



Programme and Abstracts



General Information

Registration will begin at 10 am on Tuesday morning in the Canada Room.

Talks will take place Council Chamber on Tuesday afternoon, Wednesday morning and Thursday morning, and will each be 15 minutes long with a few minutes of questions afterwards. Speakers are asked to load their talks before the session starts.

Lunch and tea / coffee breaks will be held in the Canada Room each day.

The **Poster Session** and **Wine Reception** will be held in the Canada Room on Tuesday evening, starting at 1715. Posters should be put up on the boards as soon as possible after arrival and be removed first thing on Thursday morning.

Dinner on Tuesday night will be in Deane's at Queen's, following the Poster Session.

The **EGG-Heads Pub Quiz** will be held upstairs in the Parlour Bar, following dinner.

The **Field Trip to Glenariff** will take place on Wednesday afternoon. The bus will leave from outside the Lanyon Building at 1300. We will aim to be back by 1715. Remember to bring suitable footwear and clothing.

The **Conference Dinner** will be held on Wednesday evening in the Great Hall, which is on the ground floor of the Lanyon Building (venue for the talks), preceded by a **Wine Reception** at 1845.

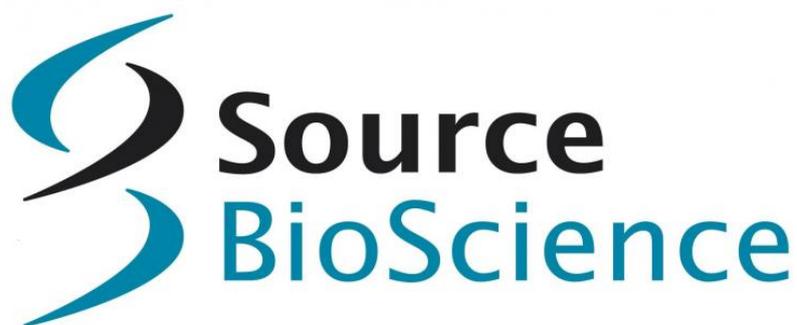
The **Ceili** will be held upstairs in the Parlour Bar, following the Conference Dinner.

Sponsors

We are extremely grateful to all our sponsors



British Ecological Society



Tuesday 2nd April

- 1300-1310 **Jim Provan**
Welcome / introduction / housekeeping
- 1310-1400 **Laurent Excoffier (University of Berne)**
Evolution of genetic diversity in neutral and functional regions during range expansions
- Session: Changes in ranges (Chair: Jim Provan)
- 1400-1420 **Ian Montgomery (Queen's University Belfast)**
Landscape genetics during species replacement: individual genotypes in an invaded population
- 1420-1440 **Colin Kelleher (National Botanic Gardens of Ireland)**
Saxifrages on the edge – was Ireland a refuge for arctic species during past glacial advances?
- 1440-1500 Tea / coffee break
- Session: Genetics of fragmented populations (Chair: Kirsten Wolff)
- 1500-1520 **Amanda Wilson (James Hutton Institute)**
How does population substructure of a common agricultural species change throughout the growing season?
- 1520-1540 **Charlie Long (Aberystwyth University)**
Decoding the mystery and history of the Spreading bellflower
- 1540-1600 **Sammy Logan (Newcastle University)**
Molecular ecology of lime (*Tilia*) populations
- 1600-1620 **Kate Johnson (Queen's University Belfast)**
Lack of genetic structure in fragmented populations of the Monkey-puzzle tree (*Araucaria araucana*)
- 1620-1640 **Jim Provan (Queen's University Belfast)**
Retrospective genetic monitoring of the threatened Yellow marsh saxifrage (*Saxifraga hirculus*) reveals genetic erosion but provides valuable insights for conservation strategies
- 1715-1830 **Wine Reception and Poster Session (Canada Room)**
- 1845 **Dinner (Deane's at Queen's)**
- 2100 **EGG-Heads Pub Quiz (Upstairs in The Parlour Bar)**
followed by
Jimbo's Eighties Electronic Experience Disco

Wednesday 3rd April

0915 **Jim Provan**
Housekeeping etc.

Session: Adaptation and divergence (Chair: John Warren)

0920-0940 **Mark Ravinet (Queen's University Belfast)**
On Irish sticklebacks: adaptive divergence and ecological speciation in Irish waterbodies

0940-1000 **Kevin Donnelly (University of Edinburgh)**
Exposing adaptive differentiation in ancient Scottish pinewoods (*Pinus sylvestris* L.) via the controlled application of water-stress

1000-1020 **Henry Creissen (John Innes Centre)**
Downy but not out: Using genetic mixtures to improve yield stability under disease pressure

1020-1040 Tea / coffee break

Session: NGS and bioinformatic tools (Chair: Richard Ennos)

1040-1100 **Kevin Keenan (Queen's University Belfast)**
diveRsity: An R package for the estimation and exploration of population genetics parameters and their associated errors

1100-1120 **Caroline Meharg (Queen's University Belfast)**
De novo transcriptome assembly and RNAseq of a *Holcus lanatus* L. population exhibiting a balanced polymorphism for arsenate tolerance: differential regulation of transcripts by phosphorus nutrition and phenotype

1120-1200 **Alex Twyford (Syracuse University)**
Next generation sequencing and population genomics

1200 Lunch

1300 **Field trip to Glenariff Glen**

1815 **Business meeting (The Parlour Bar)**

1845 **Wine reception (Great Hall)**

1900 **Conference dinner (Great Hall)**

2100 **Ceili (Upstairs in The Parlour Bar)**

Thursday 4th April

- 0915 **Jim Provan**
Housekeeping etc.
- Session: Biodiversity and policy (Chair: Natasha de Vere)
- 0920-0940 **Katie Frith (University of Durham)**
Incorporating genetics into conservation practice: presenting a web-based tool designed to aid conservation practitioners and policy makers in planning genetic studies of conservation relevance
- 0940-1000 **Sarah Al-Beidh (Royal Horticultural Society)**
Plants for bugs: Investigating the influence of plant provenance on garden biodiversity
- Session: Phylogeny and species delimitation (Chair: Natasha de Vere)
- 1000-1020 **Paul Ashton (Edge Hill University)**
Comparing DNA based and leaf anatomy based phylogenies in *Carex*
- 1020-1040 **Nick Levsen (Newcastle University)**
Diversification and geographic progression in *Populus* (Salicaceae)
- 1040-1100 **Tracey Hamston (University of Exeter)**
What are the ecological threats to the sustainability of *Sorbus* diversity?
- 1100-1120 Tea / Coffee break
- Session: Hybridization (and John) (Chair: Paul Ashton)
- 1120-1140 **Richard Ennos (University of Edinburgh)**
Patterns of mating, generation of diversity, and fitness of offspring in a *Geum* hybrid swarm
- 1140-1200 **Stuart Desjardains (University of Leicester)**
The evidence for *Fallopia x Muehlenbeckia* hybrids occurring in New Zealand
- 1200-1220 **Huw Jones (NIAB)**
A strategy for exploiting exotic germplasm using genetic, morphological ecological and environmental diversity: the *Aegilops tauschii* Coss. example
- 1220-12?? **John Warren (Aberystwyth University)**
Shake that Aspen!
- 1245ish Summary / Prizes / Photograph
- 1300 Lunch and Goodbye!

Talk Abstracts

Keynote talk

Evolution of genetic diversity in neutral and functional regions during range expansions

Laurent Excoffier and Stephan Peischl

CMPG, Institute of Ecology and Evolution, University of Berne

Most species have gone through recent or older range expansion since their origins. These spatial expansions have been shown to deeply affect patterns of neutral diversity, potentially leading to signatures that mimic positive selection. However, the effect of range expansion on functional regions where beneficial and deleterious mutations co-segregate has been little studied, and the evolution of individual fitness during such expansions is basically unknown. We present here results from individual-based simulations along a linear and uniform habitat, complemented with analytical approximations, for the evolution of mean fitness at the edge of the expansion. We find that deleterious mutations steadily accumulate on the wave front during range expansions thus creating an *expansion load*. This load is mainly due to the inefficiency of selection on the wave front. However, expansion load is not restricted to the wave front but may occur and persist for a long time over a large proportion of newly colonized habitats. Interestingly, a qualitatively similar phenomenon occurs during 2-dimensional expansions, and the evolution of fitness is still well approximated by 1D predictions. We finally present evidence that expansion load should have occurred during recent human expansions.

