Introduction à l'ADN environnemental

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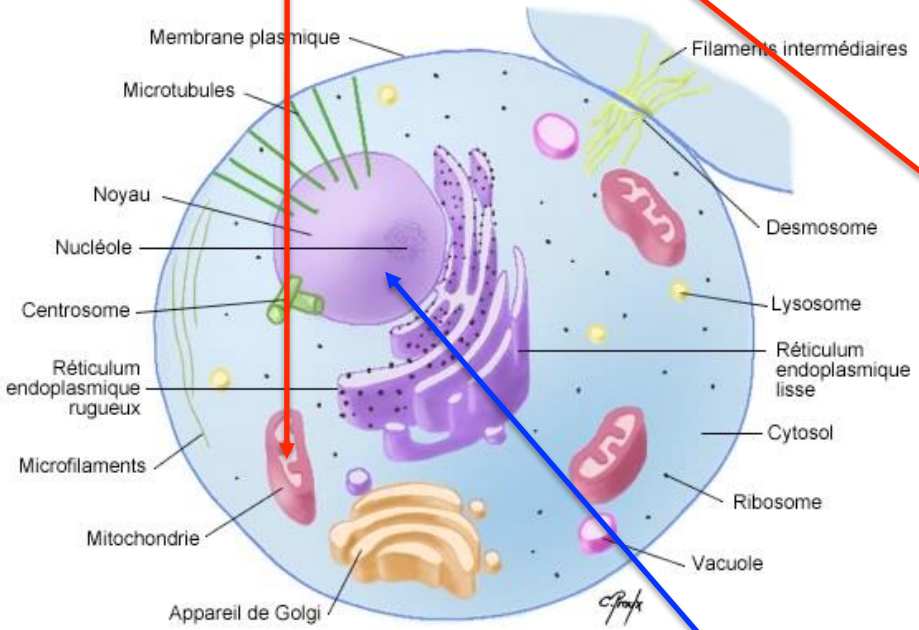
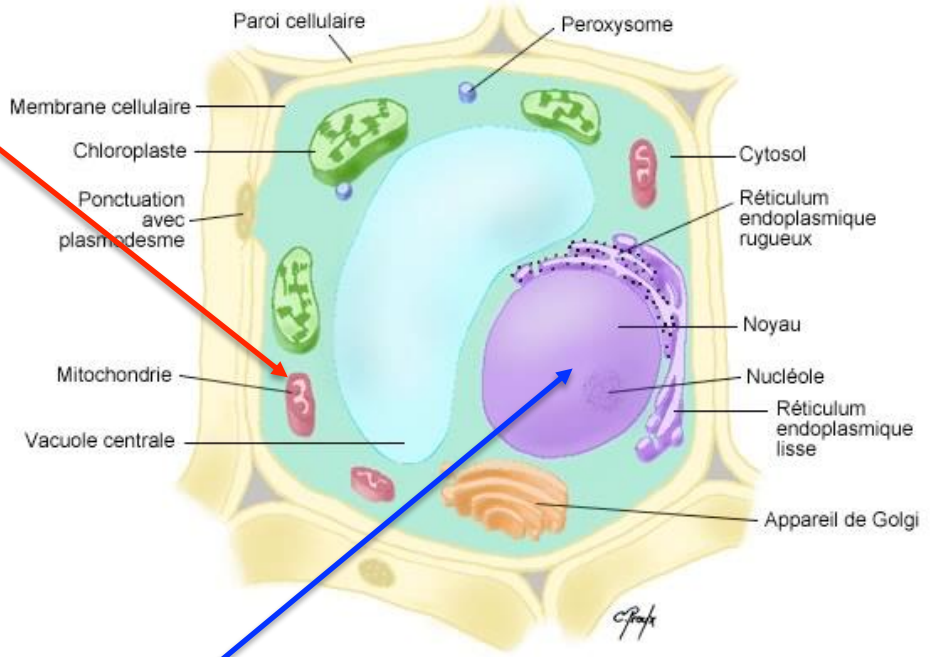
Paris, 28 Septembre 2023

L'ADN dans les cellules

ADN mitochondrial



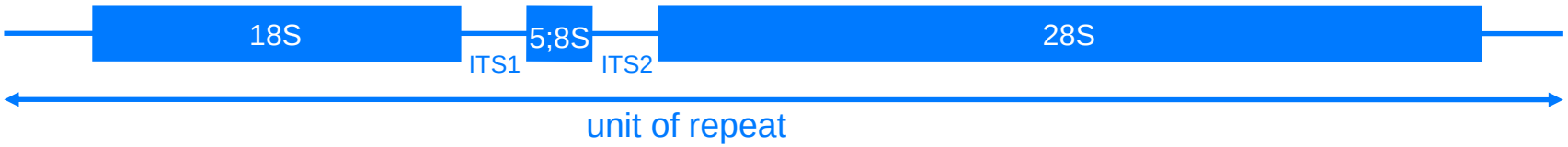
Cellule animale



Cellule végétale

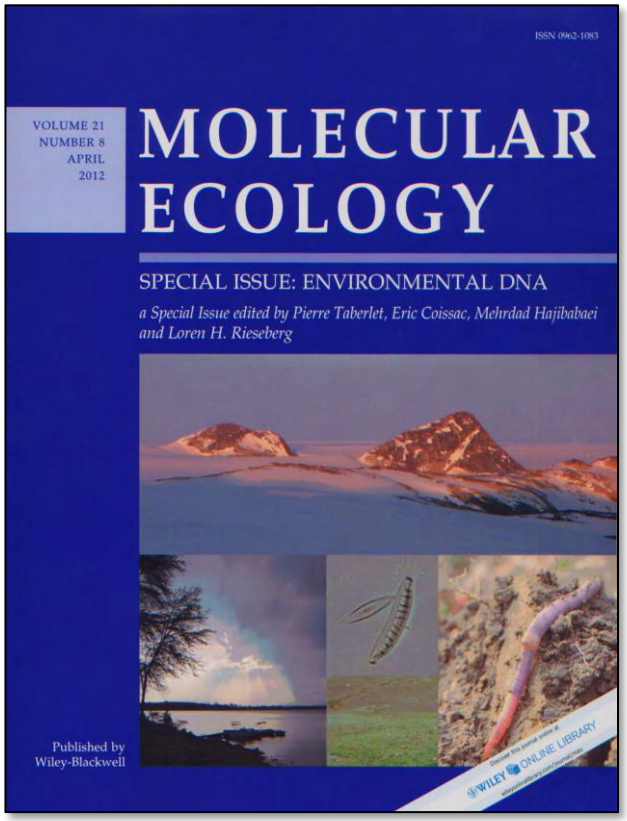
ADN nucléaire

ribosomal DNA



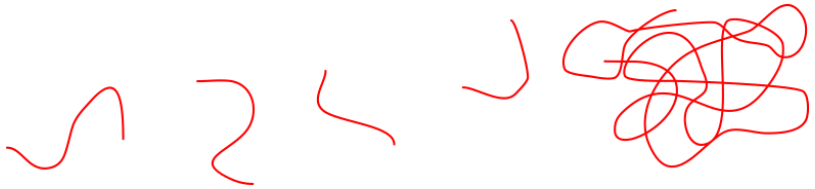
Qu'est-ce que l'ADN environnemental ?

