degree of uncertainty about the actual location of the species you are looking for (Evans & Lamberti 2018 ). Another limitation worth considering, according to Evans and Lamberti (2018), is that mitochondrial eDNA analysis is unable to distinguish hybrids from 'pure' species.

Despite these limitations there are many advantages to using eDNA as a monitoring method. It is a non-invasive method, able to detect low-abundance species often missed by traditional surveys without capture, stress or harm, which is especially important when monitoring rare or endangered species such as European eel (Duarte et al. 2025). It is also considered more cost-effective, with a reduced field effort compared to extensive fieldwork needed in current monitoring methods, and with shorter handling time and rapid results of eDNA-analysis (Duarte et al. 2025, Ramírez-Amaro et al. 2022). Because of this, eDNA can be applied at a larger scale than other methods (Duarte et al. 2025).

## 4.2 Knowledge gaps

There are some limitations to the eDNA method caused by a lack of information. Of the articles analysed in this study, several mention aspects of eDNA research that need development before eDNA can be implemented as a commonly used tool for monitoring of European eel, or fish in general.

One such aspect is how eDNA interacts with the environment, e.g. how stratification would affect eDNA dispersal in lakes during different seasons (Weldon et al. 2020), how tidal floods affect eDNA dispersal in marine waters (Fernandez et al. 2026), or how different hydrographic factors affect the

downstream transport of eDNA in rivers (Fernandez et al. 2023). When studying anthropogenically affected rivers, it can also be important to gain a better understanding of how structures such as pumps affect eDNA dispersal in highly variable environments (Griffiths et al. 2020).

Another such aspect is how fish ecology and behaviour affect the sampling of eDNA, e.g. how one should account for the patchy distribution of fish within a lake, especially since European eel is a benthic and demersal fish (Weldon et al. 2020). To quantify eDNA and estimate biomass or abundance is limited by a wide variety of biotic and abiotic factors that we do not completely understand yet (Hallam et al. 2023), and using eDNA to monitor entire fish communities is limited by incomplete metabarcoding libraries and primer bias (Schenekar et al. 2020). Beyond what is mentioned in the articles analysed in this study there seems to be a need to standardise eDNA-sampling and to make comparing results easier by agreeing on what constitutes a positive detection (Rees et al. 2014). This is complicated by the difference in local conditions regarding e.g. salinity and tidal fluctuations, and how these abiotic factors affect eDNA degradation. This, in turn, leads to a need for local validation of sampling protocols to minimize false negatives and false positives (Duarte et al. 2025). False negatives refer to when the target-species is present in the system but is undetected in the eDNA analysis. False positives refer to when water samples are contaminated with eDNA from outside the system, or organisms leave the system but their viable eDNA remains to be detected (Evans & Lamberti 2018). A false positive detection of eel could be caused by exogenous DNA from e.g. dead fish carcasses or faeces from fish-eating animals, which is hard to determine, and even harder to know how to account for in eDNA sampling. Similarly to any other ecological field survey, it is also difficult to know if a negative result actually means that species is not present, but this can be counteracted with more sampling (Rishan et al. 2023).

### 4.3 Limitations of study and future research

The very limited time frame (10 weeks) for this study prevented a more exhaustive search and analysis of relevant literature within the area of research. It is highly likely that the number of keywords and the criteria used to narrow down search results resulted in relevant literature not being included in the analysis of this study, which in turn affected the results. Publishing bias could also be a limiting factor to this study. Most articles analysed here presented positive results regarding the use of eDNA in monitoring of European eel, with several authors suggesting the method as a complementary or even an alternative method to more traditional monitoring methods. Researchers are less likely to publish negative results, which in turn affects the results of this study.

Despite using search words and phrases such as “*Anguilla anguilla* AND eDNA” or “(eDNA OR “environmental DNA”) AND (“anguilla anguilla” OR “European eel”) AND monitor\*” research concerning eDNA and other anguillid species, such as Japanese eel (*Anguilla japonica*), often showed up in the resulting matches, especially when using the Scopus AI-function. This could be due to lacking search language, misuse of filtering functions, or AI-tools not producing narrow enough searches. These studies were not included in the analysis; however, a future literature review could compare studies done concerning eDNA and European eel, and eDNA and Japanese eel, or other anguillid species. It would be interesting to see in which ways these studies are similar to or differ from one another, which areas the researchers choose to focus on and why. Results from a study concerning Japanese eel or American eel (*Anguilla rostrata*) may aid in the monitoring of European eel using eDNA. Given more time, a proper literature review would also benefit from more strictly followed criteria when choosing what studies to include in the resulting analysis. In this study, the process was dynamic, which makes it harder to produce the same results if one would like to repeat the study. Additionally, if given the opportunity to do a field study, I would focus my research on how to use eDNA to estimate eel abundance and/or biomass. The lack of research within this area seems to be the largest barrier to utilizing eDNA more widely in monitoring today. The focus of one such field study could be on how abiotic factors affect eDNA-concentration and its’ correlation to biomass or abundance. I also think it would be very interesting to attempt to apply the haplotype counting method, used by Halvorsen et al. (2023), at a larger scale (e.g. in a river or lake with higher eel abundance) and test its’ accuracy.

eDNA is a relatively new research field (Figure 2). All studies analysed within this study, except one (Knudsen et al. 2019), were published in 2020–2026. A possible explanation to the small number of relevant articles and the gaps of knowledge could be that more studies are to be published soon within the future, or that the research is currently being undertaken. The first study of eDNA pertaining to a macroorganism was published only 18 years ago (Ficetola et al. 2008), and with eDNA being non-invasive and highly sensitive for detecting rare species, it is likely more research will concern eDNA and the endangered species *A. anguilla* in the future.

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