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Data Article

New coastal records in northern Brittany (Plouescat, NW France): Sedimentological, palynological and paleogenomic data over the last 7.3 ka BP



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ABSTRACT

The multidisciplinary approach conducted on the coastal cores ANE-C3 and PADMé (48°38'54.5114"N; 4°10'21.3848"W; Kerallé watershed, NW Brittany, NW France) revealed paleoenvironmental trajectories under both relative sea level rise and anthropogenic dynamics during Middle to Late Holocene, in the research paper: "From a coastal plain to an anthropized fluvial valley (NW Brittany, France): 7.3 kyr of paleoenvironmental evolution from sedimentological, palynological and paleogenomic perspectives" [1]. This additional article presents all the ANE-C3 and PADMé cores dataset

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Keywords:
Holocene
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Anthropogenic pollen indicators
Sedimentary ancient DNA (sedaDNA)

discussed in [1] including sedimentological (XRF, grain size), palynological (pollen assemblages) and paleogenomic (plant and mammal sedimentary ancient DNA or sedaDNA) data. For the sedimentological data, the documents included here comprise high-resolution photographs and normalization of XRF-counts. A special emphasis was placed on characterising the modern pollinic signal in different sub-environments (i.e., salt marsh, coastal meadow, field) of the studied area. This was done to identify anthropogenic pollen indicators specific to this coastal zone, and, ultimately to detect more precisely the pollinic signature of human disturbances in the fossil record. Finally, this paper provides additional information on the methodologies developed, with a particular emphasis on sedaDNA analysis.

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Specifications table

Subject	Global and Planetary Change
Specific subject area	Landscape trajectories of a coastal system in NW Brittany (NW France) over the last 7.3 kyr based on sedimentological, palynological and paleogenomic data and related to sea level rise and anthropogenic impacts.
Data format	Raw and Analyzed
Type of data	2 Excel files (available online : https://doi.org/10.5281/zenodo.12731173) 6 Figures, 4 Tables
Data collection	Coring: Cobra (Eijkjerkamp) percussion corer AMS-¹⁴C datation: - final age model: rbacon package in R version 4.12 Pollinic data: - determination and counting: microscope Leica DMC 2900 at x630 magnification - data treatment: Psimpoll / Past program v 4.03 XRF data: Avaatech core-scanning Granulometric data: - acquisition: laser diffractometer Malvern Mastersizer 2000 - data treatment: GRADISTAT v 8.0 software Ancient sedimentary DNA (sedaDNA): - DNA libraries amplification: CFX touch real-time thermocycler (Biorad) - DNA libraries characterisation by capillary electrophoresis: Labchip GX Touch 24 (Perkin-Elmer) - Sequencing: Illumina NovaSeq 6000 SP lane - Post-sequencing analysis: Cutadapt v4.9, FastP v0.23.3, Geneious Prime 2023.1.2, BBTools - Taxa classification: Kraken2 v2.1.3, BlastN, BWA-0.7.18 (r1243) - Analysis of post-mortem damages: mapDamage2 Cluster analysis: Past program v 4.03 Correlation matrix: "rcorr" function from "Hmisc" package in R studio software

(continued on next page)

Data source location	<p>Coring:</p> <ul style="list-style-type: none"> - Location of ANE-C3 and PADMé cores: 48°38'54.5114"N; 4°10'21.3848"W - archived by Geo-Ocean / LETG laboratories at the IUEM (Plouzané, France) (ANE-C3 PI: P. Stéphan / PADMé PI: M. Vidal) <p>Surface samples for modern calibration of pollen signal: (O. David / M. Vidal)</p> <ul style="list-style-type: none"> - retrieved in Plouescat (Brittany, NW France) - archived by Geo-Ocean laboratory (UMR 6538 UBO, CNRS, Ifremer, Plouzané, France) <p>AMS-¹⁴C datations:</p> <ul style="list-style-type: none"> - sampling: 19 and 8 samples were collected on ANE-C3 and PADMé cores, respectively, in IUEM (Plouzané, France) (O. David / A. Gorczyńska) - laboratory analysis: ANE-C3 core: 5 dates from Beta-Analytics and 14 from ARTEMIS / PADMé core: 6 dates from Beta-Analytics and 2 from ARTEMIS (Table 1 and 2 in [1]) <p>Pollinic data:</p> <ul style="list-style-type: none"> - Sediment core treatment (core ANE-C3) - pollen extraction: EPOC palynological laboratory (UMR 5805 CNRS, Bordeaux University) - Modern samples treatment - pollen extraction: Geo-Ocean laboratory (UMR 6538 UBS, UBO, CNRS, Ifremer, Vannes, France) (O. David) - Palynological determination: Geo-Ocean laboratory (UMR 6538 UBO, CNRS, Ifremer, Plouzané, France) (O. David) <p>Granulometric data: ANE-C3 and PADMé cores, IUEM (Plouzané, France) (O. David / M. Vidal)</p> <p>XRF data: Geo-Ocean laboratory (UMR 6538 UBO, CNRS, Ifremer, Plouzané, France) (O. David)</p> <p>Total organic carbon analysis: LETG laboratory (UMR 6554, UBO, CNRS, Plouzané, France) (A. Gorczyńska)</p> <p>Ancient sedimentary DNA (sedaDNA):</p> <ul style="list-style-type: none"> - Core sub-sampling: IUEM (Plouzané, France) (N. Martin / O. David) - Ancient DNA extraction: P2GM platform (MNHN, Paris) (R. Debruyne / N. Martin) - Genomic Libraries preparation: P2GM platform (MNHN, Paris) (R. Debruyne / M. Ollivier) - Sequencing: ICM sequencing platform, Paris - sedaDNA quality pipeline: ECOBIO laboratory (UMR 6553, Univ. Rennes) (P. Garcia-Ladieu / M. Goor) - sedaDNA data analysis and interpretation: ECOBIO laboratory (UMR 6553, Univ. Rennes1) (F. Barloy- Hubler / M. Ollivier)
Data accessibility	<p>Repository name: <i>New coastal records in northern Brittany (Plouescat, NW France): Sedimentological, palynological and paleogenomic data over the last 7.3 ka BP [Data set]</i>. Data identification number: 10.5281/zenodo.12731173 Direct URL to data: https://doi.org/10.5281/zenodo.12731173</p>
Related research article	<p>[1] David, O., Vidal, M., Gorczyńska, A., Penaud, A., Pailler, Y., Clément, N., Goubert E., Stéphan, P., Ollivier M., Barloy-Hubler, F. 2024. From a coastal plain to an anthropized fluvial valley (NW Brittany, France): 7.3 kyr of paleoenvironmental evolution from sedimentological, palynological and paleogenomic perspectives. <i>Quaternary Sciences Review</i>, 344, 108983. https://doi.org/10.1016/j.quascirev.2024.108983</p>

1. Value of the Data

- Novel high-resolution (~100 years) and long-term (last 7.3 kyr) multi-proxy analyses for understanding paleoenvironmental changes of a coastal system in northern Brittany.
- The sedimentological, palynological, and paleogenomic data combined in a multiproxy approach allow to depict natural and anthropogenic dynamics on Brittany's landscape evolution over the Holocene.

- This data paper presents a complementary study of the modern pollinic signal of the studied area in order to calibrate the anthropogenic pollinic signal in the fossil record analyzed in [1].
- This data paper provides additional information about the methodology developed in [1].
- Any researcher wishing to compare some data with those of this study will be able to retrieve the original work files and reuse them for alternative interpretations.

2. Background

The original research paper [1] integrates multiproxy data to investigate paleoenvironmental changes in a NW Brittany coastal system (Kerallé valley in Plouescat). This approach involves multiple methodologies, data acquisitions, treatments and results, which are repositored in this data article supplementing the research paper. It provides details on data processing, notably the additional statistical analyses carried out on sedimentological data (i.e., XRF), as well as the calibration of the anthropogenic pollinic signal. Furthermore, it includes more information about the methodology deployed for the palynological and ancient sedimentary DNA acquisition, along with the raw results.