Session: Changes in ranges

Landscape genetics during species replacement: individual genotypes in an invaded population

Elodie Modave¹, Neil Reid², Ian Montgomery³ and Paulo Prodöhl³

¹ *University of Liege*

² *Quercus, School of Biological Sciences, Queen's University Belfast*

³ *School of Biological Sciences, Queen's University Belfast*

The bank vole in Ireland has spread over 85 years decreasing the numbers of the indigenous wood mouse. A second AIS the greater white toothed shrew is also present in the same but more limited part of the island, creating a unique opportunity to evaluate cumulative effects of AIS on population genetic diversity and structure of an invaded population. We test the hypotheses that: (1) genetic diversity decreases with population size of wood mouse due to presence of bank vole; (2) genetic diversity in mice decreases with the length of time bank vole has been present; and (3) population genetic structure in mice is associated with landscape features and presence of AIS. Mice were typed for 9 polymorphic microsatellite loci. Sampling bias was removed by regression before landscape genetic analyses. Genetic diversity was a positively correlated with environmental richness and negatively correlated with a fragmented landscape and distance from the point of introduction of the invader. More genetically diverse mice were found where both AIS were present. No association was apparent between the geographic distribution of the samples and genetic clustering. Samples deviated from the Hardy-Weinberg equilibrium for three microsatellite *loci* suggesting presence of sub-structuring. Our results are inconsistent with hypotheses 1 and 2, and consistent with hypothesis 3 suggesting that the impact of AIS on population density of mice is associated with the survival of more genetically diverse mice.

Saxifrages on the edge – was Ireland a refuge for arctic species during past glacial advances?

Colin T. Kelleher and Evelyn Gallagher

DBN Herbarium and Plant Molecular Laboratory, National Botanic Gardens of Ireland Dublin

The arctic-alpine element of the Irish flora accounts for approximately 2% of the entire flora. Ever since the initial description of the arctic-alpine flora there has always been debate as to the possible origins of these populations. However, recent studies on certain species are revealing that these small populations in Ireland are proving important in our understanding of the phylogeography of arctic-alpine plants. We are studying a group of arctic-alpine *Saxifraga* species to try to understand their presence and restricted distribution in Ireland. One site in Ben Bulbin, Co. Sligo holds a diverse array of Ireland's arctic-alpine flora and is the only site in Ireland for *Saxifraga nivalis*. *S. nivalis*, although a rarity in Ireland is common throughout its circumpolar range. Samples of *S. nivalis* were sampled at this site and gathered throughout most of its range. A set of 24 cpDNA regions were screened for variation in a variety of *Saxifraga* species to reveal species-specific variation. Out of the 24 regions screened for *Saxifraga nivalis* only 2 showed population level variation. The initial findings show a very limited genetic diversity within the populations, with most populations being fixed for a single haplotype. However, the pattern of this distribution reveals a potential refugial population in Ireland and a concentration of diversity in the Nordic countries, including Britain and Ireland.

Session: Genetics of fragmented populations

How does population substructure of a common agricultural species change throughout the growing season?

Amanda Wilson, Brian Boag, Gaynor Malloch, Steve Hubbard, Brian Fenton and Graham Begg

The James Hutton Institute, Invergowrie, Dundee

With large proportions of the earth's surface now devoted to agriculture, it is important to consider how food production affects wildlife populations. There has been some effort to investigate how agriculture affects the spatial distribution of wildlife within agricultural habitat but there has been much less effort to determine how the instability of the agricultural system drives temporal changes in spatial distribution. With this in mind, we asked how populations of a species common to agricultural habitat changed throughout the year. The wood mouse is found throughout Europe and the scale at which individuals ordinarily move around makes it a practical species to use to investigate population structure changes. We considered wood mouse population structure pre-harvest and post-harvest on a 42 hectare study plot to the west of Dundee in Scotland. Using nine microsatellite markers we investigated population substructure and how this varied with agricultural season. We hypothesise that the observed breakdown of population substructure may be driven by agricultural disturbance.

Decoding the mystery and history of the Spreading bellflower.

Charlie E. Long^{1,2}, Laura Jones², Katie Cleary², Joël Allainguillaume³, Matt J. Hegarty¹, Wayne Powell¹ and Natasha de Vere^{1,2}

¹ *IBERS, Aberystwyth University*

² *National Botanic Garden of Wales*

³ *Department of Applied Sciences, University of the West of England*

Habitat loss frequently results in small populations, which are subject to reduced genetic diversity and risk inbreeding depression. Do fragmented populations show a meta-population structure? How are they connected and what affects their gene flow? The spreading bellflower (*Campanula patula* subsp. *patula* L.), an elusive species native to hedgebanks and woodland borders in the UK, is the perfect example to investigate these questions. In recent years its abundance has dramatically declined to an

endangered status; it is of high conservation importance yet its ecology is largely unknown. Here we place the genetic diversity of remaining *C. patula* plants in time and space. Initial comparisons between extant individuals and specimens from UK and European herbaria indicate decreased genetic diversity over 177 years, using microsatellite loci designed for *C. patula* for the project. These initial data also suggest our *C. patula* are polyploid, contrary to previous assumptions of diploidy, which will significantly contribute to our understanding of the species' ecology. We aim to combine further microsatellite coverage with SNP loci genotyped using restriction-associated DNA (RAD) sequencing to assess the genetic structure of today's individuals and their reproductive connectivity, on a scale at which management can be considered.

Molecular ecology of lime (*Tilia*) populations

Samuel A. Logan and Kirsten Wolff

School of Biology, Newcastle University

Tilia (lime trees) are widely distributed throughout Europe. Two species are found in the UK, *Tilia cordata* Mill. (Small-leaved lime), and *T. platyphyllos* Scop. (Broad-leaved lime). *Tilia x europaea* L. (Common lime), is the naturally occurring hybrid of the two. Natural occurring limes in the UK are fragmented and may be remnants of ancient populations, many of which remain as old coppice stools. These individuals may harbour genetic variation many thousands of years old. Little, if any, natural regeneration has occurred within populations, particularly in the north of their UK range. Thirteen microsatellite markers were used to determine; (1) the genetic diversity of ten ancient UK populations of *T. cordata*, and three populations of *T. platyphyllos*; (2) the genetic structure of four lime woods at lower UK latitudes; (3) the cultivar types of *T x europaea* used at different times since the 17th Century across three ancient lime avenues in Oxfordshire. Initial results show less genetic variation in UK populations compared to their European counterparts. There is evidence of clonal structuring within northern populations. Lime woodlands at lower UK latitudes are mixed consisting of the two species, *T. cordata*, & *T. platyphyllos*, as well as the hybrid *T. x europaea*. The outcome of this study will have a multi-discipline utility, benefiting various areas of research, conservation, and general interest.

Lack of genetic structure in fragmented populations of the Monkey-puzzle tree (*Araucaria araucana*)

Kate Johnson

School of Geography, Archaeology and Palaeoecology, Queen's University Belfast

Araucaria araucana (the Pehuén or Monkey Puzzle tree) is a protected species in southern South America. The modern day distribution lies across central Argentina and Chile (ca. 37 - 42° S) but is fragmented, with isolated patches occurring up to 70 km from other *A. araucana* forests. Despite its significant cultural and economic significance, the species is currently under threat from human pressures, such as clearance, overgrazing and the introduction of exotic conifers. A phylogeographic / population genetic analysis of the modern day distribution was conducted on around 150 samples of fresh and herbarium needles, using chloroplast, nuclear and mitochondrial DNA. A palaeoecological study was carried out on a short sediment core from Laguna Villa Pehuenia, Neuquén, Argentina to establish the environmental history of the region. The results of this highlight that *A. araucana* has been present in the region throughout the last 3,000 years. Microsatellite analysis revealed four genetic clusters, but no geographical structuring of these groups. The results are in agreement with those from palaeodistribution models, which suggest that *A. araucana* persisted through the Last Glacial Maximum in a single coastal refugium.

