

budgets, preferably spanning an entire glacial cycle, remain the most accurate for extrapolating glacial erosion rates to the entire Pleistocene and for assessing their impact on crustal uplift. In the Carlit massif, where topographic conditions have allowed the majority of Würmian sediments to remain trapped within the catchment, clastic volumes preserved and widespread ^{10}Be nuclide inheritance on ice-scoured bedrock steps in the path of major iceways reveal that mean catchment-scale glacial denudation depths were low (5 m in ~ 100 ka), non-uniform across the landscape, and unsteady through time. Extrapolating to the Pleistocene, the transformation of Cenozoic landscapes by glaciers has thus been limited, many cirques and valleys being pre-glacial landforms merely modified by glacial scour. Such conclusions are applicable to at least the eastern half of the Pyrenees, where (i) a morphometric analysis of 1066 cirques shows an absence of statistical correlation between size parameters, palaeoclimatic conditions and the duration of glacier presence; and where (ii) (U–Th)/He-dated Miocene summit plateau surfaces covered by thick in situ saprolite are well preserved despite the Pleistocene ice caps. In a class of mountain range such as the Pyrenees, any role for glaciation in significantly raising summit elevations through isostatic response to mass removal is doubtful, as perhaps in other mountains that likewise exhibit well preserved Cenozoic summit landforms amidst glacial scenery.

MINERAL DUST IN EAST ANTARCTICA: ASSESSING THE CONTRIBUTION FROM REMOTE AND LOCAL DUST SOURCES FROM THE LAST GLACIAL MAXIMUM TO PRESENT-DAY

Barbara Delmonte. *DISAT, Dept. Environmental Science, University Mil, Italy*
E-mail address: barbara.delmonte@unimib.it

Mineral dust windblown from the southern Hemisphere continental areas to East Antarctica and archived in snow and ice layers represents an important proxy for the understanding of present and past atmospheric circulation patterns. Over the last decade, the development of new analytical techniques and the recovery of deep ice core sequences lead to substantial improvements to the understanding of dust provenance and dust-climate coupling over the last 800,000 years. The comparison of different ice core records from central East Antarctica revealed a uniform dust flux and a common South American provenance over the last climatic cycle.

In the framework of the Talos Dome Ice Core (TALDICE) project, a new 1620 m deep ice core has been drilled at the peripheral site of Talos Dome ($159^\circ 11' \text{ E}$, $72^\circ 49' \text{ S}$; 2315 m a.s.l.), located on the Ross Sea sector of the East Antarctic ice sheet, on the opposite side with respect to South America. The first ~ 1550 m of the TALDICE ice core provide a palaeoclimate record covering the past 250 kyr back to Marine Isotope Stage 7.5. The remarkably similar Sr–Nd isotopic composition of dust windblown to Talos Dome and to central East Antarctic sites during MIS 2, 3, 4 and 6 points to a dominant South American dust provenance during cold Pleistocene periods. This hypothesis is supported also by the similarity between the Talos Dome stratigraphic dust record and those from EPICA-Dome C and Vostok.

For the Holocene and for modern (pre-industrial) times, conversely, the mineral dust flux, size and Sr–Nd isotopic composition shows marked differences in the Talos Dome–Mid Point–Dome C–Vostok transect. Comparison with samples from the neighbouring ice-free areas of Victoria Land highlights that high-altitude dust sources, mainly represented by glacial deposits and regoliths, are important for the periphery of the ice sheet during the Holocene and the present-day, when dust input from remote continental areas is extremely low.

A CHAIN OF PEPTIDES: A NEW MASS SPECTROMETRIC TOOL FOR MODELLING PROTEIN DIAGENESIS

Beatrice Demarchi. *University of York, United Kingdom*
E-mail address: beatrice.demarchi@york.ac.uk

Understanding the mechanisms of protein breakdown has long been a major focus of research in the AAR scientific community. The models of protein diagenesis proposed have generally been based on the extensive use of high temperature experiments to track the kinetics of the reaction

by chiral amino acid analysis. However, this knowledge has not yet been able to produce a model which is fully able to explain the patterns of breakdown at low (burial) temperatures. By performing high temperature experiments on a range of biominerals (e.g. corals and marine gastropods) and comparing the racemisation patterns with those obtained in fossil samples of known age, some of our studies have highlighted a range of discrepancies in the datasets which we attribute to the interplay of a network of diagenesis reactions which are not yet fully understood. In particular, an accurate knowledge of the temperature sensitivity of the two main observable diagenetic reactions (hydrolysis and racemisation) is still elusive. This is mainly due to lack of data on the primary structure of the proteins which are targeted for dating purposes, e.g. in mollusc shells or avian eggshell.

The amino acid sequence of struthiocalcin (SCA), the main protein of ostrich eggshell, has recently been determined (Mann & Siedler, 2004). This offers a major opportunity for degradation studies, as the primary chemical environment of each amino acid is known. We are coupling soft-ionization mass spectrometry (MALDI TOF-TOF) and liquid chromatography (RP-HPLC) to investigate the degradation pathways of four peptides from the sequence of SCA-1. The extents of racemisation and hydrolysis are coupled to the mass shifts of the peptides observed over time and at different temperature. Informed by this data, we aim to build a model of struthiocalcin breakdown and test its ability to mimic the natural breakdown observed in archaeological struthiocalcin of known age.

MAARITIME: MARINE AMINO ACID RACEMISATION INVESTIGATION OF THE MEDITERRANEAN

Beatrice Demarchi. *University of York, United Kingdom*
E-mail address: beatrice.demarchi@york.ac.uk

Because of its extended temporal span, AAR geochronology has the potential to answer specific but vital questions of human evolution. This project (mAARITIME) aims to use AAR dating to shed light on two main unresolved problems: when did early humans become “modern”, and is “modern” behaviour isolated to our own species? Behavioural modernity has fortuitously left traces in the archaeological record as molluscan remains, one of the best substrates for AAR dating. Molluscs were exploited as a food resource and shells were used as personal ornaments, providing some of the earliest evidence of symbolic thinking displayed by humans. The Mediterranean archaeological record is important to our understanding of the development of behavioural modernity. Controversially, in this area the exploitation of marine resources has recently been associated with both Neanderthals (Stringer *et al.*, 2008; Zilhao *et al.*, 2010) and *Homo sapiens*. By applying a closed-system method of AAR dating, mAARITIME is building stratigraphical frameworks, which combined with new independent geochronology aims to provide a reliable dating control for the Mediterranean. This study presents the closed system tests for three key marine genera and compares the AAR data from fossil shells with independent age information for the pilot chronological frameworks in southern Europe and northern Africa.

MULTI-DISCIPLINARY APPROACHES TO UNDERSTANDING THE LIFE AND DEATH OF AMINO ACIDS IN BIOMINERALS

Beatrice Demarchi. *University of York, United Kingdom*
E-mail address: beatrice.demarchi@york.ac.uk

Biominerals are key to preserving amino acids in the fossil record. A deeper investigation of the proteins offers the potential to expand our understanding of the mechanisms of biomineralization and the processes it involves. We are investigating the interaction of proteins with the inorganic skeleton of the biomineral by performing a range of experiments, including the growth of synthetic calcium carbonate crystals by incorporating amino acids and peptides into the inorganic framework. Combining these with the imaging of both the ultrastructure and the nanostructure of the biominerals will provide useful insights on the role played by proteins, applicable not only to protein geochronology but also to the process of biomineralisation itself.