3. Data Description

3.1. Sedimentological dataset

3.1.1. High resolution photographs of ANE-C3 and PADMé cores (Figs. 1 and 2)

The study of the Kerallé valley paleoenvironments relies on the acquisition of two twin cores (ANE-C3 and PADMé) retrieved in the inner part of the valley. Both studied cores were subjected to high-resolution pictures allowing a complementary visualization of sedimentary facies (Figs. 1 and 2). On these pictures all sampled levels (for dating, grain size, palynological, or sedaDNA analyses) are indicated.

Core ANE-C3

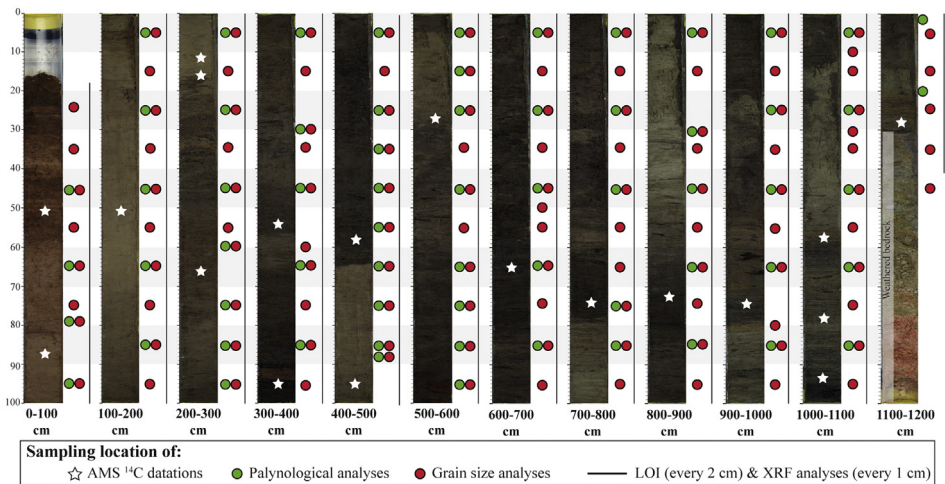


Fig. 1. High-definition pictures of the ANE-C3 core and location of various sampling (stars: AMS-¹⁴C dates / green dots: palynological analyses / red dots: grain-size analyses / black strip: core portion subjected to Loss On Ignition and XRF analyses).

Core PADMé

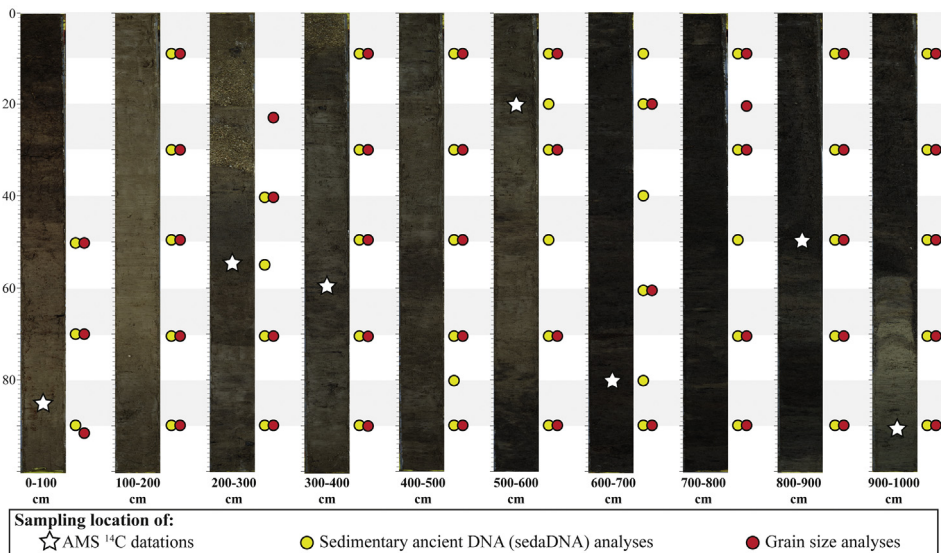


Fig. 2. High-definition pictures of the PADMé core and location of various sampling (stars: AMS-¹⁴C dates / yellow dots: sedaDNA analyses / red dots: grain-size analyses).

3.1.2. Grain size and Loss On Ignition analyses (refer supplementary data online)

Results from the grain size analyses (median D50, distribution in granulometric classes from [1]) carried out on ANE-C3 and PADMé cores are available online (“ANE-C3 core” and “PADMé core” excel file).

Loss On Ignition data (carbonate and total organic carbon contents, from [1]) are available online (“ANE-C3 core” excel file).

3.1.3. X-Ray Fluorescence (refer supplementary data online and Fig. 3)

Raw data from XRF analysis are available online (“ANE-C3 core” excel file).

The correlation matrix of XRF count shows strong correlations between two major sets of elements (Fig. 3):

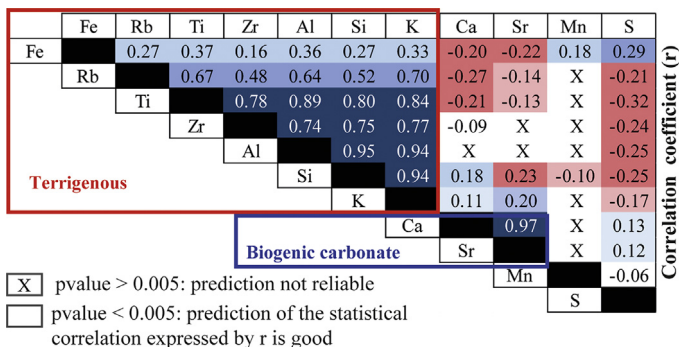


Fig. 3. Correlation matrix performed on XRF data for ANE-C3 core. It was performed under “rcorr” function from “Hmisc” package in R studio software (R Development Core Team, 2021; <http://www.r-project.org>).

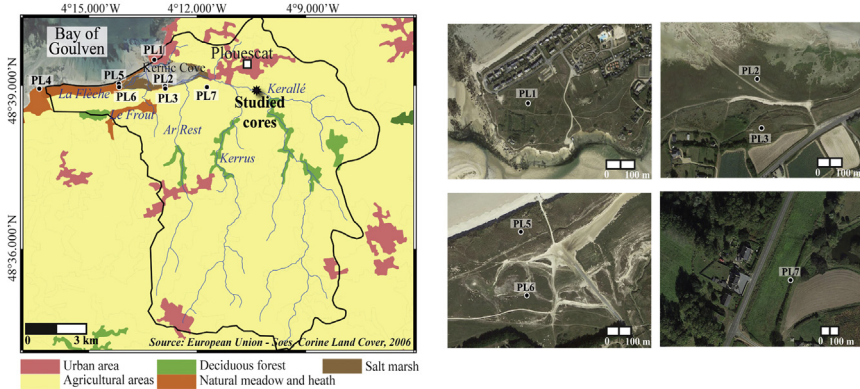
3.2.2. Sub-surface pollen assemblages (Fig. 5 + Table 1)

A complementary palynological study was carried out on modern sub-surface samples, i.e., soils and mosses, considered to be pollen-rain collectors. The aim of this additional study was to analyse the modern palynological record around Kernic Cove (Plouescat, Fig. 5a) in close relation to present-day environments, in order to interpret more accurately the fossil data from the ANE-C3 core and better characterize the pollinic signature of human disturbances.