Retrospective genetic monitoring of the threatened Yellow marsh saxifrage (*Saxifraga hirculus*) reveals genetic erosion but provides valuable insights for conservation strategies

Jim Provan¹, Gemma E. Beatty¹ and Neil Reid²

¹ *School of Biological Sciences, Queen's University Belfast*

² *Quercus, School of Biological Sciences, Queen's University Belfast*

Knowledge of levels and patterns of intraspecific genetic diversity represents a fundamental aspect of modern conservation biology. Using retrospective genetic monitoring, where the genetic diversity of extant populations is compared directly with data obtained from historical samples, valuable, and often unique, insights into evolutionary processes can be obtained that can inform conservation programmes. In the present study, we compared the genetic diversity of all extant populations of the threatened plant species *Saxifraga hirculus* in Ireland with levels and patterns observed in historical samples from herbarium collections. The most threatened population, which currently numbers only 13 individuals, exhibited greatly reduced genetic diversity compared to historical samples as a result of both lineage replacement via genetic drift and population extinction. As the currently dominant genetic lineage in this population is very rare elsewhere, care needs to be taken when formulating any potential reintroduction programme. Species distribution modelling suggested that habitat at one site where the species is extinct may also be suitable for reintroduction. Our findings highlight both the need for genetic monitoring of threatened populations, but also for its swift implementation before levels of diversity become critically low.

Session: Adaptation and divergence

On Irish sticklebacks: adaptive divergence and ecological speciation in Irish waterbodies

Mark Ravinet^{1,2} Chris Harrod^{1,3} and Paulo Prodöhl¹

¹ *School of Biological Sciences, Queen's University Belfast*

² *Ecological Genetics Laboratory, National Institute of Genetics, Mishima, Japan*

³ *Facultad de Recursos del Mar, Instituto de Investigaciones Oceanológicas, Universidad Antofagasta*

Over the last two decades, the three-spined stickleback (*Gasterosteus aculeatus* L.) has become a 'supermodel' species for studying adaptation and speciation. Characterised by repeated, independent colonisation of freshwater environments from ancestral marine populations, the stickleback species complex has evolved remarkable phenotypic and genomic diversity. Situated at the western fringe of Northern Europe, Ireland likely represents one of the first landmasses recolonised from the Atlantic Ocean following major deglaciation. Furthermore, as a species-poor post-glacial landscape with a high density of waterbodies, Ireland represents a region of considerable interest for research on sticklebacks. Here we present a summary of our work using ecological and genetic approaches to examine diversity and divergence in Irish stickleback populations. We demonstrate that Ireland likely contains three distinct evolutionary lineages of sticklebacks. Our results also show a strong role for parallel selection driving habitat-specific adaptation at both regional and catchment scales. Adaptive divergence is also apparent within Irish systems where ecological divergence is strongly positively correlated with neutral genetic differentiation. Finally, we suggest that a novel catchment topography in Western Ireland may have led to three reproductively isolated forms occurring in sympatry in a single system.

Exposing adaptive differentiation in ancient Scottish pinewoods (*Pinus sylvestris* L.) via the controlled application of water-stress

Kevin Donnelly¹, Stephen Cavers², Joan Cottrell³ and Richard Ennos¹

¹ *Institute of Evolutionary Biology, University of Edinburgh*

² *Centre for Ecology and Hydrology, Edinburgh*

³ *Centre for Human and Ecological Sciences, Forest Research*

The Scottish Highlands represent a small, but climatically diverse geographical area, and native pinewoods are found on sites with marked variation in altitude, seasonal precipitation, and soil drainage. We wish to determine whether native pinewood fragments are locally adapted to their environments, as the discovery of adaptive variation will benefit forest management and conservation policy, particularly in the midst of ongoing climate change. Presently, we are evaluating possible adaptive differentiation between native populations in response to soil waterlogging by means of a glasshouse based randomised block design progeny-provenance trial. Via the controlled application of stress, it may be possible to identify genetic differences between populations that would be otherwise elusive. The trial consists of 432 four year-old saplings originating from nine remnant populations located across an environmental gradient in Scotland. Half of the saplings have been waterlogged (continuously submerged to 1 cm below soil surface); half grown under normal watering. To acquire data at the population level, we have employed a fast physiological phenotyping technique to characterise stress responses to waterlogging in terms of photochemical capacity (via chlorophyll fluorescence). Additionally, by means of carbon isotope analysis, provenances have been screened for genetically-determined differences in water regime, both prior to and following the stress treatment. The completed data set provides evidence that the Scotland's native pinewood remnants are genetically differentiated from one another, and furthermore that adaptive differences between populations in the glasshouse can be attributed to the prevailing conditions in their home provenances.

Downy but not out: Using genetic mixtures to improve yield stability under disease pressure

Henry E. Creissen^{1,2}, Tove H. Jorgensen² and James K.M. Brown¹

¹ *Crop Genetics Department, John Innes Centre*

² *School of Biological Sciences, University of East Anglia*

Plant genotypic mixtures have the potential to increase yield stability in variable, often unpredictable environments, yet knowledge of the specific mechanisms underlying enhanced yield stability remains limited. Field studies are constrained by environmental conditions, which are not completely controllable and therefore not fully reproducible. A suitable model system would allow reproducible experiments on processes operating within crop genetic mixtures under disease pressure. Genotypic diversity of *Arabidopsis thaliana* was manipulated under growing conditions with high levels of competition. Four phenotypically dissimilar genotypes were grown in monocultures and mixtures under high levels of competition in the presence or absence of the pathogen *Hyaloperonospora arabidopsidis*. Seed production, flowering time and rosette size were recorded for multiple replications of glasshouse experiments. Disease reduced the competitive ability of susceptible genotypes, decreasing rosette size and seed production in mixtures. The effect of disease on plant fitness was greater when there was more intense competition between plants. Yield stability was achieved in mixtures under disease pressure because more resistant genotypes compensated for lost seed production by susceptible genotypes. This study indicates that the mixing ability of plant genotypes can be predicted from phenotypic traits such as rosette size, seed production, and host-pathogen compatibility, and implies that a phenotypic screen of cultivars could improve the selection of suitable components of genotypic mixtures in agriculture intended to be resilient to diverse environmental stresses.

Session: NGS and bioinformatic tools

diveRsity: An R package for the estimation and exploration of population genetics parameters and their associated errors

Kevin Keenan

School of Biological Sciences, Queen's University Belfast

Statistical tools for the analysis of population genetics data are abundant. Often these methods are spread across multiple software programs, most of which have their own specific input/output data format. This is most evident when calculating basic frequentist type population genetic parameters such as θ , G_{ST} , allelic richness, or Hardy-Weinberg equilibrium. Consequently, this can result in what should be a routine task in the analysis process, becoming unreasonably time consuming. In an effort to facilitate a more user friendly, efficient and informed approach to basic population genetics analysis, we present the R package *diveRsity*. This software, which accepts a single input data format (GENEPOP), allows for the calculation of some of the most popular frequentist statistics in addition to the inspection of results and their associated estimation errors, using various plotting tools. These features, as well as the ongoing development of a population genomics version of the software are discussed.

De novo transcriptome assembly and RNAseq of a *Holcus lanatus* L. population exhibiting a balanced polymorphism for arsenate tolerance: differential regulation of transcripts by phosphorus nutrition and phenotype

Caroline Meharg¹, Andy Meharg¹, Baezid Khan², Gareth Norton², Mark MacNair³ and Quentin Crumbes⁴

¹ *Institute for Global Food Security, Queen's University Belfast*

² *School of Biological Sciences, University of Aberdeen*

³ *School of Biological Sciences, University of Exeter*

⁴ *Max Planck Institute For Plant Breeding*

De novo Transcriptome sequencing (Roche-454) and assembly of a *Holcus lanatus* L. transcriptome, and RNAseq (Illumina), was used to investigate differential gene expression between arsenate tolerant and non-tolerant phenotypes screened from the same population, and response of these phenotypes to phosphorus nutrition. Illumina reads for phosphorous starved (P-) and phosphorous treated (P+) genovars of tolerant (T) and non-tolerant (N) phenotype (n=4) were mapped to the reference transcriptome (~22000 isotigs). Heatmaps of the gene expression data showed clustering of each P+ /P- treated plant genovar, as well as clustering by N/T. Statistical analysis identified 87 isotigs to be significantly differentially expressed between N and T phenotypes and 258 between P+ and P- treated plants. There was no overlap between P+/P- and N/T effect. Differentially regulated transcripts identified for the N/T phenotype included a putative arsenite transporter, aquaporin, resistance protein, retrotransposons, transposons, proteinases, kinases and ubiquitin-like protein indicating that post-translational modification may play a role in the N/T phenotype. In contrast to that, differentially regulated transcripts identified for P+/P- treatment where, as to be expected, dominated by genes involved in phosphate transport and metabolism including phosphate transporters, phosphatases and SPX domain containing protein.

