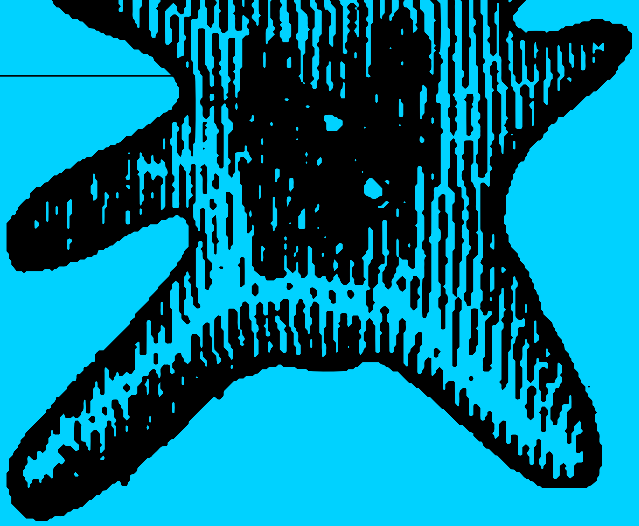
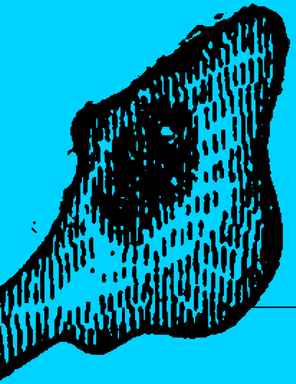
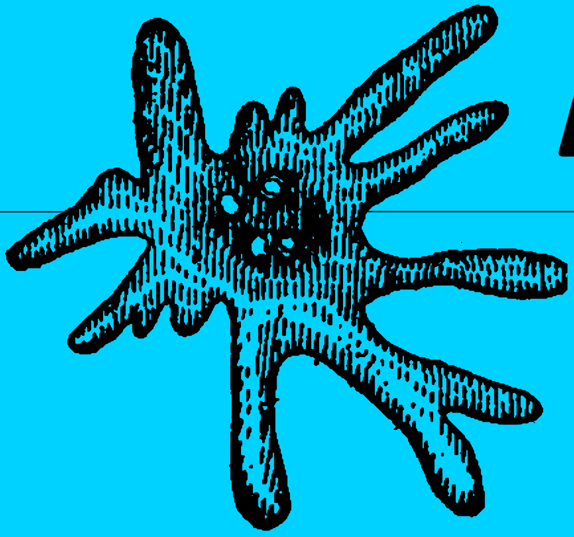




CELL BIOLOGY ABSTRACTS



3

C1 PALAEOGENOMICS AND ANCIENT DNA

ORGANISED BY: LAURA PARDUCCI (UPPSALA UNIVERSITY, SWEDEN), RICHARD TENNANT (UNIVERSITY OF EXETER, UK) AND JOHN LOVE (UNIVERSITY OF EXETER, UK)

C1.1 SEQUENCING AND COMPUTATIONAL CHALLENGES IN THE ANALYSIS OF ANCIENT DNA

WEDNESDAY 5 JULY, 2017 **09:00**

MICHAEL HOFREITER (UNIVERSITÄT POTSDAM, GERMANY)

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Paleogenomic analyses have the potential to be highly informative with regard to the population history of the species investigated, but so far, paleo-population genomic studies have been largely restricted to humans and domesticated species. We have investigated a range of extinct and extant species with regard to their mitogenomic as well as in several cases nuclear genomic diversity. Our data show that mitochondrial and nuclear DNA data often show strikingly different patterns, requiring complex population histories to reconcile the data sets. Similarly, when comparing data sets based solely on modern DNA data to those including paleogenomes, the population scenarios emerging from the latter are in general substantially more complex than the ones inferred from the former data sets, echoing findings from human paleopopulation genomic data sets. Even within single species, population dynamics may be different in different regional settings. On the other hand, we find that the population genomic data of spotted and cave hyenas mirror those of modern humans, Neandertals and Denisovans in surprising detail. Our results overwhelmingly show that, when based on incomplete data sets, which modern-only data sets are by definition, the most parsimonious explanation for any species' population dynamics has a high likelihood of being incorrect. Although no better principle for explanation exists, parsimonious explanations should be viewed with extreme caution when used for explaining population dynamics in any species.