Description of modern pollinic assemblages: Considering modern samples, 47 taxa were identified, reaching a mean diversity of 20 taxa, except for two samples PL4 and PL5, with less than 10 identified taxa (Fig. 5b). These two samples were sampled in the Keremma dune system in areas covered by *Ammophila arenaria* (Figs. 5a, b). A preservation bias caused by sandy substrate can be involved, explaining the low content and low diversity of the PL4 sample. Moreover, Poaceae are over-represented in the PL5 sample (85%). Considering their very low diversity these two samples (PL4 and PL5) were not included in the analysis.

- The PL1 sample was taken in an anthropized coastal meadow, marked by trampling (Fig. 5a and b). The arboreal pollen signal (21%; Fig. 5c) is mainly driven by *Alnus* (11%) and *Corylus* (6%). The herbaceous signal (79%) is more diversified (16 identified taxa) and dominated by Poaceae (23%; Fig. 5b and d). Plantaginaceae are well represented with *Plantago lanceolata* (21%), *Plantago coronopus* (6%) and *Plantago* sp. (7%). A relative increase of these species is generally associated to trampling [3–5] which is consistent with the sampling area. The other recorded taxa can grow naturally on sandy substrate, and more generally on coastal dune systems (Asteroideae 3%: e.g., *Helichrysum stoechas*; Brassicaceae 3%: e.g., *Cakile maritimum*; Cyperaceae 3%: e.g., *Carex arenaria*; Amaranthaceae 2%: e.g., *Atriplex laciniata*; Apiaceae 2%; [4]). Ranunculaceae (3%; Fig. 5d) are reported along the coastal fringe, in dune environment (e.g., *Ranunculus bulbosus*, *R. parviflorus*; [4]) or in trampling area (e.g., *Ranunculus sadous*, *R. parviflorus*; [4]).
- The PL2 sample, carried out in a salt marsh, is obviously dominated by Amaranthaceae (22%) and Poaceae (17%), accompanied by some occurrences of Brassicaceae (2%) and *Armeria maritima* (1.3%; Fig. 5d), taxa currently found in this type of environment [4]. Urticaceae observed in anthropized area (e.g., alongside dwellings, roads, or cultivated fields; [3–5]) reached 3% in this sample accompanied by scarce occurrences of *Artemisia* and *P. coronopus* (1%; Fig. 5d). The arboreal signal (42%) is well represented and is mainly dominated by *Alnus* (19%), *Pinus* (11%) and *Corylus* (7%).
- The PL3 sample was retrieved from a coastal meadow located on a small dune system at the end of the Kernic Cove. As expected, the herbaceous signal is dominated by Poaceae (15%; Fig. 5d). The trampling markers are well represented (*P. lanceolata* 8%; *P. coronopus* 3%; *Plantago* sp. 3%) while Urticaceae reach 5%, reflecting human disturbance, clearly visible through the paths and fields surrounding the site (Fig. 5a). The other recorded taxa can grow naturally in particular on sandy substrates (e.g., Brassicaceae 5%; Amaranthaceae 2%; Apiaceae 2%; [4]). Although very open, this environment records significant percentages of arboreal taxa reaching 48% (Fig. 5c), mainly represented by *Alnus* (16%), *Pinus* (14%) and *Corylus* (13%).
- The PL6 sample is located in a coastal meadow, at the transition between the salt marsh and the sandy dune system, near a dried channel (Fig. 5a). As expected, grains of Poaceae are dominant (49%). Given the high diversity (24 identified taxa; Fig. 5b) no preservation bias could explain this Poaceae over-representation, which reflects the surrounding vegetation cover. It is accompanied by taxa typical of back-dune environments (e.g., Brassicaceae, 4% / Asteroideae 4%; [4]) and spores of *Equisetum* sp. (10%) that can naturally grow in coastal marshes (e.g., *Equisetum arvense*, *E. telmatia*; [4]). *P. lanceolata* (2%), *Plantago* sp. (1%) are weakly recorded, while Urticaceae and *Trifolium* (<1%) are only noticed as occurrences (Fig. 5d). Arboreal taxa (22%; Fig. 5c) are mainly represented by *Alnus* (10%), *Pinus* (5%), *Quercus* (4%) and *Corylus* (3%).
- Finally, in the PL7 sample, carried out in a wet meadow surrounded by cultivated fields, Poaceae reach 10% while trampling indicators are well represented by *P. coronopus* (15%), *P. lanceolata* (8%), and *Plantago* sp. (10%). Cichorioideae (15%) and Asteroideae (5%) are well rep-

a) Vegetation cover on the Kerallé watershed and location of modern samples studied

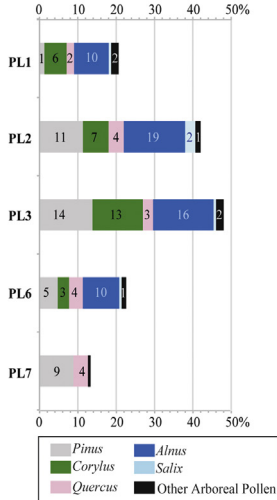


b) Sample characteristics and pollen data

Samples	Environmental characteristics	Sedimentological context	Number of pollen counted	Diversity		
				Arboreal taxa	Herbaceous taxa	Total
PL1	Anthropized coastal meadow	Dune sand deposit	155	8	16	24
PL2	Maritime marsh (Schorre with <i>Halimione, Armeria</i>)	Silty salt marsh	150	7	16	23
PL3	Costal meadow on dune system	Dune sand deposit	152	7	14	21
PL4	Keremna dune (with <i>Ammophila arenaria</i>)	Sandy dune	9	3	4	7
PL5	Top of Ode Vras dune (with <i>Ammophila arenaria</i>)	Sandy dune	168 with 143 Poaceae	3	6	9
PL6	Transition between dune and salt marsh, close to a dry channel	Transition between coastal dune and silty salt marsh	168	7	17	24
PL7	Agricultural area - Wet meadow	Silty and clay of polders	158	3	14	17

Low diversity

c) Arboreal taxa %



d) Herbaceous taxa %

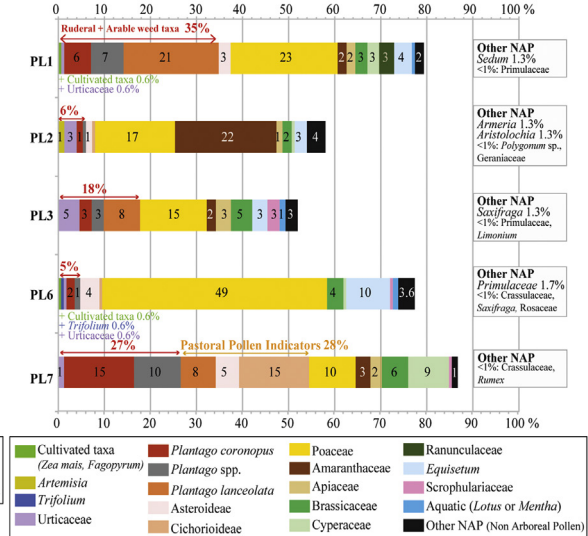


Fig. 5. a) Vegetation cover around Kernic Cove (Plouescat, NW Finistère, NW Brittany) (from Corine Land Cover database, 2006) and location of retrieved mosses and modern soils samples. b) Environmental characteristics for each sample (including vegetation cover and sedimentary substrate) and pollinic data (number of pollen grains counted and diversity). Pollen percentages for c) arboreal taxa and d) herbaceous taxa.

resented in this site (Fig. 5d), which corresponds to a frequent signature of grazing pressure in Europe [3,6,7]. Other taxa frequently associated with human disturbance as Cyperaceae (9%), Apiaceae (2%) (e.g., wet meadows in [3]) as well as Brassicaceae (6%) and Amaranthaceae (3%) (e.g., arable indicators in [3,5]) are also recorded in this station. Last, the arboreal signal is weaker in this sample than in others (13%; Fig. 5c) and mainly composed of *Pinus* (9%) and *Quercus* (4%).