- Il s'agit de l'ADN qui peut être extrait d'un échantillon environnemental sans isoler *a priori* d'organismes cibles
- Exemple d'échantillons environnementaux:
  - Sol
  - Eau
  - Sédiment
  - Air
  - Fèces

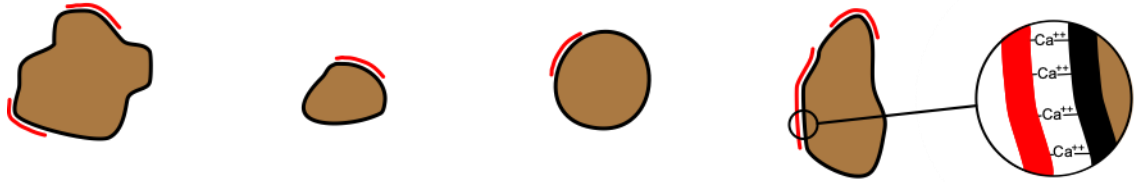


Trois formes différentes pour l'ADN environnemental

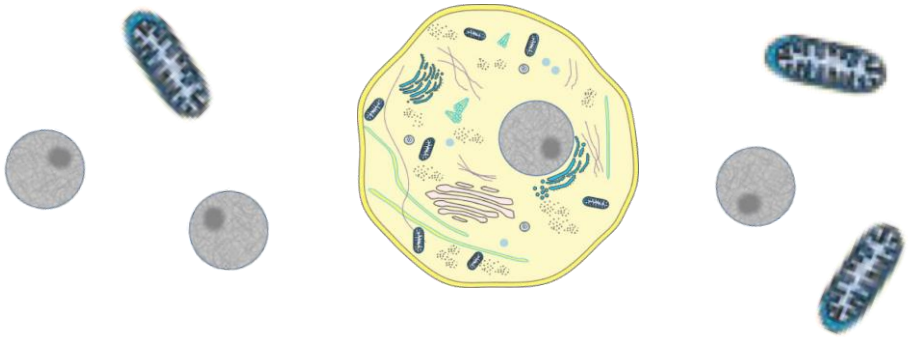
- ADN libre



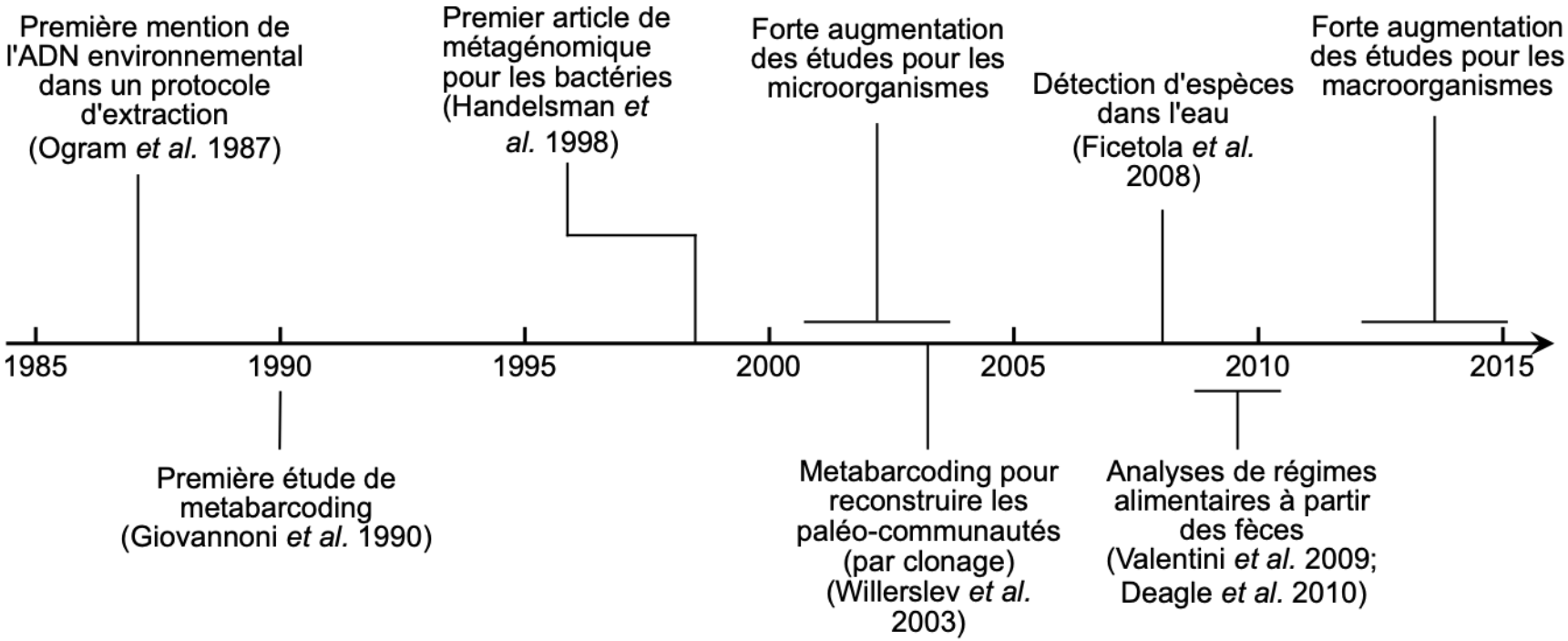
- ADN adsorbé sur des particules minérales ou organiques