C1.2 INVESTIGATING ADAPTATION TO NORTHERN LATITUDE BY COMPARING ANCIENT AND MODERN NORTHERN EUROPEANS

WEDNESDAY 5 JULY, 2017 **09:40**

TORSTEN GÜNTHER (UPPSALA UNIVERSITY, SWEDEN), HELENA MALMSTRÖM (UPPSALA UNIVERSITY, SWEDEN), EMMA SVENSSON (UPPSALA UNIVERSITY, SWEDEN), AYÇA OMRAK (STOCKHOLM UNIVERSITY, SWEDEN), FEDERICO SÁNCHEZ-QUINTO (UPPSALA UNIVERSITY, SWEDEN), GÜLŞAH KILINÇ (MIDDLE EAST TECHNICAL UNIVERSITY, TURKEY), MAJA KRZEWINSKA (STOCKHOLM UNIVERSITY, SWEDEN), MIHAI NETEA (RADBOUD UNIVERSITY MEDICAL CENTER, NETHERLANDS), JAN STORÅ (STOCKHOLM UNIVERSITY, SWEDEN), ANDERS GÖTHERSTRÖM (STOCKHOLM UNIVERSITY, SWEDEN), MATTIAS JAKOBSSON (UPPSALA UNIVERSITY, SWEDEN)

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Northern Europe was the last part of the continent to become ice-free after the last glaciation. Human populations colonized Scandinavia only 11,000 - 10,000 years before present. The environmental conditions were quite harsh which challenged the populations to adapt their behaviour and also posed a selective pressure for adaptation on a physiological and genetic level. High latitudes are associated with strong variations in seasonal light levels and low mean temperatures still representing a special habitat for populations living in these areas. We compared the genomes of early Northern Europeans to contemporary surrounding populations as well as modern populations. By combining allele frequency differences and haplotype differentiation among the populations, we scan the genome for candidate regions contributing to adaptation to high latitude conditions. We identify a number of candidate genes involved in different physiological and metabolic traits. This genome wide scan is complemented by studying the allele frequency changes in specific candidate genes such as pigmentation loci which are characterized by high derived allele frequencies in modern Northern Europeans. Finally, we extend our analysis to variants involved in pathogen response. Our study highlights the potential for combining palaeogenomic and modern genomic data in order to understand how populations adapt to extreme environments.

C1.3 A PALAEOGENOMIC PERSPECTIVE OF NEAR-EXTINCTION POPULATION DYNAMICS

WEDNESDAY 5 JULY, 2017 **09:55**

DAVID DÍEZ DEL MOLINO (SWEDISH MUSEUM OF NATURAL HISTORY, SWEDEN), PATRICIA PEČNEROVÁ (SWEDISH MUSEUM OF NATURAL HISTORY, SWEDEN), LOVE DALÉN (SWEDISH MUSEUM OF NATURAL HISTORY, SWEDEN)

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Processes leading up to species extinction are typically characterized by habitat fragmentation and decline in geographic distribution, both related to a reduction in population size. With the transition from traditional ancient DNA methods to palaeogenomics we have now the tools to assess and characterize the genomic responses to dramatic demographic declines and to identify signatures of genetic erosion across such declines by using serial sampled data to track genome-wide changes in real time. We present evidence that the expected loss of genome-wide heterozygosity and increase in inbreeding due to small population size in genomes sampled near-extinction are accompanied by an accumulation of genomic deletions and detrimental mutations, thus following the expectation of relaxed purifying selection. These results provide incomparable testimony of the value of datasets integrating heterochronous complete genomes at allowing to characterize evolutionary processes, such as near-extinction genomic dynamics, in real time and can be useful to better understand modern-day species facing similar threats as extinct species did during their final demise.