Understanding modern pollen assemblages to calibrate the pollinic signal of anthropization: this part focuses on the pollen grains of herbaceous taxa currently present in anthropized area.

- According to modern palynological signal record around Kernic Cove (Plouescat), *Plantago lanceolata* is the main indicator of human disturbance (i.e., trampling areas, paths and grazing areas; respectively samples PL1, PL3 and PL7). However, the simultaneous presence of *P. lanceolata*, Cichorioideae, and Asteroideae is clearly associated with wet meadows at the local scale of Plouescat (PL7 in Fig. 5d). Their joint occurrence is common in both mown and grazed vegetation across European regions [3,6–8]). Also, Cichorioideae is recognized as one of the main pollen indicators reflecting animal breeding and pasturelands in northern (Finland; [9]) and Mediterranean (Italy; [7]) regions. Synchronous increase of *P. lanceolata*, Cichorioideae, and Asteroideae in fossil assemblages is consequently assumed to indicate local grazing activities, allowing them to be considered as Pastoral Pollen Indicators (PPI; [6]).
- Moreover, around the Kernic Cove, *P. coronopus*, *Plantago* sp. and Urticaceae are frequently present in the vicinity of anthropized areas (PL1, 2 and 3 in Fig. 5d). Plantaginaceae are commonly attributed to ruderal communities along footpaths [3]. The nitrophilous Urticaceae family occurs in varied anthropized environments, belonging to both ruderal (i.e., paths, dwellings) and arable weed (i.e., cultivated land) communities [3–5]. Not well recorded in our modern samples, *Trifolium* and *Rumex acetosa/acetosella* (<0.6%) are also reported in various anthropized environments (wet meadows, pastures, paths, arable lands; [3]). Only detected in fossil records of the ANE-C3 core, *Centaurea cyanus*, *Polygonum aviculare* and Cannabaceae (Fig. 5) are strictly associated to farming activities [5].

Calibration of the pollinic signal of anthropization in fossil records: To visualize the anthropogenic influence in fossil records, the ruderal and arable weed taxa (i.e., *Plantago coronopus*, *Plantago* sp., *Rumex acetosa*-type, *Rumex* sp., Urticaceae, *Trifolium*, *Polygonum aviculare*, *Centaurea cyanus*, Cannabaceae; Fig. 5 and Table 1) have been summed. On the contrary, potential PPI including *Plantago lanceolata* and Asteraceae (i.e., Cichorioideae and Asteroideae) are represented separately (Fig. 4 and Table 1). Other taxa are assigned to pastureland and/or ruderal communities in exclusively continental environments, such as Brassicaceae, Amaranthaceae, Apiaceae or Cyperaceae [3,5,6,8]. Given that these taxa grow naturally in a variety of coastal habitats [4] (PL1, 2, 3 in Fig. 5d), their anthropogenic signature must be interpreted with caution in our studied case. Therefore, these families have not been included among the ruderal and arable weed group in [1] (summarize in Table 1).

Table 1

The principal anthropogenic pollen indicators recorded in Plouescat (in both modern and fossil samples) and their occurrence in various anthropized and/or natural environment (according to previous classification [3–9]).

		Pasture/Grazing	Footpath and ruderal communities	Arable Indicators	Fallow land	Grow naturally in coastal area
Taxa record in modern palynological signal of Plouescat	** <i>Plantago lanceolata</i>	++	++			
	** <i>Plantago coronopus</i>		+			Rocky cliffs
	** <i>Plantago sp.</i>		+			
	Cichorioideae	+++				
	Asteroideae	++				
	**Urticaceae		+	+		
	Cyperaceae					Dune grassland
	Brassicaceae					Dune grassland
	Apiaceae					Dune grassland
	Ranunculaceae					Dune grassland
	Amaranthaceae					Salt marsh
	** <i>Trifolium</i> (scaree <1%)		+	+		
	** <i>Artemisia</i> (scaree <1%)			+		
<i>Cultivated taxa</i> (scaree <1%: <i>Zea mays</i> , <i>Fagopyrum</i>)			+			
Taxa only present in Plouescat fossil record (ANE-C3 core)	<i>Rumex acetosa/acetosella</i>		+	+		
	<i>Centaurea Cyanus</i>			++		
	<i>Polygonum aviculare</i>			++		
	<i>Cerealia-type</i>			+++		
	Cannabaceae			+		

PPI: Pastoral Pollen Indicators

** Ruderal and arable weed taxa

Cultivated-taxa

3.3. Ancient sedimentary DNA (sedaDNA)

Raw genomic sequence data are available only on request (to M. Ollivier or F. Barloy-Hubler).

The number of reads assigned to the different mammals and Viridiplantae taxa, after the BLAST analysis, is reported in Tables 2 and 3, respectively.

Table 2
Numbers of reads assigned to the different mammals after the BLAST analysis.

Samples depth (cm)	Camelidae	RUMINANTIA												Equidae	Suidae				Sum		
		Canidae				Bovidae									Equus	Suidae sp.	Sus scrofa	sus scrofa		Sus	
		Canidae sp.	Canis	Canis lupus	Canis miliaris	Rumin antia sp.	Bovidae sp.	Capri nae sp.	Capra	Ovis	Bovi nae sp.	Bos	Cervi nae								Cervus nae
50		2			2																4
70			1		1									1					1		4
90		1	1		1																3
110	1																				1
130		1	1											2							4
150		1												1				2	1		5
170		1	1											1							3
190														2				1	1		4
240		2					1		1	4				8				6	2		27
255		1	2			3	1		1	2				29				1	1		45
270					1					1				1							3
290						3	1											2			6
310		2	1			3	3		2		10			42				4	3		79
330		2	2			3	1														8
350		2				3															5
370		1			1																4
390		3	3											1				2	1		11
410			2			2															4
430						1															1
450		1	1															2			4
470		2			1	2												2	2		9
480														1				1			2

(continued on next page)

Table 3

Numbers of reads assigned to the different Viridiplantae taxa after the BLAST analysis.

Samples depth (cm)	Fagaceae			Betulaceae					Rosaceae				Poaceae		Equisetaceae	Callitricaceae	Cyperaceae
	Indetermined	<i>Quercus</i>	<i>Fagus</i>	Indetermined	<i>Alnus</i>	<i>Betula</i>	<i>Carpinus</i>	<i>Corylus</i>	Indetermined	<i>Malus</i>	<i>Prunus</i>	<i>Rubus</i>	<i>Phragmites</i>	Poaceae sp.	<i>Equisetum</i>	<i>Callitriche</i>	
50	0	0	0	0	0	0	0	0	0	0	0	0	0	77	0	0	0
70	0	0	0	0	0	0	0	0	0	0	0	0	0	20	0	0	0
90	0	1	0	0	0	0	0	0	0	0	0	0	0	13	448	0	1
110	1	0	0	0	0	0	0	0	0	0	1	0	0	14	214	0	1
130	0	2	1	0	1	0	0	0	0	0	0	0	0	80	282	0	3
150	0	2	1	0	0	0	0	0	0	1	0	0	0	39	1081	0	0
170	0	0	1	3	1	0	0	2	0	2	0	0	0	49	255	0	1
190	0	3	0	13	4	1	0	6	1	2	0	0	0	26	0	0	4
240	26	149	7	472	622	58	145	374	47	5	118	20	0	126	0	126	3
255	20	82	4	416	282	30	108	318	69	17	20	32	0	245	0	360	8
270	0	0	1	61	20	3	4	12	0	2	13	0	0	122	0	112	2
290	1	3	0	15	12	4	7	17	0	1	0	0	0	43	0	2	0
310	57	172	13	1218	1075	267	331	695	160	8	70	59	0	197	0	365	17
330	0	2	0	2	0	0	0	1	0	0	2	0	0	28	0	0	3
350	0	5	0	3	1	0	0	3	0	0	0	2	0	17	0	0	1
370	0	3	1	37	19	0	7	15	0	0	0	0	0	10	0	0	2
390	0	1	0	4	1	0	0	2	0	0	1	0	0	46	0	0	3
410	0	3	0	1	0	0	2	2	1	1	0	0	0	13	0	0	1
430	0	6	0	3	2	0	3	5	0	0	0	0	0	15	0	0	0
450	2	4	0	2	2	0	3	16	0	0	0	0	0	10	0	0	0
470	1	8	0	43	27	9	7	27	1	3	3	4	0	12	0	2	1
480	0	10	0	15	23	1	8	23	5	1	8	1	0	18	0	2	0
490	1	18	0	14	6	0	9	39	5	1	1	0	0	11	0	0	0
510	0	2	0	2	4	0	1	3	0	0	2	0	0	6	7	0	0
520	0	1	0	6	1	0	2	6	2	1	1	0	0	12	2	0	0
530	0	2	0	1	0	0	0	2	0	0	1	0	0	27	2	1	0
550	1	0	0	7	10	0	1	2	1	1	0	0	0	5	0	1	0
570	96	168	6	725	281	17	41	297	60	18	28	9	0	15	0	24	2
590	26	331	16	687	362	60	335	1619	54	131	46	9	0	485	0	30	0

