IQUA

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1. Introduction

Dear IQUA member,
Welcome to newsletter No. 44.

The Annual Symposium at the GSI brought 2009 to a successful conclusion for IQUA, with a terrific set of talks (see extended abstracts below), discussion and attendance making the event a highly stimulating and enjoyable one. Again, our thanks go to all the speakers and organisers of the event, in particular Fraser Mitchell, and the GSI for facilitating the meeting once again.

We have every hope that this year will be marked by other enjoyable events, including the upcoming (27th March) Spring Meeting and AGM to be held in Mary Immaculate College, U. of Limerick. Our thanks go to Angela Hayes and the Dept. of Geography there for agreeing to host the event. Angela (MI) and Robin Edwards (TCD) are co-convening the meeting.

Item 4 announces a significant advance in IQUA's efforts to encourage and enable graduate research within the Quaternary Science in Ireland. An exciting new set of 'Postgraduate Radiocarbon Dating Awards' will be launched this year at the AGM, following a very generous offer by the world-class Carbon Dating facility within the ^{14}Chrono Centre for Climate, Environment and Chronology at QUB (http://www.chrono.qub.ac.uk/). The nature of the Awards and the likely competition process is details below and will be discussed at the AGM. We would encourage all intending applicants to use the Spring Meeting as an opportunity to advertise their research to the wider IQUA community (and the Awards Committee!).

My thanks again to all contributors to this Newsletter.
Best regards,
Stephen McCarron, Dept. of Geography, NUIM, March 2010

2. IQUA Committee, 2009/10

The IQUA Committee, following the 2009 AGM is as follows:
President: Prof. Pete Coxon, TCD (continuing)
Secretary: Dr. Stephen McCarron, NUIM (continuing)
Treasurer: Mr Francis Ludlow TCD (elected)
Postgrad rep: Gayle Mc Glynn, TCD (continuing)
Website manager: Dr Robin Edwards, TCD. (continuing)
Publications Secretary: Dr. Stephen McCarron, NUIM (continuing)
Ordinary members: Donal Mullane (continuing), Dr Graeme Swindles (U. of Bradford) (continuing), Dr Bettini Steffani (elected).

Offers to stand as an Ordinary Member (3 yr post) at the upcoming AGM are welcomed by the Secretary. No other posts are open for election in 2010.

3. IQUA Spring Meeting and AGM 2010

A call for papers remains open for the 2010 IQUA Spring Meeting, hosted this year by the Dept. of Geography, Mary Immaculate College, U. of Limerick on Saturday, 27th March. More details on the venue location and submitting an abstract are available through the IQUA Meetings webpage. (http://www.tcd.ie/Geography/IQUA/Index.htm).

The Annual AGM will follow the Spring Meeting. The Secretary welcomes suggestions for Agenda Items up to 25th March, 2010.

The IQUA committee strongly encourages all members to attend the Spring Meeting and AGM, to show support and appreciation of the organiser's efforts and help plan out IQUA activity for the year ahead. Postgraduate members are particularly encouraged to use the opportunity to present their work to date or thesis findings and discuss it in a

friendly environment whilst building valuable network contacts.

4. IQUA 2010 Annual Fieldtrip and Symposium

Additional offers to help organise an IQUA Fieldtrip in Sept 2010 are welcomed by the IQUA Committee (through the Secretary) for discussion at the upcoming AGM.

Suggestions for an Autumn Symposium theme by potential convenors are also welcome (through the Secretary) for discussion at the AGM.

5. IQUA 2009 Autumn Symposium

Abstracts from IQUA Symposium 2009: Quaternary Genetics

Date: Friday 27 November 2009

Keynote Address:
Megafaunal extinction and megafaunal expansion: using ancient DNA to infer population responses to environmental change
Ian Barnes with contributions from Love Dalen, Meirav Meiri and Selina Brace
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Regional mammal faunas are generally recognised to be a critical element of biodiversity; often ecologically and economically important, they also serve as umbrella species for entire communities. Globally, and particularly in Europe, there is widespread concern about the long-term survival of many mammalian species. Around 15% of European species are threatened, and 27% are in decline (IUCN 2007). The situation is likely to become significantly worse over the next century, as climate-driven environmental change becomes increasingly important. In order to avoid extinction many mammal populations, and some whole species, will be forced to migrate into new regions.