C1.4 ANCIENT DNA IN TRACING THE SPREAD OF LEPROSY IN THE PAST

WEDNESDAY 5 JULY, 2017 **10:10**

AMMIELLE A KERUDIN (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), ROMY MULLER (UNIVERSITY OF MANCHESTER, UNITED KINGDOM), JO BUCKBERRY (UNIVERSITY OF BRADFORD, UNITED KINGDOM), TERRY BROWN (UNIVERSITY OF MANCHESTER, UNITED KINGDOM)

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As contrary to ancient belief that sin is responsible for causing leprosy in human, it was later discovered that *Mycobacterium leprae* is the infectious pathogen. The ability to isolate ancient *M. leprae* DNA from archaeological remains opened a new pathway towards better understanding of the disease in the past. In Britain, the earliest palaeopathological evidence for leprosy is from the 4th century AD but prevalence did not peak until the 11th-14th century before the inexplicable and gradual decline of the disease from the 14th-16th century. Molecular studies have revealed that leprosy could have originated in East Africa or the Near East. SNP typing separates the pathogen into type one to four and subsequently 16 subtypes that strongly correlate to distinct geographical locations. DNA analysis of leprosy might therefore answer historical questions, particularly the movement patterns of humans in the past, inferred by looking at the spread of the disease. We detected ancient *M. leprae* DNA in two skeletal remains recovered from a cemetery that belonged to a hospital which housed leprosy patients and one skeleton from an Anglo-Saxon churchyard in the south of England. The ages of the skeletal remains are believed to range from around mid-900 AD to 1700 AD. We have carried out target enrichment via in-solution hybridization capture in an attempt to obtain *M. leprae* genome sequences. Subtyping revealed association of human activities such as exploration and trading to be among the possible routes of leprosy spread in the past.

C1.5 POPULATION GENOMICS OF HUNTER-GATHERERS AND FARMERS IN SCANDINAVIA

WEDNESDAY 5 JULY, 2017 **11:00**

HELENA MALMSTRÖM (UPPSALA UNIVERSITY, SWEDEN)

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The archeological record shows that Scandinavia was one of the last geographic regions in Europe to be colonized by Mesolithic hunter-gatherers after the latest glaciation, and consistent signs of human habitation appear approximately 11,000 BP. The first signs of agriculture appear around 6,000 BP, with the Neolithic Funnel Beaker culture (FBC). FBC was partly contemporaneous with the hunter-gatherer Pitted Ware culture (PWC) and was later replaced by the farming/herding Battle Axe culture (BAC), a regional variant of the Corded Ware culture (CWC). Questions relating to who these people were, where they came from and how they relate to each other have been long debated. Recently, analyses of genomic data generated from ancient human remains from Scandinavia and Eurasia, have increased our understanding of these past societies immensely. It has for example been shown that Mesolithic Scandinavian hunter-gatherers had a mixed ancestry from both Western and Eastern European hunter-gatherers, that the Neolithic FBC farmers were immigrants with some level of biological interaction with the hunter-gatherers and genetic similarities to their Central European and Anatolian counterparts, and that BAC/CWC represent another wave of immigrants with genetic affiliations to the Yamnaya steppe herders. I will review the population history of Mesolithic and Neolithic Scandinavia using previously published as well as newly generated ancient DNA data.

C1.6 UKRAINIAN ENEOLITHIC (3500 BCE) TRYPILLIAN AGROPASTORALISTS AND THEIR GENETIC ASSOCIATION WITH NEOLITHIC FARMERS FROM SOUTHERN EUROPE AND THE NEAR EAST

WEDNESDAY 5 JULY, 2017 **11:30**

RYAN W SCHMIDT (UNIVERSITY COLLEGE DUBLIN, IRELAND), DANIEL FERNANDES (UNIVERSITY COLLEGE DUBLIN, IRELAND), KEN WAKABAYASHI (SCHOOL OF MEDICINE DEPARTMENT OF ANATOMY KITASATO UNIVERSITY, JAPAN), KAE KOGANEBUCHI (SCHOOL OF MEDICINE DEPARTMENT OF ANATOMY KITASATO UNIVERSITY, JAPAN), TAKASHI GAKUHARI (CENTER FOR CULTURAL RESOURCE STUDIES KANAZAWA UNIVERSITY, JAPAN), JORDAN KARSTEN (DEPARTMENT OF ANTHROPOLOGY UNIVERSITY OF WISCONSIN-OSHKOSH, UNITED STATES), KAYLA KUBEHL (DEPARTMENT OF ANTHROPOLOGY UNIVERSITY OF WISCONSIN-OSHKOSH, UNITED STATES), GWYN MADDEN (DEPARTMENT OF ANTHROPOLOGY GRAND VALLEY STATE UNIVERSITY, UNITED STATES), MYKHAILO SOKHATSKY (BORSCHIV REGIONAL MUSEUM, UKRAINE), HIROKI OOTA (SCHOOL OF MEDICINE DEPARTMENT OF ANATOMY KITASATO UNIVERSITY, JAPAN), RON PINHASI (UNIVERSITY COLLEGE DUBLIN, IRELAND)

