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Detection of a Diverse Marine Fish Fauna Using Environmental DNA from Seawater Samples

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Abstract

Marine ecosystems worldwide are under threat with many fish species and populations suffering from human over-exploitation. This is greatly impacting global biodiversity, economy and human health. Intriguingly, marine fish are largely surveyed using selective and invasive methods, which are mostly limited to commercial species, and restricted to particular areas with favourable conditions. Furthermore, misidentification of species represents a major problem. Here, we investigate the potential of using metabarcoding of environmental DNA (eDNA) obtained directly from seawater samples to account for marine fish biodiversity. This eDNA approach has recently been used successfully in freshwater environments, but never in marine settings. We isolate eDNA from ½-litre seawater samples collected in a temperate marine ecosystem in Denmark. Using next-generation DNA sequencing of PCR amplicons, we obtain eDNA from 15 different fish species, including both important consumption species, as well as species rarely or never recorded by conventional monitoring. We also detect eDNA from a rare vagrant species in the area; European pilchard (Sardina pilchardus). Additionally, we detect four bird species. Records in national databases confirmed the occurrence of all detected species. To investigate the efficiency of the eDNA approach, we compared its performance with 9 methods conventionally used in marine fish surveys. Promisingly, eDNA covered the fish diversity better than or equal to any of the applied conventional methods. Our study demonstrates that even small samples of seawater contain eDNA from a wide range of local fish species. Finally, in order to examine the potential dispersal of eDNA in oceans, we performed an experiment addressing eDNA degradation in seawater, which shows that even small (100-bp) eDNA fragments degrades beyond detectability within days. Although further studies are needed to validate the eDNA approach in varying environmental conditions, our findings provide a strong proof-of-concept with great perspectives for future monitoring of marine biodiversity and resources.

Introduction

The marine environment represents considerable value in terms of biodiversity [1] and economics through fisheries and other products derived from the sea [2,3]. Fish are the most species-rich group of vertebrates and constitute a keystone in present-day monitoring of environmental health of marine ecosystems. Nevertheless, fish species and populations worldwide are under threat and suffer from over-exploitation [4–7] with considerable impact on human health [8]. Contemporary monitoring of marine fish biodiversity and resources is largely dependent on invasive and selective methods, such as bottom trawls and rotenone poisoning [9], which can only be carried out in particular areas where conditions are favourable. Furthermore, correct identification of many species across both non-commercial (e.g. Syngnathidae) and commercial (e.g. Ammodytidae) groups is problematic using traditional methods; leaving databases flawed with errors [10] and checklists incomplete [11,12].

An alternative approach for monitoring marine fish is that of environmental DNA (eDNA), i.e. the extraction and analysis of genetic material obtained directly from environmental samples [13]. For macro-organisms, the approach was first applied to terrestrial sediment samples revealing ecosystems of extinct and extant mammals, birds, and plants [14]. Later the same approach was successfully used on ancient cave sediments [15] and ice cores [16] as well as ancient and contemporary sediments across a variety of taxa, habitats and climates [17–28]. Recently, eDNA from Bull frogs was successfully retrieved from contemporary pond water samples [29]. This approach has since been used to detect other amphibians [30] and invasive fish species [31] in freshwater. Furthermore, it has been demonstrated that rare and endangered freshwater insects, crustaceans, amphibians, fish and mammals can be monitored and quantified using eDNA, and that such an approach can account for entire lake faunas [32]. Despite these successful applications, the detection of macro-organisms by
eDNA has to our knowledge never been reported from marine water samples.

In this study we present the first recording of marine fish biodiversity using eDNA from seawater samples.

Results

Three seawater samples were collected in a temperate marine ecosystem in Denmark (Fig. 1). Samples were filtered, DNA amplified and sequenced (see Materials and Methods section). A comparison with the GenBank sequence database revealed DNA from 15 different fish species, representing a diversity of 9 orders and 11 families (Fig. 1, Table 1). These include both important consumption species, such as Atlantic cod (Gadus morhua), European eel (Anguilla anguilla), European plaice (Pleuronectes platessa) and Atlantic herring (Clupea harengus), as well as non-commercial species like Goldsinny-wrasse (Ctenolabrus rupestris) and Atlantic herring (Clupea harengus). Myoxocephalus scorpius.

