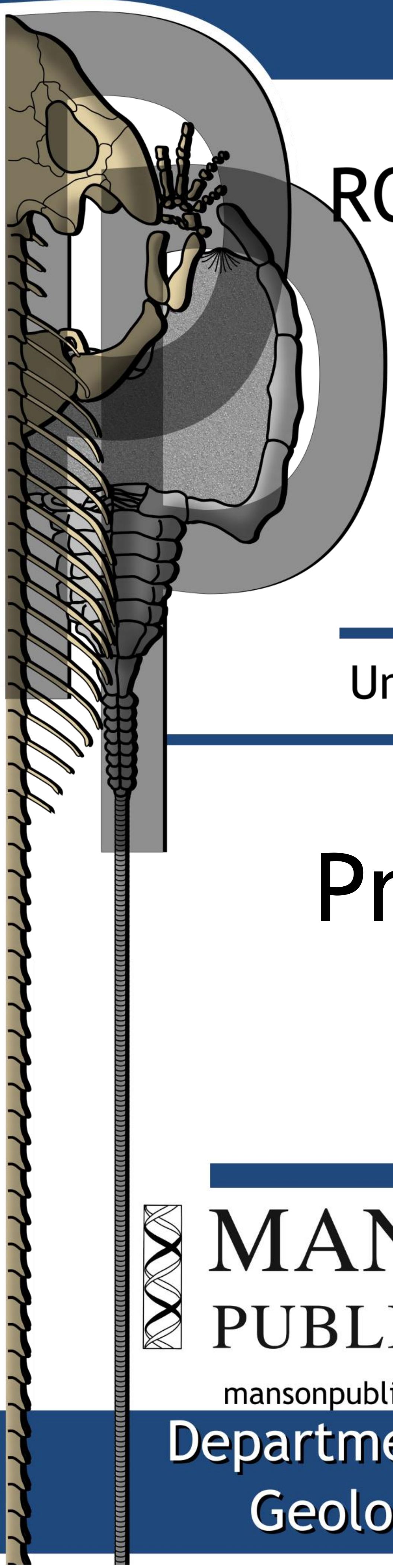

ROGRESSIVE

ALAEONTOLOGY

THE PALAEONTOLOGICAL ASSOCIATION

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Welcome and acknowledgements

We are glad to welcome you to the Department of Geology of the University of Leicester and this year's edition of Progressive Palaeontology. We look forward to another stimulating conference and would like to thank in advance all presenters.

Anybody who participated in previous Progressive palaeontology meetings will be able to tell you that talks and posters are but one element of the whole experience. We will start the meeting on Wednesday with an ice-breaker reception in the Old Horse pub, renowned for its unique decoration and tea pot collection. Presentations on Thursday will be followed by a much-anticipated dinner in the Taj Mahal restaurant, one of the oldest Indian dining places in Leicester and a nigh-on unavoidable place for any visiting palaeontologist. Friday will be the opportunity to (hopefully) get a tan and enjoy fieldwork in Ketton Quarry, collecting fossils from middle-Jurassic limestone.

We would like to thank the following for their help and support:
The Palaeontological Association for funding the conference. Manson Publishing and the University of Leicester Bookshop for providing prizes and support. The staff of the Department of Geology at the University of Leicester for their help, advice and patience. Mark Sutton for his help designing the website. Dave Jones and Dave Baines for their Prog Pal organising experience and advice. Professor Mark Purnell for first suggesting we organised the event in Leicester. The staff at the Old Horse, Taj Mahal and Ketton Quarry for welcoming us.

We would also like to thank Fanny Pouyet and Rachel Warnock for presenting their works at the last minute in replacement of people who were unable attend.

Finally, we wish next year's organisers the best of luck !

Nicola Clark, Laurent Darras, Oliver Knevitt, David Riley and Alison Tasker
The Progressive Palaeontology 2011 organising committee

Abstracts of oral presentations

Sampling and completeness of the fossil record:

A case study from the Lower Jurassic of the Dorset Coast, UK

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The majority of studies investigating the adequacy of the fossil record are carried out at a global or continental scale, and use sampling proxies that most likely do not accurately represent all aspects of sampling, to detect and correct for bias in the fossil record. These studies have identified correlations between apparent diversity and various proxies for sampling. This has led to the conclusion that patterns in the fossil record are a result of sampling biases or a common-cause scenario, or that the covariance is a result of redundancy between apparent diversity and sampling proxies. In this investigation, we compare a number of proxies representing three aspects of sampling, (1) sedimentary rock volume, (2) rock accessibility and (3) worker effort, with apparent diversity in a geographically and stratigraphically constrained data set, the marine Lower Jurassic of the Dorset and East Devon Coast. The results show that the proxies for rock volume do not correlate well with the other sampling proxies or apparent diversity, suggesting that the total amount of sedimentary rock preserved does not influence apparent diversity on a regional scale. However, correlations are observed between proxies for accessibility and worker effort with apparent diversity. The fact that all the proxies do not correlate with each other suggests that none can be regarded as an all-encompassing sampling proxy that covers all aspects of sampling bias. The presence of some correlations between sampling proxies and diversity most probably indicates a mix of bias and bonanza, as palaeontologists have preferentially sampled the most accessible and richest rock units.