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The transition from hunting and gathering to farming in Eastern Europe is not well understood. The shift began during the Eneolithic with the populations of the Cucuteni-Trypillian (CT) cultural complex of Ukraine, Romania, and Moldova. In Ukraine, the Trypillian culture existed from ~4800-2700 BCE with its distinct archaeological signatures of pottery, figurines, and large, densely populated settlements known as 'megasites'. However, due to the scarcity of excavated CT graves little is known of their burial customs. An exceptional site is Verteba Cave, which yielded a wealth of human remains and associated artifacts. The site is located in Western Ukraine along an eco-cultural steppe-forest boundary that witnessed the interaction of various local Neolithic and Early Bronze Age (Corded Ware) groups. Peak occupation and activity at the cave is dated to ~3500 BCE, based on ceramic typology and radiocarbon dating, though the cave was also occupied during later periods. Here, we report genome-wide SNP variation for 12 individuals from a single chamber in the cave during peak Tripolye cultural occupation time. Ancient DNA extractions and libraries were prepared in dedicated clean room laboratories at UCD. Libraries were shotgun sequenced on an Illumina NextSeq. Our results confirm previous analyses using partial mtDNA haplogroup information that Trypillian nuclear DNA variation is consistently more closely related to Early and Middle Neolithic Farmer groups. However, one Eneolithic individual, VC.HR.2047, shares similarity with DNA from Mesolithic hunter-gatherers (based on D-statistics, f_3 – outgroup statistics, and model-based clustering). This observation may indicate population structure for these late Neolithic agropastoralists.

C1.7 USING PALAEOGENOMIC APPROACHES WITH PLANT REMAINS

WEDNESDAY 5 JULY, 2017 **13:50**

TERRY BROWN (UNIVERSITY OF MANCHESTER, UNITED KINGDOM)

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Preserved plant remains, which are found at many archaeological sites, provide a record of the origins, spread and development of prehistoric agriculture. The extent to which palaeogenomic methods can be used with archaeobotanical samples depends on the way in which the material has been preserved. In arid environments, which include some cave sites, plant macrofossils such as seeds can be preserved by desiccation. Remains of this type often contain well-preserved nucleic acids enabling palaeogenomic studies of both DNA and RNA. Genome sequences, as well as transcriptome data, have been obtained from desiccated maize and barley, enabling the nature and timing of genetic changes associated with domestication to be studied. Unfortunately, this type of work is limited in scope because desiccated remains are only found in certain parts of the world. Most archaeobotanical material, including virtually all Eurasian crop remains, is charred, having been preserved by burning, for example during the accidental combustion of a grain store. Short DNA sequences have been obtained by PCR from various charred specimens, but so far next generation sequencing methods have been less successful, most of the reads from charred samples being identified as bacterial and assumed to be environmental contaminants. Recent work suggests that many of these 'bacterial' reads are in fact endogenous plant sequences that have accumulated miscoding lesions that result in their misidentification. A better understanding of the degradation processes occurring during charring might therefore enable palaeogenomic data to be obtained from this type of material.

C1.8 FUEL FOR EVOLUTIONARY AND ARCHEOLOGICAL STUDIES ON TEMPERATE TREE SPECIES - aDNA FROM WOOD

WEDNESDAY 5 JULY, 2017 **14:30**

STEFANIE WAGNER (BIOGECO INRA UNIV. BORDEAUX, FRANCE), FRÉDÉRIC LAGANE (BIOGECO INRA UNIV. BORDEAUX, FRANCE), WILLY TEGEL (INSTITUTE FOR FOREST GROWTH IWW UNIVERSITY OF FREIBURG, GERMANY), ANDAINE SEGUIN-ORLANDO (CENTRE FOR GEOGENETICS, NATURAL HISTORY MUSEUM OF DENMARK UNIVERSITY OF COPENHAGEN, DENMARK), YVES BILLAUD (2MCCDRASSM EDYTEM UNIV. SAVOIE, FRANCE), CHRISTOPHE PLOMION (BIOGECO INRA UNIV. BORDEAUX, FRANCE), ANTOINE KREMER (BIOGECO INRA UNIV. BORDEAUX, FRANCE), LUDOVIC ORLANDO (CENTRE FOR GEOGENETICS, NATURAL HISTORY MUSEUM OF DENMARK, UNIVERSITY OF COPENHAGEN, DENMARK)