The correct design of wildlife reserves and migration corridors is therefore a vital component of conservation strategy, requiring robust and accurate prediction of changes in the spatial patterning of biodiversity. At present, the most commonly used approach is to employ species distribution models (SDM's), which can be used to (i) identify where suitable habitats will occur under different climate change scenarios and (ii) predict if a species will be able to shift its distribution following these changes (Guisan and Thuiller 2005). Recent SDM-based forecasts (Thomas et al. 2004) predict high rates of extinction for the coming 100 years. However, such predictions are controversial, due largely to the uncertainties in how species respond to changes in habitat availability (Botkin et al. 2007). Central to this problem is the habitat tracking hypothesis (Eldredge 1989), which states that populations will respond to changes in habitat availability by altering their distributions accordingly; either through expansions, contractions or shifts in range. Although there is evidence that habitat tracking occurs during habitat expansions (Hewitt 1999, but see Valdiosera et al. 2007), recent analyses reject its general applicability for contractions and shifts in habitat availability (Dalén et al. 2007). When the factors determining species ability to track changes in habitat are so poorly understood, there is a fundamental limit on the accuracy of forecasting using SDM's.

We have recently initiated a project that explores the potential to use ancient DNA to infer the extent of habitat tracking in mammals, across the last 40 000 years of habitat change. By using ancient DNA, we are able to explore population movements, and extinctions, at a greater degree of resolution than traditional skeletal analyses would typically allow. In this presentation, I will review our aims for this project, and show some of the preliminary data we have generated thus far, which supports the notion that while habitat tracking does occur, it is likely under only certain conditions.

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L. Dalén et al., PNAS 104, 6726 (2007).

Ancient DNA analysis of brown bear (Ursus arctos): temporal and spatial phylogeography in Ireland.

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Little is known about the migration processes and mammalian population foundation events in Ireland – for example, did populations survive successive major and minor cold episodes in situ, or did repopulation occur throughout time? Are levels of genetic diversity consistent with substantial immigration across a major landbridge connection with Britain and the continent, or were the majority of mammals introduced, whether accidentally or deliberately, by man, from other locations?

One recurring pattern of recolonisation of Europe is best described by the phylogeography of the brown bear (Ursus arctos), where mitochondrial DNA analysis reveals distinct Western and Eastern lineages, originating from Iberian, Balkan and Caucasian refuges. In this well-studied species, modern data provide a valuable context in which to draw inference from ancient DNA results, and archaeological Irish bear specimens may be expected to give a valuable perspective of migration into peripheral Europe.

In this study, mtDNA and stable isotope data were analysed from a number of Pleistocene and Holocene Ursus arctos samples from Ireland, with the aim of answering specific questions about the survival of this large mammal through the Last Glacial Maximum and Younger Dryas (Glenavy and Nahanagan stadials respectively).

Skulls, teeth, and the spread of agriculture into Europe.

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Recent studies indicate that the spread of farming in Europe was a not a single event but rather involved a series of population movements and a wide range of dispersal processes such as demic diffusion, folk migration, frontier mobility, and leapfrog colonisation. Both genetic and palaeogenetic studies, which examine contemporary and past variations in the frequencies of various genetic markers have managed to provide a glimpse into this complex process. The analysis of cranial and dental metric data of Early Neolithic human populations from the Near East, Anatolia and Europe can provide new insights about the timing, nature and complexity of this process. This presentation reports results of studies of craniometric variations between and within Neolithic specimens and diachronic microveolutionary reduction processes in the size of the permanent dentition within and between pre-agricultural and agricultural populations. These results are then addressed in the broader context of the integration of human skeletal data with genetic and archaeological data.

Food fit for a mammoth? Teasing DNA out of dead plants - problems and prospects.