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Table 3 (continued)

Samples depth (cm)	Fagaceae			Betulaceae					Rosaceae				Poaceae		Equisetaceae Equisetum	Callitricaceae Callitriche	Cyperaceae
	Indetermined Fagaceae	Quercus	Fagus	Indetermined Betulaceae	Alnus	Betula	Carpinus	Corylus	Indetermined Rosaceae	Malus	Prunus	Rubus	Phragmites	Poaceae sp.			
610	49	537	25	1591	1163	93	831	3210	137	189	58	9	0	1046	0	39	4
620	51	157	7	1752	976	130	162	511	38	11	3	10	6	121	0	1	0
640	27	173	3	515	520	105	105	466	28	12	8	5	0	24	0	4	0
660	12	153	5	266	157	12	103	745	4	6	18	0	0	10	0	0	0
680	1	4	0	7	9	0	4	22	0	2	0	0	0	4	0	0	0
690	7	39	0	164	162	5	16	88	9	4	38	0	0	9	0	2	2
710	6	53	17	283	216	9	68	247	15	7	25	0	0	22	0	3	4
730	1	3	1	61	9	0	30	69	3	0	0	0	0	13	0	0	1
750	3	6	1	15	2	0	0	9	0	1	0	2	0	77	0	25	272
770	6	12	0	28	47	3	3	42	9	6	2	1	0	162	0	118	384
790	6	22	1	59	5	1	0	12	0	0	1	0	535	1848	0	9	253
810	5	41	3	223	156	33	34	146	8	6	0	2	1	64	9	22	18
830	71	95	9	668	442	12	62	299	12	10	62	4	0	193	0	23	27
850	9	41	0	31	9	3	0	208	2	4	2	2	110	915	0	96	344
870	8	87	1	172	55	5	50	261	8	14	4	1	920	4899	2	21	64
890	2	18	11	100	16	0	0	74	4	4	2	0	361	822	0	133	393
910	13	52	1	457	370	24	55	158	12	7	5	3	8	166	0	25	18
930	2	75	3	182	210	5	23	102	15	8	11	5	25	228	0	61	215
950	10	26	1	116	35	3	4	82	4	4	3	0	1299	2381	0	207	365
970	7	53	2	173	9	4	26	420	10	13	8	0	2126	5519	0	52	94
990	1	4	0	44	24	3	5	102	0	0	0	0	1620	5619	0	2	40

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Table 3 (Continued)

Samples depth (cm)	Junca ceae	Ranuncu laceae	Faba ceae	Astera ceae	Plantaginaceae			Jugland aceae	Urtica ceae	Linea ceae	Euphorbi aceae	Vita ceae	Polygonaceae	
	<i>Juncus</i>				Plantag inaceae sp.	<i>Plantago</i>	<i>Digitalis</i>						Polygon aceae sp.	<i>Persicaria</i>
50	0	0	0	0	0	0	0	0	0	0	0	0	14	61
70	0	0	0	0	0	0	0	0	0	2	0	0	0	0
90	3	0	0	0	0	0	0	0	0	15	0	0	0	0
110	0	0	0	0	0	0	0	0	0	9	0	0	0	0
130	9	0	0	0	0	0	0	0	0	1	0	0	0	0
150	17	0	1	1	0	0	0	0	0	0	0	0	0	0
170	127	1	1	1	0	0	0	0	0	3	0	0	0	0
190	71	0	3	0	0	0	0	1	2	7	4	0	6	0
240	23	0	30	24	20	3	5	32	25	7	2	1	8	6
255	13	0	20	29	4	10	3	4	19	5	0	8	11	8
270	43	10	1	0	47	1	0	0	5	5	0	7	1	0
290	7	3	5	0	2	2	0	1	0	0	0	0	9	8
310	90	8	153	71	55	59	11	10	26	10	0	0	13	12
330	2	0	0	0	0	0	0	0	0	7	0	17	0	0
350	4	0	0	0	0	0	0	0	1	10	0	5	2	1
370	0	0	0	1	0	0	0	0	0	0	0	5	0	0
390	0	0	0	0	0	0	0	0	0	0	0	0	0	0
410	0	0	0	1	0	0	0	0	0	0	0	1	0	1
430	2	0	1	0	0	0	0	1	0	5	0	0	0	0
450	4	0	4	0	0	0	0	0	0	2	0	1	0	0
470	14	1	1	0	0	0	0	0	0	0	0	0	1	0
480	16	1	1	1	0	0	0	1	0	0	0	0	2	0
490	13	0	0	0	0	0	0	1	0	1	0	1	0	0
510	8	1	0	0	0	0	0	0	0	3	0	0	0	0
520	4	1	0	0	0	0	0	0	0	1	0	0	1	0
530	1	0	1	0	0	0	0	0	0	2	0	0	0	0
550	8	0	0	0	0	0	0	0	0	4	0	0	0	1

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Table 3 (continued)

Samples depth (cm)	Junca ceae	Ranuncu laceae	Faba ceae	Astera ceae	Plantaginaceae			Jugland aceae	Urtica ceae	Linea ceae	Euphorbi aceae	Vita ceae	Polygonaceae	
	<i>Juncus</i>				Plantag inaceae sp.	<i>Plantago</i>	<i>Digitalis</i>						Polygon aceae sp.	<i>Persicaria</i>
570	1	26	0	5	0	0	0	20	0	2	0	6	0	0
590	3	24	3	4	0	1	4	8	1	5	2	0	24	24
610	1	100	12	7	10	4	8	21	2	0	4	2	24	32
620	0	410	0	12	3	1	2	5	10	0	16	9	12	2
640	0	356	18	3	0	5	0	10	41	0	10	6	3	0
660	0	12	4	2	0	0	0	4	5	7	4	1	2	0
680	0	1	2	0	0	0	0	1	0	1	0	5	0	0
690	0	41	1	0	0	0	0	4	1	4	1	2	2	0
710	2	51	2	0	0	0	0	1	1	0	2	0	7	0
730	0	0	1	2	0	0	0	0	0	4	1	11	0	0
750	18	0	1	0	0	0	0	0	0	8	0	0	0	0
770	2	0	1	2	0	1	0	0	0	0	0	0	0	0
790	489	0	1	3	0	0	0	1	0	0	0	0	0	0
810	1	30	4	1	0	0	2	0	5	0	0	2	3	2
830	21	69	5	2	8	0	0	39	0	0	0	2	4	6
850	1	0	5	2	0	1	0	0	0	6	0	3	1	0
870	3	9	2	0	0	0	0	1	1	2	0	1	1	0
890	0	8	2	5	0	1	0	0	11	12	2	6	2	0
910	6	45	3	1	15	0	4	0	0	0	1	1	0	2
930	62	32	4	2	0	0	1	1	2	0	1	1	1	6
950	0	0	4	119	0	0	0	1	0	8	0	2	0	0
970	0	0	3	12	0	0	0	0	0	7	0	1	0	0
990	0	2	6	24	0	0	0	2	1	9	0	2	0	0

4. Experimental Design, Materials and Methods

4.1. Sedimentological analysis

Methodologies used for grain-size, Loss on Ignition and XRF data acquisition are fully described in [1].