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Long-lived tree species build up global forest ecosystems and have been exploited by humans for thousands of years. They are presently of particular concern as their long generation times may limit their adaptability to fast-changing environments. Temporal-series from ancient tree populations can provide a unique perspective on tree evolutionary and forest use history, that may not be detected by studies relying exclusively on extant populations. This information, and a better knowledge of the interplay between forest tree species, humans and climate will likely be paramount for anticipating the potential consequences of ongoing environmental changes. In this study, we took European white oaks (Quercus robur and Q. petraea) as a tree model species group with the aim to use ancient DNA to track past population dynamics and selective trajectories in the face of major environmental changes. Since ancient DNA studies on trees, in particular in temperate regions, are still in their infancy, we first investigated subfossil and archeological wooden remains from different taphonomical and temporal contexts to define conditions that optimize access to authentic ancient DNA. Following optimized aDNA extraction methods and shotgun sequencing, we succeeded in authenticating genetic data retrieved from 141 ancient oak DNA samples aged between 550 and 9,500 years. We will present the first analyses on this extensive dataset, focusing on key drivers for aDNA preservation, temporal insights on DNA degradation and postglacial haplotype distribution patterns.

C1.9 UNEARTHING PAST ENVIRONMENTS USING ALGAL PALEOGENOMICS

WEDNESDAY 5 JULY, 2017 **14:45**

RICHARD K TENNANT (UNIVERSITY OF EXETER, UNITED KINGDOM), RICHARD T JONES (UNIVERSITY OF EXETER, UNITED KINGDOM), ROB LEE (UNIVERSITY OF EXETER, UNITED KINGDOM), JOHN LOVE (UNIVERSITY OF EXETER, UNITED KINGDOM)

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Microscopic fossils are used routinely to date sedimentary deposits, discover potential reserves of fossil energy and investigate environmental change. Conventionally, microfossils are identified by laborious and time-consuming methods that yield relatively few representatives, thereby limiting analytical precision. We developed new protocols for rapid analysis and purification of microfossils from ancient sediments using fluorescent activated cell sorting (FACS). Not only has FACS dramatically reduced the time to characterise entire populations of microfossils from months to days, the high-throughput offered by FACS enabled us to acquire microfossil samples of sufficient purity and concentration to enable more refined, downstream analyses than possible by microscopy alone.

Using FACS, we identified and purified representatives of a single species of algae from lake sediment cores dating 12,000 years BP. DNA was extracted from the purified algal cells and sequenced by Illumina next generation sequencing. Analysis of the ancient sequence enabled us to confirm that the algae that existed in the lake at the retreat of the ice sheet are virtually identical to those living there, today. Furthermore a metagenomic approach was employed to identify the microalgae within the Holocene sediment record, enabling not only the identification of the alga but also the biotic community in which it thrived.

C1.10 STUDYING aDNA DAMAGE IN MARINE SEDIMENTS

WEDNESDAY 5 JULY, 2017 **15:00**

ROSELYN L WARE (UNIVERSITY OF WARWICK, UNITED KINGDOM), LOGAN J KISTLER (SMITHSONIAN INSTITUTION NATIONAL MUSEUM OF NATURAL HISTORY, UNITED STATES), ROBIN G ALLABY (UNIVERSITY OF WARWICK, UNITED KINGDOM)

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Plant and animal remains have been widely used in ancient DNA studies, however these remains are often hugely valuable as they are limited in the archaeological record. The ubiquity of sediment sources, from which sediment DNA (sedaDNA) can be extracted, and the favourable conditions for DNA preservation afforded by some sediment types has led to an increase its exploitation as a source of aDNA. sedaDNA can be used as a tool for the development of palaeoenvionmental reconstructions, the study of human-environment interactions, studying catastrophic geographical events, and the study of mass floral or faunal extinction events. sedaDNA analysis can be confounded by contamination from modern DNA sources, which can arise from leaching between the sediment strata, or during sampling and analysis. Typically, characteristic DNA breakdown patterns, including strand fragmentation and cytosine deamination, are used to authenticate the age of the ancient DNA. Many DNA damage profiles are based upon DNA extracted from macroremains, rather than from the free DNA typically exploited when using sediment samples. As a result of the wide range of sediment types, and environmental biotic and abiotic factors (such as temperature and salinity), different sediments can show a wide range of damage profiles, that do not simply reflect the age of the sample. We discuss the impact of salinity on DNA degradation, and the impact on sedaDNA analysis.

