A history of advances in sedaDNA research

Peter D. Heintzman
The Arctic University Museum of Norway

@PalaeoPete
What is sedimentary ancient DNA?
“Modern DNA molecule”

“Ancient DNA molecules”

Occurrences

DNA fragment length (base pairs)

Proportion deaminated

Distance from 5’ end of read (bp)

Distance from 3’ end of read (bp)
The strength of sedimentary ancient DNA

- Taxonomic breadth
- High temporal resolution
- High taxonomic precision

@PalaeoPete
A history of advances in the field
Analysis of Subfossil Molecular Remains of Purple Sulfur Bacteria in a Lake Sediment

MARCO J. L. COOLEN AND JÖRG OVERMANN

Applied Enviro. Microbio. 64, 4513
### Table 3.

<table>
<thead>
<tr>
<th>New Zealand</th>
<th>Region (mtDNA)</th>
<th>Sequence length (bp)</th>
<th>Taxa with highest sequence similarity</th>
<th>Seq. similarity (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cave 0.6</td>
<td>10.4 19 20 to 30</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>cyt b</td>
<td>Mammutthus primigenius (mammoth)†</td>
<td>98 to 99</td>
</tr>
<tr>
<td>7</td>
<td></td>
<td>cyt b</td>
<td>Mammutthus primigenius (mammoth)†</td>
<td>99 to 100</td>
</tr>
<tr>
<td>8</td>
<td>4</td>
<td>16S</td>
<td>Mammutthus primigenius (mammoth)†</td>
<td>97 to 100</td>
</tr>
<tr>
<td>12</td>
<td>4</td>
<td>16S</td>
<td>Equus caballus (horse)</td>
<td>98 to 100</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>16S</td>
<td>Lemus lemus (lemming)</td>
<td>97†</td>
</tr>
<tr>
<td>2</td>
<td></td>
<td>Control region 124 to 125</td>
<td>Bison spp. (bison)†</td>
<td>98 to 100*</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>16S</td>
<td>Ovibos moschatus (musk ox)</td>
<td>100</td>
</tr>
<tr>
<td>1</td>
<td></td>
<td>Control region 129</td>
<td>Ovibos moschatus (musk ox)</td>
<td>82‡</td>
</tr>
<tr>
<td>1</td>
<td></td>
<td>Control region 124</td>
<td>Rangifer tarandus (reindeer)</td>
<td>98</td>
</tr>
<tr>
<td>15</td>
<td></td>
<td>Control region 202 to 203</td>
<td>Megalapteryx didinus (Upland moa)†</td>
<td>97 to 100*</td>
</tr>
<tr>
<td>2</td>
<td></td>
<td>Control region 204</td>
<td>Pachyornis elephantopus (Heavy-footed moa)†</td>
<td>99*</td>
</tr>
<tr>
<td>10</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>11</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Σ = 30</td>
<td>Σ = 10</td>
<td>Σ = 14</td>
<td>Σ = 2</td>
<td></td>
</tr>
</tbody>
</table>

*References:† Sequence similarity (32E); ‡ Sequence similarity (12E).
Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments

Eske Willerslev,1* Anders J. Hansen,1*† Jonas Binladen,1 Tina B. Brand,1 M. Thomas P. Gilbert,2 Beth Shapiro,2 Michael Bunce,2 Carsten Wiuf,3 David A. Gilichinsky,4 Alan Cooper2

*Corresponding author. E-mail: ewill1@phys.uoa.gr
†To whom correspondence should be addressed. E-mail: binladen@phys.uoa.gr
© 2003. Published by the American Association for the Advancement of Science.

Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments

Eske Willerslev,1* Anders J. Hansen,1*† Jonas Binladen,1 Tina B. Brand,1 M. Thomas P. Gilbert,2 Beth Shapiro,2 Michael Bunce,2 Carsten Wiuf,3 David A. Gilichinsky,4 Alan Cooper2

*Corresponding author. E-mail: ewill1@phys.uoa.gr
†To whom correspondence should be addressed. E-mail: binladen@phys.uoa.gr
© 2003. Published by the American Association for the Advancement of Science.

Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments

Eske Willerslev,1* Anders J. Hansen,1*† Jonas Binladen,1 Tina B. Brand,1 M. Thomas P. Gilbert,2 Beth Shapiro,2 Michael Bunce,2 Carsten Wiuf,3 David A. Gilichinsky,4 Alan Cooper2

*Corresponding author. E-mail: ewill1@phys.uoa.gr
†To whom correspondence should be addressed. E-mail: binladen@phys.uoa.gr
© 2003. Published by the American Association for the Advancement of Science.

Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments

Eske Willerslev,1* Anders J. Hansen,1*† Jonas Binladen,1 Tina B. Brand,1 M. Thomas P. Gilbert,2 Beth Shapiro,2 Michael Bunce,2 Carsten Wiuf,3 David A. Gilichinsky,4 Alan Cooper2

*Corresponding author. E-mail: ewill1@phys.uoa.gr
†To whom correspondence should be addressed. E-mail: binladen@phys.uoa.gr
© 2003. Published by the American Association for the Advancement of Science.

Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments

Eske Willerslev,1* Anders J. Hansen,1*† Jonas Binladen,1 Tina B. Brand,1 M. Thomas P. Gilbert,2 Beth Shapiro,2 Michael Bunce,2 Carsten Wiuf,3 David A. Gilichinsky,4 Alan Cooper2

*Corresponding author. E-mail: ewill1@phys.uoa.gr
†To whom correspondence should be addressed. E-mail: binladen@phys.uoa.gr
© 2003. Published by the American Association for the Advancement of Science.

Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments

Eske Willerslev,1* Anders J. Hansen,1*† Jonas Binladen,1 Tina B. Brand,1 M. Thomas P. Gilbert,2 Beth Shapiro,2 Michael Bunce,2 Carsten Wiuf,3 David A. Gilichinsky,4 Alan Cooper2

*Corresponding author. E-mail: ewill1@phys.uoa.gr
†To whom correspondence should be addressed. E-mail: binladen@phys.uoa.gr
© 2003. Published by the American Association for the Advancement of Science.

Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments

Eske Willerslev,1* Anders J. Hansen,1*† Jonas Binladen,1 Tina B. Brand,1 M. Thomas P. Gilbert,2 Beth Shapiro,2 Michael Bunce,2 Carsten Wiuf,3 David A. Gilichinsky,4 Alan Cooper2

*Corresponding author. E-mail: ewill1@phys.uoa.gr
†To whom correspondence should be addressed. E-mail: binladen@phys.uoa.gr
© 2003. Published by the American Association for the Advancement of Science.

Diverse Plant and Animal Genetic Records from Holocene and Pleistocene Sediments

Eske Willerslev,1* Anders J. Hansen,1*† Jonas Binladen,1 Tina B. Brand,1 M. Thomas P. Gilbert,2 Beth Shapiro,2 Michael Bunce,2 Carsten Wiuf,3 David A. Gilichinsky,4 Alan Cooper2

*Corresponding author. E-mail: ewill1@phys.uoa.gr
†To whom correspondence should be addressed. E-mail: binladen@phys.uoa.gr
© 2003. Published by the American Association for the Advancement of Science.
2003

Table 1.

<table>
<thead>
<tr>
<th>ID</th>
<th>Families, no. different</th>
<th>Bootstrap %</th>
<th>Next closest match Family/order</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>0</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>12S 1</td>
<td>Megatheridea</td>
<td>NID</td>
<td>94</td>
</tr>
<tr>
<td>2</td>
<td>NID</td>
<td>Cathartidae</td>
<td>47</td>
</tr>
<tr>
<td>3</td>
<td>NID</td>
<td>Procyonidae</td>
<td>87</td>
</tr>
<tr>
<td>4</td>
<td>Sciuridae</td>
<td>NID</td>
<td>97</td>
</tr>
<tr>
<td>5</td>
<td>Hominidae</td>
<td>Hominidae</td>
<td>NA</td>
</tr>
<tr>
<td>16S A</td>
<td>Megatheridea</td>
<td>NID</td>
<td>NA</td>
</tr>
<tr>
<td>B</td>
<td>NID</td>
<td>NID</td>
<td>NA</td>
</tr>
</tbody>
</table>

Molecular caving

Michael Hofreiter¹, Jim I. Mead², Paul Martin³ and Hendrik N. Poinar¹,⁴
Ancient DNA Chronology within Sediment Deposits: Are Paleobiological Reconstructions Possible and Is DNA Leaching a Factor?

James Haile,* Richard Holdaway,† Karen Oliver,* Michael Bunce,‡ M. Thomas P. Gilbert,§ Rasmus Nielsen,§ Kasper Munch,§ Simon Y. W. Ho,* Beth Shapiro,* and Eske Willerslev*§

Mol. Biol. & Evol. 24(4), 982
Sampling, DNA Extraction, and Amplification

Contamination with extraneous DNA is an ever-present concern in any aDNA study, and it is the responsibility of the researcher to demonstrate that adequate experimental and authentication procedures are carried out (Cooper and Poinar 2000; Gilbert et al. 2005). Samples were taken from freshly excavated sections in the 2 shelters, beginning at the bottom of each section and proceeding to more recent levels (fig. 2). Disposable tools were used and changed between samples to avoid cross-contamination. All manipulation of ancient samples before polymerase chain reaction (PCR) amplification were performed in dedicated aDNA laboratories at the Henry Wellcome Ancient Biomolecules Centre at the University of Oxford and the Centre for Ancient Genetics at the University of Copenhagen, in areas free from other molecular research. One negative extraction and 1 amplification control was used for every 8 samples extracted, and each positive result cloned a minimum of 8 times in agreement with suggested aDNA criteria (Handt et al. 1994; Willerslev et al. 1999; Hansen et al. 2001; Gilbert et al. 2003, 2005; Willerslev and Cooper 2005).