The trunk segmentation of trilobites and its phylogenetic implications: insights from a pill millipede

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Trilobites arguably represent one of the most successful arthropod groups that has ever lived, with several thousand described species and an evolutionary history that spans through the entire Palaeozoic (542 – 251 Ma). Despite the wealth of data available from the trilobite fossil record, the most basic aspects behind the underlying somatic segmentation of this group remains a controversial matter, as there is uncertainty on whether the number and disposition of the segmental units can be inferred from the exoskeletal anatomy exclusively. Here I will review the key features of trilobite exoskeleton, and propose that some of the more problematic aspects of their organization can be explained by drawing comparison to segmentation mechanisms described in model arthropod species, and the permanence of several plesiomorphic intersegmental markers in the arthropod body plan. By tracing the highly conserved expression patterns of the segment polarity genes *engrailed* and *hedgehog* on the ventral side of exceptionally preserved trilobites and other closely related taxa, it becomes evident that the disposition of the dorsal exoskeletal components does not match directly that of the segmental units. I discuss morphological analogues of dorsoventral segmental mismatch between trilobites and the pill millipede *Glomeris marginata*, and suggest that these phenotypic similarities are both regulated by a gene cassette inherent to all members of the total-group Mandibulata. The presence of characters shared with trilobites and some crustaceans in putative stem-euarthropods, like *Fuxianhuia*, suggest a stem-mandibulate affinity for the latter and prompt a re-evaluation of basal arthropod phylogeny.

A bivalve proxy for Neogene Antarctic shelf marine environments

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Bivalves occur in Early Pliocene sedimentary deposits of the Antarctic Peninsula and East Antarctic. Despite their often fragmentary nature, many bivalves are still articulated, suggesting minimal transport or reworking, and this is confirmed by Sr-dating and by comparison with Ar-ages from associated volcanics. Thin section petrographical and geochemical analyses of the shells also suggest minimal post-mortem diagenesis. Morphological and chemical signatures in the shells appear to record seasonal signals, including sea water temperature variation. In the Cockburn Island Formation of the northern Antarctic Peninsula (4.7 Ma) shells signal continuous growth through the year and the probable absence of sea ice, consistent with other proxies that suggest minimal sea ice for the Early Pliocene. Similar seasonality and sea temperatures (about -1 to +3°C) are suggested by approximately contemporaneous shells from glacigenic deposits at Cascade Cliffs on James Ross Island. More difficult to interpret are sea temperature reconstructions from bivalves (pectenids, hiatellids and *Cyclocardia*) recovered from Early Pliocene (4.5-3.8 Ma) shallow marine deposits of the Larsemann Hills region, East Antarctica. These suggest peak sea temperatures above 5°C that are consistent with some earlier temperature suggestions from silicoflagellate data, but which are difficult to interpret for Early Pliocene Antarctic climate.

Congruence between cranial and postcranial characters in vertebrate palaeontology

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Phylogenetic tests of partition homogeneity are routinely applied to matrices amalgamating data from more than one molecular marker, or combining molecular and morphological evidence. Incongruent phylogenetic signals from different partitions are variously explicable in terms of different evolutionary histories (in the case of genes), different selective pressures, and/or different signal strengths and levels of noise. However, this approach has rarely been applied to partitions of morphological data sets. Here we investigate the homogeneity of signal from cranial and postcranial characters in over 50 published morphological vertebrate data matrices. Cranial and postcranial characters are often claimed to be under differing magnitudes and directions of selection. We test this assertion here, not least because palaeontologists often have access to strongly biased samples of characters (or lack data from one partition altogether). Firstly, we compared levels of homoplasy and synapomorphy in cranial and postcranial partitions. Secondly we applied two randomization tests of congruence based on numbers of steps, namely the incongruence length difference (ILD) test, and topological incongruence length difference (TILD) test. Finally, we explored a new randomization approach using tree to tree distance metrics rather than tree length. Our results show that it is not uncommon for cranial and postcranial characters to contain significantly incongruent signals. Also, because missing entries are often preferentially distributed in one or other partition, this may have implications for the way in which incomplete fossils are resolved.

Fitting fossil arthropods into modern phylogenies

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Arthropods are a diverse group of animals including spiders, scorpions, centipedes, millipedes, insects and crustaceans. With over 1,000,000 described species they outnumber all other extant (living) phyla combined, and have been the dominant contributor to species diversity for the last 520 million

years. They are also commonly used as model organisms for evolutionary studies. Despite all this, we understand very little about their actual relationships, either to each other or other animal groups. Nearly every possible arrangement of the arthropod subgroups has been proposed and each is largely dependent on the type of evidence used, i.e. morphological vs. molecular (DNA) data. Recently a "total evidence" approach has been utilised which includes all available data, including information from extant and extinct species. Fossil data has been shown to be of particular importance in phylogenetic studies as they tend to resolve major character conflicts created by extant taxa and provide a "snapshot" of evolution. The aim of this talk is to provide an overview of recent works attempting to resolve arthropod interrelations and will demonstrate the importance of fossil data for resolving this issue.