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The maintenance of genetic diversity during periods of rapid climate change and tree species range adjustment is a matter of current concern, as future ranges of many species are forecast to alter significantly this century. Inferences about the effects of Quaternary glaciations on present genetic structure have previously been drawn from genetic studies of present-day populations of plants and animals but analysis of ancient DNA (aDNA) has yielded snapshots of sequence variation from the past and is now contributing to conceptual advances in phylogeography and the legacy of Quaternary glaciations on the distribution of genetic diversity.

This paper will briefly review aspects of the development of plant aDNA research, which include examples from archaeobotanical material, permafrost and ice cores, sub-fossil wood, pollen, French wine barrels and plant macrofossils. The research field has lagged behind the study of animal aDNA owing to various technical difficulties, but appears to be now poised for take-off.

We present an ongoing study designed to assess the genetic contribution of so-called 'cryptic refugia' and long-distance founding events (LDFE) on the modern genetic structure of European beech (Fagus sylvatica). Cryptic refugia are sites where species survived the Last Glacial Maximum, but in

populations too small or dispersed to be detected using conventional palaeoecological analyses. Evidence for the existence of cryptic refugia is growing, based on both genetic inference and specialised palaeoecological data of high spatial resolution. Forests in high latitude regions became established during the Holocene following invasions from predominantly southern glacial refugia, together with local expansions of small tree populations that survived the Last Glacial Maximum in cryptic refugia. This predominantly southern origin of Holocene populations has contributed to the paradigm of "southern richness and northern purity", but processes such as LDFE in the early Holocene could potentially transfer genetic material from the major refugial populations far in advance of a broader spreading species front and contribute to northern diversity. LDFE are a means by which species can appear soon after deglaciation in formerly ice-covered regions and are a likely explanation for present genetic structure in Acer rubrum and Fagus grandifolia in the USA, where a significant proportion of total diversity is observed at high latitudes. A more complex picture of Holocene reforestation is now emerging that justifies a reassessment of the development of genetic structure at the continental scale.

Cryptic refugia and LDFE are likely to have contributed to modern genetic diversity, but the fate of specific alleles when a small population merges with an invading large population is complex and influenced by relative population size and breeding system. Analysis of aDNA, which until now has primarily been used for the study of phylogenetic relationships, extinct species and loss of genetic diversity, should be able to clarify the genetic contribution of small advanced populations to present genetic structure. A major aim of our current research is to discover the current genetic contribution of a recently discovered, small, advanced population of beech in Denmark that was separated from the main, southern population centre for at least 6000 years during the Holocene, but has left a clear palaeoecological record in a small, wet forest hollow.

Both cryptic refugia and LDFE have potential importance for the maintenance of genetic diversity away from larger glacial refugia, but they also have major implications for estimation of species dispersal rates. Past migration rates for trees ranging from hundreds to thousands of metres per year have been estimated from palaeoecological data. The validity of these migration rates has been questioned for two major reasons. Firstly, the incorporation of genetic studies has led to significant reinterpretation of palaeoecological data and almost exclusively led to a downscaling in how fast species spread since the start of the current interglacial period. Secondly, the ability of standard palaeoecological sites to record small, founding populations is in doubt. However, modern day observations of how fast a species can spread still do not match with estimates of spread derived from revised palaeoecological evidence; described as Reid's Paradox. The new evidence for LDFE and the availability of long time series of aDNA samples from beech in northern Europe invite questions about the contribution of small outlying populations to current genetic diversity, analysis of genetic exchange processes when large and small populations merge and study of local site adaptation processes at the millennial time scale.