Next generation sequencing and population genomics (Discussion topic)

Alex Twyford

Department of Biology, Syracuse University

Advances in DNA sequencing technologies have opened up major new research opportunities in evolutionary and ecological genetics. This includes population genomics of non-model organisms, allowing patterns of differentiation to be compared across the genome. In this talk, I consider developments in marker discovery and high-throughput genotyping assays that have been facilitated by next-generation sequencing. The most promising approaches for population genomics and quantitative trait locus (QTL) mapping are reduced representation libraries, where many thousands of homologous loci are scored at a reasonable cost. Researchers embarking on such studies must choose between competing techniques [such as restriction-site associated DNA sequencing (RAD) and genotyping by sequencing (GBS)], and consider how appropriate they are given population and species-specific attributes (heterozygosity, levels of genetic divergence, extent of linkage disequilibrium, genome size). I consider examples of phylogeographic and population genetic studies that have used these approaches to their best effect.

Session: Biodiversity and policy

Incorporating genetics into conservation practice: presenting a web-based tool designed to aid conservation practitioners and policy makers in planning genetic studies of conservation relevance

Katie Frith

Department of Biological and Biomedical Sciences, University of Durham

It is widely recognised that the erosion of genetic diversity plays a major factor in contributing to species decline and extinction risk. Despite this genetic biodiversity is poorly represented at the policy level compared to species and ecosystems. The ConGRESS (conservation of genetic diversity for effective species survival) consortium aims to rectify this situation by delivering web-based dissemination tools which policy makers and conservation managers can conveniently use to incorporate genetic biodiversity into their policy framework. As part of the ConGRESS project we developed a decision tool which allows the user to explore specific management issues and discover the conservation genetic methods, tools and concepts that will help them address those problems. The decision tool was designed through consultation among researchers and conservation professionals across the EU. This led to the identification of key conservation issues which genetic methods can help to address. It also allowed us to understand the practical information conservation professionals require when considering a conservation genetic study. Here we present the ConGRESS site and discuss how collaboration among academics, policy makers and managers guided design and development of the project.

Plants for Bugs: Investigating the influence of plant provenance on garden biodiversity

Sarah Al-Beidh

Royal Horticultural Society

Domestic gardens provide a wealth of benefits from moderating urban temperatures and reducing flooding to supporting garden wildlife and improving human health and psychological well-being. Added together, gardens occupy approximately a quarter of the land area of most UK cities and almost half the total urban green space which means that what we grow in our gardens can have a significant impact on the wider ecosystem services they provide. Many gardeners are keen to encourage biodiversity by choosing plants that best support wildlife; however, very little scientific

evidence exists to direct plant choice. With approximately 70% of plants in a typical UK garden being non-native, we investigate the value of non-native plants to support wildlife. Using a multidisciplinary approach to invertebrate sampling, the RHS Plants for Bugs project is a designed field experiment which tests the influence of plant geographic origin on invertebrate abundance and diversity. I summarise this research, reiterating the importance of engaging the wider gardening public so that we can make more informed choices when gardening for wildlife.

Session: Phylogeny and species delimitation

Diversification and Geographic Progression in *Populus* (Salicaceae)

Nicholas Levens¹, Yuxia Wu², Li Wang³, and Matthew Olson³

¹ *School of Biology, Newcastle University*

² *Molecular Ecology Group, Key Laboratory of Arid and Grassland Ecology, Lanzhou University*

³ *Department of Biological Sciences, Texas Tech University*

The flowering plant genus *Populus* comprises ~30 species of deciduous, dioecious trees. Despite the economic, ecologic, and scientific importance of the genus, understanding of patterns of diversification within *Populus* remains poor. The difficulty in resolving relationships is attributable to widespread interspecific gene flow, recent and rapid diversification, and the previous application of a small number of insufficiently variable sequence markers. Using the published poplar genome to develop a large number of sequence markers, we generated and analyzed data from the chloroplast, mitochondrial, and nuclear genomes to estimate sectional and interspecific relationships, dates of divergence for major clades, lineage-specific substitution rates, patterns of geographic progression, and diversification rates within *Populus*.

Comparing DNA based and Leaf Anatomy based Phylogenies in *Carex*.

Paul Ashton

Biology Department, Edge Hill University

During the last ten years DNA-based phylogenies have been developed for large numbers of plant families and genera, including speciose genera such as *Carex* (Cyperaceae), the largest sedge genus. These phylogenies have been instrumental in resolving taxonomy and ancestral relationships, but have also given a new impetus to the study of the evolution of particular characters. Mapping single traits, such as flower colour, onto molecular phylogenies to identify the number of occasions a feature has evolved is a common approach. However the evolutionary relationships of more complex suites of inter-dependant physical traits likely to contain a useful phylogenetic signal, but also under strong selection pressure (eg leaf anatomy) has been little considered. This study aims to make a preliminary investigation into this area.

From an original consideration of 45 leaf anatomical characters only a number of these have been shown to be consistent within a species. Hence the characters that are phenotypically plastic have been identified and eliminated from further consideration. The remaining anatomical characters were then used to develop a phylogeny which was compared to a phylogeny for the same species based on the ITS sequences determined by Hendrichs *et al*, (2004a, b). Patterns of congruence between the two trees reveal the predominance of the phylogenetic signal within certain anatomical features. Areas where the trees are dissimilar point to characteristics that are under strong selection pressure with resultant rapid evolution. Thus the study raises the possibility that the evolution of complex interrelated structures can be used to better understand phylogeny and adaptation.

What are the ecological threats to the sustainability of *Sorbus* diversity?

Tracey Hamston¹, James Cresswell¹ and Natasha de Vere²

¹ Biosciences, College of Life and Environmental Sciences, University of Exeter

² National Botanic Garden of Wales & IBERS, Aberystwyth University

Much research on the mechanisms of speciation within the *Sorbus* genus has focussed on the origins of the polyploid taxa. Whilst this helps us understand the role of polyploidy in the speciation process there has been less work to investigate the influence of the natural environment on this process. This knowledge is crucial to the development and implementation of conservation actions to preserve this evolutionary process and its resulting diversity. In order to unravel the nature of the endemic *Sorbus* species in Devon and North Somerset, genetic markers (plastid DNA and nuclear microsatellites) and ecological observations were employed to investigate the interaction of ecology and evolution. We confirmed the genetic identity of seven morphologically distinct *Sorbus* taxa and used flow cytometry to establish the ploidy level of the individual trees sampled. Six taxa were confirmed to be tetraploid and one triploid in addition to the sexual diploids *S. aria* and *S. torminalis*. These seven polyploid taxa are thought to reproduce mainly asexually (apomixis) and generally occur on few sites. Reproduction rates are low with few seedlings found in the wild so this study focuses on identifying environmental factors that influence reproductive output and thus the long term sustainability of these populations.

Session: Hybridization

Patterns of mating, generation of diversity, and fitness of offspring in a *Geum* hybrid swarm

Markus Ruhsam^{1,2} and Richard A. Ennos²

¹ Royal Botanic Garden Edinburgh

² Institute of Evolutionary Biology, University of Edinburgh

To understand the evolutionary consequences of hybridisation between the outcrossing plant *Geum rivale* and the selfer *G. urbanum* we tested a simple model in which we assume that hybrids reproduce only as female parents, are fertilised exclusively by pollen from the outcrossing parental taxon, and produce progeny that show no reduction in fitness. The model predicts the presence of four genotypic classes (*G. rivale*, *G. rivale* backcross BC_R, F₁ and *G. urbanum*) in the hybrid swarm and asymmetric introgression from the inbreeding to the outcrossing species. AFLP analysis confirmed that only the predicted genotypic classes occurred in the hybrid swarm adults. However, microsatellite analysis of parent-progeny arrays demonstrated that both F₁ and BC_R hybrid maternal parents produce selfed offspring and receive outcross pollen from both F₁ and BC_R individuals as well as the outcrossing parent. AFLP and morphological analysis showed that the offspring generation comprises genotypes and phenotypes covering the entire spectrum of variation between the two parental species. A common garden experiment indicated no systematic reduction in fitness of offspring derived from hybrid parents. The genetic structure of the *Geum* hybrid swarm is not explained by restricted mating patterns but by ecological selection acting on a diverse offspring population.