DNA from a total of 1 g of wet weight sediment per sample was extracted in 2 subsamples of 0.5 g sediment, dissolved in 600 l lysis buffer (Bulat et al. 2000) 400 g/ml proteinase K (Roche Applied Science, Mannheim, Germany) disrupted with 4 runs of a FastPrep 120 (BIO 101) at speed 6.5 for 45 s, with 2 min on ice between runs and incubated at 65/176 C for at least 4 h under agitation. The solution was adjusted with NaCl to 1.15 M, treated with 1/2 volume of chloroform/octanol (24:1), and agitated slowly overnight at room temperature, and the water phase isolated with centrifugation at 12,000 g for 2 min and transferred to a separate microtube for incubation at 2–3/176 C for at least 1 h. The precipitate was centrifuged at 12,000 g for 2 min and the supernatant purified using silica spin columns and binding buffer (Qiagen DNA purification kit II), followed by washes in 0.5 ml Salton wash 1 and 2 (BIO 101) and 0.5 ml AW1 and AW2 (Qiagen tissue kit). The DNA was eluted twice with 100 l l elution buffer (Qiagen purification kit II) and stored at /176 C. PCR was used to amplify an 88 bp (moa) and 60 bp (sheep) fragment of control region mitochondrial DNA (mtDNA), avian 153 bp fragment of 12S mtDNA, and plant rbcL and trnL chloroplast DNA using primers listed in table S1 (Supplementary Material online), using 5 l l of DNA extractions, 35–55 cycles of PCR (1.5 min initial denaturation at 94 /176 C, 45 s at 94 /176 C, 45 s at 45–60 /176 C, 1.5 min at 68 /176 C, and a final cycle of 10 min at 68 /176 C). PCR products were cleaned using a QIAquick PCR Purification Kit (Qiagen, Crawley, UK). Amplification products from the 2 separate extracts of each sample were pooled, cloned, purified, and sequenced on both strands (Willerslev et al. 1999). Sequences were aligned using ClustalW in BioEdit (Hall 1999) and possible recombination among the clone sequences investigated (Willerslev et al. 1999).

Quantitative Real-Time PCR (qPCR)

A SYBRGreen based qPCR assay was used to determine the relative quantity of sheep DNA within the Hukanui Pool DNA extracts. Amplifications targeted a 71 bp fragment of the sheep mtDNA control region, using qPCR primers Sheep-87F and Sheep-157R (table S1, Supplementary Material online). Before the qPCR analysis, the primers were prescreened on both sheep DNA-positive and -negative soil extracts and blanks, to ensure that they generated a single correct product, with no primer–dimer or nonspecific products that might contribute to erroneous results.
Genetic markers (samples analyzed for DNA, amino acid racemization/luminescence (underlined), and \(^{10}\text{Be}^{36}\text{Cl}\) also shown.

W21°14′W) in Greenland as well as the John Evans Glacier (JEG) (79°49′N, 74°30′W) on Ellesmere Island, near Inuknngorvik in northern Greenland, indicate a forested southern boreal forest ecosystem at Dye 3.

Order Marker Clones Support (%) Family Marker Clones Support (%) Genus Marker Clones Support (%)

<table>
<thead>
<tr>
<th>JEG sample</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Rosales</td>
<td>(rbcL) 3</td>
<td>90–99</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Malpighiales</td>
<td>(rbcL) 2</td>
<td>99–100</td>
<td>Salicaceae</td>
<td>(rbcL) 2</td>
<td>99–100</td>
<td>Picea</td>
<td>(rbcL) 2</td>
<td>99–100</td>
<td></td>
</tr>
<tr>
<td></td>
<td>(trnL) 5</td>
<td>99–100</td>
<td></td>
<td>(trnL) 4</td>
<td>100</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Saxifragales</td>
<td>(rbcL) 3</td>
<td>92–94</td>
<td>Saxifragaceae</td>
<td>(rbcL) 2</td>
<td>92</td>
<td>Saxifraga</td>
<td>(rbcL) 2</td>
<td>91</td>
<td></td>
</tr>
<tr>
<td>Dye 3 sample</td>
<td>Coniferales</td>
<td>97–100</td>
<td>Pinaceae*</td>
<td>(rbcL) 20</td>
<td>100</td>
<td>Picea</td>
<td>(rbcL) 20</td>
<td>99–100</td>
<td></td>
</tr>
<tr>
<td></td>
<td>(trnL) 27</td>
<td>100</td>
<td></td>
<td>(trnL) 25</td>
<td>100</td>
<td>Pinus†</td>
<td>(trnL) 17</td>
<td>90–99</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Taxaceae‡</td>
<td>(rbcL) 23</td>
<td>91–98</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>(trnL) 2</td>
<td>100</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Poales§</td>
<td>(rbcL) 67</td>
<td>99–100</td>
<td>Poaceae§</td>
<td>(rbcL) 67</td>
<td>99–100</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>(trnL) 17</td>
<td>97–100</td>
<td></td>
<td>(trnL) 13</td>
<td>100</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Asterales</td>
<td>(rbcL) 18</td>
<td>90–100</td>
<td>Asteraceae</td>
<td>(rbcL) 2</td>
<td>91</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>(trnL) 27</td>
<td>100</td>
<td></td>
<td>(trnL) 27</td>
<td>100</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fabales</td>
<td>(rbcL) 10</td>
<td>99–100</td>
<td>Fabaceae</td>
<td>(rbcL) 10</td>
<td>99–100</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>(trnL) 3</td>
<td>99</td>
<td></td>
<td>(trnL) 3</td>
<td>99</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fagales</td>
<td>(rbcL) 10</td>
<td>95–99</td>
<td>Betulaceae</td>
<td>(rbcL) 8</td>
<td>93–97</td>
<td>Alnus</td>
<td>(rbcL) 7</td>
<td>91–95</td>
<td></td>
</tr>
<tr>
<td></td>
<td>(trnL) 12</td>
<td>100</td>
<td></td>
<td>(trnL) 11</td>
<td>98–100</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lepidoptera</td>
<td>COI 12</td>
<td>97–99</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The results of recent models suggest that the maximum age estimate for the Dye 3 silty sample was likely between 800,000 and 130,000 years ago, providing direct evidence of a forested southern boreal forest ecosystem at Dye 3.