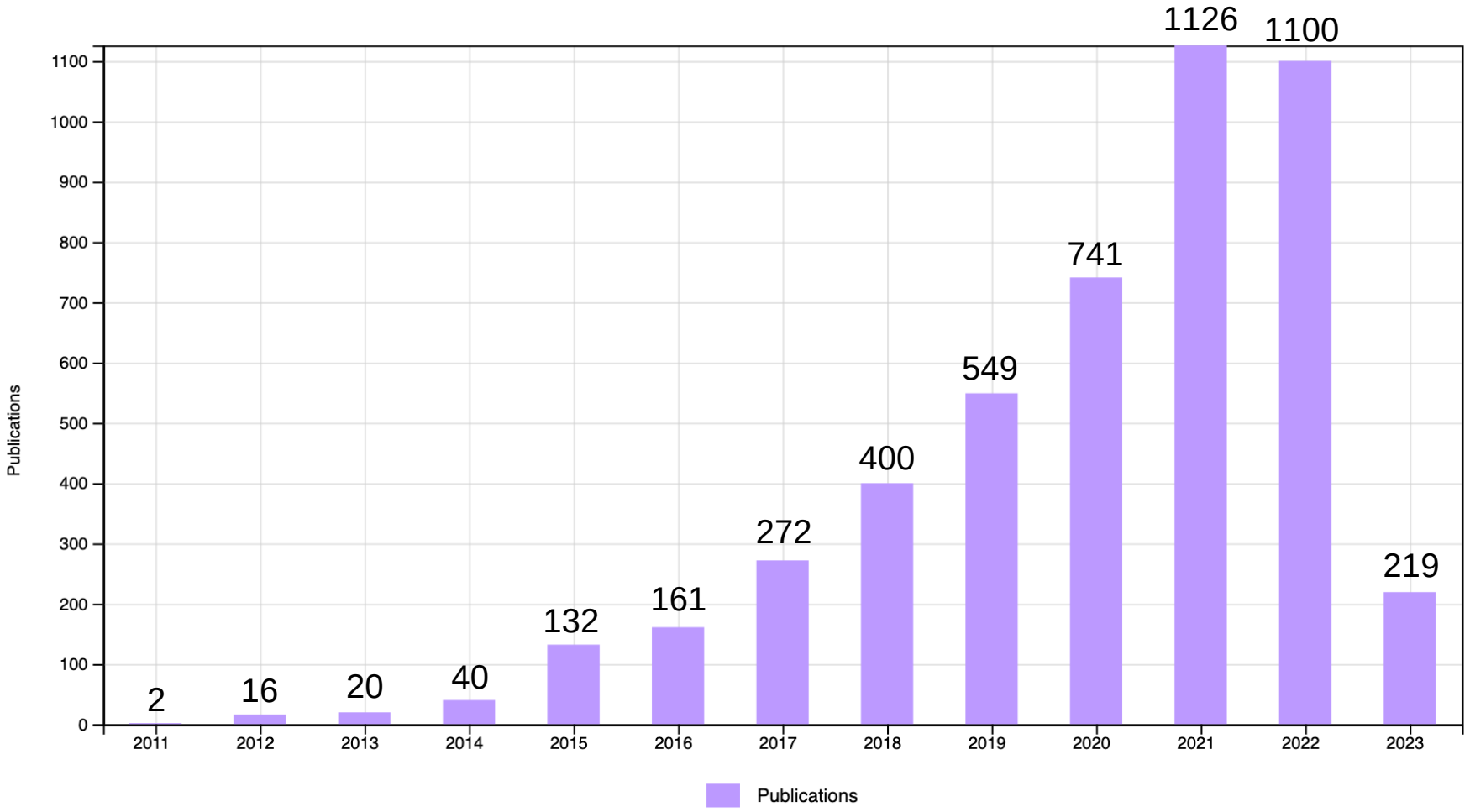
- Cellules ou débris cellulaires



Emergence de l'ADN environnemental

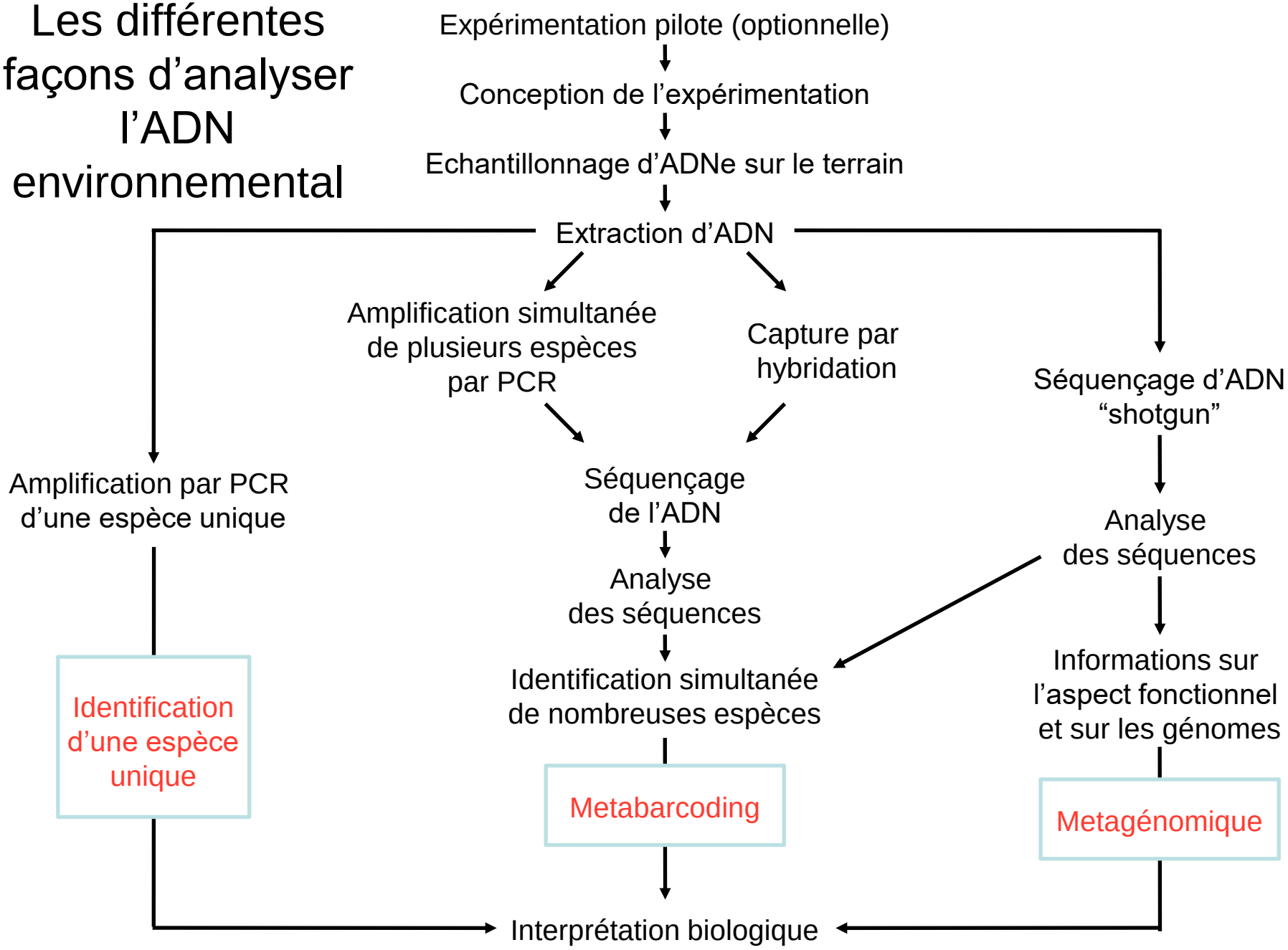


Emergence de l'ADN environnemental

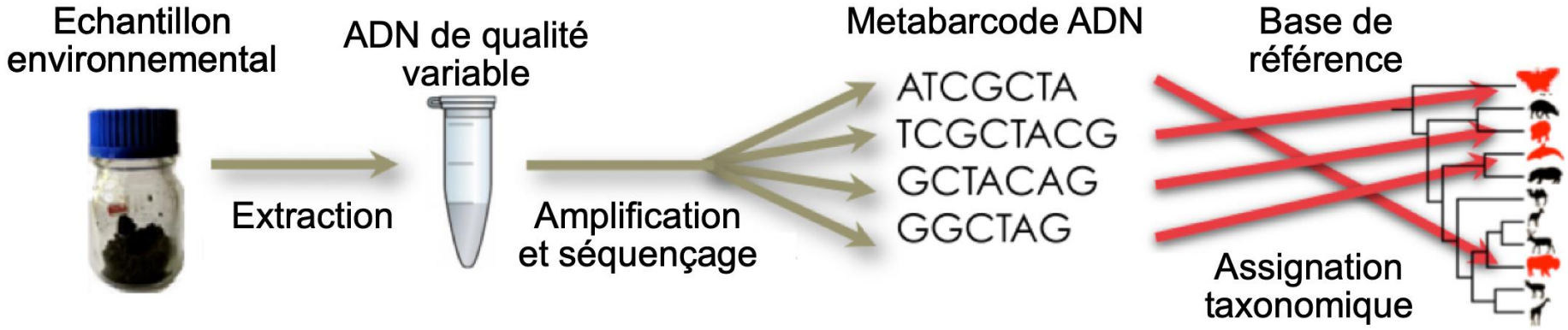


Source: "metabarcoding" dans le Web of Science, 19 Mars 2023

Les différentes façons d'analyser l'ADN environnemental



Metabarcoding: identification simultanée de plusieurs espèces à partir de leurs ADN



Le paradoxe du metabarcoding:

- Chaque étape est très simple au niveau technique
- Mais globalement, c'est difficile de concevoir une expérimentation solide

Régimes alimentaires

TECHNICAL ADVANCES

New perspectives in diet analysis based on DNA barcoding and parallel pyrosequencing: the *trn*L approach

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**Laboratoire d'Ecologie Alpine, CNRS UMR 5553, Université Joseph Fourier, BP 53, F-38041 Grenoble cedex 9, France, †Dipartimento di Ecologia e Sviluppo Economico Sostenibile, Università degli Studi della Tuscia, via S. Giovanni Decollato 1, I-01100 Viterbo, Italy, ‡Department of Ecology and Natural Resource Management, Norwegian University of Life Sciences, Post Box 5003, NO-1432 Ås, Norway, §Himalayan Wildlife Foundation, 01, Park Road, Sector F-8/1 Islamabad 44000, Pakistan, ¶Genoscope — CNS, 2 rue Gaston Crémieux, BP 5706, F-91057 Evry cedex, France, **Norwegian Institute for Nature Research, NO-7485 Trondheim, Norway*

Abstract

