# Improving Marine Megafauna Knowledge with eDNA: A French Story

Rachel Haderlé[‡], Alice Valentini[§], Visotheary Ung[|], Jean-Luc Jung[‡]

‡ ISYEB UMR 7205, Dinard, France
§ Spygen, Cexed, France
| UMR 7205 CNRS-MNHN-SU-EPHE-UA, PARIS, France

Corresponding author: Rachel Haderlé (rachel.haderle@mnhn.fr), Visotheary Ung (visotheary.ung@mnhn.fr)

## Abstract

In the current context of large-scale biodiversity loss (Díaz et al. 2019), it is urgent to carry out biodiversity inventories in order to investigate spatial and temporal variations. Among the available methods, environmental DNA (eDNA) (Taberlet et al. 2018) combined with molecular metabarcoding (Valentini et al. 2009) bring new insights in drafting inventories of taxa present in an environment.

Approaches based on eDNA facilitate the study of remote ecosystems and the detection of rare, cryptic or invasive species in a non-invasive way (Bohmann et al. 2014). In the marine realm, the study of mobile fauna, including mammals particularly, can greatly benefit from these new techniques.

Here, we present a case study carried out in the northeast and northwest Atlantic, within the boundaries of marine protected areas. The Iroise Natural Marine Park[*1] was the first French marine natural park created in France in 2007 (Fig. 1). The first campaign in the Iroise Natural Marine Park successfully detected several species of cetacean (e.g., *Phocoena phocoena*, *Tursiops truncatus*) and four species of elasmobranchs (e.g., *Scyliorhinus canicula*, *Torpedo marmorata*, *Raja undulata* and *Mustelus asterias*). This study was extended to the Martinique Natural Marine Park[*2], where similar analyses identified three cetacean species (*Stenella attenuata*, *Lagenodelphis hosei* and *Tursiops truncatus*) and 193 teleost taxa (Riou 2022), representing more than half of the species expected in Martinique. The analyses carried out in Martinique highlighted several remarkable sites for fish biodiversity. In Guadeloupe, in the heart of the Agoa Marine Mammals Sanctuary[*3] (corresponding to the French Antilles exclusive economic zone), the taxonomic composition of different eDNA samples made in 2021 and 2022 was compared. The samples were analyzed using different primer sets, specific to vertebrates, teleosts and mammals. Comparison of the results obtained with vertebrate-specific primers and those specific to teleosts showed complementary results. For cetaceans, the analyses distinguished ten distinct cetacean taxonomic units and at least 3 distinct species from four samples. In addition, the eDNA samples were used to discriminate between the two

recently recognised bottlenose dolphin ecotypes, based on the observation of a fixed nucleotide difference on the barcode targeted by the mammal-specific primers. New primers are currently being developed to make it easier to distinguish species of Delphinidae, which are still complex to identify.

Environmental DNA and metabarcoding offer new possibilities for the inventories of marine megafauna and support adequate conservation decision-making processes. It is a major step towards better monitoring of marine mammal populations of the Atlantic Ocean. Moreover, our datasets will be freely available through open platforms following the FAIR (Findable, Accessible, Interoperable, and Reusable) principles.

## Keywords

environmental DNA, biodiversity, marine fauna, marine mammals, databases, marine protected area, FAIR data

## Presenting author

Rachel Haderlé

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## Author contributions

Rachel HADERLE: led the study, ran analyses and interpreted the results

Alice VALENTINI: performed and supervised the analyses of eDNA at SPYGEN

Jean-Luc JUNG: had the original idea, led the study and supervised the project

Visotheary UNG: advisor for data standards

## Conflicts of interest

The authors have declared that no competing interests exist.

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## Endnotes

[*1] https://parc-marin-iroise.fr/
[*2] https://parc-marin-martinique.fr/
[*3] https://www.guadeloupe-islands.com/agoa-the-sanctuary/

Figure 1.

Mer d'Iroise marine natural parc and sampling sites.