**Ancient Biomolecules from Deep Ice Cores Reveal a Forested Southern Greenland**


Science 317, 111
Ancient DNA reveals late survival of mammoth and horse in interior Alaska

James Haile\textsuperscript{a}, Duane G. Froese\textsuperscript{b}, Ross D. E. MacPhee\textsuperscript{c}, Richard G. Roberts\textsuperscript{d}, Lee J. Arnold\textsuperscript{d,1}, Alberto V. Reyes\textsuperscript{b}, Morten Rasmussen\textsuperscript{a}, Rasmus Nielsen\textsuperscript{a}, Barry W. Brook\textsuperscript{f}, Simon Robinson\textsuperscript{b}, Martina Demuro\textsuperscript{d}, M. Thomas P. Gilbert\textsuperscript{a}, Kasper Munch\textsuperscript{a}, Jeremy J. Austin\textsuperscript{g}, Alan Cooper\textsuperscript{g}, Ian Barnes\textsuperscript{h}, Per Möller\textsuperscript{i}, and Eske Willerslev\textsuperscript{a,2}

\textbf{PNAS 106(52), 22352
Long livestock farming history and human landscape shaping revealed by lake sediment DNA

Charline Giguet-Covex¹,²,*, Johan Pansu¹,*, Fabien Arnaud², Pierre-Jérôme Rey², Christophe Griggo², Ludovic Gielly¹, Isabelle Domaizon³, Eric Coissac¹, Fernand David⁴, Philippe Choler¹,⁵, Jérôme Poulenard² & Pierre Taberlet¹

Nat. Comms. ncomms4211.
Fifty thousand years of Arctic vegetation and megafaunal diet

Minimizing polymerase biases in metabarcoding

Ruth V. Nichols | Christopher Vollmers | Lee A. Newsom | Yue Wang | Peter D. Heintzman | McKenna Leighton | Richard E. Green | Beth Shapiro

FROM THE COVER

2018 Mol. Ecol. Resour. 18(5), 927

©2014 Wiley

Molecular Ecology Resources
Sedimentary DNA from a submerged site reveals wheat in the British Isles 8000 years ago

Oliver Smith, Garry Momber, Richard Bates, Paul Garwood, Simon Fitch, Mark Pallen, Vincent Gaffney, Robin G. Allaby
Contesting the presence of wheat in the British Isles 8,000 years ago by assessing ancient DNA authenticity from low-coverage data

Clemens L Weiß¹, Michael Dannemann², Kay Prüfer², Hernán A Burbano¹*

TECHNICAL COMMENT

ARCHAEOLOGY

Comment on “Sedimentary DNA from a submerged site reveals wheat in the British Isles 8000 years ago”

K. D. Bennett¹,²

Science 349, 247b.

eLife 4, e10005.
Timing and causes of mid-Holocene mammoth extinction on St. Paul Island, Alaska

Russell W. Graham, Soumaya Belmecheri, Kyungcheol Choy, Brendan J. Culleton, Lauren J. Davies, Duane Froese, Peter D. Heintzman, Carrie Hritz, Joshua D. Kapp, Lee A. Newsom, Ruth Rawcliffe, Emilie Saulnier-Talbot, Beth Shapiro, Yue Wang, John W. Williams, and Matthew J. Wooller

PNAS 113(33), 9310
Timing and causes of mid-Holocene mammoth extinction on St. Paul Island, Alaska