C1.11 NOVEL BIOINFORMATIC TECHNIQUES IN PALAEOGENOMICS

THURSDAY 6 JULY, 2017 **09:00**

LUDOVIC ORLANDO (NATURAL HISTORY MUSEUM OF DENMARK, DENMARK)

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The development of High-Throughput Sequencing has unlocked access to genome-scale data from ancient populations and extinct species. The volumes of data, however, require proper management and processing strategies as well as dedicated tools handling the specificities of ancient DNA. My group has developed a series of open-source, automated computational packages tailor-made to ancient DNA sequence data and handling most of the major analytical steps. PALEOMIX takes as input raw sequence reads and reference genomes of interest, to provide read alignments, genotype calls and statistical modeling of post-mortem DNA damage signatures. It embeds AdapterRemoval for read trimming/collapsing, and mapDamage, which quantifies post-mortem DNA damage and recalibrate base quality-scores accordingly. Optional analyses include the reconstruction of super-matrix phylogenomic trees (phylo-pipeline) and the identification of F1-hybrids (ZONKEY). Starting from ancient DNA read alignment files, be produced by PALEOMIX or not, epiPALEOMIX performs a full suite of computational analysis to provide genome-wide methylation and nucleosome maps. metaBIT takes as input trimmed and/or collapsed reads, be AdapterRemoval outputs or not, and performs read alignment against the metaPhlAn(2) database to provide a thorough analysis of the microbial content often dominating shotgun data. Finally, gargammel is a high-throughput read simulator reproducing some of the most central features of ancient DNA sequence datasets, including DNA damage, and contamination from human and various other environmental microbes. I will present how these tools can be integrated to enable a full suite of analysis on a single ancient DNA dataset.

C1.12 SHOTGUN ANCIENT DNA ANALYSIS IN LATEGLACIAL LAKE SEDIMENTS FROM SWEDEN

THURSDAY 6 JULY, 2017 **09:40**

LAURA PARDUCCI (ECOLOGY AND GENETICS, UPPSALA UNIVERSITY, SWEDEN), ENGY AHMED (GEOLOGICAL SCIENCES, STOCKHOLM UNIVERSITY, SWEDEN), RASMUS ÅGREN (SCIENCE FOR LIFE LABORATORY STOCKHOLM UNIVERSITY, SWEDEN), PER UNNEBERG (SCIENCE FOR LIFE LABORATORY STOCKHOLM UNIVERSITY, SWEDEN), FREDRIK SCHENK (GEOLOGICAL SCIENCES STOCKHOLM UNIVERSITY, SWEDEN), JAYNE RATTRAY (GEOLOGICAL SCIENCES STOCKHOLM UNIVERSITY, SWEDEN), LU HAN (COLLEGE OF LIFE SCIENCES JILIN UNIVERSITY, CHINA), KWEKU AFRIFA YAMOAH (GEOLOGICAL SCIENCES STOCKHOLM UNIVERSITY, SWEDEN), FRANCESCO MUSCHITIELLO (GEOLOGICAL SCIENCES STOCKHOLM UNIVERSITY, SWEDEN), MIKKEL WINTHER PEDERSEN (CENTRE FOR GEOGENETICS UNIVERSITY OF COPENHAGEN, DENMARK), TANJA SLOTTE (SCIENCE FOR LIFE LABORATORY STOCKHOLM UNIVERSITY, SWEDEN), BARBARA WOHLFARTH (GEOLOGICAL SCIENCES STOCKHOLM UNIVERSITY, SWEDEN)

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The final stages of the Last Glacial in the Northern Hemisphere, between 19 and 11.7 thousand years before present, were punctuated by distinct and alternating warmer and colder climate states before Interglacial temperatures were attained, which in turn strongly influenced past vegetation. One of the best studied Lateglacial lake sedimentary record in Sweden is derived from the ancient lake of Hässeldala Port where several recent multi-proxy sediment studies and detailed chronological frameworks allowed reconstructing local and regional environmental conditions and summer temperatures between specific periods in great detail.