European beech is a tree of considerable silvicultural, conservation and economic significance in Europe, whose genetic diversity based on current knowledge is not uniformly distributed throughout its range. As with several other plant and animal species, nuclear and organelle genetic diversity is concentrated in presumed glacial refuge areas or regions where mixing of different refugial lines occurred during the early Holocene. This asymmetric distribution of diversity is particularly marked in chloroplast haplotype diversity for beech and may pose difficulties for the species as extreme forecasts of future distribution do not include regions with high genetic diversity. The spread of beech from its glacial refugia has been documented using pollen and plant macrofossils and it spread northwards during the Holocene rather more slowly than other temperate deciduous trees. The earliest dated presence and presumed immigration of beech in Denmark was previously dated to 1500 BC and it gradually became a dominant tree in subsequent millennia. The recent discovery of palaeoecological evidence of a continuous, small beech population that became established 9000 years ago is exciting evidence for a LDFE. A similar LDFE population has also been provisionally identified from southern England and there is emerging evidence for another population in S. Sweden. Ancient beech DNA has already been recovered and positively identified as beech from another pristine Danish beech forest and from north-western Italy, close to glacial refuge areas, although conclusions are tentative owing to some contamination in control samples. Refinement of laboratory protocols and use of highly specific beech primers designed from the recently fully sequenced beech chloroplast genome should soon allow us to assess the genetic contribution of an LDFE to current genetic diversity.

Genomic analyses of a British Mesolithic aurochs (Bos primigenius) using conventional and second-generation DNA sequencing technologies.

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Archaezoological investigations have confirmed the now extinct aurochs (Bos primigenius)—a large, formidable ox that ranged throughout much of Eurasia during the late Pleistocene—as the wild ancestor of modern domesticated cattle. Although these studies point towards the Near East as being the primary centre of domestication for modern European B. taurus, the wide geographical range of the aurochs has prompted suggestions for the existence of a secondary domestication centre within Europe. More recently, surveys of partial mitochondrial DNA (mtDNA) control region sequences generated from modern B. taurus and European aurochs samples have supported a Near Eastern origin for European B. taurus with little or no genetic contributions from local aurochsen populations. Here, we present DNA sequence analysis of a complete mtDNA genome generated from an exceptionally well-preserved Palaeolithic British aurochs sample. These mtDNA sequence data were generated using both conventional Sanger-sequencing methodology and a next-generation sequencing approach (Illumina® Genome Analyzer). This B. primigenius mtDNA sequence can be used to assess pre- and post-domestic patterns of genetic variation of a major domestic livestock species and will add a novel layer of genetic information regarding the ancestry of European B. taurus. In addition, these results signpost future efforts to determine the complete genome sequence of a wild ancestor of domestic cattle.

Fossil evidence, phylogeography and conservation planning.

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Ireland has a depauperate vascular plant flora, with around 950 species generally considered to be native. Despite this, there is considerable biogeographic interest in the flora of Ireland, especially in the hyperoceanic or Atlantic elements. Several plant species are restricted to the extreme western part of Europe, most notably the so-called 'Lusitanian' element which occurs in western Ireland, the western part of the Iberian peninsula, and in same cases the extreme western parts of France and England. Good examples of species with these distributions may be found in a number of members of the Ericaceae, including Daboecia cantabrica and Erica mackaiana.

Some authors have suggested that some of these taxa have been deliberately or accidentally introduced into Ireland by humans. For example, the lack of fossil pollen records for Erica erigena before the middle ages has been cited as evidence of its relatively recent introduction to Ireland, elsewhere the species is scattered in several parts of the Iberian peninsula. However, fossil evidence for several Atlantic species goes back to the mid-Pleistocene 'Gortian' deposits. Though these are now considered to represent several distinct interglacial periods, these fossils generally indicate the presence of these taxa in Irish interglacials. This is especially true of macrofossils, but not always true of fossil pollen. For example, while macrofossils of Daboecia leaves clearly indicate the presence of this taxon as there is no closely related species (aside from D. azorica), for E. mackaiana the evidence is less clear. Erica mackaiana is very similar to the closely related E. tetralix; though there are slight differences in leaf morphology, the presence of ovaries are required to conclusively prove which of the two species occur. Identification of pollen at species level in the genus Erica is very difficult, and with pollen there is always a greater possibility of reworking pollen through sediments.