The development of DNA barcoding (species identification using a standardized DNA sequence), and the availability of recent DNA sequencing techniques offer new possibilities in diet analysis. DNA fragments shorter than 100–150 bp remain in a much higher proportion in degraded DNA samples and can be recovered from faeces. As a consequence, by using universal primers that amplify a very short but informative DNA fragment, it is possible to reliably identify the plant taxon that has been eaten. According to our experience and using this identification system, about 50% of the taxa can be identified to species using the *trn*L approach, that is, using the P6 loop of the chloroplast *trn*L (UAA) intron. We demonstrated that this new method is fast, simple to implement, and very robust. It can be applied for diet analyses of a wide range of phytophagous species at large scales. We also demonstrated that our approach is efficient for mammals, birds, insects and molluscs. This method opens new perspectives in ecology, not only by allowing large-scale studies on diet, but also by enhancing studies on resource partitioning among competing species, and describing food webs in ecosystems.

Valentini *et al.* (2009) *Molecular Ecology Resources*, **9**, 51-60.



Mollusques

Deroceras reticulatum (1)
Arion rufus (1)
Helix aspera (1)


Insectes

Gonfophocerippus rufus (2)
Chorthippus biguttulus (1)

Oiseaux

Tetrao urogallus aquitanicus (4)
Tetrao urogallus major (2)


Mammifères

Ursus arctos (12)
Marmota caudata (12)

MOLECULAR ECOLOGY

Molecular Ecology (2012) **21**, 1951–1965 doi: 10.1111/j.1365-294X.2011.05424.x

Carnivore diet analysis based on next-generation sequencing: application to the leopard cat (*Prionailurus bengalensis*) in Pakistan

WASIM SHEHZAD,* TIAYYBA RIAZ,* MUHAMMAD A. NAWAZ,*† CHRISTIAN MIQUEL,* CAROLE POILLOT,* SAFDAR A. SHAH,‡ FRANÇOIS POMPANON,* ERIC COISSAC* and PIERRE TABERLET*