Discussion

While it has been widely demonstrated that microbial (prokaryotic and eukaryotic) biodiversity can be studied by sequencing DNA from filtered seawater samples (e.g. [33–36]), we show here, for the first time, that seawater contain a high density of detectable eDNA from macro-organisms, such as fish. At the same time, it has now been demonstrated that also eDNA from whales can be obtained from seawater [37]. Targeting DNA from macro-organisms in environmental water samples is not comparable to targeting microbial organisms, as the former is present only as true eDNA (cellular debris or free DNA), whereas the latter may be detected by DNA deriving from whole, living organisms present in the water samples. The fish eDNA detected in this study most likely derives from intestinal cells, sloughed skin, scales or mucus and may consists of both free DNA, cellular debris and particle bound DNA. Animal cells exposed to the environment will quickly undergo lyses, but the specific source and relative ratio of cellular bound and free DNA is mostly studied in soil and sediment samples (e.g. [38,39,40]), but remains unclear in aquatic environmental samples. The filter matrix size of 0.45 µm, used in this study and [30] as well as 1.5 µm filters [31] and even 3.0 µm filters [41] have been used previously to isolate eDNA from freshwater. Considering the size of a DNA molecule, it is thus quite likely that some of the detected eDNA is particle or cellular bound.

Despite recent successful applications of eDNA detection in freshwater systems [29–32,41] we find it surprising how well the approach performs on marine water samples considering: i) the larger water-volume to biomass ratio of marine ecosystems compared to that of freshwater, ii) the effects of sea-currents and wave action, and iii) the impact of salinity on the preservation and extraction of eDNA. These factors likely mean that eDNA in marine water is much less concentrated, more quickly dispersed, and may be less efficiently extracted from the water column. Still, our data reveals that marine water samples of just 0.5 litres yield eDNA from a variety of fish taxa, ranging from highly abundant species, such as the European plaice, to the rarely recorded vagrant species; European pilchard (Fig. 1). We found a small difference in the fish species compositions recovered by eDNA from the three different sites sampled at a very localised scale (Fig. 1). However, it remains unclear whether these differences were due to stochasticity in PCR amplification, insufficient depth of sequencing or a truly patchy occurrence of fish assemblages and their eDNA in the environment.

Importantly, when comparing results obtained with eDNA to those obtained from an array of 9 different conventional methods used in fish surveys, the eDNA approach performed remarkably well (Fig. 2). It should be noted that snorkeling, trawl and seine, which represents the methods with efficiencies closest to the eDNA approach, are either heavily dependent on competent experts in fish identification on-site (snorkeling), or only possible where seabed conditions allow it (trawl and seine). Stratified randomized bottom trawl surveys represent a cornerstone for marine monitoring in the framework of the International Council for the Exploration of the Sea [3]. These surveys cannot be carried out in shallow waters, areas with rocks, reefs, kelp or other obstacles on the seabed, and are also difficult in areas with soft sediment [42,43]. This leaves a bias in the way marine fish faunas are monitored today, excluding important areas for biodiversity and fisheries. In contrast to many conventional methods, the eDNA method can be performed in virtually any marine habitat, and require little expertise or effort in sampling. Additionally, the molecular identification is more confident and objective than visual identification of species, which is in many cases difficult even for experts. Conversely, DNA based species identification rely on knowledge of species-specific sequences compiled by taxonomic experts. However, global initiatives addressing this need have been established, and databases are rapidly growing (http://www.boldsystems.org). A specific initiative to provide DNA barcodes of all the world’s fish species was launched in 2005, and has today covered more than a third of all described species [44,45]. It is
clear that this remaining gap in knowledge will for some time impair the usefulness of eDNA monitoring in faunas where all species have not yet been DNA barcoded. On the other hand, the most complex and species-rich systems are also the most challenging to monitor with conventional methods, and likely where the advantage of eDNA will represent the most significant improvement for future monitoring.

It is obvious that sea currents may move eDNA beyond the area where species actually occur, leaving the possibility for false positive records. Also, fish predators such as birds, mammals or other fish species may distribute DNA from prey items across marine localities through defection. Importantly however, our results from the fish eDNA degradation experiment convincingly show, that even small (100-bp) eDNA fragments in seawater persists for only a few days above detection threshold of approximately 25 molecules pr 400 ml seawater at 15°C (Fig. 3).

In freshwater, the decay of eDNA beyond the threshold of detectability has been demonstrated to happen at a scale of days or weeks [32,46]. Notably, however, DNA degradation in seawater has previously been suggested to be substantially faster with an empirical turnover rate as low as 10 hours [47], which supports our findings and indicate lower probability of long distance dispersal of eDNA in marine ecosystems. Using an approximate degradation time of eDNA beyond detectability of minimum 12 hours and maximum 1 week, and given a rough average speed of ocean currents of 1 m/sec (normal in the Sound of Elsinore, sampled in this study), we estimate that eDNA could in this case travel between ca. 40 km–600 km in the oceans before degraded beyond detectability.