There is clear evidence that several Atlantic taxa have been recovered from Irish interglacial material, however this evidence does not of course indicate that these species have been present in Ireland continuously since the mid Pleistocene. They may of course have repeatedly colonised following extinction in full glacial periods, or, more tantalisingly, they may have persisted in small refugia within or proximal to Ireland. No fossil evidence is currently available to indicate the presence of such refugia.

Suggestions that rare Irish plants have been introduced by human agency are not restricted to Atlantic species; similar charges have been levelled at other threatened species, including amphi-Atlantic species (whose distribution spans the Atlantic) and other rare taxa. No fossil evidence is available for many of these taxa, yet determination of their biogeographic origins, and in particular whether or not they have been introduced, is essential if scarce resources are justified in being directed at the conservation of these species.

What is ideally required is some form of corroborating evidence, and fortunately this has become available with the widespread use of molecular techniques. These techniques enable historical relationships among populations to be uncovered: the study of phylogeography. Molecular techniques also allow the testing of several hypotheses regarding possible relatively recent introductions to Ireland. Such introductions would be expected to show little divergence between introduced and potential source populations, because relatively little time will have elapsed to facilitate genetic divergence. Introduced populations would also be expected to have a greatly reduced genetic diversity compared with a native population, because in general a small number of founding genotypes are likely to be introduced.

We have looked at molecular genetic variation in several species to try and elucidate their phylogeography, and to determine the genetic diversity within and divergence between populations. Amplified Fragment Length Polymorphism is a useful and reliable technique to examine genetic diversity in taxa whose genetic make up is rather poorly known. The technique generally reveals numerous markers scattered throughout the genome, and individuals can be scored for the presence/absence of particular markers. Individuals that share a high proportion of the scored markers are likely to be genetically similar, whereas those that share relatively few of these markers are more genetically distinct.

We found that genetic diversity in Daboecia cantabrica was comparable in Irish, French and Spanish populations, moreover the Irish individuals were all genetically distinct from those sampled from French and Spanish populations. This indicates that the Irish material has been genetically isolated from the continental populations for some considerable time, and is very unlikely to be introduced. One drawback of AFLP is that it is difficult to apply molecular clock techniques to the data – more precise markers (DNA sequences, microsatellites) are required. For Erica mackaiana, we again determined a large amount of variation in Irish material, though this was nested within Spanish populations. This may suggest a more recent divergence of Irish E. mackaiana from the continental populations, however two additional factors need to be considered here. Firstly, E. mackaiana rarely sets seed in Ireland; though this may not always have been the case, reduced rates of sexual reproduction would likely reduce the genetic divergence of isolated Irish populations. Additionally, E. mackaiana hybridises freely with the more widespread E. tetralix in Ireland, and this may further cloud the phylogeographic signal. More molecular work needs to be undertaken on these species to estimate an approximate divergence date (Daboecia) and to determine the impact of hybridisation (Erica).

We also looked at the genetic variation in Colchicum autumnale, a species considered to have been introduced to Ireland for medicinal reasons. No fossil evidence for Colchicum has been discovered in Ireland, but AFLP showed Irish and British populations to contain large amounts of genetic variation, suggesting the species is unlikely to have been introduced. Furthermore, the Irish and British populations were genetically closest to populations from north-west Spain, very distinct from those found in France and in the Spanish Pyrenees. This suggests colonisation of Ireland by a western route, and this has also been shown for Irish Quercus, Juniperus communis and Hedera helix. These data indicate the close, natural biogeographic links between the Iberian peninsula and Ireland, and suggest that for at least Daboecia and Colchicum, these are native Irish species worthy of conservation effort.

Finally, perhaps the greatest advantage can be gained from the combination of detailed palaeoecology data and molecular phylogeography. Pine (Pinus sylvestris) is widely regarded as

becoming extinct in Ireland by the middle ages, based on abundant Holocene fossil records. New data however suggests that isolated popluations of pine may have persisted in the periphery of the Burren, fossil pollen does not show any marked decline with time at one site. This raises the possibility of Irish native pine persisting, and this would be of great conservation and landscape importance. Hypotheses about the genetic distinction of possible native Irish pine populations, and the ensuing genetic bottleneck that must have resulted following its widespread if not complete extirpation in Ireland, urgently require testing.