Russell W. Graham, Soumya Belmecheri, Kyungcheol Choy, Brendan J. Culleton, Lauren J. Davies, Duane Froese, Peter D. Heintzman, Carrie Hritz, Joshua D. Kapp, Lee A. Newsom, Ruth Rawcliffe, Émilie Saulnier-Talbot, Beth Shapiro, Yue Wang, John W. Williams, and Matthew J. Wooller

PNAS 113(33), 9310
Timing and causes of mid-Holocene mammoth extinction on St. Paul Island, Alaska

Russell W. Graham, Soumaya Belmacher, Kyungcheol Choy, Brendan J. Culleton, Lauren J. Davies, Duane Froese, Peter D. Heintzman, Carrie Hritz, Joshua D. Kapp, Lee A. Newsom, Ruth Rawcliffe, Émilie Saulnier-Talbot, Beth Shapiro, Yue Wang, John W. Williams, and Matthew J. Wooller

PNAS 113(33), 9310
Postglacial viability and colonization in North America’s ice-free corridor

Mikkel W. Pedersen1, Anthony Ruter1, Charles Schweger2, Harvey Friebe2, Richard A. Staff3, Kristian K. Kjeldsen1,4, Marie L. Z. Mendoza1, Alwynne B. Beaudoin5, Cynthia Zutter6, Nicolaj K. Larsen1,7, Ben A. Potter8, Rasmus Nielsen1,9,10, Rebecca A. Rainville1, Ludovic Orlando1, David J. Meltzer1,12, Kurt H. Kjær1 & Eske Willerslev1,11,14

2016 Nature 537, 45
DNA evidence of bowhead whale exploitation by Greenlandic Paleo-Inuit 4,000 years ago

Frederik Valeur Seersholm¹,²,†, Mikkel Winther Pedersen¹, Martin Jensen Søe¹,³, Hussein Shokry¹, Sarah Siu Tze Mak¹, Anthony Ruter¹, Maanasa Raghavan¹,⁴,†, William Fitzhugh⁵, Kurt H. Kjær¹, Eske Willerslev¹,⁴, Morten Meldgaard¹,⁶, Christian M.O. Kapel³ & Anders Johannes Hansen¹

Nat. Comm. ncomms13389

@PalaeoPete
Neandertal and Denisovan DNA from Pleistocene sediments

Viviane Slon,1,8 Charlotte Hopfe,1 Clemens L. Weiβ,2 Fabrizio Mafessoni,1 Marco de la Rasilla,3 Carles Latueza-Fox,4 Antonio Rosas,2 Marie Soressi,6,7 Monika V. Knui,8 Rebecca Miller,9 John R. Stewart,8 Anatoly P. Derevianko,10,11 Zenobia Jacobs,12,13 Bo Li,13 Richard G. Roberts,12,13 Michael V. Shunkov,10,14 Henry de Lumley,15,16 Christian Perrenoud,15,17 Ivan Gušić,18 Željko Kučan,18 Pavao Rudan,18 Ayinuer Aximu-Petri,19 Elena Essel,1 Sarah Nagel,1 Birgit Nickel,1 Anna Schmidt,1 Kay Prüfer,1 Janet Kelso,1 Hernán A. Burbano,2 Svante Pääbo,1 Matthias Meyer1*
Persistence of arctic-alpine flora during 24,000 years of environmental change in the Polar Urals


Then we had 2021-present...
Hybridisation capture allows DNA damage analysis of ancient marine eukaryotes

L. Armbrecht, G. Hallegraeff, C. J. S. Bolch, C. Woodward & A. Cooper

Hybridization capture of larch (Larix Mill.) chloroplast genomes from sedimentary ancient DNA reveals past changes of Siberian forest

Luise Schulte, Nadine Bernhardt, Kathleen Stoeff-Leichsenring, Heike H. Zimmermann, Luidmila A. Pestryakova, Laura S. Epp, Ulrike Herczschn

Optimizing extraction and targeted capture of ancient environmental DNA for reconstructing past environments using the PalaeoChip Arctic-1.0 bait-set


2021

2020

Sci. Rep. 11, 3220

Mol. Ecol. Resour. 21, 801

Quat. Res. 99, 305

@PalaeoPete
Ancient plant DNA reveals High Arctic greening during the Last Interglacial

Sarah E. Crump\textsuperscript{a,b,1}, Bianca Fréchette\textsuperscript{c}, Matthew Power\textsuperscript{d}, Sam Cutler\textsuperscript{b}, Gregory de Wet\textsuperscript{a,e}, Martha K. Raynolds\textsuperscript{f,1}, Jonathan H. Raberg\textsuperscript{a}, Jason P. Briner\textsuperscript{g}, Elizabeth K. Thomas\textsuperscript{g}, Julio Sepúlveda\textsuperscript{a}, Beth Shapiro\textsuperscript{b,h}, Michael Bunce\textsuperscript{d,i}, and Gifford H. Miller\textsuperscript{a}

