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Patrick Jacques, Sarah Maman, Régis Debruyne, Brice Ephrem, Aurélie Manicki, et al.. Decoding ancient genomes: Genomics approaches and innovative species recognition pipeline for diadromous fish. The 20th Portugaliæ Genetica: DNA - Ancient and New (21-22 March 2024), Mar 2024, Porto (Portugal), France. 2024, 10.13140/RG.2.2.12906.53442 . hal-04568047

HAL Id: hal-04568047

<https://hal.inrae.fr/hal-04568047>

Submitted on 3 May 2024

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Decoding ancient genomes: Genomics approaches and innovative species recognition pipeline for diadromous fish

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ABSTRACT

Understanding the evolution of wild species is crucial for developing effective population management strategies and predicting their future trajectories. In my doctoral research, we opted for genomics approaches to explore the demographic history of two iconic diadromous fishes: *Anguilla anguilla* (European eel) and *Salmo salar* (Atlantic salmon). We aim to elucidate their adaptive responses to environmental changes. Setting this project apart is the sequencing and genotyping of both archaeological (aDNA) and modern DNAs samples. Our study encompasses archaeological samples from various locations across Europe, spanning a temporal range of 17,000 years – from the Paleolithic to the modern era. To accurately assign species to each sample, we developed DeFiS (*Detect Fish Species*), a pipeline relying on reference genomes and samples to analyze k-mers: fixed-size nucleotide sub-strings. The list of k-mers and their occurrences from specific dictionaries for both reference genomes and samples. By comparing the dictionaries of the samples with those of the references, we could assign each sample to a specific species. We are currently validating the pipeline using freely available modern samples of all European diadromous fish species found in public databases (NCBI, Essembl, and scientific paper). The aim is to provide a valuable resource for biological scientists. Our method offers a significant advancement in the species identification process for aDNA research. By accelerating and refining this crucial step we aim to contribute to future aDNA-based investigations by facilitating the work of biologists studying wild species evolutions.

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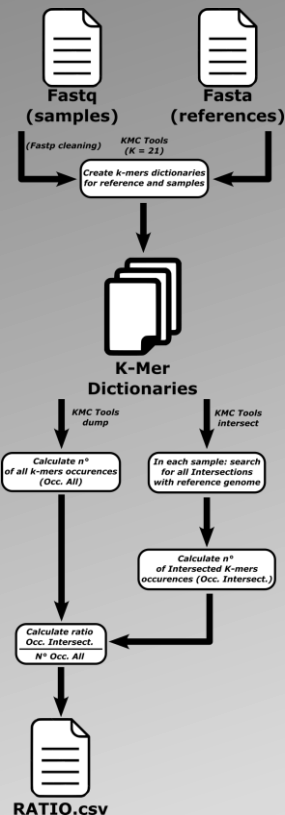
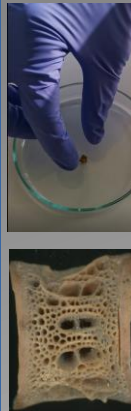
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Introduction and study context

Understanding the evolution of wild species is crucial for developing effective population management strategies and predicting their future trajectories. Ancient DNA (aDNA), DNA collected from archaeological samples, has the potential to serve as a window into the demographic history of species. But **Ancient DNA suffers from three major issues** : it is fragmented, degraded, and contaminated.

Taxonomic assignation of aDNA samples is thus a complex affair. To meet this challenge, we are developing **DeFiS**, a pipeline for aDNA taxonomic assignation based on **K-mers** : fixed-size nucleotide sub-strings.



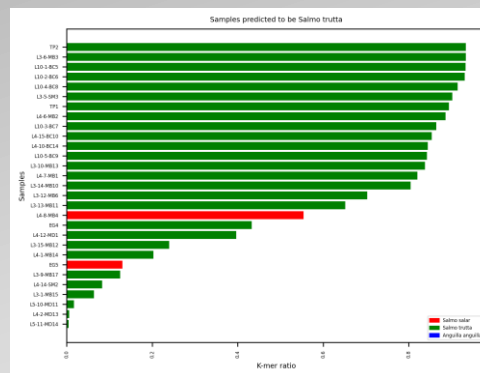
Method

A dictionary is a list of **k-mers occurrences** found in a genome. We can link a reference genome to our sample thanks to the **DeFiS pipeline** which can determine samples' species with a **k-mers ratio**:

$$\frac{Nb_{Occ^{\circ}} Kmers\ Intersect^{\circ}}{Nb_{Occ^{\circ}} Kmers\ total}$$

The highest ratio shows the sample' species.

At the end, the tool will enable the **determination of the taxonomy** of an ancient or modern DNA sequence by comparing it with the dictionary of reference databases



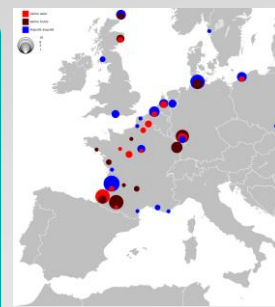
Results

Our method offers a significant advancement in the species identification process for aDNA research on **diadromous fishes**. By accelerating and refining this crucial step we aim to contribute to future aDNA-based investigations by facilitating the work of biologists studying wild species evolution.

We are currently validating the pipeline using freely available modern samples of all European diadromous fish species found in public databases (NCBI, Ensembl, and scientific papers). The aim is to provide a **valuable resource for biological scientists**.

On the left: one example of results regarding the identification of presumed diadromous fish species by archaeoichthyologists, such as Atlantic salmon, brown trout, or European eel.

Our results first demonstrate that archaeoichthyologists make few errors, and secondly, that we assign the species correctly for the majority of samples.



Map of samples used to test the pipeline on aDNA.

Thanks to our partners : BARBAZA Michel (TRACES), CLAVEL Benoît (AASPE), DACHARY Morgane (TRACES, SRA Nouv. Aquitaine), DAUJEARD Camille (HNHP), GEY Delphine (MNHN), GUILLAUD Émilie (AASPE), HAMILTON-DYER Sheila (Bournemouth Uni.), HARLAND Jennifer (Archeology Institute, UHI), HINGUANT Stéphan (INRAP), HORARD-HERBIN Marie-Pierre (CITERES), HUMMEL Esmee (Cultural Heritage Agency of the Netherlands), VAN DER JAGT Inge (ditto), JONSSON Leif (Gothenburg NHM), MADELAINE Stéphane (Musée National de la Préhistoire), MAKOWIECKI Daniel (Ins. Of Archeology, Poland), PERRIN Thomas (TRACES), PRIMAULT Jérôme (TRACES, ArScAn), QUINLAN Liz (Uni. Of York), SCHMÖLCKE Ulrich (Munich State Zoological Collection)