However, many other factors such as water temperature, wind speed, wind direction and local changes in currents will have great impact on the potential distance that eDNA can be transported in oceans. The average initial concentration of DNA molecules pr 400 ml seawater in the three original collected samples used for sequencing, showed similar (446 vs. 48) or very similar (215 vs. 214) values as seen in the eDNA degradation experiment for Gasterosteus aculeatus and Platichthys flesus, respectively. Given the different time that the water samples were collected for the two purposes (October 2011 vs. May 2012), it is obvious that seasonal and yearly variation as well as species phylogeny of G. aculeatus could easily account for the observed difference in eDNA for this species.

Most importantly, as a consequence of continuous dilution, the probability of detecting eDNA in marine waters very likely decreases rapidly with distance to its source, making recovery of eDNA of local origin much more plausible. Therefore, we feel convinced that eDNA obtained from marine water samples should represent only local fish fauna. This may also be the reason why we do not detect any truly exotic species (i.e. species living in deeper waters, different salinity or different latitude). Apart from the European pilchard, we only recovered eDNA from species resident to the area, suggesting that either there is no eDNA from non-resident species present, or that such DNA is too dilute to be detected.

**Table 1. Summary of species-specific eDNA sequences recovered in this study.**

<table>
<thead>
<tr>
<th>Taxon</th>
<th>Order</th>
<th>Family</th>
<th>Species</th>
<th>Sequence (5’-3’)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fish</td>
<td>Pleuronectiformes</td>
<td>Pleuronectidae</td>
<td>Pleuronectes platessa</td>
<td>CGGCTGTCAGCCGACACATCAAGCCCAGGTGATACT</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Limanda lindana</td>
<td></td>
<td>ACCTCTTTCCATCCACGTACTCTATCAAGCCCAGGTGATACT</td>
</tr>
<tr>
<td>Pleuronectiformes</td>
<td>Pleuronectidae</td>
<td>Platicthys flesus</td>
<td></td>
<td>CCACCTCTTCAGCCACATTAAGCCCAGGTGATACT</td>
</tr>
<tr>
<td>Perciformes</td>
<td>Zoarcidae</td>
<td>Zoarcus viviparus</td>
<td></td>
<td>CACTAGTCACCCACATCAAGCCCAGGTGATACT</td>
</tr>
<tr>
<td></td>
<td>Labridae</td>
<td>Ctenolabrus rupestris</td>
<td></td>
<td>TGACTATATTGTTGCTCCATCCATACACACTTCTCA</td>
</tr>
<tr>
<td></td>
<td>Trachinidae</td>
<td>Trachinus draco</td>
<td></td>
<td>CCCTCTAGTACTCTTCCTATATTTAAGGGTAGTTACT</td>
</tr>
<tr>
<td>Anguilliformes</td>
<td>Anguillidae</td>
<td>Anguilla anguilla</td>
<td></td>
<td>CCAATAGTTACTCGCCACACATTAAGGGAGGTGATT</td>
</tr>
<tr>
<td>Salmoniformes</td>
<td>Salmonidae</td>
<td>Salmo trutta</td>
<td></td>
<td>ACCCCCTAGTACCCACCTCTACCATCAAGCCCAGGTGATACT</td>
</tr>
<tr>
<td>Gadiformes</td>
<td>Gadidae</td>
<td>Gadus morhua</td>
<td></td>
<td>CCCAGCGTACCCACCTACTGTTAAGGGCCAGGTGATT</td>
</tr>
<tr>
<td>Gasterosteiformes</td>
<td>Gasterosteidae</td>
<td>Gasterostes aculeatus</td>
<td></td>
<td>CCAATTGACTCTCCACCTACCATCAAGGGCCAGGTGATT</td>
</tr>
<tr>
<td>Gasterosteiformes</td>
<td>Gasterosteidae</td>
<td>Spinachia spinachia</td>
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<td>CCAATATTACCTTCCCTATTTAAGGGAGGTGATT</td>
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<tr>
<td>Syngnathiformes</td>
<td>Syngnathidae</td>
<td>Syngnathus acus</td>
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<td>CCTTATGTTACT CCTTACATACCAACACCAAGGTGATT</td>
</tr>
<tr>
<td>Clupeiformes</td>
<td>Clupeidae</td>
<td>Sardina pilchardus</td>
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<td>CCCATGTTACCCACCCACACATTAAGGGCCAGGTGATT</td>
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<td>Clupeiformes</td>
<td>Clupeidae</td>
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<td>Scorpaeniformes</td>
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<td>Birds</td>
<td>Gaviformes</td>
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<td></td>
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<tr>
<td>Columbiformes</td>
<td>Columbidae</td>
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<td>Anseriformes</td>
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<td></td>
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</tr>
<tr>
<td>Pelecaniformes</td>
<td>Phalacrocoracidae</td>
<td>Phalacrocorax carbo</td>
<td></td>
<td>CTAAGAGCACATCTAGGTTTCATACACTCTTCCTTCTTACACACAAATA</td>
</tr>
</tbody>
</table>