PNAS 118, e2019069118
ECOLOGY

Sedimentary ancient DNA shows terrestrial plant richness continuously increased over the Holocene in northern Fennoscandia

Dilli P. Rijal1,2*,†, Peter D. Heintzman1*,†, Youri Lammers1, Nigel G. Yoccoz2, Kelsey E. Lorberau2, Iva Pitelkova1, Tomasz Goslar3,4, Francisco J. A. Murguzur2, J. Sakari Salonen5, Karin F. Helmens6,7, Jostein Bakke8, Mary E. Edwards1,9,10, Torbjørn Alm1, Kari Anne Bråthen2, Antony G. Brown1,9, Inger G. Alsos1*†
Anthropogenic and environmental drivers of vegetation change in southeastern Norway during the Holocene

Quat. Sci. Rev. 107175

A.T.M. ter Schure a,*, M. Bajard b,c, K. Loftsgarden d, H.I. Høeg d, E. Ballo b,c, J. Bakke e, E.W.N. Støren e, F. Iversen d, A.K. Brysting a, K. Krüger b,c, S. Boessenkool a,*
Collapse of the mammoth-steppe in central Yukon as revealed by ancient environmental DNA

Tyler J. Murchie1,2,3, Alistair J. Monteath3,4, Matthew E. Mahony3, George S. Long1,5, Scott Cocker5,3, Tara Sadoway1,6, Emil Karpinski1,5, Grant Zazula7,8, Ross D. E. MacPhee9, Duane Froese3,5 & Hendrik N. Poinar1,2,10,11,12

Nat. Comms. 12, 7120.
Collapse of the mammoth-steppe in central Yukon as revealed by ancient environmental DNA

Tyler J. Murchie1,2, Alistair J. Monteath3,4, Matthew E. Mahony3, George S. Long5,1,5, Scott Cocker3, Tara Sadoway1, Emil Karpinski1,5, Grant Zazula7,8, Ross D. E. MacPhee9, Duane Froese3,5 & Hendrik N. Poinar1,2,10,11,12

Nat. Comms. 12, 7120.
Late Quaternary dynamics of Arctic biota from ancient environmental genomics


Nature 600, 86-92.
Late Quaternary dynamics of Arctic biota from ancient environmental genomics

Environmental palaeogenomic reconstruction of an Ice Age algal population

Youri Lammers 1✉, Peter D. Heintzman 1,2 & Inger Greve Alsos 1,2

1 The Arctic University Museum of Norway, UiT–The Arctic University of Norway, Tromsø, Norway. 2 These authors contributed equally: Peter D. Heintzman, Inger Greve Alsos.

✉ email: youri.lammers@uit.no

Comms. Biol. 4, 220
Pleistocene mitogenomes reconstructed from the environmental DNA of permafrost sediments

Tyler J. Murchie,1−10 Emil Karpinski,1,8 Katherine Eaton,1,8 Ana T. Duggan,1,8 Sina Baleka,1 Grant Zazula,1,8 Ross D.E. MacPhee,8 Duane Froese,8* and Hendrik N. Poinar1,2,9,10,*

Current Biology 32, 1.
Pleistocene sediment DNA reveals hominin and faunal turnovers at Denisova Cave

Nature

595, 399

Elena I. Zavala, Zenobia Jacobs, Benjamin Vernot, Michael V. Shunkov, Maxim B. Kozlikin, Anatoly P. Derevianko, Elena Essel, Cesare de Filippo, Sarah Nagel, Julia Richter, Frédéric Romagné, Anna Schmidt, Bo Li, Kieran O’Gorman, Viviane Slon, Janet Kelso, Svante Pääbo, Richard G. Roberts & Matthias Meyer
Nature
595, 399

@Paiaeofete
PALEOGENOMICS

Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments

Benjamin Vernot1, Elena I. Zavala1, Asier Gómez-Olivencia2,3,4, Zenobia Jacobs5,6, Viviane Slon1,7,8, Fabrizio Mafessoni1, Frédéric Romagne2, Alice Pearson1, Martin Petr1, Noémie Sala4,9, Adrián Pablos4,9, Arantza Aranburu2,3, José María Bermúdez de Castro9, Eudald Carbonell10,11, Bo Li5,6, Maciej T. Krajcarz12, Andrey I. Krivoshapkin3,14, Kseniya A. Kolobova13, Maxim B. Kozlikin13, Michael V. Shunkov13, Anatoly P. Derevianko13, Bence Viola15, Steffi Grote1, Elena Essel1, David López Herráez2, Sarah Nagel1, Birgit Nickel1, Julia Richter1, Anna Schmidt1, Benjamin Peter1, Janet Kelso1, Richard G. Roberts5,6, Juan-Luis Arsuaga3,16, Matthias Meyer16