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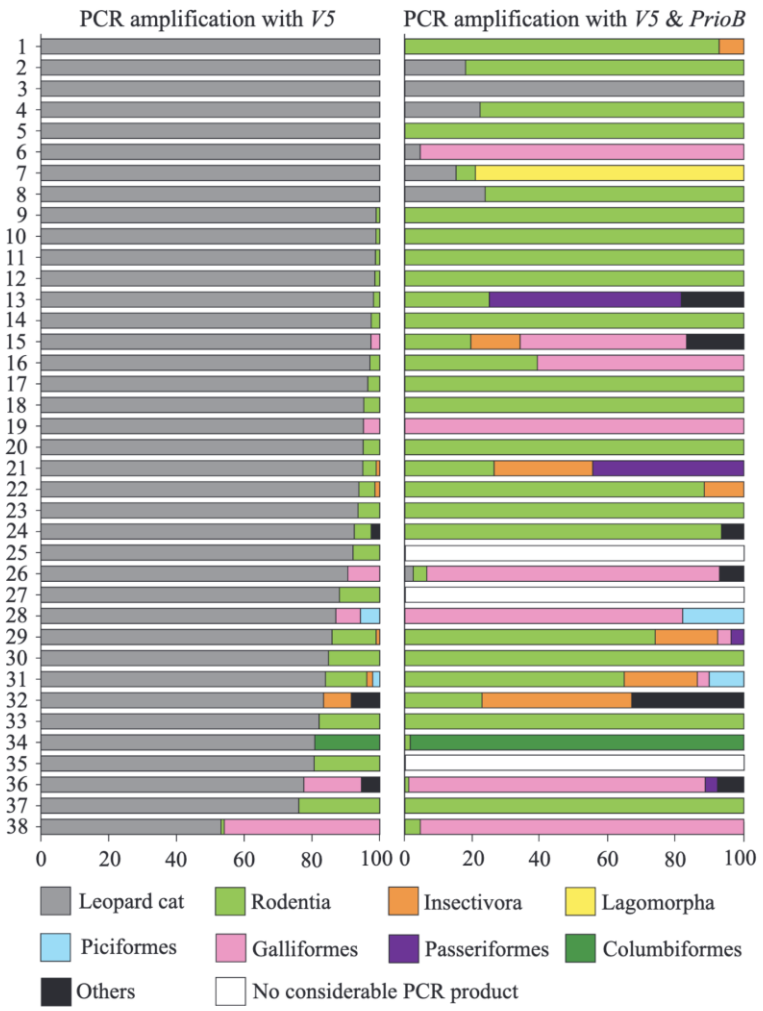
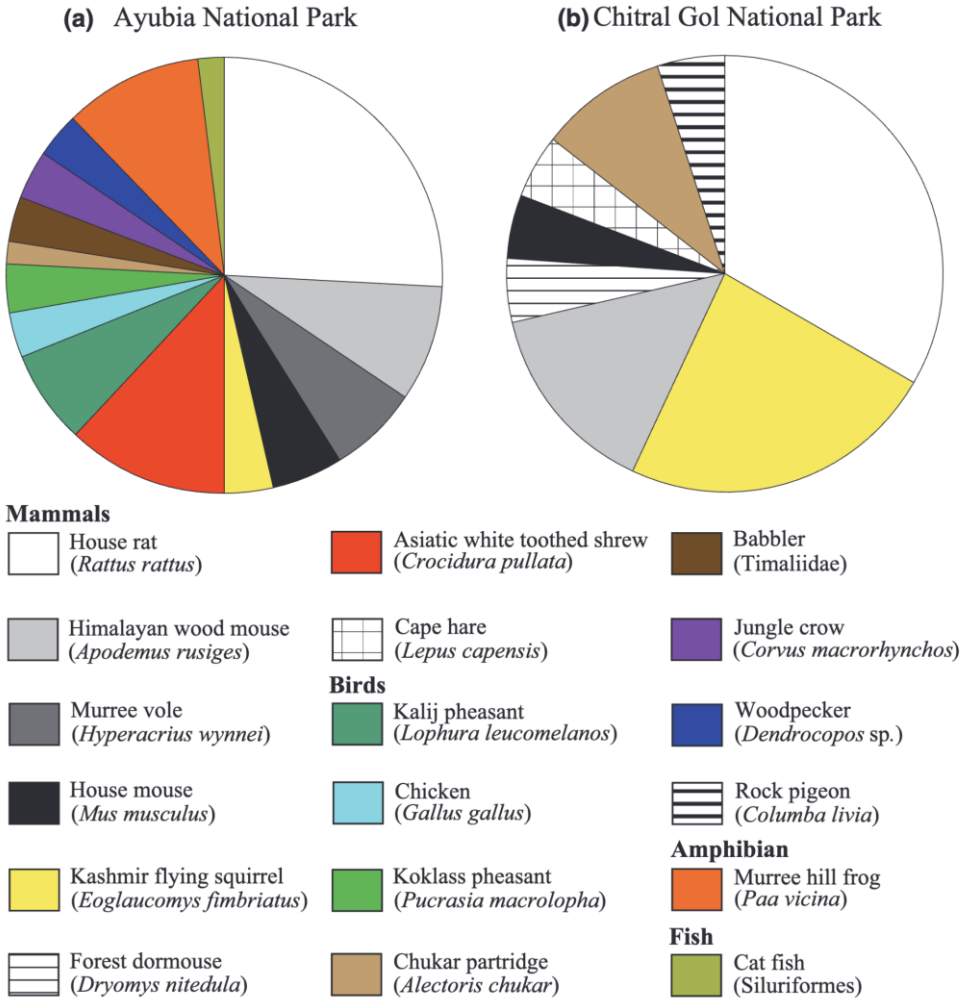
Régime alimentaire du chat léopard





Shehzad *et al.* (2012) *Molecular Ecology*, **21**, 1951-1965.

Analyse de l’eau

biology letters

Biol. Lett. (2008) **4**, 423–425
doi:10.1098/rsbl.2008.0118
Published online 9 April 2008

Population genetics

Species detection using environmental DNA from water samples

Gentile Francesco Ficetola[1,2,*], Claude Miaud[2], François Pompanon[1] and Pierre Taberlet[1]

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The assessment of species distribution is a first critical phase of biodiversity studies and is necessary to many disciplines such as biogeography, conservation biology and ecology. However, several species are difficult to detect, especially during particular time periods or developmental stages, potentially biasing study outcomes. Here we present a novel approach, based on the limited persistence of DNA in the environment, to detect the presence of a species in fresh water. We used specific primers that amplify short mitochondrial DNA sequences to track the presence of a frog (*Rana catesbeiana*) in controlled environments and natural wetlands. A multi-sampling approach allowed for species detection in all environments where it was present, even at low densities. The reliability of the results was demonstrated by the identification of amplified DNA fragments, using traditional sequencing and parallel pyrosequencing techniques. As the environment can retain the molecular imprint of inhabiting species, our approach allows the reliable detection of secretive organisms in wetlands without direct observation. Combined with massive sequencing and the development of DNA barcodes that enable species identification, this approach opens new perspectives for the assessment of current biodiversity from environmental samples.