Fossil leaves from the Miocene of Ixtapa locality, Chiapas, Mexico

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Cenozoic palaeobotanical studies in Chiapas, México, have reported flowers included in amber, pollen and fossil woods. The present work adds new plant evidence based on leaves from the Ixtapa locality, dated as ca. 14 Ma. The morphological diversity found is high, consisting in more than 40 morphotypes. The fossils have been grouped based on leaf architecture features, highlighting the presence of Myrtaceae, Dilleniaceae and Leguminosae. From these groups, two taxa have been identified by their leaf morphological characters; the first one has features present in Eugenia, *Calyptranthes* and in less proportion in *Myrcia* (Myrtaceae), such as the elliptic shape of the lamina, presence of an intramarginal vein formed by the fusion of secondary veins, random reticulate third vein order, acuminate apex and presence of glands over the entire lamina. The new leaves related to *Tetracera* (Dilleniaceae) have elliptic-oblong laminar shape, craspedodromous secondary venation, serrate margin and thick petiole. The taxa studied in this work represent two new fossil species. The abundance, diversity and size of the leaves found suggest they formed part of a tropical community, however further analyses beyond the present work are needed to confirm this hypothesis. Nevertheless it is believed that the climate was similar to those proposed for other tropical Cenozoic localities of Chiapas.

Panamanian Pompeii: A 16 million year old tropical forest buried by a hot pyroclastic flow

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A spectacular 16 million year old tropical forest has been discovered in Panama. The fossil forest occurs in the Middle Miocene Cucaracha Formation. Exposed in the course of excavations to widen the Panama Canal, the forest layer is known from three sites (Contractor Hill, Centenario Bridge and Hodges Hill) spread over a distance of 3 km. Although these are disjunct outcrops, the forest layer is correlated by means of a distinctive welded ignimbrite unit (radiometric dates are in the process of being obtained) that entombs and preserves the forest in growth position. This pyroclastic flow was emplaced at high temperature because the tree stumps, and the paleosol in which they are rooted, are charred to a depth of 0.12 m. Charred logs entrained within the overlying flow are orientated NNE-SSW, and partly uprooted stumps suggest the blast wave came from the north. There are several volcanic plugs, at a distance of 5-7 km north, which represent candidate volcanic sources for the pyroclastic flow. Geochemical studies are in progress to fingerprint the volcanic cone responsible while reflectance measurements of the charred stumps and trunks aim to constrain the temperature of the flow. Preliminary analysis of wood anatomy suggests the forest was dominated by dicots (80-90%), including Annonaceae, together with a few palms (remaining 10-20%). Megafaunal remains, including rhinos and protoceratid cameloids, found only 2-3 m below the forest layer at one site (Hodges Hill) provide a tantalizing glimpse of the communities that inhabited this ancient tropical forest.

The evolution of tail stiffness in thyreophoran dinosaurs

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Using experimentally-supported determinants of the passive flexibility of intervertebral joints, we applied a simple biomechanical approach to infer the capabilities and evolutionary histories of stegosaurian and ankylosaurian tails.

The common ancestor of stegosaurs and ankylosaurs (Thyreophora) had a tail suited for support against gravity, but not for mediolateral swinging (low flexibility). The tail of Stegosauria exapted these capabilities which were useful for supporting the tail plates and spikes. Along the stegosaur lineage the tail became more suited for supporting its weight but became less flexible for mediolateral tail swinging, although weapon usage remains plausible.

Similarly, the tails of Ankylosauria remained suited for support against gravity but mediolateral movement was restricted by ossified middle and distal tail tendons.

Ankylosaurid tails were distinct from other ankylosaurs' because the middle and distal tail was dorsoventrally low, mediolaterally narrow, and co-ossified into a single structural unit supported by fused caudal centra. Zygapophyses, neural spines and ossified tail tendons provided surface bracing that increased middle and distal tail rigidity allowing the tail club to be supported passively (against gravity). This allowed weight to be effectively transferred to the proximal tail which was suited to supporting the entire tail. In the proximal tail ankylosaurids had low mediolateral flexibility, but again a weapon function remains plausible.

Stars in their eyes: New sensory structure or epibiont?

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Limuloides limuloides (Arthropoda: Chelicerata) is a Late Silurian synziphosuran from the Lower Leintwardine Formation of Church Hill, Shropshire. Originally described by Woodward (1885), *L. limuloides* represents one of the best-preserved and phylogenetically significant 'merostome' (aquatic chelicerate) specimens. Despite this, this taxon has been largely ignored for almost a century, with only the occasional mention in relatively recent phylogenetic analyses and reviews. The detailed morphology of this taxon has not been restudied since its original description and as such, unique stellate ornamentation upon the prosoma (head shield) has gone unnoticed or ignored, bar a footnote by the original author. A comparative study has shown these structures to have a consistent morphology amongst well preserved specimens, however the theory of Woodward that they represent sensory organs is considered unlikely due to the lack of any homologous or analogous structures in any other known arthropods. Modern horseshoe crabs are well known for being a 'mobile substrate' and host a wide array of epibionts. *L. limuloides* is recognised to be the oldest species preserved with this relationship through the presence of bryozoans growing on its dorsal cuticle. This also leads to the possibility that the stellar ornamentation could represent a previously unknown epibiont; however this interpretation is also contentious due to the consistent positioning of these structures. Presently the exact nature of these stellate structures remains enigmatic.