Here we used shotgun DNA sequencing of the full metagenome preserved in the Hässeldala sedimentary record to investigate the whole diversity of taxonomic groups present in the lake sediment. We combine sedimentary aDNA, pollen and macrofossil studies and succeeded in correlating the relative abundances of plant communities to distinct climatic shifts that occurred between 14 and 10.5 ka BP.

C1.13 DETERMINING THE TIMING OF EXTINCTION FOR A LATE-SURVIVING ISLAND MAMMOTH POPULATION USING SEDIMENTARY ANCIENT DNA

THURSDAY 6 JULY, 2017 **09:55**

PETER D HEINTZMAN (TROMSØ UNIVERSITY MUSEUM UIT - THE ARCTIC UNIVERSITY OF NORWAY, NORWAY), JOSHUA D KAPP (UNIVERSITY OF CALIFORNIA SANTA CRUZ, UNITED STATES), BETH SHAPIRO (UNIVERSITY OF CALIFORNIA SANTA CRUZ, UNITED STATES), RUSSELL W GRAHAM (PENNSYLVANIA STATE UNIVERSITY, UNITED STATES), SOUMAYA BELMECHERI (UNIVERSITY OF ARIZONA, UNITED STATES), KYUNGCHEOL CHOY (UNIVERSITY OF ALASKA FAIRBANKS, UNITED STATES), BRENDAN J CULLETON (PENNSYLVANIA STATE UNIVERSITY, UNITED STATES), LAUREN J DAVIES (UNIVERSITY OF ALBERTA, CANADA), DUANE G FROESE (UNIVERSITY OF ALBERTA, CANADA), CARRIE HRITZ (NATIONAL SCIENCE FOUNDATION, UNITED STATES), LEE NEWSOM (PENNSYLVANIA STATE UNIVERSITY, UNITED STATES), RUTH RAWCLIFFE (UNIVERSITY OF ALASKA FAIRBANKS, UNITED STATES), ÉMILIE SAULNIER-TALBOT (UNIVERSITY OF ALASKA FAIRBANKS, UNITED STATES), YUE WANG (UNIVERSITY OF WISCONSIN-MADISON, UNITED STATES), JOHN W WILLIAMS (UNIVERSITY OF WISCONSIN-MADISON, UNITED STATES), MATTHEW J WOOLLER (UNIVERSITY OF ALASKA FAIRBANKS, UNITED STATES)

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The woolly mammoth became extinct on mainland Asia and North America ~11,500 years ago. However, relict populations survived on two islands for millennia after these mainland extinctions. The last known population survived on Wrangel Island until ~4,000 years ago, coinciding with the arrival of humans. Another late-surviving population endured on the island of St. Paul until at least 6,500 years ago. There is no evidence for human occupation of this island prior to the 18th Century CE, and the mammoth extinction was therefore likely driven solely by non-anthropogenic factors. To explore potential extinction drivers, it is crucial to first understand the precise timing of the extinction. The limited record of mammoth fossils on St. Paul does not provide the temporal resolution to determine a precise timing. Instead, we used a multiproxy approach to compliment the palaeontological data, which included isolating ancient mammoth DNA from a dated crater lake sediment record. The steady accumulation of lake sediments through time make this approach ideal for precisely constraining the timing of mammoth disappearance from St. Paul Island. Our results show that mammoth disappears from the sediment record at 5,600 years ago, around a millennium later than the youngest published radiocarbon date from a mammoth fossil. This result is highly congruent with other proxies, which include spore abundances of coprophilous fungi in the sediment and radiocarbon dates of newly discovered mammoth fossils. Altogether, our results provide a robust and precise timing of extinction for the late-surviving mammoth population of St. Paul Island.

C1.14 PALEO-ENVIRONMENT RECONSTRUCTION USING ANCIENT DNA FROM LAKE SEDIMENTS

THURSDAY 6 JULY, 2017 **10:55**

MIKKEL WINTHER PEDERSEN (DEPARTMENT OF ZOOLOGY, UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM)

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Traditionally ancient flora and faunal reconstruction have relied on finding and identification of fossil remains. But within the past decade, DNA imbedded in ancient soil, ice and sediments have proven to be a good and additional source for ancient plant and animal DNA. While this method primarily focusses on the extraction and amplification of short DNA barcodes, a newer alternative, focussing on shotgun sequencing the full genomic content, are emerging. This new method has several advantages, as it is for example is possible to get an independent authentication of ancient origin by looking at the degree of damage on the DNA. In addition, it can retrieve full genomic information which potentially gives lower taxonomic resolution, but also identification of a broader diversity of organisms from all trophic layers. But, as with other new methods, it also has limitations. Here, I will present and discuss shotgun sequencing DNA from ancient lake sediment by using a recently published data set as a starting point. The results show the succession of plants and animals in a recently deglaciated landscape and the environmental change occurring during climatic amelioration.