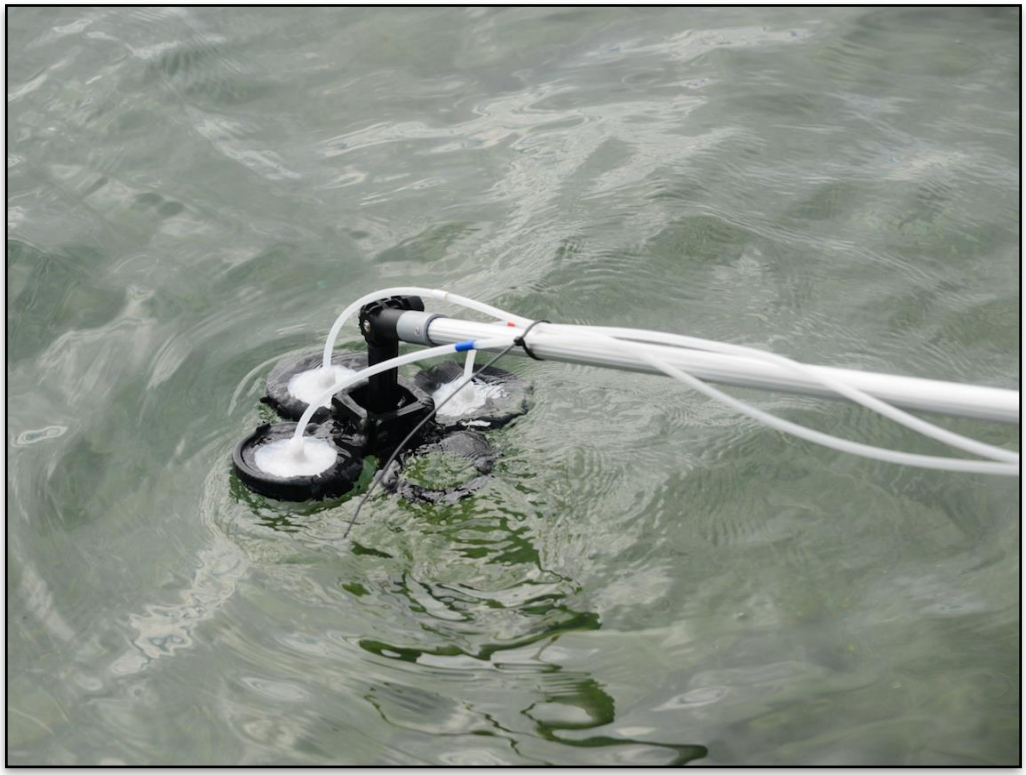
Lithobates catesbeianus

MOLECULAR ECOLOGY

Molecular Ecology (2016) **25**, 929–942 doi: 10.1111/mec.13428

Next-generation monitoring of aquatic biodiversity using environmental DNA metabarcoding

ALICE VALENTINI,* PIERRE TABERLET,†‡ CLAUDE MIAUD,§ RAPHAËL CIVADE,¶ JELGER HERDER,** PHILIP FRANCIS THOMSEN,†† EVA BELLEMAIN,* AURÉLIEN BESNARD,§ ERIC COISSAC,†‡ FRÉDÉRIC BOYER,†‡ COLINE GABORIAUD,* PAULINE JEAN,* NICOLAS POULET,‡‡ NICOLAS ROSET,§§ GORDON H. COPP,¶¶*** PHILIPPE GENIEZ,§ DIDIER PONT,¶ CHRISTINE ARGILLIER,††† JEAN-MARC BAUDOIN,††† TIPHAINE PEROUX,††† ALAIN J. CRIVELLI,‡‡‡ ANTHONY OLIVIER,‡‡‡ MANON ACQUEBERGE,§§§ MATTHIEU LE BRUN,¶¶¶ PETER R. MØLLER,**** ESKE WILLERSLEV†† and TONY DEJEAN*



Analyse des sols

MOLECULAR ECOLOGY

Molecular Ecology (2012) **21**, 3647–3655 doi: 10.1111/j.1365-294X.2012.05545.x

FROM THE COVER

DNA from soil mirrors plant taxonomic and growth form diversity

N. G. YOCCOZ,* K. A. BRÅTHEN,* L. GIELLY,† J. HAILE,‡§ M. E. EDWARDS,¶ T. GOSLAR,** H. VON STEDINGK,¶ A. K. BRYSTING,†† E. COISSAC,† F. POMPANON,† J. H. SØNSTEBØ,†† C. MIQUEL,† A. VALENTINI,† F. DE BELLO,†,‡‡ J. CHAVE,§§ W. THUILLER,† P. WINCKER,¶¶ C. CRUAUD,¶¶ F. GAVORY,¶¶ M. RASMUSSEN,‡ M. T. P. GILBERT,‡ L. ORLANDO‡ C. BROCHMANN,††[1] E. WILLERSLEV,‡[1] and P. TABERLET,†[1]

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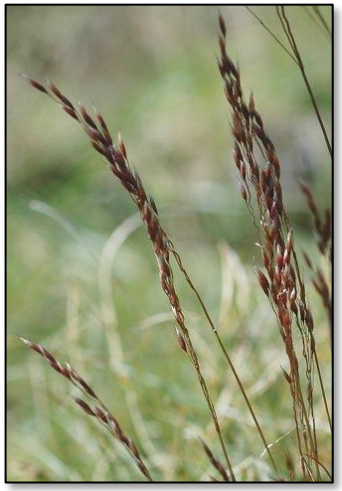
Yoccoz *et al.* (2012) *Molecular Ecology*, **21**, 3647-3655.

Relevés botaniques traditionnels versus metabarcoding sur le sol

Relevés botaniques traditionnels

Avenella flexuosa



Poa sp.

Taraxacum sp.

Anthoxanthum nipponicum

Carex sp.

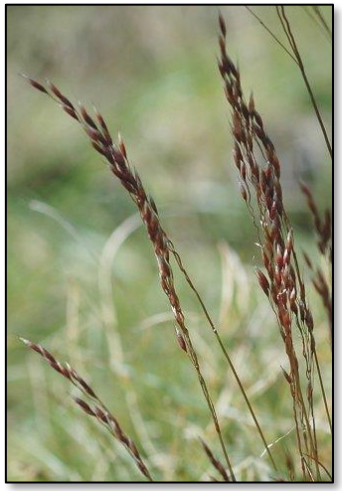
Festuca sp.

Deschampsia sp.

Rumex sp.

Calamagrostris sp.

Metabarcoding sur le sol



Bistorta vivipara

Salix sp.

Alchemilla sp.

Viola biflora

Equisetum sp.