All sequences are generated by pyrosequencing using Roche GS FLX 454 platform, except the 5 sequences obtained with species-specific primers (see Table 2), which are generated by cloning and subsequent Sanger sequencing. All sequences are full-length 100% match to the particular species only, identified by BLAST to the Genbank nucleotide database. Sequences are given without primers.

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picked up with the applied sampling procedure. The recovery of eDNA from the European pilchard, which is normally regarded as a warm-temperate species, is somewhat surprising given that the species is only rarely sighted in the sampling area. However, this species is getting increasingly more common in the northern North Sea and adjacent waters possibly due to warmer climate [48]. Furthermore, it is a species that is easily overlooked by conventional surveys due to similarity to common resident taxa. Therefore, we find it likely that the eDNA detection of European pilchard is due to authentic occurrence of the species in the area, rather than eDNA originating far from the sampling site. The recovery of eDNA from Red-throated loon (Gavia stellata) was also unexpected, but this finding could be authenticated by exact records in the national bird watching database (http://www.dobbasen.dk/) showing the species to be locally present at the time of sampling. We exclude the possibility of a laboratory contamination, based on negative PCR controls, extraction blanks and since no work has ever been performed on the particular species in the settings where this study was carried out. Hence, these findings illustrate how the eDNA approach may be useful in detecting unexpected species.

Despite our promising findings, it is important to emphasize that a number of issues need to be thoroughly addressed before eDNA can be considered a reliable tool for monitoring biodiversity in marine ecosystems. In particular the dispersal of eDNA in marine water must be better understood. This includes to what extent abiotic factors, like temperature and salinity, affect results. Similarly, an understanding of the phenology, changing metabolism and DNA excretion of target species may well have implications for the use of eDNA in monitoring.

It also remains untested whether the amount of eDNA molecules in marine water reflects population sizes and/or biomass of the local fauna as seen is freshwater [32,41]. This has large applications for monitoring of marine biodiversity and in particular fisheries, where data beyond species presence is essential.

Another potential limitation for the eDNA approach is PCR primer design. It is inherent to the use of generic primers that there is a trade-off between targeting higher taxonomic levels and detecting rare sequences. Primer affinity bias leads to certain sequences (species) amplifying less efficiently than others, potentially limiting the monitoring results to species, which are expected to be locally present and are therefore used in primer design, or in general simply to species-specific sequences with the best primer affinity. However, this limitation will continuously become less crucial due to optimization and publication of primers for eDNA studies, as well as significant increase in sequencing depth and rapid advances in sequencing technology, some of which are independent of initial PCR amplification.

Regardless of many potential present limitations and a need for more basic knowledge, the eDNA approach in marine environments have widespread perspectives in terms of biodiversity monitoring and fisheries. This study provides the first evidence that a very simple eDNA based survey may offer a coverage of local marine fish faunas, which is comparatively better than, or at least as good as, any single conventional method used here. Importantly, we also demonstrate experimentally that eDNA degrades rapidly in seawater, indicating that detectable DNA is most likely of local origin. We believe that eDNA based surveys
may in the future fill an important gap in broad-scale monitoring of marine biodiversity and resources.

**Materials and Methods**

**Sampling locality**
The study was carried out at The Sound of Elsinore, Denmark (56.04387°N, 12.61309°E) (Fig. 1).

**Conventional fish surveys**
Occurrence data of fish species in the study area was obtained in late August in 2009, 2010 and 2011 by experiments led by fish expert PRM (Table S1). In order to find as many species as possible, a wide range of methods were applied each year: five fish pots, two fyke-nets, one beach-seine (width 6 m) dragged for about 100 m near shore, one multi-mesh gillnet (100*1.5 m, mesh sizes 6.5–110 mm), two hours of push netting (width 68 cm, mesh size 8 mm), two hours of angling with lures, two hours of snorkeling during the day, two hours of snorkeling at night, and half an hour of bottom trawling (width 4 m, height 1.5 m, cod-end mesh size 10 mm) from R/V Ophelia.