The evidence for *Fallopia* x *Muehlenbeckia* hybrids occurring in New Zealand.

SD Desjardins, TS Schwarzacher and JP Bailey

Department of Biology, University of Leicester

The plant species Japanese Knotweed (*Fallopia japonica* var. *japonica*) was introduced from Japan to Europe in the 19th century. A key feature of the following invasion of the West is that this colonisation was accomplished vegetatively by a female clone of a gynodioecious species (2n=8x=88). The absence of males in the adventive range has meant that the female flowers are thus without

conspecific pollen. This can be viewed as an enormous inadvertent breeding experiment in which anything that could potentially pollinate Japanese Knotweed, will have inevitably done so. In Europe the first hybridisations were with the closely-related *F. sachalinensis* (Giant Knotweed; $2n=4x=44$) to produce the now widespread *F. x bohémica* ($2n=6x=66$). More unexpected was the ubiquitous hybridisation with the garden plant *F. baldschuanica* (Russian Vine; $2n=2x=20$) to produce *F. x conollyana* ($2n=5x=54$) at a time when the two parental species were ascribed to different genera. Furthermore, another putative inter-generic hybrid ($2n=5x=54$) has been recently reported as open-pollinated seed and established seedlings from Japanese Knotweed populations in New Zealand. This latest hybrid is thought to be the result of a cross between the European female clone of *F. japonica* and pollen from an indigenous taxa called *Muehlenbeckia*. Support for the existence of these *xMuehlopia* hybrids has been acquired using genomic *in situ* hybridisation, in which labelled total genomic probes of *M. australis* and *F. japonica* were able to discriminate between the two parental genomes in the hybrid ($2n=2x=20$). A PCR-RFLP of a low-copy nuclear gene is also being developed to further identify the paternal species of the hybrid.

A strategy for exploiting exotic germplasm using genetic, morphological ecological and environmental diversity: the *Aegilops tauschii* Coss. example

H. Jones¹, N. Gosman^{1†}, R. Horsnell¹, G.A. Rose¹, L.A. Everest¹, A.R. Bentley¹, S. Tha², C. Uauy^{1,2}, A. Kowalski², D. Novoselovic³, R. Simek³, B. Kobiljski⁴, A. Kondic-Spika⁴, L. Brbaklic⁴, O. Mitrofanova⁵, Y. Chesnokov⁵, D. Bonnett⁶ and A. Greenland¹

¹ NIAB, UK

² John Innes Centre, UK

³ Agricultural Institute of Osijek, Croatia

⁴ Institute of Field and Vegetable Crops, Serbia

⁵ Vavilov Institute of Plant Industry, Russia

⁶ CIMMYT, México

Hexaploid bread wheat evolved from a rare hybridisation which resulted in a loss of genetic diversity in the wheat D-genome with respect to the ancestral donor, *Aegilops tauschii*. Novel genetic variation can be introduced into modern wheat by recreating the above hybridization, however the information associated with the *Ae. tauschii* accessions in germplasm collections is limited, making rational selection of accessions into a re-synthesis programme difficult. We describe methodologies to identify novel diversity from *Ae. tauschii* accessions that combines Bayesian analysis of genotypic data, subspecies diversity and geographic information that summarises variation in climate and habitat at the collection point for each accession. Comparisons were made between diversity discovered amongst a panel of *Ae. tauschii* accessions, bread wheat varieties and lines from the CIMMYT-SHW programme. The selection of *Ae. tauschii* accessions based on differing approaches had significant effect on diversity within each set. Our results suggest that a strategy that combines several criteria will be most effective in maximizing the sampled variation across multiple parameters. The analysis of multiple layers of variation in ex-situ *Ae. tauschii* collections allows for an informed and rational approach to the inclusion of wild relatives into crop breeding programmes.

Shaking that Aspen!

John Warren

IBERS, Aberystwyth University

Plants are generally considered to be stationary, however, on most days casual observations reveal that plants are in a state of constant, if passive motion. The potential ecological significance of wind mediate leaf movement was investigated because it has recently been suggested that leaf movement may deter herbivory. Direct observations were made of the levels of invertebrate herbivore damage on leaves of different mobility. The Biological Records Centre database was used to compare the invertebrate communities associated with pairs of tree species known to hybridize, that have contrasting leaf mobility. Finally simple experiments were performed to investigate the likely effect of leaf form and mobility on invertebrates' ability to adhere to them. Hopefully we can replicate these at

EGG. Plants with more mobile leaves were found to suffer less herbivore damage, support fewer species of invertebrates, including proportionally more leaf miners and fewer surface grazers. The experiments clearly demonstrate that more mobile leaves are likely to be more challenging to remain attached to for external feeding phytophagous invertebrates. Field observation, biological records and these amazing high tech experiments combine to suggest that leaf form and hence mobility appear to explain highly significant differences in the invertebrate communities associated with closely related and functionally similar species of plants.

Poster Abstracts

Niche separation between Small leaved lime (*Tilia cordata*) and Large leaved lime (*T. platyphyllos*)

Carl Barker, Paul Ashton and Mark Ashton

Biology Department, Edge Hill University

Two members of the genus *Tilia* are native to the UK: *T. cordata* (Small leaved lime) and *T. platyphyllos* (Large leaved lime). Both have scattered and fragmented distributions, being relict species of ancient woodlands. *T. platyphyllos* is the least abundant of the two and is almost always found in sympatry with *T. cordata*. Evolutionary theory states that sympatric closely related species must occupy different niches, this being a product of interspecific competition. Studying over 100 lime trees across 10 populations we investigate potential niche separation with a variety of physiographic and edaphic variables.

Gene flow between birch species of differing ploidy levels in the UK: Implications for conservation of dwarf birch

James Borrell, Nian Wang and Richard J. Buggs

School of Biological and Chemical Sciences, Queen Mary University of London

On the basis of morphological studies, inter-specific gene flow has often been suggested to occur in closely related Birch species in the UK. However this has been little studied at the molecular level. We used 14 microsatellite loci to genotype populations of *B. nana*, *B. pubescens* and *B. pendula* across Britain. Here we present PCO analysis of 631 individuals, identifying the three distinct species with high confidence. STRUCTURE analysis revealed a South to North gradient of gene flow from *B. nana* (2x) to *B. pubescens* (4x). Extensive, but varying levels of gene flow were found between *B. pubescens* (4x) and *B. pendula* (2x). In contrast, less gene flow was found between *B. nana* (2x) and *B. pendula* (2x), perhaps due to altitudinal separation. Small and highly fragmented populations of *B. nana* are currently threatened by gene flow from abundant *B. pubescens* populations. Species management strategies will need to take account of this process if they aim to effectively conserve the genetic diversity of *B. nana*.

What causes limestone grassland to be resistant to climate forcing?

Sarah M. Buckland, T.A. Burke and J.P. Grime

Department of Plant and Animal Sciences, University of Sheffield

Being able to predict the contrasting rates of change among different plant communities in response to climate change will improve ecological understanding and thereby help towards better land management. This study involves one of the longest running field experiments (twenty years of continuous climate manipulations) through which to study the mechanisms of species persistence in the face of climate forcing. Two species, *Briza media* and *Carex flacca*, widespread across the UK, have responded differently to the experimental treatments. Soil heterogeneity (soil depth and pH) gives rise to a variety of microsites and has already been found to be crucial for allowing some species, at a community scale, resistance to climate change. The poster describes an investigation to characterize the role that phenotypic plasticity and contemporary evolution might play in these two clonal species. A pot experiment has been designed to examine the influence of soil heterogeneity (deep and vegetated adjacent to shallow and bare) on their response to the summer drought treatment. Microsatellite analysis has been employed to identify genotypes with a view to conducting further work on the potential changes in genetic diversity of populations establishing in the contrasted microsites in the field plots.