Science 372, 6542

@PalaeoPete
PALEOGENOMICS

Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments

Benjamin Vernot¹, Elena I. Zavala¹, Asier Gómez-Olivencia²,³,⁴, Zenobia Jacobs⁵,⁶, Viviane Slon¹,⁷,⁸, Fabrizio Mafessoni³, Frédéric Romagné³, Alice Pearson¹, Martin Petr³, Nohemi Sala⁴,⁹, Adrián Pablos⁴,⁹, Arantza Aranburu²,³, José María Bermúdez de Castro⁹, Eudald Carbonell¹⁰,¹¹, Bo Li⁵,⁶, Maciej T. Krajcarz¹², Andrey I. Krivoshapkin¹³,¹⁴, Kseniya A. Kolobova¹⁵, Maxim B. Kozlikin¹³, Michael V. Shunkov¹⁵, Anatoly P. Derevianko¹⁶, Bence Viola¹⁵, Steffi Grote¹, Elena Essel¹, David López Herráez¹, Sarah Nagel¹, Birgit Nickel¹, Julia Richter¹, Anna Schmidt¹, Benjamin Peter¹, Janet Kelso¹, Richard G. Roberts⁵,⁶, Juan-Luis Arsuaga³,¹⁶, Matthias Meyer¹⁶

Science 372, 6542
Eastern American black bears (Figure 4A). We recovered genomic data from ancient bears directly from cave sediments (D) environmental genome of the extinct giant short-faced bear (Arctodus). We observed two lower-coverage giant short-faced bear DNA extracted from cave sediments (C) PSMC plot for YG 546.562. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).
Genome-scale sequencing and analysis of human, wolf, and bison DNA from 25,000-year-old sediment

Pere Gelabert,1,11,13,* Susanna Sawyer,1,11 Anders Bergström,2,11,* Ashot Margaryan,3 Thomas C. Collin,4 Tengiz Meshveliani,5 Anna Belfer-Cohen,6 David Lordkipanidze,5 Nino Jakeli,5 Zinovi Matskevich,7 Guy Bar-Oz,8 Daniel M. Fernandes,1,9 Olivia Cheronet,1 Kadir T. Özdogan,1 Victoria Oberreiter,1 Robin N.M. Feeney,4 Mareike C. Stahlschmidt,10 Pontus Skoglund,2,12,* and Ron Pinhasi1,12,*

1Department of Evolutionary Anthropology, University of Vienna, Vienna, Austria
2Ancient Genomics Laboratory, Francis Crick Institute, London, UK
3Center for Evolutionary Hologenomics, University of Copenhagen, Copenhagen, Denmark
4School of Medicine, University College Dublin, Dublin, Ireland
5Georgian National Museum, Institute of Paleoanthropology and Paleobiology, Tbilisi, Georgia
6Institute of Archaeology, The Hebrew University of Jerusalem, Jerusalem, Israel
7Israel Antiquities Authority, Jerusalem, Israel
8Zinman Institute of Archaeology, University of Haifa, Haifa, Israel
9CIAS, Department of Life Sciences, University of Coimbra, Coimbra, Portugal
10Department of Human Evolution, Max-Planck-Institute for Evolutionary Anthropology, Leipzig, Germany
11These authors contributed equally
12These authors contributed equally
13Lead contact
*Correspondence: pere.gelabert@univie.ac.at (P.G.), anders.bergstrom@crick.ac.uk (A.B.), pontus.skoglund@crick.ac.uk (P.S.), ron.pinhasi@univie.ac.at (R.P.)

https://doi.org/10.1016/j.cub.2021.06.023

SUMMARY
Cave sediments have been shown to preserve ancient DNA but so far have not yielded the genome-scale information of skeletal remains. We retrieved and analyzed human and mammalian nuclear and mitochondrial environmental ''shotgun'' genomes from a single 25,000-year-old Upper Paleolithic sediment sample from Satsurblia cave, western Georgia:first, a human environmental genome with substantial basal Eurasian ancestry, which was an ancestral component of the majority of post-Ice Age people in the Near East, North Africa, and parts of Europe; second, a wolf environmental genome that is basal to extant Eurasian wolves and dogs and represents a previously unknown, likely extinct, Caucasian lineage; and third, a European bison environmental genome that is basal to present-day populations, suggesting that population structure has been substantially reshaped since the Last Glacial Maximum. Our results provide new insights into the Late Pleistocene genetic histories of these three species and demonstrate that direct shotgun sequencing of sediment DNA, without target enrichment methods, can yield genome-wide data informative of ancestry and phylogenetic relationships.