Permission for scientific fishing was provided by the Danish Ministry for Food, Agriculture and Fishery (journal no. 2009-02530-23088).

**Water sampling**
Three 1.5-litre seawater samples were collected on October 1st 2011. Samples were collected along the inner pier, along the outer pier and on open beach (Fig. 1). Samples were collected from surface water at depths of 1.5–6 m. Each sample was a pool of 30 sub-samples of each 50 ml collected along a 145 m transect, taking one sub-sample every 5 m. All samples were immediately stored at −20°C until extracted.

For the eDNA degradation experiment, a total of 50 l of seawater was collected as twenty-five 2-l samples May 16th 2012 in The Sound of Elsinore (outer pier and open beach), where the original samples, used for sequencing, were also collected. The samples were pooled into a 54 l aquarium and an initial sub-sample of 400 ml was taken within one hour after sampling (t = 0). The aquarium was set up to mimic natural conditions, kept at a constant 15°C, with a 12-hour daylight cycle (standard household 15 watt neon tube) and equipped with a circulation pump powerhead (600 l/hour) ensuring full admixture and oxygenation. Subsamples of 400 ml water were taken from the aquarium at close intervals (hours – days) from May 16th to May 31st 2012, and all samples were immediately stored at −20°C until DNA extraction.

**DNA extraction**
½ litre of each of the three 1.5-litre seawater samples was vacuum-filtered onto 47 mm diameter 0.45-µm pore size nylon filters (Osmonics, Penang, Malaysia). Immediately after, DNA was extracted from the filters using bead beating and Qiagen DNeasy Blood & Tissue Kit (using spin-column protocol). Filters were rolled up, cut into ca. 1 mm slices and placed in 2 ml tubes. 0.3 g of 0.5 mm Zirconia/Silica Beads (Biospec Products, Bartlesville,
Table 2. Primers and probe details showing sequences, target taxa and fragment sizes.

<table>
<thead>
<tr>
<th>Name</th>
<th>Sequence (5’-3’)</th>
<th>Target taxon</th>
<th>Fragment</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fish2CBR</td>
<td>GATGGCGTAGGCAAAACAGAA</td>
<td>Fish</td>
<td>80</td>
</tr>
<tr>
<td>Fish2CBL</td>
<td>ACAACTTCACCCCTGCAAAC</td>
<td>Fish</td>
<td>80</td>
</tr>
<tr>
<td>Fish2degCBL</td>
<td>AAACACCATCCCTGCAAAY</td>
<td>Fish</td>
<td>80</td>
</tr>
<tr>
<td>Fish2CBR</td>
<td>GATGCGTAGGCAAAACAGGA</td>
<td>Clupea harensgus</td>
<td>85</td>
</tr>
<tr>
<td>ClupeaCBL</td>
<td>CATAGCCGATTCTCAGTCA</td>
<td>Myoxo ceaphalus</td>
<td>72</td>
</tr>
<tr>
<td>MyoxoCBR</td>
<td>AAGGGGAAAGGAAAGTGAGAA</td>
<td>Salmo trutta</td>
<td>87</td>
</tr>
<tr>
<td>SalmoCBL</td>
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<td>Clionalabrus rupestris</td>
<td>76</td>
</tr>
<tr>
<td>LabrusCBL</td>
<td>CGCCTCTATCTCTCCTATCC</td>
<td>Ctenaurocras carbo</td>
<td>92</td>
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<tr>
<td>TrachuCBL</td>
<td>CGTTCCACCCATCTCC</td>
<td>Gasterosteus aculeatus</td>
<td>101</td>
</tr>
<tr>
<td>GaacCBL</td>
<td>ACGCCACCTTAAACAGTTC</td>
<td>Ctenophorus carbo</td>
<td>101</td>
</tr>
<tr>
<td>Gaac.probe</td>
<td>CTGTGCGACACCTTGTTAC</td>
<td>Plathichthys flesus</td>
<td>104</td>
</tr>
<tr>
<td>PIFCB</td>
<td>CCGCAACGTTACCCACCTAA</td>
<td>Platichthys flesus</td>
<td>104</td>
</tr>
<tr>
<td>PIFCB.probe</td>
<td>CCGCAACGTTACCCACCTAA</td>
<td>Platichthys flesus</td>
<td>104</td>
</tr>
</tbody>
</table>

Sequence Identification

Extracted sequences (trimmed for primers) were compared with GenBank Nucleotide database using BLAST [49]. Taxon identification was made using MEGAN 4 [50], with following LCA settings: Min. Support = 2, Min. Score = 50, Top Percent = 2.