MOLECULAR ECOLOGY

Molecular Ecology (2012) **21**, 2017–2030 doi: 10.1111/j.1365-294X.2011.05407.x

Tracking earthworm communities from soil DNA

FRIEDERIKE BIENERT,* SÉBASTIEN DE DANIELI,† CHRISTIAN MIQUEL,* ERIC COISSAC,* CAROLE POILLOT,* JEAN-JACQUES BRUN† and PIERRE TABERLET*

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Analyse des sédiments

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ARTICLE

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Long livestock farming history and human landscape shaping revealed by lake sediment DNA

Charline Giguet-Covex[1,2,*], Johan Pansu[1,*], Fabien Arnaud[2], Pierre-Jérôme Rey[2], Christophe Griggo[2], Ludovic Gielly[1], Isabelle Domaizon[3], Eric Coissac[1], Fernand David[4], Philippe Choler[1,5], Jérôme Poulenard[2] & Pierre Taberlet[1]

MOLECULAR ECOLOGY

Molecular Ecology (2015) **24**, 1485–1498 doi: 10.1111/mec.13136

Reconstructing long-term human impacts on plant communities: an ecological approach based on lake sediment DNA

JOHAN PANSU,*†[1] CHARLINE GIGUET-COVEX,*†‡§¶[1] GENTILE FRANCESCO FICETOLA,*† LUDOVIC GIELLY,*† FRÉDÉRIC BOYER,*† LUCIE ZINGER,** FABIEN ARNAUD,‡§¶ JÉRÔME POULENARD,‡§¶ PIERRE TABERLET*† and PHILIPPE CHOLER*†††‡‡

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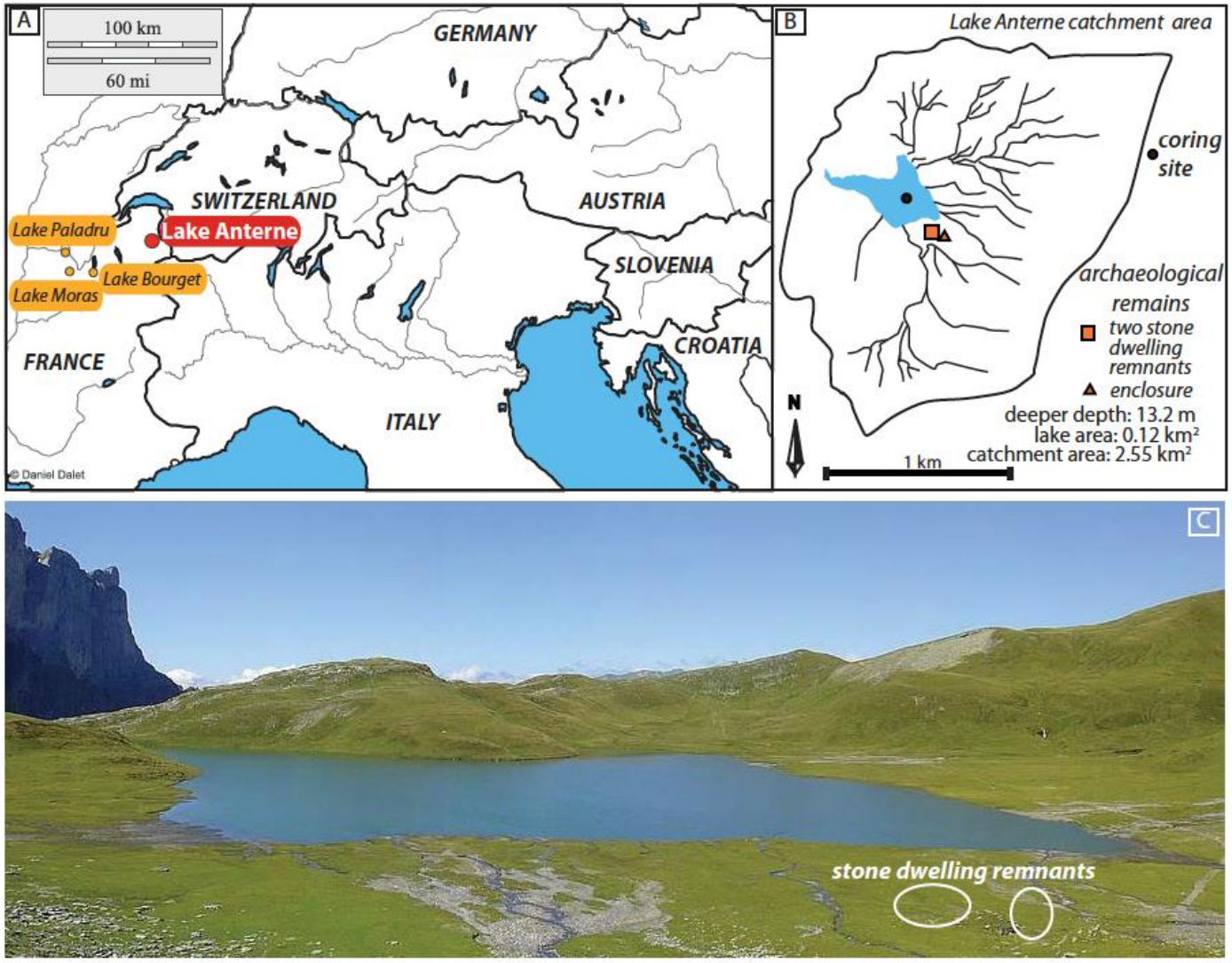
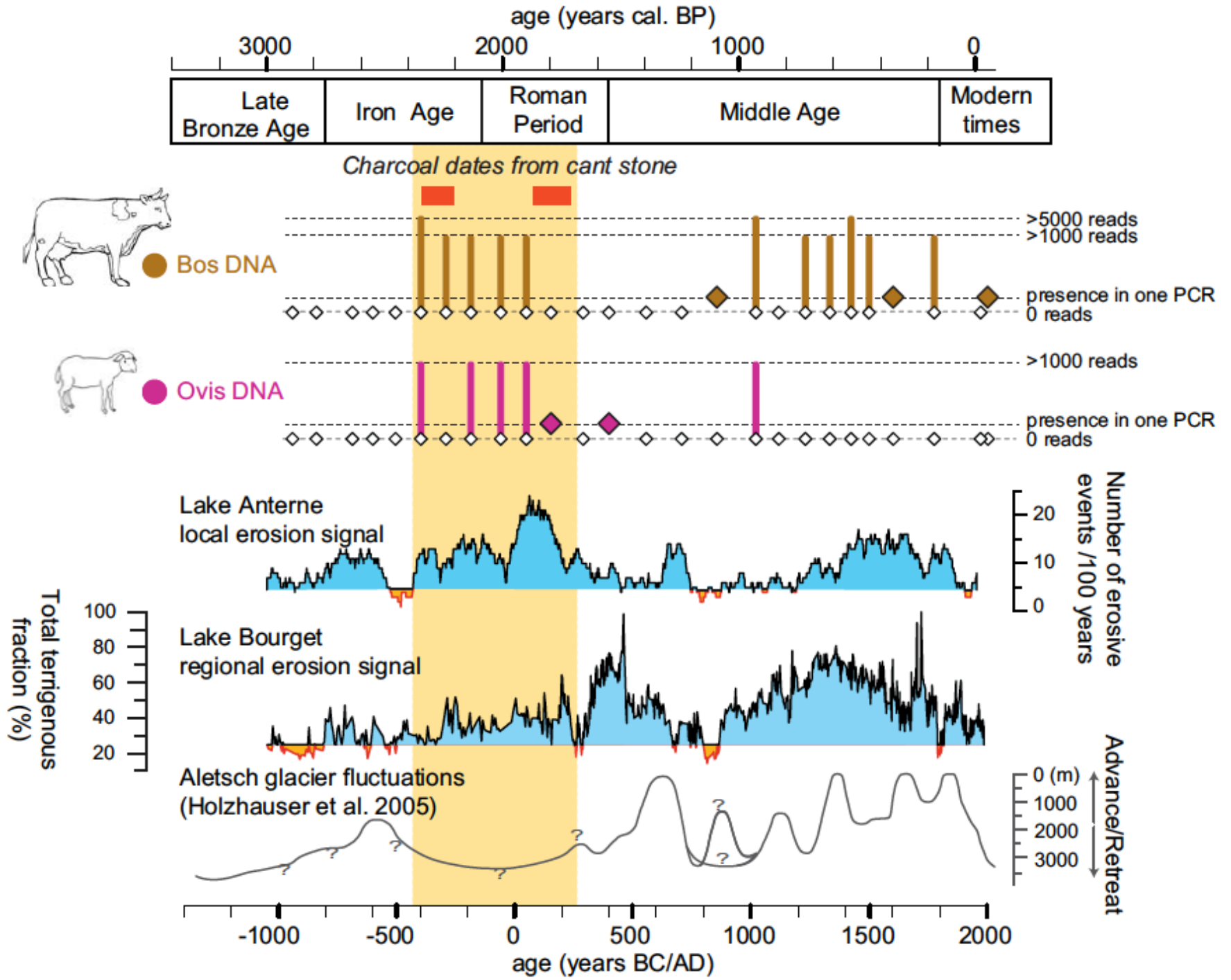
Sediments du lac d'Anterne