4.2. Palynological analyses

4.2.1. ANE-C3 core samples [1]

Palynological treatments carried out on ANE-C3 core samples are fully described in [1].

4.2.2. Modern sub-surface samples (this DiB paper)

Sampling: Sub-surface samples were taken from strictly coastal (i.e., maritime marshes, coastal meadows) and anthropized (i.e., in the vicinity of paths, roads or in pastoral lands) areas. A total of 7 samples (6 mosses and 1 sub-surface soil) were collected in Marsh 2021, in the vicinity of Kernic Cove. Sites were chosen according to environmental characteristics, such as sedimentological substrate and vegetation cover (location and descriptive information are given in Fig. 5a and b). Sampling was generally carried out on moss cushions, allowing to track pollen rain of the last 2 years [10] or up to 10-15 years [11], making a suitable analogue for the comparison of fossil pollen spectra.

Pollen extraction: For mosses, pollen grains were extracted thanks to an acetolysis (in Geo-Ocean laboratory, Univ. Bretagne Sud, Vannes). Two chemical treatments were carried out with acetic acid (CH_3COOH) following by addition of acetic anhydride ($\text{C}_4\text{H}_6\text{O}_3$) and sulfuric acid (H_2SO_4). After being placed in a water bath (90°C) for around 8 minutes, the reaction is stopped by adding acetic acid. After centrifugation, the concentrated pollen grain pellet was rinsed several times with distilled water, before being recovered. When mosses were not available, a sub-surface silty soil was sampled (PL7 sample; Fig. 5a). Pollen grains were extracted according to the procedure of de Vernal et al. [12], with chemical (cold 10% HCl and 40-70% HF) and physical (sieving with a $10\ \mu\text{m}$ mesh size nylon) treatments. For this modern sub-surface soil sample, KOH was added to destroy the remaining organic matter.

Pollen determination and counting: Pollen determinations were made using a Leica microscope DM2500 at x630 magnification. A minimum of 150 pollen grains were counted per samples to ensure statistically reliable data.

4.3. Ancient sedimentary DNA analysis [1]

4.3.1. Sampling strategy

The PADMé core was opened and sampled for DNA samples in a dedicated sterile room (IUEM, Plouzané, France). We removed the surface sediment (5-10 mm) using sterile scalpels. Subsequently, a new sterile scalpel was utilized to sample inner uncontaminated sediments, then transferred to sterile tubes and stored at -20°C until DNA extraction. This operation was carried out on 50 levels, for which two replicates were sampled.

4.3.2. DNA extractions

The laboratory work was conducted in a cleanroom dedicated to ancient DNA at the Musée de l'Homme in Paris (P2GM platform). It is subdivided into dedicated facilities for sample preparation, stock solution setup, and DNA extraction through library preparation.

Subsamples were extracted following a modified version of Dabney's et al [13] extraction protocol consisting in a cold spin extraction method [14]. The DNA was extracted from 200-250 mg of sediment as follows. First, we performed a pre-lysis step adding 500 μL of SLB1 solution

(50mM Tris-Cl, 1,25% SDS, 25mM CaCl₂, 6,25% PVP, 100mM DTT) to a PowerBead tube containing 750 μ L of lysis buffer (Powersoil DNA extraction kit, QIAGEN), shaken at 25/s in a TissueLyzer for 5 minutes. Then, we digested at 35°C overnight under slight agitation in an orbital shaker by adding proteinase K (final concentration of 0.25 mg/mL). After a centrifugation of 5 minutes at 10,000 g to pellet the debris, we transferred 1100 μ L of clear lysate to 13 volumes of binding buffer (5 M Guanidinium Hydrochloride, 40% isopropanol, 120 mM sodium acetate pH 5.2 and 0.05% tween-20) and centrifuged for 3 hours at 3,000 g and 4°C. Supernatants were transferred into a large volume column (High Pure Viral Nucleic Acid Large Volume Kit, Roche). We centrifuged the columns at 1,000 g for 2 minutes and then processed the detachable silica filter in 2 ml microtubes. We rinsed the columns (1 minute at 6,500 g) once with 500 μ L of inhibitor removal buffer and twice with 450 μ L of wash buffer from the kit. We performed a final centrifugation in two rounds of 1 minute at 15,000 g to dry the silica membrane and eluted the extracted DNA twice in 25 μ L of warm EBT buffer (EB buffer from Qiagen supplemented with 0.05% of tween-20) for a final extraction volume of 50 μ L. DNA extractions were performed per batch of 16 (15 samples plus 1 extraction blank).

4.3.3. Libraries preparation

Ten microliters of DNA extract were processed for each sample and extraction blank. We performed the double-stranded DNA end-polishing using the NEBnext End-Repair module (NEB) in 45 μ L reaction volumes as per manufacturer recommendations. We then performed the truncated P5/P7 adapter ligation by using the NEBnext Quick Ligation module (NEB) with 10 U of T4 DNA ligase and 500 nM of both adapters per 40 μ L reaction (1 hour at 22°C). Purifications after both end repair and ligations steps were performed using minelute purification columns (Qiagen) with EB buffer supplemented with 60 mM Sodium acetate pH 5.3 (as per manufacturer recommendation) and using EBT buffer for final elution. We performed the fill-in reaction of ligation products using 8 U of Bst large fragments in 30 μ L reaction volumes at 37°C for 20 minutes and then inactivated the enzyme by heating the reaction at 80°C for 20 minutes. Indexing was performed from 6 μ L of the library through a qPCR indexing reaction in a final volume of 40 μ L (1X SsOAdvanced supermix, 500 nM of each indexing primer i5 and i7), allowing an adjustment of the number of cycles needed. Libraries were all sequenced on a partial Illumina NovaSeq 6000 SP lane (100 cycles) at the ICM (Paris Brain Institute).

Duplicates for each sample (and blanks) were pooled in order to constitute a single file to facilitate the subsequent analyses. Adapters were removed in three consecutive rounds using cutadapt [15], with maximum error rate set at 0.5 (-e 0.5 parameter) and exclusion of empty reads (-m 1 parameter), FastP (version 0.23.1) [16] and mapping using Geneious (version 2023.1.2, <https://www.geneious.com>) in order to retrieve any residual adapter though manual biocuration process. Reads were then paired using BBTools (repair.sh version 38.90) (sourceforge.net/projects/bbmap/) and filtered to keep only those with an average quality greater than Q20 (-average_qual 20 restriction), no homopolymer, no homopolymer (-trim_poly_g and -trim_poly_x options) and cut on the 3' part (-cut_right -cut_right_mean_quality 20 options). The sequences that successfully passed through these filters were subsequently merged, with a minimum overlap of 5 and deduplicated (optical duplicates) using FastP. After completing these steps, we retained reads with a minimum length of 35 bp.

Scripts used to analyse the raw sedimentary DNA reads can be found on the github page: https://github.com/Gaia32/padme_project_Metagenomics.

4.3.4. Taxa classification and verification of aDNA damage (Table 4 + Fig. 6)

The methodology used for sedaDNA taxa classification is fully described in [1]. Table 4 presents additional data, i.e., the targets choose for mapping.