Only sequences with full-length 100% match to a single species were considered.

Quantitative PCR (qPCR)

For the eDNA degradation experiment, TaqMan qPCRs were performed on a Stratagene MX3000P.

Two species-specific sets of primers and TaqMan minor groove binding (MGB) probes were developed to target small (101–104 bp) fragments of the mitochondrial gene cytochrome b (cytb) in Platichthys flesus and Gasterosteus aculeatus, respectively (Table 2). The cytb gene was used again for the reasons given above. 25 μl qPCR reactions were performed using 2 μl DNA extract, 10 μl TaqMan® Environmental Master Mix 2.0 (Life Technologies), 1 μl of each primer (10 μM), 1 μl probe (2.5 μM) and 10 μl ddH₂O under thermal cycling: 50 °C for 5 min and 95 °C for 10 min, followed by 53 cycles of 95 °C for 30 sec and 60 °C for 1 min.

Cloning and Sanger sequencing

PCR products from amplifications using species-specific primers (see Table 2) were purified as above, cloned using Topo TA cloning kit (Invitrogen), and commercially sequenced (Macrogen, Europe).
The primer/probe systems were both validated, and tested negative on a total of 20 common saltwater fish species occurring in the area of sampling, and tested positive on the respective target species. To enable a clear quantitative interpretation of eDNA degradation, we applied species-specific TaqMan systems, which, unlike generic primers, ensures that only eDNA of the two selected target taxa were amplified. qPCR standards were prepared at a dilution series (10⁻¹⁰⁻¹⁰⁻³) of purified PCR products on tissue-derived DNA with concentration measured on a Qubit fluorometer (Invitrogen).

Each sample was replicated in 8 independent qPCR reactions, and all positive amplifications were used in the estimation of DNA concentrations. Final concentrations in DNA molecules per 400 ml seawater sample were calculated from the standards, setting the molecular weight of DNA to 660 g/mol/base-pair.

Efficiency of all qPCR standard curves was 90–100%.

### eDNA decay model for seawater

An exponential decay model was fitted to the qPCR data, as this is the relationship one would expect for molecular decay also used previously for similar purposes [51].

The model is the following:

\[
\frac{dN}{dt} = -\beta N
\]

Solving this gives

\[
N(t) = N_0 e^{-\beta t}
\]

\(N(t)\) is the DNA concentration at time \(t\) days.

The two parameters \(N_0\) (initial DNA concentration at time \(t = 0\)) and \(\beta\) (decay constant) were estimated by the nls function in R, resulting in the values \(N_0 = 214\) and \(\beta = 0.322\), for *Platichthys flesus* and \(N_0 = 48\) and \(\beta = 0.701\) for *Gasterosteus aculeatus*. We find a highly significant \((p < 0.001)\) or significant \((p < 0.05)\) fit to the decay models for *Platichthys flesus* and *Gasterosteus aculeatus*, respectively.

Using the parameters to calculate \(t\) for \(N(t) = 25\) (i.e. the empirically observed detection threshold), suggests that eDNA will degrade to sub-detectable levels after approximately 6.7 days for *Platichthys flesus* and 0.9 days for *Gasterosteus aculeatus*, in case of the observed initial DNA concentrations.

All statistics were performed in R ver. 2.13.1.

### Supporting Information

### Table S1 Species list and details for conventional fish surveys.

(PDF)

### Acknowledgments

We thank the Danish National Research Foundation and the Aage V. Jensen Charity Foundation for economic support, and Pernille Selmer Olsen, Lillian A. Petersen and the Danish National Sequencing centre for help with laboratory work and sequencing. We thank Johan Weidl Nielsen (Aquamind) for helpful input. We also thank Marcus Krøg, Jakob Larsen,Thomas Christensen and students from the University of Copenhagen for help with conventional fish surveys.

### Author Contributions

Conceived and designed the experiments: PFT JK EW. Performed the experiments: PFT JK PRM MR. Analyzed the data: PFT JK LIJ PRM MR. Contributed reagents/materials/analysis tools: PFT JK LIJ PRM MR. Wrote the paper: PFT JK PRM EW.

### References