Downy but not out: Using genetic mixtures to improve yield stability under disease pressure

Henry E. Creissen^{1,2}, Tove H. Jorgensen² and James K.M. Brown¹

¹ *Crop Genetics Department, John Innes Centre*

² *School of Biological Sciences, University of East Anglia*

Plant genotypic mixtures have the potential to increase yield stability in variable, often unpredictable environments, yet knowledge of the specific mechanisms underlying enhanced yield stability remains limited. Field studies are constrained by environmental conditions, which are not completely controllable and therefore not fully reproducible. A suitable model system would allow reproducible experiments on processes operating within crop genetic mixtures under disease pressure. Genotypic diversity of *Arabidopsis thaliana* was manipulated under growing conditions with high levels of competition. Four phenotypically dissimilar genotypes were grown in monocultures and mixtures under high levels of competition in the presence or absence of the pathogen *Hyaloperonospora arabidopsidis*. Seed production, flowering time and rosette size were recorded for multiple replications of glasshouse experiments. Disease reduced the competitive ability of susceptible genotypes, decreasing rosette size and seed production in mixtures. The effect of disease on plant fitness was greater when there was more intense competition between plants. Yield stability was achieved in mixtures under disease pressure because more resistant genotypes compensated for lost seed production by susceptible genotypes. This study indicates that the mixing ability of plant genotypes can be predicted from phenotypic traits such as rosette size, seed production, and host-pathogen compatibility, and implies that a phenotypic screen of cultivars could improve the selection of suitable components of genotypic mixtures in agriculture intended to be resilient to diverse environmental stresses.

Conservation genetics of an isolated population of alder buckthorn (*Frangula alnus*) and implications for management

Caroline Finlay¹, Caroline R. Bradley^{1,2}, S. Jane Preston^{1,2} and Jim Provan¹

¹ *School of Biological Sciences, Queen's University Belfast*

² *Quercus, School of Biological Sciences, Queen's University Belfast*

Surprisingly little is known about the effects of fragmentation on gene flow in insect-pollinated temperate tree species. This study looks at a fragmented population of *Frangula alnus*, also known as alder buckthorn, in Northern Ireland, to elucidate the effect of fragmentation on the genetic variability of this isolated population. Given that there are no other populations of *Frangula alnus* in Northern Ireland, this enabled us to clearly identify pollination events between individuals by genotyping all the trees, as well as seeds from their berries. A comparison between seeds and trees showed a reduction of heterozygosity and an increase in inbreeding in the next generation, but no significant loss of alleles. The population showed a small degree of genetic structuring between fragments in both the trees ($\phi_{ST}=0.045$; $P<0.001$) and the seeds ($\phi_{ST}=0.082$; $P<0.001$), but gene flow was not completely absent between fragments, probably due to the high quality of habitat for insects that surrounds the population. We discuss the implications of our findings for management of the population.

Hidden dispersal in an urban world: limited dispersal barriers for Dutch pine martens

Arjen de Groot¹, Tim Hofmeester^{1,2}, Maurice la Haye¹, Hugh Jansman¹, Maribel Perez-Haro^{1,3} and Hans-Peter Koelewijn^{1,4}

1 *ALTERRA, Wageningen UR*

2 *Resource Ecology Group, Wageningen University*

3 *Avenida Borbon*

4 *Nunhems BV*

Especially in urbanized landscapes, habitat fragmentation and increasing numbers of infrastructural features may limit genetic exchange among wildlife populations. Yet, the effects of such urban barriers have only been studied for a limited number of species, and rarely at a spatial scale that truly reflects the distances over which the study species may regularly disperse. We analysed genotypic data from 270 pine martens (*Martes martes*) sampled from locations scattered across the Netherlands, one of the most densely populated areas in the world. We assessed levels of variation and tested for spatial genetic structure using a variety of Bayesian clustering models. We find very low levels of genetic differentiation, and clear indications of long-distance dispersal. Any substructure detected by the models is likely due to confounding effects of isolation by distance and sampling of close relatives. Our results indicate that genetic exchange among Dutch pine martens has, until now, not been limited by the countries' dense infrastructural network. The species is likely able to maintain its current high levels of diversity even in a highly urbanized landscape. This surprising conclusion supports the idea that the effects of habitat fragmentation may strongly differ between (groups of) species, and that prioritization and optimization of management decisions thus requires direct study of the targeted species.

Black Alder in Ireland, putting it in a European context

Philippe Cubry¹, Evelyn Gallagher¹, Ellen O'Connor² and Colin T. Kelleher¹

¹ *DBN Herbarium and Plant Molecular Laboratory, National Botanic Gardens of Ireland, Dublin*

² *Teagasc, Ireland*

Forest habitat in Ireland accounts for approximately 11% of the land surface. The majority of forest cover is composed of coniferous plantations, while native woodlands are very limited in size (ca. 1% of the land surface) and are highly disconnected. The ForGen project aims to describe genetic resources in a selection of native tree species, including the black alder, *Alnus glutinosa* (L.) Gaertn. The primary aims for the black alder study are to establish provenance of Irish populations in a European context and to assess levels of genetic diversity and gene flow. Samples were obtained from a Teagasc tree improvement collection and were supplemented with wild collections throughout Ireland. Putative native or naturalised sites were chosen for sampling based on a survey of native woodlands published by NPWS. Primers were designed for HRM analysis on cpDNA regions that were used in a previous phylogeographic study of black alder in Europe. Nuclear microsatellites were also used to assess genetic diversity and population dynamics in the populations. No evidence for specific chlorotypes was found in Ireland and the two main chlorotypes found in western Europe were also found in Irish populations. DNA sequencing of other cpDNA regions revealed additional cpSSR variation between Irish and Scottish samples. These regions are a useful set of markers that could be used to assess other European populations. Structure analysis of the nuclear markers reveals no evidence for genetic structure among Irish samples and no apparent differentiation with Scottish population.

Ecological coherence in marine reserve network design: an empirical evaluation of sequential site selection using genetic structure

Caitríona E. McInerney¹, A. Louise Allcock², Mark P. Johnson² and Paulo A. Prodöhl³

¹ *University of Sheffield*

² *NUI Galway*

³ *School of Biological Sciences, Queen's University Belfast*

Networks of marine protected areas (MPAs) are key components to protect marine biodiversity. Consequently, for every EU member state, the establishment of 'ecologically coherent' MPA networks is a legal requirement by 2020. A general definition for ecological coherence does not exist, but it is accepted that this is a multifaceted conservation objective that includes some potentially conflicting concepts. For example, the most genetically distinctive site to complement an existing network is likely to be at some distance from currently protected sites, but a closer site is likely to be better placed to improve network connectivity. Thus, conflicting concepts include the extent to which the MPA network maximises diversity (including genetic diversity) and the extent to which protected areas interact with non-reserve locations (genetic connectivity). In this study, the preferred location to complement protected sites in an MPA network was estimated using genetic structure of three intertidal mollusc species with different dispersal capacities. Samples were analysed using microsatellite markers from sites inside and at four locations around each of two marine protected areas: Strangford Lough and Lough Hyne, Ireland. Three different measures of genetic distance: F_{ST} , D_{est} and a measure of allelic dissimilarity, along with a direct assessment of the total number of alleles in different candidate networks were compared as standardized site scores, across different methods and selection criteria. Results indicate that apparently conflicting criteria for 'ecological coherence' could be reconciled using genetic measures, leading to a clear choice of site in the region with the strongest genetic structuring. Similar patterns were found across species with different dispersal capacities. This suggests that it will be possible to make quantitative statements about the ecological coherence of different networks with relatively straightforward genetic information.

The NERC Biomolecular Analysis Facility at Sheffield

Caitríona E. McInerney

University of Sheffield

The NERC Biomolecular Analysis Facility comprises five nodes (Sheffield, Edinburgh, Liverpool, Birmingham and Wallingford) which collectively provide a range of biomolecular support. The Facility is supported by the Natural Environment Research Council (NERC) and was established in 1998. The node at Sheffield has successfully supported 189 projects and 108 PhD students. Our users have published over 200 publications from Facility-supported studies, including large numbers in high-ranking journals such as Nature and Science. At Sheffield we provide state-of-the-art molecular genetics facilities and training to the UK community in the science areas that fall under the remit of NERC. The application process is straightforward and applicants do not need to be NERC-funded. We support studies of genes, individuals, behaviour, mating strategies, populations and phylogeny:

- Genes and chromosomes: QTL identification, linkage mapping, evolutionary genetics;
- Individuals: individual identification, identification of clones, ploidy, abundance and distribution, species and hybrid identification;
- Behaviour: behavioural ecology, mating strategies, mate choice, reproductive behaviour, dispersal, kin and sexual selection;
- Populations: effective population size, genetic bottlenecks, population structure, landscape genetics (e.g. habitat fragmentation), spatial ecology;
- Phylogeny: molecular systematics, biodiversity, conservation biology.