Biodiversity crisis and recovery during the Triassic-Jurassic greenhouse interval: testing the ocean acidification hypotheses

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The Triassic-Jurassic interval witnessed one of the major biodiversity crises of the Phanerozoic. Palaeoclimate studies have demonstrated that it was associated with a four-fold rise in atmospheric CO_2 which is hypothesised to have caused global ocean acidification. Recent and ongoing experimental studies are currently being conducted in an effort to predict how present marine organisms will respond to ocean acidification. The fossil record provides long term data from past ocean acidification events and can be used to test these predictions. This project examines the fossil record of the Triassic-Jurassic high-CO_2 interval from Lyme Regis and St. Audries Bay. In this study the lengths and widths of different bivalve taxa (*Liostrea* and *Plagiostoma*) have been measured to produce a geometric size for each specimen. These data have been plotted against published estimates of atmospheric CO_2 levels. Previous authors have predicted that ocean acidification will result in a reduction in bivalve size through the Triassic-Jurassic high CO_2 interval, but the new data collected thus far show that at both locations shell size in *Liostrea* and *Plagiostoma* increases as pCO_2 increases. It is possible that other factors may be influencing shell size through the study interval, but modern experimental studies have also shown that some bivalve taxa continue to grow, just at a slower rate as CO_2 rises. The response of benthic marine organisms to high atmospheric CO_2 is therefore complex and not straightforward to predict. The hypothesis that Triassic-Jurassic CO_2 rise led to body size reduction in all bivalve taxa is rejected.

Spatial Analysis of Species Distributions on Ediacaran Bedding Planes

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The Ediacaran Biota are the first complex macroscopic organisms in the fossil record, occurring at the end of the Protozoic. The oldest of the Ediacaran Biota are from the Avalon assemblage, and my work looks at bedding planes of these fossils from Mistaken Point, Newfoundland, Canada. The bedding planes are a succession of volcanic ash flows, preserving entire ecosystems in situ. Their morphology is significantly different from any Phanerozoic organism so their ecology much harder to assess.

Spatial distributions of these fossils reflects their life interactions. In order to analyse the spatial distributions of the fossils to understand their interactions, I used differentiated GPS to map the two most important bedding planes at Mistaken Point, I first considered any preservational bias by analysising how physical features of the bedding planes could contribute to patterns in the fossils. I then looked at Ediacaran species spatial interactions in two different ways. I advanced nearest neighbour techniques to provide a more accurate analysis of the pairwise interactions discussed by Clapham et al. I then used Bayesian network inference to look at the ecosystem as a whole, and found the most probable ecological networks for different spatial scales.

I found that one species – *Thectardis* had a very different set of ecological interactions than all the other species present, and since its morphology is unique among species I conclude that *Thectardis* has a different phylogeny.

Patterns of extinction and recovery among Permian-Triassic sharks

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Sharks are predominantly marine top predators that are believed by some to have been relatively unaffected by the end-Permian mass extinction, supported by an apparent radiation of fish families across the boundary, while most of their supporting ecosystem collapsed. In contrast, it has been stated that chondrichthyan diversity has always closely followed diversity fluctuations in other marine and freshwater organisms, including the drastic decline during the Late Permian and also the subsequent recovery phase. With better reconstruction of local elasmobranch records from the Permian and Triassic, and therefore of faunas from the different oceanic basins, we can start to identify significant evolutionary developments as a result of the two-phased late Permian extinction event and link them to the changes in the global marine community. The current study is firstly based on a global literature survey, and additional field data is available for the Permian-Triassic elasmobranch fauna of Oman (western Neothethys)—which has not previously been studied—and Japan (mid-Panthalassa), and also includes Greenland (Boreal). Preliminary data show that the Middle Permian fauna of Oman mainly consists of one ctenacanthiform taxon (*Glikmanius* cf. *occidentalis*) and four new hybodontiform taxa (including *Lissodus*-like). This faunal composition is largely dissimilar to the Early Triassic fauna from the same region, but again comparable to the Middle Permian fauna from

Japan. Detailed reconstruction and comparison of such occurrence data, is expected to reveal global evolutionary patterns and the true nature of the extinction among this dominant marine group.