The verification of ancient DNA molecular damage was made under mapDamaged 2.0, some of the results acquired are presented in Fig. 6.

Table 4

List of reference genome sequences of species of interest used for mapping.

	Taxon	Species	Reference sequence accessions		
			Genome	Chloroplast	Mitochondrion
Asteroideae	<i>Aster</i> spp.	<i>Aster indicus</i>	/	NC_040126.1	/
	<i>Cirsium</i> spp.	<i>Cirsium arvense</i>	/	NC_036965.1	/
	<i>Tanacetum</i> spp.	<i>Tanacetum coccineum</i>	GCA_026074375.1	NC_047308.1	/
	<i>Helianthus</i> spp.	<i>Helianthus annuus</i>	GCF_002127325.2		
	<i>Cynara</i> spp.	<i>Cynara cardunculus</i>	GCF_001531365.2	NC_066017.1	/
Cichorioideae	<i>Sonchus</i> spp.	<i>Sonchus pustulatus</i>	/	NC_063463.1	/
	<i>Hypochaeris</i> spp.	<i>Hypochaeris radicata</i>	/	NC_044795.1	/
	<i>Lactuca</i> spp.	<i>Lactuca sativa</i>	GCF_002870075.4		
Betulaceae	<i>Alnus</i> spp.	<i>Alnus glutinosa</i>	GCA_003254965.1	MG386363	/
	<i>Corylus</i> spp.	<i>Corylus avellana</i>	GCA_901000735.2	MN082371	/
	<i>Betula</i> spp.	<i>Betula pendula</i>	GCA_900184695.1	LT855378.1	LT855379.1
	<i>Carpinus</i> spp.	<i>Carpinus viminea</i>	GCA_013348765.1	NC_039939.1	/
	<i>Ostrya</i> spp.	<i>Ostrya trichocarpa</i>	/	KY088271.1	/
	<i>Ostryopsis</i> spp.	<i>Ostryopsis nobilis</i>	/	NC_040001.1	/
	<i>Euphorbia</i> spp.	<i>Euphorbia peplus</i>	GCA_028411795.1	NC_058989.1	/
Euphorbiaceae	<i>Ricinus</i> spp.	<i>Ricinus communis</i>	GCF_019578655.1	GCF_000151685.1	NC_015141.1
	<i>Lupinus</i> spp.	<i>Lupinus angustifolius</i> / <i>Lupinus luteus</i>	GCF_001865875.1	NC_023090.1	/
Fabaceae	<i>Vicia</i> spp.	<i>Vicia sativa</i>	GCA_021764765.1	KC189947.1	
	<i>Lotus</i> spp.	<i>Lotus japonicus</i>	GCA_012489685.2		
	<i>Medicago</i> spp.	<i>Medicago trunculata</i>	GCF_003473485.1		
	<i>Melilotus</i> spp.	<i>Melilotus officinalis</i>	/	NC_070051.1	/
	<i>Trifolium</i> spp.	<i>Trifolium pratense</i>	GCF_020283565.1		
	<i>Quercus</i> spp.	<i>Quercus robur</i>	GCF_932294415.1	NC_046388	OW028777.1
Fagaceae	<i>Castanea</i> spp.	<i>Castanea mollissima</i>	GCA_014183005.1	MW044606	OP895669/OP895670
	<i>Fagus</i> spp.	<i>Fagus sylvatica</i>	GCA_907173295.1		OU015761.1/OU015762.1
	<i>Juglans</i> spp.	<i>Juglans regia</i>	GCF_001411555.2	/	
	<i>Juncus</i> spp.	<i>Juncus effusus</i>	GCA_024447645.1	NC_059754.1	NC_069588.1
Juncaceae	<i>Linum</i> spp.	<i>Linum usitatissimum</i>	GCA_010665275.2	NC_036356.1	/
Linaceae	<i>Callitriche</i> spp.	<i>Callitriche palustris</i>	/	MW774642.1	/
	<i>Digitalis</i> spp.	<i>Digitalis purpurea</i>	/	NC_068046.1	/
	<i>Plantago</i> spp.	<i>Plantago lanceolata</i>	GCA_028659135.1	NC_068049.1	/

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Table 4 (continued)

	Taxon	Species	Reference sequence accessions		
			Genome	Chloroplast	Mitochondrion
Equisetaceae	<i>Equisetum</i> spp.	<i>Equisetum arvense</i>	/	NC_014699.1	
Polygonaceae	<i>Rumex</i> spp.	<i>Rumex acetosa</i>	/	NC_042390.1	/
	<i>Persicaria</i> spp.	<i>Persicaria amphibia</i>	/	NC_071233.1	/
	<i>Fagopyrum</i> spp.	<i>Fagopyrum esculentum</i>	/	NC_010776.1	/
	<i>Rheum</i> spp.	<i>Rheum nobile</i>	GCA_027886185.1	NC_046506.1	/
Ranunculaceae	<i>Ranunculus</i> spp.	<i>Ranunculus occidentalis</i>	/	NC_031651.1	/
	<i>Anemone</i> spp.	<i>Anemone nemorosa</i>	/	NC_066446.1	/
	<i>Oxygraphis</i> spp.	<i>Oxygraphis glacialis</i>	/	NC_041538.1	/
Rosaceae	<i>Malus</i> spp.	<i>Malus domestica</i>	GCF_002114115.1	OX352779.1	NC_018554.1
	<i>Pyrus</i> spp.	<i>Pyrus communis</i>	GCA_008932095.1	MN577870	OM763766.1
	<i>Prunus</i> spp.	<i>Prunus persica</i>	GCF_000346465.2	MT984561.1	/
	<i>Rubus</i> spp.	<i>Rubus idaeus</i>	GCA_030142095.1	MW801330.1	/
	<i>Sorbus</i> spp.	<i>Sorbus aucuparia</i>	/	NC_052878	ON478177.1
	Urticaceae	<i>Urtica</i> spp.	<i>Urtica dioica</i>	/	NC_064948.1
Vitaceae	<i>Vitis vinifera</i>	<i>Vitis vinifera</i>			
	<i>Vitis riparia</i>	<i>Vitis riparia</i>	GCF_000003745.3_12X_genomic /		
			GCF_004353265.1_EGFV_Vit.rip.1.0_genomic		
Cyperaceae	<i>Bolboschoenus</i> spp.	<i>Bolboschoenus planiculmis</i>	/	NC_058998.1	OK539702.1
	<i>Carex</i> spp.	<i>Carex myosuroides</i>	GCA_028015225.1	NC_063519.1	/
	<i>Cyperus</i> spp.	<i>Cyperus difformis</i>	/	NC_061302.1	/
	<i>Eleocharis</i> spp.	<i>Eleocharis cellulosa</i>	/	NC_047448.1	/
	<i>Isolepis</i> spp.	<i>Isolepis setacea</i>	/	NC_056187.1	/

(continued on next page)

Table 4 (continued)