The service is based on a well-proven arrangement in which, usually, a researcher (often a PhD student) visits the laboratory at Sheffield to complete their own analyses under the supervision of our experienced staff. Training and consumables are provided but applicants are responsible for their own accommodation or travel costs. For more details please visit our homepage (<http://www.shef.ac.uk/nbaf-s/>) or if you wish to make informal enquiries regarding the feasibility of applying for access to the Facility please contact Deborah Dawson (D.A.Dawson@Sheffield.ac.uk).

Microsatellite analysis supports the existence of three cryptic species within *Bombus lucorum* s.l.

Lorraine McKendrick, Jim Provan, Una Fitzpatrick, Mark J.F. Brown, Tomás E. Murray, Stolle E and Robert J. Paxton

School of Biological Sciences, Queen's University Belfast

We have earlier shown that the common and widespread European bumble bee *Bombus lucorum* s.l. contains three distinct mitochondrial DNA lineages that likely represent three species, namely: *Bombus cryptarum*, *Bombus lucorum* s.s. and *Bombus magnus* (Murray, Fitzpatrick, Brown & Paxton 2008 *Conservation Genetics* 9, 653-666). Though these three lineages exhibit considerable interspecific DNA sequence divergence at mitochondrial cytochrome oxidase I ($\geq 2.3\%$) compared to intra-taxon sequence variability ($\leq 1.3\%$), the use of this or any other mitochondrial DNA marker does not permit the detection of hybrids between taxa. We have now genotyped 304 sympatric members of the *B. lucorum* s.l. group from 11 localities spread across the island of Ireland at 7 (nuclear) microsatellite loci. Our samples comprise 54 *B. cryptarum* females, 170 *B. lucorum* s.s. females and 80 *B. magnus* females, as defined using mtDNA COI sequences. Our multilocus genotypes fall into three discrete clusters that conform to the three mtDNA lineages *B. cryptarum*, *B. lucorum* s.s. and *B. magnus*. That there is an excellent fit of mitochondrial (COI sequence) to nuclear (microsatellite genotypic) genetic data supports the view that these three bumble bee taxa are reproductively isolated species. These data are also a vindication of species identity using so-called DNA barcodes.

Self- incompatibility and seed viability in ruderal species

Elisha Peers

Biology Department, Edge Hill University

An investigation of self- incompatibility (SI) and seed viability in the Asteraceae was carried out from populations in North West England. SI was measured in *Senecio squalidus*, *Senecio viscosus* and *Tripleurospermum inodorum* using controlled pollination techniques, and seed set was recorded under various pollination manipulations. SI was determined by the presence of callus deposits using standardized fluorescent microscopy methods. The results of the study showed that *S. squalidus*, *S. viscosus* and *T. inodorum* are self- compatible (SC) species. However, seed set was only found in open pollinated plants. This suggests that SI may have a seasonal element, and that cross-pollination success is influenced by the precise mechanisms used.

Genetic diversity and population structure in *T. cordata* and *T. platyphyllos*

Prattana Phuekvilai

School of Biology, Newcastle University

T. cordata (small leaved lime) and *T. platyphyllos* (large leaved lime) are the two species that are widely distributed in Europe. Lime trees were a common species 5,000 years ago and some of the trees in Western Europe are generally considered to be ancient trees, yet we know nothing about their evolutionary history. To increase our understanding of genetic diversity and geographical patterns of the distribution in *Tilia*, 13 microsatellite markers were developed. These loci show a high level of polymorphism in both *T. cordata* and *T. platyphyllos* from across Europe. AMOVA analysis indicated that the genetic variation between species is relatively high (38%), while the variation among populations within species is 8%. The populations in the south have a higher genetic diversity than those in the northern part of Europe. Population genetic differentiation was greater but genetic diversity was lower within *T. cordata* than within *T. platyphyllos*. Using STRUCTURE and a PCO analysis, the individuals of *T. cordata* and *T. platyphyllos* were clearly grouped into two clusters according to their species. The variation within *T. cordata* (23 populations) was largely distributed into 6 clusters, while individuals from 13 populations of *T. platyphyllos* were grouped into 3 clusters.

Although there was considerable overlap among populations, these clustering results support the hypothesis of plant migration routes and post glacial colonization.

Genetics of flowering time in *Setaria italica* and its wild progenitor *Setaria viridis*

Natalia Przelomska¹, Harriet Hunt¹, Frances Bligh², James Cockram³ and Martin Jones¹

¹ *Department of Archaeology and Anthropology, University of Cambridge*

² *Plant Science Division, Unilever*

³ *NIAB, Cambridge*

Foxtail millet (*Setaria italica*) displays high levels of genetic diversity compared to most cereal crop species. It is uncertain to what extent introgression from its wild progenitor green foxtail (*S. viridis*) might be contributing to this diversity and resultant adaptive potential. It is an exciting time for research on *Setaria*, which is being developed as a model for the economically important Panicoideae subfamily of C₄ grasses. Furthermore, it has been suggested that as a drought tolerant and highly nutritional crop, *S. italica* could play an important role in future food security. Flowering time is a key adaptive trait in plants, as a determinant of successful pollination, seed development and dispersal. Characterisation of the flowering time network in *Setaria* is in its infancy, but the recent sequencing of the genomes of both species will accelerate this. The aim of my PhD research is to discover genes involved in the control of flowering time in *S. italica*, using several complementary methods: association mapping, candidate gene analysis and creation of a mapping population. I am using a collection of 408 *S. italica* and 34 *S. viridis* accessions of a broad geographical distribution, making this the first study of flowering time genetics in *Setaria* in an ecological context.

Weeds in the protected environment

Sam Thomas^{1,2}, Natasha de Vere^{1,2}, John Warren² and Dylan Gwynn-Jones²

¹ *National Botanic Garden of Wales*

² *IBERS, Aberystwyth University*

Humans have an increasing impact on the distribution of species. The movement of organisms associated with global travel and trade has resulted in the introduction of innumerable species across countries and continents. A key issue arising from this is the ecological damage caused by alien invasive species. The control of well-established invasive species is ineffective and resource-heavy. Monitoring novel alien species for early warning signs of invasive potential could help avoid many of these problems, both ecological and economic. This could be of particular importance as climate change opens new areas to invasive species while concurrently exerting stress on indigenous plant populations. The agricultural and gardening industries are responsible for most plant introduction events. The regular movement of material such as potted plants and used compost between the greenhouses and polytunnels of gardeners and commercial growers provides convenient transport for weed species. Despite this very little research has been conducted on the adventive flora of the protected environment. Through targeted surveys and public involvement we hope to gain an understanding of the diversity and distribution of weeds in the protected environment and, in doing so, begin to answer questions relating to their movements and population trends.