The polar planktonic foraminifer species *Neogloboquadrina pachyderma* sinistral – a study from different views

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This study will provide much information about the species *Neogloboquadrina pachyderma* sinistral its morphotypes and its ecology. It is the only known recent polar planktonic foraminifer and therefore a valuable tracer for paleoceanography in these regions. Three different morphotypes of this species are known today: a crystalline, a reticulate and a transitional type. However, the biometry of these morphotypes is not well known yet. In addition many authors do not consider possible impacts on their analyses when using randomly picked specimens of *N. pachyderma* sinistral (e. g. EGGINS et al., 2003; HELMKE and BAUCH, 2002; HELMKE et al., 2003; HUBER et al., 2000a; 2000b; JENSEN, 1998; KOHFELD et al., 1996; MELAND et al., 2005). This study will show that a separation by morphotype is necessary. This was achieved by investigating the biometric data, i.e. their size and weight. In addition, the $\delta^{18}O$ and $\delta^{13}C$ values of the different morphotypes were compared to each other, leading to the conclusion that weight and size influence the isotope values of $\delta^{18}O$, but do not seem to have an effect on $\delta^{13}C$ values. Considering the amplitude of the effect on $\delta^{18}O$ by test biometry, ignoring the size of the analysed specimens may, in worst cases, lead to a misinterpretation of glacial and interglacial periods.

Life and Death in the First Complex Ecosystem: A Study of the Ediacara Biota from Mistaken Point, Newfoundland.

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The first complex ecosystems arose with the enigmatic Ediacara Biota. Their biological affinities remain one the most exciting unsolved problems in palaeontology, having great bearing on the origin of animals and the Cambrian Explosion. Currently only one model is published regarding the ecology of these unique creatures, suggesting that the fossils are found in life assemblages and that the creatures were tiered much like an animal community. Recently, as part of a major conservation project, a complete cast was made of one of the most important Ediacaran surfaces in the world, Mistaken Point E surface, from Newfoundland, Canada. This now allows study of these extraordinary organisms at a resolution impossible when working in the field yet still with their context intact. It is emerging that the Ediacaran organisms often suffered extensive post-mortem decay before burial in the Mistaken Point Formation. Here we examine this taphonomic model and extend its significance to models concerning ecology. These new data confirm that fossil assemblages on individual horizons are not living 'census' populations, potentially eroding the concept of animal like ecological tiering at Mistaken Point. Extensive mapping of this material is beginning to constrain possible models of ecology, while re-evaluation of newly categorised 'census' populations according to stages of decay will confirm or expel the hypothesis of metazoan-like epifaunal tiering. The immediate future will bring direct organism decay experiments and simulation of Ediacaran ocean conditions to further our understanding of the taphonomy of these biotas that hold such significance for understanding the rise of complex ecosystems.

Postglacial recolonisation mode of North American *Amara alpina* (Carabidae: Coleoptera) using museum and ancient DNA

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Predicted future climatic change is likely to result in the colonisation of new regions by species. Historical colonisation events can be used to predict the mode and tempo of these future events. This study investigated the mechanism by which the arctic beetle *Amara alpina* recolonised Canada at the end of the last ice age, utilising information from both modern and ancient representatives. Previous work had suggested that recolonising individuals originated from the western (Beringian) and southern (northern lower 48 US states) refugia. The results described here show a more complex pattern of recolonisation than originally thought. A distinctive haplogroup has been identified in Canada, which did not originate from either of the two aforementioned refugia. This raises the possibilities of a refugium in northeast North America or a postglacial immigration event to North America by individuals from Europe.

Original eumelanin pigment preservation in the feathers of the early Cretaceous bird *Gansus yumenensis* as revealed by morphological and geochemical analyses

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The identification of melanosomes and interpretation of pigmentation in fossilised soft tissues has thus far been largely based on morphological analyses. This study uses both morphological and geochemical analyses to examine two isolated and exceptionally preserved feathers of *Gansus yumenensis* from the early Cretaceous of China. Elongate structures consistent with those identified as eumelanosomes in previous studies were found in the feathers using environmental scanning electron microscopy (ESEM). The elongate structures were restricted to visibly dark areas of the feathers, but were absent from lighter areas and also the matrices. Fourier transform infrared spectroscopy (FTIR) of these dark areas demonstrated the presence of functional groups indicative of melanin as shown by the analyses of modern *Sepia officinalis* eumelanin. Such structures were again not present in lighter areas of the feather nor the matrix as shown in an infrared map of the ketone group in the barbules of one of the feathers. Different organic free radical signals were demonstrated between one feather and its matrix using electron paramagnetic resonance spectroscopy (EPR), however the technique was unable to resolve the eumelanin signal within the feather. Pyrolysis gas chromatography mass spectrometry (Py-GCMS) showed a similar distribution pattern of aliphatics in both the fossil feathers that differed from that of their respective matrices, however melanin breakdown products were not observed. The combination of these techniques clearly demonstrates the presence of endogenous organic material in the fossil feathers. However only FTIR was successful at identifying melanin breakdown products. This is the first time that organic geochemical analyses have been used in conjunction with traditional morphological techniques to provide clear evidence of the preservation of original eumelanic pigmentation in fossil feathers.