6. Quaternary Research News

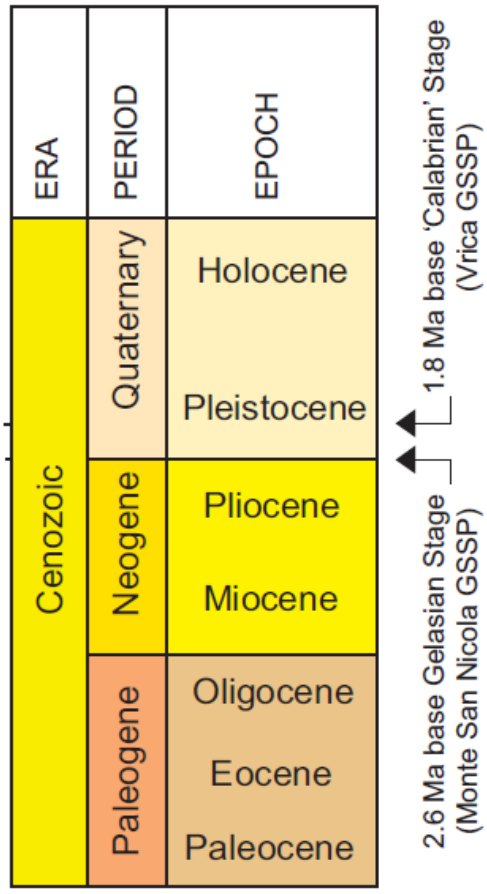
Formal ratification of the Quaternary

After a period of extensive debate and controversy, the status of the Quaternary was finally resolved in June 2009, when the International Union of Geological Sciences (IUGS) formally ratified the proposal presented by the International Commission on Stratigraphy. This confirms the status of the Quaternary as a full system/period as shown in the timescale pictured below (from Gibbard et al., 2009), The Quaternary now extends back to 2.58 Ma, which corresponds to marine oxygen isotope stage 103.

In this new scheme, the base of the Quaternary System/Period, the Pleistocene Series/Epoch, and the Gelasian Stage/Age all share the same Global Stratotype Section and Point (GSSP) which is located at Monte San Nicola in Sicily. The GSSP at Vrica in southern Italy, which was formerly used as the base of the Pleistocene, will be proposed as the base of the 'Calabrian Stage' (the new second stage of the Pleistocene Epoch) is a future submission to the IUGS. The Holocene is retained as a distinct series/epoch with its base defined by the GSSP recently established in the NGRIP ice core (Walker et al., 2009) and dated to 11 700 calendar yr b2 k (before AD 2000).

Further details concerning the ratification of the Quaternary, including the proposed stage names of the Pleistocene, are available in Gibbard et al. (2009).

R. J. Edwards, TCD, Feb. 2010.



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7. Notices

Establishment of the Irish Environmental History Network, October 2009

Francis Ludlow, Research Fellow, Trinity Long Room Hub.

The Irish Environmental History Network is hosted by the Trinity Long Room Hub, Trinity College's

Humanities Research Institute (www.tcd.ie/longroomhub), which aims to facilitate multidisciplinary initiatives like the Network. The primary goal of the Network is the provision of a point of contact for researchers working on areas and themes relevant to Irish environmental history. A related goal of the Network, and the Network website in particular, is to help in bringing relevant work on aspects of Irish environmental history to the attention of researchers working in related disciplines and the general public.
The definition of environmental history adopted by the Network is extremely broad, and therefore so is the remit of the Network. Work in any discipline employing any method (e.g. scientific, archaeological, historic, literary) that examines how humanity has studied, perceived, managed and influenced the natural environment, and been influenced in return by the environment, in any period of the past, is considered relevant to the concerns of Irish environmental history. Under natural environment is included all aspects of the natural world, oceans and landscape.