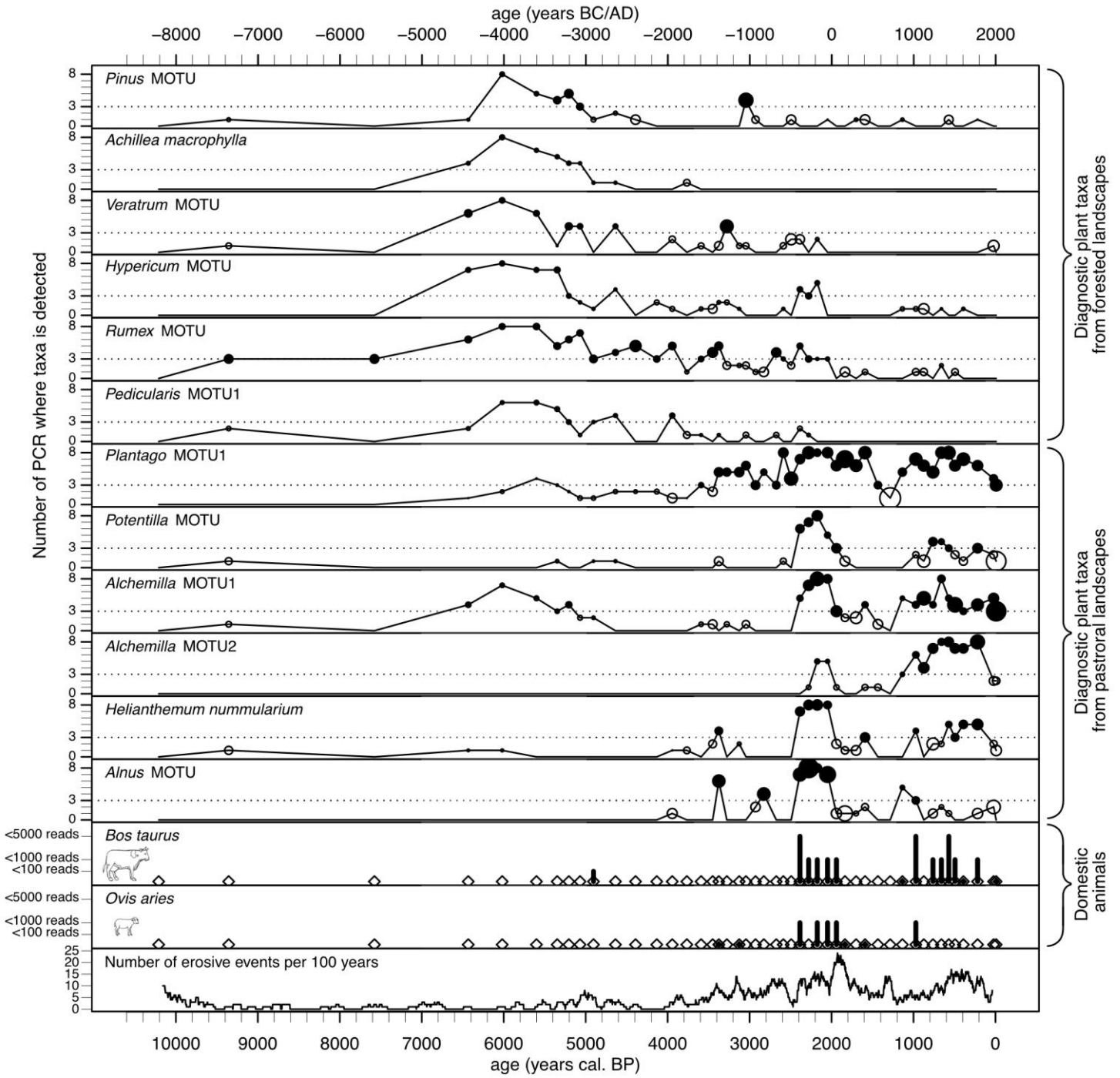


Sediments du Lac d'Anterne

- Analyse de 47 tranches d'une carotte de 20 m correspondant aux derniers 10.000 ans
- Marqueurs ADN utilisés
  - Intron du *trn*L (ADN chloroplastique) pour les plantes (amorces Sper01)
  - Court fragment du gène 16S (ADN mitochondrial) pour les mammifères (amorces Mamm02)
- 2 extractions d'ADN par tranche
- 4 PCRs par extraction


age (years cal. BP)
3000
2000
1000
0
Late Bronze Age
Iron Age
Roman Period
Middle Age
Modern times
Charcoal dates from cant stone
Bos DNA
>5000 reads
>1000 reads
presence in one PCR
0 reads
Ovis DNA
>1000 reads
presence in one PCR
0 reads
Lake Anterne
local erosion signal
Number of erosive events /100 years
20
10
0
Lake Bourget
regional erosion signal
Total terrigenous fraction (%)
100
80
60
40
20
Aletsch glacier fluctuations
(Holzhauser et al. 2005)
Advance/Retreat
0 (m)
1000
2000
3000
-1000
-500
0
500
1000
1500
2000
age (years BC/AD)

eDNA from lake Anterne




Merci pour votre attention