The impact of fossil calibrations on Bayesian estimation of divergence times

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Molecular clocks have usurped the traditional role of the fossil record in providing a timescale for evolutionary history. However, it is of critical importance that fossil data are correctly represented in any molecular clock study. Bayesian methods have become increasingly popular but no protocols have yet been established for implementing prior probability distributions that reflect the degree to which fossil minima approximate the true time of divergence. Instead, clock analyses have adopted expeditious solutions such as normal, log-normal and uniform probability distributions that assume some general relation between fossil minima and divergence dates, but are not informed by any paleontological data. We examine the consequences of this base strategy on the estimation of divergence times among the major lineages of Arthropods, plants and Testudines. Results demonstrate that calibration priors can have a profound impact on the posterior age estimates within this group. We also show that although the inclusion of informative fossil maxima can ameliorate the impact and increase concordance with raw palaeontological estimates, posterior estimates always remain sensitive to the prior distribution of ages. This highlights the urgent need for innovative ways of incorporating detailed palaeontological knowledge into molecular dating of divergence times.

Abstracts of poster presentations

Evolutionary origins of animal skeletal biomineralization

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The evolutionary history of biomineralization in animals is crucial to our understanding of modern mineralized tissues. Traditional methods of unravelling this history have aimed to derive a theory of the development of biomineralization through evolution by the comparison of mineralized systems in model organisms. This has lead to the recognition of the 'biomineralization toolkit' and raised the question of homology of mineralized tissues versus convergent or parallel evolution. However, without phylogenetic context these inferences can be problematic. The 'new animal phylogeny' reveals that many of the groups known to biomineralize sit among close relatives that do not and favours an interpretation of convergent or parallel evolution for biomineralization in animals. In addition, the fossil record of the earliest mineralized skeletons, the SSFs, presents a rapid proliferation of biomineralization across a range of animal phyla, with fossil representatives of many modern biomineralizing phyla rather than sister taxa to higher taxonomic groups. A synthesis of molecular, developmental, phylogenetic and fossil evidence, demonstrates the convergent or parallel evolution of biomineralization in animals at the phylum level, perhaps through the co-option of pre-existing unmineralized structures and molecular mechanisms. The fossil record of the Cambrian explosion not only provides vital evidence for the evolution of animal mineralized tissues but also suggests a mechanism for its rapid, and synchronous convergent origin.

The Phylogeny of Marrellomorph Arthropods

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The marrellomorphs are a small group of Palaeozoic arthropods noted for their aberrant morphology, which has precluded resolution of their phylogenetic position. Marrellomorpha includes two clades, the marrellids and the acerostracans, allied by the shared possession of numerous (>25) trunk somites with appendages that reduce in size posteriorly. The marrellids are characterised by the possession of extensive anteriolateral head spines and typified by the Burgess Shale taxon *Marrella*; the acerostracans are characterised by the possession of a dorsal "shield" that covers their entire body and appendages. Recent work on marrellomorph anatomy, including descriptions of unpublished material, has augmented our understanding of the morphology of the group, and enabled us to identify potential homologies with other arthropod taxa. A cladistic analysis was undertaken including all currently recognised marrellomorphs and a variety of extinct and extant arthropods. Preliminary results indicate that the marrellomorphs are monophyletic that includes: marrellids; acerostracans; and "skaniids", a paraphyletic group of Cambrian arthropods that, like the acerostracans, possess a dorsal "shield". This analysis also indicates that the marrellomorphs form part of a stem-mandibulate lineage that includes megacheirans, trilobites and various "orsten" taxa.

An empirical study of potential biases to stratigraphic congruence metrics

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Unsurprisingly, many studies report congruence between the order in which taxa branch within cladograms and their stratigraphic sequence in the fossil record. The strength and significance of this congruence varies greatly, both across higher taxa and through geological time. For example, arthropods tend to have poorer congruence than vertebrates, while congruence in the Mesozoic is typically superior to that at other times. Do these differences reflect the quality of the fossil record and the accuracy of cladograms, or are they a function of other parameters? Published measures of stratigraphic congruence are logically and empirically biased by tree size, tree balance, taxonomic level and the temporal extent of clades. Many of these parameters are not uniformly distributed

through time or among higher taxa. Using statistical modeling methods, we ask whether the influence of these biases is sufficient to explain the patterns reported in the literature. We focus on the Gap Excess Ratio (GER) and the Stratigraphic Consistency Index (SCI) as they address different concepts of congruence (ghost ranges and nodes respectively). We find that some higher taxa continue to show a congruence signature that probably owes much to their preservation potential. However, temporal trends in congruence are much less robust.

Problems in the Systematics and Biogeographical History of Salamanders

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Living salamanders represent a diverse and abundant clade of Lissamphibians, the group that also includes frogs and caecilians. With the exception of two recent southward migrations into South America and North Africa, their distribution is limited to northern continents. After more than a century of morphological and molecular analysis, some degree of consensus has been reached regarding the interrelationships of salamanders; however the relationships of some clades (e.g. sirenids) remain controversial, in part because of widely prevalent paedomorphosis.

The earliest fossil salamanders date from the Middle Jurassic (165 million years ago), with crown group taxa appearing shortly after. Most fossil remains are fragmentary, making determination of taxonomic affinities difficult, but exceptionally well preserved material from the Early Cretaceous of China and Spain offers the potential for a better understanding of their early evolutionary history and enables more rigorous phylogenetic analysis.