A recent audit identified nearly 120 researchers engaged in work highly relevant to the concerns of Irish environmental history, drawn from disciplines as diverse as the study of written literature representing)how authors in the past represented and perceived the natural world) to those studying how aspects of the environment impacted upon the health of people in the past. More than 400 further researchers where identified for whom the concerns of environmental history would be directly relevant, including, for example, those researching issues of contemporary natural resource management in Ireland that might benefit from an historic perspective into the utilisation and management of these resources.
The Network has the potential to involve significant numbers of individuals in disciplines such as archaeology, botany, zoology, ecology, engineering, the physical sciences, anthropology, sociology, geography, economics, history, architecture, English and Irish literature, art and media studies, amongst others. The main content of the Network website (see link below) are brief profiles of members. News of events of interest to Irish environmental history and a growing collection of links to websites and resources of relevance are also provided.

The Network is open to and welcomes all persons with research interests falling under the broad definition given above.

Further details can be requested from Francis Ludlow at ludlowf@tcd.ie.
Network website:
http://www.tcd.ie/longroomhub/iehn/

8. Recent PhD completions

The vegetation ecology and native status of Scots pine (*P. sylvestris* L.) in Ireland

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This PhD study examined the vegetation ecology, native status and biodiversity value of Scots pine (*Pinus sylvestris* L.) in Ireland, using a variety of biogeographical, palaeoecological and ecological approaches at different spatial and temporal scales. *P. sylvestris* is known to have colonised Ireland relatively early in the postglacial, becoming an important component of certain marginal habitats before undergoing a dramatic decline (Bradshaw & Browne, 1987). The species is widely believed to have been extirpated during the early medieval period (McAulay & Watts, 1961) but had been reintroduced by the eighteenth century (Pococke, 1891). It is currently widespread and naturalising in semi-natural habitats. Ireland's Native Woodland Scheme provides financial incentives for the planting of native trees of local provenance (Forest Service, 2001). Despite its uncertain native status, *P. sylvestris* has been included in this scheme and is being widely planted in semi-natural habitats. Few studies have addressed the autecology and vegetation ecology of the species in the Irish context. Information on its native status, ecological requirements and biodiversity value is urgently required to inform conservation and forest management strategies.

A database of site attributes and *Pinus* pollen frequencies from 84 palynological sampling sites throughout Ireland was compiled and added to a Geographic Information System. Isopoll maps were prepared at 500 year intervals in order to illustrate the dynamics of *Pinus* in Ireland throughout the Holocene. Spearman's rank correlation coefficients for mean *Pinus* pollen frequencies and site attributes were calculated for each time interval. The arrival, expansion, decline and reintroduction of *Pinus* were clearly illustrated by the isopoll maps. *Pinus* pollen frequencies were significantly correlated with altitude and location during various

periods of the Holocene. These results generally supported previously described patterns. However, the isopoll maps suggested that high *Pinus* pollen frequencies persisted in localised areas of western Ireland during the period when *Pinus* was thought to be extinct in Ireland.

The vegetation history of an apparently naturalised pinewood in the Burren over the last 2000 years was examined, with particular reference to the *Pinus* decline. A relatively stable vegetation history was recorded, despite considerable human activity. The dominant vegetation type was an open pinewood with abundant *Corylus*. Remarkably, no *Pinus* decline was recorded. *Pinus* pollen frequencies consistently exceeded 38% and macrofossil evidence demonstrated the local presence of *Pinus* at about AD 840. This indicated that a relict population of *P. sylvestris* has persisted in the Burren to the present day.

Botanical surveys were conducted in 20 *P. sylvestris* woodland plots in Ireland and seven in the Scottish Highlands. Vegetation, structural and environmental data were analysed using non-parametric and multivariate statistical techniques and synoptic tables were prepared. In the Irish context, *P. sylvestris* was found to tolerate a wide range of environmental conditions. Soil pH, altitude and slope had important roles in partitioning four reasonably well defined vegetation communities, some of which corresponded to habitats of international conservation importance. Irish pinewoods were found to form an important resource for the conservation of native botanical and habitat diversity (Roche *et al.*, 2009). The Irish plots were compared quantitatively with native pinewoods of high biological quality in Scotland and qualitatively with native pinewood types in continental Europe. The species composition of each Irish pinewood type was found to correspond, to a greater or lesser extent, to that of its native counterparts.