INTRODUCTION
Ancient DNA fragments sequenced from bone,1 teeth,2 and hair3 have revolutionized our understanding of natural history and the human past.4,5 When skeletal material is not available, ancient environmental DNA has been used to determine the presence or absence of different species. Several studies based on PCR methods demonstrated the presence of ancient DNA in sediments,6 including in caves,7 and more recently, high throughput sequencing techniques have been applied.8–11 Cave sediment ancient DNA has been used to track the presence or absence of species across a range of environments and time periods, primarily through targeted amplification or capture of single genetic regions.12 A ground-breaking study showed DNA preservation in clay-rich sediments since 240 ky13 and used targeted enrichment to recover sufficient numbers of fragments to reconstruct mtDNA phylogenies of Neanderthals and Denisovans. A similar study recovered Denisovan mitochondrial DNA from sediments deposited 100 kya and 60 kya from Baishya Karst Cave on the Tibetan Plateau.14 A recent study used targeted enrichment of 1.6 million loci to recover Neanderthal and Denisovan nuclear DNA from three Paleolithic sites. This yielded enough DNA to allow for some analyses of genome-wide ancestry, including the finding of a Neanderthal population replacement at one of the sites, thereby demonstrating the possibility of large-scale nuclear DNA recovery from sediments.15

Here, we report results from shotgun sequencing and genomic analysis of a sediment sample from the Upper Paleolithic site of
Microstratigraphic preservation of ancient faunal and hominin DNA in Pleistocene cave sediments

Diyendo Massilani¹, Mike W. Morley⁵,¹, Susan M. Mentzer⁴,¹, Vera Aldeias³,², Benjamin Vernot⁵,³, Christopher Miller⁴,², Mareike Stahlsmith⁴,², Maxim B. Kozlikin⁵,², Michael V. Shunkov⁵,², Anatoly P. Derevianko⁵,², Nicholas J. Conard⁴,², Sarah Wurz⁴,², Christopher S. Henshilwood⁴,², Javi Vasquez⁴, Elena Essel⁴, Sarah Nagel⁴, Julia Richter⁴, Birgit Nickel⁴, Richard G. Roberts⁴,², Svante Pääbo⁴,², Viviane Slon⁴,⁵,⁶,⁷,⁸, Paul Goldberg⁴,²,⁹, and Matthias Meyer⁴,²

PNAS 119, e2113666118.
Microstratigraphic preservation of ancient faunal and hominin DNA in Pleistocene cave sediments

Diyendo Massilanstreeting, Mike W. Morley, Susan M. Mentzer, Vera Aldeias, Benjamin Vernot, Christopher Miller, Mareike Stahlschmidt, Maxim B. Kozlikin, Michael V. Shunkov, Anatoly P. Derevianko, Nicholas J. Conard, Sarah Wurz, Christopher S. Henshilwood, Javi Vasquez, Elena Essel, Sarah Nagel, Julia Richter, Birgit Nickel, Richard G. Roberts, Svante Pääbo, Viviane Slon, Paul Goldberg, and Matthias Meyer

PNAS 119, e2113666118.
Ongoing issues in sedaDNA
Taphonomy

Source processes | Transfer processes | Deposit and preservation processes

DNA production (biomass)
DNA incorporation in soils

Connectivity between DNA sources and lake (hydrographic web and soil erodibility)

1. Mixing equation
2. Dilution equation
3. Degradation equation

2019 Scientific Reports 9, 14676

@PalaeoPete
Bioinformatic refinements

1 Database landscape
   A Fairly well-populated
   - Specific sequence and/or strict filter
   - Conserved sequence and/or wide filter
   - Two hits
   - Low taxon; contains real taxon

2 BLAST search
   - Many hits
   - High taxon; contains real taxon

3 Phylogenetic intersection or LCA
   - Zero hits
   - None

B Sparsely-populated
   - Specific sequence and/or strict filter
   - Conserved sequence and/or wide filter
   - Two hits
   - Low taxon; does not contain real taxon

Legend:
- Represented taxon
- Unrepresented taxon
- Real taxon, also unrepresented, with hit radius
- Scope of phylogenetic intersection

2020 Front. Ecol. Evol. 8, 84
@PalaeoPete
Reference databases

EARTH BIOGENOME PROJECT

2018 PNAS 115, 4325

@PalaeoPete
Data integration

The two sites in pine forest, Horntjernet (Figs. 1J and 4B), and at Nordvivatnet and birch forest (Figs. 1H and section S1). Accumulated richness was also high at Gauptjern, which is at the border between glacier in its upper reaches (Fig. 1H and section S1). Accumulated

Fig. 4D), which today drains a catchment that has a Late Holocene

The proportion of reads identified as terrestrial plant \( (\) increases through time. Data in black, samples that passed QC; blue, samples that failed QC; red, negative controls.

A Sample age minimally affects MTQ \( (\) Fig. 3. Correlations between taxonomic richness (left) and time (right) against six measures of sedaDNA data quality.

B Mean proportion of weighted PCR replicates \( (\) scores, total raw read count \( (\) across the entire dataset, although

C Total raw read count

D Mean barcode sequence length \( (\)
Data integration

Remains

Ancient DNA

Sediments


@PalaeoPete
Summary

• Ancient DNA from sediment can be used to reconstruct past environments over hundreds of thousands of years.
• Unknowns remain but progress is rapidly being made.
• Huge potential for environmental palaeogenomics applications.
• Many palaeoecological, environmental, and evolutionary questions still to explore!