Like living taxa, fossil salamanders are mainly restricted to northern continents (ancient Laurasia) suggesting a northern origin for the clade. However, a small number of aberrant fossil salamanders are known from the Cretaceous and Palaeogene of Africa and South America (ancient Gondwana) raising the question as to whether early salamanders, like frogs, might once have had a more global distribution.

Here I set out the problems faced in this field and the methods I will be using to gain a better understanding of the evolutionary and biogeographical history of salamanders.

Global patterns of Cretaceous forest distribution and productivity inferred from fossil wood

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Global patterns of Cretaceous forest distribution and productivity are analyzed based on a comprehensive fossil wood database. To ascertain patterns, fossil wood records (n=1424) were classified by botanical affinity and results plotted on palaeomaps. Results confirm previous conjecture that araucarian conifers were globally dominant in Early Cretaceous times, but reduced in numbers and geographic range during the Late Cretaceous, coincident with the rapid expansion of angiosperms. Podocarpoid conifers were restricted to Gondwanan fragments, where they were co-dominant with araucarians. Cupressoid conifers were most common in arid mid-latitudes. Pinoid conifers were mostly restricted to the Northern Hemisphere, suggesting that their modern distribution was established in Cretaceous times. To ascertain productivity patterns, mean tree-ring width data (n=259) were obtained by thin section analysis and plotted by palaeolatitude. Comparison with modern data shows that Cretaceous forest productivity was greatly elevated, especially in high-latitudes and to a lesser degree in mid- to low-latitudes. Elevated productivity may reflect the extreme Greenhouse warmth that characterized the Cretaceous Period and offers an analogue for the effects of future global warming. Results reveal global patterns of conifer distribution and productivity in the Cretaceous Greenhouse climate mode.

Sclerobionts from the K-T boundary of Alabama and Mississippi

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The Cretaceous-Tertiary (K-T) mass extinction had a dramatic impact on marine life, due to the removal of large proportions of taxa and its influence on shaping the subsequent biota. It is widely acknowledge that the K-T event is associated with a significant decline in primary production, which is likely to have particularly affected suspension-feeding epibionts inhabiting hard substrates.

Hard substrate faunas provide a unique insight into past communities; their in situ preservation allows a "snapshot" view of interactions within communities that may not be preserved elsewhere. By comparing hard substrate fauna before and after the K-T event, the influence of the mass extinction on the ecologies of these communities can be assessed. It can be predicted that low-diversity communities will dominate hard substrates in the immediate aftermath of the mass extinction, especially as relatively few taxa may be able to survive in the harsh living conditions. Over time, diversity is likely to increase, as opportunists diversify alongside improving environmental conditions.

The K-T boundary is exposed at a number of localities in Alabama and Mississippi, USA. A variety of encrusted hard substrates (e.g. oyster shells) were collected from the latest Cretaceous (Maastrichtian) and earliest Tertiary (Danian). Encrusting taxa were identified to the lowest possible taxonomic level and variations in abundance and diversity analysed. Encrusting bryozoans, foraminifera, bivalves and annelid worms are all present, as well as evidence of borings made by sponges in particular. The diversity of these sclerobionts varies between localities, with Danian hard substrates dominated by foraminifera. The proportion of hard substrates colonised by epibionts has also been assessed and appears to decline after the K-T boundary. Such analyses provide an insight into the dynamics of shallow marine communities at this critical moment in time.

Shark teeth from the Middle Permian-Triassic Arabian continental shelf area of Oman

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Elasmobranchs are newly reported from Middle Permian-Triassic deposits representing a variety of depositional environments exposed in the northern regions of Oman. Conodont residues obtained by processing limestone samples in buffered acetic acid have yielded numerous well-preserved elasmobranch remains. The well-exposed, low-palaeolatitude (boundary) sections represent both autochthonous shallow marine deposits outcropping in the interior Huqf area along the eastern coast (Khuff Fm, Wordian), and the allochthonous Oman Exotics, which consist of autochthonous olistoliths that have been redeposited in younger strata throughout the Oman Mountains: Wadi Alwa in the Ba'id region (Alwa Fm, Olenekian) and Jabel Safra (exotics within Guwayza Fm, Olenekian). Preliminary data show that the Permian fauna consists of at least four taxa (e.g., Eugeneodontiformes, Symmoriiformes) and the Triassic of three or more (e.g., *Synechodus*, *Hybodus*), and whilst the faunas are largely dissimilar, Hybodontidae seem to occur in both. Besides focusing on the description and identification of the material, this study also addresses ecological and taxonomic aspects of the Permian-Triassic shark community. Ongoing work is currently aimed at obtaining a detailed reconstruction of the elasmobranch fauna in the region.

Why do Neogene marine sediments of Italy host a diverse and rich fossil record of cetaceans?