P. sylvestris is well established and naturalising in Ireland and pinewoods are a common feature in the Irish landscape, although they are fragmented and limited in extent compared to their former range. Despite their reintroduced status, Irish pinewoods were found to function as native ecosystems. For practical conservation purposes, the species should therefore be managed as a native species in woodland habitats in Ireland. With its forestry potential, capacity to support native biodiversity and apparently native status, *P. sylvestris* has the potential to make a significant positive contribution to biodiversity conservation and sustainable forest management in Ireland.

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9. New Research projects

RIDGES : investigating glacial landscapes in the Irish-UK Celtic Sea

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S. McCarron, NUI Maynooth.
M. Stoker, BGS, Edinburgh.

The Irish-UK Celtic Sea was the target of an International Polar Year campaign in August 2009, of the Italian research vessel OGS Explora. The campaign was undertaken in the context of the IPY project GLAMAR (GLAcial Meltwater and continental MARgins, P.I. D. Praeg), led by the Italian National Institute OGS, in collaboration with partners from Ireland (INFOMAR, NUI Maynooth, UCD) and Britain (BGS, NOCS).

The objective of the GLAMAR campaign was to investigate a vast system of seabed ridges in the Celtic Sea, currently interpreted as tidal sand ridges formed by reworking of glacial outwash during post-glacial marine transgression. The GLAMAR campaign considered an alternative hypothesis: that the ridges are glaciofluvial features, formed by meltwater drainage beneath an ice sheet much more extensive than previously thought. The 3 week geophysical campaign examined the ridges along c. 100 km of the mid-shelf Irish-UK borderline, acquiring the first multibeam seabed imagery (c. 2500 km^2 area), as well as Chirp and sparker profiles (c. 4200 km and 750 km, respectively) that provide stratigraphic ties to BGS vibrocores containing subglacial tills.

Preliminary results confirm the ridges are overlain by till and show them to be associated with transverse ribs, interpreted as subglacial landforms that extend at least 65 km SW of the limit of sampled tills. These results support the hypothesised glaciofluvial origin of the ridges and raise the question of how far seaward subglacial bedforms extend. The submerged glacial landscape of the Celtic Sea is now being examined by the INFOMAR funded project RIDGES, a collaboration led by Maynooth, OGS and BGS.

For more information:
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10. Forthcoming Talks, Workshops Seminars & Conferences

Carbon Capture and Storage: Bridging the Transition from Fossil Fuels to Renewables: Conference and Public Debate.

Dublin Castle Conference Centre
11-12 March 2010

This conference will review recent international research and developments in carbon capture and storage (CCS), while at the same time providing a forum to assess technical and investment opportunities in Ireland and Northern Ireland. It will be an important occasion for communicating the benefits and impacts of implementing CCS.

The conference will be of vital interest to those who are involved in CCS developments, including government departments, local authorities, state agencies, energy companies, the research and environmental communities and the general public.

Fees and Registration:

- €100 – Academic Registrants (Registrants from a recognised Third Level Academic Institute in Ireland and Northern Ireland may register up to two postgraduate students free of charge for the conference. Names and contact details to be emailed to ccs@ria.ie)
- €100 – early registration
- €100 – concessions (students and unwaged)
- €150 – standard registrations

To register, please visit www.ria.ie

This conference is supported by the Royal Irish Academy, Geological Survey of Ireland, Geological Survey of Northern Ireland, Shell Ireland, and ESB

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Prices are the same as for those joining/renewing by post, namely, €15 Waged or €10 for students/unwaged per year.

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http://www.tcd.ie/Geography/IQUA/Member/Mem_Home.htm

Francis Ludlow, TCD.

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S. McCarron, IQUA-L Moderator

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