C1.15 VEGETATION DYNAMICS AT BOL'SHOY LYAKHOVSKY ISLAND (NEW SIBERIAN ISLANDS) SINCE THE LAST INTERGLACIAL

THURSDAY 6 JULY, 2017 **11:25**

HEIKE H ZIMMERMANN (ALFRED-WEGENER-INSTITUTE FOR POLAR AND MARINE RESEARCH, GERMANY), LAURA S EPP (ALFRED-WEGENER-INSTITUTE FOR POLAR AND MARINE RESEARCH, GERMANY), KATHLEEN R STOOF-LEICHSENRING (ALFRED-WEGENER-INSTITUTE FOR POLAR AND MARINE RESEARCH, GERMANY), GEORG SCHWAMBORN (ALFRED-WEGENER-INSTITUTE FOR POLAR AND MARINE RESEARCH, GERMANY), LUTZ SCHIRRMEISTER (ALFRED-WEGENER-INSTITUTE FOR POLAR AND MARINE RESEARCH, GERMANY), ULRIKE HERZSCHUH (ALFRED-WEGENER-INSTITUTE FOR POLAR AND MARINE RESEARCH, GERMANY)

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Climate models project an annual average temperature increase of about 3-5°C in the terrestrial Arctic until the year 2100, which corresponds to the reconstructed temperatures of the last interglacial (Eemian, ~130-110 kyr BP). Hence, the past vegetation composition might provide an analogue for the future. Bol'shoy Lyakhovsky is a treeless island, framed by the Laptev and East Siberian Seas. Our goal was to reconstruct the vegetation history from four permafrost sediment cores, focusing on terrestrial vegetation during warm phases since the last interglacial. We used sedimentary ancient DNA metabarcoding of the trnL p6-loop. A total of 264 taxa were detected with 39% being assigned to species and 37% to genus level. During several potentially warmer phases tree and shrub taxa were detected. The Eemian was the most diverse phase, also in recording three different tree taxa (Picea, Larix, Populus), whereas Larix was the only tree taxon recorded afterwards. During the Bølling-Allerød interstadial complex (~14.7-12.7 kyr BP), soon after the Last Glacial Maximum (LGM), Larix had already re-colonized Bol'shoy Lyakhovsky, suggesting the persistence of larches at high latitudes throughout the LGM. Despite warmer temperatures of the Holocene, Larix was not detected. Increasing humidity combined with the disconnection of the island from the mainland due to the global sea level rise might have made persistence and/or re-colonization impossible. As the current coastline position has been suggested to differ from the one of the last interglacial, it is however uncertain to which degree the vegetation composition represents a potential future analogue for north-eastern Siberia.

C1.16 TIMING SPECIES COLONIZATIONS USING DNA IN LAKE SEDIMENT

WEDNESDAY 5 JULY, 2017 **POSTER SESSION**

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Detection of DNA from lake sediments holds promise as a tool to study processes like extinction, colonization, adaptation and evolutionary divergence. However, low concentrations make sediment DNA difficult to detect, leading to high false negative rates and gaps in the chronology that are difficult to interpret. Additionally, successful recovery of ancient DNA is difficult to distinguish from small amounts of DNA introduced by contamination, which further complicates the interpretation of records of sediment DNA. Careful laboratory procedures can reduce false positive and negative rates, but should not be assumed to completely eliminate them. Therefore, methods are needed that identify potential false positive and negative results, and use this information to judge the plausibility of different interpretations of DNA data from natural archives. Here we present a Bayesian algorithm to infer the colonization history of the European whitefish (Coregonus lavaretus) from sediment cores from two central Swedish lakes. The method analyzes PCR amplifications using three primers at different depths in the sediment, explicitly labeling some results as false positive or false negative. We conclude that whitefish colonized Stora Lögdasjön in Västerbotten immediately after the ice melt ca 9500 years ago, and the lake Hotagen in Jämtland 2200-2500 years ago.