	Taxon	Species	Reference sequence accessions			
			Genome	Chloroplast	Mitochondrion	
Poaceae	<i>Aegilops</i> spp.	<i>Aegilops tauschii</i>	GCF_002575655.2	NC_022133.1	/	
	<i>Triticum</i> spp.	<i>Triticum aestivum</i>	GCF_018294505.1	MN605257	GU985444.1	
	<i>Avena</i> spp.	<i>Avena sativa</i>	GCA_916181665.1	MK336398	/	
	<i>Hordeum</i> spp.	<i>Hordeum vulgare</i>	GCF_904849725.1	MN171383.1	MN127974.1	
	<i>Secale</i> spp.	<i>Secale cereale</i>	GCA_902687465.1	OL688773.1	/	
	<i>Phragmites</i> spp.	<i>Phragmites australis</i>	GCA_958298935.1	MW287626.1	OY282636.1	
	<i>Agrostis</i> spp.	<i>Agrostis stolonifera</i>	/	NC_008591.1	OQ695465	
	<i>Brachypodium</i> spp.	<i>Brachypodium distachyon</i>	GCF_000005505.3	NC_011032.1	/	
	<i>Digitaria</i> spp.	<i>Digitaria exilis</i>	JACEFO000000000	OK637269.1	/	
	<i>Glyceria</i> sp	<i>Glyceria septentrionalis</i>	/	MN983110.1	/	
	<i>Lolium</i> sp	<i>Lolium perenne</i>	GCF_019359855.1	AM777385.2	JX999996.1	
	<i>Setaria</i> spp.	<i>Setaria digitata</i>	GCA_003640385.1	NC_028075.1	/	
	<i>Sporobolus</i> spp.	<i>Sporobolus alterniflorus</i>	GCA_008808055.3	MT311317.1	MT471321.1	
	<i>Eleusine</i> spp.	<i>Eleusine indica</i>	GCA_030378355.1	NC_030486.1	/	
	Amaranthaceae	<i>Amaranthus</i> spp.	<i>Amaranthus tricolor</i>	GCF_026212465.1	OP177685.1, OP177684.1, OP177683.1	
	Mammals	<i>Bos</i> spp.	<i>Bos taurus</i>	GCF_002263795.2	/	NC_006853.1
		<i>Ovis</i> spp.	<i>Ovis aries</i>	GCF_016772045.1	/	NC_001941.1
<i>Capra</i> spp.		<i>Capra hircus</i>	GCF_001704415.2	/	NC_005044.2	
<i>Canis</i> spp.		<i>Canis lupus familiaris</i>	GCF_000002285.5	/	NC_002008.4	
<i>Equus</i> spp.		<i>Equus caballus</i>	GCF_002863925.1	/	NC_001640.1	
<i>Capreolus</i> spp.		<i>Capreolus capreolus</i>	GCA_951849835.1	/	NC_020684.1	
<i>Cervus</i> spp.		<i>Cervus elaphus</i>	GCF_910594005.1	/	NC_007704.2	
<i>Sus</i> spp.		<i>Sus scrofa</i>	GCF_000003025.6	/	NC_000845.1	

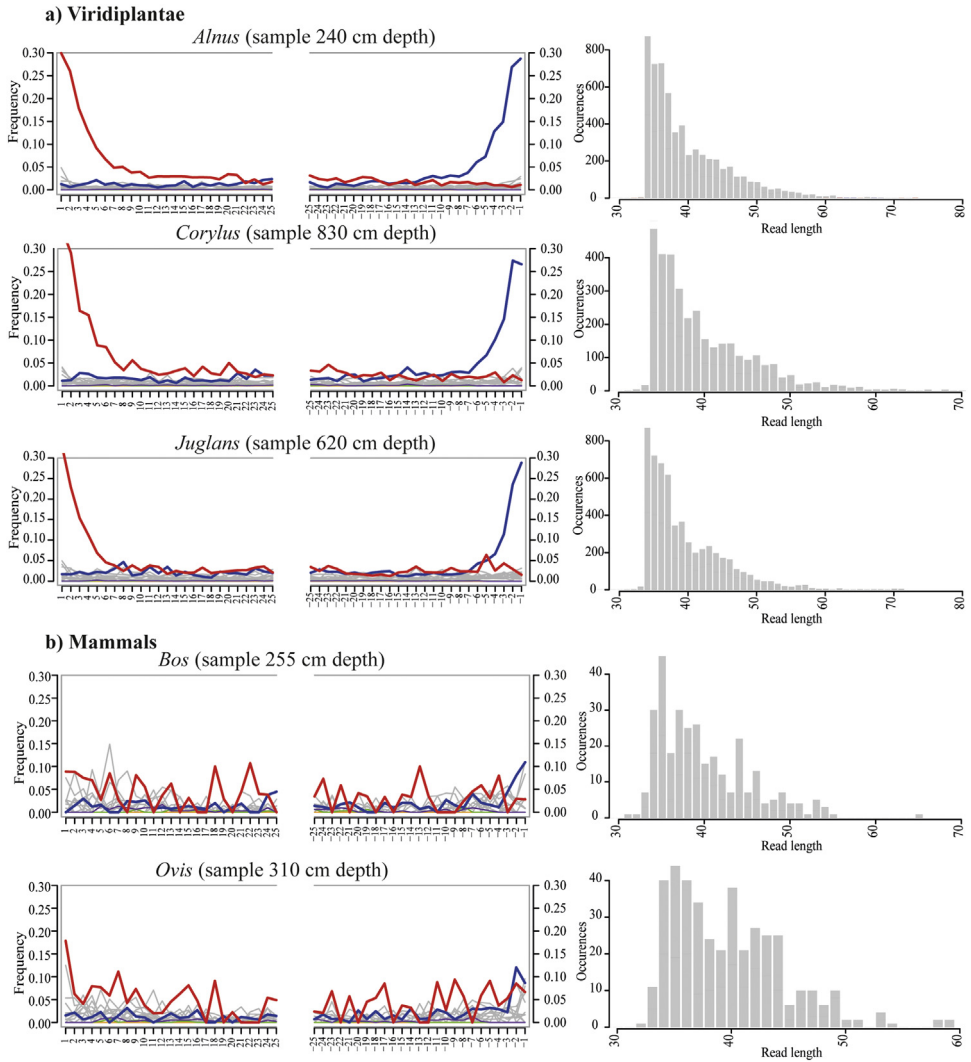


Fig. 6. Example of *mapDamage* plots showing aDNA characteristic terminal deamination patterns and short fragment length distributions (FLD) for a) Viridiplantae and b) Mammals.

4.4. Statistical analyses (this DiB paper)

4.4.1. Correlation matrix

A correlation matrix on XRF measurements acquired on core ANE-C3 (Fig. 3), was performed using the “*rcorr*” function from “*Hmisc*” package in R studio software (R Development Core Team, 2021; <http://www.r-project.org/>). The matrix consists of Pearson correlation coefficient (r), ranging from -1 to 1, attributed between each variable. If $r = -1$ no correlation exists between the two compared elements, while the closer r is to the value 1 the stronger is the correlation between the two compared elements. p-Values allow to express the confidence in the statistical

correlation. If $p\text{-value} \leq 0.05$ the correlation confidence in r coefficient is good. The objective is to detect major element co-occurrences, in order to establish ratios for XRF data normalization.

Limitations

None

Ethics Statement

The authors have read and follow the ethical requirements for publication in Data in Brief. The current dataset does not involve human subjects, animal experiments, or any data collected from social media platforms.

Credit Author Statement

Details of individual contributions: **David Ophélie** (Conceptualization, Formal analysis, Investigation, Visualization, Writing - original draft); **Vidal Muriel** (Project administration, Funding acquisition, Conceptualization, Writing - original draft); **Gorczyńska Aneta** (Investigation, Writing - review and editing); **Penaud Aurélie** (Writing - review and editing); **Pailler Yvan** (Writing - review and editing); **Nicolas Clément** (Writing - review and editing); **Debruyne Régis** (Methodology, Writing - review and editing); **Martin Nathan** (Investigation, Writing - review and editing); **Garcia-Ladieu Pauline** (Methodology, Writing - review and editing); **Goor Mahaut** (Methodology, Writing - review and editing); **Goubert Evelyne** (Writing - review and editing); **Stéphan Pierre** (Funding acquisition, Writing - review and editing); **Ollivier Morgane** (Formal analysis, Methodology, Investigation, Writing - original draft); **Barloy-Hubler Frédérique** (Formal analysis, Methodology, Investigation, Writing - original draft).

Data Availability

<https://doi.org/10.5281/zenodo.13992357> (Zenodo).

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Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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