Leaf morphology characteristics in individuals of *Tilia cordata* (Small leaved lime) for ramet identification

John Tomkinson, Paul Ashton

Edge Hill University

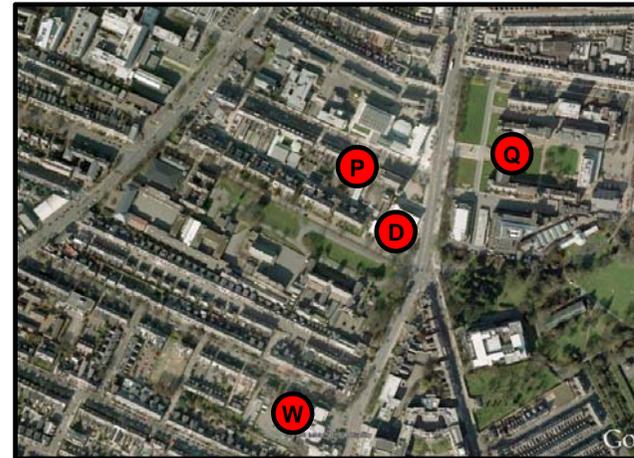
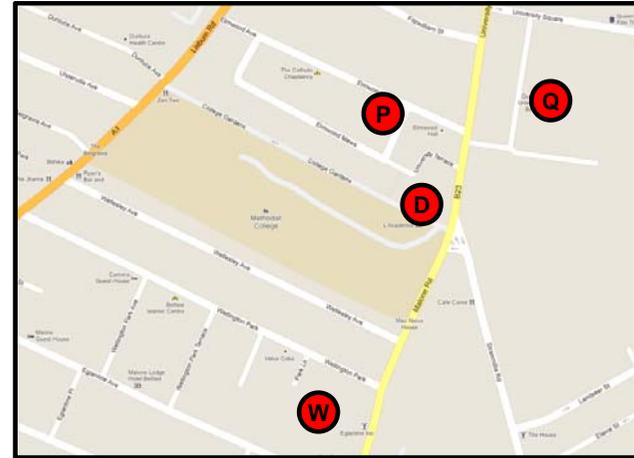
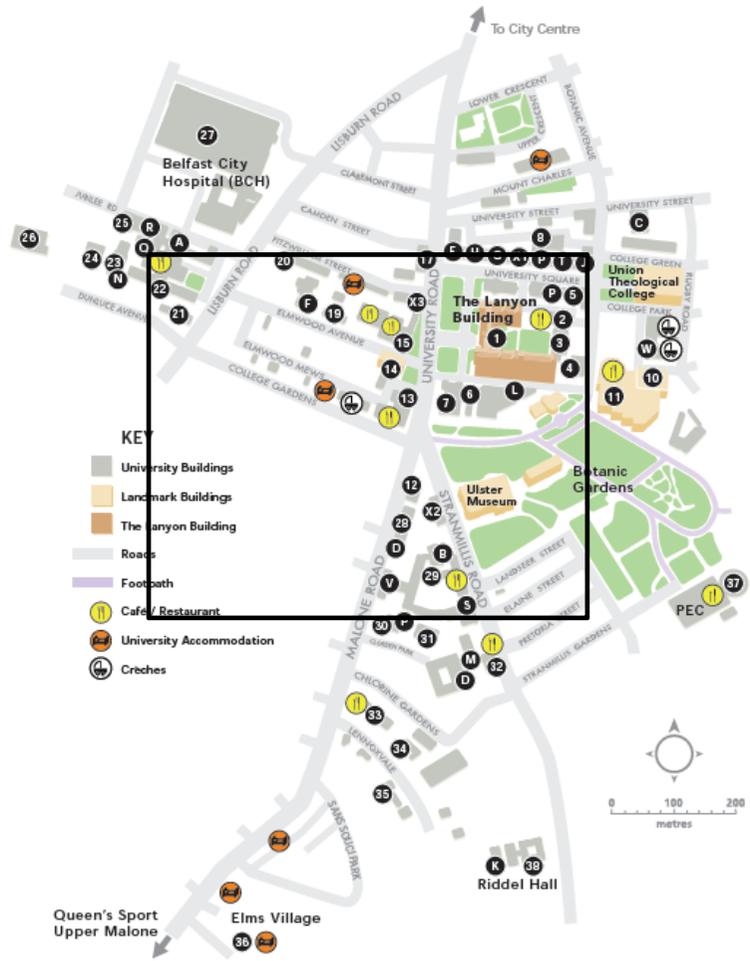
Cloning is an asexual method in which some plant species can reproduce without the need of another individual. *Tilia cordata* is a tree species which has variable capacity for sexual reproduction, the extent of sexual reproduction determined by climatic factors. It also has the ability to clone. It has been suggested that clones are easily recognisable by distinctive leaf features. Within this study two populations were sampled, one site within the Lake District at Roudsea Wood, the second site in the

midlands at Collyweston Great Wood. Forty individuals per site had ten leaves collected with ten morphological measurements per leaf taken and analysed using PCA alongside DNA analysis. The results show that clones cannot be identified using leaf characteristics and proximity alone. The Lakes population shows a similar level of clonal reproduction to that in the midlands.

Participants

Name	Affiliation	Email
Sarah Al-Beidh	Royal Horticulture Society	sarahalbeidh@rhs.org.uk
Paul Ashton	Edge Hill University	ashtonp@edgehill.ac.uk
Carl Barker	Edge Hill University	crl.barker@googlemail.com
Gemma Beatty	Queen's University Belfast	gbeatty03@qub.ac.uk
James Borrell	Queen Mary University of London	j.s.borrell@qmul.ac.uk
Gabrielle Brown	University Of Nottingham	gabrielle.brown@nottingham.ac.uk
Sarah Buckland	University of Sheffield	s.buckland@sheffield.ac.uk
Henry Creissen	John Innes Centre	Henry.Creissen@jic.ac.uk
Katie Crossen	Queen's University Belfast	kcrossen01@qub.ac.uk
Stuart Desjardins	University of Leicester	sd226@leicester.ac.uk
Kevin Donnelly	University of Edinburgh	K.Donnelly-4@sms.ed.ac.uk
Richard Ennos	University of Edinburgh	rennos@ed.ac.uk
Laurent Excoffier	University of Bern	laurent.excoffier@iee.unibe.ch
Caroline Finlay	Queen's University Belfast	cfinlay05@qub.ac.uk
Katie Frith	Durham University	k.e.frith@durham.ac.uk
Arjen de Groot	Wageningen UR	g.a.degroot@wur.nl
Tracey Hamston	University of Exeter	tjh209@exeter.ac.uk
Kate Johnson	Queen's University Belfast	kjohnson03@qub.ac.uk
Huws Jones	NIAB	huw.jones@niab.com
Kevin Keenan	Queen's University Belfast	kkeenan02@qub.ac.uk
Colin Kelleher	National Botanic Gardens of Ireland Dublin	colin.kelleher@opw.ie
David Kipling	Cardiff University	kiplingd@cardiff.ac.uk
Jack Lennon	Queen's University Belfast	j.lennon@qub.ac.uk
Nicholas Levsen	Newcastle University	nlevsen@gmail.com
Samual Logan	Newcastle University	s.logan@newcastle.ac.uk
Charlie Long	Aberystwyth University	cel12@aber.ac.uk
Ashley Lyons	Edge Hill University	Ashley.Lyons@edgehill.ac.uk
Helen Martin	Newcastle University	helen.martin2@ncl.ac.uk
Mark McCullough	Queen's University Belfast	mmccullough14@qub.ac.uk
Caitriona McInerney	University of Sheffield	c.mcinerney@sheffield.ac.uk
Lorraine McKendrick	Queen's University Belfast	lmckendrick01@qub.ac.uk
Peter McKeown	University of Galway	Peter.mckeown@nuigalway.ie
Ian Montgomery	Queen's University Belfast	i.montgomery@qub.ac.uk
Elisha Peers	Edge Hill University	Elisha.peers@go.edgehill.ac.uk
Prattana Phuekvilai	Newcastle University	p.phuekvilai@newcastle.ac.uk
Paulo Prodöhl	Queen's University Belfast	P.Prodohl@qub.ac.uk
Jim Provan	Queen's University Belfast	J.Provan@qub.ac.uk
Natalia Przelomska	University of Cambridge	np403@cam.ac.uk
Mark Ravinet	Queen's University Belfast	mravinet01@qub.ac.uk
Siobhan Simpson	University of Nottingham	stxss23@nottingham.ac.uk
Sam Thomas	Aberystwyth University	sjt9@aber.ac.uk
Jon Tomkinson	Edge Hill University	jon.tomkinson@go.edgehill.ac.uk
Alex Twyford	Syracuse University	adtwyfor@syr.edu
Natasha de Vere	National Botanic Garden of Wales	Natasha.devere@gardenofwales.org.uk
Margaret Wallace	NIAB	Margaret.Wallace@niab.com
John Warren	Aberystwyth University	jhw@aber.ac.uk
Amanda Wilson	James Hutton Institute	Amanda.Wilson@hutton.ac.uk
Kirsten Wolff	Newcastle University	kirsten.wolff@newcastle.ac.uk

Queen's University Belfast Campus Map



- Q** Queen's University - Talks / Posters / Conference Dinner
- P** Parlour Bar - Quiz / Ceili / General Drinking
- D** Deane's at Queen's - Dinner (Tuesday)
- W** Wellington Park Hotel - Accommodation