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Fossil cetaceans are abundant and diverse in Neogene shallow marine sediments of central and northern Italy. To verify which environmental factors favoured the preservation of Italian marine vertebrates in the fossil record we studied in detail the sedimentary successions from where seven nearly-complete skeletons were previously recovered. The taxonomic composition of marine benthic assemblages was used as an indirect measure of environmental gradients, among which water depth is known to be the main influencing factor. Bulk samples were collected from both the bone beds and the sediments immediately above and below, and were analyzed for their mollusc content. These new data were merged with Italian Pliocene to early Pleistocene literature-derived mollusc samples. The final dataset (312.904 individuals, 330 genera) was analyzed using detrended correspondence analysis (DCA), a multivariate statistical technique widely used to ordinate taxa and disclose underlying ecological gradients. To interpret the ordination in terms of absolute depth, the average life depths of extant mollusc genera abundant in our dataset (n=47) were calculated.

In our DCA plot, depth controls the distribution of benthic communities along the main axis of ordination (DC1), with samples ranging from intertidal to bathyal depth. According to independent geological data, we interpreted DC2 as controlled by nutrient levels. As a result, we found that all the whale carcasses settled in open shelf settings under high nutrient conditions. This result is consistent with the positive correlation between primary productivity and marine animal abundance, although other factors like sea water temperature might be important. We thus hypothesize that the rich and diverse record of fossil cetaceans in the Pliocene of Italy could be partly linked to eutrophic conditions in the water column, which favoured the development of large cetacean populations.

Landmark analysis of tridactyl dinosaur footprints from the Middle Jurassic of the Yorkshire Coast, UK.

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Methods of analysing and comparing the form and shape of dinosaur footprints have primarily relied on linear dimension measurements and ratios, with more sophisticated methods such as geometric morphometrics used sparingly. Landmark analysis offers a powerful tool for the analysis and comparison of dinosaur footprint form and shape. Like much of the Middle Jurassic worldwide, dinosaur body fossils are extremely rare on the Yorkshire Coast, with palaeocommunity reconstructions depending heavily on the abundant track data. This investigation subjected a sample of tridactyl tracks from the Yorkshire Coast, including a number of morphotype specimens, to a series of landmark and cluster analyses in an attempt to assess the validity of existing morphotypes. A number of named dinosaurian and avian ichnotaxa from the scientific literature were also added to the analysis to help determine the types of dinosaurs that roamed the Yorkshire Coast during the Middle Jurassic. Landmark analysis suggests a higher diversity of tracks than previously thought with most of the tracks being attributed to theropods. Although landmark analysis provides an excellent quantitative method for the analysis and comparison of dinosaur footprint shape, caution must still be taken when interpreting any vertebrate tracks as preservational and sedimentological factors often have a greater effect on morphology than the taxonomy of the track-maker.

Palaeoecological response of marine invertebrate communities to the Late Triassic mass extinction event

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The Late Triassic (LTr) mass extinction event (200 Ma) is considered to be one of the "big 5" mass extinctions events with extinction of 41% of the marine genera. Despite previous study, aspects of the duration, intensity and the ecological impact of this event remain unclear. To address this, samples were taken from approximately 1 m intervals through the Triassic-Jurassic section at Larne, Northern Ireland. Species abundance by sample was estimated and each species was classified according to autoecological information derived from the literature. In order to assess changes in the structure and composition of the assemblages through the LTr interval, the beta diversity index was calculated, dominance and richness were estimated through rarefaction techniques, and the data were tested against five rank abundance (RAC) models. Ecospace modelling was used to estimate the loss in ecological diversity. During the LTr event, richness decreased by 70%, the abundance of species dropped by >90%, and semi-infaunal modes of life decreased significantly. Changes in rank abundance were best explained by the Geometric RAC model. Finally the beta index showed a significant turnover in species composition during the extinction event. Although the causes of the LTr event are not clear, these results show that at a local scale environmental disruption changed species composition in a relative short time period and clearly generated deep changes in diversity which decreased the ecological functionality of the invertebrate marine assemblage.

Did Whole Genome Duplication events drive vertebrate history?

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Gen(om)e duplication is important evolutionary processes leading to the formation of new genes. Three WGD (Whole Genome Duplication) events (1R-3R) occured at significant points in vertebrate evolution, where there are substantial increases in diversity or complexity (jaws, sclerotic ring, etc.) of living vertebrates and hence, WGD have been causally implicated. Nevertheless, seven extinct taxa, phylogenetically intermediate of the cyclostomes and the clade of the living jawed vertebrates, show there were no jumps in complexity. What is not established is the role that WGDs have played in effecting phenotypic evolution during these episodes of vertebrate phylogeny. If WGDs are causal, they must have occured before the increase in body plan complexity. The permissive model supports the idea that WGD facilitates adaptations whereas the deterministic model suggest a direct causal link between WGD and phenotypic innovations. However, the DDC model (Duplication-Degeneration-Complementation) predicts complexity came first and partitioning of functions among descendant paralogues (sub-functionalization) explains why so many novel paralogues were retained after WGD. We use Bayesian molecular clock analyses to date WGD events relative to fossil divergences, we will determine whether these events occurred early or late relative to the evolution of phenotypic traits and assess; ultimately whether or not WGD events are important drivers in vertebrate evolution.

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